



US 20060134189A1

(19) **United States**

(12) **Patent Application Publication** (10) **Pub. No.: US 2006/0134189 A1**
MacLachlan et al. (43) **Pub. Date: Jun. 22, 2006**

(54) **SIRNA SILENCING OF APOLIPOPROTEIN B**

Related U.S. Application Data

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(60) Provisional application No. 60/703,226, filed on Jul.
27, 2005. Provisional application No. 60/629,808,
filed on Nov. 17, 2004.

Publication Classification

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(51) **Int. Cl.**
A61K 48/00 (2006.01)
A61K 9/127 (2006.01)
C12N 15/88 (2006.01)
C07H 21/02 (2006.01)
(52) **U.S. Cl.** **424/450**; 435/458; 514/44;
536/23.1

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(57) **ABSTRACT**

(21) Appl. No.: **11/283,550**
(22) Filed: **Nov. 17, 2005**

The present invention provides nucleic acid-lipid particles comprising siRNA molecules that silence ApoB expression and methods of using such nucleic acid-lipid particles to silence ApoB expression.

Figure 1
Plasma IFN-alpha Concentrations

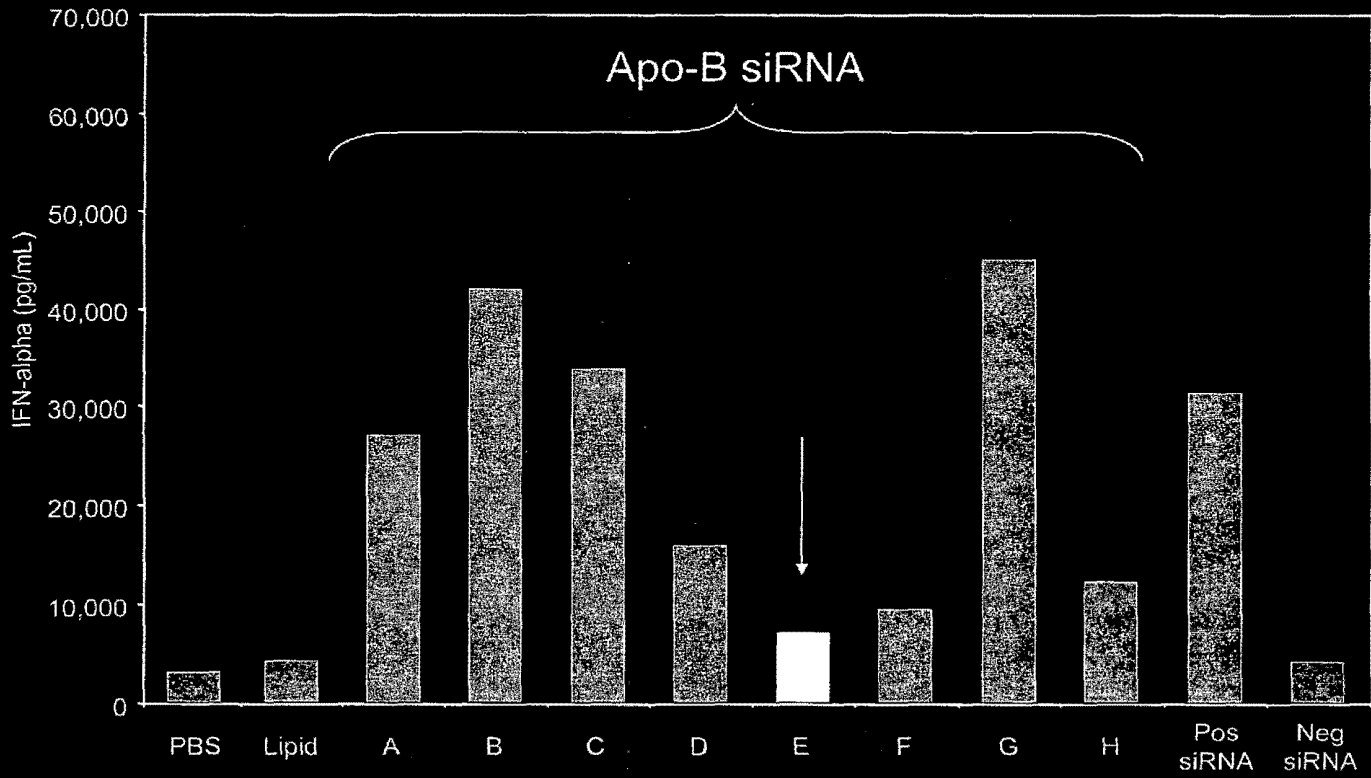


Figure 2
Plasma IFN-alpha Concentrations

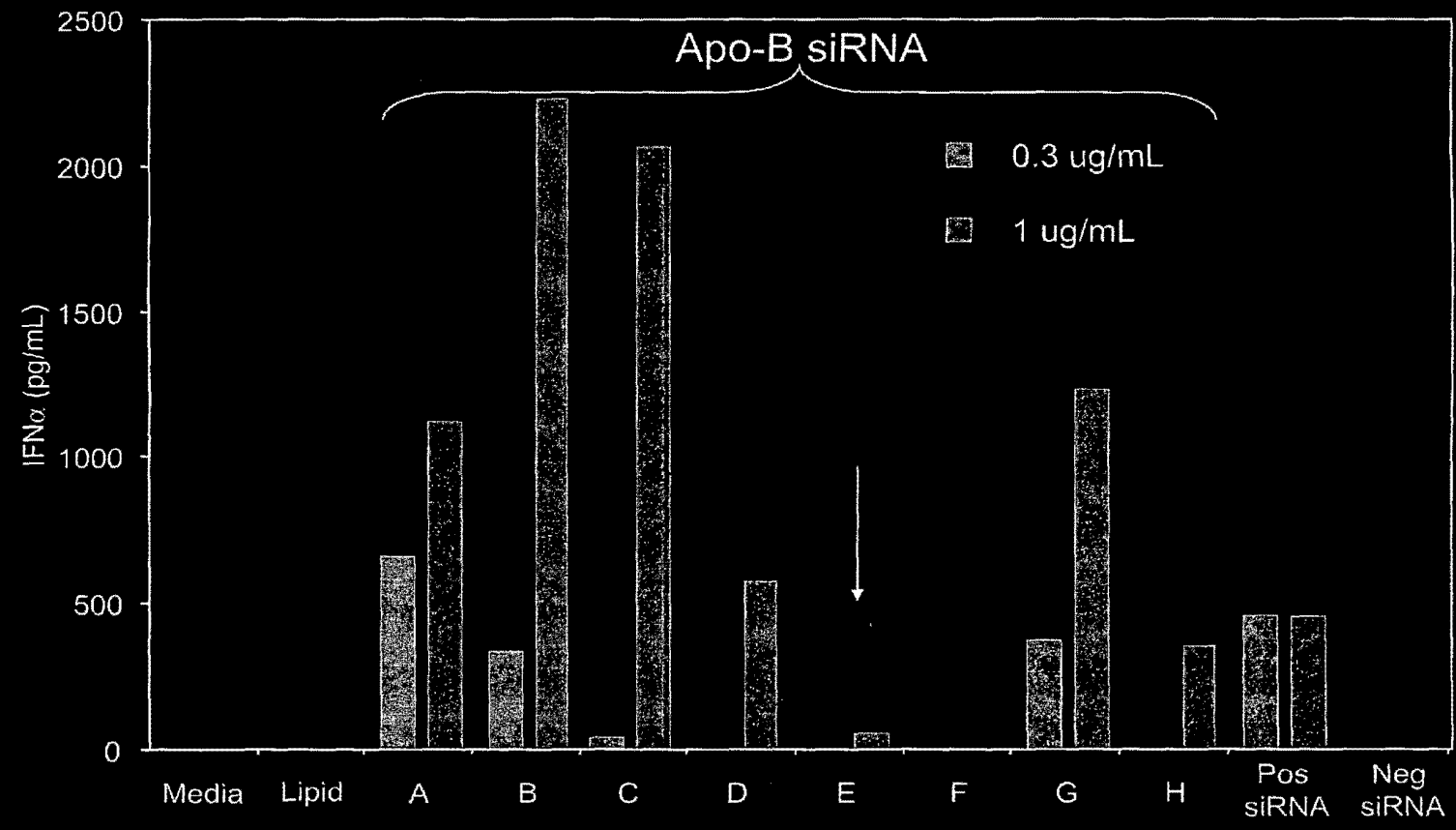


Figure 3
In Vitro Apo B Silencing

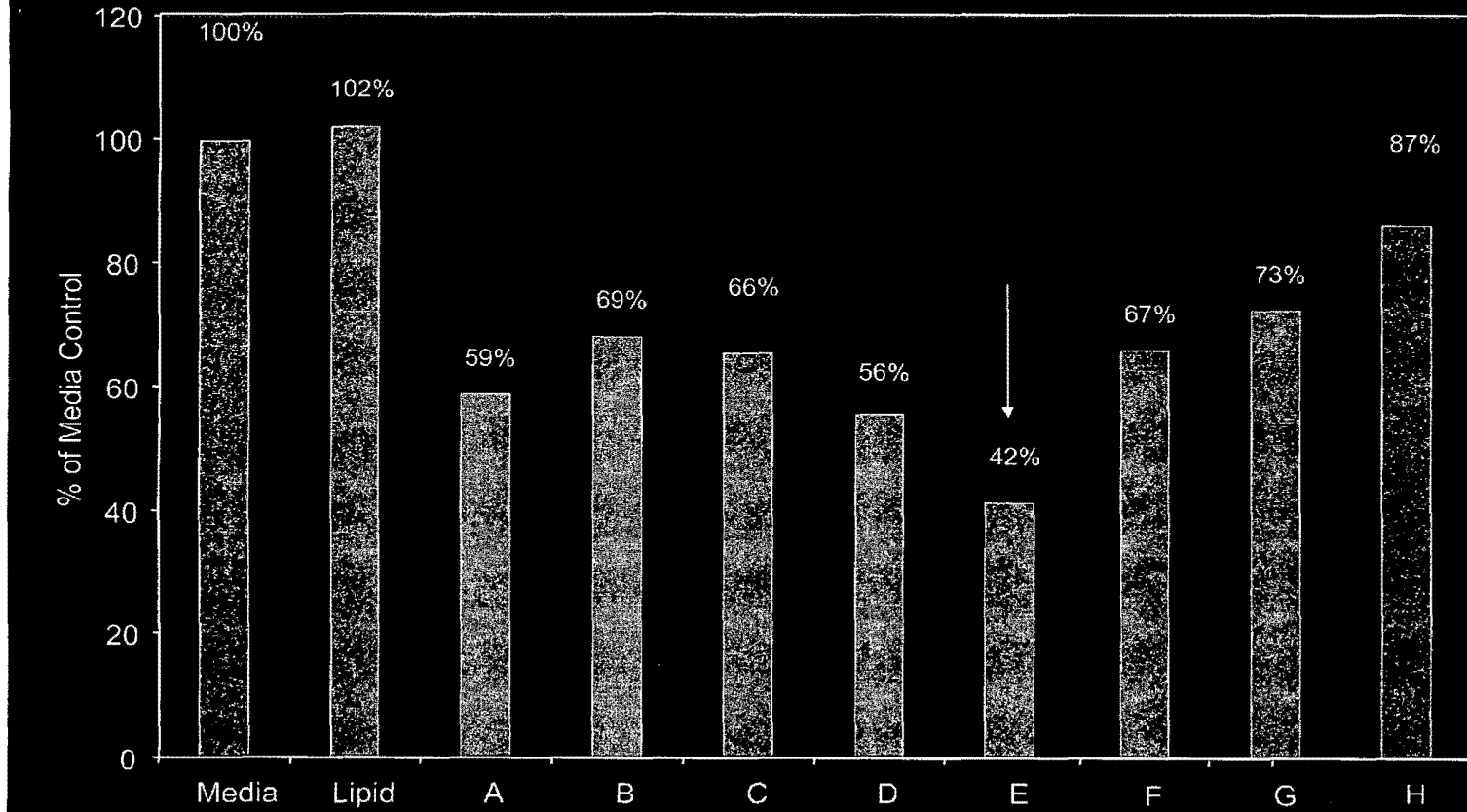
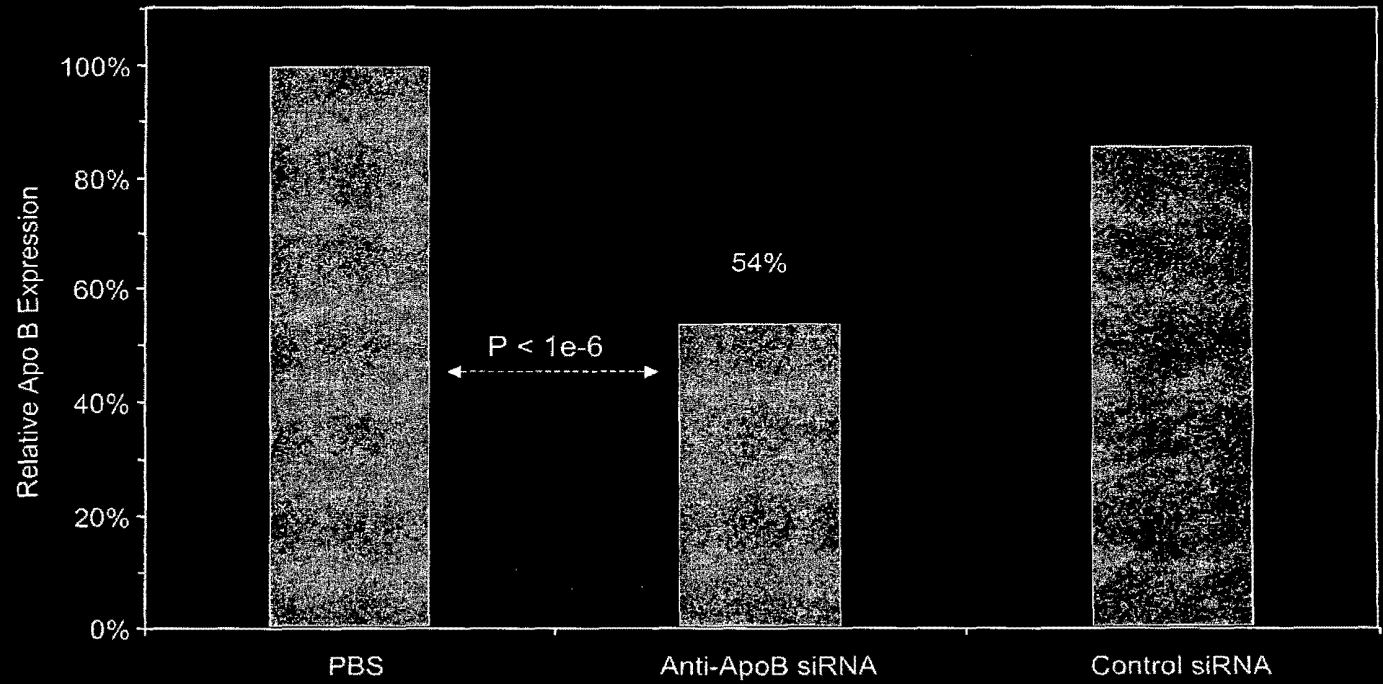


Figure 4
In Vivo Apo B Silencing



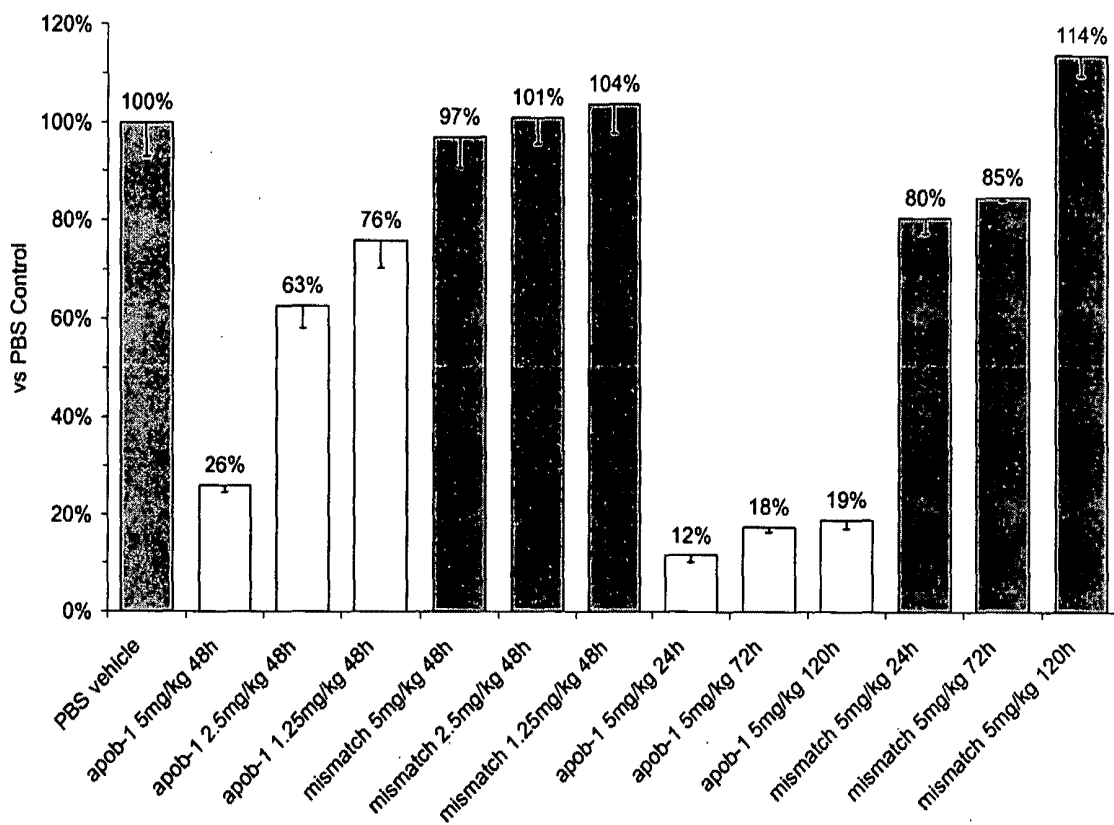


Figure 5

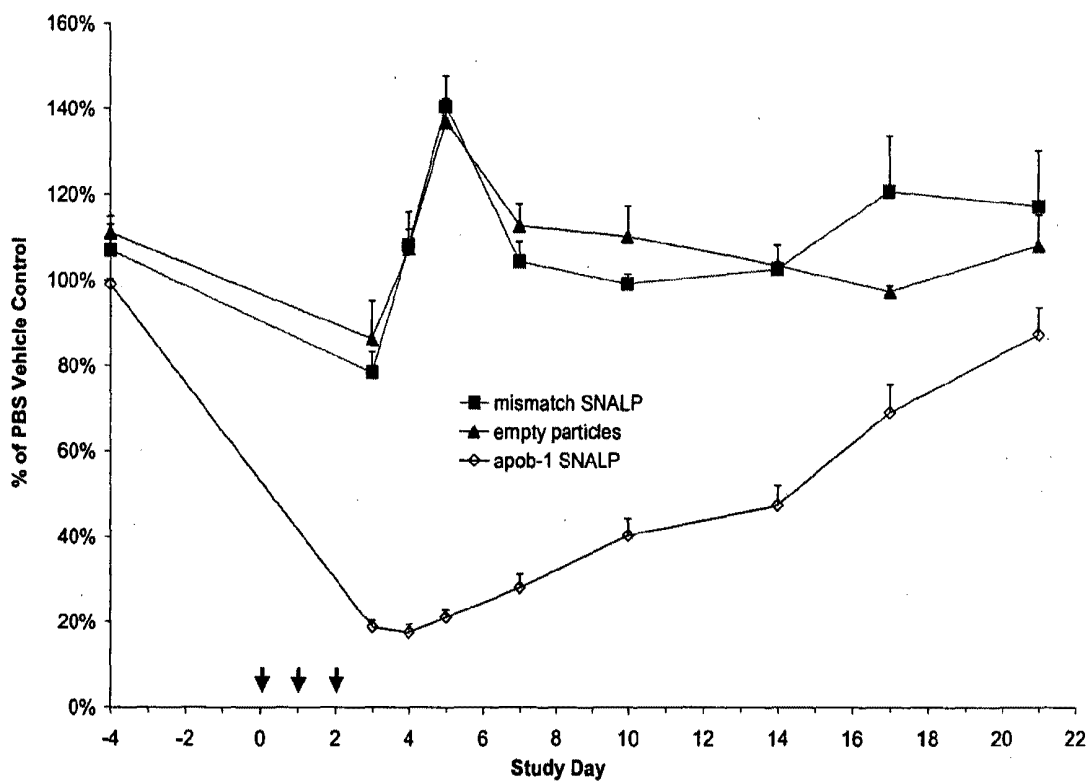


Figure 6

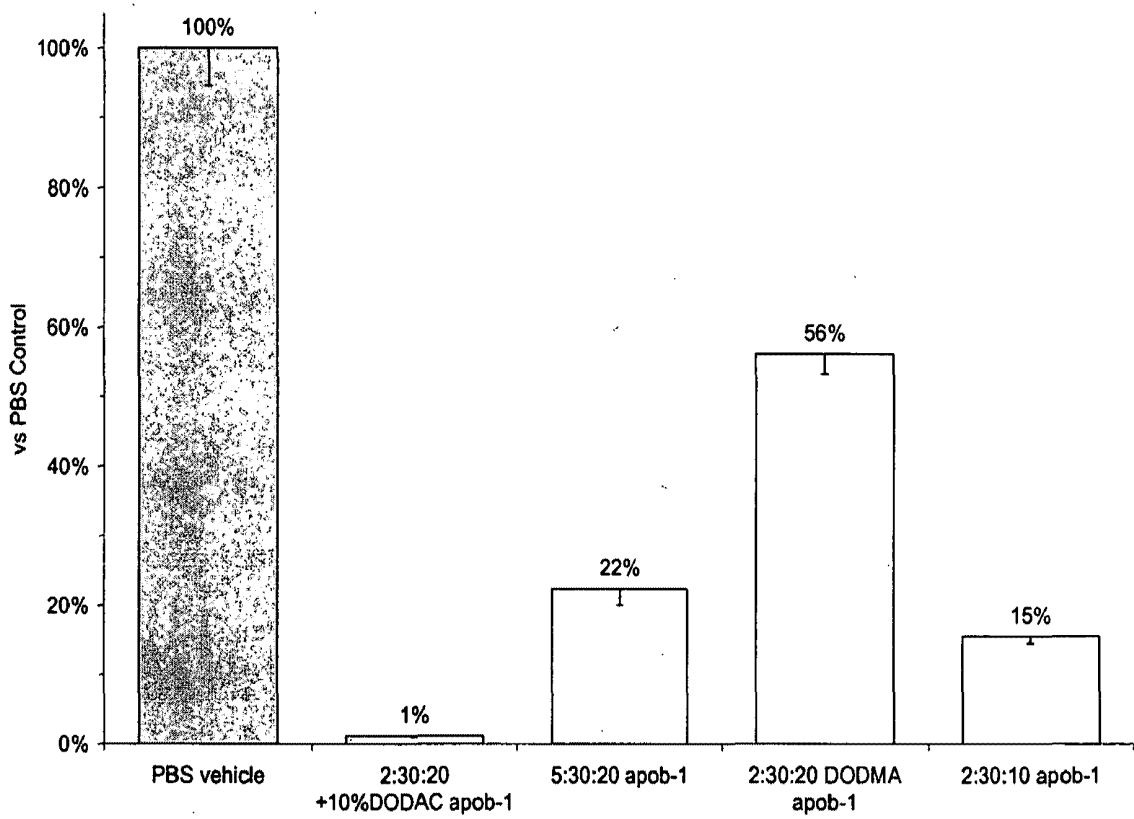


Figure 7

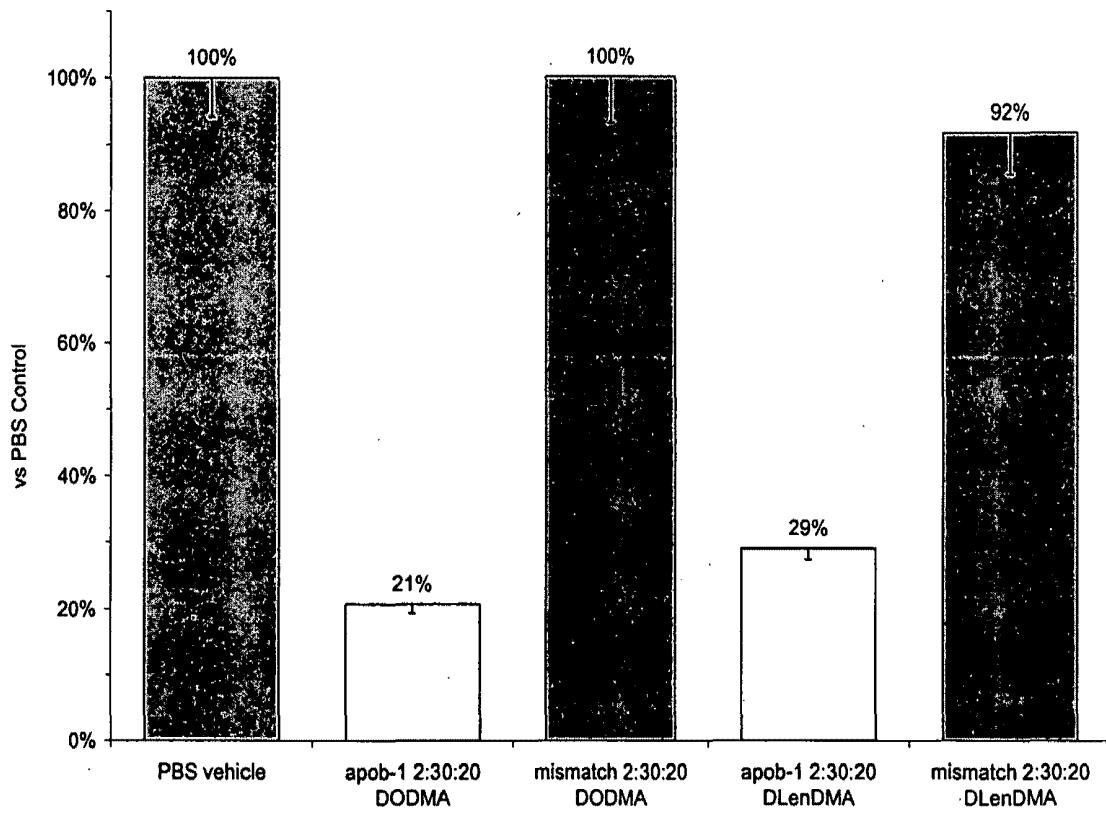


Figure 8

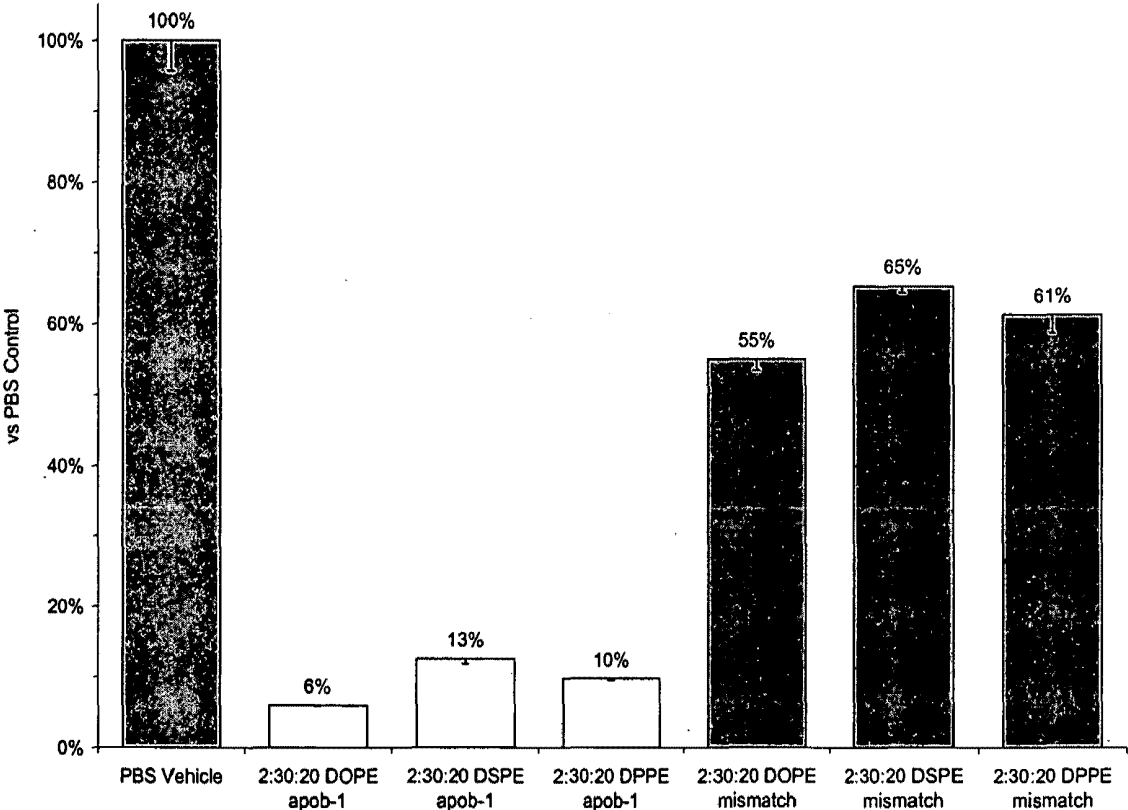


Figure 9

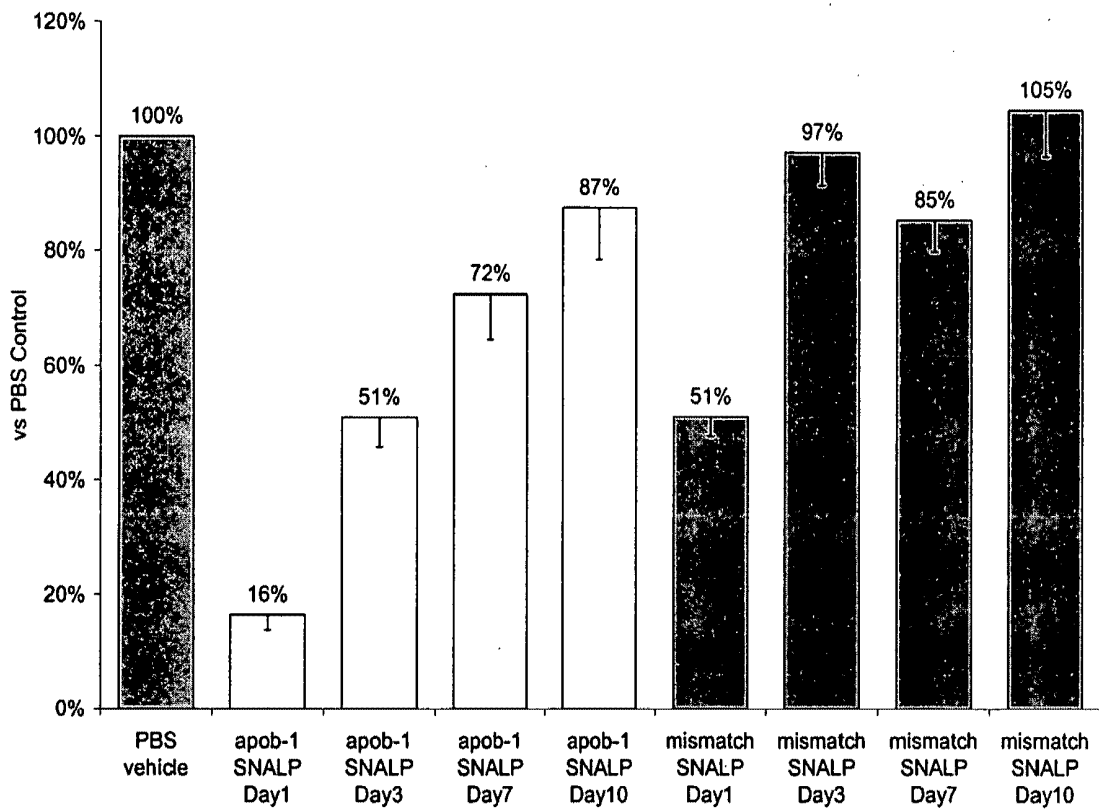


Figure 10

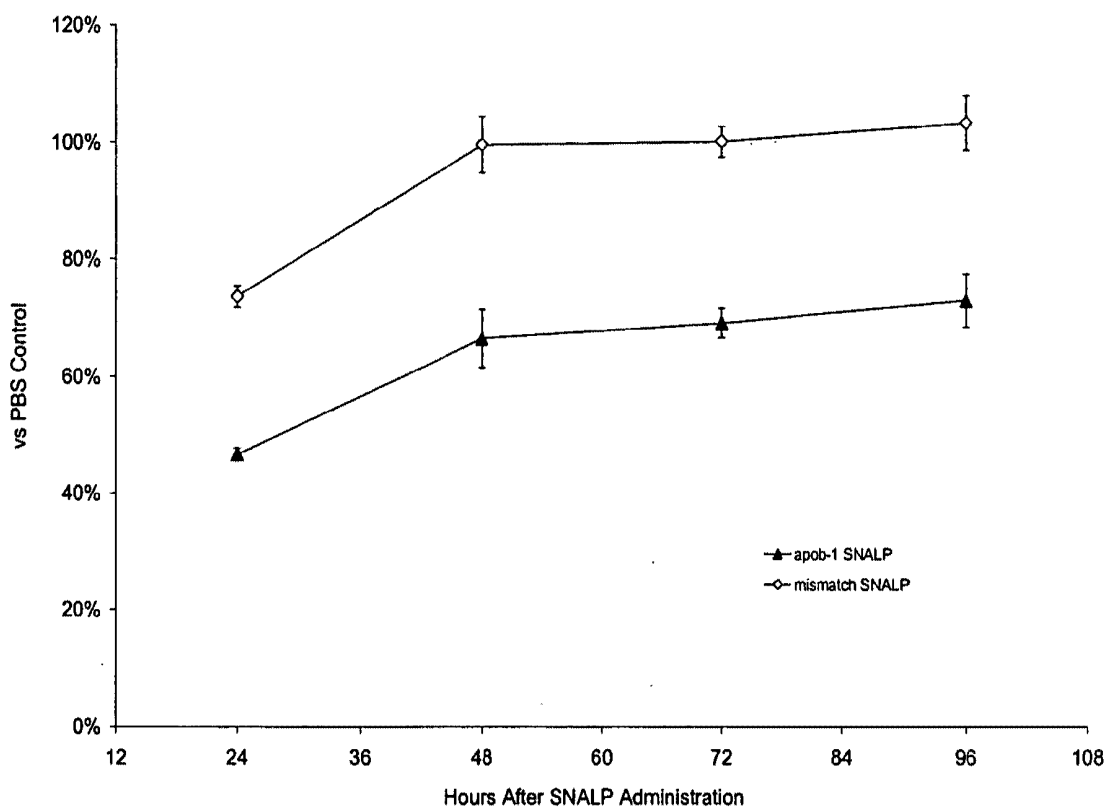


Figure 11

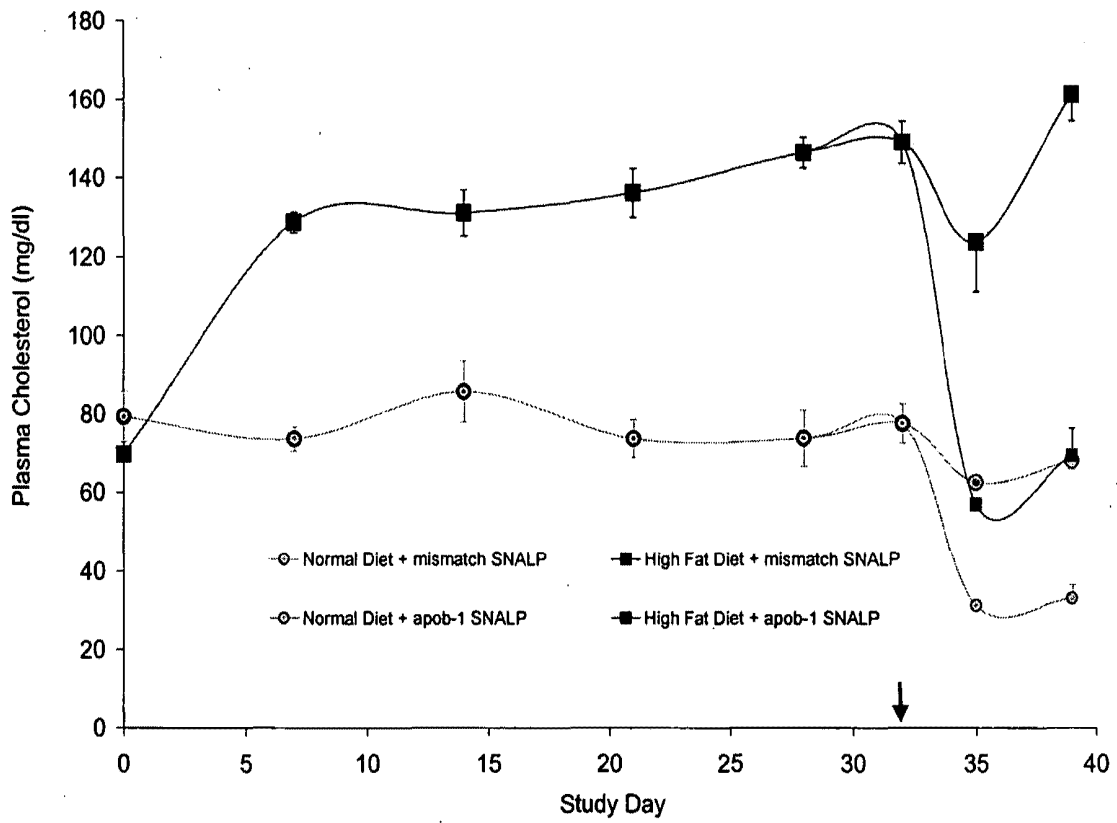


Figure 12

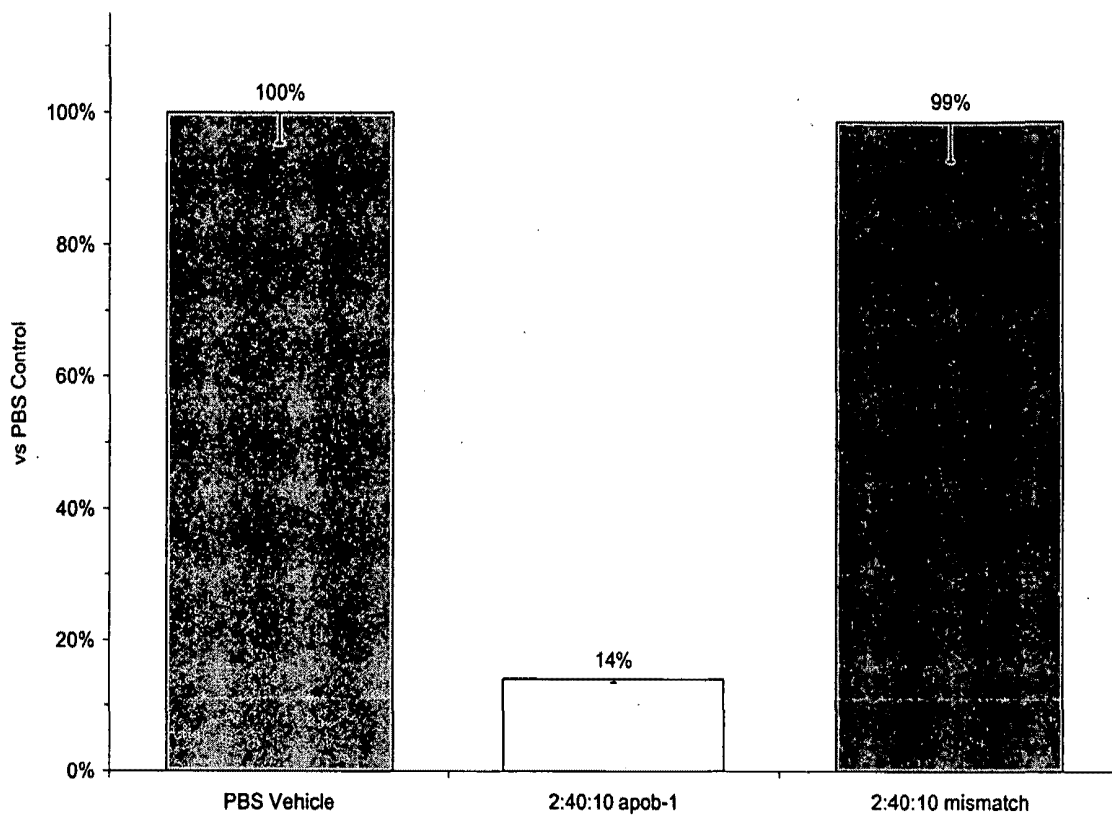


Figure 13

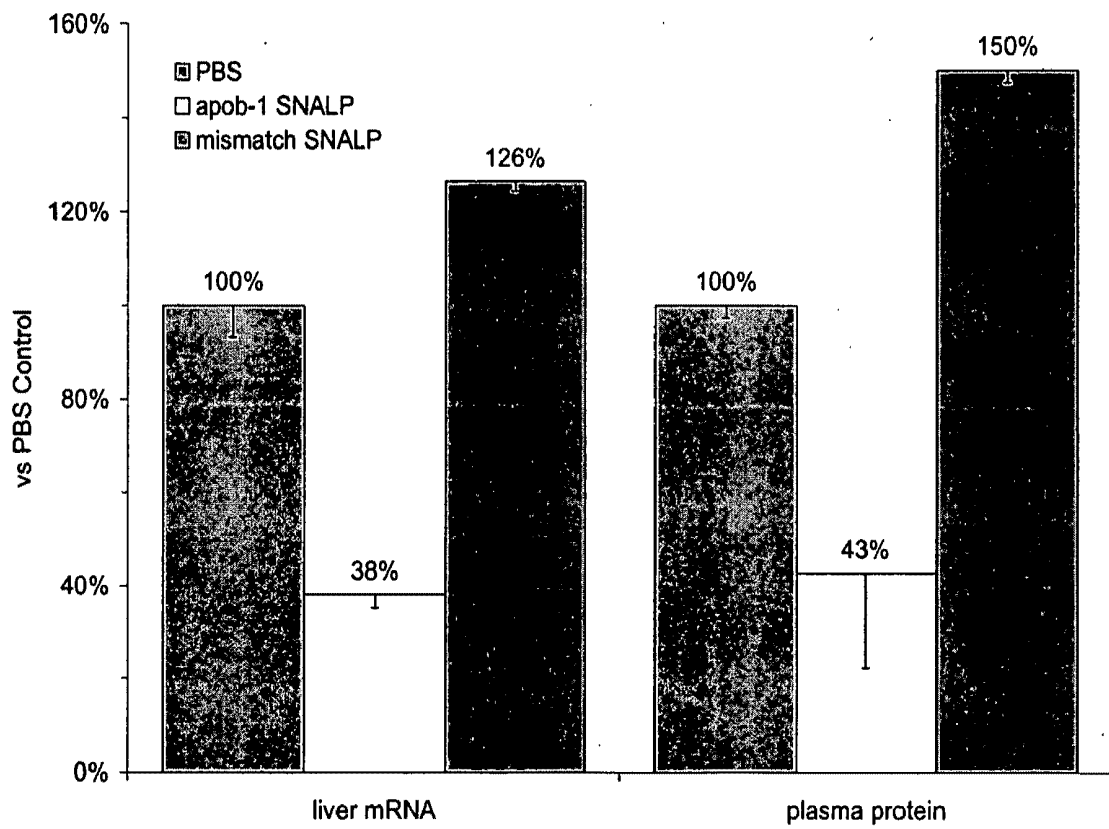


Figure 14

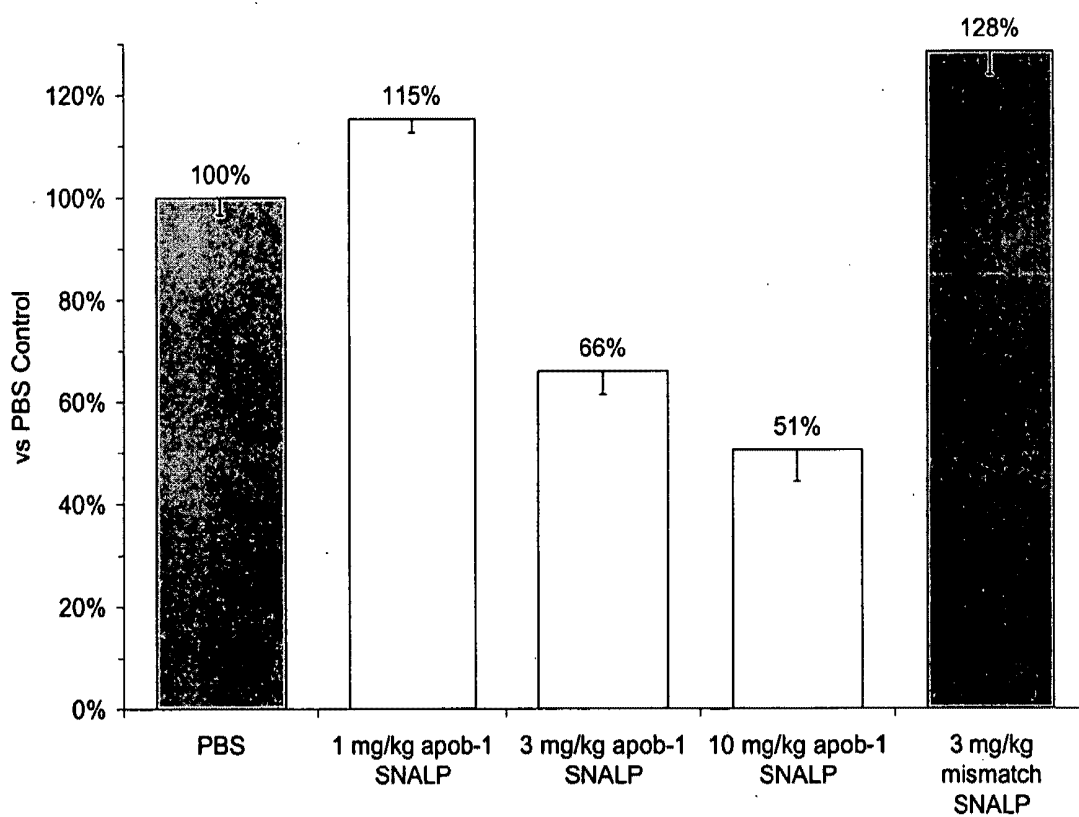


Figure 15

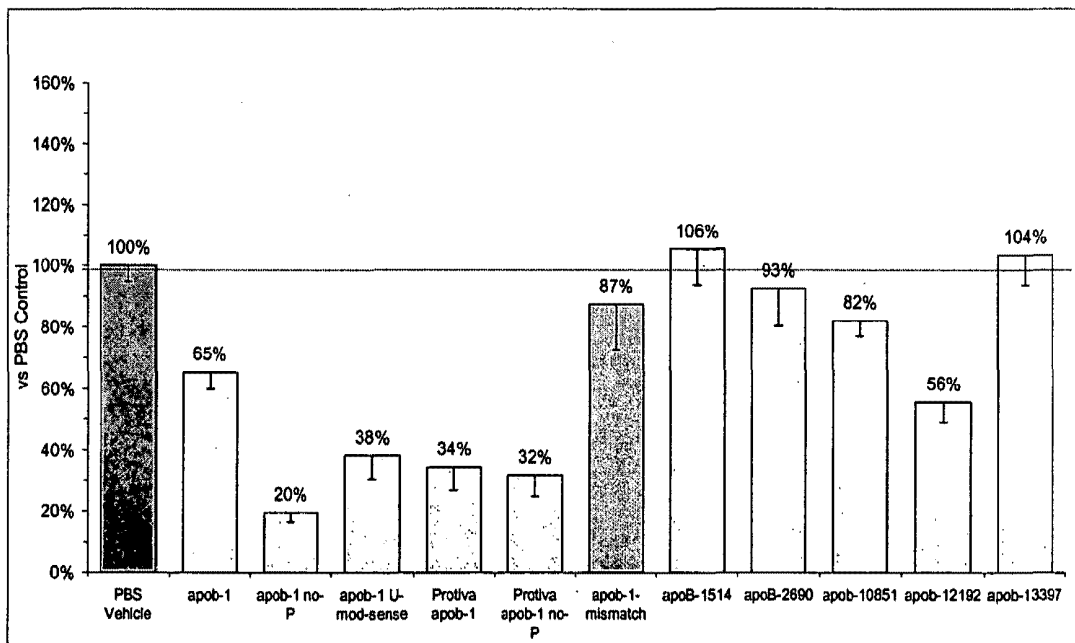


Figure 16

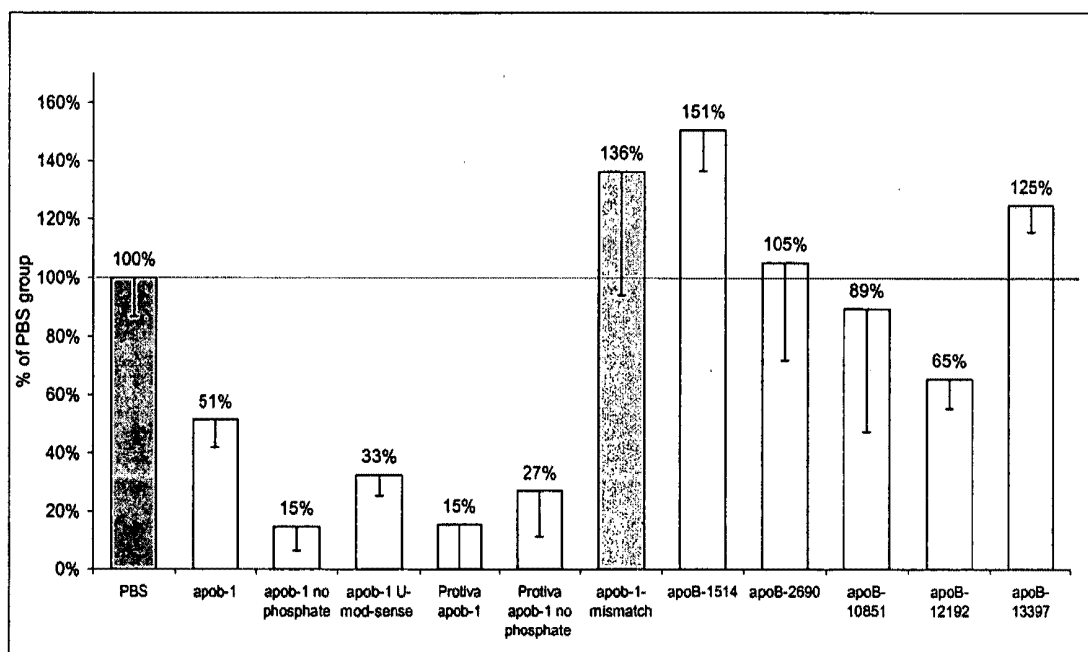


Figure 17

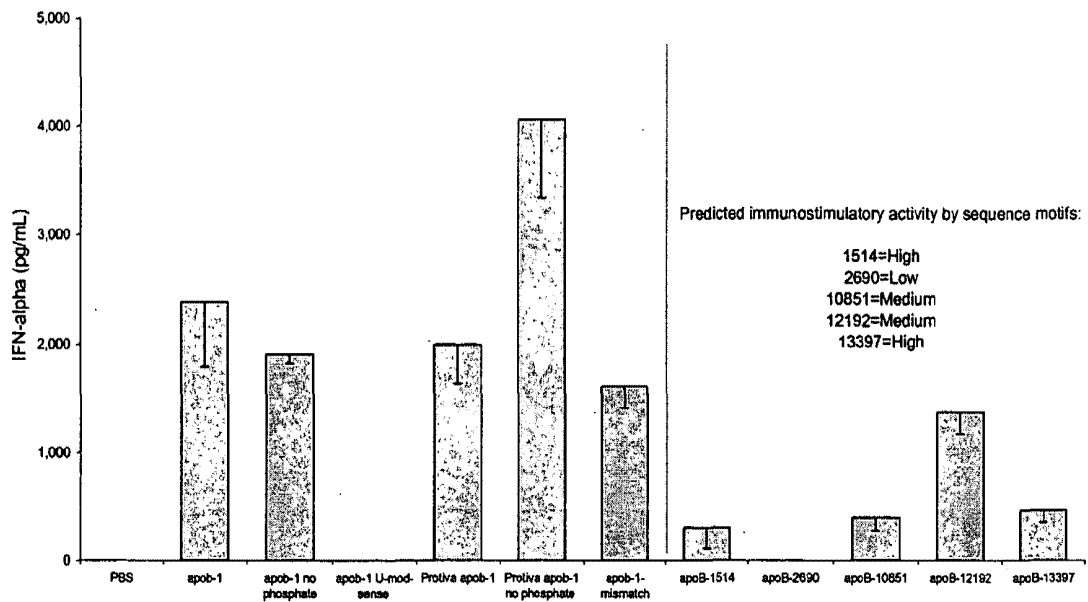


Figure 18

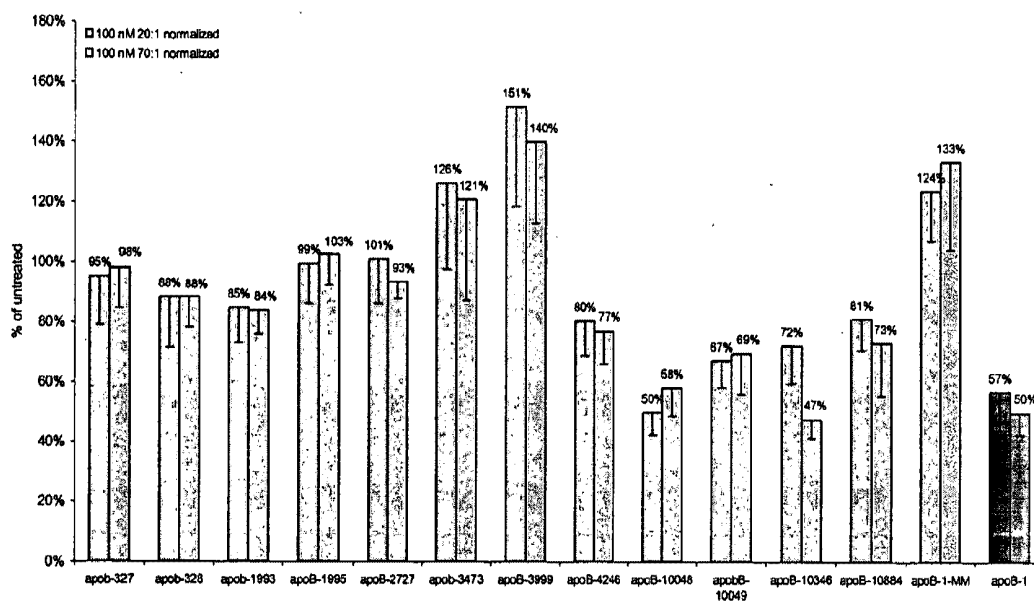


Figure 19

Figure 20
Table 5

Position	SiRNA target sequence	Immunostimulatory activity
254	TGCGACCCGATTCAAGCACCTCC	Low
344	TGCCACCAGGATCAACTGCAAGG	Med
575	ACCTACTTACATCCTGAACATCA	Low
686	CTCCACTCACTTTACCGTCAAGA	Low
791	CATCAGCCCACTTGCTCTCATCA	Med
1040	GAAGATGGGCCTCGCATTGAGA	Med
1566	GGGGATGAAGATTACACCTATTT	Med
2043	CTCTACAAATCTGTTTCTCTTCC	Med
2118	AATAACTACCTTCCTAAAGAAAG	Med
2653	CTGGATTACAGTTGCAAATATCT	High
2789	GGGCATCATCATTCCGGACTTCG	Low
2859	CTGGAGGCTCATGTTGCCCTAAA	Med
2942	AGGCAACACATTACATTTGGTCT	High
3450	GGCCACCTAAGTTGTGACACAAA	High
3486	ATCAAGGGTGTTATTTCCATACC	Med
3557	TGCCAAACTGCTTCTCCAATGG	med
3668	AGGCACCAATGTAGATACCAAAA	high
4046	CTCCAGAGATCTAAAGATGTTAG	low
4202	CTCCACGAATGTCTACAGCAACT	Med
4317	GTTGACCTGCTTTCCTACAATGT	Med
4932	TATCAGGCTGATTACGAGTCATT	Low
6058	AGACAGGCACCTGGAAACTCAAG	Med
6077	CAAGACCCAATTTAACAACAATG	High
6422	CCTGAAGCACATCAATATTGATC	High
6426	AAGCACATCAATATTGATCAATT	Low
6765	GATGAGCACTATCATATCCGTGT	Med
6963	CAGCACCTAGCTGGAAAGTAAA	Low
7256	GCTAAGCAATGTCCTACAACAAG	High
7259	AAGCAATGTCCTACAACAAGTTA	High
7757	TAGCACACTTGTCACCTACATTT	High
7824	GAGCAATATTCCTATCCAAGATTG	Low
8111	TACAATTGACTTTGTGCAAATGA	Med
8240	GAGAATCACCTGCCAGACTTCC	Low
8253	CCAGACTTCCGTTTACCAGAAAT	Med
8560	ATGCACAACCTCAAACCCTAAG	High
8846	GCGCAACGAGATCAAGACACTGT	High
9326	GAAGATAGACTTCCTGAATAACT	Low
9339	CTGAATAACTATGCACTGTTTCT	Med
9376	AGCAAGCAAGTTGGCAAGTAAGT	Med
9917	CACCATAGAGATGTCGGCATTTCG	High
10200	AACCAGTCAGATATTGTTGCTCA	High
10344	GTGGAGGGTAGTCATAACAGTAC	Med
10560	GACCACAAGCTTAGCTTGGAAG	High
10602	ATTGAGTCATCTACCAAAGGAGA	Med
12326	GCTAACCTCTCTGAAAGACAACG	Med
12831	GTCCATAATGGTTCAGAAATACT	Med
12932	GTATAGGGAACCTGTTGAAAGATT	Med
13436	CTCAAGTCAAGTTGAGCAATTTTC	Med
13473	CAGGAATATCTTAGCATCCTTAC	Low
13602	CACCAGCAGTTTAGATATAAACT	High

Figure 21
Table 6

Position	SiRNA target sequence	Immunostimulatory activity
24	GCGGACGCCGTTACTGCTGCTGT	Med
174	CCGAAAGTACGTGTACAACTATG	High
307	ACCAACCAGTGTACCCTTAAAGA	High
861	CATGACACGTGTTACACAGAAAC	High
1002	TTTGAAGACCCTTCAAGAACTGA	Med
1187	AGCCACAGTGCTATACTCACATC	Med
1257	TGTCACCTACCTGATGGCTCTGA	Low
1363	AGCCACGCAGTTAACAGCTATTT	Low
1512	GGGAAGAACCATGGAACAAGTAA	High
1837	GAAGAACTGTATGTCCAAGATCT	Med
1882	CTGGAGAATTCTCAATTTCCAAC	Med
2016	AAGCAGTTATCTTCCCAGAGAAA	Med
2089	TTTGAGATTGGTTTAGAAGGAAA	High
2230	GTGGACCACTTTGGCTATACTAC	Med
2432	GTGCACAAACTTTGCAGGGAATC	Med
2688	GGGCATCATCATCCCAGACTTCG	Low
2814	AAAGAGGCCAGTCAAGCTGTTCA	Med
2841	CAGCAACACACTGCATCTGGTCT	High
2960	CAGGAGCTTACTCCAACGCCAGC	Med
3058	GTGGAGCAGTATTCTGCCACTGC	Low
3151	GTGCAGCAGTCTGAAGCTACTGT	Med
3784	GATCACCTCAATAGCCTCTCAGA	Low
4101	TTCCACAAATGTCTACAGCAATT	Med
4540	TGTGAGAGAGATGTTACAACCTGG	High
4693	AAGAACACAGCTTCCTTGAAATA	High
5312	TCTCACTGGACTTCTTCTCAAAA	Low
5387	AGCTACAGCCCTATTCTTTCATA	Low
5389	CTACAGCCCTATTCTTTCATAAC	Low
5803	GGGCAGCTATATAGTAAGTTTCT	Med
5979	CAAGACCAAACCTGAATGACAAAG	High
6022	GCCTACAACACTAAAGACAAAAT	High
6142	TTAGAGGTAAATGATGCTGTTGA	High
6225	CACCATCAACCTCCCATTCTTCA	High
6265	TTGGAGAGAAATCGAAGAGGAAT	Low
6379	CCTCAGCAGATTCATCATTATCT	Low
6664	GAACAGTATCATATCCGTGTAAG	Med
7278	ATTGACTGACATGTTGGTGAAGA	High
7284	TGACATGTTGGTGAAGAAGTTGA	High
7531	ATGAAAGACCATTTCCAAGATAC	Med
7702	GCAGAGCAATATTCCATCCAAAA	Med
7807	TTTGAGGTCAGTCTCCGTGCTCT	Med
7956	ATTCACCTTCTCAACACCTTCC	High
7992	TACAATTGACTTGCTGGAAATAA	Med
8025	CATTAGAACTATCGACCAAATTT	Med
8622	TGGTATGACTGTCAAAGTAAACA	High
8828	GCATACATTCGTCCCAAATTAGC	Med
9276	GAGTACCAGATTCAATCAGTACA	Med
9470	AAGAAACAGGCTTGAAAGAATTT	Med
10248	CACCATTAGTTTAACCAAGAAAA	High
10297	GCCAACCTCCATGCTCCCATATT	Med

Figure 22

Table 7

Apo B siRNA sequences

Position	Sequence
1-23	ATTCCACCGGGACCTGCGGGGC
2-24	TCCACCGGGACCTGCGGGGCT
3-25	TCCACCGGGACCTGCGGGGCTG
4-26	CCCACCGGGACCTGCGGGGCTGA
5-27	CCACCGGGACCTGCGGGGCTGAG
6-28	CACCGGGACCTGCGGGGCTGAGT
7-29	ACCGGGACCTGCGGGGCTGAGTG
8-30	CCGGGACCTGCGGGGCTGAGTGC
9-31	CGGGACCTGCGGGGCTGAGTGCC
10-32	GGGACCTGCGGGGCTGAGTGCCC
11-33	GGACCTGCGGGGCTGAGTGCCCT
12-34	GACCTGCGGGGCTGAGTGCCCTT
13-35	ACCTGCGGGGCTGAGTGCCCTTC
14-36	CCTGCGGGGCTGAGTGCCCTTCT
15-37	CTGCGGGGCTGAGTGCCCTTCTC
16-38	TGCGGGGCTGAGTGCCCTTCTCG
17-39	GCGGGGCTGAGTGCCCTTCTCGG
18-40	CGGGGCTGAGTGCCCTTCTCGGT
19-41	GGGGCTGAGTGCCCTTCTCGGTT
20-42	GGGCTGAGTGCCCTTCTCGGTTG
21-43	GGCTGAGTGCCCTTCTCGGTTGC
22-44	GCTGAGTGCCCTTCTCGGTTGCT
23-45	CTGAGTGCCCTTCTCGGTTGCTG
24-46	TGAGTGCCCTTCTCGGTTGCTGC
25-47	GAGTGCCCTTCTCGGTTGCTGCC
26-48	AGTGCCCTTCTCGGTTGCTGCCG
27-49	GTGCCCTTCTCGGTTGCTGCCGC
28-50	TGCCCTTCTCGGTTGCTGCCGCT
29-51	GCCCTTCTCGGTTGCTGCCGCTG
30-52	CCCTTCTCGGTTGCTGCCGCTGA
31-53	CCTTCTCGGTTGCTGCCGCTGAG
32-54	CTTCTCGGTTGCTGCCGCTGAGG
33-55	TTCTCGGTTGCTGCCGCTGAGGA
34-56	TCTCGGTTGCTGCCGCTGAGGAG
35-57	CTCGGTTGCTGCCGCTGAGGAGC
36-58	TCGGTTGCTGCCGCTGAGGAGCC
37-59	CGGTTGCTGCCGCTGAGGAGCCC
38-60	GGTTGCTGCCGCTGAGGAGCCCG
39-61	GTTGCTGCCGCTGAGGAGCCCGC
40-62	TTGCTGCCGCTGAGGAGCCCGCC
41-63	TGCTGCCGCTGAGGAGCCCGCCC
42-64	GCTGCCGCTGAGGAGCCCGCCCA
43-65	CTGCCGCTGAGGAGCCCGCCAG
44-66	TGCCGCTGAGGAGCCCGCCAGC
45-67	GCCGCTGAGGAGCCCGCCAGCC
46-68	CCGCTGAGGAGCCCGCCAGCCA
47-69	CGCTGAGGAGCCCGCCAGCCAG
48-70	GCTGAGGAGCCCGCCAGCCAGC
49-71	CTGAGGAGCCCGCCAGCCAGCC
50-72	TGAGGAGCCCGCCAGCCAGCCA
51-73	GAGGAGCCCGCCAGCCAGCCAG
52-74	AGGAGCCCGCCAGCCAGCCAGG
53-75	GGAGCCCGCCAGCCAGCCAGGG
54-76	GAGCCCGCCAGCCAGCCAGGGC
55-77	AGCCCGCCAGCCAGCCAGGGCC
56-78	GCCCGCCAGCCAGCCAGGGCCG
57-79	CCCGCCAGCCAGCCAGGGCCGC
58-80	CCGCCAGCCAGCCAGGGCCGCG
59-81	CGCCAGCCAGCCAGGGCCGCGA
60-82	GCCAGCCAGCCAGGGCCGCGAG
61-83	CCAGCCAGCCAGGGCCGCGAGG
62-84	CCAGCCAGCCAGGGCCGCGAGGC

10333	AAGCAGGAACTTAATGGAAATAC	Med
10380	ATCCATTGAACTAACTATGACT	Med
10417	CTGCACTCTACTGCAACAGGAGG	Med
10528	TCTCAGGAATATTCAGGAAGTGT	Med
10800	GTCAACCTTGCTACAGGTTTCATG	Med
10849	CTCCATCACTTTGACCAGGAAGT	Med
11353	TTTGAGGCAACTATACCTGAAAT	Med
11439	TCTGAATAAGTTGGCCAACATGA	High
11451	GGCCAACATGATTGCCGATGTTG	High
11452	GCCAACATGATTGCCGATGTTGA	High
11767	CTTCAACACTGTGACTTCAATGT	High
11788	GTGGAGTATAATGAAGATGGTCT	Med
11868	ACTGACTGACTTTCATCTGACT	Low
12190	CTGGAATACGTTTCTTCAGAACT	Med
12243	TGCCAGAAGGATGGTTGATGAAA	High
12363	GAAGAGGGTGTTAGACAGTATAG	Med
12715	GGCCAACAGGATATCAAGTTTAC	Med
12925	AATGACTTTCCTTCAATCCATACT	Med
13192	AGAGAGTATCTTAGCATGCTTAC	Low
13200	TCTTAGCATGCTTACTGATATAA	Low
13357	GACCAACTCTCTAGCTACTATGA	Med
13395	GTCCACAAGATTGATTGACCTGT	High
13440	TCTCAGATACATCACCGAGTTAC	Med
13449	CATCACCGAGTTACTGAGAAAGC	Low
13595	GTAGACTACTATAAAGACCATCC	Med
13671	TGCAACCAAGCTGGCATAAGAAC	High

13638	GACCAACTCTCTGATTACTATGA	Med
13935	AGGCAGTAGACTATAAGCAGAAG	Low

Position	Sequence
63-85	CAGCCAGCCAGGGCCGAGGCC
64-86	AGCCAGCCAGGGCCGAGGCCG
65-87	GCCAGCCAGGGCCGAGGCCGA
66-88	CCAGCCAGGGCCGAGGCCGAG
67-89	CAGCCAGGGCCGAGGCCGAGG
68-90	AGCCAGGGCCGAGGCCGAGGC
69-91	GCCAGGGCCGAGGCCGAGGCC
70-92	CCAGGGCCGAGGCCGAGGCCA
71-93	CAGGGCCGAGGCCGAGGCCAG
72-94	AGGGCCGAGGCCGAGGCCAGG
73-95	GGGCCGAGGCCGAGGCCAGGC
74-96	GGCCGAGGCCGAGGCCAGGCC
75-97	GCCCGAGGCCGAGGCCAGGCCG
76-98	CCGCGAGGCCGAGGCCAGGCCG
77-99	CGCGAGGCCGAGGCCAGGCCGA
78-100	GCGAGGCCGAGGCCAGGCCGAG
79-101	CGAGGCCGAGGCCAGGCCGAGC
80-102	GAGGCCGAGGCCAGGCCGAGCC
81-103	AGGCCGAGGCCAGGCCGAGCCC
82-104	GGCCGAGGCCAGGCCGAGCCCA
83-105	GCCGAGGCCAGGCCGAGCCAG
84-106	CCGAGGCCAGGCCGAGGCCAGG
85-107	CGAGGCCAGGCCGAGGCCAGGA
86-108	GAGGCCAGGCCGAGGCCAGGAG
87-109	AGGCCAGGCCGAGGCCAGGAGC
88-110	GGCCAGGCCGAGGCCAGGAGCC
89-111	GCCAGGCCGAGGCCAGGAGCCG
90-112	CCAGGCCGAGGCCAGGAGCCGC
91-113	CAGGCCGAGGCCAGGAGCCGCC
92-114	AGGCCGAGGCCAGGAGCCGCC
93-115	GGCCGAGGCCAGGAGCCGCC
94-116	GCCCGAGGCCAGGAGCCGCCCA
95-117	CCGCGAGGCCAGGAGCCGCCCAC
96-118	CGCAGGCCAGGAGCCGCCACC
97-119	GCAGGCCAGGAGCCGCCACCAG
98-120	CAGGCCAGGAGCCGCCACCAGC
99-121	AGCCAGGAGCCGCCACCAGCA
100-122	GCCAGGAGCCGCCACCAGCAG
101-123	CCCAGGAGCCGCCACCAGCAGC
102-124	CCAGGAGCCGCCACCAGCAGCT
103-125	CAGGAGCCGCCACCAGCAGCTG
104-126	AGGAGCCGCCACCAGCAGCTGG
105-127	GGAGCCGCCACCAGCAGCTGGC
129-151	ATGGACCCGCGAGGCCGCGCT
141-163	AGGCCGCGCTGCTGGCGCTGCT
142-164	GGCCGCGCTGCTGGCGCTGCTG
143-165	GCCCGCGCTGCTGGCGCTGCTGG
144-166	CCCGCGCTGCTGGCGCTGCTGGC
145-167	CCGCGCTGCTGGCGCTGCTGGCG
146-168	CGCGCTGCTGGCGCTGCTGGCGC
147-169	GCGCTGCTGGCGCTGCTGGCGCT
148-170	CGCTGCTGGCGCTGCTGGCGCTG
149-171	GCTGCTGGCGCTGCTGGCGCTGC
150-172	CTGCTGGCGCTGCTGGCGCTGCC
151-173	TGCTGGCGCTGCTGGCGCTGCCT
152-174	GCTGGCGCTGCTGGCGCTGCCTG
153-175	CTGGCGCTGCTGGCGCTGCCTGC
154-176	TGGCGCTGCTGGCGCTGCCTGCG
155-177	GGCGCTGCTGGCGCTGCCTGCGC
156-178	GCGCTGCTGGCGCTGCCTGCGCT
157-179	CGCTGCTGGCGCTGCCTGCGCTG
158-180	GCTGCTGGCGCTGCCTGCGCTGC
159-181	CTGCTGGCGCTGCCTGCGCTGCT
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Position	Sequence
163-185	TGGCGCTGCCTGCGTGCTGCTG
164-186	GGCGCTGCCTGCGTGCTGCTG
165-187	CGCGCTGCCTGCGTGCTGCTG
166-188	CGCTGCCTGCGTGCTGCTGCTG
167-189	GCTGCCTGCGTGCTGCTGCTG
168-190	CTGCCTGCGTGCTGCTGCTG
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177-199	CTGCTGCTGCTGCTGCTGGCGGG
178-200	TGCTGCTGCTGCTGCTGGCGGGC
179-201	GCTGCTGCTGCTGCTGGCGGGCG
180-202	CTGCTGCTGCTGCTGGCGGGCGC
181-203	TGCTGCTGCTGCTGGCGGGCGCC
194-216	GGCGGGCGCCAGGGCCGAAGAGG
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206-228	GGCCGAAGAGGAAATGCTGGAAA
207-229	GCCGAAGAGGAAATGCTGGAAAA
208-230	CCGAAGAGGAAATGCTGGAAAT
209-231	CGAAGAGGAAATGCTGGAAATG
210-232	GAAGAGGAAATGCTGGAAATGT
211-233	AAGAGGAAATGCTGGAAATGTC
212-234	AGAGGAAATGCTGGAAATGTCA
213-235	GAGGAAATGCTGGAAATGTCAG
214-236	AGGAAATGCTGGAAATGTCAGC
215-237	GGAAATGCTGGAAATGTCAGCC
216-238	GAAATGCTGGAAATGTCAGCCT
217-239	AAATGCTGGAAATGTCAGCCTG
218-240	AATGCTGGAAATGTCAGCCTGG
219-241	ATGCTGGAAATGTCAGCCTGGT
220-242	TGCTGGAAATGTCAGCCTGGTC
221-243	GCTGGAAATGTCAGCCTGGTCT
222-244	CTGGAAATGTCAGCCTGGTCTG
223-245	TGGAAATGTCAGCCTGGTCTGT
224-246	GGAAATGTCAGCCTGGTCTGTG
225-247	GAAATGTCAGCCTGGTCTGTGCC
226-248	AAAATGTCAGCCTGGTCTGTCCA
227-249	AAATGTCAGCCTGGTCTGTCCAA
228-250	AATGTCAGCCTGGTCTGTCCAAA
229-251	ATGTCAGCCTGGTCTGTCCAAAA
230-252	TGTCAGCCTGGTCTGTCCAAAAG
231-253	GTCAGCCTGGTCTGTCCAAAAGA
232-254	TCAGCCTGGTCTGTCCAAAAGAT
233-255	CAGCCTGGTCTGTCCAAAAGATG
234-256	AGCCTGGTCTGTCCAAAAGATGC
235-257	GCCTGGTCTGTCCAAAAGATGCG
236-258	CCTGGTCTGTCCAAAAGATGCGA
237-259	CTGGTCTGTCCAAAAGATGCGAC
238-260	TGGTCTGTCCAAAAGATGCGACC
239-261	GGTCTGTCCAAAAGATGCGACCC
240-262	GTCTGTCCAAAAGATGCGACCCG

Position	Sequence
241-263	TCTGTCCAAAAGATGCGACCCGA
242-264	CTGTCCAAAAGATGCGACCCGAT
243-265	TGTCCAAAAGATGCGACCCGATT
244-266	GTCCAAAAGATGCGACCCGATTC
245-267	TCCAAAAGATGCGACCCGATTCA
246-268	CCAAAAGATGCGACCCGATTCAA
247-269	CAAAGATGCGACCCGATTCAAG
248-270	AAAAGATGCGACCCGATTCAAGC
249-271	AAAGATGCGACCCGATTCAAGCA
250-272	AAGATGCGACCCGATTCAAGCAC
251-273	AGATGCGACCCGATTCAAGCACC
252-274	GATGCGACCCGATTCAAGCACCT
253-275	ATGCGACCCGATTCAAGCACCTC
254-276	TGCGACCCGATTCAAGCACCTCC
255-277	GCGACCCGATTCAAGCACCTCCG
256-278	CGACCCGATTCAAGCACCTCCGG
257-279	GACCCGATTCAAGCACCTCCGGA
258-280	ACCCGATTCAAGCACCTCCGGAA
259-281	CCCGATTCAAGCACCTCCGGAAG
260-282	CCGATTCAAGCACCTCCGGAAGT
261-283	CGATTCAAGCACCTCCGGAAGTA
262-284	GATTCAAGCACCTCCGGAAGTAC
263-285	ATTCAAGCACCTCCGGAAGTACA
264-286	TTCAAGCACCTCCGGAAGTACAC
265-287	TCAAGCACCTCCGGAAGTACACA
266-288	CAAGCACCTCCGGAAGTACACAT
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272-294	CCTCCGGAAGTACACATACAAC
273-295	CTCCGGAAGTACACATACAAC
274-296	TCCGGAAGTACACATACAAC
275-297	CCGGAAGTACACATACAAC
276-298	CGGAAGTACACATACAAC
277-299	GGAAGTACACATACAAC
278-300	GAAGTACACATACAAC
279-301	AAGTACACATACAAC
280-302	AGTACACATACAAC
281-303	GTACACATACAAC
282-304	TACACATACAAC
283-305	ACACATACAAC
284-306	CACATACAAC
285-307	ACATACAAC
286-308	CATACAAC
287-309	ATACAAC
288-310	TACAAC
289-311	ACAAC
290-312	CAAC
291-313	AAC
292-314	ACT
293-315	CT
294-316	TAT
295-317	AT
296-318	TG
297-319	GAG
298-320	AGG
299-321	GGT
300-322	GCT
301-323	CTG
302-324	TG
303-325	GAG
304-326	AG
305-327	GAG
306-328	AGT

Position	Sequence
307-329	GTTCCAGTGGAGTCCCTGGGACT
308-330	TTCCAGTGGAGTCCCTGGGACTG
309-331	TCCAGTGGAGTCCCTGGGACTGC
310-332	CCAGTGGAGTCCCTGGGACTGCT
311-333	CAGTGGAGTCCCTGGGACTGCTG
312-334	AGTGGAGTCCCTGGGACTGCTGA
313-335	GTGGAGTCCCTGGGACTGCTGAT
314-336	TGGAGTCCCTGGGACTGCTGATT
315-337	GGAGTCCCTGGGACTGCTGATTC
316-338	GAGTCCCTGGGACTGCTGATTCA
317-339	AGTCCCTGGGACTGCTGATTCAA
318-340	GTCCCTGGGACTGCTGATTCAAG
319-341	TCCCTGGGACTGCTGATTCAAGA
320-342	CCCTGGGACTGCTGATTCAAGAA
321-343	CCTGGGACTGCTGATTCAAGAAG
322-344	CTGGGACTGCTGATTCAAGAAGT
323-345	TGGGACTGCTGATTCAAGAAGTG
324-346	GGGACTGCTGATTCAAGAAGTGC
325-347	GGACTGCTGATTCAAGAAGTGCC
326-348	GACTGCTGATTCAAGAAGTGCCA
327-349	ACTGCTGATTCAAGAAGTGCCAC
328-350	CTGCTGATTCAAGAAGTGCCACC
329-351	TGCTGATTCAAGAAGTGCCACCA
330-352	GCTGATTCAAGAAGTGCCACCAG
331-353	CTGATTCAAGAAGTGCCACCAGG
332-354	TGATTCAAGAAGTGCCACCAGGA
333-355	GATTCAAGAAGTGCCACCAGGAT
334-356	ATTCAAGAAGTGCCACCAGGATC
335-357	TTCAAGAAGTGCCACCAGGATCA
336-358	TCAAGAAGTGCCACCAGGATCAA
337-359	CAAGAAGTGCCACCAGGATCAAC
338-360	AAGAAGTGCCACCAGGATCAACT
339-361	AGAAGTGCCACCAGGATCAACTG
340-362	GAAGTGCCACCAGGATCAACTGC
341-363	AAGTGCCACCAGGATCAACTGCA
342-364	AGTGCCACCAGGATCAACTGCAA
343-365	GTGCCACCAGGATCAACTGCAAG
344-366	TGCCACCAGGATCAACTGCAAGG
345-367	GCCACCAGGATCAACTGCAAGGT
346-368	CCACCAGGATCAACTGCAAGGTT
347-369	CACCAGGATCAACTGCAAGGTTG
348-370	ACCAGGATCAACTGCAAGGTTGA
349-371	CCAGGATCAACTGCAAGGTTGAG
350-372	CAGGATCAACTGCAAGGTTGAGC
351-373	AGGATCAACTGCAAGGTTGAGCT
352-374	GGATCAACTGCAAGGTTGAGCTG
353-375	GATCAACTGCAAGGTTGAGCTGG
354-376	ATCAACTGCAAGGTTGAGCTGGA
355-377	TCAACTGCAAGGTTGAGCTGGAG
356-378	CAACTGCAAGGTTGAGCTGGAGG
357-379	AACTGCAAGGTTGAGCTGGAGGT
358-380	ACTGCAAGGTTGAGCTGGAGGTT
359-381	CTGCAAGGTTGAGCTGGAGGTTT
360-382	TGCAAGGTTGAGCTGGAGGTTCC
361-383	GCAAGGTTGAGCTGGAGGTTCCC
362-384	CAAGGTTGAGCTGGAGGTTCCCC
363-385	AAGGTTGAGCTGGAGGTTCCCCA
364-386	AGGTTGAGCTGGAGGTTCCCCAG
365-387	GGTTGAGCTGGAGGTTCCCCAGC
366-388	GTTGAGCTGGAGGTTCCCCAGCT
367-389	TTGAGCTGGAGGTTCCCCAGCTC
368-390	TGAGCTGGAGGTTCCCCAGCTCT
369-391	GAGCTGGAGGTTCCCCAGCTCTG
370-392	AGCTGGAGGTTCCCCAGCTCTGC
371-393	GCTGGAGGTTCCCCAGCTCTGCA
372-394	CTGGAGGTTCCCCAGCTCTGCAG

Position	Sequence
373-395	TGGAGGTTC CCCAGCTCTGCAGC
374-396	GGAGGTTC CCCAGCTCTGCAGCT
375-397	GAGGTTC CCCAGCTCTGCAGCTT
376-398	AGGTTC CCCAGCTCTGCAGCTTC
377-399	GGTTC CCCAGCTCTGCAGCTTCA
378-400	GTTTC CCCAGCTCTGCAGCTTCAT
379-401	TTCC CAGCTCTGCAGCTTCATC
380-402	TCC CAGCTCTGCAGCTTCATCC
381-403	CCC CAGCTCTGCAGCTTCATCCT
382-404	CCCAGCTCTGCAGCTTCATCCTG
383-405	CCAGCTCTGCAGCTTCATCCTGA
384-406	CAGCTCTGCAGCTTCATCCTGAA
385-407	AGCTCTGCAGCTTCATCCTGAAG
386-408	GCTCTGCAGCTTCATCCTGAAGA
387-409	CTCTGCAGCTTCATCCTGAAGAC
388-410	TCTGCAGCTTCATCCTGAAGACC
389-411	CTGCAGCTTCATCCTGAAGACCA
390-412	TGCAGCTTCATCCTGAAGACCAG
391-413	GCAGCTTCATCCTGAAGACCAGC
392-414	CAGCTTCATCCTGAAGACCAGCC
393-415	AGCTTCATCCTGAAGACCAGCCA
394-416	GCTTCATCCTGAAGACCAGCCAG
395-417	CTTCATCCTGAAGACCAGCCAGT
396-418	TTCATCCTGAAGACCAGCCAGTG
397-419	TCATCCTGAAGACCAGCCAGTGC
398-420	CATCCTGAAGACCAGCCAGTGCA
399-421	ATCCTGAAGACCAGCCAGTGCAC
400-422	TCCTGAAGACCAGCCAGTGCAACC
401-423	CCTGAAGACCAGCCAGTGCAACCC
402-424	CTGAAGACCAGCCAGTGCAACCT
403-425	TGAAGACCAGCCAGTGCAACCTG
404-426	GAAGACCAGCCAGTGCAACCTGA
405-427	AAGACCAGCCAGTGCAACCTGAA
406-428	AGACCAGCCAGTGCAACCTGAAA
407-429	GACCAGCCAGTGCAACCTGAAAG
408-430	ACCAGCCAGTGCAACCTGAAAGA
409-431	CCAGCCAGTGCAACCTGAAAGAG
410-432	CAGCCAGTGCAACCTGAAAGAGG
411-433	AGCCAGTGCAACCTGAAAGAGGT
412-434	GCCAGTGCAACCTGAAAGAGGTG
413-435	CCAGTGCAACCTGAAAGAGGTGT
414-436	CAGTGCAACCTGAAAGAGGTGTA
415-437	AGTGCAACCTGAAAGAGGTGTAT
416-438	GTGCAACCTGAAAGAGGTGTATG
417-439	TGCAACCTGAAAGAGGTGTATGG
418-440	GCACCTGAAAGAGGTGTATGGC
419-441	CACCTGAAAGAGGTGTATGGCT
420-442	ACCCTGAAAGAGGTGTATGGCTT
421-443	CCCTGAAAGAGGTGTATGGCTTC
422-444	CCTGAAAGAGGTGTATGGCTTCA
423-445	CTGAAAGAGGTGTATGGCTTCAA
424-446	TGAAAGAGGTGTATGGCTTCAAC
425-447	GAAAGAGGTGTATGGCTTCAACC
426-448	AAAGAGGTGTATGGCTTCAACCC
427-449	AAGAGGTGTATGGCTTCAACCCT
428-450	AGAGGTGTATGGCTTCAACCCTG
429-451	GAGGTGTATGGCTTCAACCCTGA
430-452	AGGTGTATGGCTTCAACCCTGAG
431-453	GGTGTATGGCTTCAACCCTGAGG
432-454	GTGTATGGCTTCAACCCTGAGGG
433-455	TGTATGGCTTCAACCCTGAGGGC
434-456	GTATGGCTTCAACCCTGAGGGCA
435-457	TATGGCTTCAACCCTGAGGGCAA
436-458	ATGGCTTCAACCCTGAGGGCAAA
437-459	TGGCTTCAACCCTGAGGGCAAAG
438-460	GGCTTCAACCCTGAGGGCAAAGC

Position	Sequence
439-461	GCTCAACCCCTGAGGGCAAAGCC
440-462	CTTCAACCCCTGAGGGCAAAGCCT
441-463	TTCAACCCCTGAGGGCAAAGCCTT
442-464	TCAACCCCTGAGGGCAAAGCCTTG
443-465	CAACCCCTGAGGGCAAAGCCTTGC
444-466	AACCCCTGAGGGCAAAGCCTTGCT
445-467	ACCCTGAGGGCAAAGCCTTGCTG
446-468	CCCTGAGGGCAAAGCCTTGCTGA
447-469	CCTGAGGGCAAAGCCTTGCTGAA
448-470	CTGAGGGCAAAGCCTTGCTGAAG
449-471	TGAGGGCAAAGCCTTGCTGAAGA
450-472	GAGGGCAAAGCCTTGCTGAAGAA
451-473	AGGGCAAAGCCTTGCTGAAGAAA
452-474	GGCAAAGCCTTGCTGAAGAAAA
453-475	GGCAAAGCCTTGCTGAAGAAAAC
454-476	GCAAAGCCTTGCTGAAGAAAACC
455-477	CAAAGCCTTGCTGAAGAAAACCA
456-478	AAAGCCTTGCTGAAGAAAACCAA
457-479	AAGCCTTGCTGAAGAAAACCAAG
458-480	AGCCTTGCTGAAGAAAACCAAGA
459-481	GCCTTGCTGAAGAAAACCAAGAA
460-482	CCTTGCTGAAGAAAACCAAGAAC
461-483	CTTGCTGAAGAAAACCAAGAACT
462-484	TTGCTGAAGAAAACCAAGAACTC
463-485	TGCTGAAGAAAACCAAGAACTCT
464-486	GCTGAAGAAAACCAAGAACTCTG
465-487	CTGAAGAAAACCAAGAACTCTGA
466-488	TGAAGAAAACCAAGAACTCTGAG
467-489	GAAGAAAACCAAGAACTCTGAGG
468-490	AAGAAAACCAAGAACTCTGAGGA
469-491	AGAAAACCAAGAACTCTGAGGAG
470-492	GAAAACCAAGAACTCTGAGGAGT
471-493	AAAACCAAGAACTCTGAGGAGTT
472-494	AAACCAAGAACTCTGAGGAGTTT
473-495	AACCAAGAACTCTGAGGAGTTTG
474-496	ACCAAGAACTCTGAGGAGTTTGC
475-497	CCAAGAACTCTGAGGAGTTTGCT
476-498	CAAGAACTCTGAGGAGTTTGCTG
477-499	AAGAACTCTGAGGAGTTTGCTGC
478-500	AGAACTCTGAGGAGTTTGCTGCA
479-501	GAACTCTGAGGAGTTTGCTGCAG
480-502	AACTCTGAGGAGTTTGCTGCAGC
481-503	ACTCTGAGGAGTTTGCTGCAGCC
482-504	CTCTGAGGAGTTTGCTGCAGCCA
483-505	TCTGAGGAGTTTGCTGCAGCCAT
484-506	CTGAGGAGTTTGCTGCAGCCATG
485-507	TGAGGAGTTTGCTGCAGCCATGT
486-508	GAGGAGTTTGCTGCAGCCATGTC
487-509	AGGAGTTTGCTGCAGCCATGTCC
488-510	GGAGTTTGCTGCAGCCATGTCCA
489-511	GAGTTTGCTGCAGCCATGTCCAG
490-512	AGTTTGCTGCAGCCATGTCCAGG
491-513	GTTTGCTGCAGCCATGTCCAGGT
492-514	TTTGCTGCAGCCATGTCCAGGTA
493-515	TTGCTGCAGCCATGTCCAGGTAT
494-516	TGCTGCAGCCATGTCCAGGTATG
495-517	GCTGCAGCCATGTCCAGGTATGA
496-518	CTGCAGCCATGTCCAGGTATGAG
497-519	TGCAGCCATGTCCAGGTATGAGC
498-520	GCAGCCATGTCCAGGTATGAGCT
499-521	CAGCCATGTCCAGGTATGAGCTC
500-522	AGCCATGTCCAGGTATGAGCTCA
501-523	GCCATGTCCAGGTATGAGCTCAA
502-524	CCATGTCCAGGTATGAGCTCAAG
503-525	CATGTCCAGGTATGAGCTCAAGC
504-526	ATGTCCAGGTATGAGCTCAAGCT

Position	Sequence
505-527	TGTCCAGGTATGAGCTCAAGCTG
506-528	GTCCAGGTATGAGCTCAAGCTGG
507-529	TCCAGGTATGAGCTCAAGCTGGC
508-530	CCAGGTATGAGCTCAAGCTGGCC
509-531	CAGGTATGAGCTCAAGCTGGCCA
510-532	AGGTATGAGCTCAAGCTGGCCAT
511-533	GGTATGAGCTCAAGCTGGCCATT
512-534	GTATGAGCTCAAGCTGGCCATTC
513-535	TATGAGCTCAAGCTGGCCATTCC
514-536	ATGAGCTCAAGCTGGCCATTCCA
515-537	TGAGCTCAAGCTGGCCATTCCAG
516-538	GAGCTCAAGCTGGCCATTCCAGA
517-539	AGCTCAAGCTGGCCATTCCAGAA
518-540	GCTCAAGCTGGCCATTCCAGAAG
519-541	CTCAAGCTGGCCATTCCAGAAGG
520-542	TCAAGCTGGCCATTCCAGAAGGG
521-543	CAAGCTGGCCATTCCAGAAGGGA
522-544	AAGCTGGCCATTCCAGAAGGGAA
523-545	AGCTGGCCATTCCAGAAGGGAAG
524-546	GCTGGCCATTCCAGAAGGGAAAGC
525-547	CTGGCCATTCCAGAAGGGAAAGCA
526-548	TGGCCATTCCAGAAGGGAAAGCAG
527-549	GGCCATTCCAGAAGGGAAAGCAGG
528-550	GCCATTCCAGAAGGGAAAGCAGGT
529-551	CCATTCCAGAAGGGAAAGCAGGTT
530-552	CATTCCAGAAGGGAAAGCAGGTTT
531-553	ATTCCAGAAGGGAAAGCAGGTTTT
532-554	TCCAGAAGGGAAAGCAGGTTTTTC
533-555	TCCAGAAGGGAAAGCAGGTTTTTCC
534-556	CCAGAAGGGAAAGCAGGTTTTTCCT
535-557	CAGAAGGGAAAGCAGGTTTTTCCTT
536-558	AGAAGGGAAAGCAGGTTTTTCCTTT
537-559	GAAGGGAAAGCAGGTTTTTCCTTTA
538-560	AAGGGAAAGCAGGTTTTTCCTTTAC
539-561	AGGGAAAGCAGGTTTTTCCTTTACC
540-562	GGGAAGCAGGTTTTTCCTTTACCC
541-563	GGAAGCAGGTTTTTCCTTTACCCG
542-564	GAGCAGGTTTTTCCTTTACCCGG
543-565	AAGCAGGTTTTTCCTTTACCCGGGA
544-566	AGCAGGTTTTTCCTTTACCCGGGAG
545-567	GCAGGTTTTTCCTTTACCCGGGAGA
546-568	CAGGTTTTTCCTTTACCCGGGAGAA
547-569	AGGTTTTTCCTTTACCCGGGAGAAA
548-570	GGTTTTTCCTTTACCCGGGAGAAAAG
549-571	GTTTTTCCTTTACCCGGGAGAAAAGA
550-572	TTTTTCCTTTACCCGGGAGAAAAGAT
551-573	TTTCCTTTACCCGGGAGAAAAGATG
552-574	TTCCTTTACCCGGGAGAAAAGATGA
553-575	TCCTTTACCCGGGAGAAAAGATGAA
554-576	CCTTTACCCGGGAGAAAAGATGAAC
555-577	CTTTACCCGGGAGAAAAGATGAACC
556-578	TTTACCCGGGAGAAAAGATGAACCT
557-579	TTACCCGGGAGAAAAGATGAACCTA
558-580	TACCCGGGAGAAAAGATGAACCTAC
559-581	ACCCGGGAGAAAAGATGAACCTACT
560-582	CCCGGAGAAAAGATGAACCTACTT
561-583	CCGGAGAAAAGATGAACCTACTTA
562-584	CGGAGAAAAGATGAACCTACTTAC
563-585	GGAGAAAAGATGAACCTACTTACA
564-586	GAGAAAAGATGAACCTACTTACAT
565-587	AGAAAAGATGAACCTACTTACATC
566-588	GAAAAGATGAACCTACTTACATCC
567-589	AAAGATGAACCTACTTACATCCT
568-590	AAGATGAACCTACTTACATCCTG
569-591	AGATGAACCTACTTACATCCTGA
570-592	GATGAACCTACTTACATCCTGAA

Position	Sequence
571-593	ATGAACCTACTTACATCCTGAAC
572-594	TGAACCTACTTACATCCTGAACA
573-595	GAACCTACTTACATCCTGAACAT
574-596	AACCTACTTACATCCTGAACATC
575-597	ACCTACTTACATCCTGAACATCA
576-598	CCTACTTACATCCTGAACATCAA
577-599	CTACTTACATCCTGAACATCAAG
578-600	TACTTACATCCTGAACATCAAGA
579-601	ACTTACATCCTGAACATCAAGAG
580-602	CTTACATCCTGAACATCAAGAGG
581-603	TTACATCCTGAACATCAAGAGGG
582-604	TACATCCTGAACATCAAGAGGGG
583-605	ACATCCTGAACATCAAGAGGGGC
584-606	CATCCTGAACATCAAGAGGGGCA
585-607	ATCCTGAACATCAAGAGGGGCAT
586-608	TCCTGAACATCAAGAGGGGCATC
587-609	CCTGAACATCAAGAGGGGCATCA
588-610	CTGAACATCAAGAGGGGCATCAT
589-611	TGAACATCAAGAGGGGCATCATT
590-612	GAACATCAAGAGGGGCATCATTT
591-613	AACATCAAGAGGGGCATCATTTT
592-614	ACATCAAGAGGGGCATCATTTCT
593-615	CATCAAGAGGGGCATCATTTCTG
594-616	ATCAAGAGGGGCATCATTTCTGC
595-617	TCAAGAGGGGCATCATTTCTGCC
596-618	CAAGAGGGGCATCATTTCTGCCC
597-619	AAGAGGGGCATCATTTCTGCCCT
598-620	AGAGGGGCATCATTTCTGCCCTC
599-621	GAGGGGCATCATTTCTGCCCTCC
600-622	AGGGGCATCATTTCTGCCCTCCT
601-623	GGGGCATCATTTCTGCCCTCCTG
602-624	GGGCATCATTTCTGCCCTCCTGG
603-625	GGCATCATTTCTGCCCTCCTGGT
604-626	GCATCATTTCTGCCCTCCTGGTT
605-627	CATCATTTCTGCCCTCCTGGTTC
606-628	ATCATTTCTGCCCTCCTGGTTCC
607-629	TCATTTCTGCCCTCCTGGTTCCC
608-630	CATTTCTGCCCTCCTGGTTCCCC
609-631	ATTTCTGCCCTCCTGGTTCCCCC
610-632	TTTCTGCCCTCCTGGTTCCCCCA
611-633	TTCTGCCCTCCTGGTTCCCCCAG
612-634	TCTGCCCTCCTGGTTCCCCCAGA
613-635	CTGCCCTCCTGGTTCCCCCAGAG
614-636	TGCCCTCCTGGTTCCCCCAGAGA
615-637	GCCCTCCTGGTTCCCCCAGAGAC
616-638	CCCTCCTGGTTCCCCCAGAGACA
617-639	CCTCCTGGTTCCCCCAGAGACAG
618-640	CTCCTGGTTCCCCCAGAGACAGA
619-641	TCTCCTGGTTCCCCCAGAGACAGAA
620-642	CCTGGTTCCCCCAGAGACAGAAG
621-643	CTGGTTCCCCCAGAGACAGAAGA
622-644	TGGTTCCCCCAGAGACAGAAGAA
623-645	GGTTCCCCCAGAGACAGAAGAAG
624-646	GTTCCCCCAGAGACAGAAGAAGC
625-647	TTCCCCCAGAGACAGAAGAAGCC
626-648	TCCCCCAGAGACAGAAGAAGCCA
627-649	CCCCCAGAGACAGAAGAAGCCAA
628-650	CCCCAGAGACAGAAGAAGCCAAG
629-651	CCCAGAGACAGAAGAAGCCAAGC
630-652	CCAGAGACAGAAGAAGCCAAGCA
631-653	CAGAGACAGAAGAAGCCAAGCAA
632-654	AGAGACAGAAGAAGCCAAGCAAG
633-655	GAGACAGAAGAAGCCAAGCAAGT
634-656	AGACAGAAGAAGCCAAGCAAGTG
635-657	GACAGAAGAAGCCAAGCAAGTGT
636-658	ACAGAAGAAGCCAAGCAAGTGT

Position	Sequence
637-659	CAGAAGAAGCCAAGCAAGTGTG
638-660	AGAAGAAGCCAAGCAAGTGTGT
639-661	GAAGAAGCCAAGCAAGTGTGTT
640-662	AAGAAGCCAAGCAAGTGTGTTT
641-663	AGAAGCCAAGCAAGTGTGTTTC
642-664	GAAGCCAAGCAAGTGTGTTTCT
643-665	AAGCCAAGCAAGTGTGTTTCTG
644-666	AGCCAAGCAAGTGTGTTTCTGG
645-667	GCCAAGCAAGTGTGTTTCTGGA
646-668	CCAAGCAAGTGTGTTTCTGGAT
647-669	CAAGCAAGTGTGTTTCTGGATA
648-670	AAGCAAGTGTGTTTCTGGATAC
649-671	AGCAAGTGTGTTTCTGGATACC
650-672	GCAAGTGTGTTTCTGGATACCG
651-673	CAAGTGTGTTTCTGGATACCGT
652-674	AAGTGTGTTTCTGGATACCGTG
653-675	AGTGTGTTTCTGGATACCGTGT
654-676	GTGTGTTTCTGGATACCGTGTA
655-677	TGTTGTTTCTGGATACCGTGAT
656-678	GTTGTTTCTGGATACCGTGATG
657-679	TTGTTTCTGGATACCGTGATGG
658-680	TGTTTCTGGATACCGTGATGGA
659-681	GTTTCTGGATACCGTGATGGAA
660-682	TTTCTGGATACCGTGATGGAAA
661-683	TTCTGGATACCGTGATGGAAAC
662-684	TCTGGATACCGTGATGGAAACT
663-685	CTGGATACCGTGATGGAAACTG
664-686	TGGATACCGTGATGGAAACTGC
665-687	GGATACCGTGATGGAAACTGCT
666-688	GATACCGTGATGGAAACTGCTC
667-689	ATACCGTGATGGAAACTGCTCC
668-690	TACCGTGATGGAAACTGCTCCA
669-691	ACCGTGATGGAAACTGCTCCAC
670-692	CCGTGATGGAAACTGCTCCACT
671-693	CGTGATGGAAACTGCTCCACTC
672-694	GTGTATGGAAACTGCTCCACTCA
673-695	TGTATGGAAACTGCTCCACTCAC
674-696	GTATGGAAACTGCTCCACTCACT
675-697	TATGGAAACTGCTCCACTCACTT
676-698	ATGGAAACTGCTCCACTCACTTT
677-699	TGGAAACTGCTCCACTCACTTTA
678-700	GGAAACTGCTCCACTCACTTTAC
679-701	GAAACTGCTCCACTCACTTTACC
680-702	AAACTGCTCCACTCACTTTACCG
681-703	AACTGCTCCACTCACTTTACCGT
682-704	ACTGCTCCACTCACTTTACCGTC
683-705	CTGCTCCACTCACTTTACCGTCA
684-706	TGCTCCACTCACTTTACCGTCAA
685-707	GCTCCACTCACTTTACCGTCAAG
686-708	CTCCACTCACTTTACCGTCAAGA
687-709	TCCACTCACTTTACCGTCAAGAC
688-710	CCACTCACTTTACCGTCAAGACG
689-711	CACTCACTTTACCGTCAAGACGA
690-712	ACTCACTTTACCGTCAAGACGAG
691-713	CTCACTTTACCGTCAAGACGAGG
692-714	TCACTTTACCGTCAAGACGAGGA
693-715	CACTTTACCGTCAAGACGAGGAA
694-716	ACTTTACCGTCAAGACGAGGAAG
695-717	CTTTACCGTCAAGACGAGGAAGG
696-718	TTTACCGTCAAGACGAGGAAGGG
697-719	TTACCGTCAAGACGAGGAAGGGC
698-720	TACCGTCAAGACGAGGAAGGGCA
699-721	ACCGTCAAGACGAGGAAGGGCAA
700-722	CCGTCAAGACGAGGAAGGGCAAT
701-723	CGTCAAGACGAGGAAGGGCAATG
702-724	GTCAGACGAGGAAGGGCAATGT

Position	Sequence
703-725	TCAAGACGAGGAAGGGCAATGTG
704-726	CAAGACGAGGAAGGGCAATGTGG
705-727	AAGACGAGGAAGGGCAATGTGGC
706-728	AGACGAGGAAGGGCAATGTGGCA
707-729	GACGAGGAAGGGCAATGTGGCAA
708-730	ACGAGGAAGGGCAATGTGGCAAC
709-731	CGAGGAAGGGCAATGTGGCAACA
710-732	GAGGAAGGGCAATGTGGCAACAG
711-733	AGGAAGGGCAATGTGGCAACAGA
712-734	GGAAGGGCAATGTGGCAACAGAA
713-735	GAAGGGCAATGTGGCAACAGAAA
714-736	AAGGGCAATGTGGCAACAGAAAT
715-737	AGGGCAATGTGGCAACAGAAATA
716-738	GGGCAATGTGGCAACAGAAATAT
717-739	GGCAATGTGGCAACAGAAATATC
718-740	GCAATGTGGCAACAGAAATATCC
719-741	CAATGTGGCAACAGAAATATCCA
720-742	AATGTGGCAACAGAAATATCCAC
721-743	ATGTGGCAACAGAAATATCCACT
722-744	TGTGGCAACAGAAATATCCACTG
723-745	GTGGCAACAGAAATATCCACTGA
724-746	TGGCAACAGAAATATCCACTGAA
725-747	GGCAACAGAAATATCCACTGAAA
726-748	GCAACAGAAATATCCACTGAAAG
727-749	CAACAGAAATATCCACTGAAAGA
728-750	AACAGAAATATCCACTGAAAGAG
729-751	ACAGAAATATCCACTGAAAGAGA
730-752	CAGAAATATCCACTGAAAGAGAC
731-753	AGAAATATCCACTGAAAGAGACC
732-754	GAAATATCCACTGAAAGAGACCT
733-755	AAATATCCACTGAAAGAGACCTG
734-756	AATATCCACTGAAAGAGACCTGG
735-757	ATATCCACTGAAAGAGACCTGGG
736-758	TATCCACTGAAAGAGACCTGGGG
737-759	ATCCACTGAAAGAGACCTGGGGC
738-760	TCCACTGAAAGAGACCTGGGGCA
739-761	CCACTGAAAGAGACCTGGGGCAG
740-762	CACTGAAAGAGACCTGGGGCAGT
741-763	ACTGAAAGAGACCTGGGGCAGTG
742-764	CTGAAAGAGACCTGGGGCAGTGT
743-765	TGAAAGAGACCTGGGGCAGTGTG
744-766	GAAAGAGACCTGGGGCAGTGTGA
745-767	AAAGAGACCTGGGGCAGTGTGAT
746-768	AAGAGACCTGGGGCAGTGTGATC
747-769	AGAGACCTGGGGCAGTGTGATCG
748-770	GAGACCTGGGGCAGTGTGATCGC
749-771	AGACCTGGGGCAGTGTGATCGCT
750-772	GACCTGGGGCAGTGTGATCGCTT
751-773	ACCTGGGGCAGTGTGATCGCTTC
752-774	CCTGGGGCAGTGTGATCGCTTCA
753-775	CTGGGGCAGTGTGATCGCTTCAA
754-776	TGGGGCAGTGTGATCGCTTCAAG
755-777	GGGGCAGTGTGATCGCTTCAAGC
756-778	GGGCAGTGTGATCGCTTCAAGCC
757-779	GGCAGTGTGATCGCTTCAAGCCC
758-780	GCAGTGTGATCGCTTCAAGCCCA
759-781	CAGTGTGATCGCTTCAAGCCCAT
760-782	AGTGTGATCGCTTCAAGCCCATC
761-783	GTGTGATCGCTTCAAGCCCATCC
762-784	TGTGATCGCTTCAAGCCCATCCG
763-785	GTGATCGCTTCAAGCCCATCCGC
764-786	TGATCGCTTCAAGCCCATCCGCA
765-787	GATCGCTTCAAGCCCATCCGCAC
766-788	ATCGCTTCAAGCCCATCCGCACA
767-789	TCGCTTCAAGCCCATCCGCACAG
768-790	CGCTTCAAGCCCATCCGCACAGG

Position	Sequence
769-791	GCTTCAAGCCCATCCGCACAGGC
770-792	CTTCAAGCCCATCCGCACAGGCA
771-793	TTCAAGCCCATCCGCACAGGCAT
772-794	TCAAGCCCATCCGCACAGGCATC
773-795	CAAGCCCATCCGCACAGGCATCA
774-796	AAGCCCATCCGCACAGGCATCAG
775-797	AGCCCATCCGCACAGGCATCAGC
776-798	GCCCATCCGCACAGGCATCAGCC
777-799	CCCATCCGCACAGGCATCAGCCC
778-800	CCATCCGCACAGGCATCAGCCCA
779-801	CATCCGCACAGGCATCAGCCAC
780-802	ATCCGCACAGGCATCAGCCCACT
781-803	TCCGCACAGGCATCAGCCCACTT
782-804	CCGCACAGGCATCAGCCCACTTG
783-805	CGCACAGGCATCAGCCCACTTGC
784-806	GCACAGGCATCAGCCCACTTGCT
785-807	CACAGGCATCAGCCCACTTGCTC
786-808	ACAGGCATCAGCCCACTTGCTCT
787-809	CAGGCATCAGCCCACTTGCTCTC
788-810	AGGCATCAGCCCACTTGCTCTCA
789-811	GGCATCAGCCCACTTGCTCTCAT
790-812	GCATCAGCCCACTTGCTCTCATC
791-813	CATCAGCCCACTTGCTCTCATCA
792-814	ATCAGCCCACTTGCTCTCATCAA
793-815	TCAGCCCACTTGCTCTCATCAA
794-816	CAGCCCACTTGCTCTCATCAAAG
795-817	AGCCCACTTGCTCTCATCAAAGG
796-818	GCCCACTTGCTCTCATCAAAGGC
797-819	CCCACTTGCTCTCATCAAAGGCA
798-820	CCACTTGCTCTCATCAAAGGCAT
799-821	CACTTGCTCTCATCAAAGGCATG
800-822	ACTTGCTCTCATCAAAGGCATGA
801-823	CTTGCTCTCATCAAAGGCATGAC
802-824	TTGCTCTCATCAAAGGCATGACC
803-825	TGCTCTCATCAAAGGCATGACCC
804-826	GCTCTCATCAAAGGCATGACCCG
805-827	CTCTCATCAAAGGCATGACCCGC
806-828	TCTCATCAAAGGCATGACCCGCC
807-829	CTCATCAAAGGCATGACCCGCC
808-830	TCATCAAAGGCATGACCCGCC
809-831	CATCAAAGGCATGACCCGCCCT
810-832	ATCAAAGGCATGACCCGCCCTT
811-833	TCAAAGGCATGACCCGCCCTTG
812-834	CAAAGGCATGACCCGCCCTTGT
813-835	AAAGGCATGACCCGCCCTTGTG
814-836	AAGGCATGACCCGCCCTTGTCA
815-837	AGGCATGACCCGCCCTTGTCAA
816-838	GGCATGACCCGCCCTTGTCAAC
817-839	GCATGACCCGCCCTTGTCAACT
818-840	CATGACCCGCCCTTGTCAACTC
819-841	ATGACCCGCCCTTGTCAACTCT
820-842	TGACCCGCCCTTGTCAACTCTG
821-843	GACCCGCCCTTGTCAACTCTGA
822-844	ACCCGCCCTTGTCAACTCTGAT
823-845	CCCGCCCTTGTCAACTCTGATC
824-846	CCGCCCTTGTCAACTCTGATCA
825-847	CGCCCTTGTCAACTCTGATCAG
826-848	GCCCTTGTCAACTCTGATCAGC
827-849	CCCCTTGTCAACTCTGATCAGCA
828-850	CCCTTGTCAACTCTGATCAGCAG
829-851	CCTTGTCAACTCTGATCAGCAGC
830-852	CTTGTCAACTCTGATCAGCAGCA
831-853	TTGTCAACTCTGATCAGCAGCAG
832-854	TGTCAACTCTGATCAGCAGCAGC
833-855	GTCAACTCTGATCAGCAGCAGCC
834-856	TCAACTCTGATCAGCAGCAGCCA

Position	Sequence
835-857	CAACTCTGATCAGCAGCAGCCAG
836-858	AACTCTGATCAGCAGCAGCCAGT
837-859	ACTCTGATCAGCAGCAGCCAGTC
838-860	CTCTGATCAGCAGCAGCCAGTCC
839-861	TCTGATCAGCAGCAGCCAGTCCT
840-862	CTGATCAGCAGCAGCCAGTCCTG
841-863	TGATCAGCAGCAGCCAGTCCTGT
842-864	GATCAGCAGCAGCCAGTCCTGTC
843-865	ATCAGCAGCAGCCAGTCCTGTCA
844-866	TCAGCAGCAGCCAGTCCTGTGTCAG
845-867	CAGCAGCAGCCAGTCCTGTGTCAGT
846-868	AGCAGCAGCCAGTCCTGTGTCAGTA
847-869	GCAGCAGCCAGTCCTGTGTCAGTAC
848-870	CAGCAGCCAGTCCTGTGTCAGTACA
849-871	AGCAGCCAGTCCTGTGTCAGTACAC
850-872	GCAGCCAGTCCTGTGTCAGTACACA
851-873	CAGCCAGTCCTGTGTCAGTACACAC
852-874	AGCCAGTCCTGTGTCAGTACACACT
853-875	GCCAGTCCTGTGTCAGTACACACTG
854-876	CCAGTCCTGTGTCAGTACACACTGG
855-877	CAGTCCTGTGTCAGTACACACTGGA
856-878	AGTCCTGTGTCAGTACACACTGGAC
857-879	GTCTGTGTCAGTACACACTGGACG
858-880	TCCTGTGTCAGTACACACTGGACGC
859-881	CCTGTGTCAGTACACACTGGACGCT
860-882	CTGTGTCAGTACACACTGGACGCTA
861-883	TGTGTCAGTACACACTGGACGCTAA
862-884	GTCAGTACACACTGGACGCTAAG
863-885	TCAGTACACACTGGACGCTAAGA
864-886	CAGTACACACTGGACGCTAAGAG
865-887	AGTACACACTGGACGCTAAGAGG
866-888	GTACACACTGGACGCTAAGAGGA
867-889	TACACACTGGACGCTAAGAGGAA
868-890	ACACACTGGACGCTAAGAGGAAG
869-891	CACACTGGACGCTAAGAGGAAGC
870-892	ACACTGGACGCTAAGAGGAAGCA
871-893	CACTGGACGCTAAGAGGAAGCAT
872-894	ACTGGACGCTAAGAGGAAGCATG
873-895	CTGGACGCTAAGAGGAAGCATGT
874-896	TGGACGCTAAGAGGAAGCATGTG
875-897	GGACGCTAAGAGGAAGCATGTGG
876-898	GACGCTAAGAGGAAGCATGTGGC
877-899	ACGCTAAGAGGAAGCATGTGGCA
878-900	CGCTAAGAGGAAGCATGTGGCAG
879-901	GCTAAGAGGAAGCATGTGGCAGA
880-902	CTAAGAGGAAGCATGTGGCAGAA
881-903	TAAGAGGAAGCATGTGGCAGAAG
882-904	AAGAGGAAGCATGTGGCAGAAGC
883-905	AGAGGAAGCATGTGGCAGAAGCC
884-906	GAGGAAGCATGTGGCAGAAGCCA
885-907	AGGAAGCATGTGGCAGAAGCCAT
886-908	GAAGCATGTGGCAGAAGCCATC
887-909	GAAGCATGTGGCAGAAGCCATCT
888-910	AAGCATGTGGCAGAAGCCATCTG
889-911	AGCATGTGGCAGAAGCCATCTGC
890-912	GCATGTGGCAGAAGCCATCTGCA
891-913	CATGTGGCAGAAGCCATCTGCAA
892-914	ATGTGGCAGAAGCCATCTGCAAG
893-915	TGTGGCAGAAGCCATCTGCAAGG
894-916	GTGGCAGAAGCCATCTGCAAGGA
895-917	TGGCAGAAGCCATCTGCAAGGAG
896-918	GGCAGAAGCCATCTGCAAGGAGC
897-919	GCAGAAGCCATCTGCAAGGAGCA
898-920	CAGAAGCCATCTGCAAGGAGCAA
899-921	AGAAGCCATCTGCAAGGAGCAAC
900-922	GAAGCCATCTGCAAGGAGCAACA

Position	Sequence
901-923	AAGCCATCTGCAAGGAGCAACAC
902-924	AGCCATCTGCAAGGAGCAACACC
903-925	GCCATCTGCAAGGAGCAACACCT
904-926	CCATCTGCAAGGAGCAACACCTC
905-927	CATCTGCAAGGAGCAACACCTCT
906-928	ATCTGCAAGGAGCAACACCTCTT
907-929	TCTGCAAGGAGCAACACCTCTTC
908-930	CTGCAAGGAGCAACACCTCTTCC
909-931	TGCAAGGAGCAACACCTCTTCTCT
910-932	GCAAGGAGCAACACCTCTTCTCTG
911-933	CAAGGAGCAACACCTCTTCTCTGC
912-934	AAGGAGCAACACCTCTTCTCTGCC
913-935	AGGAGCAACACCTCTTCTCTGCCT
914-936	GGAGCAACACCTCTTCTCTGCCTT
915-937	GAGCAACACCTCTTCTCTGCCTTT
916-938	AGCAACACCTCTTCTCTGCCTTTC
917-939	GCAACACCTCTTCTCTGCCTTTCT
918-940	CAACACCTCTTCTCTGCCTTTCTC
919-941	AACACCTCTTCTCTGCCTTTCTCC
920-942	ACACCTCTTCTCTGCCTTTCTCCT
921-943	CACCTCTTCTCTGCCTTTCTCCTA
922-944	ACCTCTTCTCTGCCTTTCTCCTAC
923-945	CCTCTTCTCTGCCTTTCTCCTACA
924-946	CTCTTCTCTGCCTTTCTCCTACAA
925-947	TCTTCTCTGCCTTTCTCCTACAAC
926-948	CTTCTCTGCCTTTCTCCTACAACA
927-949	TTCTCTCTGCCTTTCTCCTACAACAA
928-950	TCCTGCCTTTCTCCTACAACAATA
929-951	CCTGCCTTTCTCCTACAACAATAA
930-952	CTGCCTTTCTCCTACAACAATAAA
931-953	TGCCTTTCTCCTACAACAATAAAG
932-954	GCCTTTCTCCTACAACAATAAAGT
933-955	CCTTTCTCCTACAACAATAAAGTA
934-956	CTTTCTCCTACAACAATAAAGTAT
935-957	TTTCTCCTACAACAATAAAGTATG
936-958	TTCTCCTACAACAATAAAGTATGG
937-959	TCTCCTACAACAATAAAGTATGGG
938-960	CTCCTACAACAATAAAGTATGGGA
939-961	TCCTACAACAATAAAGTATGGGAT
940-962	CCTACAACAATAAAGTATGGGATG
941-963	CTACAACAATAAAGTATGGGATGG
942-964	TACAACAATAAAGTATGGGATGGT
943-965	ACAACAATAAAGTATGGGATGGTA
944-966	CAACAATAAAGTATGGGATGGTAG
945-967	AACAATAAAGTATGGGATGGTAGC
946-968	ACAATAAAGTATGGGATGGTAGCA
947-969	CAATAAAGTATGGGATGGTAGCAC
948-970	AATAAAGTATGGGATGGTAGCACA
949-971	ATAAAGTATGGGATGGTAGCACAA
950-972	TAAGTATGGGATGGTAGCACAAAG
951-973	AAGTATGGGATGGTAGCACAAAGT
952-974	AGTATGGGATGGTAGCACAAAGTG
953-975	GTATGGGATGGTAGCACAAAGTGA
954-976	TATGGGATGGTAGCACAAAGTGAC
955-977	ATGGGATGGTAGCACAAAGTGACA
956-978	TGGGATGGTAGCACAAAGTGACAC
957-979	GGGATGGTAGCACAAAGTGACACA
958-980	GGATGGTAGCACAAAGTGACACAG
959-981	GATGGTAGCACAAAGTGACACAGA
960-982	ATGGTAGCACAAAGTGACACAGAC
961-983	TGGTAGCACAAAGTGACACAGACT
962-984	GGTAGCACAAAGTGACACAGACTT
963-985	GTAGCACAAAGTGACACAGACTTT
964-986	TAGCACAAAGTGACACAGACTTTG
965-987	AGCACAAAGTGACACAGACTTTGA
966-988	GCACAAGTGACACAGACTTTGAA

Position	Sequence
967-989	CACAAGTGACACAGACTTTGAAA
968-990	ACAAGTGACACAGACTTTGAAAC
969-991	CAAGTGACACAGACTTTGAAACT
970-992	AAGTGACACAGACTTTGAAACTT
971-993	AGTGACACAGACTTTGAAACTTG
972-994	GTGACACAGACTTTGAAACTTGA
973-995	TGACACAGACTTTGAAACTTGAA
974-996	GACACAGACTTTGAAACTTGAAAG
975-997	ACACAGACTTTGAAACTTGAAAGA
976-998	CACAGACTTTGAAACTTGAAAGAC
977-999	ACAGACTTTGAAACTTGAAAGACA
978-1000	CAGACTTTGAAACTTGAAAGACAC
979-1001	AGACTTTGAAACTTGAAAGACACA
980-1002	GACTTTGAAACTTGAAAGACACAC
981-1003	ACTTTGAAACTTGAAAGACACACC
982-1004	CTTTGAAACTTGAAAGACACACCA
983-1005	TTGAAACTTGAAAGACACACCAA
984-1006	TTGAAACTTGAAAGACACACCAA
985-1007	TGAAACTTGAAAGACACACCAAAG
986-1008	GAAACTTGAAAGACACACCAAAGA
987-1009	AAACTTGAAAGACACACCAAAGAT
988-1010	AACTTGAAAGACACACCAAAGATC
989-1011	ACTTGAAAGACACACCAAAGATCA
990-1012	CTTGAAAGACACACCAAAGATCAA
991-1013	TTGAAAGACACACCAAAGATCAAC
992-1014	TGAAGACACACCAAAGATCAACA
993-1015	GAAGACACACCAAAGATCAACAG
994-1016	AAGACACACCAAAGATCAACAGC
995-1017	AGACACACCAAAGATCAACAGCC
996-1018	GACACACCAAAGATCAACAGCCG
997-1019	ACACACCAAAGATCAACAGCCGC
998-1020	CACACCAAAGATCAACAGCCGCT
999-1021	ACACCAAAGATCAACAGCCGCTT
1000-1022	CACCAAAGATCAACAGCCGCTTC
1001-1023	ACCAAAGATCAACAGCCGCTTCT
1002-1024	CCAAAGATCAACAGCCGCTTCTT
1003-1025	CAAAGATCAACAGCCGCTTCTTT
1004-1026	AAAGATCAACAGCCGCTTCTTTG
1005-1027	AAGATCAACAGCCGCTTCTTTGG
1006-1028	AGATCAACAGCCGCTTCTTTGGT
1007-1029	GATCAACAGCCGCTTCTTTGGTG
1008-1030	ATCAACAGCCGCTTCTTTGGTGA
1009-1031	TCAACAGCCGCTTCTTTGGTGAA
1010-1032	CAACAGCCGCTTCTTTGGTGAAG
1011-1033	AACAGCCGCTTCTTTGGTGAAGG
1012-1034	ACAGCCGCTTCTTTGGTGAAGGT
1013-1035	CAGCCGCTTCTTTGGTGAAGGTA
1014-1036	AGCCGCTTCTTTGGTGAAGGTAC
1015-1037	GCCGCTTCTTTGGTGAAGGTACT
1016-1038	CCGCTTCTTTGGTGAAGGTACTA
1017-1039	CGCTTCTTTGGTGAAGGTACTAA
1018-1040	GCTTCTTTGGTGAAGGTACTAAG
1019-1041	CTTCTTTGGTGAAGGTACTAAGA
1020-1042	TTCTTTGGTGAAGGTACTAAGAA
1021-1043	TCTTTGGTGAAGGTACTAAGAAG
1022-1044	CTTTGGTGAAGGTACTAAGAAGA
1023-1045	TTTGGTGAAGGTACTAAGAAGAT
1024-1046	TTGGTGAAGGTACTAAGAAGATG
1025-1047	TGGTGAAGGTACTAAGAAGATGG
1026-1048	GGTGAAGGTACTAAGAAGATGGG
1027-1049	GTGAAGGTACTAAGAAGATGGGC
1028-1050	TGAAGGTACTAAGAAGATGGGCC
1029-1051	GAAGGTACTAAGAAGATGGGCCT
1030-1052	AAGGTACTAAGAAGATGGGCCTC
1031-1053	AGGTACTAAGAAGATGGGCCTCG
1032-1054	GGTACTAAGAAGATGGGCCTCGC

Position	Sequence
1033-1055	GTAAGAAGAAGATGGGCCTCGCA
1034-1056	TACTAAGAAGATGGGCCTCGCAT
1035-1057	ACTAAGAAGATGGGCCTCGCATT
1036-1058	CTAAGAAGATGGGCCTCGCATT
1037-1059	TAAGAAGATGGGCCTCGCATTG
1038-1060	AAGAAGATGGGCCTCGCATTGA
1039-1061	AGAAGATGGGCCTCGCATTGAG
1040-1062	GAAGATGGGCCTCGCATTGAGA
1041-1063	AAGATGGGCCTCGCATTGAGAG
1042-1064	AGATGGGCCTCGCATTGAGAGC
1043-1065	GATGGGCCTCGCATTGAGAGCA
1044-1066	ATGGGCCTCGCATTGAGAGCAC
1045-1067	TGGGCCTCGCATTGAGAGCACC
1046-1068	GGGCCTCGCATTGAGAGCACCA
1047-1069	GGCCTCGCATTGAGAGCACCAA
1048-1070	GCCTCGCATTGAGAGCACCAA
1049-1071	CCTCGCATTGAGAGCACCAAAT
1050-1072	CTCGCATTGAGAGCACCAAATC
1051-1073	TCGCATTGAGAGCACCAAATCC
1052-1074	CGCATTGAGAGCACCAAATCCA
1053-1075	GCATTGAGAGCACCAAATCCAC
1054-1076	CATTGAGAGCACCAAATCCACA
1055-1077	ATTTGAGAGCACCAAATCCACAT
1056-1078	TTTGAAGAGCACCAAATCCACATC
1057-1079	TTGAGAGCACCAAATCCACATCA
1058-1080	TGAGAGCACCAAATCCACATCAC
1059-1081	GAGAGCACCAAATCCACATCAC
1060-1082	AGAGCACCAAATCCACATCACCT
1061-1083	GAGCACCAAATCCACATCACCTC
1062-1084	AGCACCAAATCCACATCACCTCC
1063-1085	GCACCAAATCCACATCACCTCCA
1064-1086	CACCAAATCCACATCACCTCCAA
1065-1087	ACCAAATCCACATCACCTCCAAA
1066-1088	CCAAATCCACATCACCTCCAAAG
1067-1089	CAAATCCACATCACCTCCAAAGC
1068-1090	AAATCCACATCACCTCCAAAGCA
1069-1091	AATCCACATCACCTCCAAAGCAG
1070-1092	ATCCACATCACCTCCAAAGCAGG
1071-1093	TCCACATCACCTCCAAAGCAGGC
1072-1094	CCACATCACCTCCAAAGCAGGCC
1073-1095	CACATCACCTCCAAAGCAGGCCG
1074-1096	ACATCACCTCCAAAGCAGGCCGA
1075-1097	CATCACCTCCAAAGCAGGCCGAA
1076-1098	ATCACCTCCAAAGCAGGCCGAAG
1077-1099	TCACCTCCAAAGCAGGCCGAAGC
1078-1100	CACCTCCAAAGCAGGCCGAAGCT
1079-1101	ACCTCCAAAGCAGGCCGAAGCTG
1080-1102	CCTCCAAAGCAGGCCGAAGCTGT
1081-1103	CTCCAAAGCAGGCCGAAGCTGTT
1082-1104	TCCAAAGCAGGCCGAAGCTGTTT
1083-1105	CCAAAGCAGGCCGAAGCTGTTTT
1084-1106	CAAAGCAGGCCGAAGCTGTTTTG
1085-1107	AAAGCAGGCCGAAGCTGTTTTGA
1086-1108	AAGCAGGCCGAAGCTGTTTTGAA
1087-1109	AGCAGGCCGAAGCTGTTTTGAAG
1088-1110	GCAGGCCGAAGCTGTTTTGAAGA
1089-1111	CAGGCCGAAGCTGTTTTGAAGAC
1090-1112	AGGCCGAAGCTGTTTTGAAGACT
1091-1113	GGCCGAAGCTGTTTTGAAGACTC
1092-1114	GCCGAAGCTGTTTTGAAGACTCT
1093-1115	CCGAAGCTGTTTTGAAGACTCTC
1094-1116	CGAAGCTGTTTTGAAGACTCTCC
1095-1117	GAAGCTGTTTTGAAGACTCTCCA
1096-1118	AAGCTGTTTTGAAGACTCTCCAG
1097-1119	AGCTGTTTTGAAGACTCTCCAGG
1098-1120	GCTGTTTTGAAGACTCTCCAGGA

Position	Sequence
1099-1121	CTGTTTTGAAGACTCTCCAGGAA
1100-1122	TGTTTTGAAGACTCTCCAGGAAC
1101-1123	GTTTTGAAGACTCTCCAGGAAC
1102-1124	TTTGAAGACTCTCCAGGAAC
1103-1125	TTTGAAGACTCTCCAGGAAC
1104-1126	TTGAAGACTCTCCAGGAAC
1105-1127	TGAAGACTCTCCAGGAAC
1106-1128	GAAGACTCTCCAGGAAC
1107-1129	AAGACTCTCCAGGAAC
1108-1130	AGACTCTCCAGGAAC
1109-1131	GAAGACTCTCCAGGAAC
1110-1132	ACTCTCCAGGAAC
1111-1133	CTCTCCAGGAAC
1112-1134	TCTCCAGGAAC
1113-1135	CTCCAGGAAC
1114-1136	TCCAGGAAC
1115-1137	CCAGGAAC
1116-1138	CAGGAAC
1117-1139	AGGAAC
1118-1140	GGAAC
1119-1141	GAAC
1120-1142	AACTGAAAAACTAACCATCTCT
1121-1143	ACTGAAAAACTAACCATCTCTG
1122-1144	CTGAAAAACTAACCATCTCTGA
1123-1145	TGAAAAACTAACCATCTCTGAG
1124-1146	GAAAAACTAACCATCTCTGAGC
1125-1147	AAAAACTAACCATCTCTGAGCA
1126-1148	AAAAACTAACCATCTCTGAGCAA
1127-1149	AAAACTAACCATCTCTGAGCAA
1128-1150	AACTAACCATCTCTGAGCAA
1129-1151	AACTAACCATCTCTGAGCAA
1130-1152	ACTAACCATCTCTGAGCAA
1131-1153	CTAACCATCTCTGAGCAA
1132-1154	TAACCATCTCTGAGCAA
1133-1155	AACCATCTCTGAGCAA
1134-1156	ACCATCTCTGAGCAA
1135-1157	CCATCTCTGAGCAA
1136-1158	CATCTCTGAGCAA
1137-1159	ATCTCTGAGCAA
1138-1160	TCTCTGAGCAA
1139-1161	CTCTGAGCAA
1140-1162	TCTGAGCAA
1141-1163	CTGAGCAA
1142-1164	TGAGCAA
1143-1165	GAGCAA
1144-1166	AGCAA
1145-1167	GCAA
1146-1168	CAA
1147-1169	AA
1148-1170	AA
1149-1171	AA
1150-1172	ATATCCAGAGGCTAATCTCTT
1151-1173	TATCCAGAGGCTAATCTCTTCA
1152-1174	ATCCAGAGGCTAATCTCTTCAA
1153-1175	TCCAGAGGCTAATCTCTTCAAT
1154-1176	CCAGAGGCTAATCTCTTCAATA
1155-1177	CAGAGGCTAATCTCTTCAATAA
1156-1178	AGAGGCTAATCTCTTCAATAAG
1157-1179	GAGGCTAATCTCTTCAATAAGC
1158-1180	AGGCTAATCTCTTCAATAAGCT
1159-1181	GAGCTAATCTCTTCAATAAGCTG
1160-1182	AGCTAATCTCTTCAATAAGCTGG
1161-1183	GCTAATCTCTTCAATAAGCTGGT
1162-1184	CTAATCTCTTCAATAAGCTGGTT
1163-1185	TAATCTCTTCAATAAGCTGGTTA
1164-1186	AATCTCTTCAATAAGCTGGTTAC

Position	Sequence
1165-1187	ATCTCTCAATAAGCTGGTTACT
1166-1188	TCTCTCAATAAGCTGGTTACTG
1167-1189	CTCTTCAATAAGCTGGTTACTGA
1168-1190	TCTTCAATAAGCTGGTTACTGAG
1169-1191	CTTCAATAAGCTGGTTACTGAGC
1170-1192	TTCAATAAGCTGGTTACTGAGCT
1171-1193	TCAATAAGCTGGTTACTGAGCTG
1172-1194	CAATAAGCTGGTTACTGAGCTGA
1173-1195	AATAAGCTGGTTACTGAGCTGAG
1174-1196	ATAAGCTGGTTACTGAGCTGAGA
1175-1197	TAAGCTGGTTACTGAGCTGAGAG
1176-1198	AAGCTGGTTACTGAGCTGAGAGG
1177-1199	AGCTGGTTACTGAGCTGAGAGGC
1178-1200	GCTGGTTACTGAGCTGAGAGGCC
1179-1201	CTGGTTACTGAGCTGAGAGGCCT
1180-1202	TGGTTACTGAGCTGAGAGGCCTC
1181-1203	GTTACTGAGCTGAGAGGCCTCA
1182-1204	GTTACTGAGCTGAGAGGCCTCAG
1183-1205	TTACTGAGCTGAGAGGCCTCAGT
1184-1206	TACTGAGCTGAGAGGCCTCAGTG
1185-1207	ACTGAGCTGAGAGGCCTCAGTGA
1186-1208	CTGAGCTGAGAGGCCTCAGTGAT
1187-1209	TGAGCTGAGAGGCCTCAGTGATG
1188-1210	GAGCTGAGAGGCCTCAGTGATGA
1189-1211	AGCTGAGAGGCCTCAGTGATGAA
1190-1212	GCTGAGAGGCCTCAGTGATGAAG
1191-1213	CTGAGAGGCCTCAGTGATGAAGC
1192-1214	TGAGAGGCCTCAGTGATGAAGCA
1193-1215	GAGAGGCCTCAGTGATGAAGCAG
1194-1216	AGAGGCCTCAGTGATGAAGCAGT
1195-1217	GAGGCCTCAGTGATGAAGCAGTC
1196-1218	AGGCCTCAGTGATGAAGCAGTCA
1197-1219	GGCCTCAGTGATGAAGCAGTCAC
1198-1220	GCCTCAGTGATGAAGCAGTCACA
1199-1221	CCTCAGTGATGAAGCAGTCACAT
1200-1222	CTCAGTGATGAAGCAGTCACATC
1201-1223	TCAGTGATGAAGCAGTCACATCT
1202-1224	CAGTGATGAAGCAGTCACATCTC
1203-1225	AGTGATGAAGCAGTCACATCTCT
1204-1226	GTGATGAAGCAGTCACATCTCTC
1205-1227	TGATGAAGCAGTCACATCTCTCT
1206-1228	GATGAAGCAGTCACATCTCTCTT
1207-1229	ATGAAGCAGTCACATCTCTCTTG
1208-1230	TGAAGCAGTCACATCTCTCTTGC
1209-1231	GAAGCAGTCACATCTCTCTTGCC
1210-1232	AAGCAGTCACATCTCTCTTGCCA
1211-1233	AGCAGTCACATCTCTCTTGCCAC
1212-1234	GCAGTCACATCTCTCTTGCCACA
1213-1235	CAGTCACATCTCTCTTGCCACAG
1214-1236	AGTCACATCTCTCTTGCCACAGC
1215-1237	GTCACATCTCTCTTGCCACAGCT
1216-1238	TCACATCTCTCTTGCCACAGCTG
1217-1239	CACATCTCTCTTGCCACAGCTGA
1218-1240	ACATCTCTCTTGCCACAGCTGAT
1219-1241	CATCTCTCTTGCCACAGCTGATT
1220-1242	ATCTCTCTTGCCACAGCTGATTG
1221-1243	TCTCTCTTGCCACAGCTGATTGA
1222-1244	CTCTCTTGCCACAGCTGATTGAG
1223-1245	TCTCTTGCCACAGCTGATTGAGG
1224-1246	CTCTTGCCACAGCTGATTGAGGT
1225-1247	TCTTGCCACAGCTGATTGAGGTG
1226-1248	CTTGCCACAGCTGATTGAGGTGT
1227-1249	TTGCCACAGCTGATTGAGGTGTC
1228-1250	TGCCACAGCTGATTGAGGTGTCC
1229-1251	GCCACAGCTGATTGAGGTGTCCA
1230-1252	CCACAGCTGATTGAGGTGTCCAG

Position	Sequence
1231-1253	CACAGCTGATTGAGGTGTCCAGC
1232-1254	ACAGCTGATTGAGGTGTCCAGCC
1233-1255	CAGCTGATTGAGGTGTCCAGCCC
1234-1256	AGCTGATTGAGGTGTCCAGCCCC
1235-1257	GCTGATTGAGGTGTCCAGCCCCA
1236-1258	CTGATTGAGGTGTCCAGCCCCAT
1237-1259	TGATTGAGGTGTCCAGCCCCATC
1238-1260	GATTGAGGTGTCCAGCCCCATCA
1239-1261	ATTGAGGTGTCCAGCCCCATCAC
1240-1262	TTGAGGTGTCCAGCCCCATCACT
1241-1263	TGAGGTGTCCAGCCCCATCACTT
1242-1264	GAGGTGTCCAGCCCCATCACTTT
1243-1265	AGGTGTCCAGCCCCATCACTTTA
1244-1266	GGTGTCCAGCCCCATCACTTTAC
1245-1267	GTGTCCAGCCCCATCACTTTACA
1246-1268	TGTCCAGCCCCATCACTTTACAA
1247-1269	GTCCAGCCCCATCACTTTACAAG
1248-1270	TCCAGCCCCATCACTTTACAAGC
1249-1271	CCAGCCCCATCACTTTACAAGCC
1250-1272	CAGCCCCATCACTTTACAAGCCT
1251-1273	AGCCCCATCACTTTACAAGCCTT
1252-1274	GCCCCATCACTTTACAAGCCTTG
1253-1275	CCCCATCACTTTACAAGCCTTGG
1254-1276	CCCATCACTTTACAAGCCTTGGT
1255-1277	CCATCACTTTACAAGCCTTGGTT
1256-1278	CATCACTTTACAAGCCTTGGTTC
1257-1279	ATCACTTTACAAGCCTTGGTTCA
1258-1280	TCACTTTACAAGCCTTGGTTCAG
1259-1281	CACTTTACAAGCCTTGGTTCAGT
1260-1282	ACTTTACAAGCCTTGGTTCAGTG
1261-1283	CTTTACAAGCCTTGGTTCAGTGT
1262-1284	TTTACAAGCCTTGGTTCAGTGTG
1263-1285	TTACAAGCCTTGGTTCAGTGTGG
1264-1286	TACAAGCCTTGGTTCAGTGTGGA
1265-1287	ACAAGCCTTGGTTCAGTGTGGAC
1266-1288	CAAGCCTTGGTTCAGTGTGGACA
1267-1289	AAGCCTTGGTTCAGTGTGGACAG
1268-1290	AGCCTTGGTTCAGTGTGGACAGC
1269-1291	GCCTTGGTTCAGTGTGGACAGCC
1270-1292	CCTTGGTTCAGTGTGGACAGCCT
1271-1293	CTTGGTTCAGTGTGGACAGCCTC
1272-1294	TGGTTCAGTGTGGACAGCCTCA
1273-1295	TGGTTCAGTGTGGACAGCCTCAG
1274-1296	GGTTCAGTGTGGACAGCCTCAGT
1275-1297	GTTTCAGTGTGGACAGCCTCAGTG
1276-1298	TTTCAGTGTGGACAGCCTCAGTGC
1277-1299	TCAGTGTGGACAGCCTCAGTGCT
1278-1300	CAGTGTGGACAGCCTCAGTGCTC
1279-1301	AGTGTGGACAGCCTCAGTGCTCC
1280-1302	GTGTGGACAGCCTCAGTGCTCCA
1281-1303	TGTGGACAGCCTCAGTGCTCCAC
1282-1304	GTGGACAGCCTCAGTGCTCCACT
1283-1305	TGGACAGCCTCAGTGCTCCACTC
1284-1306	GGACAGCCTCAGTGCTCCACTCA
1285-1307	GACAGCCTCAGTGCTCCACTCAC
1286-1308	ACAGCCTCAGTGCTCCACTCACA
1287-1309	CAGCCTCAGTGCTCCACTCACAT
1288-1310	AGCCTCAGTGCTCCACTCACATC
1289-1311	GCCTCAGTGCTCCACTCACATCC
1290-1312	CCTCAGTGCTCCACTCACATCCT
1291-1313	CTCAGTGCTCCACTCACATCCTC
1292-1314	TCAGTGCTCCACTCACATCCTCC
1293-1315	CAGTGCTCCACTCACATCCTCCA
1294-1316	AGTGCTCCACTCACATCCTCCAG
1295-1317	GTGCTCCACTCACATCCTCCAGT
1296-1318	TGCTCCACTCACATCCTCCAGTG

Position	Sequence
1297-1319	GCTCCACTCACATCCTCCAGTGG
1298-1320	CTCCACTCACATCCTCCAGTGGC
1299-1321	TCCACTCACATCCTCCAGTGGCT
1300-1322	CCACTCACATCCTCCAGTGGCTG
1301-1323	CACTCACATCCTCCAGTGGCTGA
1302-1324	ACTCACATCCTCCAGTGGCTGAA
1303-1325	CTCACATCCTCCAGTGGCTGAAA
1304-1326	TCACATCCTCCAGTGGCTGAAAC
1305-1327	CACATCCTCCAGTGGCTGAAACG
1306-1328	ACATCCTCCAGTGGCTGAAACGT
1307-1329	CATCCTCCAGTGGCTGAAACGTG
1308-1330	ATCCTCCAGTGGCTGAAACGTGT
1309-1331	TCCTCCAGTGGCTGAAACGTGTG
1310-1332	CCTCCAGTGGCTGAAACGTGTGC
1311-1333	CTCCAGTGGCTGAAACGTGTGCA
1312-1334	TCCAGTGGCTGAAACGTGTGCAT
1313-1335	CCAGTGGCTGAAACGTGTGCATG
1314-1336	CAGTGGCTGAAACGTGTGCATGC
1315-1337	AGTGGCTGAAACGTGTGCATGCC
1316-1338	GTGGCTGAAACGTGTGCATGCCA
1317-1339	TGGCTGAAACGTGTGCATGCCAA
1318-1340	GGCTGAAACGTGTGCATGCCAAC
1319-1341	GCTGAAACGTGTGCATGCCAACC
1320-1342	CTGAAACGTGTGCATGCCAACCC
1321-1343	TGAAACGTGTGCATGCCAACCCC
1322-1344	GAAACGTGTGCATGCCAACCCCC
1323-1345	AAACGTGTGCATGCCAACCCCCCT
1324-1346	AACGTGTGCATGCCAACCCCCCTT
1325-1347	ACGTGTGCATGCCAACCCCCCTTC
1326-1348	CGTGTGCATGCCAACCCCCCTTCT
1327-1349	GTGTGCATGCCAACCCCCCTTCTG
1328-1350	TGTGCATGCCAACCCCCCTTCTGA
1329-1351	GTGCATGCCAACCCCCCTTCTGAT
1330-1352	TGCATGCCAACCCCCCTTCTGATA
1331-1353	GCATGCCAACCCCCCTTCTGATAG
1332-1354	CATGCCAACCCCCCTTCTGATAGA
1333-1355	ATGCCAACCCCCCTTCTGATAGAT
1334-1356	TGCCAACCCCCCTTCTGATAGATG
1335-1357	GCCAACCCCCCTTCTGATAGATGT
1336-1358	CCAACCCCCCTTCTGATAGATGTG
1337-1359	CAACCCCCCTTCTGATAGATGTGG
1338-1360	AACCCCCCTTCTGATAGATGTGGT
1339-1361	ACCCCCCTTCTGATAGATGTGGTC
1340-1362	CCCCCTTCTGATAGATGTGGTCA
1341-1363	CCCCTTCTGATAGATGTGGTCAC
1342-1364	CCCTTCTGATAGATGTGGTCACC
1343-1365	CCTTCTGATAGATGTGGTCACCT
1344-1366	CTTCTGATAGATGTGGTCACCTA
1345-1367	TTCTGATAGATGTGGTCACCTAC
1346-1368	TCTGATAGATGTGGTCACCTACC
1347-1369	CTGATAGATGTGGTCACCTACCT
1348-1370	TGATAGATGTGGTCACCTACCTG
1349-1371	GATAGATGTGGTCACCTACCTGG
1350-1372	ATAGATGTGGTCACCTACCTGGT
1351-1373	TAGATGTGGTCACCTACCTGGTG
1352-1374	AGATGTGGTCACCTACCTGGTGG
1353-1375	GATGTGGTCACCTACCTGGTGGC
1354-1376	ATGTGGTCACCTACCTGGTGGCC
1355-1377	TGTGGTCACCTACCTGGTGGCCC
1356-1378	GTGGTCACCTACCTGGTGGCCCT
1357-1379	TGGTCACCTACCTGGTGGCCCTG
1358-1380	GGTCACCTACCTGGTGGCCCTGA
1359-1381	GTCACCTACCTGGTGGCCCTGAT
1360-1382	TCACCTACCTGGTGGCCCTGATC
1361-1383	CACCTACCTGGTGGCCCTGATCC
1362-1384	ACCTACCTGGTGGCCCTGATCCC

Position	Sequence
1363-1385	CCTACCTGGTGGCCCTGATCCCC
1364-1386	CTACCTGGTGGCCCTGATCCCCG
1365-1387	TACCTGGTGGCCCTGATCCCCGA
1366-1388	ACCTGGTGGCCCTGATCCCCGAG
1367-1389	CCTGGTGGCCCTGATCCCCGAGC
1368-1390	CTGGTGGCCCTGATCCCCGAGCC
1369-1391	TGGTGGCCCTGATCCCCGAGCCC
1370-1392	GGTGGCCCTGATCCCCGAGCCCT
1371-1393	GTGGCCCTGATCCCCGAGCCCTC
1372-1394	TGGCCCTGATCCCCGAGCCCTCA
1373-1395	GGCCCTGATCCCCGAGCCCTCAG
1374-1396	GCCCTGATCCCCGAGCCCTCAGC
1375-1397	CCCTGATCCCCGAGCCCTCAGCA
1376-1398	CCTGATCCCCGAGCCCTCAGCAC
1377-1399	CTGATCCCCGAGCCCTCAGCACA
1378-1400	TGATCCCCGAGCCCTCAGCACAG
1379-1401	GATCCCCGAGCCCTCAGCACAGC
1380-1402	ATCCCCGAGCCCTCAGCACAGCA
1381-1403	TCCCCGAGCCCTCAGCACAGCAG
1382-1404	CCCCGAGCCCTCAGCACAGCAGC
1383-1405	CCCGAGCCCTCAGCACAGCAGCT
1384-1406	CGAGCCCTCAGCACAGCAGCTG
1385-1407	CGAGCCCTCAGCACAGCAGCTGC
1386-1408	GAGCCCTCAGCACAGCAGCTGCC
1387-1409	AGCCCTCAGCACAGCAGCTGCCA
1388-1410	GCCCTCAGCACAGCAGCTGCCGAG
1389-1411	CCCTCAGCACAGCAGCTGCCGAGA
1390-1412	CCTCAGCACAGCAGCTGCCGAGAG
1391-1413	CTCAGCACAGCAGCTGCCGAGAGA
1392-1414	TCAGCACAGCAGCTGCCGAGAGAT
1393-1415	CAGCACAGCAGCTGCCGAGAGATC
1394-1416	AGCACAGCAGCTGCCGAGAGATCT
1395-1417	GCACAGCAGCTGCCGAGAGATCTT
1396-1418	CACAGCAGCTGCCGAGAGATCTTC
1397-1419	ACAGCAGCTGCCGAGAGATCTTCA
1398-1420	CAGCAGCTGCCGAGAGATCTTCAA
1399-1421	AGCAGCTGCCGAGAGATCTTCAAC
1400-1422	GCAGCTGCCGAGAGATCTTCAACA
1401-1423	CAGCTGCCGAGAGATCTTCAACAT
1402-1424	AGCTGCCGAGAGATCTTCAACATG
1403-1425	GCTGCCGAGAGATCTTCAACATGG
1404-1426	CTGCCGAGAGATCTTCAACATGGC
1405-1427	TGCCGAGAGATCTTCAACATGGCG
1406-1428	GCGAGAGATCTTCAACATGGCGA
1407-1429	CGAGAGATCTTCAACATGGCGAG
1408-1430	GAGAGATCTTCAACATGGCGAGG
1409-1431	AGAGATCTTCAACATGGCGAGGG
1410-1432	GAGATCTTCAACATGGCGAGGGA
1411-1433	AGATCTTCAACATGGCGAGGGAT
1412-1434	GATCTTCAACATGGCGAGGGATC
1413-1435	ATCTTCAACATGGCGAGGGATCA
1414-1436	TCTTCAACATGGCGAGGGATCAG
1415-1437	CTTCAACATGGCGAGGGATCAGC
1416-1438	TTCAACATGGCGAGGGATCAGCG
1417-1439	TCAACATGGCGAGGGATCAGCGC
1418-1440	CAACATGGCGAGGGATCAGCGCA
1419-1441	AACATGGCGAGGGATCAGCGCAG
1420-1442	ACATGGCGAGGGATCAGCGCAGC
1421-1443	CATGGCGAGGGATCAGCGCAGCC
1422-1444	ATGGCGAGGGATCAGCGCAGCCG
1423-1445	TGGCGAGGGATCAGCGCAGCCGA
1424-1446	GGCGAGGGATCAGCGCAGCCGAG
1425-1447	GCGAGGGATCAGCGCAGCCGAGC
1426-1448	CGAGGGATCAGCGCAGCCGAGCC
1427-1449	GAGGGATCAGCGCAGCCGAGCCA
1428-1450	AGGGATCAGCGCAGCCGAGCCAC

Position	Sequence
1429-1451	GGGATCAGCGCAGCCGAGCCACC
1430-1452	GGATCAGCGCAGCCGAGCCACCT
1431-1453	GATCAGCGCAGCCGAGCCACCTT
1432-1454	ATCAGCGCAGCCGAGCCACCTTG
1433-1455	TCAGCGCAGCCGAGCCACCTTGT
1434-1456	CAGCGCAGCCGAGCCACCTTGTA
1435-1457	AGCGCAGCCGAGCCACCTTGTAT
1436-1458	GCGCAGCCGAGCCACCTTGTATG
1437-1459	CGCAGCCGAGCCACCTTGTATGC
1438-1460	GCAGCCGAGCCACCTTGTATGCG
1439-1461	CAGCCGAGCCACCTTGTATGCGC
1440-1462	AGCCGAGCCACCTTGTATGCGCT
1441-1463	GCCGAGCCACCTTGTATGCGCTG
1442-1464	CCGAGCCACCTTGTATGCGCTGA
1443-1465	CGAGCCACCTTGTATGCGCTGAG
1444-1466	GAGCCACCTTGTATGCGCTGAGC
1445-1467	AGCCACCTTGTATGCGCTGAGCC
1446-1468	GCCACCTTGTATGCGCTGAGCCA
1447-1469	CCACCTTGTATGCGCTGAGCCAC
1448-1470	CACCTTGTATGCGCTGAGCCACG
1449-1471	ACCTTGTATGCGCTGAGCCACGC
1450-1472	CCTTGTATGCGCTGAGCCACGCG
1451-1473	CTTGTATGCGCTGAGCCACGCGG
1452-1474	TTGTATGCGCTGAGCCACGCGGT
1453-1475	TGTATGCGCTGAGCCACGCGGTC
1454-1476	GTATGCGCTGAGCCACGCGGTCA
1455-1477	TATGCGCTGAGCCACGCGGTCAA
1456-1478	ATGCGCTGAGCCACGCGGTCAAC
1457-1479	TGCGCTGAGCCACGCGGTCAACA
1458-1480	GCGCTGAGCCACGCGGTCAACAA
1459-1481	CGCTGAGCCACGCGGTCAACAAC
1460-1482	GCTGAGCCACGCGGTCAACAACT
1461-1483	CTGAGCCACGCGGTCAACAACTA
1462-1484	TGAGCCACGCGGTCAACAACTAT
1463-1485	GAGCCACGCGGTCAACAACTATC
1464-1486	AGCCACGCGGTCAACAACTATCA
1465-1487	GCCACGCGGTCAACAACTATCAT
1466-1488	CCACGCGGTCAACAACTATCATA
1467-1489	CACGCGGTCAACAACTATCATAA
1468-1490	ACGCGGTCAACAACTATCATAAG
1469-1491	CGCGGTCAACAACTATCATAAGA
1470-1492	GCGGTCAACAACTATCATAAGAC
1471-1493	CGGTCAACAACTATCATAAGACA
1472-1494	GGTCAACAACTATCATAAGACAA
1473-1495	GTCACAACACTATCATAAGACAAA
1474-1496	TCAACAACACTATCATAAGACAAAC
1475-1497	CAACAACACTATCATAAGACAAACC
1476-1498	AACAACACTATCATAAGACAAACCC
1477-1499	ACAACACTATCATAAGACAAACCCT
1478-1500	CAACTATCATAAGACAAACCCTA
1479-1501	AACTATCATAAGACAAACCCTAC
1480-1502	ACTATCATAAGACAAACCCTACA
1481-1503	CTATCATAAGACAAACCCTACAG
1482-1504	TATCATAAGACAAACCCTACAGG
1483-1505	ATCATAAGACAAACCCTACAGGG
1484-1506	TCATAAGACAAACCCTACAGGGA
1485-1507	CATAAGACAAACCCTACAGGGAC
1486-1508	ATAAGACAAACCCTACAGGGACC
1487-1509	TAAGACAAACCCTACAGGGACCC
1488-1510	AAGACAAACCCTACAGGGACCCA
1489-1511	AGACAAACCCTACAGGGACCCAG
1490-1512	GACAAACCCTACAGGGACCCAGG
1491-1513	ACAAACCCTACAGGGACCCAGGA
1492-1514	CAAACCCTACAGGGACCCAGGAG
1493-1515	AAACCCTACAGGGACCCAGGAGC
1494-1516	AACCCTACAGGGACCCAGGAGCT

Position	Sequence
1495-1517	ACCCTACAGGGACCCAGGAGCTG
1496-1518	CCCTACAGGGACCCAGGAGCTGC
1497-1519	CCTACAGGGACCCAGGAGCTGCT
1498-1520	CTACAGGGACCCAGGAGCTGCTG
1499-1521	TACAGGGACCCAGGAGCTGCTGG
1500-1522	ACAGGGACCCAGGAGCTGCTGGA
1501-1523	CAGGGACCCAGGAGCTGCTGGAC
1502-1524	AGGGACCCAGGAGCTGCTGGACA
1503-1525	GGGACCCAGGAGCTGCTGGACAT
1504-1526	GGACCCAGGAGCTGCTGGACATT
1505-1527	GACCCAGGAGCTGCTGGACATTG
1506-1528	ACCAGGAGCTGCTGGACATTGC
1507-1529	CCCAGGAGCTGCTGGACATTGCT
1508-1530	CCAGGAGCTGCTGGACATTGCTA
1509-1531	CAGGAGCTGCTGGACATTGCTAA
1510-1532	AGGAGCTGCTGGACATTGCTAAT
1511-1533	GGAGCTGCTGGACATTGCTAATT
1512-1534	GAGCTGCTGGACATTGCTAATTA
1513-1535	AGCTGCTGGACATTGCTAATTAC
1514-1536	GCTGCTGGACATTGCTAATTACC
1515-1537	CTGCTGGACATTGCTAATTACCT
1516-1538	TGCTGGACATTGCTAATTACCTG
1517-1539	GCTGGACATTGCTAATTACCTGA
1518-1540	CTGGACATTGCTAATTACCTGAT
1519-1541	TGGACATTGCTAATTACCTGATG
1520-1542	GGACATTGCTAATTACCTGATGG
1521-1543	GACATTGCTAATTACCTGATGGA
1522-1544	ACATTGCTAATTACCTGATGGAA
1523-1545	CATTGCTAATTACCTGATGGAAC
1524-1546	ATTGCTAATTACCTGATGGAAACA
1525-1547	TTGCTAATTACCTGATGGAACAG
1526-1548	TGCTAATTACCTGATGGAACAGA
1527-1549	GCTAATTACCTGATGGAACAGAT
1528-1550	CTAATTACCTGATGGAACAGATT
1529-1551	TAATTACCTGATGGAACAGATTC
1530-1552	AATTACCTGATGGAACAGATTCA
1531-1553	ATTACCTGATGGAACAGATTCAA
1532-1554	TTACCTGATGGAACAGATTCAAG
1533-1555	TACCTGATGGAACAGATTCAAGA
1534-1556	ACCTGATGGAACAGATTCAAGAT
1535-1557	CCTGATGGAACAGATTCAAGATG
1536-1558	CTGATGGAACAGATTCAAGATGA
1537-1559	TGATGGAACAGATTCAAGATGAC
1538-1560	GATGGAACAGATTCAAGATGACT
1539-1561	ATGGAACAGATTCAAGATGACTG
1540-1562	TGGAACAGATTCAAGATGACTGC
1541-1563	GGAACAGATTCAAGATGACTGCA
1542-1564	GAACAGATTCAAGATGACTGCAC
1543-1565	AACAGATTCAAGATGACTGCACT
1544-1566	ACAGATTCAAGATGACTGCACTG
1545-1567	CAGATTCAAGATGACTGCACTGG
1546-1568	AGATTCAAGATGACTGCACTGGG
1547-1569	GATTCAAGATGACTGCACTGGGG
1548-1570	ATTCAAGATGACTGCACTGGGGA
1549-1571	TTCAAGATGACTGCACTGGGGAT
1550-1572	TCAAGATGACTGCACTGGGGATG
1551-1573	CAAGATGACTGCACTGGGGATGA
1552-1574	AAGATGACTGCACTGGGGATGAA
1553-1575	AGATGACTGCACTGGGGATGAAG
1554-1576	GATGACTGCACTGGGGATGAAGA
1555-1577	ATGACTGCACTGGGGATGAAGAT
1556-1578	TGACTGCACTGGGGATGAAGATT
1557-1579	GACTGCACTGGGGATGAAGATTA
1558-1580	ACTGCACTGGGGATGAAGATTAC
1559-1581	CTGCACTGGGGATGAAGATTACA
1560-1582	TGCACTGGGGATGAAGATTACAC

Position	Sequence
1561-1583	GCACTGGGGATGAAGATTACACC
1562-1584	CACTGGGGATGAAGATTACACCT
1563-1585	ACTGGGGATGAAGATTACACCTA
1564-1586	CTGGGGATGAAGATTACACCTAT
1565-1587	TGGGGATGAAGATTACACCTATF
1566-1588	GGGGATGAAGATTACACCTATTF
1567-1589	GGGATGAAGATTACACCTATTTG
1568-1590	GGATGAAGATTACACCTATTTGA
1569-1591	GATGAAGATTACACCTATTTGAT
1570-1592	ATGAAGATTACACCTATTTGATT
1571-1593	TGAAGATTACACCTATTTGATTC
1572-1594	GAAGATTACACCTATTTGATTCT
1573-1595	AAGATTACACCTATTTGATTCTG
1574-1596	AGATTACACCTATTTGATTCTGC
1575-1597	GATTACACCTATTTGATTCTGCG
1576-1598	ATTACACCTATTTGATTCTGCGG
1577-1599	TTACACCTATTTGATTCTGCGGG
1578-1600	TACACCTATTTGATTCTGCGGGT
1579-1601	ACACCTATTTGATTCTGCGGGTC
1580-1602	CACCTATTTGATTCTGCGGGTCA
1581-1603	ACCTATTTGATTCTGCGGGTCAT
1582-1604	CCTATTTGATTCTGCGGGTCATT
1583-1605	CTATTTGATTCTGCGGGTCATTG
1584-1606	TATTTGATTCTGCGGGTCATTGG
1585-1607	ATTTGATTCTGCGGGTCATTGGA
1586-1608	TTGATTCTGCGGGTCATTGGAA
1587-1609	TGATTCTGCGGGTCATTGGAAA
1588-1610	TGATTCTGCGGGTCATTGGAAAT
1589-1611	GATTCTGCGGGTCATTGGAAATA
1590-1612	ATTCTGCGGGTCATTGGAAATAT
1591-1613	TTCTGCGGGTCATTGGAAATATG
1592-1614	TCTGCGGGTCATTGGAAATATGG
1593-1615	CTGCGGGTCATTGGAAATATGGG
1594-1616	TGCGGGTCATTGGAAATATGGGC
1595-1617	GCGGGTCATTGGAAATATGGGCC
1596-1618	CGGGTCATTGGAAATATGGGCCA
1597-1619	GGGTCATTGGAAATATGGGCCAA
1598-1620	GGTCATTGGAAATATGGGCCAAA
1599-1621	GTCATTGGAAATATGGGCCAAAC
1600-1622	TCATTGGAAATATGGGCCAAACC
1601-1623	CATTGGAAATATGGGCCAAACCA
1602-1624	ATTGGAAATATGGGCCAAACCAT
1603-1625	TTGGAAATATGGGCCAAACCATG
1604-1626	TGGAAATATGGGCCAAACCATGG
1605-1627	GAAATATGGGCCAAACCATGGGA
1606-1628	GAAATATGGGCCAAACCATGGAG
1607-1629	AAATATGGGCCAAACCATGGAGC
1608-1630	AATATGGGCCAAACCATGGAGCA
1609-1631	ATATGGGCCAAACCATGGAGCAG
1610-1632	TATGGGCCAAACCATGGAGCAGT
1611-1633	ATGGGCCAAACCATGGAGCAGTT
1612-1634	TGGGCCAAACCATGGAGCAGTTA
1613-1635	GGGCCAAACCATGGAGCAGTTAA
1614-1636	GGCCAAACCATGGAGCAGTTAAC
1615-1637	GCCAAACCATGGAGCAGTTAACT
1616-1638	CCAAACCATGGAGCAGTTAACTC
1617-1639	CAAACCATGGAGCAGTTAACTCC
1618-1640	AAACCATGGAGCAGTTAACTCCA
1619-1641	AACCATGGAGCAGTTAACTCCAG
1620-1642	ACCATGGAGCAGTTAACTCCAGA
1621-1643	CCATGGAGCAGTTAACTCCAGAA
1622-1644	CATGGAGCAGTTAACTCCAGAAC
1623-1645	ATGGAGCAGTTAACTCCAGAACT
1624-1646	TGGAGCAGTTAACTCCAGAACTC
1625-1647	GGAGCAGTTAACTCCAGAACTCA
1626-1648	GAGCAGTTAACTCCAGAACTCAA

Position	Sequence
1627-1649	AGCAGTAACTCCAGAACTCAAG
1628-1650	GCAGTAACTCCAGAACTCAAGT
1629-1651	CAGTAACTCCAGAACTCAAGTC
1630-1652	AGTTAACTCCAGAACTCAAGTCT
1631-1653	GTTAACTCCAGAACTCAAGTCTT
1632-1654	TTAACTCCAGAACTCAAGTCTTC
1633-1655	TAACTCCAGAACTCAAGTCTTCA
1634-1656	AACTCCAGAACTCAAGTCTTCAA
1635-1657	ACTCCAGAACTCAAGTCTTCAAT
1636-1658	CTCCAGAACTCAAGTCTTCAATC
1637-1659	TCCAGAACTCAAGTCTTCAATCC
1638-1660	CCAGAACTCAAGTCTTCAATCCT
1639-1661	CAGAACTCAAGTCTTCAATCCTC
1640-1662	AGAACTCAAGTCTTCAATCCTCA
1641-1663	GAACTCAAGTCTTCAATCCTCAA
1642-1664	AACTCAAGTCTTCAATCCTCAAA
1643-1665	ACTCAAGTCTTCAATCCTCAAAT
1644-1666	CTCAAGTCTTCAATCCTCAAATG
1645-1667	TCAAGTCTTCAATCCTCAAATGT
1646-1668	CAAGTCTTCAATCCTCAAATGTG
1647-1669	AAGTCTTCAATCCTCAAATGTGT
1648-1670	AGTCTTCAATCCTCAAATGTGTC
1649-1671	GTCTTCAATCCTCAAATGTGTCC
1650-1672	TCTTCAATCCTCAAATGTGTCCA
1651-1673	CTTCAATCCTCAAATGTGTCCAA
1652-1674	TTCATCCTCAAATGTGTCCAAA
1653-1675	TCAATCCTCAAATGTGTCCAAAG
1654-1676	CAATCCTCAAATGTGTCCAAAGT
1655-1677	AATCCTCAAATGTGTCCAAAGTA
1656-1678	ATCCTCAAATGTGTCCAAAGTAC
1657-1679	TCCTCAAATGTGTCCAAAGTACA
1658-1680	CCTCAAATGTGTCCAAAGTACAA
1659-1681	CTCAAATGTGTCCAAAGTACAAA
1660-1682	TCAAATGTGTCCAAAGTACAAAG
1661-1683	CAAATGTGTCCAAAGTACAAAGC
1662-1684	AAATGTGTCCAAAGTACAAAGCC
1663-1685	AATGTGTCCAAAGTACAAAGCCA
1664-1686	ATGTGTCCAAAGTACAAAGCCAT
1665-1687	TGTGTCCAAAGTACAAAGCCATC
1666-1688	GTGTCCAAAGTACAAAGCCATCA
1667-1689	TGTCCAAAGTACAAAGCCATCAC
1668-1690	GTCCAAAGTACAAAGCCATCACT
1669-1691	TCCAAAGTACAAAGCCATCACTG
1670-1692	CCAAAGTACAAAGCCATCACTGA
1671-1693	CAAAGTACAAAGCCATCACTGAT
1672-1694	AAAGTACAAAGCCATCACTGATG
1673-1695	AAGTACAAAGCCATCACTGATGA
1674-1696	AGTACAAAGCCATCACTGATGAT
1675-1697	GTACAAAGCCATCACTGATGATC
1676-1698	TACAAAGCCATCACTGATGATCC
1677-1699	ACAAAGCCATCACTGATGATCCA
1678-1700	CAAAGCCATCACTGATGATCCAG
1679-1701	AAAGCCATCACTGATGATCCAGA
1680-1702	AAGCCATCACTGATGATCCAGAA
1681-1703	AGCCATCACTGATGATCCAGAAA
1682-1704	GCCATCACTGATGATCCAGAAAG
1683-1705	CCATCACTGATGATCCAGAAAGC
1684-1706	CATCACTGATGATCCAGAAAGCT
1685-1707	ATCACTGATGATCCAGAAAGCTG
1686-1708	TCACTGATGATCCAGAAAGCTGC
1687-1709	CACTGATGATCCAGAAAGCTGCC
1688-1710	ACTGATGATCCAGAAAGCTGCCA
1689-1711	CTGATGATCCAGAAAGCTGCCAT
1690-1712	TGATGATCCAGAAAGCTGCCATC
1691-1713	GATGATCCAGAAAGCTGCCATCC
1692-1714	ATGATCCAGAAAGCTGCCATCCA

Position	Sequence
1693-1715	TGATCCAGAAAGCTGCCATCCAG
1694-1716	GATCCAGAAAGCTGCCATCCAGG
1695-1717	ATCCAGAAAGCTGCCATCCAGGC
1696-1718	TCCAGAAAGCTGCCATCCAGGCT
1697-1719	CCAGAAAGCTGCCATCCAGGCTC
1698-1720	CAGAAAGCTGCCATCCAGGCTCT
1699-1721	AGAAAGCTGCCATCCAGGCTCTG
1700-1722	GAAAGCTGCCATCCAGGCTCTGC
1701-1723	AAAGCTGCCATCCAGGCTCTGCG
1702-1724	AAGCTGCCATCCAGGCTCTGCGG
1703-1725	AGCTGCCATCCAGGCTCTGCGGA
1704-1726	GCTGCCATCCAGGCTCTGCGGAA
1705-1727	CTGCCATCCAGGCTCTGCGGAAA
1706-1728	TGCCATCCAGGCTCTGCGGAAAA
1707-1729	GCCATCCAGGCTCTGCGGAAAAT
1708-1730	CCATCCAGGCTCTGCGGAAAATG
1709-1731	CATCCAGGCTCTGCGGAAAATGG
1710-1732	ATCCAGGCTCTGCGGAAAATGGA
1711-1733	TCCAGGCTCTGCGGAAAATGGAG
1712-1734	CCAGGCTCTGCGGAAAATGGAGC
1713-1735	CAGGCTCTGCGGAAAATGGAGCC
1714-1736	AGGCTCTGCGGAAAATGGAGCCT
1715-1737	GGCTCTGCGGAAAATGGAGCCTA
1716-1738	GCTCTGCGGAAAATGGAGCCTAA
1717-1739	CTCTGCGGAAAATGGAGCCTAAA
1718-1740	TCTGCGGAAAATGGAGCCTAAAG
1719-1741	CTGCGGAAAATGGAGCCTAAAGA
1720-1742	TGCGGAAAATGGAGCCTAAAGAC
1721-1743	GCGGAAAATGGAGCCTAAAGACA
1722-1744	CGGAAAATGGAGCCTAAAGACAA
1723-1745	GGAAAATGGAGCCTAAAGACAAG
1724-1746	GAAAATGGAGCCTAAAGACAAGG
1725-1747	AAAATGGAGCCTAAAGACAAGGA
1726-1748	AAATGGAGCCTAAAGACAAGGAC
1727-1749	AATGGAGCCTAAAGACAAGGACC
1728-1750	ATGGAGCCTAAAGACAAGGACCA
1729-1751	TGGAGCCTAAAGACAAGGACCAG
1730-1752	GGAGCCTAAAGACAAGGACCAGG
1731-1753	GAGCCTAAAGACAAGGACCAGGA
1732-1754	AGCCTAAAGACAAGGACCAGGAG
1733-1755	GCCTAAAGACAAGGACCAGGAGG
1734-1756	CCTAAAGACAAGGACCAGGAGGT
1735-1757	CTAAAGACAAGGACCAGGAGGTT
1736-1758	TAAAGACAAGGACCAGGAGGTTT
1737-1759	AAAGACAAGGACCAGGAGGTTCT
1738-1760	AAGACAAGGACCAGGAGGTTCTT
1739-1761	AGACAAGGACCAGGAGGTTCTTC
1740-1762	GACAAGGACCAGGAGGTTCTTCT
1741-1763	ACAAGGACCAGGAGGTTCTTCTT
1742-1764	CAAGGACCAGGAGGTTCTTCTTC
1743-1765	AAGGACCAGGAGGTTCTTCTTCA
1744-1766	AGGACCAGGAGGTTCTTCTTCAG
1745-1767	GGACCAGGAGGTTCTTCTTCAGA
1746-1768	GACCAGGAGGTTCTTCTTCAGAC
1747-1769	ACCAGGAGGTTCTTCTTCAGACT
1748-1770	CCAGGAGGTTCTTCTTCAGACTT
1749-1771	CAGGAGGTTCTTCTTCAGACTTT
1750-1772	AGGAGGTTCTTCTTCAGACTTTC
1751-1773	GGAGGTTCTTCTTCAGACTTTCC
1752-1774	GAGGTTCTTCTTCAGACTTTCCCT
1753-1775	AGGTTCTTCTTCAGACTTTCCCTT
1754-1776	GGTTCTTCTTCAGACTTTCCCTTG
1755-1777	GTTCTTCTTCAGACTTTCCCTTGA
1756-1778	TTCTTCTTCAGACTTTCCCTTGAT
1757-1779	TCTTCTTCAGACTTTCCCTTGATG
1758-1780	CTTCTTCAGACTTTCCCTTGATGA

Position	Sequence
1759-1781	TTCTTCAGACTTCCTTGATGAT
1760-1782	TCTTCAGACTTCCTTGATGATG
1761-1783	CTTCAGACTTCCTTGATGATGC
1762-1784	TTCAGACTTCCTTGATGATGCT
1763-1785	TCAGACTTCCTTGATGATGCTT
1764-1786	CAGACTTCCTTGATGATGCTTC
1765-1787	AGACTTCCTTGATGATGCTTCT
1766-1788	GACTTCCTTGATGATGCTTCTC
1767-1789	ACTTCCTTGATGATGCTTCTCC
1768-1790	CTTCCTTGATGATGCTTCTCCG
1769-1791	TTTCCTTGATGATGCTTCTCCGG
1770-1792	TTCCTTGATGATGCTTCTCCGGG
1771-1793	TCCTTGATGATGCTTCTCCGGGA
1772-1794	CCTTGATGATGCTTCTCCGGGAG
1773-1795	CTTGATGATGCTTCTCCGGGAGA
1774-1796	TTGATGATGCTTCTCCGGGAGAT
1775-1797	TGATGATGCTTCTCCGGGAGATA
1776-1798	GATGATGCTTCTCCGGGAGATAA
1777-1799	ATGATGCTTCTCCGGGAGATAAG
1778-1800	TGATGCTTCTCCGGGAGATAAGC
1779-1801	GATGCTTCTCCGGGAGATAAGCG
1780-1802	ATGCTTCTCCGGGAGATAAGCGA
1781-1803	TGCTTCTCCGGGAGATAAGCGAC
1782-1804	GCTTCTCCGGGAGATAAGCGACT
1783-1805	CTTCTCCGGGAGATAAGCGACTG
1784-1806	TTCTCCGGGAGATAAGCGACTGG
1785-1807	TCTCCGGGAGATAAGCGACTGGC
1786-1808	CTCCGGGAGATAAGCGACTGGCT
1787-1809	TCCGGGAGATAAGCGACTGGCTG
1788-1810	CCGGGAGATAAGCGACTGGCTGC
1789-1811	CGGGAGATAAGCGACTGGCTGCC
1790-1812	GGGAGATAAGCGACTGGCTGCCT
1791-1813	GGAGATAAGCGACTGGCTGCCTA
1792-1814	GAGATAAGCGACTGGCTGCCTAT
1793-1815	AGATAAGCGACTGGCTGCCTATC
1794-1816	GATAAGCGACTGGCTGCCTATCT
1795-1817	ATAAGCGACTGGCTGCCTATCTT
1796-1818	TAAGCGACTGGCTGCCTATCTTA
1797-1819	AAGCGACTGGCTGCCTATCTTAT
1798-1820	AGCGACTGGCTGCCTATCTTATG
1799-1821	GCGACTGGCTGCCTATCTTATGT
1800-1822	CGACTGGCTGCCTATCTTATGTT
1801-1823	GACTGGCTGCCTATCTTATGTTG
1802-1824	ACTGGCTGCCTATCTTATGTTGA
1803-1825	CTGGCTGCCTATCTTATGTTGAT
1804-1826	TGGCTGCCTATCTTATGTTGATG
1805-1827	GGCTGCCTATCTTATGTTGATGA
1806-1828	GCTGCCTATCTTATGTTGATGAG
1807-1829	CTGCCTATCTTATGTTGATGAGG
1808-1830	TGCCTATCTTATGTTGATGAGGA
1809-1831	GCCTATCTTATGTTGATGAGGAG
1810-1832	CCTATCTTATGTTGATGAGGAGT
1811-1833	CTATCTTATGTTGATGAGGAGTC
1812-1834	TATCTTATGTTGATGAGGAGTCC
1813-1835	ATCTTATGTTGATGAGGAGTCCT
1814-1836	TCTTATGTTGATGAGGAGTCCTT
1815-1837	CTTATGTTGATGAGGAGTCCTTC
1816-1838	TTATGTTGATGAGGAGTCCTTCA
1817-1839	TATGTTGATGAGGAGTCCTTCA
1818-1840	ATGTTGATGAGGAGTCCTTCA
1819-1841	TGTTGATGAGGAGTCCTTCA
1820-1842	GTTGATGAGGAGTCCTTCA
1821-1843	TTGATGAGGAGTCCTTCA
1822-1844	TGATGAGGAGTCCTTCA
1823-1845	GATGAGGAGTCCTTCA
1824-1846	ATGAGGAGTCCTTCA

Position	Sequence
1825-1847	TGAGGAGTCCTTCACAGGCAGAT
1826-1848	GAGGAGTCCTTCACAGGCAGATA
1827-1849	AGGAGTCCTTCACAGGCAGATAT
1828-1850	GGAGTCCTTCACAGGCAGATATT
1829-1851	GAGTCCTTCACAGGCAGATATTA
1830-1852	AGTCCTTCACAGGCAGATATTAA
1831-1853	GTCCTTCACAGGCAGATATTAC
1832-1854	TCCTTCACAGGCAGATATTAACA
1833-1855	CCTTCACAGGCAGATATTAACAA
1834-1856	CTTCACAGGCAGATATTAACAAA
1835-1857	TTCACAGGCAGATATTAACAAAA
1836-1858	TCACAGGCAGATATTAACAAAAT
1837-1859	CACAGGCAGATATTAACAAAATT
1838-1860	ACAGGCAGATATTAACAAAATTG
1839-1861	CAGGCAGATATTAACAAAATTGT
1840-1862	AGGCAGATATTAACAAAATTGTC
1841-1863	GGCAGATATTAACAAAATTGTCC
1842-1864	GCAGATATTAACAAAATTGTCCA
1843-1865	CAGATATTAACAAAATTGTCCAA
1844-1866	AGATATTAACAAAATTGTCCAAA
1845-1867	GATATTAACAAAATTGTCCAAAT
1846-1868	ATATTAACAAAATTGTCCAAAT
1847-1869	TATTAACAAAATTGTCCAAATTC
1848-1870	ATTAACAAAATTGTCCAAATTC
1849-1871	TTAACAAAATTGTCCAAATTC
1850-1872	TAACAAAATTGTCCAAATTC
1851-1873	AACAAAATTGTCCAAATTC
1852-1874	ACAAAATTGTCCAAATTC
1853-1875	CAAAAATTGTCCAAATTC
1854-1876	AAAATTGTCCAAATTC
1855-1877	AAATTGTCCAAATTC
1856-1878	AATTGTCCAAATTC
1857-1879	ATTGTCCAAATTC
1858-1880	TTGTCCAAATTC
1859-1881	TGTCCAAATTC
1860-1882	GTCCAAATTC
1861-1883	TCCAAATTC
1862-1884	CCAAATTC
1863-1885	CAAATTC
1864-1886	AAATTC
1865-1887	AATTC
1866-1888	ATTCTACCATGGGAACAGAATG
1867-1889	TTCTACCATGGGAACAGAATGAG
1868-1890	TCTACCATGGGAACAGAATGAGC
1869-1891	CTACCATGGGAACAGAATGAGCA
1870-1892	TACCATGGGAACAGAATGAGCAA
1871-1893	ACCATGGGAACAGAATGAGCAAG
1872-1894	CCATGGGAACAGAATGAGCAAGT
1873-1895	CATGGGAACAGAATGAGCAAGTG
1874-1896	ATGGGAACAGAATGAGCAAGTGA
1875-1897	TGGGAACAGAATGAGCAAGTGAA
1876-1898	GGGAACAGAATGAGCAAGTGAAG
1877-1899	GGAACAGAATGAGCAAGTGAAGA
1878-1900	GAACAGAATGAGCAAGTGAAGAA
1879-1901	AACAGAATGAGCAAGTGAAGAAC
1880-1902	ACAGAATGAGCAAGTGAAGAACT
1881-1903	CAGAATGAGCAAGTGAAGAACTT
1882-1904	AGAATGAGCAAGTGAAGAACTTT
1883-1905	GAATGAGCAAGTGAAGAACTTTG
1884-1906	AATGAGCAAGTGAAGAACTTTGT
1885-1907	ATGAGCAAGTGAAGAACTTTGTG
1886-1908	TGAGCAAGTGAAGAACTTTGTGG
1887-1909	GAGCAAGTGAAGAACTTTGTGGC
1888-1910	AGCAAGTGAAGAACTTTGTGGCT
1889-1911	GCAAGTGAAGAACTTTGTGGCTT
1890-1912	CAAGTGAAGAACTTTGTGGCTTC

Position	Sequence
1891-1913	AAGTGAAGAACTTTGTGGCTTCC
1892-1914	AGTGAAGAACTTTGTGGCTTCCC
1893-1915	GTGAAGAACTTTGTGGCTTCCCA
1894-1916	TGAAGAACTTTGTGGCTTCCCAT
1895-1917	GAAGAACTTTGTGGCTTCCCATA
1896-1918	AAGAACTTTGTGGCTTCCCATAT
1897-1919	AGAACTTTGTGGCTTCCCATATT
1898-1920	GAACCTTTGTGGCTTCCCATATTG
1899-1921	AACTTTGTGGCTTCCCATATTGC
1900-1922	ACTTTGTGGCTTCCCATATTGCC
1901-1923	CTTTGTGGCTTCCCATATTGCCA
1902-1924	TTTGTGGCTTCCCATATTGCCAA
1903-1925	TTGTGGCTTCCCATATTGCCAAT
1904-1926	TGTGGCTTCCCATATTGCCAATA
1905-1927	GTGGCTTCCCATATTGCCAATAT
1906-1928	TGGCTTCCCATATTGCCAATATC
1907-1929	GGCTTCCCATATTGCCAATATCT
1908-1930	GCTTCCCATATTGCCAATATCTT
1909-1931	CTCCCATATTGCCAATATCTTG
1910-1932	TCCCATATTGCCAATATCTTGA
1911-1933	TCCCATATTGCCAATATCTTGAA
1912-1934	CCCATATTGCCAATATCTTGAAC
1913-1935	CCATATTGCCAATATCTTGAACT
1914-1936	CATATTGCCAATATCTTGAACTC
1915-1937	ATATTGCCAATATCTTGAACTCA
1916-1938	TATTGCCAATATCTTGAACTCAG
1917-1939	ATTGCCAATATCTTGAACTCAGA
1918-1940	TTGCCAATATCTTGAACTCAGAA
1919-1941	TGCCAATATCTTGAACTCAGAAG
1920-1942	GCCAATATCTTGAACTCAGAAGA
1921-1943	CCAATATCTTGAACTCAGAAGAA
1922-1944	CAATATCTTGAACTCAGAAGAAT
1923-1945	AATATCTTGAACTCAGAAGAATT
1924-1946	ATATCTTGAACTCAGAAGAATTG
1925-1947	TATCTTGAACTCAGAAGAATTGG
1926-1948	ATCTTGAACTCAGAAGAATTGGA
1927-1949	TCTTGAACTCAGAAGAATTGGAT
1928-1950	CTTGAACTCAGAAGAATTGGATA
1929-1951	TTGAACTCAGAAGAATTGGATAT
1930-1952	TGAACTCAGAAGAATTGGATATC
1931-1953	GAACTCAGAAGAATTGGATATCC
1932-1954	AACTCAGAAGAATTGGATATCCA
1933-1955	ACTCAGAAGAATTGGATATCCAA
1934-1956	CTCAGAAGAATTGGATATCCAAG
1935-1957	TCAGAAGAATTGGATATCCAAGA
1936-1958	CAGAAGAATTGGATATCCAAGAT
1937-1959	AGAAGAATTGGATATCCAAGATC
1938-1960	GAAGAATTGGATATCCAAGATCT
1939-1961	AAGAATTGGATATCCAAGATCTG
1940-1962	AGAATTGGATATCCAAGATCTGA
1941-1963	GAATTGGATATCCAAGATCTGAA
1942-1964	AATTGGATATCCAAGATCTGAAA
1943-1965	ATTGGATATCCAAGATCTGAAAA
1944-1966	TTGGATATCCAAGATCTGAAAAA
1945-1967	TGGATATCCAAGATCTGAAAAAG
1946-1968	GGATATCCAAGATCTGAAAAAGT
1947-1969	GATATCCAAGATCTGAAAAAGTT
1948-1970	ATATCCAAGATCTGAAAAAGTTA
1949-1971	TATCCAAGATCTGAAAAAGTTAG
1950-1972	ATCCAAGATCTGAAAAAGTTAGT
1951-1973	TCCAAGATCTGAAAAAGTTAGTG
1952-1974	CCAAGATCTGAAAAAGTTAGTGA
1953-1975	CAAGATCTGAAAAAGTTAGTGAA
1954-1976	AAGATCTGAAAAAGTTAGTGAAA
1955-1977	AGATCTGAAAAAGTTAGTGAAAG
1956-1978	GATCTGAAAAAGTTAGTGAAAGA

Position	Sequence
1957-1979	ATCTGAAAAGTTAGTGAAAGAA
1958-1980	TCTGAAAAGTTAGTGAAAGAAG
1959-1981	CTGAAAAGTTAGTGAAAGAAGC
1960-1982	TGAAAAGTTAGTGAAAGAAGCT
1961-1983	GAAAAGTTAGTGAAAGAAGCTC
1962-1984	AAAAGTTAGTGAAAGAAGCTCT
1963-1985	AAAAGTTAGTGAAAGAAGCTCTG
1964-1986	AAAGTTAGTGAAAGAAGCTCTGA
1965-1987	AAGTTAGTGAAAGAAGCTCTGAA
1966-1988	AGTTAGTGAAAGAAGCTCTGAAA
1967-1989	GTTAGTGAAAGAAGCTCTGAAAG
1968-1990	TTAGTGAAAGAAGCTCTGAAAGA
1969-1991	TAGTGAAAGAAGCTCTGAAAGAA
1970-1992	AGTGAAAGAAGCTCTGAAAGAAT
1971-1993	GTGAAAGAAGCTCTGAAAGAATC
1972-1994	TGAAAGAAGCTCTGAAAGAATCT
1973-1995	GAAAGAAGCTCTGAAAGAATCTC
1974-1996	AAAGAAGCTCTGAAAGAATCTCA
1975-1997	AAGAAGCTCTGAAAGAATCTCAA
1976-1998	AGAAGCTCTGAAAGAATCTCAAC
1977-1999	GAAGCTCTGAAAGAATCTCAACT
1978-2000	AAGCTCTGAAAGAATCTCAACTT
1979-2001	AGCTCTGAAAGAATCTCAACTTC
1980-2002	GCTCTGAAAGAATCTCAACTTCC
1981-2003	CTCTGAAAGAATCTCAACTTCCA
1982-2004	TCTGAAAGAATCTCAACTTCCAA
1983-2005	CTGAAAGAATCTCAACTTCCAAC
1984-2006	TGAAAGAATCTCAACTTCCAACT
1985-2007	GAAAGAATCTCAACTTCCAACTG
1986-2008	AAAGAATCTCAACTTCCAACTGT
1987-2009	AAGAATCTCAACTTCCAACTGTC
1988-2010	AGAATCTCAACTTCCAACTGTCA
1989-2011	GAATCTCAACTTCCAACTGTCAT
1990-2012	AATCTCAACTTCCAACTGTCATG
1991-2013	ATCTCAACTTCCAACTGTCATGG
1992-2014	TCTCAACTTCCAACTGTCATGGA
1993-2015	CTCAACTTCCAACTGTCATGGAC
1994-2016	TCAACTTCCAACTGTCATGGACT
1995-2017	CAACTTCCAACTGTCATGGACTT
1996-2018	AACTTCCAACTGTCATGGACTTC
1997-2019	ACTTCCAACTGTCATGGACTTCA
1998-2020	CTTCCAACTGTCATGGACTTCAG
1999-2021	TTCCAACTGTCATGGACTTCAGA
2000-2022	TCCAACTGTCATGGACTTCAGAA
2001-2023	CCAACTGTCATGGACTTCAGAAA
2002-2024	CAACTGTCATGGACTTCAGAAAA
2003-2025	AACTGTCATGGACTTCAGAAAAT
2004-2026	ACTGTCATGGACTTCAGAAAATF
2005-2027	CTGTCATGGACTTCAGAAAATTC
2006-2028	TGTCATGGACTTCAGAAAATTCT
2007-2029	GTCATGGACTTCAGAAAATTCTC
2008-2030	TCATGGACTTCAGAAAATTCTCT
2009-2031	CATGGACTTCAGAAAATTCTCTC
2010-2032	ATGGACTTCAGAAAATTCTCTCG
2011-2033	TGGACTTCAGAAAATTCTCTCGG
2012-2034	GGACTTCAGAAAATTCTCTCGGA
2013-2035	GACTTCAGAAAATTCTCTCGGAA
2014-2036	ACTTCAGAAAATTCTCTCGGAAC
2015-2037	CTTCAGAAAATTCTCTCGGAACT
2016-2038	TTCAGAAAATTCTCTCGGAACTA
2017-2039	TCAGAAAATTCTCTCGGAACTAT
2018-2040	CAGAAAATTCTCTCGGAACTATC
2019-2041	AGAAAATTCTCTCGGAACTATCA
2020-2042	GAAAATTCTCTCGGAACTATCAA
2021-2043	AAAATTCTCTCGGAACTATCAAC
2022-2044	AAATTCTCTCGGAACTATCAACT

Position	Sequence
2023-2045	AATTCTCTCGGAACTATCAACTC
2024-2046	ATTCTCTCGGAACTATCAACTCT
2025-2047	TTCTCTCGGAACTATCAACTCTA
2026-2048	TCTCTCGGAACTATCAACTCTAC
2027-2049	CTCTCGGAACTATCAACTCTACA
2028-2050	TCTCGGAACTATCAACTCTACAA
2029-2051	CTCGGAACTATCAACTCTACAAA
2030-2052	TCGGAACTATCAACTCTACAAAT
2031-2053	CGGAACTATCAACTCTACAAATC
2032-2054	GGAACTATCAACTCTACAAATCT
2033-2055	GAACTATCAACTCTACAAATCTG
2034-2056	AACTATCAACTCTACAAATCTGT
2035-2057	ACTATCAACTCTACAAATCTGTT
2036-2058	CTATCAACTCTACAAATCTGTTT
2037-2059	TATCAACTCTACAAATCTGTTTC
2038-2060	ATCAACTCTACAAATCTGTTTCT
2039-2061	TCAACTCTACAAATCTGTTTCTC
2040-2062	CAACTCTACAAATCTGTTTCTCT
2041-2063	AACTCTACAAATCTGTTTCTCTT
2042-2064	ACTCTACAAATCTGTTTCTCTTC
2043-2065	CTCTACAAATCTGTTTCTCTTCC
2044-2066	TCTACAAATCTGTTTCTCTTCCA
2045-2067	CTACAAATCTGTTTCTCTTCCAT
2046-2068	TACAAATCTGTTTCTCTTCCATC
2047-2069	ACAAATCTGTTTCTCTTCCATCA
2048-2070	CAAATCTGTTTCTCTTCCATCAC
2049-2071	AAATCTGTTTCTCTTCCATCACT
2050-2072	AATCTGTTTCTCTTCCATCACTT
2051-2073	ATCTGTTTCTCTTCCATCACTTG
2052-2074	TCTGTTTCTCTTCCATCACTTGA
2053-2075	CTGTTTCTCTTCCATCACTTGAC
2054-2076	TGTTTCTCTTCCATCACTTGACC
2055-2077	GTTTCTCTTCCATCACTTGACCC
2056-2078	TTTCTCTTCCATCACTTGACCCA
2057-2079	TTCTCTTCCATCACTTGACCCAG
2058-2080	TCTCTTCCATCACTTGACCCAGC
2059-2081	CTCTTCCATCACTTGACCCAGCC
2060-2082	TCTTCCATCACTTGACCCAGCCT
2061-2083	CTTCCATCACTTGACCCAGCCTC
2062-2084	TTCCATCACTTGACCCAGCCTCA
2063-2085	TCCATCACTTGACCCAGCCTCAG
2064-2086	CCATCACTTGACCCAGCCTCAGC
2065-2087	CATCACTTGACCCAGCCTCAGCC
2066-2088	ATCACTTGACCCAGCCTCAGCCA
2067-2089	TCACTTGACCCAGCCTCAGCCAA
2068-2090	CACTTGACCCAGCCTCAGCCAAA
2069-2091	ACTTGACCCAGCCTCAGCCAAAA
2070-2092	CTTGACCCAGCCTCAGCCAAAAT
2071-2093	TTGACCCAGCCTCAGCCAAAATA
2072-2094	TGACCCAGCCTCAGCCAAAATAG
2073-2095	GACCCAGCCTCAGCCAAAATAGA
2074-2096	ACCCAGCCTCAGCCAAAATAGAA
2075-2097	CCCAGCCTCAGCCAAAATAGAAG
2076-2098	CCAGCCTCAGCCAAAATAGAAGG
2077-2099	CAGCCTCAGCCAAAATAGAAGGG
2078-2100	AGCCTCAGCCAAAATAGAAGGGA
2079-2101	GCCTCAGCCAAAATAGAAGGGAA
2080-2102	CCTCAGCCAAAATAGAAGGGAAAT
2081-2103	CTCAGCCAAAATAGAAGGGAAATC
2082-2104	TCAGCCAAAATAGAAGGGAAATCT
2083-2105	CAGCCAAAATAGAAGGGAAATCTT
2084-2106	AGCCAAAATAGAAGGGAAATCTTA
2085-2107	GCCAAAATAGAAGGGAAATCTTAT
2086-2108	CCAAAATAGAAGGGAAATCTTATA
2087-2109	CAAAAATAGAAGGGAAATCTTATAT
2088-2110	AAAAATAGAAGGGAAATCTTATATT

Position	Sequence
2089-2111	AAATAGAAGGGAATCTTATATTT
2090-2112	AATAGAAGGGAATCTTATATTTG
2091-2113	ATAGAAGGGAATCTTATATTTGA
2092-2114	TAGAAGGGAATCTTATATTTGAT
2093-2115	AGAAGGGAATCTTATATTTGATC
2094-2116	GAAGGGAATCTTATATTTGATCC
2095-2117	AAGGGAATCTTATATTTGATCCA
2096-2118	AGGGAATCTTATATTTGATCCAA
2097-2119	GGGAATCTTATATTTGATCCAAA
2098-2120	GGATCTTATATTTGATCCAAAT
2099-2121	GAATCTTATATTTGATCCAAATA
2100-2122	AATCTTATATTTGATCCAAATAA
2101-2123	ATCTTATATTTGATCCAAATAAC
2102-2124	TCTTATATTTGATCCAAATAACT
2103-2125	CTTATATTTGATCCAAATAACTA
2104-2126	TTATATTTGATCCAAATAACTAC
2105-2127	TATATTTGATCCAAATAACTACC
2106-2128	ATATTTGATCCAAATAACTACCT
2107-2129	TATTTGATCCAAATAACTACCTT
2108-2130	ATTTGATCCAAATAACTACCTTC
2109-2131	TTTGATCCAAATAACTACCTTCC
2110-2132	TTGATCCAAATAACTACCTTCCT
2111-2133	TGATCCAAATAACTACCTTCCTA
2112-2134	GATCCAAATAACTACCTTCCTAA
2113-2135	ATCCAAATAACTACCTTCCTAAA
2114-2136	TCCAAATAACTACCTTCCTAAAG
2115-2137	CCAAATAACTACCTTCCTAAAGA
2116-2138	CAATAACTACCTTCCTAAAGAA
2117-2139	AAATAACTACCTTCCTAAAGAAA
2118-2140	AATAACTACCTTCCTAAAGAAAG
2119-2141	ATAACTACCTTCCTAAAGAAAGC
2120-2142	TAACTACCTTCCTAAAGAAAGCA
2121-2143	AACTACCTTCCTAAAGAAAGCAT
2122-2144	ACTACCTTCCTAAAGAAAGCATG
2123-2145	CTACCTTCCTAAAGAAAGCATGC
2124-2146	TACCTTCCTAAAGAAAGCATGCT
2125-2147	ACCTTCCTAAAGAAAGCATGCTG
2126-2148	CCTTCCTAAAGAAAGCATGCTGA
2127-2149	CTTCCTAAAGAAAGCATGCTGAA
2128-2150	TTCTAAAGAAAGCATGCTGAAA
2129-2151	TCCTAAAGAAAGCATGCTGAAA
2130-2152	CCTAAAGAAAGCATGCTGAAAAC
2131-2153	CTAAAGAAAGCATGCTGAAAACT
2132-2154	TAAAGAAAGCATGCTGAAAACTA
2133-2155	AAAGAAAGCATGCTGAAAACTAC
2134-2156	AAGAAAGCATGCTGAAAACTACC
2135-2157	AGAAAGCATGCTGAAAACTACCC
2136-2158	GAAAGCATGCTGAAAACTACCCT
2137-2159	AAAGCATGCTGAAAACTACCCTC
2138-2160	AAGCATGCTGAAAACTACCCTCA
2139-2161	AGCATGCTGAAAACTACCCTCAC
2140-2162	GCATGCTGAAAACTACCCTCACT
2141-2163	CATGCTGAAAACTACCCTCACTG
2142-2164	ATGCTGAAAACTACCCTCACTGC
2143-2165	TGCTGAAAACTACCCTCACTGCC
2144-2166	GCTGAAAACTACCCTCACTGCCT
2145-2167	CTGAAAACTACCCTCACTGCCTT
2146-2168	TGAAAACTACCCTCACTGCCTTT
2147-2169	GAAAACTACCCTCACTGCCTTTG
2148-2170	AAAACTACCCTCACTGCCTTTGG
2149-2171	AAACTACCCTCACTGCCTTTGGA
2150-2172	AACTACCCTCACTGCCTTTGGAT
2151-2173	ACTACCCTCACTGCCTTTGGATT
2152-2174	CTACCCTCACTGCCTTTGGATTT
2153-2175	TACCCTCACTGCCTTTGGATTTG
2154-2176	ACCCTCACTGCCTTTGGATTTGC

Position	Sequence
2155-2177	CCCTCACTGCCTTTGGATTGCT
2156-2178	CCTCACTGCCTTTGGATTGCTT
2157-2179	CTCACTGCCTTTGGATTGCTTC
2158-2180	TCACTGCCTTTGGATTGCTTCA
2159-2181	CACTGCCTTTGGATTGCTTCAG
2160-2182	ACTGCCTTTGGATTGCTTCAGC
2161-2183	CTGCCTTTGGATTGCTTCAGCT
2162-2184	TGCCTTTGGATTGCTTCAGCTG
2163-2185	GCCTTTGGATTGCTTCAGCTGA
2164-2186	CCTTTGGATTGCTTCAGCTGAC
2165-2187	CTTTGGATTGCTTCAGCTGACC
2166-2188	TTTGGATTGCTTCAGCTGACCT
2167-2189	TTGGATTGCTTCAGCTGACCTC
2168-2190	TGGATTGCTTCAGCTGACCTCA
2169-2191	GGATTGCTTCAGCTGACCTCAT
2170-2192	GATTTGCTTCAGCTGACCTCATC
2171-2193	ATTTGCTTCAGCTGACCTCATCG
2172-2194	TTTGCTTCAGCTGACCTCATCGA
2173-2195	TTGCTTCAGCTGACCTCATCGAG
2174-2196	TGCTTCAGCTGACCTCATCGAGA
2175-2197	GCTTCAGCTGACCTCATCGAGAT
2176-2198	CTTCAGCTGACCTCATCGAGATT
2177-2199	TTCAGCTGACCTCATCGAGATTG
2178-2200	TCAGCTGACCTCATCGAGATTGG
2179-2201	CAGCTGACCTCATCGAGATTGGC
2180-2202	AGCTGACCTCATCGAGATTGGCT
2181-2203	GCTGACCTCATCGAGATTGGCTT
2182-2204	CTGACCTCATCGAGATTGGCTTG
2183-2205	TGACCTCATCGAGATTGGCTTGG
2184-2206	GACCTCATCGAGATTGGCTTGGGA
2185-2207	ACCTCATCGAGATTGGCTTGGAA
2186-2208	CCTCATCGAGATTGGCTTGGAAG
2187-2209	CTCATCGAGATTGGCTTGGAAGG
2188-2210	TCATCGAGATTGGCTTGGAAGGA
2189-2211	CATCGAGATTGGCTTGGAAGGAA
2190-2212	ATCGAGATTGGCTTGGAAGGAAA
2191-2213	TCGAGATTGGCTTGGAAGGAAAA
2192-2214	CGAGATTGGCTTGGAAGGAAAAG
2193-2215	GAGATTGGCTTGGAAGGAAAAGG
2194-2216	AGATTGGCTTGGAAGGAAAAGGC
2195-2217	GATTGGCTTGGAAGGAAAAGGCT
2196-2218	ATTGGCTTGGAAGGAAAAGGCTT
2197-2219	TTGGCTTGGAAGGAAAAGGCTTT
2198-2220	TGGCTTGGAAGGAAAAGGCTTTG
2199-2221	GGCTTGGAAGGAAAAGGCTTTGA
2200-2222	GCTTGGAAGGAAAAGGCTTTGAG
2201-2223	CTTGGAAGGAAAAGGCTTTGAGC
2202-2224	TTGGAAGGAAAAGGCTTTGAGCC
2203-2225	TGGAAGGAAAAGGCTTTGAGCCA
2204-2226	GGAAGGAAAAGGCTTTGAGCCAA
2205-2227	GAAGGAAAAGGCTTTGAGCCAAC
2206-2228	AAGGAAAAGGCTTTGAGCCAACA
2207-2229	AGGAAAAGGCTTTGAGCCAACAT
2208-2230	GGAAAAGGCTTTGAGCCAACATT
2209-2231	GAAAAGGCTTTGAGCCAACATTG
2210-2232	AAAAGGCTTTGAGCCAACATTGG
2211-2233	AAAGGCTTTGAGCCAACATTGGA
2212-2234	AAGGCTTTGAGCCAACATTGGAA
2213-2235	AGGCTTTGAGCCAACATTGGAAG
2214-2236	GGCTTTGAGCCAACATTGGAAGC
2215-2237	GCTTTGAGCCAACATTGGAAGCT
2216-2238	CTTTGAGCCAACATTGGAAGCTC
2217-2239	TTTGAAGCTTTGAGCCAACATTG
2218-2240	TTGAGCCAACATTGGAAGCTCTT
2219-2241	TGAGCCAACATTGGAAGCTCTTT
2220-2242	GAGCCAACATTGGAAGCTCTTTT

Position	Sequence
2221-2243	AGCCAACATTGGAAGCTCTTTTT
2222-2244	GCCAACATTGGAAGCTCTTTTTG
2223-2245	CCAACATTGGAAGCTCTTTTTGG
2224-2246	CAACATTGGAAGCTCTTTTTGGG
2225-2247	AACATTGGAAGCTCTTTTTGGGA
2226-2248	ACATTGGAAGCTCTTTTTGGGAA
2227-2249	CATTGGAAGCTCTTTTTGGGAAG
2228-2250	ATGGAAGCTCTTTTTGGGAAGC
2229-2251	TTGGAAGCTCTTTTTGGGAAGCA
2230-2252	TGGAAGCTCTTTTTGGGAAGCAA
2231-2253	GGAAGCTCTTTTTGGGAAGCAAG
2232-2254	GAAGCTCTTTTTGGGAAGCAAGG
2233-2255	AAGCTCTTTTTGGGAAGCAAGGA
2234-2256	AGCTCTTTTTGGGAAGCAAGGAT
2235-2257	GCTCTTTTTGGGAAGCAAGGATT
2236-2258	CTCTTTTTGGGAAGCAAGGATTT
2237-2259	TCTTTTTGGGAAGCAAGGATTTT
2238-2260	CTTTTTGGGAAGCAAGGATTTT
2239-2261	TTTTTGGGAAGCAAGGATTTTTC
2240-2262	TTTTGGGAAGCAAGGATTTTCC
2241-2263	TTTGGGAAGCAAGGATTTTCCC
2242-2264	TGGGAAGCAAGGATTTTCCCA
2243-2265	TGGGAAGCAAGGATTTTCCCAG
2244-2266	GGGAAGCAAGGATTTTCCCAGA
2245-2267	GGAAGCAAGGATTTTCCCAGAC
2246-2268	GAAGCAAGGATTTTCCCAGACA
2247-2269	AAGCAAGGATTTTCCCAGACAG
2248-2270	AGCAAGGATTTTCCCAGACAGT
2249-2271	GCAAGGATTTTCCCAGACAGTG
2250-2272	CAAGGATTTTCCCAGACAGTGT
2251-2273	AAGGATTTTCCCAGACAGTGTCT
2252-2274	AGGATTTTCCCAGACAGTGTCTA
2253-2275	GGATTTTCCCAGACAGTGTCTAA
2254-2276	GATTTTCCCAGACAGTGTCTAAC
2255-2277	ATTTTCCCAGACAGTGTCTAACA
2256-2278	TTTTCCCAGACAGTGTCTAACAA
2257-2279	TTTCCCAGACAGTGTCTAACAAA
2258-2280	TTCCCAGACAGTGTCTAACAAAG
2259-2281	TTCCCAGACAGTGTCTAACAAAGC
2260-2282	TCCCAGACAGTGTCTAACAAAGCT
2261-2283	CCCAGACAGTGTCTAACAAAGCTT
2262-2284	CCAGACAGTGTCTAACAAAGCTTT
2263-2285	CAGACAGTGTCTAACAAAGCTTTG
2264-2286	AGACAGTGTCTAACAAAGCTTTGT
2265-2287	GACAGTGTCTAACAAAGCTTTGTA
2266-2288	ACAGTGTCTAACAAAGCTTTGTAC
2267-2289	CAGTGTCTAACAAAGCTTTGTACT
2268-2290	AGTGTCTAACAAAGCTTTGTACTG
2269-2291	GTGTCTAACAAAGCTTTGTACTGG
2270-2292	TGTCTAACAAAGCTTTGTACTGGG
2271-2293	GTCACAAAGCTTTGTACTGGGT
2272-2294	TCAACAAAGCTTTGTACTGGGTT
2273-2295	CAACAAAGCTTTGTACTGGGTTA
2274-2296	AACAAAGCTTTGTACTGGGTTAA
2275-2297	ACAAAGCTTTGTACTGGGTTAAT
2276-2298	CAAAGCTTTGTACTGGGTTAATG
2277-2299	AAAGCTTTGTACTGGGTTAATGG
2278-2300	AAGCTTTGTACTGGGTTAATGGT
2279-2301	AGCTTTGTACTGGGTTAATGGTC
2280-2302	GCTTTGTACTGGGTTAATGGTCA
2281-2303	CTTTGTACTGGGTTAATGGTCAA
2282-2304	TTTGTACTGGGTTAATGGTCAAG
2283-2305	TTGTACTGGGTTAATGGTCAAGT
2284-2306	TGTACTGGGTTAATGGTCAAGTT
2285-2307	GTACTGGGTTAATGGTCAAGTTC
2286-2308	TACTGGGTTAATGGTCAAGTTCC

Position	Sequence
2287-2309	ACTGGGTTAATGGTCAAGTTCCT
2288-2310	CTGGGTTAATGGTCAAGTTCCTG
2289-2311	TGGGTTAATGGTCAAGTTCCTGA
2290-2312	GGGTTAATGGTCAAGTTCCTGAT
2291-2313	GGTTAATGGTCAAGTTCCTGATG
2292-2314	GTTAATGGTCAAGTTCCTGATGG
2293-2315	TTAATGGTCAAGTTCCTGATGGT
2294-2316	TAATGGTCAAGTTCCTGATGGTG
2295-2317	AATGGTCAAGTTCCTGATGGTGT
2296-2318	ATGGTCAAGTTCCTGATGGTGTC
2297-2319	TGGTCAAGTTCCTGATGGTGTCT
2298-2320	GGTCAAGTTCCTGATGGTGTCTC
2299-2321	GTCAGTTCCTGATGGTGTCTCT
2300-2322	TCAAGTTCCTGATGGTGTCTCTA
2301-2323	CAAGTTCCTGATGGTGTCTCTAA
2302-2324	AAGTTCCTGATGGTGTCTCTAAG
2303-2325	AGTTCCTGATGGTGTCTCTAAGG
2304-2326	GTTCTGATGGTGTCTCTAAGGT
2305-2327	TTCTGATGGTGTCTCTAAGGTC
2306-2328	TCCTGATGGTGTCTCTAAGGTCT
2307-2329	CCTGATGGTGTCTCTAAGGTCTT
2308-2330	CTGATGGTGTCTCTAAGGTCTTA
2309-2331	TGATGGTGTCTCTAAGGTCTTAG
2310-2332	GATGGTGTCTCTAAGGTCTTAGT
2311-2333	ATGGTGTCTCTAAGGTCTTAGTG
2312-2334	TGGTGTCTCTAAGGTCTTAGTGG
2313-2335	GGTGTCTCTAAGGTCTTAGTGGA
2314-2336	GTGTCTCTAAGGTCTTAGTGGAC
2315-2337	TGTCTCTAAGGTCTTAGTGGACC
2316-2338	GTCTCTAAGGTCTTAGTGGACCA
2317-2339	TCTCTAAGGTCTTAGTGGACCAC
2318-2340	CTCTAAGGTCTTAGTGGACCACT
2319-2341	TCTAAGGTCTTAGTGGACCACTT
2320-2342	CTAAGGTCTTAGTGGACCACFTT
2321-2343	TAAGGTCTTAGTGGACCACFTTG
2322-2344	AAGGTCTTAGTGGACCACFTTGG
2323-2345	AGGTCTTAGTGGACCACFTTGGC
2324-2346	GGTCTTAGTGGACCACFTTGGCT
2325-2347	GTCTTAGTGGACCACFTTGGCTA
2326-2348	TCTTAGTGGACCACFTTGGCTAT
2327-2349	CTTAGTGGACCACFTTGGCTATA
2328-2350	TTAGTGGACCACFTTGGCTATAC
2329-2351	TAGTGGACCACFTTGGCTATACC
2330-2352	AGTGGACCACFTTGGCTATACCA
2331-2353	GTGGACCACFTTGGCTATACCAA
2332-2354	TGGACCACFTTGGCTATACCAAA
2333-2355	GGACCACFTTGGCTATACCAAAG
2334-2356	GACCACFTTGGCTATACCAAAGA
2335-2357	ACCACFTTGGCTATACCAAAGAT
2336-2358	CCACFTTGGCTATACCAAAGATG
2337-2359	CACTTGGCTATACCAAAGATGA
2338-2360	ACTTGGCTATACCAAAGATGAT
2339-2361	CTTGGCTATACCAAAGATGATA
2340-2362	TTGGCTATACCAAAGATGATAA
2341-2363	TTGGCTATACCAAAGATGATAAA
2342-2364	TGGCTATACCAAAGATGATAAAC
2343-2365	GGCTATACCAAAGATGATAAACA
2344-2366	GCTATACCAAAGATGATAAACAT
2345-2367	CTATACCAAAGATGATAAACATG
2346-2368	TATACCAAAGATGATAAACATGA
2347-2369	ATACCAAAGATGATAAACATGAG
2348-2370	TACCAAAGATGATAAACATGAGC
2349-2371	ACCAAAGATGATAAACATGAGCA
2350-2372	CCAAAGATGATAAACATGAGCAG
2351-2373	CAAAGATGATAAACATGAGCAGG
2352-2374	AAAGATGATAAACATGAGCAGGA

Position	Sequence
2353-2375	AAGATGATAAACATGAGCAGGAT
2354-2376	AGATGATAAACATGAGCAGGATA
2355-2377	GATGATAAACATGAGCAGGATAT
2356-2378	ATGATAAACATGAGCAGGATATG
2357-2379	TGATAAACATGAGCAGGATATGG
2358-2380	GATAAACATGAGCAGGATATGGT
2359-2381	ATAAACATGAGCAGGATATGGTA
2360-2382	TAAACATGAGCAGGATATGGTAA
2361-2383	AAACATGAGCAGGATATGGTAAA
2362-2384	AACATGAGCAGGATATGGTAAAT
2363-2385	ACATGAGCAGGATATGGTAAATG
2364-2386	CATGAGCAGGATATGGTAAATGG
2365-2387	ATGAGCAGGATATGGTAAATGGA
2366-2388	TGAGCAGGATATGGTAAATGGAA
2367-2389	GAGCAGGATATGGTAAATGGAAT
2368-2390	AGCAGGATATGGTAAATGGAATA
2369-2391	GCAGGATATGGTAAATGGAATAA
2370-2392	CAGGATATGGTAAATGGAATAAT
2371-2393	AGGATATGGTAAATGGAATAATG
2372-2394	GGATATGGTAAATGGAATAATGC
2373-2395	GATATGGTAAATGGAATAATGCT
2374-2396	ATATGGTAAATGGAATAATGCTC
2375-2397	TATGGTAAATGGAATAATGCTCA
2376-2398	ATGGTAAATGGAATAATGCTCAG
2377-2399	TGGTAAATGGAATAATGCTCAGT
2378-2400	GGTAAATGGAATAATGCTCAGTG
2379-2401	GTAATGGAATAATGCTCAGTGT
2380-2402	TAAATGGAATAATGCTCAGTGTT
2381-2403	AAATGGAATAATGCTCAGTGTTG
2382-2404	AATGGAATAATGCTCAGTGTTGA
2383-2405	ATGGAATAATGCTCAGTGTTGAG
2384-2406	TGGAATAATGCTCAGTGTTGAGA
2385-2407	GGAATAATGCTCAGTGTTGAGAA
2386-2408	GAATAATGCTCAGTGTTGAGAAG
2387-2409	AATAATGCTCAGTGTTGAGAAGC
2388-2410	ATAATGCTCAGTGTTGAGAAGCT
2389-2411	TAATGCTCAGTGTTGAGAAGCTG
2390-2412	AATGCTCAGTGTTGAGAAGCTGA
2391-2413	ATGCTCAGTGTTGAGAAGCTGAT
2392-2414	TGCTCAGTGTTGAGAAGCTGATT
2393-2415	GCTCAGTGTTGAGAAGCTGATTA
2394-2416	CTCAGTGTTGAGAAGCTGATTAA
2395-2417	TCAGTGTTGAGAAGCTGATTAAA
2396-2418	CAGTGTTGAGAAGCTGATTAAAG
2397-2419	AGTGTTGAGAAGCTGATTAAAGA
2398-2420	GTGTTGAGAAGCTGATTAAAGAT
2399-2421	TGTTGAGAAGCTGATTAAAGATT
2400-2422	GTTGAGAAGCTGATTAAAGATTT
2401-2423	TTGAGAAGCTGATTAAAGATTTG
2402-2424	TGAGAAGCTGATTAAAGATTTGA
2403-2425	GAGAAGCTGATTAAAGATTTGAA
2404-2426	AGAAGCTGATTAAAGATTTGAAA
2405-2427	GAAGCTGATTAAAGATTTGAAAT
2406-2428	AAGCTGATTAAAGATTTGAAATC
2407-2429	AGCTGATTAAAGATTTGAAATCC
2408-2430	GCTGATTAAAGATTTGAAATCCA
2409-2431	CTGATTAAAGATTTGAAATCCAA
2410-2432	TGATTAAAGATTTGAAATCCAAA
2411-2433	GATTAAAGATTTGAAATCCAAAG
2412-2434	ATTAAAGATTTGAAATCCAAAGA
2413-2435	TTAAAGATTTGAAATCCAAAGAA
2414-2436	TAAAGATTTGAAATCCAAAGAAG
2415-2437	AAAGATTTGAAATCCAAAGAAGT
2416-2438	AAGATTTGAAATCCAAAGAAGTC
2417-2439	AGATTTGAAATCCAAAGAAGTCC
2418-2440	GATTTGAAATCCAAAGAAGTCCC

Position	Sequence
2419-2441	ATTGAAATCCAAGAAGTCCCG
2420-2442	TTGAAATCCAAGAAGTCCCGG
2421-2443	TTGAAATCCAAGAAGTCCCGGA
2422-2444	TGAAATCCAAGAAGTCCCGGAA
2423-2445	GAAATCCAAGAAGTCCCGGAAG
2424-2446	AAATCCAAGAAGTCCCGGAAGC
2425-2447	AATCCAAGAAGTCCCGGAAGCC
2426-2448	ATCCAAGAAGTCCCGGAAGCCA
2427-2449	TCCAAGAAGTCCCGGAAGCCAG
2428-2450	CCAAGAAGTCCCGGAAGCCAGA
2429-2451	CAAAGAAGTCCCGGAAGCCAGAG
2430-2452	AAAGAAGTCCCGGAAGCCAGAGC
2431-2453	AAGAAGTCCCGGAAGCCAGAGCC
2432-2454	AGAAGTCCCGGAAGCCAGAGCCT
2433-2455	GAGTCCCGGAAGCCAGAGCCTA
2434-2456	AAGTCCCGGAAGCCAGAGCCTAC
2435-2457	AGTCCCGGAAGCCAGAGCCTACC
2436-2458	GTCCCGGAAGCCAGAGCCTACCT
2437-2459	TCCCGGAAGCCAGAGCCTACCTC
2438-2460	CCCGGAAGCCAGAGCCTACCTCC
2439-2461	CCGGAAGCCAGAGCCTACCTCCG
2440-2462	CGGAAGCCAGAGCCTACCTCCGC
2441-2463	GGAAGCCAGAGCCTACCTCCGCA
2442-2464	GAGCCAGAGCCTACCTCCGCAT
2443-2465	AAGCCAGAGCCTACCTCCGCATC
2444-2466	AGCCAGAGCCTACCTCCGCATCT
2445-2467	GCCAGAGCCTACCTCCGCATCTT
2446-2468	CCAGAGCCTACCTCCGCATCTTG
2447-2469	CAGAGCCTACCTCCGCATCTTGG
2448-2470	AGAGCCTACCTCCGCATCTTGGG
2449-2471	GAGCCTACCTCCGCATCTTGGGA
2450-2472	AGCCTACCTCCGCATCTTGGGAG
2451-2473	GCCTACCTCCGCATCTTGGGAGA
2452-2474	CCTACCTCCGCATCTTGGGAGAG
2453-2475	CTACCTCCGCATCTTGGGAGAGG
2454-2476	TACCTCCGCATCTTGGGAGAGGA
2455-2477	ACCTCCGCATCTTGGGAGAGGAG
2456-2478	CCTCCGCATCTTGGGAGAGGAGC
2457-2479	CTCCGCATCTTGGGAGAGGAGCT
2458-2480	TCCGCATCTTGGGAGAGGAGCTT
2459-2481	CCGCATCTTGGGAGAGGAGCTTG
2460-2482	CGCATCTTGGGAGAGGAGCTTGG
2461-2483	GCATCTTGGGAGAGGAGCTTGGT
2462-2484	CATCTTGGGAGAGGAGCTTGGTT
2463-2485	ATCTTGGGAGAGGAGCTTGGTTT
2464-2486	TCTTGGGAGAGGAGCTTGGTTTT
2465-2487	CTTGGGAGAGGAGCTTGGTTTTG
2466-2488	TTGGGAGAGGAGCTTGGTTTTGC
2467-2489	TGGGAGAGGAGCTTGGTTTTGCC
2468-2490	GGGAGAGGAGCTTGGTTTTGCCA
2469-2491	GGAGAGGAGCTTGGTTTTGCCAG
2470-2492	GAGAGGAGCTTGGTTTTGCCAGT
2471-2493	AGAGGAGCTTGGTTTTGCCAGTC
2472-2494	GAGGAGCTTGGTTTTGCCAGTCT
2473-2495	AGGAGCTTGGTTTTGCCAGTCTC
2474-2496	GGAGCTTGGTTTTGCCAGTCTCC
2475-2497	GAGCTTGGTTTTGCCAGTCTCCA
2476-2498	AGCTTGGTTTTGCCAGTCTCCAT
2477-2499	GCTTGGTTTTGCCAGTCTCCATG
2478-2500	CTTGGTTTTGCCAGTCTCCATGA
2479-2501	TTGGTTTTGCCAGTCTCCATGAC
2480-2502	TGGTTTTGCCAGTCTCCATGACC
2481-2503	GGTTTTGCCAGTCTCCATGACCT
2482-2504	GTTTTGCCAGTCTCCATGACCTC
2483-2505	TTTTGCCAGTCTCCATGACCTCC
2484-2506	TTTGGCAGTCTCCATGACCTCCA

Position	Sequence
2485-2507	TTGCCAGTCTCCATGACCTCCAG
2486-2508	TGCCAGTCTCCATGACCTCCAGC
2487-2509	GCCAGTCTCCATGACCTCCAGCT
2488-2510	CCAGTCTCCATGACCTCCAGCTC
2489-2511	CAGTCTCCATGACCTCCAGCTCC
2490-2512	AGTCTCCATGACCTCCAGCTCCT
2491-2513	GTCTCCATGACCTCCAGCTCCTG
2492-2514	TCTCCATGACCTCCAGCTCCTGG
2493-2515	CTCCATGACCTCCAGCTCCTGGG
2494-2516	TCCATGACCTCCAGCTCCTGGGA
2495-2517	CCATGACCTCCAGCTCCTGGGAA
2496-2518	CATGACCTCCAGCTCCTGGGAAA
2497-2519	ATGACCTCCAGCTCCTGGGAAAG
2498-2520	TGACCTCCAGCTCCTGGGAAAGC
2499-2521	GACCTCCAGCTCCTGGGAAAGCT
2500-2522	ACCTCCAGCTCCTGGGAAAGCTG
2501-2523	CCTCCAGCTCCTGGGAAAGCTGC
2502-2524	CTCCAGCTCCTGGGAAAGCTGCT
2503-2525	TCCAGCTCCTGGGAAAGCTGCTT
2504-2526	CCAGCTCCTGGGAAAGCTGCTTC
2505-2527	CAGCTCCTGGGAAAGCTGCTTCT
2506-2528	AGCTCCTGGGAAAGCTGCTTCTG
2507-2529	GCTCCTGGGAAAGCTGCTTCTGA
2508-2530	CTCCTGGGAAAGCTGCTTCTGAT
2509-2531	TCCTGGGAAAGCTGCTTCTGATG
2510-2532	CCTGGGAAAGCTGCTTCTGATGG
2511-2533	CTGGGAAAGCTGCTTCTGATGGG
2512-2534	TGGGAAAGCTGCTTCTGATGGGT
2513-2535	GGGAAAGCTGCTTCTGATGGGTG
2514-2536	GGAAAGCTGCTTCTGATGGGTGC
2515-2537	GAAAGCTGCTTCTGATGGGTGCC
2516-2538	AAAGCTGCTTCTGATGGGTGCC
2517-2539	AAGCTGCTTCTGATGGGTGCCCG
2518-2540	AGCTGCTTCTGATGGGTGCCCGC
2519-2541	GCTGCTTCTGATGGGTGCCCGCA
2520-2542	CTGCTTCTGATGGGTGCCCGCAC
2521-2543	TGCTTCTGATGGGTGCCCGCACT
2522-2544	GCTTCTGATGGGTGCCCGCACTC
2523-2545	CTTCTGATGGGTGCCCGCACTCT
2524-2546	TTCTGATGGGTGCCCGCACTCTG
2525-2547	TCTGATGGGTGCCCGCACTCTGC
2526-2548	CTGATGGGTGCCCGCACTCTGCA
2527-2549	TGATGGGTGCCCGCACTCTGCAG
2528-2550	GATGGGTGCCCGCACTCTGCAGG
2529-2551	ATGGGTGCCCGCACTCTGCAGGG
2530-2552	TGGGTGCCCGCACTCTGCAGGGG
2531-2553	GGGTGCCCGCACTCTGCAGGGGA
2532-2554	GGTGCCCGCACTCTGCAGGGGAT
2533-2555	GTGCCCGCACTCTGCAGGGGATC
2534-2556	TGCCCGCACTCTGCAGGGGATCC
2535-2557	GCCCGCACTCTGCAGGGGATCCC
2536-2558	CCCGCACTCTGCAGGGGATCCCC
2537-2559	CCGCACTCTGCAGGGGATCCCC
2538-2560	CGCACTCTGCAGGGGATCCCCCA
2539-2561	GCACTCTGCAGGGGATCCCCCAG
2540-2562	CACTCTGCAGGGGATCCCCCAGA
2541-2563	ACTCTGCAGGGGATCCCCCAGAT
2542-2564	CTCTGCAGGGGATCCCCCAGATG
2543-2565	TCTGCAGGGGATCCCCCAGATGA
2544-2566	CTGCAGGGGATCCCCCAGATGAT
2545-2567	TGCAGGGGATCCCCCAGATGATT
2546-2568	GCAGGGGATCCCCCAGATGATTG
2547-2569	CAGGGGATCCCCCAGATGATTGG
2548-2570	AGGGGATCCCCCAGATGATTGGA
2549-2571	GGGGATCCCCCAGATGATTGGAG
2550-2572	GGGATCCCCCAGATGATTGGAGA

Position	Sequence
2551-2573	GGATCCCCAGATGATTGGAGAG
2552-2574	GATCCCCAGATGATTGGAGAGG
2553-2575	ATCCCCAGATGATTGGAGAGGT
2554-2576	TCCCCAGATGATTGGAGAGGTC
2555-2577	CCCCAGATGATTGGAGAGGTCA
2556-2578	CCCAGATGATTGGAGAGGTTCAT
2557-2579	CCAGATGATTGGAGAGGTTCATC
2558-2580	CCAGATGATTGGAGAGGTTCATCA
2559-2581	CAGATGATTGGAGAGGTTCATCAG
2560-2582	AGATGATTGGAGAGGTTCATCAGG
2561-2583	GATGATTGGAGAGGTTCATCAGGA
2562-2584	ATGATTGGAGAGGTTCATCAGGAA
2563-2585	TGATTGGAGAGGTTCATCAGGAAG
2564-2586	GATTGGAGAGGTTCATCAGGAAGG
2565-2587	ATTGGAGAGGTTCATCAGGAAGGG
2566-2588	TTGGAGAGGTTCATCAGGAAGGGC
2567-2589	TGGAGAGGTTCATCAGGAAGGGCT
2568-2590	GGAGAGGTTCATCAGGAAGGGCTC
2569-2591	GAGAGGTTCATCAGGAAGGGCTCA
2570-2592	AGAGGTTCATCAGGAAGGGCTCAA
2571-2593	GAGGTTCATCAGGAAGGGCTCAA
2572-2594	AGGTTCATCAGGAAGGGCTCAAAG
2573-2595	GGTCATCAGGAAGGGCTCAAAGA
2574-2596	GTCATCAGGAAGGGCTCAAAGAA
2575-2597	TCATCAGGAAGGGCTCAAAGAAT
2576-2598	CATCAGGAAGGGCTCAAAGAATG
2577-2599	ATCAGGAAGGGCTCAAAGAATGA
2578-2600	TCAGGAAGGGCTCAAAGAATGAC
2579-2601	CAGGAAGGGCTCAAAGAATGACT
2580-2602	AGGAAGGGCTCAAAGAATGACTT
2581-2603	GGAAGGGCTCAAAGAATGACTTT
2582-2604	GAAGGGCTCAAAGAATGACTTTT
2583-2605	AAGGGCTCAAAGAATGACTTTTT
2584-2606	AGGGCTCAAAGAATGACTTTTTT
2585-2607	GGGCTCAAAGAATGACTTTTTTC
2586-2608	GGCTCAAAGAATGACTTTTTTCT
2587-2609	GCTCAAAGAATGACTTTTTTCTT
2588-2610	CTCAAAGAATGACTTTTTTCTTC
2589-2611	TCAAAGAATGACTTTTTTCTTCA
2590-2612	CAAAGAATGACTTTTTTCTTCAC
2591-2613	AAAGAATGACTTTTTTCTTCACT
2592-2614	AAGAATGACTTTTTTCTTCACTA
2593-2615	AGAATGACTTTTTTCTTCACTAC
2594-2616	GAATGACTTTTTTCTTCACTACA
2595-2617	AATGACTTTTTTCTTCACTACAT
2596-2618	ATGACTTTTTTCTTCACTACATC
2597-2619	TGACTTTTTTCTTCACTACATCT
2598-2620	GACTTTTTTCTTCACTACATCTT
2599-2621	ACTTTTTTCTTCACTACATCTTC
2600-2622	CTTTTTTCTTCACTACATCTTCA
2601-2623	TTTTTCTTCACTACATCTTCAT
2602-2624	TTTTTCTTCACTACATCTTCATG
2603-2625	TTTTTCTTCACTACATCTTCATGG
2604-2626	TTTCTTCACTACATCTTCATGGA
2605-2627	TTCTTCACTACATCTTCATGGAG
2606-2628	TCTTCACTACATCTTCATGGAGA
2607-2629	CTTCACTACATCTTCATGGAGAA
2608-2630	TCTCACTACATCTTCATGGAGAAT
2609-2631	TCACTACATCTTCATGGAGAATG
2610-2632	CACTACATCTTCATGGAGAATGC
2611-2633	ACTACATCTTCATGGAGAATGCC
2612-2634	CTACATCTTCATGGAGAATGCCT
2613-2635	TACATCTTCATGGAGAATGCCTT
2614-2636	ACATCTTCATGGAGAATGCCTTT
2615-2637	CATCTTCATGGAGAATGCCTTTG
2616-2638	ATCTTCATGGAGAATGCCTTTGA

Position	Sequence
2617-2639	TCTTCATGGAGAATGCCTTTGAA
2618-2640	CTTCATGGAGAATGCCTTTGAAC
2619-2641	TTCATGGAGAATGCCTTTGAACT
2620-2642	TCATGGAGAATGCCTTTGAACTC
2621-2643	CATGGAGAATGCCTTTGAACTCC
2622-2644	ATGGAGAATGCCTTTGAACTCCC
2623-2645	TGGAGAATGCCTTTGAACTCCCC
2624-2646	GGAGAATGCCTTTGAACTCCCCA
2625-2647	GAGAATGCCTTTGAACTCCCCAC
2626-2648	AGAATGCCTTTGAACTCCCCACT
2627-2649	GAATGCCTTTGAACTCCCCACTG
2628-2650	AATGCCTTTGAACTCCCCACTGG
2629-2651	ATGCCTTTGAACTCCCCACTGGA
2630-2652	TGCCCTTTGAACTCCCCACTGGAG
2631-2653	GCCTTTGAACTCCCCACTGGAGC
2632-2654	CCTTTGAACTCCCCACTGGAGCT
2633-2655	CTTTGAACTCCCCACTGGAGCTG
2634-2656	TTTGAATCCCCACTGGAGCTGG
2635-2657	TTGAATCCCCACTGGAGCTGGA
2636-2658	TGAATCCCCACTGGAGCTGGAT
2637-2659	GAATCCCCACTGGAGCTGGATT
2638-2660	AACTCCCCACTGGAGCTGGATTA
2639-2661	ACTCCCCACTGGAGCTGGATTAC
2640-2662	CTCCCCACTGGAGCTGGATTACA
2641-2663	TCCCCACTGGAGCTGGATTACAG
2642-2664	CCCCACTGGAGCTGGATTACAGT
2643-2665	CCCACTGGAGCTGGATTACAGTT
2644-2666	CCACTGGAGCTGGATTACAGTTG
2645-2667	CACTGGAGCTGGATTACAGTTGC
2646-2668	ACTGGAGCTGGATTACAGTTGCA
2647-2669	CTGGAGCTGGATTACAGTTGCAA
2648-2670	TGGAGCTGGATTACAGTTGCAAA
2649-2671	GGAGCTGGATTACAGTTGCAAAAT
2650-2672	GAGCTGGATTACAGTTGCAAAATA
2651-2673	AGCTGGATTACAGTTGCAAAATAT
2652-2674	GCTGGATTACAGTTGCAAAATATC
2653-2675	CTGGATTACAGTTGCAAAATATCT
2654-2676	TGGATTACAGTTGCAAAATATCTT
2655-2677	GGATTACAGTTGCAAAATATCTTC
2656-2678	GATTACAGTTGCAAAATATCTTCA
2657-2679	ATTACAGTTGCAAAATATCTTCAT
2658-2680	TTACAGTTGCAAAATATCTTCATC
2659-2681	TACAGTTGCAAAATATCTTCATCT
2660-2682	ACAGTTGCAAAATATCTTCATCTG
2661-2683	CAGTTGCAAAATATCTTCATCTGG
2662-2684	AGTTGCAAAATATCTTCATCTGGA
2663-2685	GTTGCAAAATATCTTCATCTGGAG
2664-2686	TTGCAAAATATCTTCATCTGGAGT
2665-2687	TGCAAAATATCTTCATCTGGAGTC
2666-2688	GCAAAATATCTTCATCTGGAGTCA
2667-2689	CAAATATCTTCATCTGGAGTCAT
2668-2690	AAATATCTTCATCTGGAGTCATT
2669-2691	AATATCTTCATCTGGAGTCATTG
2670-2692	ATATCTTCATCTGGAGTCATTGC
2671-2693	TATCTTCATCTGGAGTCATTGCT
2672-2694	ATCTTCATCTGGAGTCATTGCTC
2673-2695	TCTTCATCTGGAGTCATTGCTCC
2674-2696	CTTCATCTGGAGTCATTGCTCCC
2675-2697	TTCATCTGGAGTCATTGCTCCCG
2676-2698	TCATCTGGAGTCATTGCTCCCGG
2677-2699	CATCTGGAGTCATTGCTCCCGGA
2678-2700	ATCTGGAGTCATTGCTCCCGGAG
2679-2701	TCTGGAGTCATTGCTCCCGGAGC
2680-2702	CTGGAGTCATTGCTCCCGGAGCC
2681-2703	TGGAGTCATTGCTCCCGGAGCCA
2682-2704	GGAGTCATTGCTCCCGGAGCCAA

Position	Sequence
2683-2705	GAGTCATTGCTCCCGGAGCCAAG
2684-2706	AGTCATTGCTCCCGGAGCCAAGG
2685-2707	GTCATTGCTCCCGGAGCCAAGGC
2686-2708	TCATTGCTCCCGGAGCCAAGGCT
2687-2709	CATTGCTCCCGGAGCCAAGGCTG
2688-2710	ATTGCTCCCGGAGCCAAGGCTGG
2689-2711	TTGCTCCCGGAGCCAAGGCTGGA
2690-2712	TGCTCCCGGAGCCAAGGCTGGAG
2691-2713	GCTCCCGGAGCCAAGGCTGGAGT
2692-2714	CTCCCGGAGCCAAGGCTGGAGTA
2693-2715	TCCCGGAGCCAAGGCTGGAGTAA
2694-2716	CCCGGAGCCAAGGCTGGAGTAAA
2695-2717	CCGGAGCCAAGGCTGGAGTAAAA
2696-2718	CGGAGCCAAGGCTGGAGTAAAAC
2697-2719	GGAGCCAAGGCTGGAGTAAAAC
2698-2720	GAGCCAAGGCTGGAGTAAAAC
2699-2721	AGCCAAGGCTGGAGTAAAAC
2700-2722	GCCAAGGCTGGAGTAAAAC
2701-2723	CCAAGGCTGGAGTAAAAC
2702-2724	CAAGGCTGGAGTAAAAC
2703-2725	AAGGCTGGAGTAAAAC
2704-2726	AGGCTGGAGTAAAAC
2705-2727	GGCTGGAGTAAAAC
2706-2728	GCTGGAGTAAAAC
2707-2729	CTGGAGTAAAAC
2708-2730	TGGAGTAAAAC
2709-2731	GGAGTAAAAC
2710-2732	GAGTAAAAC
2711-2733	AGTAAAAC
2712-2734	GTA AAAAC
2713-2735	TAAAAC
2714-2736	AAAAC
2715-2737	AAAC
2716-2738	AAC
2717-2739	ACT
2718-2740	CT
2719-2741	TG
2720-2742	GG
2721-2743	GA
2722-2744	AAG
2723-2745	AGT
2724-2746	GTA
2725-2747	TAG
2726-2748	AGC
2727-2749	GCA
2728-2750	CCA
2729-2751	CAAC
2730-2752	AACAT
2731-2753	ACATG
2732-2754	CATGC
2733-2755	ATGC
2734-2756	TGC
2735-2757	GC
2736-2758	CAG
2737-2759	AGG
2738-2760	GG
2739-2761	GCT
2740-2762	CTG
2741-2763	TGA
2742-2764	GA
2743-2765	AA
2744-2766	ACT
2745-2767	CTG
2746-2768	TGG
2747-2769	GGT
2748-2770	GTG

Position	Sequence
2749-2771	TGGCAAACCCCTCCGTGTCTGTG
2750-2772	GGCAAACCCCTCCGTGTCTGTGG
2751-2773	GCAAACCCCTCCGTGTCTGTGGA
2752-2774	CAAACCCCTCCGTGTCTGTGGAG
2753-2775	AAAACCCCTCCGTGTCTGTGGAGT
2754-2776	AAACCCCTCCGTGTCTGTGGAGTT
2755-2777	AACCCCTCCGTGTCTGTGGAGTTT
2756-2778	ACCCCTCCGTGTCTGTGGAGTTTG
2757-2779	CCCTCCGTGTCTGTGGAGTTTGT
2758-2780	CCTCCGTGTCTGTGGAGTTTGTG
2759-2781	CTCCGTGTCTGTGGAGTTTGTGA
2760-2782	TCCGTGTCTGTGGAGTTTGTGAC
2761-2783	CCGTGTCTGTGGAGTTTGTGACA
2762-2784	CGTGTCTGTGGAGTTTGTGACAA
2763-2785	GTGTCTGTGGAGTTTGTGACAAA
2764-2786	TGTCTGTGGAGTTTGTGACAAAT
2765-2787	GTCTGTGGAGTTTGTGACAAATA
2766-2788	TCTGTGGAGTTTGTGACAAATAT
2767-2789	CTGTGGAGTTTGTGACAAATATG
2768-2790	TGTGGAGTTTGTGACAAATATGG
2769-2791	GTGGAGTTTGTGACAAATATGGG
2770-2792	TGGAGTTTGTGACAAATATGGGC
2771-2793	GGAGTTTGTGACAAATATGGGCA
2772-2794	GAGTTTGTGACAAATATGGGCAT
2773-2795	AGTTTGTGACAAATATGGGCATC
2774-2796	GTTTGTGACAAATATGGGCATCA
2775-2797	TTTGTGACAAATATGGGCATCAT
2776-2798	TTGTGACAAATATGGGCATCATC
2777-2799	TGTGACAAATATGGGCATCATCA
2778-2800	GTGACAAATATGGGCATCATCAT
2779-2801	TGACAAATATGGGCATCATCATT
2780-2802	GACAAATATGGGCATCATCATTC
2781-2803	ACAAATATGGGCATCATCATTCC
2782-2804	CAAATATGGGCATCATCATTCCG
2783-2805	AAATATGGGCATCATCATTCCGG
2784-2806	AATATGGGCATCATCATTCCGGA
2785-2807	ATATGGGCATCATCATTCCGGAC
2786-2808	TATGGGCATCATCATTCCGGACT
2787-2809	ATGGGCATCATCATTCCGGACTT
2788-2810	TGGGCATCATCATTCCGGACTTC
2789-2811	GGGCATCATCATTCCGGACTTCG
2790-2812	GGCATCATCATTCCGGACTTCGC
2791-2813	GCATCATCATTCCGGACTTCGCT
2792-2814	CATCATCATTCCGGACTTCGCTA
2793-2815	ATCATCATTCCGGACTTCGCTAG
2794-2816	TCATCATTCCGGACTTCGCTAGG
2795-2817	CATCATTCCGGACTTCGCTAGGA
2796-2818	ATCATTCCGGACTTCGCTAGGAG
2797-2819	TCATTCCGGACTTCGCTAGGAGT
2798-2820	CATTCCGGACTTCGCTAGGAGTG
2799-2821	ATTCCGGACTTCGCTAGGAGTGG
2800-2822	TTCCGGACTTCGCTAGGAGTGGG
2801-2823	TCCGGACTTCGCTAGGAGTGGGG
2802-2824	CCGGACTTCGCTAGGAGTGGGGT
2803-2825	CGGACTTCGCTAGGAGTGGGGTC
2804-2826	GGACTTCGCTAGGAGTGGGGTCC
2805-2827	GACTTCGCTAGGAGTGGGGTCCA
2806-2828	ACTTCGCTAGGAGTGGGGTCCAG
2807-2829	CTTCGCTAGGAGTGGGGTCCAGA
2808-2830	TTCGCTAGGAGTGGGGTCCAGAT
2809-2831	TCGCTAGGAGTGGGGTCCAGATG
2810-2832	CGCTAGGAGTGGGGTCCAGATGA
2811-2833	GCTAGGAGTGGGGTCCAGATGAA
2812-2834	CTAGGAGTGGGGTCCAGATGAAC
2813-2835	TAGGAGTGGGGTCCAGATGAACA
2814-2836	AGGAGTGGGGTCCAGATGAACAC

Position	Sequence
2815-2837	GGAGTGGGGTCCAGATGAACACC
2816-2838	GAGTGGGGTCCAGATGAACACCA
2817-2839	AGTGGGGTCCAGATGAACACCAA
2818-2840	GTGGGGTCCAGATGAACACCAAC
2819-2841	TGGGGTCCAGATGAACACCAACT
2820-2842	GGGGTCCAGATGAACACCAACTT
2821-2843	GGGTCCAGATGAACACCAACTTC
2822-2844	GGTCCAGATGAACACCAACTTCT
2823-2845	GTCCAGATGAACACCAACTTCTT
2824-2846	TCCAGATGAACACCAACTTCTTC
2825-2847	CCAGATGAACACCAACTTCTTCC
2826-2848	CAGATGAACACCAACTTCTTCCA
2827-2849	AGATGAACACCAACTTCTTCCAC
2828-2850	GATGAACACCAACTTCTTCCACG
2829-2851	ATGAACACCAACTTCTTCCACGA
2830-2852	TGAACACCAACTTCTTCCACGAG
2831-2853	GAACACCAACTTCTTCCACGAGT
2832-2854	AACACCAACTTCTTCCACGAGTC
2833-2855	ACACCAACTTCTTCCACGAGTCG
2834-2856	CACCAACTTCTTCCACGAGTCGG
2835-2857	ACCAACTTCTTCCACGAGTCGGG
2836-2858	CCAACTTCTTCCACGAGTCGGGT
2837-2859	CAACTTCTTCCACGAGTCGGGTC
2838-2860	AACTTCTTCCACGAGTCGGGTCT
2839-2861	ACTTCTTCCACGAGTCGGGTCTG
2840-2862	CTTCTTCCACGAGTCGGGTCTGG
2841-2863	TTCTTCCACGAGTCGGGTCTGGA
2842-2864	TCTTCCACGAGTCGGGTCTGGAG
2843-2865	CTTCCACGAGTCGGGTCTGGAGG
2844-2866	TTCCACGAGTCGGGTCTGGAGGC
2845-2867	TCCACGAGTCGGGTCTGGAGGCT
2846-2868	CCACGAGTCGGGTCTGGAGGCTC
2847-2869	CACGAGTCGGGTCTGGAGGCTCA
2848-2870	ACGAGTCGGGTCTGGAGGCTCAT
2849-2871	CGAGTCGGGTCTGGAGGCTCATG
2850-2872	GAGTCGGGTCTGGAGGCTCATGT
2851-2873	AGTCGGGTCTGGAGGCTCATGTT
2852-2874	GTCGGGTCTGGAGGCTCATGTTG
2853-2875	TCGGGTCTGGAGGCTCATGTTGC
2854-2876	CGGGTCTGGAGGCTCATGTTGCC
2855-2877	GGGTCTGGAGGCTCATGTTGCC
2856-2878	GGTCTGGAGGCTCATGTTGCCCT
2857-2879	GTCTGGAGGCTCATGTTGCCCTA
2858-2880	TCTGGAGGCTCATGTTGCCCTAA
2859-2881	CTGGAGGCTCATGTTGCCCTAAA
2860-2882	TGGAGGCTCATGTTGCCCTAAAA
2861-2883	GGAGGCTCATGTTGCCCTAAAAG
2862-2884	GAGGCTCATGTTGCCCTAAAAGC
2863-2885	AGGCTCATGTTGCCCTAAAAGCT
2864-2886	GGCTCATGTTGCCCTAAAAGCTG
2865-2887	GCTCATGTTGCCCTAAAAGCTGG
2866-2888	CTCATGTTGCCCTAAAAGCTGGG
2867-2889	TCATGTTGCCCTAAAAGCTGGGA
2868-2890	CATGTTGCCCTAAAAGCTGGGAA
2869-2891	ATGTTGCCCTAAAAGCTGGGAAG
2870-2892	TGTTGCCCTAAAAGCTGGGAAGC
2871-2893	GTTGCCCTAAAAGCTGGGAAGCT
2872-2894	TTGCCCTAAAAGCTGGGAAGCTG
2873-2895	TGCCCTAAAAGCTGGGAAGCTGA
2874-2896	GCCCTAAAAGCTGGGAAGCTGAA
2875-2897	CCCTAAAAGCTGGGAAGCTGAAG
2876-2898	CCTAAAAGCTGGGAAGCTGAAGT
2877-2899	CTAAAAGCTGGGAAGCTGAAGTT
2878-2900	TAAAAGCTGGGAAGCTGAAGTTT
2879-2901	AAAAGCTGGGAAGCTGAAGTTTA
2880-2902	AAAGCTGGGAAGCTGAAGTTTAT

Position	Sequence
2881-2903	AAGCTGGGAAGCTGAAGTTATC
2882-2904	AGCTGGGAAGCTGAAGTTATCA
2883-2905	GCTGGGAAGCTGAAGTTATCAT
2884-2906	CTGGGAAGCTGAAGTTATCATT
2885-2907	TGGGAAGCTGAAGTTATCATT
2886-2908	GGGAAGCTGAAGTTATCATTCC
2887-2909	GGAAGCTGAAGTTATCATTCC
2888-2910	GAAGCTGAAGTTATCATTCC
2889-2911	AAGCTGAAGTTATCATTCC
2890-2912	AGCTGAAGTTATCATTCC
2891-2913	GCTGAAGTTATCATTCC
2892-2914	CTGAAGTTATCATTCC
2893-2915	TGAAGTTATCATTCC
2894-2916	GAAGTTATCATTCC
2895-2917	AAGTTATCATTCC
2896-2918	AGTTATCATTCC
2897-2919	GTTATCATTCC
2898-2920	TTATCATTCC
2899-2921	TTATCATTCC
2900-2922	TATCATTCC
2901-2923	ATCATTCC
2902-2924	TCATTCC
2903-2925	CATTCC
2904-2926	ATCC
2905-2927	TTCC
2906-2928	TC
2907-2929	CT
2908-2930	CT
2909-2931	TT
2910-2932	T
2911-2933	CCC
2912-2934	CCC
2913-2935	CC
2914-2936	CA
2915-2937	AA
2916-2938	A
2917-2939	AG
2918-2940	G
2919-2941	AG
2920-2942	G
2921-2943	ACC
2922-2944	CC
2923-2945	C
2924-2946	AG
2925-2947	G
2926-2948	T
2927-2949	CA
2928-2950	A
2929-2951	AG
2930-2952	G
2931-2953	CT
2932-2954	T
2933-2955	G
2934-2956	CT
2935-2957	T
2936-2958	C
2937-2959	AG
2938-2960	G
2939-2961	T
2940-2962	G
2941-2963	G
2942-2964	AG
2943-2965	G
2944-2966	G
2945-2967	CA
2946-2968	A

Position	Sequence
2947-2969	ACACATTACATTGGTCTCTACC
2948-2970	CACATTACATTGGTCTCTACCA
2949-2971	ACATTACATTTGGTCTCTACCAC
2950-2972	CATTACATTTGGTCTCTACCACC
2951-2973	ATTACATTTGGTCTCTACCACCA
2952-2974	TTACATTTGGTCTCTACCACCAA
2953-2975	TACATTTGGTCTCTACCACCAAAA
2954-2976	ACATTTGGTCTCTACCACCAAAA
2955-2977	CATTTGGTCTCTACCACCAAAAC
2956-2978	ATTTGGTCTCTACCACCAAAACG
2957-2979	TTTGGTCTCTACCACCAAAACGG
2958-2980	TTGGTCTCTACCACCAAAACGGA
2959-2981	TGGTCTCTACCACCAAAACGGAG
2960-2982	GGTCTCTACCACCAAAACGGAGG
2961-2983	GTCTCTACCACCAAAACGGAGGT
2962-2984	TCTCTACCACCAAAACGGAGGTG
2963-2985	CTCTACCACCAAAACGGAGGTGA
2964-2986	TCTACCACCAAAACGGAGGTGAT
2965-2987	CTACCACCAAAACGGAGGTGATC
2966-2988	TACCACCAAAACGGAGGTGATCC
2967-2989	ACCACCAAAACGGAGGTGATCCC
2968-2990	CCACCAAAACGGAGGTGATCCCA
2969-2991	CACCAAAACGGAGGTGATCCCAC
2970-2992	ACCAAAACGGAGGTGATCCACCC
2971-2993	CCAAACGGAGGTGATCCACCT
2972-2994	CAAACGGAGGTGATCCACCTC
2973-2995	AAAACGGAGGTGATCCACCTCT
2974-2996	AAACGGAGGTGATCCACCTCTC
2975-2997	AACGGAGGTGATCCACCTCTCA
2976-2998	ACGGAGGTGATCCACCTCTCAT
2977-2999	CGGAGGTGATCCACCTCTCATT
2978-3000	GGAGGTGATCCACCTCTCATTG
2979-3001	GAGGTGATCCACCTCTCATTGA
2980-3002	AGGTGATCCACCTCTCATTGAG
2981-3003	GGTGATCCACCTCTCATTGAGA
2982-3004	GTGATCCACCTCTCATTGAGAA
2983-3005	TGATCCACCTCTCATTGAGAAC
2984-3006	GATCCACCTCTCATTGAGAACA
2985-3007	ATCCACCTCTCATTGAGAACAG
2986-3008	TCCACCTCTCATTGAGAACAGG
2987-3009	CCCACCTCTCATTGAGAACAGGC
2988-3010	CCACCTCTCATTGAGAACAGGCA
2989-3011	CACCTCTCATTGAGAACAGGCAG
2990-3012	ACCTCTCATTGAGAACAGGCAGT
2991-3013	CCTCTCATTGAGAACAGGCAGTC
2992-3014	CTCTCATTGAGAACAGGCAGTCC
2993-3015	TCTCATTGAGAACAGGCAGTCC
2994-3016	CTCATTGAGAACAGGCAGTCC
2995-3017	TCATTGAGAACAGGCAGTCC
2996-3018	CATTGAGAACAGGCAGTCC
2997-3019	ATTGAGAACAGGCAGTCC
2998-3020	TTGAGAACAGGCAGTCC
2999-3021	TGAGAACAGGCAGTCC
3000-3022	GAGAACAGGCAGTCC
3001-3023	AGAACAGGCAGTCC
3002-3024	GAACAGGCAGTCC
3003-3025	AACAGGCAGTCC
3004-3026	ACAGGCAGTCC
3005-3027	CAGGCAGTCC
3006-3028	AGGCAGTCC
3007-3029	GCAGTCC
3008-3030	GCAGTCC
3009-3031	CAGTCC
3010-3032	AGTCC
3011-3033	GTCC
3012-3034	TCCTGGTCAGTTGCAAGCAAGT

Position	Sequence
3013-3035	CCTGGTCAGTTTGCAAGCAAGTC
3014-3036	CTGGTCAGTTTGCAAGCAAGTCT
3015-3037	TGGTCAGTTTGCAAGCAAGTCTT
3016-3038	GGTCAGTTTGCAAGCAAGTCTTT
3017-3039	GTCAGTTTGCAAGCAAGTCTTTC
3018-3040	TCAGTTTGCAAGCAAGTCTTTCC
3019-3041	CAGTTTGCAAGCAAGTCTTTCCCT
3020-3042	AGTTTGCAAGCAAGTCTTTCCCTG
3021-3043	GTTTGCAAGCAAGTCTTTCCCTGG
3022-3044	TTTGCAAGCAAGTCTTTCCCTGGC
3023-3045	TTGCAAGCAAGTCTTTCCCTGGCC
3024-3046	TGCAAGCAAGTCTTTCCCTGGCCT
3025-3047	GCAAGCAAGTCTTTCCCTGGCCTG
3026-3048	CAAGCAAGTCTTTCCCTGGCCTGA
3027-3049	AAGCAAGTCTTTCCCTGGCCTGAA
3028-3050	AGCAAGTCTTTCCCTGGCCTGAAT
3029-3051	GCAAGTCTTTCCCTGGCCTGAATT
3030-3052	CAAGTCTTTCCCTGGCCTGAATTA
3031-3053	AAGTCTTTCCCTGGCCTGAATTAC
3032-3054	AGTCTTTCCCTGGCCTGAATTACT
3033-3055	GTCTTTCCCTGGCCTGAATTACTG
3034-3056	TCTTTCCCTGGCCTGAATTACTGC
3035-3057	CTTTCCCTGGCCTGAATTACTGCA
3036-3058	TTTCCCTGGCCTGAATTACTGCAC
3037-3059	TTCCCTGGCCTGAATTACTGCACC
3038-3060	TCCTGGCCTGAATTACTGCACCT
3039-3061	CCTGGCCTGAATTACTGCACCTC
3040-3062	CTGGCCTGAATTACTGCACCTCA
3041-3063	TGGCCTGAATTACTGCACCTCAG
3042-3064	GGCCTGAATTACTGCACCTCAGG
3043-3065	GCCTGAATTACTGCACCTCAGGC
3044-3066	CCTGAATTACTGCACCTCAGGCG
3045-3067	CTGAATTACTGCACCTCAGGCGC
3046-3068	TGAATTACTGCACCTCAGGCGCT
3047-3069	GAATTACTGCACCTCAGGCGCTT
3048-3070	AATTACTGCACCTCAGGCGCTTA
3049-3071	ATTACTGCACCTCAGGCGCTTAC
3050-3072	TTACTGCACCTCAGGCGCTTACT
3051-3073	TACTGCACCTCAGGCGCTTACTC
3052-3074	ACTGCACCTCAGGCGCTTACTCC
3053-3075	CTGCACCTCAGGCGCTTACTCCA
3054-3076	TGCACCTCAGGCGCTTACTCCAA
3055-3077	GCACCTCAGGCGCTTACTCCAAC
3056-3078	CACCTCAGGCGCTTACTCCAACG
3057-3079	ACCTCAGGCGCTTACTCCAACGC
3058-3080	CCTCAGGCGCTTACTCCAACGCC
3059-3081	CTCAGGCGCTTACTCCAACGCCA
3060-3082	TCAGGCGCTTACTCCAACGCCAG
3061-3083	CAGGCGCTTACTCCAACGCCAGC
3062-3084	AGGCGCTTACTCCAACGCCAGCT
3063-3085	GGCGCTTACTCCAACGCCAGCTC
3064-3086	GCGCTTACTCCAACGCCAGCTCC
3065-3087	CGCTTACTCCAACGCCAGCTCCA
3066-3088	GCTTACTCCAACGCCAGCTCCAC
3067-3089	CTTACTCCAACGCCAGCTCCACA
3068-3090	TTACTCCAACGCCAGCTCCACAG
3069-3091	TACTCCAACGCCAGCTCCACAGA
3070-3092	ACTCCAACGCCAGCTCCACAGAC
3071-3093	CTCCAACGCCAGCTCCACAGACT
3072-3094	TCCAACGCCAGCTCCACAGACTC
3073-3095	CCAACGCCAGCTCCACAGACTCC
3074-3096	CAACGCCAGCTCCACAGACTCCG
3075-3097	AACGCCAGCTCCACAGACTCCGC
3076-3098	AGCCAGCTCCACAGACTCCGCC
3077-3099	CGCCAGCTCCACAGACTCCGCCCT
3078-3100	GCCAGCTCCACAGACTCCGCCCTC

Position	Sequence
3079-3101	CCAGCTCCACAGACTCCGCCTCC
3080-3102	CAGCTCCACAGACTCCGCCTCCT
3081-3103	AGCTCCACAGACTCCGCCTCCTA
3082-3104	GCTCCACAGACTCCGCCTCCTAC
3083-3105	CTCCACAGACTCCGCCTCCTACT
3084-3106	TCCACAGACTCCGCCTCCTACTA
3085-3107	CCACAGACTCCGCCTCCTACTAT
3086-3108	CACAGACTCCGCCTCCTACTATC
3087-3109	ACAGACTCCGCCTCCTACTATCC
3088-3110	CAGACTCCGCCTCCTACTATCCG
3089-3111	AGACTCCGCCTCCTACTATCCGC
3090-3112	GACTCCGCCTCCTACTATCCGCT
3091-3113	ACTCCGCCTCCTACTATCCGCTG
3092-3114	CTCCGCCTCCTACTATCCGCTGA
3093-3115	TCCGCCTCCTACTATCCGCTGAC
3094-3116	CCGCCTCCTACTATCCGCTGACC
3095-3117	CGCCTCCTACTATCCGCTGACCG
3096-3118	GCCTCCTACTATCCGCTGACCGG
3097-3119	CCTCCTACTATCCGCTGACCGGG
3098-3120	CTCCTACTATCCGCTGACCGGGG
3099-3121	TCCTACTATCCGCTGACCGGGGA
3100-3122	CCTACTATCCGCTGACCGGGGAC
3101-3123	CTACTATCCGCTGACCGGGGACA
3102-3124	TACTATCCGCTGACCGGGGACAC
3103-3125	ACTATCCGCTGACCGGGGACACC
3104-3126	CTATCCGCTGACCGGGGACACCA
3105-3127	TATCCGCTGACCGGGGACACCAG
3106-3128	ATCCGCTGACCGGGGACACCAGA
3107-3129	TCCGCTGACCGGGGACACCAGAT
3108-3130	CCGCTGACCGGGGACACCAGATT
3109-3131	CGCTGACCGGGGACACCAGATTA
3110-3132	GCTGACCGGGGACACCAGATTAG
3111-3133	CTGACCGGGGACACCAGATTAGA
3112-3134	TGACCGGGGACACCAGATTAGAG
3113-3135	GACCGGGGACACCAGATTAGAGC
3114-3136	ACCGGGGACACCAGATTAGAGCT
3115-3137	CCGGGGACACCAGATTAGAGCTG
3116-3138	CGGGGACACCAGATTAGAGCTGG
3117-3139	GGGGACACCAGATTAGAGCTGGA
3118-3140	GGGACACCAGATTAGAGCTGGA
3119-3141	GGACACCAGATTAGAGCTGGAAC
3120-3142	GACACCAGATTAGAGCTGGAAC
3121-3143	ACACCAGATTAGAGCTGGAAC
3122-3144	CACCAGATTAGAGCTGGAAC
3123-3145	ACCAGATTAGAGCTGGAAC
3124-3146	CCAGATTAGAGCTGGAAC
3125-3147	CAGATTAGAGCTGGAAC
3126-3148	AGATTAGAGCTGGAAC
3127-3149	GATTAGAGCTGGAAC
3128-3150	ATTAGAGCTGGAAC
3129-3151	TTAGAGCTGGAAC
3130-3152	TAGAGCTGGAAC
3131-3153	AGAGCTGGAAC
3132-3154	GAGCTGGAAC
3133-3155	AGCTGGAAC
3134-3156	GCTGGAAC
3135-3157	CTGGAAC
3136-3158	TGGAAC
3137-3159	GGAAC
3138-3160	GAAC
3139-3161	AACTGAGGCCTACAGGAGAGAT
3140-3162	ACTGAGGCCTACAGGAGAGATTG
3141-3163	CTGAGGCCTACAGGAGAGATTGA
3142-3164	TGAGGCCTACAGGAGAGATTGAG
3143-3165	GAGGCCTACAGGAGAGATTGAGC
3144-3166	AGGCCTACAGGAGAGATTGAGCA

Position	Sequence
3145-3167	GGCCTACAGGAGAGATTGAGCAG
3146-3168	GCCTACAGGAGAGATTGAGCAGT
3147-3169	CCTACAGGAGAGATTGAGCAGTA
3148-3170	CTACAGGAGAGATTGAGCAGTAT
3149-3171	TACAGGAGAGATTGAGCAGTATT
3150-3172	ACAGGAGAGATTGAGCAGTATTC
3151-3173	CAGGAGAGATTGAGCAGTATTCT
3152-3174	AGGAGAGATTGAGCAGTATTCTG
3153-3175	GGAGAGATTGAGCAGTATTCTGT
3154-3176	GAGAGATTGAGCAGTATTCTGTC
3155-3177	AGAGATTGAGCAGTATTCTGTCA
3156-3178	GAGATTGAGCAGTATTCTGTCCAG
3157-3179	AGATTGAGCAGTATTCTGTCCAGC
3158-3180	GATTGAGCAGTATTCTGTCCAGCG
3159-3181	ATTGAGCAGTATTCTGTCCAGCGC
3160-3182	TTGAGCAGTATTCTGTCCAGCGCA
3161-3183	TGAGCAGTATTCTGTCCAGCGCAA
3162-3184	GAGCAGTATTCTGTCCAGCGCAAC
3163-3185	AGCAGTATTCTGTCCAGCGCAACC
3164-3186	GCAGTATTCTGTCCAGCGCAACCT
3165-3187	CAGTATTCTGTCCAGCGCAACCTA
3166-3188	AGTATTCTGTCCAGCGCAACCTAT
3167-3189	GTATTCTGTCCAGCGCAACCTATG
3168-3190	TATTCTGTCCAGCGCAACCTATGA
3169-3191	ATTCTGTCCAGCGCAACCTATGAG
3170-3192	TTCTGTCCAGCGCAACCTATGAGC
3171-3193	TCTGTCCAGCGCAACCTATGAGCT
3172-3194	CTGTCCAGCGCAACCTATGAGCTC
3173-3195	TGTCCAGCGCAACCTATGAGCTCC
3174-3196	GTCAGCGCAACCTATGAGCTCCA
3175-3197	TCAGCGCAACCTATGAGCTCCAG
3176-3198	CAGCGCAACCTATGAGCTCCAGA
3177-3199	AGCGCAACCTATGAGCTCCAGAG
3178-3200	GCGCAACCTATGAGCTCCAGAGA
3179-3201	CGCAACCTATGAGCTCCAGAGAG
3180-3202	GCAACCTATGAGCTCCAGAGAGA
3181-3203	CAACCTATGAGCTCCAGAGAGAG
3182-3204	AACCTATGAGCTCCAGAGAGAGG
3183-3205	ACCTATGAGCTCCAGAGAGAGGA
3184-3206	CCTATGAGCTCCAGAGAGAGGAC
3185-3207	CTATGAGCTCCAGAGAGAGGACA
3186-3208	TATGAGCTCCAGAGAGAGGACAG
3187-3209	ATGAGCTCCAGAGAGAGGACAGA
3188-3210	TGAGCTCCAGAGAGAGGACAGAG
3189-3211	GAGCTCCAGAGAGAGGACAGAGC
3190-3212	AGCTCCAGAGAGAGGACAGAGCC
3191-3213	GCTCCAGAGAGAGGACAGAGCCT
3192-3214	CTCCAGAGAGAGGACAGAGCCTT
3193-3215	TCCAGAGAGAGGACAGAGCCTTG
3194-3216	CCAGAGAGAGGACAGAGCCTTGG
3195-3217	CAGAGAGAGGACAGAGCCTTGGT
3196-3218	AGAGAGAGGACAGAGCCTTGGTG
3197-3219	GAGAGAGGACAGAGCCTTGGTGG
3198-3220	AGAGAGGACAGAGCCTTGGTGGA
3199-3221	GAGAGGACAGAGCCTTGGTGAT
3200-3222	AGAGGACAGAGCCTTGGTGATA
3201-3223	GAGGACAGAGCCTTGGTGATAC
3202-3224	AGGACAGAGCCTTGGTGATACC
3203-3225	GGACAGAGCCTTGGTGATACCC
3204-3226	GACAGAGCCTTGGTGATACCCT
3205-3227	ACAGAGCCTTGGTGATACCCTG
3206-3228	CAGAGCCTTGGTGATACCCTGA
3207-3229	AGAGCCTTGGTGATACCCTGAA
3208-3230	GAGCCTTGGTGATACCCTGAAG
3209-3231	AGCCTTGGTGATACCCTGAAGT
3210-3232	GCCTTGGTGATACCCTGAAGTT

Position	Sequence
3211-3233	CCTGGTGGATACCCTGAAGTTT
3212-3234	CTTGGTGGATACCCTGAAGTTTG
3213-3235	TTGGTGGATACCCTGAAGTTTGT
3214-3236	TGGTGGATACCCTGAAGTTTGTA
3215-3237	GGTGGATACCCTGAAGTTTGTA
3216-3238	GTGGATACCCTGAAGTTTGTAAC
3217-3239	TGGATACCCTGAAGTTTGTAAC
3218-3240	GGATACCCTGAAGTTTGTAAC
3219-3241	GATACCCTGAAGTTTGTAAC
3220-3242	ATACCCTGAAGTTTGTAAC
3221-3243	TACCCTGAAGTTTGTAAC
3222-3244	ACCCTGAAGTTTGTAAC
3223-3245	CCCTGAAGTTTGTAAC
3224-3246	CCTGAAGTTTGTAAC
3225-3247	CTGAAGTTTGTAAC
3226-3248	TGAAGTTTGTAAC
3227-3249	GAAGTTTGTAAC
3228-3250	AAGTTTGTAAC
3229-3251	AGTTTGTAAC
3230-3252	GTTTGTAAC
3231-3253	TTTGTAAC
3232-3254	TTGTAAC
3233-3255	TGTAAC
3234-3256	GTAAC
3235-3257	TAAC
3236-3258	AACTCAAGCAGAAGGTGCGAAGC
3237-3259	ACTCAAGCAGAAGGTGCGAAGCA
3238-3260	CTCAAGCAGAAGGTGCGAAGCAG
3239-3261	TCAAGCAGAAGGTGCGAAGCAGA
3240-3262	CAAGCAGAAGGTGCGAAGCAGAC
3241-3263	AAGCAGAAGGTGCGAAGCAGACT
3242-3264	AGCAGAAGGTGCGAAGCAGACTG
3243-3265	GCAGAAGGTGCGAAGCAGACTGA
3244-3266	CAGAAGGTGCGAAGCAGACTGAG
3245-3267	AGAAGGTGCGAAGCAGACTGAGG
3246-3268	GAAGGTGCGAAGCAGACTGAGGC
3247-3269	AAGGTGCGAAGCAGACTGAGGCT
3248-3270	AGGTGCGAAGCAGACTGAGGCTA
3249-3271	GGTGCGAAGCAGACTGAGGCTAC
3250-3272	GTGCGAAGCAGACTGAGGCTACC
3251-3273	TGCGAAGCAGACTGAGGCTACCA
3252-3274	GCGAAGCAGACTGAGGCTACCAT
3253-3275	CGAAGCAGACTGAGGCTACCATG
3254-3276	GAAGCAGACTGAGGCTACCATGA
3255-3277	AAGCAGACTGAGGCTACCATGAC
3256-3278	AGCAGACTGAGGCTACCATGACA
3257-3279	GCAGACTGAGGCTACCATGACAT
3258-3280	CAGACTGAGGCTACCATGACATT
3259-3281	AGACTGAGGCTACCATGACATT
3260-3282	GACTGAGGCTACCATGACATTCA
3261-3283	ACTGAGGCTACCATGACATTCAA
3262-3284	CTGAGGCTACCATGACATTCAAA
3263-3285	TGAGGCTACCATGACATTCAAAT
3264-3286	GAGGCTACCATGACATTCAAATA
3265-3287	AGGCTACCATGACATTCAAATAT
3266-3288	GGCTACCATGACATTCAAATATA
3267-3289	GCTACCATGACATTCAAATATAA
3268-3290	CTACCATGACATTCAAATATAAT
3269-3291	TACCATGACATTCAAATATAATC
3270-3292	ACCATGACATTCAAATATAATCG
3271-3293	CCATGACATTCAAATATAATCGG
3272-3294	CATGACATTCAAATATAATCGGC
3273-3295	ATGACATTCAAATATAATCGGCA
3274-3296	TGACATTCAAATATAATCGGCAG
3275-3297	GACATTCAAATATAATCGGCAGA
3276-3298	ACATTCAAATATAATCGGCAGAG

Position	Sequence
3277-3299	CATTCAAATATAATCGGCAGAGT
3278-3300	ATTCAAATATAATCGGCAGAGTA
3279-3301	TTCAAATATAATCGGCAGAGTAT
3280-3302	TCAAATATAATCGGCAGAGTATG
3281-3303	CAAATATAATCGGCAGAGTATGA
3282-3304	AAATATAATCGGCAGAGTATGAC
3283-3305	AATATAATCGGCAGAGTATGACC
3284-3306	ATATAATCGGCAGAGTATGACCT
3285-3307	TATAATCGGCAGAGTATGACCTT
3286-3308	ATAATCGGCAGAGTATGACCTTG
3287-3309	TAATCGGCAGAGTATGACCTTGT
3288-3310	AATCGGCAGAGTATGACCTTGTC
3289-3311	ATCGGCAGAGTATGACCTTGTC
3290-3312	TCGGCAGAGTATGACCTTGCCA
3291-3313	CGGCAGAGTATGACCTTGCCAG
3292-3314	GGCAGAGTATGACCTTGCCAGT
3293-3315	GCAGAGTATGACCTTGCCAGTG
3294-3316	CAGAGTATGACCTTGCCAGTGA
3295-3317	AGAGTATGACCTTGCCAGTGAA
3296-3318	GAGTATGACCTTGCCAGTGAAG
3297-3319	AGTATGACCTTGCCAGTGAAGT
3298-3320	GTATGACCTTGCCAGTGAAGTC
3299-3321	TATGACCTTGCCAGTGAAGTCC
3300-3322	ATGACCTTGCCAGTGAAGTCCA
3301-3323	TGACCTTGCCAGTGAAGTCCAA
3302-3324	GACCTTGCCAGTGAAGTCCAAA
3303-3325	ACCTTGCCAGTGAAGTCCAAAT
3304-3326	CCTTGCCAGTGAAGTCCAAATT
3305-3327	CTTGCCAGTGAAGTCCAAATTC
3306-3328	TTTGCCAGTGAAGTCCAAATTC
3307-3329	TGTCCAGTGAAGTCCAAATTC
3308-3330	GTCCAGTGAAGTCCAAATTC
3309-3331	TCCAGTGAAGTCCAAATTC
3310-3332	CCAGTGAAGTCCAAATTC
3311-3333	CAGTGAAGTCCAAATTC
3312-3334	AGTGAAGTCCAAATTC
3313-3335	GTGAAGTCCAAATTC
3314-3336	TGAAGTCCAAATTC
3315-3337	GAAGTCCAAATTC
3316-3338	AAGTCCAAATTC
3317-3339	AGTCCAAATTC
3318-3340	GTCCAAATTC
3319-3341	TCCAAATTC
3320-3342	CCAAATTC
3321-3343	CAAATTC
3322-3344	AAATTC
3323-3345	AATTC
3324-3346	ATTTC
3325-3347	TTC
3326-3348	TCC
3327-3349	CCG
3328-3350	CGG
3329-3351	GGA
3330-3352	GATT
3331-3353	ATTT
3332-3354	TTTT
3333-3355	TTTG
3334-3356	TTGAT
3335-3357	TGATG
3336-3358	GATGTT
3337-3359	ATGTT
3338-3360	TGTT
3339-3361	GTT
3340-3362	TTG
3341-3363	TG
3342-3364	G

Position	Sequence
3343-3365	ACCTCGGAACAATCCTCAGAGTT
3344-3366	CCTCGGAACAATCCTCAGAGTTA
3345-3367	CTCGGAACAATCCTCAGAGTTAA
3346-3368	TCGGAACAATCCTCAGAGTTAAT
3347-3369	CGGAACAATCCTCAGAGTTAATG
3348-3370	GGAACAATCCTCAGAGTTAATGA
3349-3371	GAACAATCCTCAGAGTTAATGAT
3350-3372	AACAATCCTCAGAGTTAATGATG
3351-3373	ACAATCCTCAGAGTTAATGATGA
3352-3374	CAATCCTCAGAGTTAATGATGAA
3353-3375	AATCCTCAGAGTTAATGATGAAT
3354-3376	ATCCTCAGAGTTAATGATGAATC
3355-3377	TCCTCAGAGTTAATGATGAATCT
3356-3378	CCTCAGAGTTAATGATGAATCTA
3357-3379	CTCAGAGTTAATGATGAATCTAC
3358-3380	TCAGAGTTAATGATGAATCTACT
3359-3381	CAGAGTTAATGATGAATCTACTG
3360-3382	AGAGTTAATGATGAATCTACTGA
3361-3383	GAGTTAATGATGAATCTACTGAG
3362-3384	AGTTAATGATGAATCTACTGAGG
3363-3385	GTTAATGATGAATCTACTGAGGG
3364-3386	TTAATGATGAATCTACTGAGGGC
3365-3387	TAATGATGAATCTACTGAGGGCA
3366-3388	AATGATGAATCTACTGAGGGCAA
3367-3389	ATGATGAATCTACTGAGGGCAAA
3368-3390	TGATGAATCTACTGAGGGCAAAA
3369-3391	GATGAATCTACTGAGGGCAAAAC
3370-3392	ATGAATCTACTGAGGGCAAAACG
3371-3393	TGAATCTACTGAGGGCAAAACGT
3372-3394	GAATCTACTGAGGGCAAAACGTC
3373-3395	AATCTACTGAGGGCAAAACGTCT
3374-3396	ATCTACTGAGGGCAAAACGTCTT
3375-3397	TCTACTGAGGGCAAAACGTCTTA
3376-3398	CTACTGAGGGCAAAACGTCTTAC
3377-3399	TACTGAGGGCAAAACGTCTTACA
3378-3400	ACTGAGGGCAAAACGTCTTACAG
3379-3401	CTGAGGGCAAAACGTCTTACAGA
3380-3402	TGAGGGCAAAACGTCTTACAGAC
3381-3403	GAGGGCAAAACGTCTTACAGACT
3382-3404	AGGGCAAAACGTCTTACAGACTC
3383-3405	GGGCAAAACGTCTTACAGACTCA
3384-3406	GGCAAAACGTCTTACAGACTCAC
3385-3407	GCAAAACGTCTTACAGACTCACC
3386-3408	CAAAACGTCTTACAGACTCACCC
3387-3409	AAAACGTCTTACAGACTCACCCCT
3388-3410	AAACGTCTTACAGACTCACCCCTG
3389-3411	AACGTCTTACAGACTCACCCCTGG
3390-3412	ACGTCTTACAGACTCACCCCTGGA
3391-3413	CGTCTTACAGACTCACCCCTGGAC
3392-3414	GTCTTACAGACTCACCCCTGGACA
3393-3415	TCTTACAGACTCACCCCTGGACAT
3394-3416	CTTACAGACTCACCCCTGGACATT
3395-3417	TTACAGACTCACCCCTGGACATTC
3396-3418	TACAGACTCACCCCTGGACATTCA
3397-3419	ACAGACTCACCCCTGGACATTTCAG
3398-3420	CAGACTCACCCCTGGACATTTCAGA
3399-3421	AGACTCACCCCTGGACATTTCAGAA
3400-3422	GACTCACCCCTGGACATTTCAGAAC
3401-3423	ACTCACCCCTGGACATTTCAGAACA
3402-3424	CTCACCCCTGGACATTTCAGAACAA
3403-3425	TCACCCCTGGACATTTCAGAACAAG
3404-3426	CACCCCTGGACATTTCAGAACAAGA
3405-3427	ACCCTGGACATTTCAGAACAAGAA
3406-3428	CCCTGGACATTTCAGAACAAGAAA
3407-3429	CCTGGACATTTCAGAACAAGAAAA
3408-3430	CTGGACATTTCAGAACAAGAAAAAT

Position	Sequence
3409-3431	TGGACATTCAGAACAAGAAAATT
3410-3432	GGACATTCAGAACAAGAAAATTA
3411-3433	GACATTCAGAACAAGAAAATTAC
3412-3434	ACATTCAGAACAAGAAAATTACT
3413-3435	CATTCAGAACAAGAAAATTACTG
3414-3436	ATTCAGAACAAGAAAATTACTGA
3415-3437	TTCAGAACAAGAAAATTACTGAG
3416-3438	TCAGAACAAGAAAATTACTGAGG
3417-3439	CAGAACAAGAAAATTACTGAGGT
3418-3440	AGAACAAGAAAATTACTGAGGTC
3419-3441	GAACAAGAAAATTACTGAGGTCG
3420-3442	AACAAGAAAATTACTGAGGTCGC
3421-3443	ACAAGAAAATTACTGAGGTCGCC
3422-3444	CAAGAAAATTACTGAGGTCGCC
3423-3445	AAGAAAATTACTGAGGTCGCCCT
3424-3446	AGAAAATTACTGAGGTCGCCCTC
3425-3447	GAAAATTACTGAGGTCGCCCTCA
3426-3448	AAAATTACTGAGGTCGCCCTCAT
3427-3449	AAATTACTGAGGTCGCCCTCATG
3428-3450	AATTACTGAGGTCGCCCTCATGG
3429-3451	ATTACTGAGGTCGCCCTCATGGG
3430-3452	TTACTGAGGTCGCCCTCATGGGC
3431-3453	TACTGAGGTCGCCCTCATGGGCC
3432-3454	ACTGAGGTCGCCCTCATGGGCCA
3433-3455	CTGAGGTCGCCCTCATGGGCCAC
3434-3456	TGAGGTCGCCCTCATGGGCCACC
3435-3457	GAGGTCGCCCTCATGGGCCACCT
3436-3458	AGGTCGCCCTCATGGGCCACCTA
3437-3459	GGTCGCCCTCATGGGCCACCTAA
3438-3460	GTCGCCCTCATGGGCCACCTAAG
3439-3461	TGCCCTCATGGGCCACCTAAGT
3440-3462	CGCCCTCATGGGCCACCTAAGTT
3441-3463	GCCCTCATGGGCCACCTAAGTTG
3442-3464	CCCTCATGGGCCACCTAAGTTGT
3443-3465	CCTCATGGGCCACCTAAGTTGTG
3444-3466	CTCATGGGCCACCTAAGTTGTGA
3445-3467	TCATGGGCCACCTAAGTTGTGAC
3446-3468	CATGGGCCACCTAAGTTGTGACA
3447-3469	ATGGGCCACCTAAGTTGTGACAC
3448-3470	TGGGCCACCTAAGTTGTGACACA
3449-3471	GGGCCACCTAAGTTGTGACACAA
3450-3472	GGCCACCTAAGTTGTGACACAAA
3451-3473	GCCACCTAAGTTGTGACACAAAG
3452-3474	CCACCTAAGTTGTGACACAAAGG
3453-3475	CACCTAAGTTGTGACACAAAGGA
3454-3476	ACCTAAGTTGTGACACAAAGGAA
3455-3477	CCTAAGTTGTGACACAAAGGAAG
3456-3478	CTAAGTTGTGACACAAAGGAAGA
3457-3479	TAAGTTGTGACACAAAGGAAGAA
3458-3480	AAGTTGTGACACAAAGGAAGAAA
3459-3481	AGTTGTGACACAAAGGAAGAAAG
3460-3482	GTGTGACACAAAGGAAGAAAGA
3461-3483	TTGTGACACAAAGGAAGAAAGAA
3462-3484	TGTGACACAAAGGAAGAAAGAAA
3463-3485	GTGACACAAAGGAAGAAAGAAAA
3464-3486	TGACACAAAGGAAGAAAGAAAAA
3465-3487	GACACAAAGGAAGAAAGAAAAAT
3466-3488	ACACAAAGGAAGAAAGAAAAATC
3467-3489	CACAAAGGAAGAAAGAAAAATCA
3468-3490	ACAAAGGAAGAAAGAAAAATCAA
3469-3491	CAAAGGAAGAAAGAAAAATCAAG
3470-3492	AAAGGAAGAAAGAAAAATCAAGG
3471-3493	AAGGAAGAAAGAAAAATCAAGGG
3472-3494	AGGAAGAAAGAAAAATCAAGGGT
3473-3495	GGAAGAAAGAAAAATCAAGGGTG
3474-3496	GAAGAAAGAAAAATCAAGGGTGT

Position	Sequence
3475-3497	AAGAAAGAAAAATCAAGGGTGT
3476-3498	AGAAAGAAAAATCAAGGGTGTTA
3477-3499	GAAAGAAAAATCAAGGGTGTAT
3478-3500	AAAGAAAAATCAAGGGTGTATT
3479-3501	AAGAAAAATCAAGGGTGTATTT
3480-3502	AGAAAAATCAAGGGTGTATTTT
3481-3503	GAAAAATCAAGGGTGTATTTCC
3482-3504	AAAAATCAAGGGTGTATTTCCA
3483-3505	AAAATCAAGGGTGTATTTCCAT
3484-3506	AAATCAAGGGTGTATTTCCATA
3485-3507	AATCAAGGGTGTATTTCCATAC
3486-3508	ATCAAGGGTGTATTTCCATACC
3487-3509	TCAAGGGTGTATTTCCATACCC
3488-3510	CAAGGGTGTATTTCCATACCCC
3489-3511	AAGGGTGTATTTCCATACCCCG
3490-3512	AGGGTGTATTTCCATACCCCGT
3491-3513	GGGTGTATTTCCATACCCCGTT
3492-3514	GGTGTATTTCCATACCCCGTTT
3493-3515	GTGTATTTCCATACCCCGTTTG
3494-3516	TGTATTTCCATACCCCGTTTGC
3495-3517	GTTATTTCCATACCCCGTTTGCA
3496-3518	TTATTTCCATACCCCGTTTGCAA
3497-3519	TATTTCCATACCCCGTTTGCAAG
3498-3520	ATTTCCATACCCCGTTTGCAAGC
3499-3521	TTTCCATACCCCGTTTGCAAGCA
3500-3522	TTCCATACCCCGTTTGCAAGCAG
3501-3523	TCCATACCCCGTTTGCAAGCAGA
3502-3524	CCATACCCCGTTTGCAAGCAGAA
3503-3525	CATACCCCGTTTGCAAGCAGAAG
3504-3526	ATACCCCGTTTGCAAGCAGAAGC
3505-3527	TACCCCGTTTGCAAGCAGAAGCC
3506-3528	ACCCCGTTTGCAAGCAGAAGCCA
3507-3529	CCCCGTTTGCAAGCAGAAGCCAG
3508-3530	CCCGTTTGCAAGCAGAAGCCAGA
3509-3531	CCGTTTGCAAGCAGAAGCCAGAA
3510-3532	CGTTTGCAAGCAGAAGCCAGAAG
3511-3533	GTTTGCAAGCAGAAGCCAGAAGT
3512-3534	TTTGCAAGCAGAAGCCAGAAGTG
3513-3535	TTGCAAGCAGAAGCCAGAAGTGA
3514-3536	TGCAAGCAGAAGCCAGAAGTGAG
3515-3537	GCAAGCAGAAGCCAGAAGTGAGA
3516-3538	CAAGCAGAAGCCAGAAGTGAGAT
3517-3539	AAGCAGAAGCCAGAAGTGAGATC
3518-3540	AGCAGAAGCCAGAAGTGAGATCC
3519-3541	GCAGAAGCCAGAAGTGAGATCCT
3520-3542	CAGAAGCCAGAAGTGAGATCCTC
3521-3543	AGAAGCCAGAAGTGAGATCCTCG
3522-3544	GAAGCCAGAAGTGAGATCCTCGC
3523-3545	AAGCCAGAAGTGAGATCCTCGCC
3524-3546	AGCCAGAAGTGAGATCCTCGCCC
3525-3547	GCCAGAAGTGAGATCCTCGCCCA
3526-3548	CCAGAAGTGAGATCCTCGCCCAC
3527-3549	CAGAAGTGAGATCCTCGCCCACT
3528-3550	AGAAGTGAGATCCTCGCCCACTG
3529-3551	GAAGTGAGATCCTCGCCCACTGG
3530-3552	AAGTGAGATCCTCGCCCACTGGT
3531-3553	AGTGAGATCCTCGCCCACTGGTC
3532-3554	GTGAGATCCTCGCCCACTGGTCG
3533-3555	TGAGATCCTCGCCCACTGGTCGC
3534-3556	GAGATCCTCGCCCACTGGTCGCC
3535-3557	AGATCCTCGCCCACTGGTCGCCT
3536-3558	GATCCTCGCCCACTGGTCGCCTG
3537-3559	ATCCTCGCCCACTGGTCGCCTGC
3538-3560	TCCTCGCCCACTGGTCGCCTGCC
3539-3561	CCTCGCCCACTGGTCGCCTGCCA
3540-3562	CTCGCCCACTGGTCGCCTGCCAA

Position	Sequence
3541-3563	TCGCCACTGGTCGCCTGCCAAA
3542-3564	CGCCCACTGGTCGCCTGCCAAAC
3543-3565	GCCCACTGGTCGCCTGCCAAACT
3544-3566	CCCACTGGTCGCCTGCCAAACTG
3545-3567	CCACTGGTCGCCTGCCAAACTGC
3546-3568	CACTGGTCGCCTGCCAAACTGCT
3547-3569	ACTGGTCGCCTGCCAAACTGCTT
3548-3570	CTGGTCGCCTGCCAAACTGCTTC
3549-3571	TGGTCGCCTGCCAAACTGCTTCT
3550-3572	GGTCGCCTGCCAAACTGCTTCTC
3551-3573	GTCGCCTGCCAAACTGCTTCTCC
3552-3574	TCGCCTGCCAAACTGCTTCTCCA
3553-3575	CGCCTGCCAAACTGCTTCTCCAA
3554-3576	GCCTGCCAAACTGCTTCTCCAAA
3555-3577	CCTGCCAAACTGCTTCTCCAAAT
3556-3578	CTGCCAAACTGCTTCTCCAAATG
3557-3579	TGCCAAACTGCTTCTCCAAATGG
3558-3580	GCCAAACTGCTTCTCCAAATGGA
3559-3581	CCAAACTGCTTCTCCAAATGGAC
3560-3582	CAAAGCTTCTCCAAATGGACT
3561-3583	AAAGCTTCTCCAAATGGACTC
3562-3584	AACTGCTTCTCCAAATGGACTCA
3563-3585	ACTGCTTCTCCAAATGGACTCAT
3564-3586	CTGCTTCTCCAAATGGACTCATC
3565-3587	TGCTTCTCCAAATGGACTCATCT
3566-3588	GCTTCTCCAAATGGACTCATCTG
3567-3589	CTTCTCCAAATGGACTCATCTGC
3568-3590	TTCTCCAAATGGACTCATCTGCT
3569-3591	TCTCCAAATGGACTCATCTGCTA
3570-3592	CTCCAAATGGACTCATCTGCTAC
3571-3593	TCCAAATGGACTCATCTGCTACA
3572-3594	CCAAATGGACTCATCTGCTACAG
3573-3595	CAAATGGACTCATCTGCTACAGC
3574-3596	AAATGGACTCATCTGCTACAGCT
3575-3597	AATGGACTCATCTGCTACAGCTT
3576-3598	ATGGACTCATCTGCTACAGCTTA
3577-3599	TGGACTCATCTGCTACAGCTTAT
3578-3600	GGACTCATCTGCTACAGCTTATG
3579-3601	GACTCATCTGCTACAGCTTATGG
3580-3602	ACTCATCTGCTACAGCTTATGGC
3581-3603	CTCATCTGCTACAGCTTATGGCT
3582-3604	TCATCTGCTACAGCTTATGGCTC
3583-3605	CATCTGCTACAGCTTATGGCTCC
3584-3606	ATCTGCTACAGCTTATGGCTCCA
3585-3607	TCTGCTACAGCTTATGGCTCCAC
3586-3608	CTGCTACAGCTTATGGCTCCACA
3587-3609	TGCTACAGCTTATGGCTCCACAG
3588-3610	GCTACAGCTTATGGCTCCACAGT
3589-3611	CTACAGCTTATGGCTCCACAGTT
3590-3612	TACAGCTTATGGCTCCACAGTTT
3591-3613	ACAGCTTATGGCTCCACAGTTTC
3592-3614	CAGCTTATGGCTCCACAGTTTCC
3593-3615	AGCTTATGGCTCCACAGTTTCCA
3594-3616	GCTTATGGCTCCACAGTTTCCAA
3595-3617	CTTATGGCTCCACAGTTTCCAAG
3596-3618	TTATGGCTCCACAGTTTCCAAGA
3597-3619	TATGGCTCCACAGTTTCCAAGAG
3598-3620	ATGGCTCCACAGTTTCCAAGAGG
3599-3621	TGGCTCCACAGTTTCCAAGAGGG
3600-3622	GGCTCCACAGTTTCCAAGAGGGT
3601-3623	GCTCCACAGTTTCCAAGAGGGTG
3602-3624	CTCCACAGTTTCCAAGAGGGTGG
3603-3625	TCCACAGTTTCCAAGAGGGTGGC
3604-3626	CCACAGTTTCCAAGAGGGTGGCA
3605-3627	CACAGTTTCCAAGAGGGTGGCAT
3606-3628	ACAGTTTCCAAGAGGGTGGCATG

Position	Sequence
3607-3629	CAGTTTCCAAGAGGGTGGCATGG
3608-3630	AGTTTCCAAGAGGGTGGCATGGC
3609-3631	GTTTCCAAGAGGGTGGCATGGCA
3610-3632	TTTCCAAGAGGGTGGCATGGCAT
3611-3633	TTCCAAGAGGGTGGCATGGCATT
3612-3634	TCCAAGAGGGTGGCATGGCATT
3613-3635	CCAAGAGGGTGGCATGGCATTAT
3614-3636	CAAGAGGGTGGCATGGCATTATG
3615-3637	AAGAGGGTGGCATGGCATTATGA
3616-3638	AGAGGGTGGCATGGCATTATGAT
3617-3639	GAGGGTGGCATGGCATTATGATG
3618-3640	AGGGTGGCATGGCATTATGATGA
3619-3641	GGGTGGCATGGCATTATGATGAA
3620-3642	GGTGGCATGGCATTATGATGAAG
3621-3643	GTGGCATGGCATTATGATGAAGA
3622-3644	TGGCATGGCATTATGATGAAGAG
3623-3645	GGCATGGCATTATGATGAAGAGA
3624-3646	GCCATGGCATTATGATGAAGAGAA
3625-3647	CATGGCATTATGATGAAGAGAAG
3626-3648	ATGGCATTATGATGAAGAGAAGA
3627-3649	TGGCATTATGATGAAGAGAAGAT
3628-3650	GGCATTATGATGAAGAGAAGATT
3629-3651	GCATTATGATGAAGAGAAGATTG
3630-3652	CATTATGATGAAGAGAAGATTGA
3631-3653	ATTATGATGAAGAGAAGATTGAA
3632-3654	TTATGATGAAGAGAAGATTGAAT
3633-3655	TATGATGAAGAGAAGATTGAATT
3634-3656	ATGATGAAGAGAAGATTGAATTT
3635-3657	TGATGAAGAGAAGATTGAATTTG
3636-3658	GATGAAGAGAAGATTGAATTTGA
3637-3659	ATGAAGAGAAGATTGAATTTGAA
3638-3660	TGAAGAGAAGATTGAATTTGAAT
3639-3661	GAAGAGAAGATTGAATTTGAATG
3640-3662	AAGAGAAGATTGAATTTGAATGG
3641-3663	AGAGAAGATTGAATTTGAATGGA
3642-3664	GAGAAGATTGAATTTGAATGGAA
3643-3665	AGAAGATTGAATTTGAATGGAAC
3644-3666	GAAGATTGAATTTGAATGGAAACA
3645-3667	AAGATTGAATTTGAATGGAAACAC
3646-3668	AGATTGAATTTGAATGGAAACACA
3647-3669	GATTGAATTTGAATGGAAACACAG
3648-3670	ATTGAATTTGAATGGAAACACAGG
3649-3671	TTGAATTTGAATGGAAACACAGGC
3650-3672	TGAATTTGAATGGAAACACAGGCCA
3651-3673	GAATTTGAATGGAAACACAGGCAC
3652-3674	AATTTGAATGGAAACACAGGCACC
3653-3675	ATTTGAATGGAAACACAGGCACCA
3654-3676	TTTGAATGGAAACACAGGCACCAA
3655-3677	TTGAATGGAAACACAGGCACCAAT
3656-3678	TGAATGGAAACACAGGCACCAATG
3657-3679	GAATGGAAACACAGGCACCAATGT
3658-3680	AATGGAAACACAGGCACCAATGTA
3659-3681	ATGGAAACACAGGCACCAATGTAG
3660-3682	TGGAAACACAGGCACCAATGTAGA
3661-3683	GGAACACAGGCACCAATGTAGAT
3662-3684	GAACACAGGCACCAATGTAGATA
3663-3685	AACACAGGCACCAATGTAGATAC
3664-3686	ACACAGGCACCAATGTAGATACC
3665-3687	CACAGGCACCAATGTAGATACCA
3666-3688	ACAGGCACCAATGTAGATACCAA
3667-3689	CAGGCACCAATGTAGATACCAAA
3668-3690	AGGCACCAATGTAGATACCAAAA
3669-3691	GGCACCAATGTAGATACCAAAAA
3670-3692	GCACCAATGTAGATACCAAAAAA
3671-3693	CACCAATGTAGATACCAAAAAAA
3672-3694	ACCAATGTAGATACCAAAAAAAT

Position	Sequence
3673-3695	CCAATGTAGATACCAAAAAAATG
3674-3696	CAATGTAGATACCAAAAAAATGA
3675-3697	AATGTAGATACCAAAAAAATGAC
3676-3698	ATGTAGATACCAAAAAAATGACT
3677-3699	TGTAGATACCAAAAAAATGACTT
3678-3700	GTAGATACCAAAAAAATGACTTC
3679-3701	TAGATACCAAAAAAATGACTTCC
3680-3702	AGATACCAAAAAAATGACTTCCA
3681-3703	GATACCAAAAAAATGACTTCCAA
3682-3704	ATACCAAAAAAATGACTTCCAAT
3683-3705	TACCAAAAAAATGACTTCCAATT
3684-3706	ACCAAAAAAATGACTTCCAATTT
3685-3707	CCAAAAAATGACTTCCAATTTTC
3686-3708	CAAAAAAATGACTTCCAATTTCC
3687-3709	AAAAAATGACTTCCAATTTCCC
3688-3710	AAAAAATGACTTCCAATTTCCCT
3689-3711	AAAAATGACTTCCAATTTCCCTG
3690-3712	AAAATGACTTCCAATTTCCCTGT
3691-3713	AAATGACTTCCAATTTCCCTGTG
3692-3714	AATGACTTCCAATTTCCCTGTGG
3693-3715	ATGACTTCCAATTTCCCTGTGGA
3694-3716	TGACTTCCAATTTCCCTGTGGAT
3695-3717	GACTTCCAATTTCCCTGTGGATC
3696-3718	ACTTCCAATTTCCCTGTGGATCT
3697-3719	CTTCCAATTTCCCTGTGGATCTC
3698-3720	TTCCAATTTCCCTGTGGATCTCT
3699-3721	TCCAATTTCCCTGTGGATCTCTC
3700-3722	CCAATTTCCCTGTGGATCTCTCC
3701-3723	CAATTTCCCTGTGGATCTCTCCG
3702-3724	AATTTCCCTGTGGATCTCTCCGA
3703-3725	ATTTCCCTGTGGATCTCTCCGAT
3704-3726	TTCCCTGTGGATCTCTCCGATT
3705-3727	TTCCCTGTGGATCTCTCCGATTA
3706-3728	TCCCTGTGGATCTCTCCGATTAT
3707-3729	CCCTGTGGATCTCTCCGATTATC
3708-3730	CCTGTGGATCTCTCCGATTATCC
3709-3731	CTGTGGATCTCTCCGATTATCCT
3710-3732	TGTGGATCTCTCCGATTATCCTA
3711-3733	GTGGATCTCTCCGATTATCCTAA
3712-3734	TGGATCTCTCCGATTATCCTAAG
3713-3735	GGATCTCTCCGATTATCCTAAGA
3714-3736	GATCTCTCCGATTATCCTAAGAG
3715-3737	ATCTCTCCGATTATCCTAAGAGC
3716-3738	TCTCTCCGATTATCCTAAGAGCT
3717-3739	CTCTCCGATTATCCTAAGAGCTT
3718-3740	TCTCCGATTATCCTAAGAGCTTG
3719-3741	CTCCGATTATCCTAAGAGCTTGC
3720-3742	TCCGATTATCCTAAGAGCTTGCA
3721-3743	CCGATTATCCTAAGAGCTTGCAAT
3722-3744	CGATTATCCTAAGAGCTTGCAATA
3723-3745	GATTATCCTAAGAGCTTGCAATAT
3724-3746	ATTATCCTAAGAGCTTGCAATATG
3725-3747	TTATCCTAAGAGCTTGCAATATGT
3726-3748	TATCCTAAGAGCTTGCAATATGTA
3727-3749	ATCCTAAGAGCTTGCAATATGTAT
3728-3750	TCCTAAGAGCTTGCAATATGTATG
3729-3751	CCTAAGAGCTTGCAATATGTATGC
3730-3752	CTAAGAGCTTGCAATATGTATGCT
3731-3753	TAAGAGCTTGCAATATGTATGCTA
3732-3754	AAGAGCTTGCAATATGTATGCTAA
3733-3755	AGAGCTTGCAATATGTATGCTAAT
3734-3756	GAGCTTGCAATATGTATGCTAATA
3735-3757	AGCTTGCAATATGTATGCTAATAG
3736-3758	GCTTGCAATATGTATGCTAATAGA
3737-3759	CTTGCAATATGTATGCTAATAGAC
3738-3760	TTGCAATATGTATGCTAATAGACT

Position	Sequence
3739-3761	TGCATATGTATGCTAATAGACTC
3740-3762	GCATATGTATGCTAATAGACTCC
3741-3763	CATATGTATGCTAATAGACTCCT
3742-3764	ATATGTATGCTAATAGACTCCTG
3743-3765	TATGTATGCTAATAGACTCCTGG
3744-3766	ATGTATGCTAATAGACTCCTGGA
3745-3767	TGTATGCTAATAGACTCCTGGAT
3746-3768	GTATGCTAATAGACTCCTGGATC
3747-3769	TATGCTAATAGACTCCTGGATCA
3748-3770	ATGCTAATAGACTCCTGGATCAC
3749-3771	TGCTAATAGACTCCTGGATCACA
3750-3772	GCTAATAGACTCCTGGATCACAG
3751-3773	CTAATAGACTCCTGGATCACAGA
3752-3774	TAATAGACTCCTGGATCACAGAG
3753-3775	AATAGACTCCTGGATCACAGAGT
3754-3776	ATAGACTCCTGGATCACAGAGTC
3755-3777	TAGACTCCTGGATCACAGAGTCC
3756-3778	AGACTCCTGGATCACAGAGTCCC
3757-3779	GACTCCTGGATCACAGAGTCCCT
3758-3780	ACTCCTGGATCACAGAGTCCCTG
3759-3781	CTCCTGGATCACAGAGTCCCTGA
3760-3782	TCCTGGATCACAGAGTCCCTGAA
3761-3783	CCTGGATCACAGAGTCCCTGAAA
3762-3784	CTGGATCACAGAGTCCCTGAAAC
3763-3785	TGGATCACAGAGTCCCTGAAACA
3764-3786	GGATCACAGAGTCCCTGAAACAG
3765-3787	GATCACAGAGTCCCTGAAACAGA
3766-3788	ATCACAGAGTCCCTGAAACAGAC
3767-3789	TCACAGAGTCCCTGAAACAGACA
3768-3790	CACAGAGTCCCTGAAACAGACAT
3769-3791	ACAGAGTCCCTGAAACAGACATG
3770-3792	CAGAGTCCCTGAAACAGACATGA
3771-3793	AGAGTCCCTGAAACAGACATGAC
3772-3794	GAGTCCCTGAAACAGACATGACT
3773-3795	AGTCCCTGAAACAGACATGACTT
3774-3796	GTCCCTGAAACAGACATGACTTT
3775-3797	TCCCTGAAACAGACATGACTTTC
3776-3798	CCCTGAAACAGACATGACTTTCC
3777-3799	CCTGAAACAGACATGACTTTCCG
3778-3800	CTGAAACAGACATGACTTTCCGG
3779-3801	TGAAACAGACATGACTTTCCGGC
3780-3802	GAAACAGACATGACTTTCCGGCA
3781-3803	AAACAGACATGACTTTCCGGCAC
3782-3804	AACAGACATGACTTTCCGGCACG
3783-3805	ACAGACATGACTTTCCGGCACGT
3784-3806	CAGACATGACTTTCCGGCACGTG
3785-3807	AGACATGACTTTCCGGCACGTGG
3786-3808	GACATGACTTTCCGGCACGTGGG
3787-3809	ACATGACTTTCCGGCACGTGGGT
3788-3810	CATGACTTTCCGGCACGTGGGTT
3789-3811	ATGACTTTCCGGCACGTGGGTTT
3790-3812	TGACTTTCCGGCACGTGGGTTCC
3791-3813	GACTTTCCGGCACGTGGGTTCCA
3792-3814	ACTTTCCGGCACGTGGGTTCCAA
3793-3815	CTTTCCGGCACGTGGGTTCCAAA
3794-3816	TTTCCGGCACGTGGGTTCCAAAT
3795-3817	TCCGGCACGTGGGTTCCAAATT
3796-3818	TCCGGCACGTGGGTTCCAAATTA
3797-3819	CCGGCACGTGGGTTCCAAATTAA
3798-3820	CGGCACGTGGGTTCCAAATTAAT
3799-3821	GGCACGTGGGTTCCAAATTAATA
3800-3822	GCACGTGGGTTCCAAATTAATAG
3801-3823	CACGTGGGTTCCAAATTAATAGT
3802-3824	ACGTGGGTTCCAAATTAATAGTT
3803-3825	CGTGGGTTCCAAATTAATAGTTG
3804-3826	GTGGGTTCCAAATTAATAGTTGC

Position	Sequence
3805-3827	TGGGTCCAAATTAATAGTTGCA
3806-3828	GGGTCCAAATTAATAGTTGCAA
3807-3829	GGTCCAAATTAATAGTTGCAAT
3808-3830	GTTCCAAATTAATAGTTGCAATG
3809-3831	TTCCAAATTAATAGTTGCAATGA
3810-3832	TCCAAATTAATAGTTGCAATGAG
3811-3833	CCAAATTAATAGTTGCAATGAGC
3812-3834	CAAATTAATAGTTGCAATGAGCT
3813-3835	AAATTAATAGTTGCAATGAGCTC
3814-3836	AATTAATAGTTGCAATGAGCTCA
3815-3837	ATTAATAGTTGCAATGAGCTCAT
3816-3838	TTAATAGTTGCAATGAGCTCATG
3817-3839	TAATAGTTGCAATGAGCTCATGG
3818-3840	AATAGTTGCAATGAGCTCATGGC
3819-3841	ATAGTTGCAATGAGCTCATGGCT
3820-3842	TAGTTGCAATGAGCTCATGGCTT
3821-3843	AGTTGCAATGAGCTCATGGCTTC
3822-3844	GTTGCAATGAGCTCATGGCTTCA
3823-3845	TTGCAATGAGCTCATGGCTTCAG
3824-3846	TGCAATGAGCTCATGGCTTCAGA
3825-3847	GCAATGAGCTCATGGCTTCAGAA
3826-3848	CAATGAGCTCATGGCTTCAGAAG
3827-3849	AATGAGCTCATGGCTTCAGAAGG
3828-3850	ATGAGCTCATGGCTTCAGAAGGC
3829-3851	TGAGCTCATGGCTTCAGAAGGCA
3830-3852	GAGCTCATGGCTTCAGAAGGCAT
3831-3853	AGCTCATGGCTTCAGAAGGCATC
3832-3854	GCTCATGGCTTCAGAAGGCATCT
3833-3855	CTCATGGCTTCAGAAGGCATCTG
3834-3856	TCATGGCTTCAGAAGGCATCTGG
3835-3857	CATGGCTTCAGAAGGCATCTGGG
3836-3858	ATGGCTTCAGAAGGCATCTGGGA
3837-3859	TGGCTTCAGAAGGCATCTGGGAG
3838-3860	GGCTTCAGAAGGCATCTGGGAGT
3839-3861	GCTTCAGAAGGCATCTGGGAGTC
3840-3862	CTTCAGAAGGCATCTGGGAGTCT
3841-3863	TTCAGAAGGCATCTGGGAGTCTT
3842-3864	TCAGAAGGCATCTGGGAGTCTTC
3843-3865	CAGAAGGCATCTGGGAGTCTTCC
3844-3866	AGAAGGCATCTGGGAGTCTTCCT
3845-3867	GAAGGCATCTGGGAGTCTTCCTT
3846-3868	AAGGCATCTGGGAGTCTTCCTTA
3847-3869	AGGCATCTGGGAGTCTTCCTTAT
3848-3870	GGCATCTGGGAGTCTTCCTTATA
3849-3871	GCATCTGGGAGTCTTCCTTATAC
3850-3872	CATCTGGGAGTCTTCCTTATACC
3851-3873	ATCTGGGAGTCTTCCTTATACCC
3852-3874	TCTGGGAGTCTTCCTTATACCCA
3853-3875	CTGGGAGTCTTCCTTATACCCAG
3854-3876	TGGGAGTCTTCCTTATACCCAGA
3855-3877	GGGAGTCTTCCTTATACCCAGAC
3856-3878	GGAGTCTTCCTTATACCCAGACT
3857-3879	GAGTCTTCCTTATACCCAGACTT
3858-3880	AGTCTTCCTTATACCCAGACTTT
3859-3881	GTCTTCCTTATACCCAGACTTTG
3860-3882	TCTTCCTTATACCCAGACTTTGC
3861-3883	CTTCCTTATACCCAGACTTTGCA
3862-3884	TTCTTATACCCAGACTTTGCAA
3863-3885	TCCTTATACCCAGACTTTGCAAG
3864-3886	CCTTATACCCAGACTTTGCAAGA
3865-3887	CTTATACCCAGACTTTGCAAGAC
3866-3888	TTATACCCAGACTTTGCAAGACC
3867-3889	TATACCCAGACTTTGCAAGACCA
3868-3890	ATACCCAGACTTTGCAAGACCAC
3869-3891	TACCCAGACTTTGCAAGACCACC
3870-3892	ACCCAGACTTTGCAAGACCACCT

Position	Sequence
3871-3893	CCCAGACTTTGCAAGACCACCTC
3872-3894	CCAGACTTTGCAAGACCACCTCA
3873-3895	CAGACTTTGCAAGACCACCTCAA
3874-3896	AGACTTTGCAAGACCACCTCAAT
3875-3897	GACTTTGCAAGACCACCTCAATA
3876-3898	ACTTTGCAAGACCACCTCAATAG
3877-3899	CTTTGCAAGACCACCTCAATAGC
3878-3900	TTTGCAAGACCACCTCAATAGCC
3879-3901	TTGCAAGACCACCTCAATAGCCT
3880-3902	TGCAAGACCACCTCAATAGCCTG
3881-3903	GCAAGACCACCTCAATAGCCTGA
3882-3904	CAAGACCACCTCAATAGCCTGAA
3883-3905	AAGACCACCTCAATAGCCTGAAG
3884-3906	AGACCACCTCAATAGCCTGAAGG
3885-3907	GACCACCTCAATAGCCTGAAGGA
3886-3908	ACCACCTCAATAGCCTGAAGGAG
3887-3909	CCACCTCAATAGCCTGAAGGAGT
3888-3910	CACCTCAATAGCCTGAAGGAGTT
3889-3911	ACCTCAATAGCCTGAAGGAGTTC
3890-3912	CCTCAATAGCCTGAAGGAGTTCA
3891-3913	CTCAATAGCCTGAAGGAGTTCAA
3892-3914	TCAATAGCCTGAAGGAGTTCAAC
3893-3915	CAATAGCCTGAAGGAGTTCAACC
3894-3916	AATAGCCTGAAGGAGTTCAACCT
3895-3917	ATAGCCTGAAGGAGTTCAACCTC
3896-3918	TAGCCTGAAGGAGTTCAACCTCC
3897-3919	AGCCTGAAGGAGTTCAACCTCCA
3898-3920	GCCTGAAGGAGTTCAACCTCCAG
3899-3921	CCTGAAGGAGTTCAACCTCCAGA
3900-3922	CTGAAGGAGTTCAACCTCCAGAA
3901-3923	TGAAGGAGTTCAACCTCCAGAAC
3902-3924	GAAGGAGTTCAACCTCCAGAAACA
3903-3925	AAGGAGTTCAACCTCCAGAACAT
3904-3926	AGGAGTTCAACCTCCAGAACATG
3905-3927	GGAGTTCAACCTCCAGAACATGG
3906-3928	GAGTTCAACCTCCAGAACATGGG
3907-3929	AGTTCAACCTCCAGAACATGGGA
3908-3930	GTTCAACCTCCAGAACATGGGAT
3909-3931	TTCAACCTCCAGAACATGGGATT
3910-3932	TCAACCTCCAGAACATGGGATTG
3911-3933	CAACCTCCAGAACATGGGATTGC
3912-3934	AACCTCCAGAACATGGGATTGCC
3913-3935	ACCTCCAGAACATGGGATTGCCA
3914-3936	CCTCCAGAACATGGGATTGCCAG
3915-3937	CTCCAGAACATGGGATTGCCAGA
3916-3938	TCCAGAACATGGGATTGCCAGAC
3917-3939	CCAGAACATGGGATTGCCAGACT
3918-3940	CAGAACATGGGATTGCCAGACTT
3919-3941	AGAACATGGGATTGCCAGACTTC
3920-3942	GAACATGGGATTGCCAGACTTCC
3921-3943	AACATGGGATTGCCAGACTTCCA
3922-3944	ACATGGGATTGCCAGACTTCCAC
3923-3945	CATGGGATTGCCAGACTTCCACA
3924-3946	ATGGGATTGCCAGACTTCCACAT
3925-3947	TGGGATTGCCAGACTTCCACATC
3926-3948	GGGATTGCCAGACTTCCACATCC
3927-3949	GGATTGCCAGACTTCCACATCCC
3928-3950	GATTGCCAGACTTCCACATCCCA
3929-3951	ATTGCCAGACTTCCACATCCCAG
3930-3952	TTGCCAGACTTCCACATCCCAGA
3931-3953	TGCCAGACTTCCACATCCCAGAA
3932-3954	GCCAGACTTCCACATCCCAGAAA
3933-3955	CCAGACTTCCACATCCCAGAAAA
3934-3956	CAGACTTCCACATCCCAGAAAAC
3935-3957	AGACTTCCACATCCCAGAAAACC
3936-3958	GACTTCCACATCCCAGAAAACCT

Position	Sequence
3937-3959	ACTTCCACATCCCAGAAAACCTC
3938-3960	CTTCCACATCCCAGAAAACCTCT
3939-3961	TTCACATCCCAGAAAACCTCTT
3940-3962	TCCACATCCCAGAAAACCTCTTC
3941-3963	CCACATCCCAGAAAACCTCTTCT
3942-3964	CACATCCCAGAAAACCTCTTCTT
3943-3965	ACATCCCAGAAAACCTCTTCTTA
3944-3966	CATCCCAGAAAACCTCTTCTTAA
3945-3967	ATCCCAGAAAACCTCTTCTTAAA
3946-3968	TCCCAGAAAACCTCTTCTTAAAA
3947-3969	CCCAGAAAACCTCTTCTTAAAAA
3948-3970	CCAGAAAACCTCTTCTTAAAAAG
3949-3971	CAGAAAACCTCTTCTTAAAAAGC
3950-3972	AGAAAACCTCTTCTTAAAAAGCG
3951-3973	GAAAACCTCTTCTTAAAAAGCGA
3952-3974	AAAACCTCTTCTTAAAAAGCGAT
3953-3975	AAACCTCTTCTTAAAAAGCGATG
3954-3976	AACCTCTTCTTAAAAAGCGATGG
3955-3977	ACCTCTTCTTAAAAAGCGATGGC
3956-3978	CCTCTTCTTAAAAAGCGATGGCC
3957-3979	CTCTTCTTAAAAAGCGATGGCCG
3958-3980	TCTTCTTAAAAAGCGATGGCCGG
3959-3981	CTTCTTAAAAAGCGATGGCCGGG
3960-3982	TTCTTAAAAAGCGATGGCCGGGT
3961-3983	TCTTAAAAAGCGATGGCCGGGTC
3962-3984	CTTAAAAAGCGATGGCCGGGTCA
3963-3985	TAAAAAGCGATGGCCGGGTCAA
3964-3986	TAAAAAGCGATGGCCGGGTCAAA
3965-3987	AAAAAGCGATGGCCGGGTCAAAT
3966-3988	AAAAGCGATGGCCGGGTCAAATA
3967-3989	AAAGCGATGGCCGGGTCAAATAT
3968-3990	AAGCGATGGCCGGGTCAAATATA
3969-3991	AGCGATGGCCGGGTCAAATATAC
3970-3992	GCGATGGCCGGGTCAAATATACC
3971-3993	CGATGGCCGGGTCAAATATACCT
3972-3994	GATGGCCGGGTCAAATATACCTT
3973-3995	ATGGCCGGGTCAAATATACCTTG
3974-3996	TGGCCGGGTCAAATATACCTTGA
3975-3997	GGCCGGGTCAAATATACCTTGAA
3976-3998	GCCGGGTCAAATATACCTTGAAC
3977-3999	CCGGGTCAAATATACCTTGAACA
3978-4000	CGGTCAAATATACCTTGAACAA
3979-4001	GGTCAAATATACCTTGAACAAG
3980-4002	GTCAAATATACCTTGAACAAGA
3981-4003	GTCAAATATACCTTGAACAAGAA
3982-4004	TCAAATATACCTTGAACAAGAAC
3983-4005	CAAATATACCTTGAACAAGAACA
3984-4006	AAATATACCTTGAACAAGAACAG
3985-4007	AATATACCTTGAACAAGAACAGT
3986-4008	ATATACCTTGAACAAGAACAGTT
3987-4009	TATACCTTGAACAAGAACAGTTT
3988-4010	ATACCTTGAACAAGAACAGTTTG
3989-4011	TACCTTGAACAAGAACAGTTTGA
3990-4012	ACCTTGAACAAGAACAGTTTGAA
3991-4013	CCTTGAACAAGAACAGTTTGAAA
3992-4014	CTTGAACAAGAACAGTTTGAAAA
3993-4015	TTGAACAAGAACAGTTTGAAAAAT
3994-4016	TGAACAAGAACAGTTTGAAAAATT
3995-4017	GAACAAGAACAGTTTGAAAAATTG
3996-4018	AACAAGAACAGTTTGAAAAATTGA
3997-4019	ACAAGAACAGTTTGAAAAATTGAG
3998-4020	CAAGAACAGTTTGAAAAATTGAGA
3999-4021	AAGAACAGTTTGAAAAATTGAGAT
4000-4022	AGAACAGTTTGAAAAATTGAGATT
4001-4023	GAACAGTTTGAAAAATTGAGATTC
4002-4024	AACAGTTTGAAAAATTGAGATTCC

Position	Sequence
4003-4025	ACAGTTGAAAATTGAGATTCCT
4004-4026	CAGTTGAAAATTGAGATTCCTT
4005-4027	AGTTGAAAATTGAGATTCCTTT
4006-4028	GTTGAAAATTGAGATTCCTTTG
4007-4029	TTGAAAATTGAGATTCCTTTGC
4008-4030	TTGAAAATTGAGATTCCTTTGCC
4009-4031	TGAAAATTGAGATTCCTTTGCCT
4010-4032	GAAAATTGAGATTCCTTTGCCTT
4011-4033	AAAATTGAGATTCCTTTGCCTTT
4012-4034	AAATTGAGATTCCTTTGCCTTTT
4013-4035	AATTGAGATTCCTTTGCCTTTTG
4014-4036	ATTGAGATTCCTTTGCCTTTTGG
4015-4037	TTGAGATTCCTTTGCCTTTTGGT
4016-4038	TGAGATTCCTTTGCCTTTTGGTG
4017-4039	GAGATTCCTTTGCCTTTTGGTGG
4018-4040	AGATTCCTTTGCCTTTTGGTGGC
4019-4041	GATTCCTTTGCCTTTTGGTGGCA
4020-4042	ATTCCTTTGCCTTTTGGTGGCAA
4021-4043	TTCCCTTTGCCTTTTGGTGGCAA
4022-4044	TCCTTTGCCTTTTGGTGGCAAAT
4023-4045	CCTTTGCCTTTTGGTGGCAAATC
4024-4046	CTTTGCCTTTTGGTGGCAAATCC
4025-4047	TTTGCCTTTTGGTGGCAAATCCT
4026-4048	TTGCCTTTTGGTGGCAAATCCTC
4027-4049	TGCCCTTTTGGTGGCAAATCCTCC
4028-4050	GCCTTTTGGTGGCAAATCCTCCA
4029-4051	CCTTTTGGTGGCAAATCCTCCAG
4030-4052	CTTTTGGTGGCAAATCCTCCAGA
4031-4053	TTTTGGTGGCAAATCCTCCAGAG
4032-4054	TTTGGTGGCAAATCCTCCAGAGA
4033-4055	TTGGTGGCAAATCCTCCAGAGAT
4034-4056	TGGTGGCAAATCCTCCAGAGATC
4035-4057	GGTGGCAAATCCTCCAGAGATCT
4036-4058	GTGGCAAATCCTCCAGAGATCTA
4037-4059	TGGCAAATCCTCCAGAGATCTAA
4038-4060	GGCAAATCCTCCAGAGATCTAAA
4039-4061	GCAAATCCTCCAGAGATCTAAAG
4040-4062	CAAATCCTCCAGAGATCTAAAGA
4041-4063	AAATCCTCCAGAGATCTAAAGAT
4042-4064	AATCCTCCAGAGATCTAAAGATG
4043-4065	ATCCTCCAGAGATCTAAAGATGT
4044-4066	TCCTCCAGAGATCTAAAGATGTT
4045-4067	CCTCCAGAGATCTAAAGATGTTA
4046-4068	CTCCAGAGATCTAAAGATGTTAG
4047-4069	TCCAGAGATCTAAAGATGTTAGA
4048-4070	CCAGAGATCTAAAGATGTTAGAG
4049-4071	CAGAGATCTAAAGATGTTAGAGA
4050-4072	AGAGATCTAAAGATGTTAGAGAC
4051-4073	GAGATCTAAAGATGTTAGAGACT
4052-4074	AGATCTAAAGATGTTAGAGACTG
4053-4075	GATCTAAAGATGTTAGAGACTGT
4054-4076	ATCTAAAGATGTTAGAGACTGTT
4055-4077	TCTAAAGATGTTAGAGACTGTTA
4056-4078	CTAAAGATGTTAGAGACTGTTAG
4057-4079	TAAAGATGTTAGAGACTGTTAGG
4058-4080	AAAGATGTTAGAGACTGTTAGGA
4059-4081	AAGATGTTAGAGACTGTTAGGAC
4060-4082	AGATGTTAGAGACTGTTAGGACA
4061-4083	GATGTTAGAGACTGTTAGGACAC
4062-4084	ATGTTAGAGACTGTTAGGACACC
4063-4085	TGTTAGAGACTGTTAGGACACCA
4064-4086	GTTAGAGACTGTTAGGACACCAG
4065-4087	TTAGAGACTGTTAGGACACCAGC
4066-4088	TAGAGACTGTTAGGACACCAGCC
4067-4089	AGAGACTGTTAGGACACCAGCCC
4068-4090	GAGACTGTTAGGACACCAGCCCT

Position	Sequence
4069-4091	AGACTGTTAGGACACCAGCCCTC
4070-4092	GACTGTTAGGACACCAGCCCTCC
4071-4093	ACTGTTAGGACACCAGCCCTCCA
4072-4094	CTGTTAGGACACCAGCCCTCCAC
4073-4095	TGTTAGGACACCAGCCCTCCACT
4074-4096	GTTAGGACACCAGCCCTCCACTT
4075-4097	TTAGGACACCAGCCCTCCACTTC
4076-4098	TAGGACACCAGCCCTCCACTTCA
4077-4099	AGGACACCAGCCCTCCACTTCAA
4078-4100	GGACACCAGCCCTCCACTTCAAG
4079-4101	GACACCAGCCCTCCACTTCAAGT
4080-4102	ACACCAGCCCTCCACTTCAAGTC
4081-4103	CACCAGCCCTCCACTTCAAGTCT
4082-4104	ACCAGCCCTCCACTTCAAGTCTG
4083-4105	CCAGCCCTCCACTTCAAGTCTGT
4084-4106	CAGCCCTCCACTTCAAGTCTGTG
4085-4107	AGCCCTCCACTTCAAGTCTGTGG
4086-4108	GCCCTCCACTTCAAGTCTGTGGG
4087-4109	CCCTCCACTTCAAGTCTGTGGGA
4088-4110	CCTCCACTTCAAGTCTGTGGGAT
4089-4111	CTCCACTTCAAGTCTGTGGGATT
4090-4112	TCCACTTCAAGTCTGTGGGATTC
4091-4113	CCACTTCAAGTCTGTGGGATTC
4092-4114	CACTTCAAGTCTGTGGGATTCCA
4093-4115	ACTTCAAGTCTGTGGGATTCCAT
4094-4116	CTTCAAGTCTGTGGGATTCCATC
4095-4117	TTCAGTCTGTGGGATTCCATCT
4096-4118	TCAAGTCTGTGGGATTCCATCTG
4097-4119	CAAGTCTGTGGGATTCCATCTGC
4098-4120	AAGTCTGTGGGATTCCATCTGCC
4099-4121	AGTCTGTGGGATTCCATCTGCCA
4100-4122	GTCTGTGGGATTCCATCTGCCAT
4101-4123	TCTGTGGGATTCCATCTGCCATC
4102-4124	CTGTGGGATTCCATCTGCCATCT
4103-4125	TGTGGGATTCCATCTGCCATCTC
4104-4126	GTGGGATTCCATCTGCCATCTCG
4105-4127	TGGGATTCCATCTGCCATCTCGA
4106-4128	GGGATTCCATCTGCCATCTCGAG
4107-4129	GGATTCCATCTGCCATCTCGAGA
4108-4130	GATTCCATCTGCCATCTCGAGAG
4109-4131	ATTCCATCTGCCATCTCGAGAGT
4110-4132	TTCCATCTGCCATCTCGAGAGTT
4111-4133	TCCATCTGCCATCTCGAGAGTTC
4112-4134	CCATCTGCCATCTCGAGAGTTCC
4113-4135	CATCTGCCATCTCGAGAGTTCCA
4114-4136	ATCTGCCATCTCGAGAGTTCCAA
4115-4137	TCTGCCATCTCGAGAGTTCCAAG
4116-4138	CTGCCATCTCGAGAGTTCCAAGT
4117-4139	TGCCATCTCGAGAGTTCCAAGTC
4118-4140	GCCATCTCGAGAGTTCCAAGTCC
4119-4141	CCATCTCGAGAGTTCCAAGTCCC
4120-4142	CATCTCGAGAGTTCCAAGTCCCT
4121-4143	ATCTCGAGAGTTCCAAGTCCCTA
4122-4144	TCTCGAGAGTTCCAAGTCCCTAC
4123-4145	CTCGAGAGTTCCAAGTCCCTACT
4124-4146	TCGAGAGTTCCAAGTCCCTACTT
4125-4147	CGAGAGTTCCAAGTCCCTACTTT
4126-4148	GAGAGTTCCAAGTCCCTACTTTT
4127-4149	AGAGTTCCAAGTCCCTACTTTTA
4128-4150	GAGTTCCAAGTCCCTACTTTTAC
4129-4151	AGTTCCAAGTCCCTACTTTTACC
4130-4152	GTTCCAAGTCCCTACTTTTACCA
4131-4153	TTCCAAGTCCCTACTTTTACCAT
4132-4154	TCCAAGTCCCTACTTTTACCATT
4133-4155	CCAAGTCCCTACTTTTACCATTTC
4134-4156	CAAGTCCCTACTTTTACCATTCC

Position	Sequence
4135-4157	AAGTCCCTACTTTTACCATTCCC
4136-4158	AGTCCCTACTTTTACCATTCCCA
4137-4159	GTCCCTACTTTTACCATTCCCAA
4138-4160	TCCCTACTTTTACCATTCCCAAG
4139-4161	CCCTACTTTTACCATTCCCAAGT
4140-4162	CCTACTTTTACCATTCCCAAGTT
4141-4163	CTACTTTTACCATTCCCAAGTTG
4142-4164	TACTTTTACCATTCCCAAGTTGT
4143-4165	ACTTTTACCATTCCCAAGTTGTA
4144-4166	CTTTTACCATTCCCAAGTTGTAT
4145-4167	TTTTACCATTCCCAAGTTGTATC
4146-4168	TTTACCATTCCCAAGTTGTATCA
4147-4169	TTACCATTCCCAAGTTGTATCAA
4148-4170	TACCATTCCCAAGTTGTATCAAC
4149-4171	ACCATTCCCAAGTTGTATCAACT
4150-4172	CCATTCCCAAGTTGTATCAACTG
4151-4173	CATTCCCAAGTTGTATCAACTGC
4152-4174	ATCCCAAGTTGTATCAACTGCA
4153-4175	TTCCCAAGTTGTATCAACTGCAA
4154-4176	TCCCAAGTTGTATCAACTGCAAG
4155-4177	CCCAAGTTGTATCAACTGCAAGT
4156-4178	CCAAGTTGTATCAACTGCAAGTG
4157-4179	CAAGTTGTATCAACTGCAAGTGC
4158-4180	AAGTTGTATCAACTGCAAGTGCC
4159-4181	AGTTGTATCAACTGCAAGTGCC
4160-4182	GTTGTATCAACTGCAAGTGCCCTC
4161-4183	TTGTATCAACTGCAAGTGCCCTCT
4162-4184	TGTATCAACTGCAAGTGCCCTCTC
4163-4185	GTATCAACTGCAAGTGCCCTCTCC
4164-4186	TATCAACTGCAAGTGCCCTCTCCT
4165-4187	ATCAACTGCAAGTGCCCTCTCCTG
4166-4188	TCAACTGCAAGTGCCCTCTCCTGG
4167-4189	CAACTGCAAGTGCCCTCTCCTGGG
4168-4190	AACTGCAAGTGCCCTCTCCTGGGT
4169-4191	ACTGCAAGTGCCCTCTCCTGGGTG
4170-4192	CTGCAAGTGCCCTCTCCTGGGTGT
4171-4193	TGCAAGTGCCCTCTCCTGGGTGTT
4172-4194	GCAAGTGCCCTCTCCTGGGTGTTT
4173-4195	CAAGTGCCCTCTCCTGGGTGTTCT
4174-4196	AAGTGCCCTCTCCTGGGTGTTCTA
4175-4197	AGTGCCCTCTCCTGGGTGTTCTAG
4176-4198	GTGCCCTCTCCTGGGTGTTCTAGA
4177-4199	TGCCCTCTCCTGGGTGTTCTAGAC
4178-4200	GCCTCTCCTGGGTGTTCTAGACC
4179-4201	CCTCTCCTGGGTGTTCTAGACCT
4180-4202	CTCTCCTGGGTGTTCTAGACCTC
4181-4203	TCTCCTGGGTGTTCTAGACCTCT
4182-4204	CTCCTGGGTGTTCTAGACCTCTC
4183-4205	TCCTGGGTGTTCTAGACCTCTCC
4184-4206	CCTGGGTGTTCTAGACCTCTCCA
4185-4207	CTGGGTGTTCTAGACCTCTCCAC
4186-4208	TGGGTGTTCTAGACCTCTCCACG
4187-4209	GGGTGTTCTAGACCTCTCCACGA
4188-4210	GGTGTCTAGACCTCTCCACGAA
4189-4211	GTGTCTAGACCTCTCCACGAAT
4190-4212	TGTCTAGACCTCTCCACGAATG
4191-4213	GTTCTAGACCTCTCCACGAATGT
4192-4214	TTCTAGACCTCTCCACGAATGTC
4193-4215	TCTAGACCTCTCCACGAATGTCT
4194-4216	CTAGACCTCTCCACGAATGTCTA
4195-4217	TAGACCTCTCCACGAATGTCTAC
4196-4218	AGACCTCTCCACGAATGTCTACA
4197-4219	GACCTCTCCACGAATGTCTACAG
4198-4220	ACCTCTCCACGAATGTCTACAGC
4199-4221	CCTCTCCACGAATGTCTACAGCA
4200-4222	CTCTCCACGAATGTCTACAGCAA

Position	Sequence
4201-4223	TCTCCACGAATGTCTACAGCAAC
4202-4224	CTCCACGAATGTCTACAGCAACT
4203-4225	TCCACGAATGTCTACAGCAACTT
4204-4226	CCACGAATGTCTACAGCAACTTG
4205-4227	CACGAATGTCTACAGCAACTTGT
4206-4228	ACGAATGTCTACAGCAACTTGTA
4207-4229	CGAATGTCTACAGCAACTTGTAC
4208-4230	GAATGTCTACAGCAACTTGTACA
4209-4231	AATGTCTACAGCAACTTGTACAA
4210-4232	ATGTCTACAGCAACTTGTACAAC
4211-4233	TGTCTACAGCAACTTGTACAAC
4212-4234	GTCTACAGCAACTTGTACAAC
4213-4235	TCTACAGCAACTTGTACAAC
4214-4236	CTACAGCAACTTGTACAAC
4215-4237	TACAGCAACTTGTACAAC
4216-4238	ACAGCAACTTGTACAAC
4217-4239	CAGCAACTTGTACAAC
4218-4240	AGCAACTTGTACAAC
4219-4241	GCAACTTGTACAAC
4220-4242	CAACTTGTACAAC
4221-4243	AACTTGTACAAC
4222-4244	ACTTGTACAAC
4223-4245	CTTGTACAAC
4224-4246	TTGTACAAC
4225-4247	TGTACAAC
4226-4248	GTACAAC
4227-4249	TACAAC
4228-4250	ACAAC
4229-4251	CAACTGGTCCGCCTCTACAGTG
4230-4252	AACTGGTCCGCCTCTACAGTGG
4231-4253	ACTGGTCCGCCTCTACAGTGGT
4232-4254	CTGGTCCGCCTCTACAGTGGTG
4233-4255	TGGTCCGCCTCTACAGTGGTGG
4234-4256	GGTCCGCCTCTACAGTGGTGGC
4235-4257	GTCCGCCTCTACAGTGGTGGCA
4236-4258	TCCGCCTCTACAGTGGTGGCAA
4237-4259	CCGCCTCTACAGTGGTGGCAAC
4238-4260	CGCCTCTACAGTGGTGGCAACA
4239-4261	GCCTCTACAGTGGTGGCAACAC
4240-4262	CCTCTACAGTGGTGGCAACACC
4241-4263	CTCCTACAGTGGTGGCAACACCA
4242-4264	TCCTACAGTGGTGGCAACACCAG
4243-4265	CCTACAGTGGTGGCAACACCAGC
4244-4266	CTACAGTGGTGGCAACACCAGCA
4245-4267	TACAGTGGTGGCAACACCAGCAC
4246-4268	ACAGTGGTGGCAACACCAGCACACA
4247-4269	CAGTGGTGGCAACACCAGCACACAG
4248-4270	AGTGGTGGCAACACCAGCACACAGA
4249-4271	GTGGTGGCAACACCAGCACACAGAC
4250-4272	TGGTGGCAACACCAGCACACAGACC
4251-4273	GGTGGCAACACCAGCACACAGACCA
4252-4274	GTGGCAACACCAGCACAGACCAT
4253-4275	TGGCAACACCAGCACAGACCAT
4254-4276	GGCAACACCAGCACAGACCAT
4255-4277	GCAACACCAGCACAGACCAT
4256-4278	CAACACCAGCACAGACCAT
4257-4279	AACACCAGCACAGACCAT
4258-4280	ACACCAGCACAGACCAT
4259-4281	CACCAGCACAGACCAT
4260-4282	ACCAGCACAGACCAT
4261-4283	CCAGCACAGACCAT
4262-4284	CAGCACAGACCAT
4263-4285	AGCACAGACCAT
4264-4286	GCACAGACCAT
4265-4287	CACAGACCAT
4266-4288	ACAGACCAT

Position	Sequence
4267-4289	CAGACCATTTCAGCCTTCGGGCT
4268-4290	AGACCATTTCAGCCTTCGGGCTC
4269-4291	GACCATTTCAGCCTTCGGGCTCG
4270-4292	ACCATTTCAGCCTTCGGGCTCGT
4271-4293	CCATTTCAGCCTTCGGGCTCGTT
4272-4294	CATTTCAGCCTTCGGGCTCGTTA
4273-4295	ATTTCAGCCTTCGGGCTCGTTAC
4274-4296	TTCAGCCTTCGGGCTCGTTACC
4275-4297	TTCAGCCTTCGGGCTCGTTACCA
4276-4298	TCAGCCTTCGGGCTCGTTACCAC
4277-4299	CAGCCTTCGGGCTCGTTACCACA
4278-4300	AGCCTTCGGGCTCGTTACCACAT
4279-4301	GCCTTCGGGCTCGTTACCACATG
4280-4302	CCTTCGGGCTCGTTACCACATGA
4281-4303	CTTCGGGCTCGTTACCACATGAA
4282-4304	TTCGGGCTCGTTACCACATGAAG
4283-4305	TCGGGCTCGTTACCACATGAAGG
4284-4306	CGGGCTCGTTACCACATGAAGGC
4285-4307	GGGCTCGTTACCACATGAAGGCT
4286-4308	GGCTCGTTACCACATGAAGGCTG
4287-4309	GCTCGTTACCACATGAAGGCTGA
4288-4310	CTCGTTACCACATGAAGGCTGAC
4289-4311	TCGTTACCACATGAAGGCTGACT
4290-4312	CGTTACCACATGAAGGCTGACTC
4291-4313	GTACCACATGAAGGCTGACTCT
4292-4314	TTACCACATGAAGGCTGACTCTG
4293-4315	TACCACATGAAGGCTGACTCTGT
4294-4316	ACCACATGAAGGCTGACTCTGTG
4295-4317	CCACATGAAGGCTGACTCTGTGG
4296-4318	CACATGAAGGCTGACTCTGTGGT
4297-4319	ACATGAAGGCTGACTCTGTGGTT
4298-4320	CATGAAGGCTGACTCTGTGGTTG
4299-4321	ATGAAGGCTGACTCTGTGGTTGA
4300-4322	TGAAGGCTGACTCTGTGGTTGAC
4301-4323	GAAGGCTGACTCTGTGGTTGACC
4302-4324	AAGGCTGACTCTGTGGTTGACCT
4303-4325	AGGCTGACTCTGTGGTTGACCTG
4304-4326	GGCTGACTCTGTGGTTGACCTGC
4305-4327	GCTGACTCTGTGGTTGACCTGCT
4306-4328	CTGACTCTGTGGTTGACCTGCTT
4307-4329	TGACTCTGTGGTTGACCTGCTTT
4308-4330	GACTCTGTGGTTGACCTGCTTTC
4309-4331	ACTCTGTGGTTGACCTGCTTTCC
4310-4332	CTCTGTGGTTGACCTGCTTTCCCT
4311-4333	TCTGTGGTTGACCTGCTTTCCCTA
4312-4334	CTGTGGTTGACCTGCTTTCCCTAC
4313-4335	TGTGGTTGACCTGCTTTCCCTACA
4314-4336	GTGGTTGACCTGCTTTCCCTACAA
4315-4337	TGGTTGACCTGCTTTCCCTACAAT
4316-4338	GGTTGACCTGCTTTCCCTACAATG
4317-4339	GTTGACCTGCTTTCCCTACAATGT
4318-4340	TTGACCTGCTTTCCCTACAATGTG
4319-4341	TGACCTGCTTTCCCTACAATGTGC
4320-4342	GACCTGCTTTCCCTACAATGTGCA
4321-4343	ACCTGCTTTCCCTACAATGTGCAA
4322-4344	CCTGCTTTCCCTACAATGTGCAAG
4323-4345	CTGCTTTCCCTACAATGTGCAAGG
4324-4346	TGCTTTCCCTACAATGTGCAAGGA
4325-4347	GCTTTCCCTACAATGTGCAAGGAT
4326-4348	CTTTCCCTACAATGTGCAAGGATC
4327-4349	TTTCCCTACAATGTGCAAGGATCT
4328-4350	TTCCCTACAATGTGCAAGGATCTG
4329-4351	TCCCTACAATGTGCAAGGATCTGG
4330-4352	CCTACAATGTGCAAGGATCTGGA
4331-4353	CTACAATGTGCAAGGATCTGGAG
4332-4354	TACAATGTGCAAGGATCTGGAGA

Position	Sequence
4333-4355	ACAATGTGCAAGGATCTGGAGAA
4334-4356	CAATGTGCAAGGATCTGGAGAAA
4335-4357	AATGTGCAAGGATCTGGAGAAAC
4336-4358	ATGTGCAAGGATCTGGAGAAACA
4337-4359	TGTGCAAGGATCTGGAGAAACAA
4338-4360	GTGCAAGGATCTGGAGAAACAAC
4339-4361	TGCAAGGATCTGGAGAAACAACA
4340-4362	GCAAGGATCTGGAGAAACAACAT
4341-4363	CAAGGATCTGGAGAAACAACATA
4342-4364	AAGGATCTGGAGAAACAACATAT
4343-4365	AGGATCTGGAGAAACAACATATG
4344-4366	GGATCTGGAGAAACAACATATGA
4345-4367	GATCTGGAGAAACAACATATGAC
4346-4368	ATCTGGAGAAACAACATATGACC
4347-4369	TCTGGAGAAACAACATATGACCA
4348-4370	CTGGAGAAACAACATATGACCAC
4349-4371	TGGAGAAACAACATATGACCACA
4350-4372	GGAGAAACAACATATGACCACAA
4351-4373	GAGAAACAACATATGACCACAAG
4352-4374	AGAAACAACATATGACCACAAGA
4353-4375	GAAACAACATATGACCACAAGAA
4354-4376	AAACAACATATGACCACAAGAAT
4355-4377	AACAACATATGACCACAAGAATA
4356-4378	ACAACATATGACCACAAGAATAC
4357-4379	CAACATATGACCACAAGAATACG
4358-4380	AACATATGACCACAAGAATACGT
4359-4381	ACATATGACCACAAGAATACGTT
4360-4382	CATATGACCACAAGAATACGTTTC
4361-4383	ATATGACCACAAGAATACGTTCA
4362-4384	TATGACCACAAGAATACGTTTAC
4363-4385	ATGACCACAAGAATACGTTTACA
4364-4386	TGACCACAAGAATACGTTTACAC
4365-4387	GACCACAAGAATACGTTTCACT
4366-4388	ACCACAAGAATACGTTTCACTA
4367-4389	CCACAAGAATACGTTTCACTAT
4368-4390	CACAAGAATACGTTTCACTATC
4369-4391	ACAAGAATACGTTTCACTATCA
4370-4392	CAAGAATACGTTTCACTATCAT
4371-4393	AAGAATACGTTTCACTATCATG
4372-4394	AGAATACGTTTCACTATCATGT
4373-4395	GAATACGTTTCACTATCATGTG
4374-4396	AATACGTTTCACTATCATGTGA
4375-4397	ATACGTTTCACTATCATGTGAT
4376-4398	TACGTTTCACTATCATGTGATG
4377-4399	ACGTTTCACTATCATGTGATGG
4378-4400	CGTTTCACTATCATGTGATGGG
4379-4401	GTTTCACTATCATGTGATGGGT
4380-4402	TTCACACTATCATGTGATGGGTC
4381-4403	TCACACTATCATGTGATGGGTCT
4382-4404	CACACTATCATGTGATGGGTCTC
4383-4405	ACACTATCATGTGATGGGTCTCT
4384-4406	CACTATCATGTGATGGGTCTCTA
4385-4407	ACTATCATGTGATGGGTCTCTAC
4386-4408	CTATCATGTGATGGGTCTCTACG
4387-4409	TATCATGTGATGGGTCTCTACGC
4388-4410	ATCATGTGATGGGTCTCTACGCC
4389-4411	TCATGTGATGGGTCTCTACGCCA
4390-4412	CATGTGATGGGTCTCTACGCCAC
4391-4413	ATGTGATGGGTCTCTACGCCACA
4392-4414	TGTGATGGGTCTCTACGCCACAA
4393-4415	GTGATGGGTCTCTACGCCACAAA
4394-4416	TGATGGGTCTCTACGCCACAAAT
4395-4417	GATGGGTCTCTACGCCACAAATT
4396-4418	ATGGGTCTCTACGCCACAAATTT
4397-4419	TGGGTCTCTACGCCACAAATTTT
4398-4420	GGGTCTCTACGCCACAAATTTCT

Position	Sequence
4399-4421	GGTCTCTACGCCACAAATTTCTA
4400-4422	GTCTCTACGCCACAAATTTCTAG
4401-4423	TCTCTACGCCACAAATTTCTAGA
4402-4424	CTCTACGCCACAAATTTCTAGAT
4403-4425	TCTACGCCACAAATTTCTAGATT
4404-4426	CTACGCCACAAATTTCTAGATTC
4405-4427	TACGCCACAAATTTCTAGATTTCG
4406-4428	ACGCCACAAATTTCTAGATTTCGA
4407-4429	CGCCACAAATTTCTAGATTTCGAA
4408-4430	GCCACAAATTTCTAGATTTCGAAT
4409-4431	CCACAAATTTCTAGATTTCGAATA
4410-4432	CACAAATTTCTAGATTTCGAATAT
4411-4433	ACAAATTTCTAGATTTCGAATATC
4412-4434	CAAATTTCTAGATTTCGAATATCA
4413-4435	AAATTTCTAGATTTCGAATATCAA
4414-4436	AATTTCTAGATTTCGAATATCAAA
4415-4437	ATTTCTAGATTTCGAATATCAAAT
4416-4438	TTTCTAGATTTCGAATATCAAATT
4417-4439	TTCTAGATTTCGAATATCAAATTC
4418-4440	TCTAGATTTCGAATATCAAATTC
4419-4441	CTAGATTTCGAATATCAAATTCAG
4420-4442	TAGATTTCGAATATCAAATTCAGT
4421-4443	AGATTTCGAATATCAAATTCAGTC
4422-4444	GATTTCGAATATCAAATTCAGTCA
4423-4445	ATTTCGAATATCAAATTCAGTCAT
4424-4446	TTCGAATATCAAATTCAGTCATG
4425-4447	TCGAATATCAAATTCAGTCATGT
4426-4448	CGAATATCAAATTCAGTCATGTA
4427-4449	GAATATCAAATTCAGTCATGTAG
4428-4450	AATATCAAATTCAGTCATGTAGA
4429-4451	ATATCAAATTCAGTCATGTAGAA
4430-4452	TATCAAATTCAGTCATGTAGAAA
4431-4453	ATCAAATTCAGTCATGTAGAAAA
4432-4454	TCAAATTCAGTCATGTAGAAAAA
4433-4455	CAAATTCAGTCATGTAGAAAAAC
4434-4456	AAATTCAGTCATGTAGAAAAACT
4435-4457	AATTCAGTCATGTAGAAAAACTT
4436-4458	ATTCAGTCATGTAGAAAAACTTG
4437-4459	TTCAGTCATGTAGAAAAACTTGG
4438-4460	TCAGTCATGTAGAAAAACTTGGGA
4439-4461	CAGTCATGTAGAAAAACTTGGGAA
4440-4462	AGTCATGTAGAAAAACTTGGGAAA
4441-4463	GTCATGTAGAAAAACTTGGGAAAC
4442-4464	TCATGTAGAAAAACTTGGGAAACA
4443-4465	CATGTAGAAAAACTTGGGAAACAA
4444-4466	ATGTAGAAAAACTTGGGAAACAAC
4445-4467	TGTAGAAAAACTTGGGAAACAACC
4446-4468	GTAGAAAAACTTGGGAAACAACCC
4447-4469	TAGAAAAACTTGGGAAACAACCCA
4448-4470	AGAAAAACTTGGGAAACAACCCAG
4449-4471	GAAAAACTTGGGAAACAACCCAGT
4450-4472	AAAAACTTGGGAAACAACCCAGTC
4451-4473	AAAACTTGGGAAACAACCCAGTCT
4452-4474	AAACTTGGGAAACAACCCAGTCTC
4453-4475	AACTTGGGAAACAACCCAGTCTCA
4454-4476	ACTTGGGAAACAACCCAGTCTCAA
4455-4477	CTTGGGAAACAACCCAGTCTCAAAA
4456-4478	TTGGGAAACAACCCAGTCTCAAAA
4457-4479	TGGGAAACAACCCAGTCTCAAAAG
4458-4480	GGGAAACAACCCAGTCTCAAAAGG
4459-4481	GAAACAACCCAGTCTCAAAAGGT
4460-4482	AAACAACCCAGTCTCAAAAGGTT
4461-4483	AACAACCCAGTCTCAAAAGGTTT
4462-4484	ACAACCCAGTCTCAAAAGGTTTA
4463-4485	CAACCCAGTCTCAAAAGGTTTAC
4464-4486	AACCCAGTCTCAAAAGGTTTACT

Position	Sequence
4465-4487	ACCCAGTCTCAAAGGTTACTA
4466-4488	CCCAGTCTCAAAGGTTACTAA
4467-4489	CCAGTCTCAAAGGTTACTAAT
4468-4490	CAGTCTCAAAGGTTACTAATA
4469-4491	AGTCTCAAAGGTTACTAATAT
4470-4492	GTCTCAAAGGTTACTAATATT
4471-4493	TCTCAAAGGTTACTAATATTC
4472-4494	CTCAAAGGTTACTAATATTCG
4473-4495	TCAAAGGTTACTAATATTCGA
4474-4496	CAAAGGTTACTAATATTCGAT
4475-4497	AAAAGGTTACTAATATTCGATG
4476-4498	AAAGGTTACTAATATTCGATGC
4477-4499	AAGGTTACTAATATTCGATGCA
4478-4500	AGGTTACTAATATTCGATGCAT
4479-4501	GGTTACTAATATTCGATGCATC
4480-4502	GTTACTAATATTCGATGCATCT
4481-4503	TTACTAATATTCGATGCATCTA
4482-4504	TTACTAATATTCGATGCATCTAG
4483-4505	TACTAATATTCGATGCATCTAGT
4484-4506	ACTAATATTCGATGCATCTAGTT
4485-4507	CTAATATTCGATGCATCTAGTTC
4486-4508	TAATATTCGATGCATCTAGTTCC
4487-4509	AATATTCGATGCATCTAGTTCCCT
4488-4510	ATATTCGATGCATCTAGTTCCCTG
4489-4511	TATTCGATGCATCTAGTTCCCTGG
4490-4512	ATTTCGATGCATCTAGTTCCCTGGG
4491-4513	TTCGATGCATCTAGTTCCCTGGGG
4492-4514	TCGATGCATCTAGTTCCCTGGGGA
4493-4515	CGATGCATCTAGTTCCCTGGGGAC
4494-4516	GATGCATCTAGTTCCCTGGGGACC
4495-4517	ATGCATCTAGTTCCCTGGGGACCA
4496-4518	TGCATCTAGTTCCCTGGGGACCAC
4497-4519	GCATCTAGTTCCCTGGGGACCACA
4498-4520	CATCTAGTTCCCTGGGGACCACAG
4499-4521	ATCTAGTTCCCTGGGGACCACAGA
4500-4522	TCTAGTTCCCTGGGGACCACAGAT
4501-4523	CTAGTTCCCTGGGGACCACAGATG
4502-4524	TAGTTCCCTGGGGACCACAGATGT
4503-4525	AGTTCCCTGGGGACCACAGATGTC
4504-4526	GTTCCCTGGGGACCACAGATGTCT
4505-4527	TTCCCTGGGGACCACAGATGTCTG
4506-4528	TCCTGGGGACCACAGATGTCTGC
4507-4529	CCTGGGGACCACAGATGTCTGCT
4508-4530	CTGGGGACCACAGATGTCTGCTT
4509-4531	TGGGGACCACAGATGTCTGCTTC
4510-4532	GGGGACCACAGATGTCTGCTTCA
4511-4533	GGGACCACAGATGTCTGCTTCAG
4512-4534	GGACCACAGATGTCTGCTTCAGT
4513-4535	GACCACAGATGTCTGCTTCAGTT
4514-4536	ACCACAGATGTCTGCTTCAGTTC
4515-4537	CCACAGATGTCTGCTTCAGTTCA
4516-4538	CACAGATGTCTGCTTCAGTTCAT
4517-4539	ACAGATGTCTGCTTCAGTTCATT
4518-4540	CAGATGTCTGCTTCAGTTCATTT
4519-4541	AGATGTCTGCTTCAGTTCATTTG
4520-4542	GATGTCTGCTTCAGTTCATTTGG
4521-4543	ATGTCTGCTTCAGTTCATTTGGA
4522-4544	TGTCTGCTTCAGTTCATTTGGAC
4523-4545	GTCTGCTTCAGTTCATTTGGACT
4524-4546	TCTGCTTCAGTTCATTTGGACTC
4525-4547	CTGCTTCAGTTCATTTGGACTCC
4526-4548	TGCTTCAGTTCATTTGGACTCCA
4527-4549	GCTTCAGTTCATTTGGACTCCAA
4528-4550	CTTCAGTTCATTTGGACTCCAAA
4529-4551	TTCAGTTCATTTGGACTCCAAAA
4530-4552	TCAGTTCATTTGGACTCCAAAA

Position	Sequence
4531-4553	CAGTTCATTTGGACTCCAAAAAG
4532-4554	AGTTCATTTGGACTCCAAAAAGA
4533-4555	GTTTCATTTGGACTCCAAAAAGAA
4534-4556	TTCATTTGGACTCCAAAAAGAAA
4535-4557	TCATTTGGACTCCAAAAAGAAAC
4536-4558	CATTTGGACTCCAAAAAGAAACA
4537-4559	ATTTGGACTCCAAAAAGAAACAG
4538-4560	TTTGGACTCCAAAAAGAAACAGC
4539-4561	TTGGACTCCAAAAAGAAACAGCA
4540-4562	TGGACTCCAAAAAGAAACAGCAT
4541-4563	GGACTCCAAAAAGAAACAGCATT
4542-4564	GACTCCAAAAAGAAACAGCATTT
4543-4565	ACTCCAAAAAGAAACAGCATTTG
4544-4566	CTCCAAAAAGAAACAGCATTTGT
4545-4567	TCCAAAAAGAAACAGCATTTGT
4546-4568	CCAAAAAGAAACAGCATTTGT
4547-4569	CAAAAAAGAAACAGCATTTGT
4548-4570	AAAAAGAAACAGCATTTGT
4549-4571	AAAAGAAACAGCATTTGT
4550-4572	AAAGAAACAGCATTTGT
4551-4573	AAGAAACAGCATTTGT
4552-4574	AGAAACAGCATTTGT
4553-4575	GAAACAGCATTTGT
4554-4576	AAACAGCATTTGT
4555-4577	AACAGCATTTGT
4556-4578	ACAGCATTTGT
4557-4579	CAGCATTTGT
4558-4580	AGCATTTGT
4559-4581	GCATTTGT
4560-4582	CATTTGTTGTCAAAGAAGTCAA
4561-4583	ATTTGTTGTCAAAGAAGTCAAG
4562-4584	TTTGTTCAAAGAAGTCAAGA
4563-4585	TTGTTGTCAAAGAAGTCAAGAT
4564-4586	TGTTGTCAAAGAAGTCAAGATT
4565-4587	GTTGTCAAAGAAGTCAAGATTG
4566-4588	TTGTCAAAGAAGTCAAGATTGA
4567-4589	TTGTCAAAGAAGTCAAGATTGAT
4568-4590	TGTCAAAGAAGTCAAGATTGATG
4569-4591	GTCAAAGAAGTCAAGATTGATGG
4570-4592	TCAAAGAAGTCAAGATTGATGGG
4571-4593	CAAAGAAGTCAAGATTGATGGGC
4572-4594	AAAGAAGTCAAGATTGATGGGCA
4573-4595	AAGAAGTCAAGATTGATGGGCAG
4574-4596	AGAAGTCAAGATTGATGGGCAGT
4575-4597	GAAGTCAAGATTGATGGGCAGTT
4576-4598	AAGTCAAGATTGATGGGCAGTTC
4577-4599	AGTCAAGATTGATGGGCAGTTCA
4578-4600	GTCAGATTGATGGGCAGTTCAG
4579-4601	TCAAGATTGATGGGCAGTTCAGA
4580-4602	CAAGATTGATGGGCAGTTCAGAG
4581-4603	AAGATTGATGGGCAGTTCAGAGT
4582-4604	AGATTGATGGGCAGTTCAGAGTC
4583-4605	GATTGATGGGCAGTTCAGAGTCT
4584-4606	ATTGATGGGCAGTTCAGAGTCTC
4585-4607	TTGATGGGCAGTTCAGAGTCTCT
4586-4608	TGATGGGCAGTTCAGAGTCTCTT
4587-4609	GATGGGCAGTTCAGAGTCTCTTC
4588-4610	ATGGGCAGTTCAGAGTCTCTTCG
4589-4611	TGGGCAGTTCAGAGTCTCTTCGT
4590-4612	GGGCAGTTCAGAGTCTCTTCGTT
4591-4613	GGCAGTTCAGAGTCTCTTCGTTT
4592-4614	GCAGTTCAGAGTCTCTTCGTTCT
4593-4615	CAGTTCAGAGTCTCTTCGTTCTA
4594-4616	AGTTCAGAGTCTCTTCGTTCTAT
4595-4617	GTTTCAGAGTCTCTTCGTTCTATG
4596-4618	TTTCAGAGTCTCTTCGTTCTATGC

Position	Sequence
4597-4619	TCAGAGTCTCTCGTTCTATGCT
4598-4620	CAGAGTCTCTCGTTCTATGCTA
4599-4621	AGAGTCTCTCGTTCTATGCTAA
4600-4622	GAGTCTCTCGTTCTATGCTAAA
4601-4623	AGTCTCTCGTTCTATGCTAAAG
4602-4624	GTCTCTCGTTCTATGCTAAAGG
4603-4625	TCTCTCGTTCTATGCTAAAGGC
4604-4626	CTCTTCGTTCTATGCTAAAGGCA
4605-4627	TCTTCGTTCTATGCTAAAGGCAC
4606-4628	CTTCGTTCTATGCTAAAGGCACA
4607-4629	TTCGTTCTATGCTAAAGGCACAT
4608-4630	TCGTTCTATGCTAAAGGCACATA
4609-4631	CGTTCTATGCTAAAGGCACATAT
4610-4632	GTTCTATGCTAAAGGCACATATG
4611-4633	TTCTATGCTAAAGGCACATATGG
4612-4634	TCTATGCTAAAGGCACATATGGC
4613-4635	CTATGCTAAAGGCACATATGGCC
4614-4636	TATGCTAAAGGCACATATGGCCT
4615-4637	ATGCTAAAGGCACATATGGCCTG
4616-4638	TGCTAAAGGCACATATGGCCTGT
4617-4639	GCTAAAGGCACATATGGCCTGTC
4618-4640	CTAAAGGCACATATGGCCTGTCT
4619-4641	TAAAGGCACATATGGCCTGTCTT
4620-4642	AAAGGCACATATGGCCTGTCTTG
4621-4643	AAGGCACATATGGCCTGTCTTGT
4622-4644	AGGCACATATGGCCTGTCTTGTC
4623-4645	GGCACATATGGCCTGTCTTGTC
4624-4646	GCACATATGGCCTGTCTTGTCAG
4625-4647	CACATATGGCCTGTCTTGTCAGA
4626-4648	ACATATGGCCTGTCTTGTCAGAG
4627-4649	CATATGGCCTGTCTTGTCAGAGG
4628-4650	ATATGGCCTGTCTTGTCAGAGGG
4629-4651	TATGGCCTGTCTTGTCAGAGGGGA
4630-4652	ATGGCCTGTCTTGTCAGAGGGAT
4631-4653	TGGCCTGTCTTGTCAGAGGGATC
4632-4654	GGCCTGTCTTGTCAGAGGGATCC
4633-4655	GCCTGTCTTGTCAGAGGGATCCT
4634-4656	CCTGTCTTGTCAGAGGGATCCTA
4635-4657	CTGTCTTGTCAGAGGGATCCTAA
4636-4658	TGTCTTGTCAGAGGGATCCTAAC
4637-4659	GTCTTGTCAGAGGGATCCTAAC
4638-4660	TCTTGTCAGAGGGATCCTAACAC
4639-4661	CTTGTCAGAGGGATCCTAACACT
4640-4662	TTGTCAGAGGGATCCTAACACTG
4641-4663	TGTCAGAGGGATCCTAACACTGG
4642-4664	GTCAGAGGGATCCTAACACTGGC
4643-4665	TCAGAGGGATCCTAACACTGGCC
4644-4666	CAGAGGGATCCTAACACTGGCCG
4645-4667	AGAGGGATCCTAACACTGGCCGG
4646-4668	GAGGGATCCTAACACTGGCCGGC
4647-4669	AGGGATCCTAACACTGGCCGGCT
4648-4670	GGGATCCTAACACTGGCCGGCTC
4649-4671	GGATCCTAACACTGGCCGGCTCA
4650-4672	GATCCTAACACTGGCCGGCTCAA
4651-4673	ATCCTAACACTGGCCGGCTCAAT
4652-4674	TCCTAACACTGGCCGGCTCAATG
4653-4675	CCTAACACTGGCCGGCTCAATGG
4654-4676	CTAACACTGGCCGGCTCAATGGA
4655-4677	TAACACTGGCCGGCTCAATGGAG
4656-4678	AACACTGGCCGGCTCAATGGAGA
4657-4679	ACACTGGCCGGCTCAATGGAGAG
4658-4680	CACTGGCCGGCTCAATGGAGAGT
4659-4681	ACTGGCCGGCTCAATGGAGAGTC
4660-4682	CTGGCCGGCTCAATGGAGAGTCC
4661-4683	TGGCCGGCTCAATGGAGAGTCCA
4662-4684	GGCCGGCTCAATGGAGAGTCCAA

Position	Sequence
4663-4685	GCCGGCTCAATGGAGAGTCCAAC
4664-4686	CCGGCTCAATGGAGAGTCCAACC
4665-4687	CGGCTCAATGGAGAGTCCAACCT
4666-4688	GGCTCAATGGAGAGTCCAACCTG
4667-4689	GCTCAATGGAGAGTCCAACCTGA
4668-4690	CTCAATGGAGAGTCCAACCTGAG
4669-4691	TCAATGGAGAGTCCAACCTGAGG
4670-4692	CAATGGAGAGTCCAACCTGAGGT
4671-4693	AATGGAGAGTCCAACCTGAGGTT
4672-4694	ATGGAGAGTCCAACCTGAGGTTT
4673-4695	TGGAGAGTCCAACCTGAGGTTTA
4674-4696	GGAGAGTCCAACCTGAGGTTTAA
4675-4697	GAGAGTCCAACCTGAGGTTTAACT
4676-4698	AGAGTCCAACCTGAGGTTTAACT
4677-4699	GAGTCCAACCTGAGGTTTAACTC
4678-4700	AGTCCAACCTGAGGTTTAACTCC
4679-4701	GTCCAACCTGAGGTTTAACTCCT
4680-4702	TCCAACCTGAGGTTTAACTCCTC
4681-4703	CCAACCTGAGGTTTAACTCCTCC
4682-4704	CAACCTGAGGTTTAACTCCTCCT
4683-4705	AACCTGAGGTTTAACTCCTCCTA
4684-4706	ACCTGAGGTTTAACTCCTCCTAC
4685-4707	CCTGAGGTTTAACTCCTCCTACC
4686-4708	CTGAGGTTTAACTCCTCCTACCT
4687-4709	TGAGGTTTAACTCCTCCTACCTC
4688-4710	GAGGTTTAACTCCTCCTACCTCC
4689-4711	AGGTTTAACTCCTCCTACCTCCA
4690-4712	GGTTTAACTCCTCCTACCTCCAA
4691-4713	GTTTAACTCCTCCTACCTCCAAG
4692-4714	TTTAACTCCTCCTACCTCCAAGG
4693-4715	TAACTCCTCCTACCTCCAAGGC
4694-4716	TAACTCCTCCTACCTCCAAGGCA
4695-4717	AACTCCTCCTACCTCCAAGGCAC
4696-4718	ACTCCTCCTACCTCCAAGGCACC
4697-4719	CTCCTCCTACCTCCAAGGCACCA
4698-4720	TCCTCCTACCTCCAAGGCACCAA
4699-4721	CCTCCTACCTCCAAGGCACCAAC
4700-4722	CTCCTACCTCCAAGGCACCAACC
4701-4723	TCCTACCTCCAAGGCACCAACCA
4702-4724	CCTACCTCCAAGGCACCAACCAG
4703-4725	CTACCTCCAAGGCACCAACCAGA
4704-4726	TACCTCCAAGGCACCAACCAGAT
4705-4727	ACCTCCAAGGCACCAACCAGATA
4706-4728	CCTCCAAGGCACCAACCAGATAA
4707-4729	CTCCAAGGCACCAACCAGATAAC
4708-4730	TCCAAGGCACCAACCAGATAACA
4709-4731	CCAAGGCACCAACCAGATAACAG
4710-4732	CAAGGCACCAACCAGATAACAGG
4711-4733	AAGGCACCAACCAGATAACAGGA
4712-4734	AGGCACCAACCAGATAACAGGAA
4713-4735	GGCACCAACCAGATAACAGGAAG
4714-4736	GCACCAACCAGATAACAGGAAGA
4715-4737	CACCAACCAGATAACAGGAAGAT
4716-4738	ACCAACCAGATAACAGGAAGATA
4717-4739	CCAACCAGATAACAGGAAGATAT
4718-4740	CAACCAGATAACAGGAAGATATG
4719-4741	AACCAGATAACAGGAAGATATGA
4720-4742	ACCAGATAACAGGAAGATATGAA
4721-4743	CCAGATAACAGGAAGATATGAAG
4722-4744	CAGATAACAGGAAGATATGAAGA
4723-4745	AGATAACAGGAAGATATGAAGAT
4724-4746	GATAACAGGAAGATATGAAGATG
4725-4747	ATAACAGGAAGATATGAAGATGG
4726-4748	TAAACAGGAAGATATGAAGATGGA
4727-4749	AACAGGAAGATATGAAGATGGAA
4728-4750	ACAGGAAGATATGAAGATGGAAC

Position	Sequence
4729-4751	CAGGAAGATATGAAGATGGAACC
4730-4752	AGGAAGATATGAAGATGGAACCC
4731-4753	GGAAGATATGAAGATGGAACCCT
4732-4754	GAAGATATGAAGATGGAACCCTC
4733-4755	AAGATATGAAGATGGAACCCTCT
4734-4756	AGATATGAAGATGGAACCCTCTC
4735-4757	GATATGAAGATGGAACCCTCTCC
4736-4758	ATATGAAGATGGAACCCTCTCCC
4737-4759	TATGAAGATGGAACCCTCTCCCT
4738-4760	ATGAAGATGGAACCCTCTCCCTC
4739-4761	TGAAGATGGAACCCTCTCCCTCA
4740-4762	GAAGATGGAACCCTCTCCCTCAC
4741-4763	AAGATGGAACCCTCTCCCTCACC
4742-4764	AGATGGAACCCTCTCCCTCACCT
4743-4765	GATGGAACCCTCTCCCTCACCTC
4744-4766	ATGGAACCCTCTCCCTCACCTCC
4745-4767	TGGAACCCTCTCCCTCACCTCCA
4746-4768	GGAACCCTCTCCCTCACCTCCAC
4747-4769	GAACCCTCTCCCTCACCTCCACC
4748-4770	AACCCTCTCCCTCACCTCCACCT
4749-4771	ACCCTCTCCCTCACCTCCACCTC
4750-4772	CCCTCTCCCTCACCTCCACCTCT
4751-4773	CCTCTCCCTCACCTCCACCTCTG
4752-4774	CTCTCCCTCACCTCCACCTCTGA
4753-4775	TCTCCCTCACCTCCACCTCTGAT
4754-4776	CTCCCTCACCTCCACCTCTGATC
4755-4777	TCCCTCACCTCCACCTCTGATCT
4756-4778	CCCTCACCTCCACCTCTGATCTG
4757-4779	CCTCACCTCCACCTCTGATCTGTC
4758-4780	CTCACCTCCACCTCTGATCTGCA
4759-4781	TCACCTCCACCTCTGATCTGCAA
4760-4782	CACCTCCACCTCTGATCTGCAAA
4761-4783	ACCTCCACCTCTGATCTGCAAAG
4762-4784	CCTCCACCTCTGATCTGCAAAGT
4763-4785	CTCCACCTCTGATCTGCAAAGTG
4764-4786	TCCACCTCTGATCTGCAAAGTGG
4765-4787	CCACCTCTGATCTGCAAAGTGGC
4766-4788	CACCTCTGATCTGCAAAGTGGCA
4767-4789	ACCTCTGATCTGCAAAGTGGCAT
4768-4790	CCTCTGATCTGCAAAGTGGCATC
4769-4791	CTCTGATCTGCAAAGTGGCATCA
4770-4792	TCTGATCTGCAAAGTGGCATCAT
4771-4793	CTGATCTGCAAAGTGGCATCATT
4772-4794	TGATCTGCAAAGTGGCATCATTAA
4773-4795	GATCTGCAAAGTGGCATCATTAAA
4774-4796	ATCTGCAAAGTGGCATCATTAAAA
4775-4797	TCTGCAAAGTGGCATCATTAAAAA
4776-4798	CTGCAAAGTGGCATCATTAAAAAA
4777-4799	TGCAAAGTGGCATCATTAAAAAAT
4778-4800	GCAAAGTGGCATCATTAAAAATA
4779-4801	CAAAGTGGCATCATTAAAAATAC
4780-4802	AAAGTGGCATCATTAAAAATACT
4781-4803	AAGTGGCATCATTAAAAATACTG
4782-4804	AGTGGCATCATTAAAAATACTGC
4783-4805	GTGGCATCATTAAAAATACTGCT
4784-4806	TGGCATCATTAAAAATACTGCTT
4785-4807	GGCATCATTAAAAATACTGCTTC
4786-4808	GCATCATTAAAAATACTGCTTCC
4787-4809	CATCATTAAAAATACTGCTTCCC
4788-4810	ATCATTAAAAATACTGCTTCCCT
4789-4811	TCATTAAAAATACTGCTTCCCTA
4790-4812	CATTAAAAATACTGCTTCCCTAA
4791-4813	ATTAAAAATACTGCTTCCCTAAA
4792-4814	TAAAAATACTGCTTCCCTAAAG
4793-4815	TAAAAATACTGCTTCCCTAAAGT
4794-4816	AAAAATACTGCTTCCCTAAAGTA

Position	Sequence
4795-4817	AAAATACTGCTTCCCTAAAGTAT
4796-4818	AAATACTGCTTCCCTAAAGTATG
4797-4819	AATACTGCTTCCCTAAAGTATGA
4798-4820	ATACTGCTTCCCTAAAGTATGAG
4799-4821	TACTGCTTCCCTAAAGTATGAGA
4800-4822	ACTGCTTCCCTAAAGTATGAGAA
4801-4823	CTGCTTCCCTAAAGTATGAGAAC
4802-4824	TGCTTCCCTAAAGTATGAGAACT
4803-4825	GCTTCCCTAAAGTATGAGAACTA
4804-4826	CTTCCCTAAAGTATGAGAACTAC
4805-4827	TTCCCTAAAGTATGAGAACTACG
4806-4828	TCCCTAAAGTATGAGAACTACGA
4807-4829	CCCTAAAGTATGAGAACTACGAG
4808-4830	CCTAAAGTATGAGAACTACGAGC
4809-4831	CTAAAGTATGAGAACTACGAGCT
4810-4832	TAAAGTATGAGAACTACGAGCTG
4811-4833	AAAGTATGAGAACTACGAGCTGA
4812-4834	AAGTATGAGAACTACGAGCTGAC
4813-4835	AGTATGAGAACTACGAGCTGACT
4814-4836	GTATGAGAACTACGAGCTGACTT
4815-4837	TATGAGAACTACGAGCTGACTTT
4816-4838	ATGAGAACTACGAGCTGACTTTA
4817-4839	TGAGAACTACGAGCTGACTTTAA
4818-4840	GAGAACTACGAGCTGACTTTAAA
4819-4841	AGAACTACGAGCTGACTTTAAAA
4820-4842	GAACCTACGAGCTGACTTTAAAAT
4821-4843	AACTACGAGCTGACTTTAAAATC
4822-4844	ACTACGAGCTGACTTTAAAATCT
4823-4845	CTACGAGCTGACTTTAAAATCTG
4824-4846	TACGAGCTGACTTTAAAATCTGA
4825-4847	ACGAGCTGACTTTAAAATCTGAC
4826-4848	CGAGCTGACTTTAAAATCTGACA
4827-4849	GAGCTGACTTTAAAATCTGACAC
4828-4850	AGCTGACTTTAAAATCTGACACC
4829-4851	GCTGACTTTAAAATCTGACACCA
4830-4852	CTGACTTTAAAATCTGACACCAA
4831-4853	TGACTTTAAAATCTGACACCAAT
4832-4854	GACTTTAAAATCTGACACCAATG
4833-4855	ACTTTAAAATCTGACACCAATGG
4834-4856	CTTTAAAATCTGACACCAATGGG
4835-4857	TTTAAAATCTGACACCAATGGGA
4836-4858	TTAAAATCTGACACCAATGGGAA
4837-4859	TAAAATCTGACACCAATGGGAAG
4838-4860	AAAATCTGACACCAATGGGAAGT
4839-4861	AAATCTGACACCAATGGGAAGTA
4840-4862	AATCTGACACCAATGGGAAGTAT
4841-4863	ATCTGACACCAATGGGAAGTATA
4842-4864	TCTGACACCAATGGGAAGTATAA
4843-4865	CTGACACCAATGGGAAGTATAAG
4844-4866	TGACACCAATGGGAAGTATAAGA
4845-4867	GACACCAATGGGAAGTATAAGAA
4846-4868	ACACCAATGGGAAGTATAAGAAC
4847-4869	CACCAATGGGAAGTATAAGAACT
4848-4870	ACCAATGGGAAGTATAAGAACTT
4849-4871	CCAATGGGAAGTATAAGAACTTT
4850-4872	CAATGGGAAGTATAAGAACTTTG
4851-4873	AATGGGAAGTATAAGAACTTTGC
4852-4874	ATGGGAAGTATAAGAACTTTGCC
4853-4875	TGGGAAGTATAAGAACTTTGCCA
4854-4876	GGGAAGTATAAGAACTTTGCCAC
4855-4877	GGAAGTATAAGAACTTTGCCACT
4856-4878	GAAGTATAAGAACTTTGCCACTT
4857-4879	AAGTATAAGAACTTTGCCACTTC
4858-4880	AGTATAAGAACTTTGCCACTTCT
4859-4881	GTATAAGAACTTTGCCACTTCTA
4860-4882	TATAAGAACTTTGCCACTTCTAA

Position	Sequence
4861-4883	ATAAGAACTTTGCCACTTCTAAC
4862-4884	TAAGAACTTTGCCACTTCTAACA
4863-4885	AAGAACTTTGCCACTTCTAACAA
4864-4886	AGAACTTTGCCACTTCTAACAAG
4865-4887	GAACTTTGCCACTTCTAACAAGA
4866-4888	AACTTTGCCACTTCTAACAAGAT
4867-4889	ACTTTGCCACTTCTAACAAGATG
4868-4890	CTTTGCCACTTCTAACAAGATGG
4869-4891	TTTGCCACTTCTAACAAGATGGA
4870-4892	TTGCCACTTCTAACAAGATGGAT
4871-4893	TGCCACTTCTAACAAGATGGATA
4872-4894	GCCACTTCTAACAAGATGGATAT
4873-4895	CCACTTCTAACAAGATGGATATG
4874-4896	CACTTCTAACAAGATGGATATGA
4875-4897	ACTTCTAACAAGATGGATATGAC
4876-4898	CTTCTAACAAGATGGATATGACC
4877-4899	TTCTAACAAGATGGATATGACCT
4878-4900	TCTAACAAGATGGATATGACCTT
4879-4901	CTAACAAGATGGATATGACCTTC
4880-4902	TAACAAGATGGATATGACCTTCT
4881-4903	AACAAGATGGATATGACCTTCTC
4882-4904	ACAAGATGGATATGACCTTCTCT
4883-4905	CAAGATGGATATGACCTTCTCTA
4884-4906	AAGATGGATATGACCTTCTCTAA
4885-4907	AGATGGATATGACCTTCTCTAAG
4886-4908	GATGGATATGACCTTCTCTAAGC
4887-4909	ATGGATATGACCTTCTCTAAGCA
4888-4910	TGGATATGACCTTCTCTAAGCAA
4889-4911	GGATATGACCTTCTCTAAGCAAA
4890-4912	GATATGACCTTCTCTAAGCAAAA
4891-4913	ATATGACCTTCTCTAAGCAAAT
4892-4914	TATGACCTTCTCTAAGCAAATG
4893-4915	ATGACCTTCTCTAAGCAAATGC
4894-4916	TGACCTTCTCTAAGCAAATGCA
4895-4917	GACCTTCTCTAAGCAAATGCAC
4896-4918	ACCTTCTCTAAGCAAATGCACT
4897-4919	CCTTCTCTAAGCAAATGCACTG
4898-4920	CTTCTCTAAGCAAATGCACTGC
4899-4921	TTCTCTAAGCAAATGCACTGCT
4900-4922	TCTCTAAGCAAATGCACTGCTG
4901-4923	CTCTAAGCAAATGCACTGCTGC
4902-4924	TCTAAGCAAATGCACTGCTGCG
4903-4925	CTAAGCAAATGCACTGCTGCGT
4904-4926	TAAGCAAATGCACTGCTGCGTT
4905-4927	AAGCAAATGCACTGCTGCGTTC
4906-4928	AGCAAATGCACTGCTGCGTTCT
4907-4929	GCAAATGCACTGCTGCGTTCTG
4908-4930	CAAATGCACTGCTGCGTTCTGA
4909-4931	AAATGCACTGCTGCGTTCTGAA
4910-4932	AAATGCACTGCTGCGTTCTGAAT
4911-4933	AATGCACTGCTGCGTTCTGAATA
4912-4934	ATGCACTGCTGCGTTCTGAATAT
4913-4935	TGCACTGCTGCGTTCTGAATATC
4914-4936	GCACTGCTGCGTTCTGAATATCA
4915-4937	CACTGCTGCGTTCTGAATATCAG
4916-4938	ACTGCTGCGTTCTGAATATCAGG
4917-4939	CTGCTGCGTTCTGAATATCAGGC
4918-4940	TGCTGCGTTCTGAATATCAGGCT
4919-4941	GCTGCGTTCTGAATATCAGGCTG
4920-4942	CTGCGTTCTGAATATCAGGCTGA
4921-4943	TGCGTTCTGAATATCAGGCTGAT
4922-4944	GCGTTCTGAATATCAGGCTGATT
4923-4945	CGTTCTGAATATCAGGCTGATTA
4924-4946	GTTCTGAATATCAGGCTGATTAC
4925-4947	TTCTGAATATCAGGCTGATTACG
4926-4948	TCTGAATATCAGGCTGATTACGA

Position	Sequence
4927-4949	CTGAATATCAGGCTGATTACGAG
4928-4950	TGAATATCAGGCTGATTACGAGT
4929-4951	GAATATCAGGCTGATTACGAGTC
4930-4952	AATATCAGGCTGATTACGAGTCA
4931-4953	ATATCAGGCTGATTACGAGTCAT
4932-4954	TATCAGGCTGATTACGAGTCATT
4933-4955	ATCAGGCTGATTACGAGTCATTG
4934-4956	TCAGGCTGATTACGAGTCATTGA
4935-4957	CAGGCTGATTACGAGTCATTGAG
4936-4958	AGGCTGATTACGAGTCATTGAGG
4937-4959	GGCTGATTACGAGTCATTGAGGT
4938-4960	GCTGATTACGAGTCATTGAGGTT
4939-4961	CTGATTACGAGTCATTGAGGTTTC
4940-4962	TGATTACGAGTCATTGAGGTTCT
4941-4963	GATTACGAGTCATTGAGGTTCTT
4942-4964	ATTACGAGTCATTGAGGTTCTTC
4943-4965	TTACGAGTCATTGAGGTTCTTCA
4944-4966	TACGAGTCATTGAGGTTCTTCAG
4945-4967	ACGAGTCATTGAGGTTCTTCAGC
4946-4968	CGAGTCATTGAGGTTCTTCAGCC
4947-4969	GAGTCATTGAGGTTCTTCAGCCT
4948-4970	AGTCATTGAGGTTCTTCAGCCTG
4949-4971	GTCATTGAGGTTCTTCAGCCTGC
4950-4972	TCATTGAGGTTCTTCAGCCTGCT
4951-4973	CATTGAGGTTCTTCAGCCTGCTT
4952-4974	ATTGAGGTTCTTCAGCCTGCTTT
4953-4975	TTGAGGTTCTTCAGCCTGCTTTC
4954-4976	TGAGGTTCTTCAGCCTGCTTTCT
4955-4977	GAGGTTCTTCAGCCTGCTTTCTG
4956-4978	AGGTTCTTCAGCCTGCTTTCTGG
4957-4979	GGTTCTTCAGCCTGCTTTCTGGA
4958-4980	GTTCTTCAGCCTGCTTTCTGGAT
4959-4981	TTCTTCAGCCTGCTTTCTGGATC
4960-4982	TCTTCAGCCTGCTTTCTGGATCA
4961-4983	CTTCAGCCTGCTTTCTGGATCAC
4962-4984	TTCAGCCTGCTTTCTGGATCACT
4963-4985	TCAGCCTGCTTTCTGGATCACTA
4964-4986	CAGCCTGCTTTCTGGATCACTAA
4965-4987	AGCCTGCTTTCTGGATCACTAAA
4966-4988	GCCTGCTTTCTGGATCACTAAAT
4967-4989	CCTGCTTTCTGGATCACTAAATT
4968-4990	CTGCTTTCTGGATCACTAAATTC
4969-4991	TGCTTTCTGGATCACTAAATTCC
4970-4992	GCTTTCTGGATCACTAAATTCCC
4971-4993	CTTCTGGATCACTAAATCCCA
4972-4994	TTCTGGATCACTAAATCCCAT
4973-4995	TTCTGGATCACTAAATCCCATG
4974-4996	TCTGGATCACTAAATCCCATGG
4975-4997	CTGGATCACTAAATCCCATGGT
4976-4998	TGGATCACTAAATCCCATGGTC
4977-4999	GGATCACTAAATCCCATGGTCT
4978-5000	GATCACTAAATCCCATGGTCTT
4979-5001	ATCACTAAATCCCATGGTCTTG
4980-5002	TCACTAAATCCCATGGTCTTGA
4981-5003	CACTAAATCCCATGGTCTTGAG
4982-5004	ACTAAATCCCATGGTCTTGAGT
4983-5005	CTAAATCCCATGGTCTTGAGTT
4984-5006	TAAATCCCATGGTCTTGAGTTA
4985-5007	AAATCCCATGGTCTTGAGTTAA
4986-5008	AATCCCATGGTCTTGAGTTAAA
4987-5009	ATTCCCATGGTCTTGAGTTAAAT
4988-5010	TCCCATGGTCTTGAGTTAAATG
4989-5011	TCCCATGGTCTTGAGTTAAATGC
4990-5012	CCCATGGTCTTGAGTTAAATGCT
4991-5013	CCATGGTCTTGAGTTAAATGCTG
4992-5014	CATGGTCTTGAGTTAAATGCTGA

Position	Sequence
4993-5015	ATGGTCTTGAGTTAAATGCTGAC
4994-5016	TGGTCTTGAGTTAAATGCTGACA
4995-5017	GGTCTTGAGTTAAATGCTGACAT
4996-5018	GTCTTGAGTTAAATGCTGACATC
4997-5019	TCTTGAGTTAAATGCTGACATCT
4998-5020	CTTGAGTTAAATGCTGACATCTT
4999-5021	TTGAGTTAAATGCTGACATCTTA
5000-5022	TGAGTTAAATGCTGACATCTTAG
5001-5023	GAGTTAAATGCTGACATCTTAGG
5002-5024	AGTTAAATGCTGACATCTTAGGC
5003-5025	GTTAAATGCTGACATCTTAGGCA
5004-5026	TAAATGCTGACATCTTAGGCAC
5005-5027	TAAATGCTGACATCTTAGGCACT
5006-5028	AAATGCTGACATCTTAGGCACTG
5007-5029	AATGCTGACATCTTAGGCACTGA
5008-5030	ATGCTGACATCTTAGGCACTGAC
5009-5031	TGCTGACATCTTAGGCACTGACA
5010-5032	GCTGACATCTTAGGCACTGACAA
5011-5033	CTGACATCTTAGGCACTGACAAA
5012-5034	TGACATCTTAGGCACTGACAAAA
5013-5035	GACATCTTAGGCACTGACAAAAT
5014-5036	ACATCTTAGGCACTGACAAAATT
5015-5037	CATCTTAGGCACTGACAAAATTA
5016-5038	ATCTTAGGCACTGACAAAATTA
5017-5039	TCTTAGGCACTGACAAAATTAAT
5018-5040	CTTAGGCACTGACAAAATTAATA
5019-5041	TTAGGCACTGACAAAATTAATAG
5020-5042	TAGGCACTGACAAAATTAATAGT
5021-5043	AGGCACTGACAAAATTAATAGTG
5022-5044	GGCACTGACAAAATTAATAGTGG
5023-5045	GCACTGACAAAATTAATAGTGGT
5024-5046	CACTGACAAAATTAATAGTGGTG
5025-5047	ACTGACAAAATTAATAGTGGTGC
5026-5048	CTGACAAAATTAATAGTGGTGCT
5027-5049	TGACAAAATTAATAGTGGTGCTC
5028-5050	GACAAAATTAATAGTGGTGCTCA
5029-5051	ACAAAATTAATAGTGGTGCTCAC
5030-5052	CAAAAATTAATAGTGGTGCTCACA
5031-5053	AAAATTAATAGTGGTGCTCACAA
5032-5054	AAATTAATAGTGGTGCTCACAAAG
5033-5055	AATTAATAGTGGTGCTCACAAAGG
5034-5056	ATTAATAGTGGTGCTCACAAAGGC
5035-5057	TTAATAGTGGTGCTCACAAAGCG
5036-5058	TAATAGTGGTGCTCACAAAGCGGA
5037-5059	AATAGTGGTGCTCACAAAGCGGAC
5038-5060	ATAGTGGTGCTCACAAAGCGGACA
5039-5061	TAGTGGTGCTCACAAAGCGGACAC
5040-5062	AGTGGTGCTCACAAAGCGGACACT
5041-5063	GTGGTGCTCACAAAGCGGACACTA
5042-5064	TGGTGCTCACAAAGCGGACACTAA
5043-5065	GGTGCTCACAAAGCGGACACTAAG
5044-5066	GTGCTCACAAAGCGGACACTAAGG
5045-5067	TGCTCACAAAGCGGACACTAAGGA
5046-5068	GCTCACAAAGCGGACACTAAGGAT
5047-5069	CTCACAAAGCGGACACTAAGGATT
5048-5070	TCACAAAGCGGACACTAAGGATTG
5049-5071	CACAAGCGGACACTAAGGATTGG
5050-5072	ACAAGCGGACACTAAGGATTGGC
5051-5073	CAAGCGGACACTAAGGATTGGCC
5052-5074	AAGCGGACACTAAGGATTGGCCA
5053-5075	AGCGGACACTAAGGATTGGCCAA
5054-5076	GGCGGACACTAAGGATTGGCCAAG
5055-5077	GCGGACACTAAGGATTGGCCAAGA
5056-5078	CGGACACTAAGGATTGGCCAAGAT
5057-5079	GACACTAAGGATTGGCCAAGATG
5058-5080	ACACTAAGGATTGGCCAAGATGG

Position	Sequence
5059-5081	CACTAAGGATTGGCCAAGATGGA
5060-5082	ACTAAGGATTGGCCAAGATGGAA
5061-5083	CTAAGGATTGGCCAAGATGGAAT
5062-5084	TAAGGATTGGCCAAGATGGAATA
5063-5085	AAGGATTGGCCAAGATGGAATAT
5064-5086	AGGATTGGCCAAGATGGAATATC
5065-5087	GGATTGGCCAAGATGGAATATCT
5066-5088	GATTGGCCAAGATGGAATATCTA
5067-5089	ATGGCCAAGATGGAATATCTAC
5068-5090	TTGGCCAAGATGGAATATCTACC
5069-5091	TGGCCAAGATGGAATATCTACCA
5070-5092	GGCCAAGATGGAATATCTACCAG
5071-5093	GCCAAGATGGAATATCTACCAGT
5072-5094	CCAAGATGGAATATCTACCAGTG
5073-5095	CAAGATGGAATATCTACCAGTGC
5074-5096	AAGATGGAATATCTACCAGTGCA
5075-5097	AGATGGAATATCTACCAGTGCAA
5076-5098	GATGGAATATCTACCAGTGCAAC
5077-5099	ATGGAATATCTACCAGTGCAACG
5078-5100	TGGAATATCTACCAGTGCAACGA
5079-5101	GGAAATATCTACCAGTGCAACGAC
5080-5102	GAATATCTACCAGTGCAACGACC
5081-5103	AATATCTACCAGTGCAACGACCA
5082-5104	ATATCTACCAGTGCAACGACCAA
5083-5105	TATCTACCAGTGCAACGACCAAC
5084-5106	ATCTACCAGTGCAACGACCAACT
5085-5107	TCTACCAGTGCAACGACCAACTT
5086-5108	CTACCAGTGCAACGACCAACTTG
5087-5109	TACCAGTGCAACGACCAACTTGA
5088-5110	ACCAGTGCAACGACCAACTTGAA
5089-5111	CCAGTGCAACGACCAACTTGAAG
5090-5112	CAGTGCAACGACCAACTTGAAGT
5091-5113	AGTGCAACGACCAACTTGAAGTG
5092-5114	GTGCAACGACCAACTTGAAGTGT
5093-5115	TGCAACGACCAACTTGAAGTGTA
5094-5116	GCAACGACCAACTTGAAGTGTAG
5095-5117	CAACGACCAACTTGAAGTGTAGT
5096-5118	AACGACCAACTTGAAGTGTAGTCT
5097-5119	ACGACCAACTTGAAGTGTAGTCT
5098-5120	CGACCAACTTGAAGTGTAGTCTC
5099-5121	GACCAACTTGAAGTGTAGTCTCC
5100-5122	ACCAACTTGAAGTGTAGTCTCCT
5101-5123	CCAACTTGAAGTGTAGTCTCCTG
5102-5124	CAACTTGAAGTGTAGTCTCCTGG
5103-5125	AACTTGAAGTGTAGTCTCCTGGT
5104-5126	ACTTGAAGTGTAGTCTCCTGGTG
5105-5127	CTTGAAGTGTAGTCTCCTGGTGC
5106-5128	TTGAAGTGTAGTCTCCTGGTGCT
5107-5129	TGAAGTGTAGTCTCCTGGTGCTG
5108-5130	GAAGTGTAGTCTCCTGGTGCTGG
5109-5131	AAGTGTAGTCTCCTGGTGCTGGGA
5110-5132	AGTGTAGTCTCCTGGTGCTGGGAG
5111-5133	GTGTAGTCTCCTGGTGCTGGAGA
5112-5134	TGTAGTCTCCTGGTGCTGGAGAA
5113-5135	GTAGTCTCCTGGTGCTGGAGAAAT
5114-5136	TAGTCTCCTGGTGCTGGAGAAATG
5115-5137	AGTCTCCTGGTGCTGGAGAAATGA
5116-5138	GTCTCCTGGTGCTGGAGAAATGAG
5117-5139	TCTCCTGGTGCTGGAGAAATGAGC
5118-5140	CTCCTGGTGCTGGAGAAATGAGCT
5119-5141	TCCTGGTGCTGGAGAAATGAGCTG
5120-5142	CCTGGTGCTGGAGAAATGAGCTGA
5121-5143	CTGGTGCTGGAGAAATGAGCTGAA
5122-5144	TGGTGCTGGAGAAATGAGCTGAAT
5123-5145	GGTGCTGGAGAAATGAGCTGAATG
5124-5146	GTGCTGGAGAAATGAGCTGAATGC

Position	Sequence
5125-5147	TGCTGGAGAATGAGCTGAATGCA
5126-5148	GCTGGAGAATGAGCTGAATGCAG
5127-5149	CTGGAGAATGAGCTGAATGCAGA
5128-5150	TGGAGAATGAGCTGAATGCAGAG
5129-5151	GGAGAATGAGCTGAATGCAGAGC
5130-5152	GAGAATGAGCTGAATGCAGAGCT
5131-5153	AGAATGAGCTGAATGCAGAGCTT
5132-5154	GAATGAGCTGAATGCAGAGCTTG
5133-5155	AATGAGCTGAATGCAGAGCTTGG
5134-5156	ATGAGCTGAATGCAGAGCTTGGC
5135-5157	TGAGCTGAATGCAGAGCTTGGCC
5136-5158	GAGCTGAATGCAGAGCTTGGCCT
5137-5159	AGCTGAATGCAGAGCTTGGCCTC
5138-5160	GCTGAATGCAGAGCTTGGCCTCT
5139-5161	CTGAATGCAGAGCTTGGCCTCTC
5140-5162	TGAATGCAGAGCTTGGCCTCTCT
5141-5163	GAATGCAGAGCTTGGCCTCTCTG
5142-5164	AATGCAGAGCTTGGCCTCTCTGG
5143-5165	ATGCAGAGCTTGGCCTCTCTGGG
5144-5166	TGCAGAGCTTGGCCTCTCTGGGG
5145-5167	GCAGAGCTTGGCCTCTCTGGGGC
5146-5168	CAGAGCTTGGCCTCTCTGGGGCA
5147-5169	AGAGCTTGGCCTCTCTGGGGCAT
5148-5170	GAGCTTGGCCTCTCTGGGGCATC
5149-5171	AGCTTGGCCTCTCTGGGGCATCT
5150-5172	GCTTGGCCTCTCTGGGGCATCTA
5151-5173	CTTGGCCTCTCTGGGGCATCTAT
5152-5174	TTGGCCTCTCTGGGGCATCTATG
5153-5175	TGGCCTCTCTGGGGCATCTATGA
5154-5176	GGCCTCTCTGGGGCATCTATGAA
5155-5177	GCCTCTCTGGGGCATCTATGAAA
5156-5178	CCTCTCTGGGGCATCTATGAAAT
5157-5179	CTCTCTGGGGCATCTATGAAATT
5158-5180	TCTCTGGGGCATCTATGAAATTA
5159-5181	CTCTGGGGCATCTATGAAATTAA
5160-5182	TCTGGGGCATCTATGAAATTAAC
5161-5183	CTGGGGCATCTATGAAATTAACA
5162-5184	TGGGGCATCTATGAAATTAACAA
5163-5185	GGGGCATCTATGAAATTAACAAC
5164-5186	GGGCATCTATGAAATTAACAACA
5165-5187	GGCATCTATGAAATTAACAACAA
5166-5188	GCATCTATGAAATTAACAACAAA
5167-5189	CATCTATGAAATTAACAACAAAT
5168-5190	ATCTATGAAATTAACAACAAATG
5169-5191	TCTATGAAATTAACAACAAATGG
5170-5192	CTATGAAATTAACAACAAATGGC
5171-5193	TATGAAATTAACAACAAATGGCC
5172-5194	ATGAAATTAACAACAAATGGCCG
5173-5195	TGAAATTAACAACAAATGGCCGC
5174-5196	GAAATTAACAACAAATGGCCGCT
5175-5197	AAATTAACAACAAATGGCCGCTT
5176-5198	AATTAACAACAAATGGCCGCTTC
5177-5199	ATTAACAACAAATGGCCGCTTCA
5178-5200	TTAACAACAAATGGCCGCTTCAG
5179-5201	TAACAACAAATGGCCGCTTCAGG
5180-5202	AACAACAAATGGCCGCTTCAGGG
5181-5203	ACAACAAATGGCCGCTTCAGGGA
5182-5204	CAACAAATGGCCGCTTCAGGGAA
5183-5205	AACAAATGGCCGCTTCAGGGAAC
5184-5206	ACAATGGCCGCTTCAGGGAAACA
5185-5207	CAAATGGCCGCTTCAGGGAAACAC
5186-5208	AAATGGCCGCTTCAGGGAAACACA
5187-5209	AATGGCCGCTTCAGGGAAACACAA
5188-5210	ATGGCCGCTTCAGGGAAACACAAT
5189-5211	TGGCCGCTTCAGGGAAACACAATG
5190-5212	GGCCGCTTCAGGGAAACACAATGC

Position	Sequence
5191-5213	GCCGCTTCAGGGAACACAATGCA
5192-5214	CGGCTTCAGGGAACACAATGCAA
5193-5215	CGCTTCAGGGAACACAATGCAA
5194-5216	GCTTCAGGGAACACAATGCAAAA
5195-5217	CTTCAGGGAACACAATGCAAAAT
5196-5218	TTCAGGGAACACAATGCAAAAT
5197-5219	TCAGGGAACACAATGCAAAATTC
5198-5220	CAGGGAACACAATGCAAAATTC
5199-5221	AGGGAACACAATGCAAAATTCAG
5200-5222	GGAACACAATGCAAAATTCAGT
5201-5223	GGAACACAATGCAAAATTCAGTC
5202-5224	GAACACAATGCAAAATTCAGTCT
5203-5225	AACACAATGCAAAATTCAGTCTG
5204-5226	ACACAATGCAAAATTCAGTCTGG
5205-5227	CACAATGCAAAATTCAGTCTGGA
5206-5228	ACAATGCAAAATTCAGTCTGGAT
5207-5229	CAATGCAAAATTCAGTCTGGATG
5208-5230	AATGCAAAATTCAGTCTGGATGG
5209-5231	ATGCAAAATTCAGTCTGGATGGG
5210-5232	TGCAAAATTCAGTCTGGATGGGA
5211-5233	GCAAAATTCAGTCTGGATGGGAA
5212-5234	CAAAATTCAGTCTGGATGGGAAA
5213-5235	AAAATTCAGTCTGGATGGGAAAG
5214-5236	AAATTCAGTCTGGATGGGAAAGC
5215-5237	AATTCAGTCTGGATGGGAAAGCC
5216-5238	ATTCAGTCTGGATGGGAAAGCCG
5217-5239	TTCAGTCTGGATGGGAAAGCCGC
5218-5240	TCAGTCTGGATGGGAAAGCCGCC
5219-5241	CAGTCTGGATGGGAAAGCCGCC
5220-5242	AGTCTGGATGGGAAAGCCGCCCT
5221-5243	GTCTGGATGGGAAAGCCGCCCTC
5222-5244	TCTGGATGGGAAAGCCGCCCTCA
5223-5245	CTGGATGGGAAAGCCGCCCTCAC
5224-5246	TGGATGGGAAAGCCGCCCTCACA
5225-5247	GGATGGGAAAGCCGCCCTCACAG
5226-5248	GATGGGAAAGCCGCCCTCACAGA
5227-5249	ATGGGAAAGCCGCCCTCACAGAG
5228-5250	TGGGAAAGCCGCCCTCACAGAGC
5229-5251	GGGAAAGCCGCCCTCACAGAGCT
5230-5252	GGAAGCCGCCCTCACAGAGCTA
5231-5253	GAAAGCCGCCCTCACAGAGCTAT
5232-5254	AAAGCCGCCCTCACAGAGCTATC
5233-5255	AAGCCGCCCTCACAGAGCTATCA
5234-5256	AGCCGCCCTCACAGAGCTATCAC
5235-5257	GCCGCCCTCACAGAGCTATCACT
5236-5258	CCGCCCTCACAGAGCTATCACTG
5237-5259	CGCCCTCACAGAGCTATCACTGG
5238-5260	GCCTCACAGAGCTATCACTGGG
5239-5261	CCCTCACAGAGCTATCACTGGGA
5240-5262	CCTCACAGAGCTATCACTGGGAA
5241-5263	CTCACAGAGCTATCACTGGGAAG
5242-5264	TCACAGAGCTATCACTGGGAAGT
5243-5265	CACAGAGCTATCACTGGGAAGTG
5244-5266	ACAGAGCTATCACTGGGAAGTGC
5245-5267	CAGAGCTATCACTGGGAAGTGCT
5246-5268	AGAGCTATCACTGGGAAGTGCTT
5247-5269	GAGCTATCACTGGGAAGTGCTTA
5248-5270	AGCTATCACTGGGAAGTGCTTAT
5249-5271	GCTATCACTGGGAAGTGCTTATC
5250-5272	CTATCACTGGGAAGTGCTTATCA
5251-5273	TATCACTGGGAAGTGCTTATCAG
5252-5274	ATCACTGGGAAGTGCTTATCAGG
5253-5275	TCACTGGGAAGTGCTTATCAGGC
5254-5276	CACTGGGAAGTGCTTATCAGGCC
5255-5277	ACTGGGAAGTGCTTATCAGGCCA
5256-5278	CTGGGAAGTGCTTATCAGGCCAT

Position	Sequence
5257-5279	TGGGAAGTGCTTATCAGGCCATG
5258-5280	GGGAAGTGCTTATCAGGCCATGA
5259-5281	GGAAGTGCTTATCAGGCCATGAT
5260-5282	GAAGTGCTTATCAGGCCATGATT
5261-5283	AAGTGCTTATCAGGCCATGATTC
5262-5284	AGTGCTTATCAGGCCATGATTCT
5263-5285	GTGCTTATCAGGCCATGATTCTG
5264-5286	TGCTTATCAGGCCATGATTCTGG
5265-5287	GCTTATCAGGCCATGATTCTGGG
5266-5288	CTTATCAGGCCATGATTCTGGGT
5267-5289	TTATCAGGCCATGATTCTGGGTG
5268-5290	TATCAGGCCATGATTCTGGGTGT
5269-5291	ATCAGGCCATGATTCTGGGTGTC
5270-5292	TCAGGCCATGATTCTGGGTGTCG
5271-5293	CAGGCCATGATTCTGGGTGTCGA
5272-5294	AGGCCATGATTCTGGGTGTCGAC
5273-5295	GGCCATGATTCTGGGTGTCGACA
5274-5296	GCCATGATTCTGGGTGTCGACAG
5275-5297	CCATGATTCTGGGTGTCGACAGC
5276-5298	CATGATTCTGGGTGTCGACAGCA
5277-5299	ATGATTCTGGGTGTCGACAGCAA
5278-5300	TGATTCTGGGTGTCGACAGCAAA
5279-5301	GATTCTGGGTGTCGACAGCAAAA
5280-5302	ATTCTGGGTGTCGACAGCAAAAA
5281-5303	TTCTGGGTGTCGACAGCAAAAAAC
5282-5304	TCTGGGTGTCGACAGCAAAAAACA
5283-5305	CTGGGTGTCGACAGCAAAAAACAT
5284-5306	TGGGTGTCGACAGCAAAAAACATT
5285-5307	GGGTGTCGACAGCAAAAAACATTT
5286-5308	GGTGTGACAGCAAAAAACATTTT
5287-5309	GTGTGACAGCAAAAAACATTTTC
5288-5310	TGTGACAGCAAAAAACATTTTCA
5289-5311	GTCGACAGCAAAAAACATTTTCAA
5290-5312	TCGACAGCAAAAAACATTTTCAAC
5291-5313	CGACAGCAAAAAACATTTTCAACT
5292-5314	GACAGCAAAAAACATTTTCAACTT
5293-5315	ACAGCAAAAAACATTTTCAACTTC
5294-5316	CAGCAAAAAACATTTTCAACTTCA
5295-5317	AGCAAAAAACATTTTCAACTTCAA
5296-5318	GCAAAAAACATTTTCAACTTCAAG
5297-5319	CAAAAAACATTTTCAACTTCAAGG
5298-5320	AAAAACATTTTCAACTTCAAGGT
5299-5321	AAACATTTTCAACTTCAAGGTC
5300-5322	AAACATTTTCAACTTCAAGGTCA
5301-5323	AACATTTTCAACTTCAAGGTCAG
5302-5324	ACATTTTCAACTTCAAGGTCAGT
5303-5325	CATTTTCAACTTCAAGGTCAGTC
5304-5326	ATTTTCAACTTCAAGGTCAGTCA
5305-5327	TTTCAACTTCAAGGTCAGTCAA
5306-5328	TTTCAACTTCAAGGTCAGTCAAG
5307-5329	TTCAGTCAAGGTCAGTCAAGA
5308-5330	TCAACTTCAAGGTCAGTCAAGAA
5309-5331	CAACTTCAAGGTCAGTCAAGAAG
5310-5332	AACTTCAAGGTCAGTCAAGAAGG
5311-5333	ACTTCAAGGTCAGTCAAGAAGGA
5312-5334	CTTCAAGGTCAGTCAAGAAGGAC
5313-5335	TTCAGGTCAGTCAAGAAGGACT
5314-5336	TCAAGGTCAGTCAAGAAGGACTT
5315-5337	CAAGGTCAGTCAAGAAGGACTTA
5316-5338	AAGGTCAGTCAAGAAGGACTTAA
5317-5339	AGGTCAGTCAAGAAGGACTTAAG
5318-5340	GGTCAGTCAAGAAGGACTTAAGC
5319-5341	GTCAGTCAAGAAGGACTTAAGCT
5320-5342	TCAGTCAAGAAGGACTTAAGCTC
5321-5343	CAGTCAAGAAGGACTTAAGCTCT
5322-5344	AGTCAAGAAGGACTTAAGCTCTC

Position	Sequence
5323-5345	GTCAAGAAGGACTTAAGCTCTCA
5324-5346	TCAAGAAGGACTTAAGCTCTCAA
5325-5347	CAAGAAGGACTTAAGCTCTCAAA
5326-5348	AAGAAGGACTTAAGCTCTCAAAT
5327-5349	AGAAGGACTTAAGCTCTCAAATG
5328-5350	GAAGGACTTAAGCTCTCAAATGA
5329-5351	AAGGACTTAAGCTCTCAAATGAC
5330-5352	AGGACTTAAGCTCTCAAATGACA
5331-5353	GGACTTAAGCTCTCAAATGACAT
5332-5354	GACTTAAGCTCTCAAATGACATG
5333-5355	ACTTAAGCTCTCAAATGACATGA
5334-5356	CTTAAGCTCTCAAATGACATGAT
5335-5357	TTAAGCTCTCAAATGACATGATG
5336-5358	TAAGCTCTCAAATGACATGATGG
5337-5359	AAGCTCTCAAATGACATGATGGG
5338-5360	AGCTCTCAAATGACATGATGGGC
5339-5361	GCTCTCAAATGACATGATGGGCT
5340-5362	CTCTCAAATGACATGATGGGCTC
5341-5363	TCTCAAATGACATGATGGGCTCA
5342-5364	CTCAAATGACATGATGGGCTCAT
5343-5365	TCAAATGACATGATGGGCTCATA
5344-5366	CAAATGACATGATGGGCTCATAT
5345-5367	AAATGACATGATGGGCTCATATG
5346-5368	AATGACATGATGGGCTCATATGC
5347-5369	ATGACATGATGGGCTCATATGCT
5348-5370	TGACATGATGGGCTCATATGCTG
5349-5371	GACATGATGGGCTCATATGCTGA
5350-5372	ACATGATGGGCTCATATGCTGAA
5351-5373	CATGATGGGCTCATATGCTGAAA
5352-5374	ATGATGGGCTCATATGCTGAAAT
5353-5375	TGATGGGCTCATATGCTGAAATG
5354-5376	GATGGGCTCATATGCTGAAATGA
5355-5377	ATGGGCTCATATGCTGAAATGAA
5356-5378	TGGGCTCATATGCTGAAATGAAA
5357-5379	GGGCTCATATGCTGAAATGAAAT
5358-5380	GGCTCATATGCTGAAATGAAATT
5359-5381	GCTCATATGCTGAAATGAAATTT
5360-5382	CTCATATGCTGAAATGAAATTTG
5361-5383	TCATATGCTGAAATGAAATTTGA
5362-5384	CATATGCTGAAATGAAATTTGAC
5363-5385	ATATGCTGAAATGAAATTTGACC
5364-5386	TATGCTGAAATGAAATTTGACCA
5365-5387	ATGCTGAAATGAAATTTGACCAC
5366-5388	TGCTGAAATGAAATTTGACCACA
5367-5389	GCTGAAATGAAATTTGACCACAC
5368-5390	CTGAAATGAAATTTGACCACACA
5369-5391	TGAAATGAAATTTGACCACACAA
5370-5392	GAAATGAAATTTGACCACACAAA
5371-5393	AAATGAAATTTGACCACACAAAC
5372-5394	AATGAAATTTGACCACACAAACA
5373-5395	ATGAAATTTGACCACACAAACAG
5374-5396	TGAAATTTGACCACACAAACAGT
5375-5397	GAAATTTGACCACACAAACAGTC
5376-5398	AAATTTGACCACACAAACAGTCT
5377-5399	AATTTGACCACACAAACAGTCTG
5378-5400	ATTTGACCACACAAACAGTCTGA
5379-5401	TTTACCACACAAACAGTCTGAA
5380-5402	TTGACCACACAAACAGTCTGAAC
5381-5403	TGACCACACAAACAGTCTGAACA
5382-5404	GACCACACAAACAGTCTGAACAT
5383-5405	ACCACACAAACAGTCTGAACATT
5384-5406	CCACACAAACAGTCTGAACATTG
5385-5407	CACACAAACAGTCTGAACATTGC
5386-5408	ACACAAACAGTCTGAACATTGCA
5387-5409	CACAAACAGTCTGAACATTGCAG
5388-5410	ACAAACAGTCTGAACATTGCAGG

Position	Sequence
5389-5411	CAAACAGTCTGAACATTGCAGGC
5390-5412	AAACAGTCTGAACATTGCAGGCT
5391-5413	AACAGTCTGAACATTGCAGGCTT
5392-5414	ACAGTCTGAACATTGCAGGCTTA
5393-5415	CAGTCTGAACATTGCAGGCTTAT
5394-5416	AGTCTGAACATTGCAGGCTTATC
5395-5417	GTCTGAACATTGCAGGCTTATCA
5396-5418	TCTGAACATTGCAGGCTTATCAC
5397-5419	CTGAACATTGCAGGCTTATCACT
5398-5420	TGAACATTGCAGGCTTATCACTG
5399-5421	GAACATTGCAGGCTTATCACTGG
5400-5422	AACATTGCAGGCTTATCACTGGA
5401-5423	ACATTGCAGGCTTATCACTGGAC
5402-5424	CATTGCAGGCTTATCACTGGACT
5403-5425	ATTGCAGGCTTATCACTGGACTT
5404-5426	TTGCAGGCTTATCACTGGACTTC
5405-5427	TGCAGGCTTATCACTGGACTTCT
5406-5428	GCAGGCTTATCACTGGACTTCTC
5407-5429	CAGGCTTATCACTGGACTTCTCT
5408-5430	AGGCTTATCACTGGACTTCTCTT
5409-5431	GGCTTATCACTGGACTTCTCTTC
5410-5432	GCTTATCACTGGACTTCTCTTCA
5411-5433	CTTATCACTGGACTTCTCTTCAA
5412-5434	TTATCACTGGACTTCTCTTCAAA
5413-5435	TATCACTGGACTTCTCTTCAAAA
5414-5436	ATCACTGGACTTCTCTTCAAAC
5415-5437	TCACCTGGACTTCTCTTCAAAC
5416-5438	CACTGGACTTCTCTTCAAAC
5417-5439	ACTGGACTTCTCTTCAAAC
5418-5440	CTGGACTTCTCTTCAAAC
5419-5441	TGGACTTCTCTTCAAAC
5420-5442	GGACTTCTCTTCAAAC
5421-5443	GACTTCTCTTCAAAC
5422-5444	ACTTCTCTTCAAAC
5423-5445	CTTCTCTTCAAAC
5424-5446	TTCTCTTCAAAC
5425-5447	TCTCTTCAAAC
5426-5448	CTCTTCAAAC
5427-5449	TCTTCAAAC
5428-5450	CTTCAAAC
5429-5451	TTCAAAC
5430-5452	TCAAAC
5431-5453	CAAAC
5432-5454	AAAC
5433-5455	AACT
5434-5456	AACTGACAACATTTACAGCTC
5435-5457	AACTGACAACATTTACAGCTCTG
5436-5458	AACTGACAACATTTACAGCTCTGA
5437-5459	AACTGACAACATTTACAGCTCTGAC
5438-5460	AACTGACAACATTTACAGCTCTGACA
5439-5461	AACTGACAACATTTACAGCTCTGACAA
5440-5462	AACTGACAACATTTACAGCTCTGACAAG
5441-5463	AACTGACAACATTTACAGCTCTGACAAGT
5442-5464	AACTGACAACATTTACAGCTCTGACAAGTT
5443-5465	AACTGACAACATTTACAGCTCTGACAAGTTT
5444-5466	AACTGACAACATTTACAGCTCTGACAAGTTTT
5445-5467	AACTGACAACATTTACAGCTCTGACAAGTTTTA
5446-5468	AACTGACAACATTTACAGCTCTGACAAGTTTTAT
5447-5469	AACTGACAACATTTACAGCTCTGACAAGTTTTATA
5448-5470	AACTGACAACATTTACAGCTCTGACAAGTTTTATAA
5449-5471	AACTGACAACATTTACAGCTCTGACAAGTTTTATAAG
5450-5472	AACTGACAACATTTACAGCTCTGACAAGTTTTATAAGC
5451-5473	AACTGACAACATTTACAGCTCTGACAAGTTTTATAAGCA
5452-5474	AACTGACAACATTTACAGCTCTGACAAGTTTTATAAGCAA
5453-5475	AACTGACAACATTTACAGCTCTGACAAGTTTTATAAGCAAA
5454-5476	AACTGACAACATTTACAGCTCTGACAAGTTTTATAAGCAAAC

Position	Sequence
5455-5477	CTGACAAGTTTATAAGCAAACCT
5456-5478	TGACAAGTTTATAAGCAAACCTG
5457-5479	GACAAGTTTATAAGCAAACCTGT
5458-5480	ACAAGTTTATAAGCAAACCTGTT
5459-5481	CAAGTTTATAAGCAAACCTGTTA
5460-5482	AAGTTTATAAGCAAACCTGTTAA
5461-5483	AGTTTATAAGCAAACCTGTTAAT
5462-5484	GTTTATAAGCAAACCTGTTAATT
5463-5485	TTTTATAAGCAAACCTGTTAATT
5464-5486	TTTATAAGCAAACCTGTTAATTTA
5465-5487	TTATAAGCAAACCTGTTAATTTAC
5466-5488	TATAAGCAAACCTGTTAATTTACA
5467-5489	ATAAGCAAACCTGTTAATTTACAG
5468-5490	TAAGCAAACCTGTTAATTTACAGC
5469-5491	AAGCAAACCTGTTAATTTACAGCT
5470-5492	AGCAAACCTGTTAATTTACAGCTA
5471-5493	GCAAACCTGTTAATTTACAGCTAC
5472-5494	CAAACCTGTTAATTTACAGCTACA
5473-5495	AAACCTGTTAATTTACAGCTACAG
5474-5496	AACCTGTTAATTTACAGCTACAGC
5475-5497	ACTGTTAATTTACAGCTACAGCC
5476-5498	CTGTTAATTTACAGCTACAGCCC
5477-5499	TGTTAATTTACAGCTACAGCCCT
5478-5500	GTTAATTTACAGCTACAGCCCTA
5479-5501	TTAATTTACAGCTACAGCCCTAT
5480-5502	TAATTTACAGCTACAGCCCTATT
5481-5503	AATTTACAGCTACAGCCCTATTC
5482-5504	ATTTACAGCTACAGCCCTATTCT
5483-5505	TTTACAGCTACAGCCCTATTCTC
5484-5506	TTACAGCTACAGCCCTATTCTCT
5485-5507	TACAGCTACAGCCCTATTCTCTG
5486-5508	ACAGCTACAGCCCTATTCTCTGG
5487-5509	CAGCTACAGCCCTATTCTCTGGT
5488-5510	AGCTACAGCCCTATTCTCTGGTA
5489-5511	GCTACAGCCCTATTCTCTGGTAA
5490-5512	CTACAGCCCTATTCTCTGGTAAC
5491-5513	TACAGCCCTATTCTCTGGTAACT
5492-5514	ACAGCCCTATTCTCTGGTAACTA
5493-5515	CAGCCCTATTCTCTGGTAACTAC
5494-5516	AGCCCTATTCTCTGGTAACTACT
5495-5517	GCCCTATTCTCTGGTAACTACTT
5496-5518	CCCTATTCTCTGGTAACTACTTT
5497-5519	CCTATTCTCTGGTAACTACTTTA
5498-5520	CTATTCTCTGGTAACTACTTTAA
5499-5521	TATTCTCTGGTAACTACTTTAAA
5500-5522	ATTCTCTGGTAACTACTTTAAAC
5501-5523	TTCTCTGGTAACTACTTTAAACA
5502-5524	TCTCTGGTAACTACTTTAAACAG
5503-5525	CTCTGGTAACTACTTTAAACAGT
5504-5526	TCTGGTAACTACTTTAAACAGTG
5505-5527	CTGGTAACTACTTTAAACAGTGA
5506-5528	TGGTAACTACTTTAAACAGTGAC
5507-5529	GGTAACTACTTTAAACAGTGACC
5508-5530	GTAACACTTTAAACAGTGACCT
5509-5531	TAACACTTTAAACAGTGACCTG
5510-5532	AACACTTTAAACAGTGACCTGA
5511-5533	ACTACTTTAAACAGTGACCTGAA
5512-5534	CTACTTTAAACAGTGACCTGAAA
5513-5535	TACTTTAAACAGTGACCTGAAAT
5514-5536	ACTTTAAACAGTGACCTGAAATA
5515-5537	CTTTAAACAGTGACCTGAAATAC
5516-5538	TTTAAACAGTGACCTGAAATACA
5517-5539	TTAAACAGTGACCTGAAATACAA
5518-5540	TAAACAGTGACCTGAAATACAAT
5519-5541	AAACAGTGACCTGAAATACAATG
5520-5542	AACAGTGACCTGAAATACAATGC

Position	Sequence
5521-5543	ACAGTGACCTGAAATACAATGCT
5522-5544	CAGTGACCTGAAATACAATGCTC
5523-5545	AGTGACCTGAAATACAATGCTCT
5524-5546	GTGACCTGAAATACAATGCTCTG
5525-5547	TGACCTGAAATACAATGCTCTGG
5526-5548	GACCTGAAATACAATGCTCTGGA
5527-5549	ACCTGAAATACAATGCTCTGGAT
5528-5550	CCTGAAATACAATGCTCTGGATC
5529-5551	CTGAAATACAATGCTCTGGATCT
5530-5552	TGAAATACAATGCTCTGGATCTC
5531-5553	GAAATACAATGCTCTGGATCTCA
5532-5554	AAATACAATGCTCTGGATCTCAC
5533-5555	AATACAATGCTCTGGATCTCAC
5534-5556	ATACAATGCTCTGGATCTCACCA
5535-5557	TACAATGCTCTGGATCTCACCAA
5536-5558	ACAATGCTCTGGATCTCACCAAC
5537-5559	CAATGCTCTGGATCTCACCAACA
5538-5560	AATGCTCTGGATCTCACCAACAA
5539-5561	ATGCTCTGGATCTCACCAACAAT
5540-5562	TGCTCTGGATCTCACCAACAATG
5541-5563	GCTCTGGATCTCACCAACAATGG
5542-5564	CTCTGGATCTCACCAACAATGGG
5543-5565	TCTGGATCTCACCAACAATGGGA
5544-5566	CTGGATCTCACCAACAATGGGAA
5545-5567	TGGATCTCACCAACAATGGGAAA
5546-5568	GGATCTCACCAACAATGGGAAAC
5547-5569	GATCTCACCAACAATGGGAAACT
5548-5570	ATCTCACCAACAATGGGAAACTA
5549-5571	TCTCACCAACAATGGGAAACTAC
5550-5572	CTCACCAACAATGGGAAACTACG
5551-5573	TCACCAACAATGGGAAACTACGG
5552-5574	CACCAACAATGGGAAACTACGGC
5553-5575	ACCAACAATGGGAAACTACGGCT
5554-5576	CCAACAATGGGAAACTACGGCTA
5555-5577	CAACAATGGGAAACTACGGCTAG
5556-5578	AACAATGGGAAACTACGGCTAGA
5557-5579	ACAATGGGAAACTACGGCTAGAA
5558-5580	CAATGGGAAACTACGGCTAGAAC
5559-5581	AATGGGAAACTACGGCTAGAAC
5560-5582	ATGGGAAACTACGGCTAGAACCC
5561-5583	TGGGAAACTACGGCTAGAACCCC
5562-5584	GGGAAACTACGGCTAGAACCCCT
5563-5585	GGAAACTACGGCTAGAACCCCTG
5564-5586	GAAACTACGGCTAGAACCCCTGA
5565-5587	AAACTACGGCTAGAACCCCTGAA
5566-5588	AACTACGGCTAGAACCCCTGAAG
5567-5589	ACTACGGCTAGAACCCCTGAAGC
5568-5590	CTACGGCTAGAACCCCTGAAGCT
5569-5591	TACGGCTAGAACCCCTGAAGCTG
5570-5592	ACGGCTAGAACCCCTGAAGCTGC
5571-5593	CGGCTAGAACCCCTGAAGCTGCA
5572-5594	GGCTAGAACCCCTGAAGCTGCAT
5573-5595	GCTAGAACCCCTGAAGCTGCATG
5574-5596	CTAGAACCCCTGAAGCTGCATGT
5575-5597	TAGAACCCCTGAAGCTGCATGTG
5576-5598	AGAACCCCTGAAGCTGCATGTGG
5577-5599	GAACCCCTGAAGCTGCATGTGGC
5578-5600	AACCCCTGAAGCTGCATGTGGCT
5579-5601	ACCCCTGAAGCTGCATGTGGCTG
5580-5602	CCCTGAAGCTGCATGTGGCTGG
5581-5603	CCCTGAAGCTGCATGTGGCTGGT
5582-5604	CCTGAAGCTGCATGTGGCTGGTA
5583-5605	CTGAAGCTGCATGTGGCTGGTAA
5584-5606	TGAAGCTGCATGTGGCTGGTAAC
5585-5607	GAAGCTGCATGTGGCTGGTAACC
5586-5608	AAGCTGCATGTGGCTGGTAACCT

Position	Sequence
5587-5609	AGCTGCATGTGGCTGGTAACCTA
5588-5610	GCTGCATGTGGCTGGTAACCTAA
5589-5611	CTGCATGTGGCTGGTAACCTAAA
5590-5612	TGCATGTGGCTGGTAACCTAAAA
5591-5613	GCATGTGGCTGGTAACCTAAAAG
5592-5614	CATGTGGCTGGTAACCTAAAAGG
5593-5615	ATGTGGCTGGTAACCTAAAAGGA
5594-5616	TGTGGCTGGTAACCTAAAAGGAG
5595-5617	GTGGCTGGTAACCTAAAAGGAGC
5596-5618	TGGCTGGTAACCTAAAAGGAGCC
5597-5619	GGCTGGTAACCTAAAAGGAGCCT
5598-5620	GCTGGTAACCTAAAAGGAGCCTA
5599-5621	CTGGTAACCTAAAAGGAGCCTAC
5600-5622	TGGTAACCTAAAAGGAGCCTACC
5601-5623	GGTAACCTAAAAGGAGCCTACCA
5602-5624	GTAACCTAAAAGGAGCCTACCAA
5603-5625	TAACTAAAAGGAGCCTACCAA
5604-5626	AACCTAAAAGGAGCCTACCAAAA
5605-5627	ACCTAAAAGGAGCCTACCAAAAT
5606-5628	CCTAAAAGGAGCCTACCAAAATA
5607-5629	CTAAAAGGAGCCTACCAAAATAA
5608-5630	TAAAAGGAGCCTACCAAAATAAT
5609-5631	AAAAGGAGCCTACCAAAATAATG
5610-5632	AAAGGAGCCTACCAAAATAATGA
5611-5633	AAGGAGCCTACCAAAATAATGAA
5612-5634	AGGAGCCTACCAAAATAATGAAA
5613-5635	GGAGCCTACCAAAATAATGAAAT
5614-5636	GAGCCTACCAAAATAATGAAATA
5615-5637	AGCCTACCAAAATAATGAAATAA
5616-5638	GCCTACCAAAATAATGAAATAAA
5617-5639	CCTACCAAAATAATGAAATAAAA
5618-5640	CTACCAAAATAATGAAATAAAAC
5619-5641	TACCAAAATAATGAAATAAAACA
5620-5642	ACCAAAATAATGAAATAAAACAC
5621-5643	CCAAATAATGAAATAAAACACA
5622-5644	CAAATAATGAAATAAAACACAT
5623-5645	AAAATAATGAAATAAAACACATC
5624-5646	AAATAATGAAATAAAACACATCT
5625-5647	AATAATGAAATAAAACACATCTA
5626-5648	ATAATGAAATAAAACACATCTAT
5627-5649	TAATGAAATAAAACACATCTATG
5628-5650	AATGAAATAAAACACATCTATGC
5629-5651	ATGAAATAAAACACATCTATGCC
5630-5652	TGAAATAAAACACATCTATGCCA
5631-5653	GAAATAAAACACATCTATGCCAT
5632-5654	AAATAAAACACATCTATGCCATC
5633-5655	AATAAAACACATCTATGCCATCT
5634-5656	ATAAAACACATCTATGCCATCTC
5635-5657	TAAAACACATCTATGCCATCTCT
5636-5658	AAAACACATCTATGCCATCTCTT
5637-5659	AAACACATCTATGCCATCTCTTC
5638-5660	AACACATCTATGCCATCTCTTCT
5639-5661	ACACATCTATGCCATCTCTTCTG
5640-5662	CACATCTATGCCATCTCTTCTGCT
5641-5663	ACATCTATGCCATCTCTTCTGCT
5642-5664	CATCTATGCCATCTCTTCTGCTG
5643-5665	ATCTATGCCATCTCTTCTGCTGC
5644-5666	TCTATGCCATCTCTTCTGCTGCC
5645-5667	CTATGCCATCTCTTCTGCTGCCCT
5646-5668	TATGCCATCTCTTCTGCTGCCCTT
5647-5669	ATGCCATCTCTTCTGCTGCCCTTA
5648-5670	TGCCATCTCTTCTGCTGCCCTTAT
5649-5671	GCCATCTCTTCTGCTGCCCTTATC
5650-5672	CCATCTCTTCTGCTGCCCTTATCA
5651-5673	CATCTCTTCTGCTGCCCTTATCAG
5652-5674	ATCTCTTCTGCTGCCCTTATCAGC

Position	Sequence
5653-5675	TCTCTTCTGCTGCCTTATCAGCA
5654-5676	CTCTTCTGCTGCCTTATCAGCAA
5655-5677	TCTTCTGCTGCCTTATCAGCAAG
5656-5678	CTTCTGCTGCCTTATCAGCAAGC
5657-5679	TTCTGCTGCCTTATCAGCAAGCT
5658-5680	TCTGCTGCCTTATCAGCAAGCTA
5659-5681	CTGCTGCCTTATCAGCAAGCTAT
5660-5682	TGCTGCCTTATCAGCAAGCTATA
5661-5683	GCTGCCTTATCAGCAAGCTATAA
5662-5684	CTGCCTTATCAGCAAGCTATAAA
5663-5685	TGCCTTATCAGCAAGCTATAAAG
5664-5686	GCCTTATCAGCAAGCTATAAAGC
5665-5687	CCTTATCAGCAAGCTATAAAGCA
5666-5688	CTTATCAGCAAGCTATAAAGCAG
5667-5689	TTATCAGCAAGCTATAAAGCAGA
5668-5690	TATCAGCAAGCTATAAAGCAGAC
5669-5691	ATCAGCAAGCTATAAAGCAGACA
5670-5692	TCAGCAAGCTATAAAGCAGACAC
5671-5693	CAGCAAGCTATAAAGCAGACACT
5672-5694	AGCAAGCTATAAAGCAGACACTG
5673-5695	GCAAGCTATAAAGCAGACACTGT
5674-5696	CAAGCTATAAAGCAGACACTGTT
5675-5697	AAGCTATAAAGCAGACACTGTTG
5676-5698	AGCTATAAAGCAGACACTGTTGC
5677-5699	GCTATAAAGCAGACACTGTTGCT
5678-5700	CTATAAAGCAGACACTGTTGCTA
5679-5701	TATAAAGCAGACACTGTTGCTAA
5680-5702	ATAAAGCAGACACTGTTGCTAAG
5681-5703	TAAAGCAGACACTGTTGCTAAGG
5682-5704	AAAGCAGACACTGTTGCTAAGGT
5683-5705	AAGCAGACACTGTTGCTAAGGTT
5684-5706	AGCAGACACTGTTGCTAAGGTTT
5685-5707	GCAGACACTGTTGCTAAGGTTCA
5686-5708	CAGACACTGTTGCTAAGGTTTCA
5687-5709	AGACACTGTTGCTAAGGTTTCA
5688-5710	GACACTGTTGCTAAGGTTTCA
5689-5711	ACACTGTTGCTAAGGTTTCA
5690-5712	CACTGTTGCTAAGGTTTCA
5691-5713	ACTGTTGCTAAGGTTTCA
5692-5714	CTGTTGCTAAGGTTTCA
5693-5715	TGTTGCTAAGGTTTCA
5694-5716	GTGCTAAGGTTTCA
5695-5717	TTGCTAAGGTTTCA
5696-5718	TGCTAAGGTTTCA
5697-5719	GCTAAGGTTTCA
5698-5720	CTAAGGTTTCA
5699-5721	TAAGGTTTCA
5700-5722	AAGGTTTCA
5701-5723	AGGTTTCA
5702-5724	GGTTTCA
5703-5725	GTTTCA
5704-5726	TTTCA
5705-5727	TTTCA
5706-5728	TTTCA
5707-5729	TTTCA
5708-5730	TTTCA
5709-5731	TTTCA
5710-5732	TTTCA
5711-5733	TTTCA
5712-5734	TTTCA
5713-5735	TTTCA
5714-5736	TTTCA
5715-5737	TTTCA
5716-5738	TTTCA
5717-5739	TTTCA
5718-5740	TTTCA

Position	Sequence
5719-5741	TTAGCCATCGGCTCAACACAGAC
5720-5742	TAGCCATCGGCTCAACACAGACA
5721-5743	AGCCATCGGCTCAACACAGACAT
5722-5744	GCCATCGGCTCAACACAGACATC
5723-5745	CCATCGGCTCAACACAGACATCG
5724-5746	CATCGGCTCAACACAGACATCGC
5725-5747	ATCGGCTCAACACAGACATCGCT
5726-5748	TCGGCTCAACACAGACATCGCTG
5727-5749	CGGCTCAACACAGACATCGCTGG
5728-5750	GGCTCAACACAGACATCGCTGGG
5729-5751	GCTCAACACAGACATCGCTGGGC
5730-5752	CTCAACACAGACATCGCTGGGCT
5731-5753	TCAACACAGACATCGCTGGGCTG
5732-5754	CAACACAGACATCGCTGGGCTGG
5733-5755	AACACAGACATCGCTGGGCTGGC
5734-5756	ACACAGACATCGCTGGGCTGGCT
5735-5757	CACAGACATCGCTGGGCTGGCTT
5736-5758	ACAGACATCGCTGGGCTGGCTTC
5737-5759	CAGACATCGCTGGGCTGGCTTCA
5738-5760	AGACATCGCTGGGCTGGCTTCAG
5739-5761	GACATCGCTGGGCTGGCTTCAGC
5740-5762	ACATCGCTGGGCTGGCTTCAGCC
5741-5763	CATCGCTGGGCTGGCTTCAGCCA
5742-5764	ATCGCTGGGCTGGCTTCAGCCAT
5743-5765	TCGCTGGGCTGGCTTCAGCCATT
5744-5766	CGCTGGGCTGGCTTCAGCCATTG
5745-5767	GCTGGGCTGGCTTCAGCCATTGA
5746-5768	CTGGGCTGGCTTCAGCCATTGAC
5747-5769	TGGGCTGGCTTCAGCCATTGACA
5748-5770	GGGCTGGCTTCAGCCATTGACAT
5749-5771	GGCTGGCTTCAGCCATTGACATG
5750-5772	GCTGGCTTCAGCCATTGACATGA
5751-5773	CTGGCTTCAGCCATTGACATGAG
5752-5774	TGGCTTCAGCCATTGACATGAGC
5753-5775	GGCTTCAGCCATTGACATGAGCA
5754-5776	GCTTCAGCCATTGACATGAGCAC
5755-5777	CTTCAGCCATTGACATGAGCACA
5756-5778	TTCAGCCATTGACATGAGCACAAA
5757-5779	TCAGCCATTGACATGAGCACAAA
5758-5780	CAGCCATTGACATGAGCACAAAC
5759-5781	AGCCATTGACATGAGCACAAACT
5760-5782	GCCATTGACATGAGCACAAACTA
5761-5783	CCATTGACATGAGCACAAACTAT
5762-5784	CATTGACATGAGCACAAACTATA
5763-5785	ATTGACATGAGCACAAACTATAA
5764-5786	TTGACATGAGCACAAACTATAAT
5765-5787	TGACATGAGCACAAACTATAATT
5766-5788	GACATGAGCACAAACTATAATTC
5767-5789	ACATGAGCACAAACTATAATTC
5768-5790	CATGAGCACAAACTATAATTCAG
5769-5791	ATGAGCACAAACTATAATTCAGA
5770-5792	TGAGCACAAACTATAATTCAGAC
5771-5793	GAGCACAAACTATAATTCAGACT
5772-5794	AGCACAAACTATAATTCAGACTC
5773-5795	GCACAAACTATAATTCAGACTCA
5774-5796	CACAAACTATAATTCAGACTCAC
5775-5797	ACAAACTATAATTCAGACTCACT
5776-5798	CAAACATAATTCAGACTCACTG
5777-5799	AAACTATAATTCAGACTCACTGC
5778-5800	AACTATAATTCAGACTCACTGCA
5779-5801	ACTATAATTCAGACTCACTGCAT
5780-5802	CTATAATTCAGACTCACTGCATT
5781-5803	TATAATTCAGACTCACTGCATTT
5782-5804	ATAATTCAGACTCACTGCATTT
5783-5805	TAATTCAGACTCACTGCATTTCA
5784-5806	AATTCAGACTCACTGCATTTCAG

Position	Sequence
5785-5807	ATTCAGACTCACTGCATTTTCAGC
5786-5808	TTCAGACTCACTGCATTTTCAGCA
5787-5809	TCAGACTCACTGCATTTTCAGCAA
5788-5810	CAGACTCACTGCATTTTCAGCAAT
5789-5811	AGACTCACTGCATTTTCAGCAATG
5790-5812	GACTCACTGCATTTTCAGCAATGT
5791-5813	ACTCACTGCATTTTCAGCAATGTC
5792-5814	CTCACTGCATTTTCAGCAATGTCT
5793-5815	TCACTGCATTTTCAGCAATGTCTT
5794-5816	CACTGCATTTTCAGCAATGTCTTC
5795-5817	ACTGCATTTTCAGCAATGTCTTCC
5796-5818	CTGCATTTTCAGCAATGTCTTCCG
5797-5819	TGCATTTTCAGCAATGTCTTCCGT
5798-5820	GCATTTTCAGCAATGTCTTCCGTT
5799-5821	CATTTTCAGCAATGTCTTCCGTTTC
5800-5822	ATTTTCAGCAATGTCTTCCGTTCT
5801-5823	TTTCAGCAATGTCTTCCGTTCTG
5802-5824	TTCAGCAATGTCTTCCGTTCTGT
5803-5825	TCAGCAATGTCTTCCGTTCTGTA
5804-5826	CAGCAATGTCTTCCGTTCTGTAA
5805-5827	AGCAATGTCTTCCGTTCTGTAAAT
5806-5828	GCAATGTCTTCCGTTCTGTAAATG
5807-5829	CAATGTCTTCCGTTCTGTAAATGG
5808-5830	AATGTCTTCCGTTCTGTAAATGGC
5809-5831	ATGTCTTCCGTTCTGTAAATGGCC
5810-5832	TGTCTTCCGTTCTGTAAATGGCCC
5811-5833	GTCTTCCGTTCTGTAAATGGCCCC
5812-5834	TCTTCCGTTCTGTAAATGGCCCCG
5813-5835	CTTCCGTTCTGTAAATGGCCCCCGT
5814-5836	TTCCGTTCTGTAAATGGCCCCCGTT
5815-5837	FCCGTTCTGTAAATGGCCCCCGTTT
5816-5838	CCGTTCTGTAAATGGCCCCCGTTTA
5817-5839	CGTTCTGTAAATGGCCCCCGTTTAC
5818-5840	GTTCTGTAAATGGCCCCCGTTTACC
5819-5841	TTCTGTAAATGGCCCCCGTTTACCA
5820-5842	TCTGTAAATGGCCCCCGTTTACCAT
5821-5843	CTGTAAATGGCCCCCGTTTACCATG
5822-5844	TGTAATGGCCCCCGTTTACCATGA
5823-5845	GTAATGGCCCCCGTTTACCATGAC
5824-5846	TAATGGCCCCCGTTTACCATGACC
5825-5847	AATGGCCCCCGTTTACCATGACCA
5826-5848	ATGGCCCCCGTTTACCATGACCAT
5827-5849	TGGCCCCCGTTTACCATGACCATC
5828-5850	GGCCCCCGTTTACCATGACCATCG
5829-5851	GCCCCCGTTTACCATGACCATCGA
5830-5852	CCCCCGTTTACCATGACCATCGAT
5831-5853	CCCGTTTACCATGACCATCGATG
5832-5854	CCGTTTACCATGACCATCGATGC
5833-5855	CGTTTACCATGACCATCGATGCA
5834-5856	GTTTACCATGACCATCGATGCAC
5835-5857	TTTACCATGACCATCGATGCACA
5836-5858	TTACCATGACCATCGATGCACAT
5837-5859	TACCATGACCATCGATGCACATA
5838-5860	ACCATGACCATCGATGCACATAC
5839-5861	CCATGACCATCGATGCACATACA
5840-5862	CATGACCATCGATGCACATACAA
5841-5863	ATGACCATCGATGCACATACAAA
5842-5864	TGACCATCGATGCACATACAAAT
5843-5865	GACCATCGATGCACATACAAATG
5844-5866	ACCATCGATGCACATACAAATGG
5845-5867	CCATCGATGCACATACAAATGGC
5846-5868	CATCGATGCACATACAAATGGCA
5847-5869	ATCGATGCACATACAAATGGCAA
5848-5870	TCGATGCACATACAAATGGCAAT
5849-5871	CGATGCACATACAAATGGCAATG
5850-5872	GATGCACATACAAATGGCAATGG

Position	Sequence
5851-5873	ATGCACATACAAATGGCAATGGG
5852-5874	TGCACATACAAATGGCAATGGGA
5853-5875	GCACATACAAATGGCAATGGGAA
5854-5876	CACATACAAATGGCAATGGGAAA
5855-5877	ACATACAAATGGCAATGGGAAAC
5856-5878	CATACAAATGGCAATGGGAAACT
5857-5879	ATACAAATGGCAATGGGAAACTC
5858-5880	TACAAATGGCAATGGGAAACTCG
5859-5881	ACAAATGGCAATGGGAAACTCGC
5860-5882	CAAATGGCAATGGGAAACTCGCT
5861-5883	AAATGGCAATGGGAAACTCGCTC
5862-5884	AATGGCAATGGGAAACTCGCTCT
5863-5885	ATGGCAATGGGAAACTCGCTCTC
5864-5886	TGGCAATGGGAAACTCGCTCTCT
5865-5887	GGCAATGGGAAACTCGCTCTCTG
5866-5888	GCAATGGGAAACTCGCTCTCTGG
5867-5889	CAATGGGAAACTCGCTCTCTGGG
5868-5890	AATGGGAAACTCGCTCTCTGGGG
5869-5891	ATGGGAAACTCGCTCTCTGGGGA
5870-5892	TGGGAAACTCGCTCTCTGGGGAG
5871-5893	GGGAAACTCGCTCTCTGGGGAGA
5872-5894	GGAACACTCGCTCTCTGGGGAGAA
5873-5895	GAAACTCGCTCTCTGGGGAGAAC
5874-5896	AAACTCGCTCTCTGGGGAGAACAA
5875-5897	AACTCGCTCTCTGGGGAGAACAT
5876-5898	ACTCGCTCTCTGGGGAGAACATA
5877-5899	CTCGCTCTCTGGGGAGAACATAC
5878-5900	TCGCTCTCTGGGGAGAACATACT
5879-5901	CGCTCTCTGGGGAGAACATACTG
5880-5902	GCTCTCTGGGGAGAACATACTGG
5881-5903	CTCTCTGGGGAGAACATACTGGG
5882-5904	TCTCTGGGGAGAACATACTGGGC
5883-5905	CTCTGGGGAGAACATACTGGGCA
5884-5906	TCTGGGGAGAACATACTGGGCAG
5885-5907	CTGGGGAGAACATACTGGGCAGC
5886-5908	TGGGGAGAACATACTGGGCAGCT
5887-5909	GGGGAGAACATACTGGGCAGCTG
5888-5910	GGGAGAACATACTGGGCAGCTGT
5889-5911	GGAGAACATACTGGGCAGCTGTA
5890-5912	GAGAACATACTGGGCAGCTGTAT
5891-5913	AGAACATACTGGGCAGCTGTATA
5892-5914	GAACATACTGGGCAGCTGTATAG
5893-5915	AACATACTGGGCAGCTGTATAGC
5894-5916	ACATACTGGGCAGCTGTATAGCA
5895-5917	CATACTGGGCAGCTGTATAGCAA
5896-5918	ATACTGGGCAGCTGTATAGCAAA
5897-5919	TACTGGGCAGCTGTATAGCAAAT
5898-5920	ACTGGGCAGCTGTATAGCAAATT
5899-5921	CTGGGCAGCTGTATAGCAAATTC
5900-5922	TGGGCAGCTGTATAGCAAATTC
5901-5923	GGGCAGCTGTATAGCAAATTCCT
5902-5924	GGCAGCTGTATAGCAAATTCCTG
5903-5925	GCAGCTGTATAGCAAATTCCTGT
5904-5926	CAGCTGTATAGCAAATTCCTGTT
5905-5927	AGCTGTATAGCAAATTCCTGTTG
5906-5928	GCTGTATAGCAAATTCCTGTTGA
5907-5929	CTGTATAGCAAATTCCTGTTGAA
5908-5930	TGTATAGCAAATTCCTGTTGAAA
5909-5931	GTATAGCAAATTCCTGTTGAAAG
5910-5932	TATAGCAAATTCCTGTTGAAAGC
5911-5933	ATAGCAAATTCCTGTTGAAAGCA
5912-5934	TAGCAAATTCCTGTTGAAAGCAG
5913-5935	AGCAAATTCCTGTTGAAAGCAGA
5914-5936	GCAAATTCCTGTTGAAAGCAGAA
5915-5937	CAAATTCCTGTTGAAAGCAGAAC
5916-5938	AAATTCCTGTTGAAAGCAGAAC

Position	Sequence
5917-5939	AATTCCTGTTGAAAGCAGAACCT
5918-5940	ATTCCTGTTGAAAGCAGAACCTC
5919-5941	TTCCTGTTGAAAGCAGAACCTCT
5920-5942	TCCTGTTGAAAGCAGAACCTCTG
5921-5943	CCTGTTGAAAGCAGAACCTCTGG
5922-5944	CTGTTGAAAGCAGAACCTCTGGC
5923-5945	TGTTGAAAGCAGAACCTCTGGCA
5924-5946	GTTGAAAGCAGAACCTCTGGCAT
5925-5947	TGAAAGCAGAACCTCTGGCATT
5926-5948	TGAAAGCAGAACCTCTGGCATTT
5927-5949	GAAAGCAGAACCTCTGGCATTTA
5928-5950	AAAGCAGAACCTCTGGCATTTAC
5929-5951	AAGCAGAACCTCTGGCATTTACT
5930-5952	AGCAGAACCTCTGGCATTTACTT
5931-5953	GCAGAACCTCTGGCATTTACTTT
5932-5954	CAGAACCTCTGGCATTTACTTTC
5933-5955	AGAACCTCTGGCATTTACTTTCT
5934-5956	GAACCTCTGGCATTTACTTTCTC
5935-5957	AACCTCTGGCATTTACTTTCTCT
5936-5958	ACCTCTGGCATTTACTTTCTCTC
5937-5959	CCTCTGGCATTTACTTTCTCTCA
5938-5960	CTCTGGCATTTACTTTCTCTCAT
5939-5961	TCTGGCATTTACTTTCTCTCATG
5940-5962	CTGGCATTTACTTTCTCTCATGA
5941-5963	TGGCATTTACTTTCTCTCATGAT
5942-5964	GGCATTTACTTTCTCTCATGATT
5943-5965	GCATTTACTTTCTCTCATGATTA
5944-5966	CATTTACTTTCTCTCATGATTAC
5945-5967	ATTTACTTTCTCTCATGATTACA
5946-5968	TTACTTTCTCTCATGATTACAA
5947-5969	TTACTTTCTCTCATGATTACAAA
5948-5970	TACTTTCTCTCATGATTACAAAG
5949-5971	ACTTTCTCTCATGATTACAAAGG
5950-5972	CTTTCTCTCATGATTACAAAGGC
5951-5973	TTTCTCTCATGATTACAAAGGCT
5952-5974	TTCTCTCATGATTACAAAGGCTC
5953-5975	TCTCTCATGATTACAAAGGCTCC
5954-5976	CTCTCATGATTACAAAGGCTCCA
5955-5977	TCTCATGATTACAAAGGCTCCAC
5956-5978	CTCATGATTACAAAGGCTCCACA
5957-5979	TCATGATTACAAAGGCTCCACAA
5958-5980	CATGATTACAAAGGCTCCACAAG
5959-5981	ATGATTACAAAGGCTCCACAAGT
5960-5982	TGATTACAAAGGCTCCACAAGTC
5961-5983	GATTACAAAGGCTCCACAAGTCA
5962-5984	ATTACAAAGGCTCCACAAGTCAT
5963-5985	TTACAAAGGCTCCACAAGTCATC
5964-5986	TACAAAGGCTCCACAAGTCATCA
5965-5987	ACAAAGGCTCCACAAGTCATCAT
5966-5988	CAAAGGCTCCACAAGTCATCATC
5967-5989	AAAGGCTCCACAAGTCATCATCT
5968-5990	AAGGCTCCACAAGTCATCATCTC
5969-5991	AGGCTCCACAAGTCATCATCTCG
5970-5992	GGCTCCACAAGTCATCATCTCGT
5971-5993	GCTCCACAAGTCATCATCTCGTG
5972-5994	CTCCACAAGTCATCATCTCGTGT
5973-5995	TCCACAAGTCATCATCTCGTGTC
5974-5996	CCACAAGTCATCATCTCGTGTCT
5975-5997	CACAAGTCATCATCTCGTGTCTA
5976-5998	ACAAGTCATCATCTCGTGTCTAG
5977-5999	CAAGTCATCATCTCGTGTCTAGG
5978-6000	AAGTCATCATCTCGTGTCTAGGA
5979-6001	AGTCATCATCTCGTGTCTAGGAA
5980-6002	GTCATCATCTCGTGTCTAGGAAA
5981-6003	TCATCATCTCGTGTCTAGGAAAA
5982-6004	CATCATCTCGTGTCTAGGAAAAG

Position	Sequence
5983-6005	ATCATCTCGTGTCTAGGAAAAGC
5984-6006	TCATCTCGTGTCTAGGAAAAGCA
5985-6007	CATCTCGTGTCTAGGAAAAGCAT
5986-6008	ATCTCGTGTCTAGGAAAAGCATC
5987-6009	TCTCGTGTCTAGGAAAAGCATCA
5988-6010	CTCGTGTCTAGGAAAAGCATCAG
5989-6011	TCGTGTCTAGGAAAAGCATCAGT
5990-6012	CGTGTCTAGGAAAAGCATCAGTG
5991-6013	GTGTCTAGGAAAAGCATCAGTGC
5992-6014	TGTCTAGGAAAAGCATCAGTGCA
5993-6015	GTCTAGGAAAAGCATCAGTGCG
5994-6016	TCTAGGAAAAGCATCAGTGCGC
5995-6017	CTAGGAAAAGCATCAGTGCGCT
5996-6018	TAGGAAAAGCATCAGTGCGCTC
5997-6019	AGGAAAAGCATCAGTGCGCTCT
5998-6020	GGAAAAGCATCAGTGCGCTCTT
5999-6021	GAAAAGCATCAGTGCGCTCTTG
6000-6022	AAAAGCATCAGTGCGCTCTTGA
6001-6023	AAAGCATCAGTGCGCTCTTGAA
6002-6024	AAGCATCAGTGCGCTCTTGAAC
6003-6025	AGCATCAGTGCGCTCTTGAACA
6004-6026	GCATCAGTGCGCTCTTGAACAC
6005-6027	CATCAGTGCGCTCTTGAACACA
6006-6028	ATCAGTGCGCTCTTGAACACAA
6007-6029	TCAGTGCGCTCTTGAACACAAA
6008-6030	CAGTGCGCTCTTGAACACAAAG
6009-6031	AGTGCGCTCTTGAACACAAAGT
6010-6032	GTGCGCTCTTGAACACAAAGTC
6011-6033	TGCGCTCTTGAACACAAAGTCA
6012-6034	GCAGCTCTTGAACACAAAGTCAG
6013-6035	CAGCTCTTGAACACAAAGTCAGT
6014-6036	AGCTCTTGAACACAAAGTCAGTG
6015-6037	GCTCTTGAACACAAAGTCAGTGC
6016-6038	CTCTTGAACACAAAGTCAGTGCC
6017-6039	TCTTGAACACAAAGTCAGTGCCC
6018-6040	CTTGAACACAAAGTCAGTGCCCT
6019-6041	TTGAACACAAAGTCAGTGCCCTG
6020-6042	TGAACACAAAGTCAGTGCCCTGC
6021-6043	GAACACAAAGTCAGTGCCCTGCT
6022-6044	AACACAAAGTCAGTGCCCTGCTT
6023-6045	ACACAAAGTCAGTGCCCTGCTTA
6024-6046	CACAAAGTCAGTGCCCTGCTTAC
6025-6047	ACAAAGTCAGTGCCCTGCTTACT
6026-6048	CAAAGTCAGTGCCCTGCTTACTC
6027-6049	AAAGTCAGTGCCCTGCTTACTPCC
6028-6050	AAGTCAGTGCCCTGCTTACTCCA
6029-6051	AGTCAGTGCCCTGCTTACTCCAG
6030-6052	GTCAGTGCCCTGCTTACTCCAGC
6031-6053	TCAGTGCCCTGCTTACTCCAGCT
6032-6054	CAGTGCCCTGCTTACTCCAGCTG
6033-6055	AGTGCCCTGCTTACTCCAGCTGA
6034-6056	GTGCCCTGCTTACTCCAGCTGAG
6035-6057	TGCCCTGCTTACTCCAGCTGAGC
6036-6058	GCCCTGCTTACTCCAGCTGAGCA
6037-6059	CCCTGCTTACTCCAGCTGAGCAG
6038-6060	CCTGCTTACTCCAGCTGAGCAGA
6039-6061	CTGCTTACTCCAGCTGAGCAGAC
6040-6062	TGCTTACTCCAGCTGAGCAGACA
6041-6063	GCTTACTCCAGCTGAGCAGACAG
6042-6064	CTTACTCCAGCTGAGCAGACAGG
6043-6065	TTACTCCAGCTGAGCAGACAGGC
6044-6066	TACTCCAGCTGAGCAGACAGGCA
6045-6067	ACTCCAGCTGAGCAGACAGGCAC
6046-6068	CTCCAGCTGAGCAGACAGGCACC
6047-6069	TCCAGCTGAGCAGACAGGCACCT
6048-6070	CCAGCTGAGCAGACAGGCACCTG

Position	Sequence
6049-6071	CAGCTGAGCAGACAGGCACCTGG
6050-6072	AGCTGAGCAGACAGGCACCTGGA
6051-6073	GCTGAGCAGACAGGCACCTGGAA
6052-6074	CTGAGCAGACAGGCACCTGGAAA
6053-6075	TGAGCAGACAGGCACCTGGAAAC
6054-6076	GAGCAGACAGGCACCTGGAAACT
6055-6077	AGCAGACAGGCACCTGGAAACTC
6056-6078	GCAGACAGGCACCTGGAAACTCA
6057-6079	CAGACAGGCACCTGGAAACTCAA
6058-6080	AGACAGGCACCTGGAAACTCAAG
6059-6081	GACAGGCACCTGGAAACTCAAGA
6060-6082	ACAGGCACCTGGAAACTCAAGAC
6061-6083	CAGGCACCTGGAAACTCAAGACC
6062-6084	AGGCACCTGGAAACTCAAGACCC
6063-6085	GGCACCTGGAAACTCAAGACCCA
6064-6086	GCACCTGGAAACTCAAGACCCAA
6065-6087	CACCTGGAAACTCAAGACCCAAAT
6066-6088	ACCTGGAAACTCAAGACCCAAAT
6067-6089	CCTGGAAACTCAAGACCCAAATTT
6068-6090	CTGGAAACTCAAGACCCAAATTTA
6069-6091	TGGAAACTCAAGACCCAAATTTAA
6070-6092	GGAAACTCAAGACCCAAATTTAAC
6071-6093	GAAACTCAAGACCCAAATTTAACA
6072-6094	AAACTCAAGACCCAAATTTAACAA
6073-6095	AACTCAAGACCCAAATTTAACAAC
6074-6096	ACTCAAGACCCAAATTTAACAACA
6075-6097	CTCAAGACCCAAATTTAACAACAA
6076-6098	TCAAGACCCAAATTTAACAACAAT
6077-6099	CAAGACCCAAATTTAACAACAATG
6078-6100	AAGACCCAAATTTAACAACAATGA
6079-6101	AGACCCAAATTTAACAACAATGAA
6080-6102	GACCCAAATTTAACAACAATGAAT
6081-6103	ACCCAATTTAACAACAATGAATA
6082-6104	CCCAATTTAACAACAATGAATAC
6083-6105	CCAATTTAACAACAATGAATACA
6084-6106	CAATTTAACAACAATGAATACAG
6085-6107	AATTTAACAACAATGAATACAGC
6086-6108	ATTTAACAACAATGAATACAGCC
6087-6109	TTTAACAACAATGAATACAGCCA
6088-6110	TTAACAACAATGAATACAGCCAG
6089-6111	TAACAACAATGAATACAGCCAGG
6090-6112	AACAACAATGAATACAGCCAGGA
6091-6113	ACAACAATGAATACAGCCAGGAC
6092-6114	CAACAATGAATACAGCCAGGACT
6093-6115	AACAATGAATACAGCCAGGACTT
6094-6116	ACAATGAATACAGCCAGGACTTG
6095-6117	CAATGAATACAGCCAGGACTTGG
6096-6118	AATGAATACAGCCAGGACTTGGG
6097-6119	ATGAATACAGCCAGGACTTGGAT
6098-6120	TGAATACAGCCAGGACTTGGATG
6099-6121	GAATACAGCCAGGACTTGGATGC
6100-6122	AATACAGCCAGGACTTGGATGCT
6101-6123	ATACAGCCAGGACTTGGATGCTT
6102-6124	TACAGCCAGGACTTGGATGCTTA
6103-6125	ACAGCCAGGACTTGGATGCTTAC
6104-6126	CAGCCAGGACTTGGATGCTTACA
6105-6127	AGCCAGGACTTGGATGCTTACAA
6106-6128	GCCAGGACTTGGATGCTTACAAC
6107-6129	CCAGGACTTGGATGCTTACAACA
6108-6130	CAGGACTTGGATGCTTACAACAC
6109-6131	AGGACTTGGATGCTTACAACACT
6110-6132	GGACTTGGATGCTTACAACACTA
6111-6133	GACTTGGATGCTTACAACACTAA
6112-6134	ACTTGGATGCTTACAACACTAAA
6113-6135	CTTGGATGCTTACAACACTAAAG
6114-6136	TTGGATGCTTACAACACTAAAGA

Position	Sequence
6115-6137	TGGATGCTTACAACACTAAAGAT
6116-6138	GGATGCTTACAACACTAAAGATA
6117-6139	GATGCTTACAACACTAAAGATAA
6118-6140	ATGCTTACAACACTAAAGATAAA
6119-6141	TGCTTACAACACTAAAGATAAAA
6120-6142	GCTTACAACACTAAAGATAAAAT
6121-6143	CTTACAACACTAAAGATAAAATT
6122-6144	TTACAACACTAAAGATAAAATTG
6123-6145	TACAACACTAAAGATAAAATTGG
6124-6146	ACAACACTAAAGATAAAATTGGC
6125-6147	CAACACTAAAGATAAAATTGGCG
6126-6148	AACACTAAAGATAAAATTGGCGT
6127-6149	ACACTAAAGATAAAATTGGCGTG
6128-6150	CACTAAAGATAAAATTGGCGTGG
6129-6151	ACTAAAGATAAAATTGGCGTGGA
6130-6152	CTAAAGATAAAATTGGCGTGGAG
6131-6153	TAAAGATAAAATTGGCGTGGAGC
6132-6154	AAAGATAAAATTGGCGTGGAGCT
6133-6155	AAGATAAAATTGGCGTGGAGCTT
6134-6156	AGATAAAATTGGCGTGGAGCTTA
6135-6157	GATAAAATTGGCGTGGAGCTTAC
6136-6158	ATAAAATTGGCGTGGAGCTTACT
6137-6159	TAAATTTGGCGTGGAGCTTACTG
6138-6160	AAAATTTGGCGTGGAGCTTACTGG
6139-6161	AAATTTGGCGTGGAGCTTACTGGA
6140-6162	AATTTGGCGTGGAGCTTACTGGAC
6141-6163	ATTTGGCGTGGAGCTTACTGGACG
6142-6164	TTGGCGTGGAGCTTACTGGACGA
6143-6165	TGGCGTGGAGCTTACTGGACGAA
6144-6166	GGCGTGGAGCTTACTGGACGAAC
6145-6167	GCGTGGAGCTTACTGGACGAACT
6146-6168	CGTGGAGCTTACTGGACGAACTC
6147-6169	GTGGAGCTTACTGGACGAACTCT
6148-6170	TGGAGCTTACTGGACGAACTCTG
6149-6171	GGAGCTTACTGGACGAACTCTGG
6150-6172	GAGCTTACTGGACGAACTCTGGC
6151-6173	AGCTTACTGGACGAACTCTGGCT
6152-6174	GCTTACTGGACGAACTCTGGCTG
6153-6175	CTTACTGGACGAACTCTGGCTGA
6154-6176	TTACTGGACGAACTCTGGCTGAC
6155-6177	TACTGGACGAACTCTGGCTGACC
6156-6178	ACTGGACGAACTCTGGCTGACCT
6157-6179	CTGGACGAACTCTGGCTGACCTA
6158-6180	TGGACGAACTCTGGCTGACCTAA
6159-6181	GGACGAACTCTGGCTGACCTAAC
6160-6182	GACGAACTCTGGCTGACCTAACT
6161-6183	ACGAACTCTGGCTGACCTAACTC
6162-6184	CGAACTCTGGCTGACCTAACTCT
6163-6185	GAACCTCTGGCTGACCTAACTCTA
6164-6186	AACTCTGGCTGACCTAACTCTACT
6165-6187	ACTCTGGCTGACCTAACTCTACT
6166-6188	CTCTGGCTGACCTAACTCTACTA
6167-6189	TCTGGCTGACCTAACTCTACTAG
6168-6190	CTGGCTGACCTAACTCTACTAGA
6169-6191	TGGCTGACCTAACTCTACTAGAC
6170-6192	GGCTGACCTAACTCTACTAGACT
6171-6193	GCTGACCTAACTCTACTAGACTC
6172-6194	CTGACCTAACTCTACTAGACTCC
6173-6195	TGACCTAACTCTACTAGACTCCC
6174-6196	GACCTAACTCTACTAGACTCCCC
6175-6197	ACCTAACTCTACTAGACTCCCCA
6176-6198	CCTAACTCTACTAGACTCCCCAA
6177-6199	CTAACTCTACTAGACTCCCCAAT
6178-6200	TAACTCTACTAGACTCCCCAATT
6179-6201	AACTCTACTAGACTCCCCAATTA
6180-6202	ACTCTACTAGACTCCCCAATTAA

Position	Sequence
6181-6203	CTCTACTAGACTCCCCAATTAAA
6182-6204	TCTACTAGACTCCCCAATTAAAG
6183-6205	CTACTAGACTCCCCAATTAAAGT
6184-6206	TACTAGACTCCCCAATTAAAGTG
6185-6207	ACTAGACTCCCCAATTAAAGTGC
6186-6208	CTAGACTCCCCAATTAAAGTGCC
6187-6209	TAGACTCCCCAATTAAAGTGCCA
6188-6210	AGACTCCCCAATTAAAGTGCCAC
6189-6211	GACTCCCCAATTAAAGTGCCACT
6190-6212	ACTCCCCAATTAAAGTGCCACTT
6191-6213	CTCCCCAATTAAAGTGCCACTTT
6192-6214	TCCCCAATTAAAGTGCCACTTTT
6193-6215	CCCCAATTAAAGTGCCACTTTTA
6194-6216	CCCAATTAAAGTGCCACTTTTAC
6195-6217	CCAATTAAAGTGCCACTTTTACT
6196-6218	CAATTAAAGTGCCACTTTTACTC
6197-6219	AATTAAAGTGCCACTTTTACTCA
6198-6220	ATTAAGTGCCACTTTTACTCAG
6199-6221	TAAAGTGCCACTTTTACTCAGT
6200-6222	TAAAGTGCCACTTTTACTCAGTG
6201-6223	AAAGTGCCACTTTTACTCAGTGA
6202-6224	AAGTGCCACTTTTACTCAGTGAG
6203-6225	AGTGCCACTTTTACTCAGTGAGC
6204-6226	GTGCCACTTTTACTCAGTGAGCC
6205-6227	TGCCACTTTTACTCAGTGAGCCC
6206-6228	GCCACTTTTACTCAGTGAGCCCA
6207-6229	CCACTTTTACTCAGTGAGCCCAT
6208-6230	CACTTTTACTCAGTGAGCCCATC
6209-6231	ACTTTTACTCAGTGAGCCCATCA
6210-6232	CTTTTACTCAGTGAGCCCATCAA
6211-6233	TTTTTACTCAGTGAGCCCATCAAT
6212-6234	TTTACTCAGTGAGCCCATCAATA
6213-6235	TTACTCAGTGAGCCCATCAATAT
6214-6236	TACTCAGTGAGCCCATCAATATC
6215-6237	ACTCAGTGAGCCCATCAATATCA
6216-6238	CTCAGTGAGCCCATCAATATCAT
6217-6239	TCAGTGAGCCCATCAATATCATT
6218-6240	CAGTGAGCCCATCAATATCATTG
6219-6241	AGTGAGCCCATCAATATCATTGA
6220-6242	GTGAGCCCATCAATATCATTGAT
6221-6243	TGAGCCCATCAATATCATTGATG
6222-6244	GAGCCCATCAATATCATTGATGC
6223-6245	AGCCCATCAATATCATTGATGCT
6224-6246	GCCCATCAATATCATTGATGCTT
6225-6247	CCCATCAATATCATTGATGCTTT
6226-6248	CCATCAATATCATTGATGCTTTA
6227-6249	CATCAATATCATTGATGCTTTAG
6228-6250	ATCAATATCATTGATGCTTTAGA
6229-6251	TCAATATCATTGATGCTTTAGAG
6230-6252	CAATATCATTGATGCTTTAGAGA
6231-6253	AATATCATTGATGCTTTAGAGAT
6232-6254	ATATCATTGATGCTTTAGAGATG
6233-6255	TATCATTGATGCTTTAGAGATGA
6234-6256	ATCATTGATGCTTTAGAGATGAG
6235-6257	TCATTGATGCTTTAGAGATGAGA
6236-6258	CATTGATGCTTTAGAGATGAGAG
6237-6259	ATTGATGCTTTAGAGATGAGAGA
6238-6260	TTGATGCTTTAGAGATGAGAGAT
6239-6261	TGATGCTTTAGAGATGAGAGATG
6240-6262	GATGCTTTAGAGATGAGAGATGC
6241-6263	ATGCTTTAGAGATGAGAGATGCC
6242-6264	TGCTTTAGAGATGAGAGATGCCG
6243-6265	GCTTTAGAGATGAGAGATGCCGT
6244-6266	CTTTAGAGATGAGAGATGCCGTT
6245-6267	TTTAGAGATGAGAGATGCCGTTG
6246-6268	TTAGAGATGAGAGATGCCGTTGA

Position	Sequence
6247-6269	TAGAGATGAGAGATGCCGTTGAG
6248-6270	AGAGATGAGAGATGCCGTTGAGA
6249-6271	GAGATGAGAGATGCCGTTGAGAA
6250-6272	AGATGAGAGATGCCGTTGAGAAG
6251-6273	GATGAGAGATGCCGTTGAGAAGC
6252-6274	ATGAGAGATGCCGTTGAGAAGCC
6253-6275	TGAGAGATGCCGTTGAGAAGCCC
6254-6276	GAGAGATGCCGTTGAGAAGCCCC
6255-6277	AGAGATGCCGTTGAGAAGCCCCA
6256-6278	GAGATGCCGTTGAGAAGCCCCAA
6257-6279	AGATGCCGTTGAGAAGCCCCAAG
6258-6280	GATGCCGTTGAGAAGCCCCAAGA
6259-6281	ATGCCGTTGAGAAGCCCCAAGAA
6260-6282	TGCCGTTGAGAAGCCCCAAGAAT
6261-6283	GCCGTTGAGAAGCCCCAAGAATT
6262-6284	CCGTTGAGAAGCCCCAAGAATT
6263-6285	CGTTGAGAAGCCCCAAGAATT
6264-6286	GTTGAGAAGCCCCAAGAATT
6265-6287	TTGAGAAGCCCCAAGAATT
6266-6288	TGAGAAGCCCCAAGAATT
6267-6289	GAGAAGCCCCAAGAATT
6268-6290	AGAAGCCCCAAGAATT
6269-6291	GAAGCCCCAAGAATT
6270-6292	AAGCCCCAAGAATT
6271-6293	AGCCCCAAGAATT
6272-6294	GCCCCAAGAATT
6273-6295	CCCCAAGAATT
6274-6296	CCCAAGAATT
6275-6297	CCAAGAATT
6276-6298	CAAGAATT
6277-6299	AAGAATT
6278-6300	AGAATT
6279-6301	GAATT
6280-6302	AATT
6281-6303	ATT
6282-6304	TT
6283-6305	T
6284-6306	
6285-6307	
6286-6308	
6287-6309	
6288-6310	
6289-6311	
6290-6312	
6291-6313	
6292-6314	
6293-6315	
6294-6316	
6295-6317	
6296-6318	
6297-6319	
6298-6320	
6299-6321	
6300-6322	
6301-6323	
6302-6324	
6303-6325	
6304-6326	
6305-6327	
6306-6328	
6307-6329	
6308-6330	
6309-6331	
6310-6332	
6311-6333	
6312-6334	

Position	Sequence
6313-6335	AAAACCAAGATGTTCACTCCATT
6314-6336	AAACCAAGATGTTCACTCCATTA
6315-6337	AACCAAGATGTTCACTCCATTAA
6316-6338	ACCAAGATGTTCACTCCATTAAC
6317-6339	CCAAGATGTTCACTCCATTAACC
6318-6340	CAAGATGTTCACTCCATTAACCT
6319-6341	AAGATGTTCACTCCATTAACCTC
6320-6342	AGATGTTCACTCCATTAACCTCC
6321-6343	GATGTTCACTCCATTAACCTCCC
6322-6344	ATGTTCACTCCATTAACCTCCCA
6323-6345	TGTTCACTCCATTAACCTCCCAT
6324-6346	GTTCACTCCATTAACCTCCCAT
6325-6347	TTCCTCCATTAACCTCCCATTT
6326-6348	TCCTCCATTAACCTCCCATTTT
6327-6349	CACTCCATTAACCTCCCATTTTT
6328-6350	ACTCCATTAACCTCCCATTTTTT
6329-6351	CTCCATTAACCTCCCATTTTTTG
6330-6352	TCCATTAACCTCCCATTTTTTGA
6331-6353	CCATTAACCTCCCATTTTTTGAG
6332-6354	CATTAACCTCCCATTTTTTGAGA
6333-6355	ATTAACCTCCCATTTTTTGAGAC
6334-6356	TTAACCTCCCATTTTTTGAGACC
6335-6357	TAACCTCCCATTTTTTGAGACCT
6336-6358	AACCTCCCATTTTTTGAGACCTT
6337-6359	ACCTCCCATTTTTTGAGACCTTG
6338-6360	CCTCCCATTTTTTGAGACCTTGC
6339-6361	CTCCCATTTTTTGAGACCTTGCA
6340-6362	TCCCATTTTTTGAGACCTTGCAA
6341-6363	CCCATTTTTTGAGACCTTGCAAG
6342-6364	CCATTTTTTGAGACCTTGCAAGA
6343-6365	CATTTTTTGAGACCTTGCAAGAA
6344-6366	ATTTTTTGAGACCTTGCAAGAAT
6345-6367	TTTTTTGAGACCTTGCAAGAATA
6346-6368	TTTTTTGAGACCTTGCAAGAATAT
6347-6369	TTTTGAGACCTTGCAAGAATATT
6348-6370	TTTGAGACCTTGCAAGAATATTT
6349-6371	TTGAGACCTTGCAAGAATATTTT
6350-6372	TGAGACCTTGCAAGAATATTTTG
6351-6373	GAGACCTTGCAAGAATATTTTGA
6352-6374	AGACCTTGCAAGAATATTTTGAG
6353-6375	GACCTTGCAAGAATATTTTGAGA
6354-6376	ACCTTGCAAGAATATTTTGAGAG
6355-6377	CCTTGCAAGAATATTTTGAGAGG
6356-6378	CTTGCAAGAATATTTTGAGAGGA
6357-6379	TTGCAAGAATATTTTGAGAGGAA
6358-6380	TGCAAGAATATTTTGAGAGGAAT
6359-6381	GCAAGAATATTTTGAGAGGAATC
6360-6382	CAAGAATATTTTGAGAGGAATCG
6361-6383	AAGAATATTTTGAGAGGAATCGA
6362-6384	AGAATATTTTGAGAGGAATCGAC
6363-6385	GAATATTTTGAGAGGAATCGACA
6364-6386	AATATTTTGAGAGGAATCGACAA
6365-6387	ATATTTTGAGAGGAATCGACAAA
6366-6388	TATTTTGAGAGGAATCGACAAAC
6367-6389	ATTTTGAGAGGAATCGACAAACC
6368-6390	TTTTGAGAGGAATCGACAAACCA
6369-6391	TTTGAGAGGAATCGACAAACCAT
6370-6392	TTGAGAGGAATCGACAAACCATT
6371-6393	TGAGAGGAATCGACAAACCATTA
6372-6394	GAGAGGAATCGACAAACCATTAT
6373-6395	AGAGGAATCGACAAACCATTATA
6374-6396	GAGGAATCGACAAACCATTATAG
6375-6397	AGGAATCGACAAACCATTATAGT
6376-6398	GGAATCGACAAACCATTATAGTT
6377-6399	GAATCGACAAACCATTATAGTTG
6378-6400	AATCGACAAACCATTATAGTTGT

Position	Sequence
6379-6401	ATCGACAAACCATTATAGTTGTA
6380-6402	TCGACAAACCATTATAGTTGTAG
6381-6403	CGACAAACCATTATAGTTGTAGT
6382-6404	GACAAACCATTATAGTTGTAGTG
6383-6405	ACAAACCATTATAGTTGTAGTGG
6384-6406	CAAACCATTATAGTTGTAGTGGGA
6385-6407	AAACCATTATAGTTGTAGTGGAA
6386-6408	AACCATTATAGTTGTAGTGGAAA
6387-6409	ACCATTATAGTTGTAGTGGAAAA
6388-6410	CCATTATAGTTGTAGTGGAAAAC
6389-6411	CATTATAGTTGTAGTGGAAAACG
6390-6412	ATTATAGTTGTAGTGGAAAACGT
6391-6413	TTATAGTTGTAGTGGAAAACGTA
6392-6414	TATAGTTGTAGTGGAAAACGTAC
6393-6415	ATAGTTGTAGTGGAAAACGTACA
6394-6416	TAGTTGTAGTGGAAAACGTACAG
6395-6417	AGTTGTAGTGGAAAACGTACAGA
6396-6418	GTTGTAGTGGAAAACGTACAGAG
6397-6419	TTGTAGTGGAAAACGTACAGAGA
6398-6420	TGTAGTGGAAAACGTACAGAGAA
6399-6421	GTAGTGGAAAACGTACAGAGAAA
6400-6422	TAGTGGAAAACGTACAGAGAAAC
6401-6423	AGTGGAAAACGTACAGAGAAACC
6402-6424	GTGGAAAACGTACAGAGAAACCT
6403-6425	TGGAAAACGTACAGAGAAACCTG
6404-6426	GGAAAACGTACAGAGAAACCTGA
6405-6427	GAAAACGTACAGAGAAACCTGAA
6406-6428	AAAACGTACAGAGAAACCTGAAG
6407-6429	AAACGTACAGAGAAACCTGAAGC
6408-6430	AACGTACAGAGAAACCTGAAGCA
6409-6431	ACGTACAGAGAAACCTGAAGCAC
6410-6432	CGTACAGAGAAACCTGAAGCACA
6411-6433	GTACAGAGAAACCTGAAGCACAT
6412-6434	TACAGAGAAACCTGAAGCACATC
6413-6435	ACAGAGAAACCTGAAGCACATCA
6414-6436	CAGAGAAACCTGAAGCACATCAA
6415-6437	AGAGAAACCTGAAGCACATCAAT
6416-6438	GAGAAACCTGAAGCACATCAATA
6417-6439	AGAAACCTGAAGCACATCAATAT
6418-6440	GAAACCTGAAGCACATCAATATT
6419-6441	AAACCTGAAGCACATCAATATTG
6420-6442	AACCTGAAGCACATCAATATTGA
6421-6443	ACCTGAAGCACATCAATATTGAT
6422-6444	CCTGAAGCACATCAATATTGATC
6423-6445	CTGAAGCACATCAATATTGATCA
6424-6446	TGAAGCACATCAATATTGATCAA
6425-6447	GAAGCACATCAATATTGATCAAT
6426-6448	AAGCACATCAATATTGATCAATT
6427-6449	AGCACATCAATATTGATCAATTT
6428-6450	GCACATCAATATTGATCAATTTG
6429-6451	CACATCAATATTGATCAATTTGT
6430-6452	ACATCAATATTGATCAATTTGTA
6431-6453	CATCAATATTGATCAATTTGTAA
6432-6454	ATCAATATTGATCAATTTGTAAG
6433-6455	TCAATATTGATCAATTTGTAAGA
6434-6456	CAATATTGATCAATTTGTAAGAA
6435-6457	AATATTGATCAATTTGTAAGAAA
6436-6458	ATATTGATCAATTTGTAAGAAAA
6437-6459	TATTGATCAATTTGTAAGAAAAA
6438-6460	ATTGATCAATTTGTAAGAAAAATA
6439-6461	TTGATCAATTTGTAAGAAAAATAC
6440-6462	TGATCAATTTGTAAGAAAAATACA
6441-6463	GATCAATTTGTAAGAAAAATACAG
6442-6464	ATCAATTTGTAAGAAAAATACAGA
6443-6465	TCAATTTGTAAGAAAAATACAGAG
6444-6466	CAATTTGTAAGAAAAATACAGAGC

Position	Sequence
6445-6467	AATTTGTAAGAAAATACAGAGCA
6446-6468	ATTTGTAAGAAAATACAGAGCAG
6447-6469	TTGTAAGAAAATACAGAGCAGC
6448-6470	TTGTAAGAAAATACAGAGCAGCC
6449-6471	TGTAAGAAAATACAGAGCAGCCC
6450-6472	GTAAGAAAATACAGAGCAGCCCT
6451-6473	TAAGAAAATACAGAGCAGCCCTG
6452-6474	AAGAAAATACAGAGCAGCCCTGG
6453-6475	AGAAAATACAGAGCAGCCCTGGG
6454-6476	GAAAATACAGAGCAGCCCTGGGA
6455-6477	AAAATACAGAGCAGCCCTGGGAA
6456-6478	AAATACAGAGCAGCCCTGGGAAA
6457-6479	AATACAGAGCAGCCCTGGGAAAA
6458-6480	ATACAGAGCAGCCCTGGGAAAAC
6459-6481	TACAGAGCAGCCCTGGGAAAAC
6460-6482	ACAGAGCAGCCCTGGGAAAAC
6461-6483	CAGAGCAGCCCTGGGAAAAC
6462-6484	AGAGCAGCCCTGGGAAAAC
6463-6485	GAGCAGCCCTGGGAAAAC
6464-6486	AGCAGCCCTGGGAAAAC
6465-6487	GCAGCCCTGGGAAAAC
6466-6488	CAGCCCTGGGAAAAC
6467-6489	AGCCCTGGGAAAAC
6468-6490	GCCCTGGGAAAAC
6469-6491	CCCTGGGAAAAC
6470-6492	CCTGGGAAAAC
6471-6493	CTGGGAAAAC
6472-6494	TGGGAAAAC
6473-6495	GGGAAAAC
6474-6496	GGAAAAC
6475-6497	GAAAAC
6476-6498	AAAAC
6477-6499	AAAC
6478-6500	AAC
6479-6501	ACT
6480-6502	CTCC
6481-6503	TCCC
6482-6504	CCC
6483-6505	CC
6484-6506	CAC
6485-6507	ACAG
6486-6508	CAGCA
6487-6509	AGCA
6488-6510	GCA
6489-6511	CA
6490-6512	AAG
6491-6513	AGCT
6492-6514	GCT
6493-6515	CTA
6494-6516	TAAT
6495-6517	AATG
6496-6518	ATG
6497-6519	TG
6498-6520	GAT
6499-6521	ATT
6500-6522	TTAT
6501-6523	TATCT
6502-6524	ATCT
6503-6525	TCT
6504-6526	CT
6505-6527	TG
6506-6528	GA
6507-6529	AAT
6508-6530	AT
6509-6531	TT
6510-6532	TC

Position	Sequence
6511-6533	CATTCAATTGGGAGAGACAAGTT
6512-6534	ATTCAATTGGGAGAGACAAGTTT
6513-6535	TTCAATTGGGAGAGACAAGTTTC
6514-6536	TCAATTGGGAGAGACAAGTTTCA
6515-6537	CAATTGGGAGAGACAAGTTTCAC
6516-6538	AATTGGGAGAGACAAGTTTCACA
6517-6539	ATTGGGAGAGACAAGTTTCACAT
6518-6540	TTGGGAGAGACAAGTTTCACATG
6519-6541	TGGGAGAGACAAGTTTCACATGC
6520-6542	GGGAGAGACAAGTTTCACATGCC
6521-6543	GGAGAGACAAGTTTCACATGCCA
6522-6544	GAGAGACAAGTTTCACATGCCAA
6523-6545	AGAGACAAGTTTCACATGCCAAG
6524-6546	GAGACAAGTTTCACATGCCAAGG
6525-6547	AGACAAGTTTCACATGCCAAGGA
6526-6548	GACAAGTTTCACATGCCAAGGAG
6527-6549	ACAAGTTTCACATGCCAAGGAGA
6528-6550	CAAGTTTCACATGCCAAGGAGAA
6529-6551	AAGTTTCACATGCCAAGGAGAAA
6530-6552	AGTTTCACATGCCAAGGAGAAAAC
6531-6553	GTTTCACATGCCAAGGAGAAAAC
6532-6554	TTTCACATGCCAAGGAGAAAAC
6533-6555	TTCACATGCCAAGGAGAAAAC
6534-6556	TCACATGCCAAGGAGAAAAC
6535-6557	CACATGCCAAGGAGAAAAC
6536-6558	ACATGCCAAGGAGAAAAC
6537-6559	CATGCCAAGGAGAAAAC
6538-6560	ATGCCAAGGAGAAAAC
6539-6561	TGCCAAGGAGAAAAC
6540-6562	GCCAAGGAGAAAAC
6541-6563	CCAAGGAGAAAAC
6542-6564	CAAGGAGAAAAC
6543-6565	AAGGAGAAAAC
6544-6566	AGGAGAAAAC
6545-6567	GGAGAAAAC
6546-6568	GAGAAAAC
6547-6569	AGAAAAC
6548-6570	GAAAAC
6549-6571	AAAAC
6550-6572	AACTGACTGCTTCACAAAAAG
6551-6573	ACTGACTGCTTCACAAAAAGT
6552-6574	CTGACTGCTTCACAAAAAGTA
6553-6575	TGACTGCTTCACAAAAAGTAT
6554-6576	GACTGCTTCACAAAAAGTATA
6555-6577	ACTGCTTCACAAAAAGTATAG
6556-6578	CTGCTTCACAAAAAGTATAGA
6557-6579	TGCTTCACAAAAAGTATAGAA
6558-6580	GCTTCACAAAAAGTATAGAAT
6559-6581	CTTCACAAAAAGTATAGAATT
6560-6582	TTCACAAAAAGTATAGAATTA
6561-6583	CTCACAAAAAGTATAGAATTAC
6562-6584	TCACAAAAAGTATAGAATTACA
6563-6585	CACAAAAAGTATAGAATTACAG
6564-6586	ACAAAAAGTATAGAATTACAGA
6565-6587	CAAAAAAGTATAGAATTACAGAA
6566-6588	AAAAAGTATAGAATTACAGAAA
6567-6589	AAAAGTATAGAATTACAGAAAA
6568-6590	AAAAGTATAGAATTACAGAAAAT
6569-6591	AAAGTATAGAATTACAGAAAATG
6570-6592	AAGTATAGAATTACAGAAAATGA
6571-6593	AGTATAGAATTACAGAAAATGAT
6572-6594	GTATAGAATTACAGAAAATGATA
6573-6595	TATAGAATTACAGAAAATGATAT
6574-6596	ATAGAATTACAGAAAATGATATA
6575-6597	TAGAATTACAGAAAATGATATAC
6576-6598	AGAATTACAGAAAATGATATACA

Position	Sequence
6577-6599	GAATTACAGAAAATGATATACAA
6578-6600	AATTACAGAAAATGATATACAAA
6579-6601	ATTACAGAAAATGATATACAAAT
6580-6602	TTACAGAAAATGATATACAAATT
6581-6603	TACAGAAAATGATATACAAATTG
6582-6604	ACAGAAAATGATATACAAATTGC
6583-6605	CAGAAAATGATATACAAATTGCA
6584-6606	AGAAAATGATATACAAATTGCAT
6585-6607	GAAAATGATATACAAATTGCATT
6586-6608	AAAATGATATACAAATTGCATTA
6587-6609	AAATGATATACAAATTGCATTAG
6588-6610	AATGATATACAAATTGCATTAGA
6589-6611	ATGATATACAAATTGCATTAGAT
6590-6612	TGATATACAAATTGCATTAGATG
6591-6613	GATATACAAATTGCATTAGATGA
6592-6614	ATATACAAATTGCATTAGATGAT
6593-6615	TATACAAATTGCATTAGATGATG
6594-6616	ATACAAATTGCATTAGATGATGC
6595-6617	TACAAATTGCATTAGATGATGCC
6596-6618	ACAAATTGCATTAGATGATGCCA
6597-6619	CAAATTGCATTAGATGATGCCAA
6598-6620	AAATTGCATTAGATGATGCCAAA
6599-6621	AATTGCATTAGATGATGCCAAAA
6600-6622	ATTGCATTAGATGATGCCAAAAT
6601-6623	TTGCATTAGATGATGCCAAAATC
6602-6624	TGCATTAGATGATGCCAAAATCA
6603-6625	GCATTAGATGATGCCAAAATCAA
6604-6626	CATTAGATGATGCCAAAATCAAC
6605-6627	ATTAGATGATGCCAAAATCAACT
6606-6628	TTAGATGATGCCAAAATCAACTT
6607-6629	TAGATGATGCCAAAATCAACTTT
6608-6630	AGATGATGCCAAAATCAACTTTA
6609-6631	GATGATGCCAAAATCAACTTTAA
6610-6632	ATGATGCCAAAATCAACTTTAAT
6611-6633	TGATGCCAAAATCAACTTTAATG
6612-6634	GATGCCAAAATCAACTTTAATGA
6613-6635	ATGCCAAAATCAACTTTAATGAA
6614-6636	TGCCAAAATCAACTTTAATGAAA
6615-6637	GCCAAAATCAACTTTAATGAAAA
6616-6638	CCAAAATCAACTTTAATGAAAAA
6617-6639	CAAAAATCAACTTTAATGAAAAAC
6618-6640	AAAATCAACTTTAATGAAAAACT
6619-6641	AAATCAACTTTAATGAAAAACTA
6620-6642	AATCAACTTTAATGAAAAACTAT
6621-6643	ATCAACTTTAATGAAAAACTATC
6622-6644	TCAACTTTAATGAAAAACTATCT
6623-6645	CAACTTTAATGAAAAACTATCTC
6624-6646	AACTTTAATGAAAAACTATCTCA
6625-6647	ACTTTAATGAAAAACTATCTCAA
6626-6648	CTTTAATGAAAAACTATCTCAAC
6627-6649	TTAATGAAAAACTATCTCAACT
6628-6650	TTAATGAAAAACTATCTCAACTG
6629-6651	TAATGAAAAACTATCTCAACTGC
6630-6652	AATGAAAAACTATCTCAACTGCA
6631-6653	ATGAAAAACTATCTCAACTGCAG
6632-6654	TGAAAAACTATCTCAACTGCAGA
6633-6655	GAAAAACTATCTCAACTGCAGAC
6634-6656	AAAAACTATCTCAACTGCAGACA
6635-6657	AAAACTATCTCAACTGCAGACAT
6636-6658	AACTATCTCAACTGCAGACATA
6637-6659	AACTATCTCAACTGCAGACATAT
6638-6660	ACTATCTCAACTGCAGACATATA
6639-6661	CTATCTCAACTGCAGACATATAT
6640-6662	TATCTCAACTGCAGACATATATG
6641-6663	ATCTCAACTGCAGACATATATGA
6642-6664	TCTCAACTGCAGACATATATGAT

Position	Sequence
6643-6665	CTCAACTGCAGACATATATGATA
6644-6666	TCAACTGCAGACATATATGATAC
6645-6667	CAACTGCAGACATATATGATACA
6646-6668	AACTGCAGACATATATGATACAA
6647-6669	ACTGCAGACATATATGATACAAT
6648-6670	CTGCAGACATATATGATACAATT
6649-6671	TGCAGACATATATGATACAATTT
6650-6672	GCAGACATATATGATACAATTTG
6651-6673	CAGACATATATGATACAATTTGA
6652-6674	AGACATATATGATACAATTTGAT
6653-6675	GACATATATGATACAATTTGATC
6654-6676	ACATATATGATACAATTTGATCA
6655-6677	CATATATGATACAATTTGATCAG
6656-6678	ATATATGATACAATTTGATCAGT
6657-6679	TATATGATACAATTTGATCAGTA
6658-6680	ATATGATACAATTTGATCAGTAT
6659-6681	TATGATACAATTTGATCAGTATA
6660-6682	ATGATACAATTTGATCAGTATAT
6661-6683	TGATACAATTTGATCAGTATATT
6662-6684	GATACAATTTGATCAGTATATTA
6663-6685	ATACAATTTGATCAGTATATTTAA
6664-6686	TACAATTTGATCAGTATATTTAAA
6665-6687	ACAATTTGATCAGTATATTTAAAG
6666-6688	CAATTTGATCAGTATATTTAAAGA
6667-6689	AATTTGATCAGTATATTTAAAGAT
6668-6690	ATTTGATCAGTATATTTAAAGATA
6669-6691	TTTATGATCAGTATATTTAAAGATAG
6670-6692	TTGATCAGTATATTTAAAGATAGT
6671-6693	TGATCAGTATATTTAAAGATAGTT
6672-6694	GATCAGTATATTTAAAGATAGTTA
6673-6695	ATCAGTATATTTAAAGATAGTTAT
6674-6696	TCAGTATATTTAAAGATAGTTATG
6675-6697	CAGTATATTTAAAGATAGTTATGA
6676-6698	AGTATATTTAAAGATAGTTATGAT
6677-6699	GTATATTTAAAGATAGTTATGATT
6678-6700	TATATTTAAAGATAGTTATGATTT
6679-6701	ATATTTAAAGATAGTTATGATTTA
6680-6702	TATTTAAAGATAGTTATGATTTAC
6681-6703	ATTTAAAGATAGTTATGATTTACA
6682-6704	TTTAAAGATAGTTATGATTTACAT
6683-6705	TAAAGATAGTTATGATTTACATG
6684-6706	AAAGATAGTTATGATTTACATGA
6685-6707	AAGATAGTTATGATTTACATGAT
6686-6708	AGATAGTTATGATTTACATGATT
6687-6709	GATAGTTATGATTTACATGATTT
6688-6710	ATAGTTATGATTTACATGATTTG
6689-6711	TAGTTATGATTTACATGATTTGA
6690-6712	AGTTATGATTTACATGATTTGAA
6691-6713	GTTATGATTTACATGATTTGAAA
6692-6714	TTATGATTTACATGATTTGAAAA
6693-6715	TATGATTTACATGATTTGAAAAAT
6694-6716	ATGATTTACATGATTTGAAAAATA
6695-6717	TGATTTACATGATTTGAAAAATAG
6696-6718	GATTTACATGATTTGAAAAATAGC
6697-6719	ATTTACATGATTTGAAAAATAGCT
6698-6720	TTTACATGATTTGAAAAATAGCTA
6699-6721	TTACATGATTTGAAAAATAGCTAT
6700-6722	TACATGATTTGAAAAATAGCTATT
6701-6723	ACATGATTTGAAAAATAGCTATTG
6702-6724	CATGATTTGAAAAATAGCTATTGC
6703-6725	ATGATTTGAAAAATAGCTATTGCT
6704-6726	TGATTTGAAAAATAGCTATTGCTA
6705-6727	GATTTGAAAAATAGCTATTGCTAA
6706-6728	ATTTGAAAAATAGCTATTGCTAAT
6707-6729	TTTAAAAATAGCTATTGCTAATA
6708-6730	TTGAAAAATAGCTATTGCTAATAT

Position	Sequence
6709-6731	TGAAAATAGCTATTGCTAATATT
6710-6732	GAAAATAGCTATTGCTAATATTA
6711-6733	AAAATAGCTATTGCTAATATTAT
6712-6734	AAATAGCTATTGCTAATATTATT
6713-6735	AATAGCTATTGCTAATATTATTG
6714-6736	ATAGCTATTGCTAATATTATTGA
6715-6737	TAGCTATTGCTAATATTATTGAT
6716-6738	AGCTATTGCTAATATTATTGATG
6717-6739	GCTATTGCTAATATTATTGATGA
6718-6740	CTATTGCTAATATTATTGATGAA
6719-6741	TATTGCTAATATTATTGATGAAA
6720-6742	ATGCTAATATTATTGATGAAAT
6721-6743	TGCTAATATTATTGATGAAATC
6722-6744	TGCTAATATTATTGATGAAATCA
6723-6745	GCTAATATTATTGATGAAATCAT
6724-6746	CTAATATTATTGATGAAATCATT
6725-6747	TAATATTATTGATGAAATCATTG
6726-6748	AATATTATTGATGAAATCATTGA
6727-6749	ATATTATTGATGAAATCATTGAA
6728-6750	TATTATTGATGAAATCATTGAAA
6729-6751	ATTATTGATGAAATCATTGAAAA
6730-6752	TTATTGATGAAATCATTGAAAAA
6731-6753	TATTGATGAAATCATTGAAAAAT
6732-6754	ATTGATGAAATCATTGAAAAATT
6733-6755	TTGATGAAATCATTGAAAAATTA
6734-6756	TGATGAAATCATTGAAAAATTAA
6735-6757	GATGAAATCATTGAAAAATTAAA
6736-6758	ATGAAATCATTGAAAAATTAAAA
6737-6759	TGAAATCATTGAAAAATTAAAAA
6738-6760	GAAATCATTGAAAAATTAAAAAG
6739-6761	AAATCATTGAAAAATTAAAAAGT
6740-6762	AATCATTGAAAAATTAAAAAGTC
6741-6763	ATCATTGAAAAATTAAAAAGTCT
6742-6764	TCATTGAAAAATTAAAAAGTCTT
6743-6765	CATTGAAAAATTAAAAAGTCTTG
6744-6766	ATTGAAAAATTAAAAAGTCTTGA
6745-6767	TTGAAAAATTAAAAAGTCTTGAT
6746-6768	TGAAAAATTAAAAAGTCTTGATG
6747-6769	GAAAAATTAAAAAGTCTTGATGA
6748-6770	AAAAATTAAAAAGTCTTGATGAG
6749-6771	AAAATTAAAAAGTCTTGATGAGC
6750-6772	AAATTAAAAAGTCTTGATGAGCA
6751-6773	AATTAAAAAGTCTTGATGAGCAC
6752-6774	ATTA AAAAGTCTTGATGAGCACT
6753-6775	TAAAAAGTCTTGATGAGCACTA
6754-6776	TAAAAAGTCTTGATGAGCACTAT
6755-6777	AAAAAGTCTTGATGAGCACTATC
6756-6778	AAAAGTCTTGATGAGCACTATCA
6757-6779	AAAGTCTTGATGAGCACTATCAT
6758-6780	AAGTCTTGATGAGCACTATCATA
6759-6781	AGTCTTGATGAGCACTATCATAT
6760-6782	GTCTTGATGAGCACTATCATATC
6761-6783	TCTTGATGAGCACTATCATATCC
6762-6784	CTTGATGAGCACTATCATATCCG
6763-6785	TTGATGAGCACTATCATATCCGT
6764-6786	TGATGAGCACTATCATATCCGTG
6765-6787	GATGAGCACTATCATATCCGTGT
6766-6788	ATGAGCACTATCATATCCGTGTA
6767-6789	TGAGCACTATCATATCCGTGTAA
6768-6790	GAGCACTATCATATCCGTGTAAA
6769-6791	AGCACTATCATATCCGTGTAAAT
6770-6792	GCACTATCATATCCGTGTAAATT
6771-6793	CACTATCATATCCGTGTAAATTT
6772-6794	ACTATCATATCCGTGTAAATTTA
6773-6795	CTATCATATCCGTGTAAATTTAG
6774-6796	TATCATATCCGTGTAAATTTAGT

Position	Sequence
6775-6797	ATCATATCCGTGTAATTTAGTA
6776-6798	TCATATCCGTGTAATTTAGTAA
6777-6799	CATATCCGTGTAATTTAGTAAA
6778-6800	ATATCCGTGTAATTTAGTAAAA
6779-6801	TATCCGTGTAATTTAGTAAAAA
6780-6802	ATCCGTGTAATTTAGTAAAAAC
6781-6803	TCCGTGTAATTTAGTAAAAACA
6782-6804	CCGTGTAATTTAGTAAAAACAA
6783-6805	CGTGTAATTTAGTAAAAACAAT
6784-6806	GTGTAATTTAGTAAAAACAATC
6785-6807	TGTAATTTAGTAAAAACAATCC
6786-6808	GTAATTTAGTAAAAACAATCCA
6787-6809	TAAATTTAGTAAAAACAATCCAT
6788-6810	AAATTTAGTAAAAACAATCCATG
6789-6811	AATTTAGTAAAAACAATCCATGA
6790-6812	ATTTAGTAAAAACAATCCATGAT
6791-6813	TTTAGTAAAAACAATCCATGATC
6792-6814	TTAGTAAAAACAATCCATGATCT
6793-6815	TAGTAAAAACAATCCATGATCTA
6794-6816	AGTAAAAACAATCCATGATCTAC
6795-6817	GTAAAAACAATCCATGATCTACA
6796-6818	TAAAAACAATCCATGATCTACAT
6797-6819	AAAAACAATCCATGATCTACATT
6798-6820	AAAACAATCCATGATCTACATTT
6799-6821	AAACAATCCATGATCTACATTTG
6800-6822	AACAATCCATGATCTACATTTGT
6801-6823	ACAATCCATGATCTACATTTGTT
6802-6824	CAATCCATGATCTACATTTGTTT
6803-6825	AATCCATGATCTACATTTGTTTA
6804-6826	ATCCATGATCTACATTTGTTTAT
6805-6827	TCCATGATCTACATTTGTTTATT
6806-6828	CCATGATCTACATTTGTTTATTG
6807-6829	CATGATCTACATTTGTTTATTGA
6808-6830	ATGATCTACATTTGTTTATTGAA
6809-6831	TGATCTACATTTGTTTATTGAAA
6810-6832	GATCTACATTTGTTTATTGAAAA
6811-6833	ATCTACATTTGTTTATTGAAAAA
6812-6834	TCTACATTTGTTTATTGAAAAATA
6813-6835	CTACATTTGTTTATTGAAAAATAT
6814-6836	TACATTTGTTTATTGAAAAATATT
6815-6837	ACATTTGTTTATTGAAAAATATTG
6816-6838	CATTTGTTTATTGAAAAATATTGA
6817-6839	ATTTGTTTATTGAAAAATATTGAT
6818-6840	TTTGTTTATTGAAAAATATTGATT
6819-6841	TTGTTTATTGAAAAATATTGATTT
6820-6842	TGTTTATTGAAAAATATTGATTTT
6821-6843	GTTTATTGAAAAATATTGATTTTA
6822-6844	TTTATTGAAAAATATTGATTTTAA
6823-6845	TTATTGAAAAATATTGATTTTAAC
6824-6846	TATTGAAAAATATTGATTTTAACA
6825-6847	ATTGAAAAATATTGATTTTAACAA
6826-6848	TTGAAAAATATTGATTTTAACAAA
6827-6849	TGAAAAATATTGATTTTAACAAAA
6828-6850	GAAAAATATTGATTTTAACAAAAAG
6829-6851	AAAAATATTGATTTTAACAAAAAGT
6830-6852	AAATATTGATTTTAACAAAAAGTG
6831-6853	AATATTGATTTTAACAAAAAGTGG
6832-6854	ATATTGATTTTAACAAAAAGTGGA
6833-6855	TATTGATTTTAACAAAAAGTGGA
6834-6856	ATTGATTTTAACAAAAAGTGGAAG
6835-6857	TTGATTTTAACAAAAAGTGGAAGT
6836-6858	TGATTTTAACAAAAAGTGGAAGTA
6837-6859	GATTTTAACAAAAAGTGGAAGTAG
6838-6860	ATTTTAACAAAAAGTGGAAGTAGT
6839-6861	TTTTAACAAAAAGTGGAAGTAGTA
6840-6862	TTTAACAAAAAGTGGAAGTAGTAC

Position	Sequence
6841-6863	TTAACAAAAGTGAAGTAGTACT
6842-6864	TAACAAAAGTGAAGTAGTACTG
6843-6865	AACAAAAGTGAAGTAGTACTGC
6844-6866	ACAAAAGTGAAGTAGTACTGCA
6845-6867	CAAAAAGTGAAGTAGTACTGCAT
6846-6868	AAAAGTGAAGTAGTACTGCATC
6847-6869	AAAGTGAAGTAGTACTGCATCC
6848-6870	AAGTGAAGTAGTACTGCATCCT
6849-6871	AGTGAAGTAGTACTGCATCCTG
6850-6872	GTGAAGTAGTACTGCATCCTGG
6851-6873	TGAAGTAGTACTGCATCCTGGA
6852-6874	GAAGTAGTACTGCATCCTGGAT
6853-6875	GAAGTAGTACTGCATCCTGGATT
6854-6876	AAGTAGTACTGCATCCTGGATTC
6855-6877	AGTAGTACTGCATCCTGGATTCA
6856-6878	GTAGTACTGCATCCTGGATTCAA
6857-6879	TAGTACTGCATCCTGGATTCAAAA
6858-6880	AGTACTGCATCCTGGATTCAAAA
6859-6881	GTACTGCATCCTGGATTCAAAT
6860-6882	TACTGCATCCTGGATTCAAATG
6861-6883	ACTGCATCCTGGATTCAAATGT
6862-6884	CTGCATCCTGGATTCAAATGTG
6863-6885	TGCATCCTGGATTCAAATGTGG
6864-6886	GCATCCTGGATTCAAATGTGGA
6865-6887	CATCCTGGATTCAAATGTGGAT
6866-6888	ATCCTGGATTCAAATGTGGATA
6867-6889	TCCTGGATTCAAATGTGGATAC
6868-6890	CCTGGATTCAAATGTGGATACT
6869-6891	CTGGATTCAAATGTGGATACTA
6870-6892	TGGATTCAAATGTGGATACTAA
6871-6893	GGATTCAAATGTGGATACTAAG
6872-6894	GATTCAAATGTGGATACTAAGT
6873-6895	ATTCAAATGTGGATACTAAGTA
6874-6896	TTCAAATGTGGATACTAAGTAC
6875-6897	TCAAATGTGGATACTAAGTACC
6876-6898	CAAATGTGGATACTAAGTACCA
6877-6899	AAAATGTGGATACTAAGTACCAA
6878-6900	AAATGTGGATACTAAGTACCAA
6879-6901	AATGTGGATACTAAGTACCAAAT
6880-6902	ATGTGGATACTAAGTACCAAATC
6881-6903	TGTGGATACTAAGTACCAAATCA
6882-6904	GTGGATACTAAGTACCAAATCAG
6883-6905	TGGATACTAAGTACCAAATCAGA
6884-6906	GGATACTAAGTACCAAATCAGAA
6885-6907	GATACTAAGTACCAAATCAGAAT
6886-6908	ATACTAAGTACCAAATCAGAATC
6887-6909	TACTAAGTACCAAATCAGAATCC
6888-6910	ACTAAGTACCAAATCAGAATCCA
6889-6911	CTAAGTACCAAATCAGAATCCAG
6890-6912	TAAGTACCAAATCAGAATCCAGA
6891-6913	AAGTACCAAATCAGAATCCAGAT
6892-6914	AGTACCAAATCAGAATCCAGATA
6893-6915	GTACCAAATCAGAATCCAGATAC
6894-6916	TACCAAATCAGAATCCAGATACA
6895-6917	ACCAAATCAGAATCCAGATACAA
6896-6918	CCAAATCAGAATCCAGATACAAG
6897-6919	CAAATCAGAATCCAGATACAAGA
6898-6920	AAATCAGAATCCAGATACAAGAA
6899-6921	AATCAGAATCCAGATACAAGAAA
6900-6922	ATCAGAATCCAGATACAAGAAAA
6901-6923	TCAGAATCCAGATACAAGAAAAA
6902-6924	CAGAATCCAGATACAAGAAAAAC
6903-6925	AGAATCCAGATACAAGAAAAACT
6904-6926	GAATCCAGATACAAGAAAAACTG
6905-6927	AATCCAGATACAAGAAAAACTGC
6906-6928	ATCCAGATACAAGAAAAACTGCA

Position	Sequence
6907-6929	TCCAGATACAAGAAAACTGCAG
6908-6930	CCAGATACAAGAAAACTGCAGC
6909-6931	CAGATACAAGAAAACTGCAGCA
6910-6932	AGATACAAGAAAACTGCAGCAG
6911-6933	GATACAAGAAAACTGCAGCAGC
6912-6934	ATACAAGAAAACTGCAGCAGCT
6913-6935	TACAAGAAAACTGCAGCAGCTT
6914-6936	ACAAGAAAACTGCAGCAGCTTA
6915-6937	CAAGAAAACTGCAGCAGCTTAA
6916-6938	AAGAAAACTGCAGCAGCTTAAG
6917-6939	AGAAAACTGCAGCAGCTTAAGA
6918-6940	GAAAACTGCAGCAGCTTAAGAG
6919-6941	AAAACTGCAGCAGCTTAAGAGA
6920-6942	AAACTGCAGCAGCTTAAGAGAC
6921-6943	AACTGCAGCAGCTTAAGAGACA
6922-6944	AACTGCAGCAGCTTAAGAGACAC
6923-6945	ACTGCAGCAGCTTAAGAGACACA
6924-6946	CTGCAGCAGCTTAAGAGACACAT
6925-6947	TGCAGCAGCTTAAGAGACACATA
6926-6948	GCAGCAGCTTAAGAGACACATAC
6927-6949	CAGCAGCTTAAGAGACACATACA
6928-6950	AGCAGCTTAAGAGACACATACAG
6929-6951	GCAGCTTAAGAGACACATACAGA
6930-6952	CAGCTTAAGAGACACATACAGAA
6931-6953	AGCTTAAGAGACACATACAGAAT
6932-6954	GCTTAAGAGACACATACAGAATA
6933-6955	CTTAAGAGACACATACAGAATAT
6934-6956	TTAAGAGACACATACAGAATATA
6935-6957	TAAGAGACACATACAGAATATAG
6936-6958	AAGAGACACATACAGAATATAGA
6937-6959	AGAGACACATACAGAATATAGAC
6938-6960	GAGACACATACAGAATATAGACA
6939-6961	AGACACATACAGAATATAGACAT
6940-6962	GACACATACAGAATATAGACATC
6941-6963	ACACATACAGAATATAGACATCC
6942-6964	CACATACAGAATATAGACATCCA
6943-6965	ACATACAGAATATAGACATCCAG
6944-6966	CATACAGAATATAGACATCCAGC
6945-6967	ATACAGAATATAGACATCCAGCA
6946-6968	TACAGAATATAGACATCCAGCAC
6947-6969	ACAGAATATAGACATCCAGCACC
6948-6970	CAGAATATAGACATCCAGCACCT
6949-6971	AGAATATAGACATCCAGCACCTA
6950-6972	GAATATAGACATCCAGCACCTAG
6951-6973	AATATAGACATCCAGCACCTAGC
6952-6974	ATATAGACATCCAGCACCTAGCT
6953-6975	TATAGACATCCAGCACCTAGCTG
6954-6976	ATAGACATCCAGCACCTAGCTGG
6955-6977	TAGACATCCAGCACCTAGCTGGA
6956-6978	AGACATCCAGCACCTAGCTGGAA
6957-6979	GACATCCAGCACCTAGCTGGAAA
6958-6980	ACATCCAGCACCTAGCTGGAAAG
6959-6981	CATCCAGCACCTAGCTGGAAAGT
6960-6982	ATCCAGCACCTAGCTGGAAAGTT
6961-6983	TCCAGCACCTAGCTGGAAAGTTA
6962-6984	CCAGCACCTAGCTGGAAAGTTAA
6963-6985	CAGCACCTAGCTGGAAAGTTAAA
6964-6986	AGCACCTAGCTGGAAAGTTAAAA
6965-6987	GCACCTAGCTGGAAAGTTAAAAC
6966-6988	CACCTAGCTGGAAAGTTAAAAACA
6967-6989	ACCTAGCTGGAAAGTTAAAAACAA
6968-6990	CCTAGCTGGAAAGTTAAAAACAAC
6969-6991	CTAGCTGGAAAGTTAAAAACAACA
6970-6992	TAGCTGGAAAGTTAAAAACAACAC
6971-6993	AGCTGGAAAGTTAAAAACAACACA
6972-6994	GCTGGAAAGTTAAAAACAACACAT

Position	Sequence
6973-6995	CTGGAAGTTAAAACAACACATT
6974-6996	TGGAAGTTAAAACAACACATG
6975-6997	GGAAAGTTAAAACAACACATTGA
6976-6998	GAAAGTTAAAACAACACATTGAG
6977-6999	AAAGTTAAAACAACACATTGAGG
6978-7000	AAGTTAAAACAACACATTGAGGC
6979-7001	AGTTAAAACAACACATTGAGGCT
6980-7002	GTTAAAACAACACATTGAGGCTA
6981-7003	TTAAAACAACACATTGAGGCTAT
6982-7004	TAAAACAACACATTGAGGCTATT
6983-7005	AAAACAACACATTGAGGCTATTG
6984-7006	AAACAACACATTGAGGCTATTGA
6985-7007	AACAACACATTGAGGCTATTGAT
6986-7008	ACAACACATTGAGGCTATTGATG
6987-7009	CAACACATTGAGGCTATTGATGT
6988-7010	AACACATTGAGGCTATTGATGTT
6989-7011	ACACATTGAGGCTATTGATGTTA
6990-7012	CACATTGAGGCTATTGATGTTAG
6991-7013	ACATTGAGGCTATTGATGTTAGA
6992-7014	CATTGAGGCTATTGATGTTAGAG
6993-7015	ATTGAGGCTATTGATGTTAGAGT
6994-7016	TTGAGGCTATTGATGTTAGAGTG
6995-7017	TGAGGCTATTGATGTTAGAGTGC
6996-7018	GAGGCTATTGATGTTAGAGTGCT
6997-7019	AGGCTATTGATGTTAGAGTGCTT
6998-7020	GGCTATTGATGTTAGAGTGCTTT
6999-7021	GCTATTGATGTTAGAGTGCTTTT
7000-7022	CTATTGATGTTAGAGTGCTTTTA
7001-7023	TATTGATGTTAGAGTGCTTTTAG
7002-7024	ATTGATGTTAGAGTGCTTTTAGA
7003-7025	TTGATGTTAGAGTGCTTTTAGAT
7004-7026	TGATGTTAGAGTGCTTTTAGATC
7005-7027	GATGTTAGAGTGCTTTTAGATCA
7006-7028	ATGTTAGAGTGCTTTTAGATCAA
7007-7029	TGTTAGAGTGCTTTTAGATCAAT
7008-7030	GTTAGAGTGCTTTTAGATCAATT
7009-7031	TTAGAGTGCTTTTAGATCAATTG
7010-7032	TAGAGTGCTTTTAGATCAATTGG
7011-7033	AGAGTGCTTTTAGATCAATTGGG
7012-7034	GAGTGCTTTTAGATCAATTGGGA
7013-7035	AGTGCTTTTAGATCAATTGGGAA
7014-7036	GTGCTTTTAGATCAATTGGGAAC
7015-7037	TGCTTTTAGATCAATTGGGAACT
7016-7038	GCTTTTAGATCAATTGGGAACTA
7017-7039	CTTTTAGATCAATTGGGAACTAC
7018-7040	TTTTAGATCAATTGGGAACTACA
7019-7041	TTTAGATCAATTGGGAACTACAA
7020-7042	TTAGATCAATTGGGAACTACAAT
7021-7043	TAGATCAATTGGGAACTACAATT
7022-7044	AGATCAATTGGGAACTACAATTT
7023-7045	GATCAATTGGGAACTACAATTTT
7024-7046	ATCAATTGGGAACTACAATTTCA
7025-7047	TCAATTGGGAACTACAATTTTCA
7026-7048	CAATTGGGAACTACAATTTTCA
7027-7049	AATTGGGAACTACAATTTTCA
7028-7050	ATTGGGAACTACAATTTTCA
7029-7051	TTGGGAACTACAATTTTCA
7030-7052	TGGGAACTACAATTTTCA
7031-7053	GGGAACTACAATTTTCA
7032-7054	GGAACACTACAATTTTCA
7033-7055	GAACACTACAATTTTCA
7034-7056	AACTACAATTTTCA
7035-7057	ACTACAATTTTCA
7036-7058	CTACAATTTTCA
7037-7059	TACAATTTTCA
7038-7060	ACAATTTTCA

Position	Sequence
7039-7061	CAATTCATTTGAAAGAATAAAT
7040-7062	AATTCATTTGAAAGAATAAATG
7041-7063	ATTCATTTGAAAGAATAAATGA
7042-7064	TTTCATTTGAAAGAATAAATGAT
7043-7065	TTCATTTGAAAGAATAAATGATG
7044-7066	TCATTTGAAAGAATAAATGATGT
7045-7067	CATTTGAAAGAATAAATGATGTT
7046-7068	ATTTGAAAGAATAAATGATGTTC
7047-7069	TTGAAAGAATAAATGATGTCTT
7048-7070	TTGAAAGAATAAATGATGTCTT
7049-7071	TGAAAGAATAAATGATGTCTTG
7050-7072	GAAAGAATAAATGATGTCTTGA
7051-7073	AAAGAATAAATGATGTCTTGAG
7052-7074	AAGAATAAATGATGTCTTGAGC
7053-7075	AGAATAAATGATGTCTTGAGCA
7054-7076	GAATAAATGATGTCTTGAGCAT
7055-7077	AATAAATGATGTCTTGAGCATG
7056-7078	ATAAATGATGTCTTGAGCATGT
7057-7079	TAAATGATGTCTTGAGCATGTC
7058-7080	AAATGATGTCTTGAGCATGTCA
7059-7081	AATGATGTCTTGAGCATGTCAA
7060-7082	ATGATGTCTTGAGCATGTCAAA
7061-7083	TGATGTCTTGAGCATGTCAAAC
7062-7084	GATGTCTTGAGCATGTCAAACA
7063-7085	ATGTTCTTGAGCATGTCAAACAC
7064-7086	TGTTCTTGAGCATGTCAAACACT
7065-7087	GTTCTTGAGCATGTCAAACACTT
7066-7088	TTCTTGAGCATGTCAAACACTTT
7067-7089	TCTTGAGCATGTCAAACACTTTG
7068-7090	CTTGAGCATGTCAAACACTTTGT
7069-7091	TTGAGCATGTCAAACACTTTGTT
7070-7092	TGAGCATGTCAAACACTTTGTTA
7071-7093	GAGCATGTCAAACACTTTGTTAT
7072-7094	AGCATGTCAAACACTTTGTTATA
7073-7095	GCATGTCAAACACTTTGTTATAA
7074-7096	CATGTCAAACACTTTGTTATAAA
7075-7097	ATGTCAAACACTTTGTTATAAAT
7076-7098	TGTCAAACACTTTGTTATAAATC
7077-7099	GTCAAACACTTTGTTATAAATCT
7078-7100	TCAAACACTTTGTTATAAATCTT
7079-7101	CAAACACTTTGTTATAAATCTTA
7080-7102	AAACACTTTGTTATAAATCTTAT
7081-7103	AACACTTTGTTATAAATCTTATT
7082-7104	ACACTTTGTTATAAATCTTATTG
7083-7105	CACTTTGTTATAAATCTTATTGG
7084-7106	ACTTTGTTATAAATCTTATTGGG
7085-7107	CTTTGTATAAATCTTATTGGGG
7086-7108	TTTGTATAAATCTTATTGGGGGA
7087-7109	TTGTTATAAATCTTATTGGGGAT
7088-7110	TGTATAAATCTTATTGGGGATT
7089-7111	GTATAAATCTTATTGGGGATTT
7090-7112	TTATAAATCTTATTGGGGATTTT
7091-7113	TATAAATCTTATTGGGGATTTTG
7092-7114	ATAAATCTTATTGGGGATTTTGA
7093-7115	TAAATCTTATTGGGGATTTTGAA
7094-7116	AAATCTTATTGGGGATTTTGAAG
7095-7117	AATCTTATTGGGGATTTTGAAGT
7096-7118	ATCTTATTGGGGATTTTGAAGTA
7097-7119	TCTTATTGGGGATTTTGAAGTAG
7098-7120	CTTATTGGGGATTTTGAAGTAGC
7099-7121	TTATTGGGGATTTTGAAGTAGCT
7100-7122	TATTGGGGATTTTGAAGTAGCTG
7101-7123	ATTGGGGATTTTGAAGTAGCTGA
7102-7124	TTGGGGATTTTGAAGTAGCTGAG
7103-7125	TGGGGATTTTGAAGTAGCTGAGA
7104-7126	GGGGATTTTGAAGTAGCTGAGAA

Position	Sequence
7105-7127	GGGATTTTGAAGTAGCTGAGAAA
7106-7128	GGATTTTGAAGTAGCTGAGAAAA
7107-7129	GATTTTGAAGTAGCTGAGAAAAT
7108-7130	ATTTTGAAGTAGCTGAGAAAATC
7109-7131	TTTGAAGTAGCTGAGAAAATCA
7110-7132	TTTGAAGTAGCTGAGAAAATCAA
7111-7133	TTGAAGTAGCTGAGAAAATCAAT
7112-7134	TGAAGTAGCTGAGAAAATCAATG
7113-7135	GAAGTAGCTGAGAAAATCAATGC
7114-7136	AAGTAGCTGAGAAAATCAATGCC
7115-7137	AGTAGCTGAGAAAATCAATGCCT
7116-7138	GTAGCTGAGAAAATCAATGCCTT
7117-7139	TAGCTGAGAAAATCAATGCCTTC
7118-7140	AGCTGAGAAAATCAATGCCTTCA
7119-7141	GCTGAGAAAATCAATGCCTTCAG
7120-7142	CTGAGAAAATCAATGCCTTCAGA
7121-7143	TGAGAAAATCAATGCCTTCAGAG
7122-7144	GAGAAAATCAATGCCTTCAGAGC
7123-7145	AGAAAATCAATGCCTTCAGAGCC
7124-7146	GAAAATCAATGCCTTCAGAGCCA
7125-7147	AAAATCAATGCCTTCAGAGCCAA
7126-7148	AAATCAATGCCTTCAGAGCCAAA
7127-7149	AATCAATGCCTTCAGAGCCAAAG
7128-7150	ATCAATGCCTTCAGAGCCAAAGT
7129-7151	TCAATGCCTTCAGAGCCAAAGTC
7130-7152	CAATGCCTTCAGAGCCAAAGTCC
7131-7153	AATGCCTTCAGAGCCAAAGTCCA
7132-7154	ATGCCTTCAGAGCCAAAGTCCAT
7133-7155	TGCCTTCAGAGCCAAAGTCCATG
7134-7156	GCTTCAGAGCCAAAGTCCATGA
7135-7157	CCTTCAGAGCCAAAGTCCATGAG
7136-7158	CTTCAGAGCCAAAGTCCATGAGT
7137-7159	TTCAGAGCCAAAGTCCATGAGTT
7138-7160	TCAGAGCCAAAGTCCATGAGTTA
7139-7161	CAGAGCCAAAGTCCATGAGTTAA
7140-7162	AGAGCCAAAGTCCATGAGTTAAT
7141-7163	GAGCCAAAGTCCATGAGTTAATC
7142-7164	AGCCAAAGTCCATGAGTTAATCG
7143-7165	GCCAAAGTCCATGAGTTAATCGA
7144-7166	CCAAAGTCCATGAGTTAATCGAG
7145-7167	CAAAGTCCATGAGTTAATCGAGA
7146-7168	AAAGTCCATGAGTTAATCGAGAG
7147-7169	AAGTCCATGAGTTAATCGAGAGG
7148-7170	AGTCCATGAGTTAATCGAGAGGT
7149-7171	GTCCATGAGTTAATCGAGAGGTA
7150-7172	TCCATGAGTTAATCGAGAGGTAT
7151-7173	CCATGAGTTAATCGAGAGGTATG
7152-7174	CATGAGTTAATCGAGAGGTATGA
7153-7175	ATGAGTTAATCGAGAGGTATGAA
7154-7176	TGAGTTAATCGAGAGGTATGAAG
7155-7177	GAGTTAATCGAGAGGTATGAAGT
7156-7178	AGTTAATCGAGAGGTATGAAGTA
7157-7179	GTTAATCGAGAGGTATGAAGTAG
7158-7180	TTAATCGAGAGGTATGAAGTAGA
7159-7181	TAATCGAGAGGTATGAAGTAGAC
7160-7182	AATCGAGAGGTATGAAGTAGACC
7161-7183	ATCGAGAGGTATGAAGTAGACCA
7162-7184	TCGAGAGGTATGAAGTAGACCAA
7163-7185	CGAGAGGTATGAAGTAGACCAAC
7164-7186	GAGAGGTATGAAGTAGACCAACA
7165-7187	AGAGGTATGAAGTAGACCAACAA
7166-7188	GAGGTATGAAGTAGACCAACAACA
7167-7189	AGGTATGAAGTAGACCAACAACAAT
7168-7190	GGTATGAAGTAGACCAACAACAATC
7169-7191	GTATGAAGTAGACCAACAACAATCC
7170-7192	TATGAAGTAGACCAACAACAATCCA

Position	Sequence
7171-7193	ATGAAGTAGACCAACAAATCCAG
7172-7194	TGAAGTAGACCAACAAATCCAGG
7173-7195	GAAGTAGACCAACAAATCCAGGT
7174-7196	AAGTAGACCAACAAATCCAGGTT
7175-7197	AGTAGACCAACAAATCCAGGTTT
7176-7198	GTAGACCAACAAATCCAGGTTTT
7177-7199	TAGACCAACAAATCCAGGTTTTA
7178-7200	AGACCAACAAATCCAGGTTTTAA
7179-7201	GACCAACAAATCCAGGTTTTAAT
7180-7202	ACCAACAAATCCAGGTTTTAATG
7181-7203	CCAACAAATCCAGGTTTTAATGG
7182-7204	CAACAAATCCAGGTTTTAATGGA
7183-7205	AACAAATCCAGGTTTTAATGGAT
7184-7206	ACAAATCCAGGTTTTAATGGATA
7185-7207	CAAATCCAGGTTTTAATGGATAA
7186-7208	AAATCCAGGTTTTAATGGATAAA
7187-7209	AATCCAGGTTTTAATGGATAAAT
7188-7210	ATCCAGGTTTTAATGGATAAATF
7189-7211	TCCAGGTTTTAATGGATAAATTA
7190-7212	CCAGGTTTTAATGGATAAATTAG
7191-7213	CAGGTTTTAATGGATAAATTAGT
7192-7214	AGGTTTTAATGGATAAATTAGTA
7193-7215	GGTTTTAATGGATAAATTAGTAG
7194-7216	GTTTTAATGGATAAATTAGTAGA
7195-7217	TTTTAATGGATAAATTAGTAGAG
7196-7218	TTTAATGGATAAATTAGTAGAGT
7197-7219	TTAATGGATAAATTAGTAGAGTT
7198-7220	TAATGGATAAATTAGTAGAGTTG
7199-7221	AATGGATAAATTAGTAGAGTTGA
7200-7222	ATGGATAAATTAGTAGAGTTGAC
7201-7223	TGGATAAATTAGTAGAGTTGACC
7202-7224	GGATAAATTAGTAGAGTTGACCC
7203-7225	GATAAATTAGTAGAGTTGACCCA
7204-7226	ATAAATTAGTAGAGTTGACCCAC
7205-7227	TAAATTAGTAGAGTTGACCCACC
7206-7228	AAATTAGTAGAGTTGACCCACCA
7207-7229	AATTAGTAGAGTTGACCCACCAA
7208-7230	ATTAGTAGAGTTGACCCACCAAT
7209-7231	TTAGTAGAGTTGACCCACCAATA
7210-7232	TAGTAGAGTTGACCCACCAATAC
7211-7233	AGTAGAGTTGACCCACCAATACA
7212-7234	GTAGAGTTGACCCACCAATACAA
7213-7235	TAGAGTTGACCCACCAATACAAG
7214-7236	AGAGTTGACCCACCAATACAAGT
7215-7237	GAGTTGACCCACCAATACAAGTT
7216-7238	AGTTGACCCACCAATACAAGTTG
7217-7239	GTTGACCCACCAATACAAGTTGA
7218-7240	TTGACCCACCAATACAAGTTGAA
7219-7241	TGACCCACCAATACAAGTTGAAG
7220-7242	GACCCACCAATACAAGTTGAAGG
7221-7243	ACCCACCAATACAAGTTGAAGGA
7222-7244	CCCACCAATACAAGTTGAAGGAG
7223-7245	CCACCAATACAAGTTGAAGGAGA
7224-7246	CACCAATACAAGTTGAAGGAGAC
7225-7247	ACCAATACAAGTTGAAGGAGACT
7226-7248	CCAATACAAGTTGAAGGAGACTA
7227-7249	CAATACAAGTTGAAGGAGACTAT
7228-7250	AATACAAGTTGAAGGAGACTATT
7229-7251	ATACAAGTTGAAGGAGACTATTTC
7230-7252	TACAAGTTGAAGGAGACTATTCA
7231-7253	ACAAGTTGAAGGAGACTATTTCAG
7232-7254	CAAGTTGAAGGAGACTATTTCAGA
7233-7255	AAGTTGAAGGAGACTATTTCAGAA
7234-7256	AGTTGAAGGAGACTATTTCAGAAG
7235-7257	GTTGAAGGAGACTATTTCAGAAGC
7236-7258	TTGAAGGAGACTATTTCAGAAGCT

Position	Sequence
7237-7259	TGAAGGAGACTATTCAGAAGCTA
7238-7260	GAAGGAGACTATTCAGAAGCTAA
7239-7261	AAGGAGACTATTCAGAAGCTAAG
7240-7262	AGGAGACTATTCAGAAGCTAAGC
7241-7263	GGAGACTATTCAGAAGCTAAGCA
7242-7264	GAGACTATTCAGAAGCTAAGCAA
7243-7265	AGACTATTCAGAAGCTAAGCAAT
7244-7266	GACTATTCAGAAGCTAAGCAATG
7245-7267	ACTATTCAGAAGCTAAGCAATGT
7246-7268	CTATTCAGAAGCTAAGCAATGTC
7247-7269	TATTCAGAAGCTAAGCAATGTCC
7248-7270	ATTCAGAAGCTAAGCAATGTCCT
7249-7271	TTCAGAAGCTAAGCAATGTCCTA
7250-7272	TCAGAAGCTAAGCAATGTCCTAC
7251-7273	CAGAAGCTAAGCAATGTCCTACA
7252-7274	AGAAGCTAAGCAATGTCCTACAA
7253-7275	GAAGCTAAGCAATGTCCTACAAC
7254-7276	AAGCTAAGCAATGTCCTACAACA
7255-7277	AGCTAAGCAATGTCCTACAACAA
7256-7278	GCTAAGCAATGTCCTACAACAAG
7257-7279	CTAAGCAATGTCCTACAACAAGT
7258-7280	TAAGCAATGTCCTACAACAAGTT
7259-7281	AAGCAATGTCCTACAACAAGTTA
7260-7282	AGCAATGTCCTACAACAAGTTAA
7261-7283	GCAATGTCCTACAACAAGTTAAG
7262-7284	CAATGTCCTACAACAAGTTAAGA
7263-7285	AATGTCCTACAACAAGTTAAGAT
7264-7286	ATGTCCTACAACAAGTTAAGATA
7265-7287	TGTCCTACAACAAGTTAAGATAA
7266-7288	GTCTACAACAAGTTAAGATAAA
7267-7289	TCCTACAACAAGTTAAGATAAAA
7268-7290	CCTACAACAAGTTAAGATAAAAAG
7269-7291	CTACAACAAGTTAAGATAAAAAGA
7270-7292	TACAACAAGTTAAGATAAAAAGAT
7271-7293	ACAACAAGTTAAGATAAAAAGATT
7272-7294	CAACAAGTTAAGATAAAAAGATTA
7273-7295	AACAAGTTAAGATAAAAAGATTAC
7274-7296	ACAAGTTAAGATAAAAAGATTACT
7275-7297	CAAGTTAAGATAAAAAGATTACTT
7276-7298	AAGTTAAGATAAAAAGATTACTTT
7277-7299	AGTTAAGATAAAAAGATTACTTTG
7278-7300	GTTAAGATAAAAAGATTACTTTGA
7279-7301	TTAAGATAAAAAGATTACTTTGAG
7280-7302	TAAGATAAAAAGATTACTTTGAGA
7281-7303	AAGATAAAAAGATTACTTTGAGAA
7282-7304	AGATAAAAAGATTACTTTGAGAAA
7283-7305	GATAAAAAGATTACTTTGAGAAAT
7284-7306	ATAAAAAGATTACTTTGAGAAATT
7285-7307	TAAAAGATTACTTTGAGAAATTG
7286-7308	AAAAGATTACTTTGAGAAATTGG
7287-7309	AAAGATTACTTTGAGAAATTGGT
7288-7310	AAGATTACTTTGAGAAATTGGTT
7289-7311	AGATTACTTTGAGAAATTGGTTG
7290-7312	GATTACTTTGAGAAATTGGTTGG
7291-7313	ATTACTTTGAGAAATTGGTTGGA
7292-7314	TTACTTTGAGAAATTGGTTGGAT
7293-7315	TACTTTGAGAAATTGGTTGGATT
7294-7316	ACTTTGAGAAATTGGTTGGATTT
7295-7317	CTTTGAGAAATTGGTTGGATTTA
7296-7318	TTTGAGAAATTGGTTGGATTTAT
7297-7319	TTGAGAAATTGGTTGGATTTATT
7298-7320	TGAGAAATTGGTTGGATTTATTG
7299-7321	GAGAAATTGGTTGGATTTATTGA
7300-7322	AGAAATTGGTTGGATTTATTGAT
7301-7323	GAAATTGGTTGGATTTATTGATG
7302-7324	AAATTGGTTGGATTTATTGATGA

Position	Sequence
7303-7325	AATTGGTTGGATTATTGATGAT
7304-7326	ATTGGTTGGATTATTGATGATG
7305-7327	TTGGTTGGATTATTGATGATGC
7306-7328	TGGTTGGATTATTGATGATGCT
7307-7329	GGTTGGATTATTGATGATGCTG
7308-7330	GTTGGATTATTGATGATGCTGT
7309-7331	TTGGATTATTGATGATGCTGTG
7310-7332	TGGATTATTGATGATGCTGTGA
7311-7333	GGATTATTGATGATGCTGTGAA
7312-7334	GATTATTGATGATGCTGTGAAG
7313-7335	ATTATTGATGATGCTGTGAAGA
7314-7336	TTTATTGATGATGCTGTGAAGAA
7315-7337	TTATTGATGATGCTGTGAAGAAG
7316-7338	TATTGATGATGCTGTGAAGAAGC
7317-7339	ATTGATGATGCTGTGAAGAAGCT
7318-7340	TTGATGATGCTGTGAAGAAGCTT
7319-7341	TGATGATGCTGTGAAGAAGCTTA
7320-7342	GATGATGCTGTGAAGAAGCTTAA
7321-7343	ATGATGCTGTGAAGAAGCTTAAT
7322-7344	TGATGCTGTGAAGAAGCTTAATG
7323-7345	GATGCTGTGAAGAAGCTTAATGA
7324-7346	ATGCTGTGAAGAAGCTTAATGAA
7325-7347	TGCTGTGAAGAAGCTTAATGAAT
7326-7348	GCTGTGAAGAAGCTTAATGAATT
7327-7349	CTGTGAAGAAGCTTAATGAATTA
7328-7350	TGTGAAGAAGCTTAATGAATTAT
7329-7351	GTGAAGAAGCTTAATGAATTATC
7330-7352	TGAAGAAGCTTAATGAATTATCT
7331-7353	GAAGAAGCTTAATGAATTATCTT
7332-7354	AAGAAGCTTAATGAATTATCTTT
7333-7355	AGAAGCTTAATGAATTATCTTTT
7334-7356	GAAGCTTAATGAATTATCTTTTA
7335-7357	AAGCTTAATGAATTATCTTTTAA
7336-7358	AGCTTAATGAATTATCTTTTAAA
7337-7359	GCTTAATGAATTATCTTTTAAAA
7338-7360	CTTAATGAATTATCTTTTAAAC
7339-7361	TTAATGAATTATCTTTTAAACA
7340-7362	TAATGAATTATCTTTTAAAACAT
7341-7363	AATGAATTATCTTTTAAAACATT
7342-7364	ATGAATTATCTTTTAAAACATTC
7343-7365	TGAATTATCTTTTAAAACATTCA
7344-7366	GAATTATCTTTTAAAACATTTCAT
7345-7367	AATTATCTTTTAAAACATTCATT
7346-7368	ATTATCTTTTAAAACATTCATTG
7347-7369	TTATCTTTTAAAACATTCATTGA
7348-7370	TATCTTTTAAAACATTCATTGAA
7349-7371	ATCTTTTAAAACATTCATTGAAG
7350-7372	TCTTTTAAAACATTCATTGAAGA
7351-7373	CTTTTAAAACATTCATTGAAGAT
7352-7374	TTTTAAAACATTCATTGAAGATG
7353-7375	TTTAAAACATTCATTGAAGATGT
7354-7376	TTAAAACATTCATTGAAGATGTT
7355-7377	TAAAACATTCATTGAAGATGTTA
7356-7378	AAAACATTCATTGAAGATGTTAA
7357-7379	AAACATTCATTGAAGATGTTAAC
7358-7380	AACATTCATTGAAGATGTTAACA
7359-7381	ACATTCATTGAAGATGTTAACAA
7360-7382	CATTCATTGAAGATGTTAACAAA
7361-7383	ATTCATTGAAGATGTTAACA AAT
7362-7384	TTTCATTGAAGATGTTAACA AATT
7363-7385	TCATTGAAGATGTTAACA AATTC
7364-7386	CATTGAAGATGTTAACA AATTC
7365-7387	ATTGAAGATGTTAACA AATTCCT
7366-7388	TTGAAGATGTTAACA AATTCCTT
7367-7389	TGAAGATGTTAACA AATTCCTTG
7368-7390	GAAGATGTTAACA AATTCCTTGA

Position	Sequence
7369-7391	AAGATGTTAACAAATTCCTTGAC
7370-7392	AGATGTTAACAAATTCCTTGACA
7371-7393	GATGTTAACAAATTCCTTGACAT
7372-7394	ATGTTAACAAATTCCTTGACATG
7373-7395	TGTTAACAAATTCCTTGACATGT
7374-7396	GTTAACAAATTCCTTGACATGTT
7375-7397	TTAACAAATTCCTTGACATGTTG
7376-7398	TAACAAATTCCTTGACATGTTGA
7377-7399	AACAAATTCCTTGACATGTTGAT
7378-7400	ACAAATTCCTTGACATGTTGATA
7379-7401	CAAATTCCTTGACATGTTGATAA
7380-7402	AAATTCCTTGACATGTTGATAAA
7381-7403	AATTCCTTGACATGTTGATAAAG
7382-7404	ATTCCTTGACATGTTGATAAAGA
7383-7405	TTTCCTTGACATGTTGATAAAGAA
7384-7406	TCCTTGACATGTTGATAAAGAAA
7385-7407	CCTTGACATGTTGATAAAGAAAT
7386-7408	CTTGACATGTTGATAAAGAAATT
7387-7409	TTGACATGTTGATAAAGAAATTA
7388-7410	TGACATGTTGATAAAGAAATTAA
7389-7411	GACATGTTGATAAAGAAATTTAA
7390-7412	ACATGTTGATAAAGAAATTTAAG
7391-7413	CATGTTGATAAAGAAATTTAAGT
7392-7414	ATGTTGATAAAGAAATTTAAGTC
7393-7415	TGTTGATAAAGAAATTTAAGTCA
7394-7416	GTTGATAAAGAAATTTAAGTCAT
7395-7417	TTGATAAAGAAATTTAAGTCATT
7396-7418	TGATAAAGAAATTTAAGTCATTT
7397-7419	GATAAAGAAATTTAAGTCATTTG
7398-7420	ATAAAGAAATTTAAGTCATTTGA
7399-7421	TAAAGAAATTTAAGTCATTTGAT
7400-7422	AAAGAAATTTAAGTCATTTGATT
7401-7423	AAGAAATTTAAGTCATTTGATTA
7402-7424	AGAAATTTAAGTCATTTGATTAC
7403-7425	GAAATTTAAGTCATTTGATTACC
7404-7426	AAATTTAAGTCATTTGATTACCA
7405-7427	AATTTAAGTCATTTGATTACCAC
7406-7428	ATTAAAGTCATTTGATTACCACC
7407-7429	TTAAAGTCATTTGATTACCACCA
7408-7430	TAAAGTCATTTGATTACCACCAG
7409-7431	AAAGTCATTTGATTACCACCAGT
7410-7432	AAGTCATTTGATTACCACCAGTT
7411-7433	AGTCATTTGATTACCACCAGTTT
7412-7434	GTCATTTGATTACCACCAGTTTG
7413-7435	TCATTTGATTACCACCAGTTTGT
7414-7436	CATTTGATTACCACCAGTTTGTA
7415-7437	ATTTGATTACCACCAGTTTGTAG
7416-7438	TTGATTACCACCAGTTTGTAGA
7417-7439	TTGATTACCACCAGTTTGTAGAT
7418-7440	TGATTACCACCAGTTTGTAGATG
7419-7441	GATTACCACCAGTTTGTAGATGA
7420-7442	ATTACCACCAGTTTGTAGATGAA
7421-7443	TTACCACCAGTTTGTAGATGAAA
7422-7444	TACCACCAGTTTGTAGATGAAAC
7423-7445	ACCACCAGTTTGTAGATGAAACC
7424-7446	CCACCAGTTTGTAGATGAAACCA
7425-7447	CACCAGTTTGTAGATGAAACCAA
7426-7448	ACCAGTTTGTAGATGAAACCAAT
7427-7449	CCAGTTTGTAGATGAAACCAATG
7428-7450	CAGTTTGTAGATGAAACCAATGA
7429-7451	AGTTTGTAGATGAAACCAATGAC
7430-7452	GTTTGTAGATGAAACCAATGACA
7431-7453	TTTGTAGATGAAACCAATGACAA
7432-7454	TTGTAGATGAAACCAATGACAAA
7433-7455	TGTAGATGAAACCAATGACAAAA
7434-7456	GTAGATGAAACCAATGACAAAAAT

Position	Sequence
7435-7457	TAGATGAAACCAATGACAAAATC
7436-7458	AGATGAAACCAATGACAAAATCC
7437-7459	GATGAAACCAATGACAAAATCCG
7438-7460	ATGAAACCAATGACAAAATCCGT
7439-7461	TGAAACCAATGACAAAATCCGTG
7440-7462	GAAACCAATGACAAAATCCGTGA
7441-7463	AAACCAATGACAAAATCCGTGAG
7442-7464	AACCAATGACAAAATCCGTGAGG
7443-7465	ACCAATGACAAAATCCGTGAGGT
7444-7466	CCAATGACAAAATCCGTGAGGTG
7445-7467	CAATGACAAAATCCGTGAGGTGA
7446-7468	AATGACAAAATCCGTGAGGTGAC
7447-7469	ATGACAAAATCCGTGAGGTGACT
7448-7470	TGACAAAATCCGTGAGGTGACTC
7449-7471	GACAAAATCCGTGAGGTGACTCA
7450-7472	ACAAAATCCGTGAGGTGACTCAG
7451-7473	CAAAAATCCGTGAGGTGACTCAGA
7452-7474	AAAATCCGTGAGGTGACTCAGAG
7453-7475	AAATCCGTGAGGTGACTCAGAGA
7454-7476	AATCCGTGAGGTGACTCAGAGAC
7455-7477	ATCCGTGAGGTGACTCAGAGACT
7456-7478	TCCGTGAGGTGACTCAGAGACTC
7457-7479	CCGTGAGGTGACTCAGAGACTCA
7458-7480	CGTGAGGTGACTCAGAGACTCAA
7459-7481	GTGAGGTGACTCAGAGACTCAAT
7460-7482	TGAGGTGACTCAGAGACTCAATG
7461-7483	GAGGTGACTCAGAGACTCAATGG
7462-7484	AGGTGACTCAGAGACTCAATGGT
7463-7485	GGTGACTCAGAGACTCAATGGTG
7464-7486	GTGACTCAGAGACTCAATGGTGA
7465-7487	TGACTCAGAGACTCAATGGTGAA
7466-7488	GACTCAGAGACTCAATGGTGAAA
7467-7489	ACTCAGAGACTCAATGGTGAAAT
7468-7490	CTCAGAGACTCAATGGTGAAATT
7469-7491	TCAGAGACTCAATGGTGAAATTC
7470-7492	CAGAGACTCAATGGTGAAATTCA
7471-7493	AGAGACTCAATGGTGAAATTCAG
7472-7494	GAGACTCAATGGTGAAATTCAGG
7473-7495	AGACTCAATGGTGAAATTCAGGC
7474-7496	GACTCAATGGTGAAATTCAGGCT
7475-7497	ACTCAATGGTGAAATTCAGGCTC
7476-7498	CTCAATGGTGAAATTCAGGCTCT
7477-7499	TCAATGGTGAAATTCAGGCTCTG
7478-7500	CAATGGTGAAATTCAGGCTCTGG
7479-7501	AATGGTGAAATTCAGGCTCTGGA
7480-7502	ATGGTGAAATTCAGGCTCTGGAA
7481-7503	TGGTGAAATTCAGGCTCTGGAAC
7482-7504	GGTGAAATTCAGGCTCTGGAACT
7483-7505	GTGAAATTCAGGCTCTGGAACTA
7484-7506	TGAAATTCAGGCTCTGGAACTAC
7485-7507	GAAATTCAGGCTCTGGAACTACC
7486-7508	AAATTCAGGCTCTGGAACTACCA
7487-7509	AATTCAGGCTCTGGAACTACCAC
7488-7510	ATTCAGGCTCTGGAACTACCACA
7489-7511	TTCAGGCTCTGGAACTACCACAA
7490-7512	TCAGGCTCTGGAACTACCACAAA
7491-7513	CAGGCTCTGGAACTACCACAAAA
7492-7514	AGGCTCTGGAACTACCACAAAAA
7493-7515	GGCTCTGGAACTACCACAAAAAG
7494-7516	GCTCTGGAACTACCACAAAAAGC
7495-7517	CTCTGGAACTACCACAAAAAGCT
7496-7518	TCTGGAACTACCACAAAAAGCTG
7497-7519	CTGGAACTACCACAAAAAGCTGA
7498-7520	TGGAACTACCACAAAAAGCTGAA
7499-7521	GGACTACCACAAAAAGCTGAAG
7500-7522	GACTACCACAAAAAGCTGAAGC

Position	Sequence
7501-7523	AACTACCACAAAAAGCTGAAGCA
7502-7524	ACTACCACAAAAAGCTGAAGCAT
7503-7525	CTACCACAAAAAGCTGAAGCATT
7504-7526	TACCACAAAAAGCTGAAGCATTAA
7505-7527	ACCACAAAAAGCTGAAGCATTAA
7506-7528	CCACAAAAAGCTGAAGCATTAAA
7507-7529	CACAAAAAGCTGAAGCATTAAAA
7508-7530	ACAAAAAGCTGAAGCATTAAAAC
7509-7531	CAAAAAGCTGAAGCATTAAAAC
7510-7532	AAAAAGCTGAAGCATTAAAAC
7511-7533	AAAAGCTGAAGCATTAAAAC
7512-7534	AAAGCTGAAGCATTAAAAC
7513-7535	AAGCTGAAGCATTAAAAC
7514-7536	AGCTGAAGCATTAAAAC
7515-7537	GCTGAAGCATTAAAAC
7516-7538	CTGAAGCATTAAAAC
7517-7539	TGAAGCATTAAAAC
7518-7540	GAAGCATTAAAAC
7519-7541	AAGCATTAAAAC
7520-7542	AGCATTAAAAC
7521-7543	GCATTAAAAC
7522-7544	CATTAAAAC
7523-7545	ATTAATACTGTTTTAGAGGAAA
7524-7546	TTAATACTGTTTTAGAGGAAAC
7525-7547	TAAATACTGTTTTAGAGGAAACC
7526-7548	AAAATACTGTTTTAGAGGAAACCA
7527-7549	AAATACTGTTTTAGAGGAAACCAA
7528-7550	AACTGTTTTAGAGGAAACCAAG
7529-7551	ACTGTTTTAGAGGAAACCAAGG
7530-7552	CTGTTTTAGAGGAAACCAAGGC
7531-7553	TGTTTTAGAGGAAACCAAGGCC
7532-7554	GTTTTAGAGGAAACCAAGGCCA
7533-7555	TTTTAGAGGAAACCAAGGCCAC
7534-7556	TTTTAGAGGAAACCAAGGCCACA
7535-7557	TTTAGAGGAAACCAAGGCCACAG
7536-7558	TTAGAGGAAACCAAGGCCACAGT
7537-7559	TAGAGGAAACCAAGGCCACAGTT
7538-7560	AGAGGAAACCAAGGCCACAGTTG
7539-7561	GAGGAAACCAAGGCCACAGTTGC
7540-7562	AGGAAACCAAGGCCACAGTTGCA
7541-7563	GAAACCAAGGCCACAGTTGCAG
7542-7564	GAAACCAAGGCCACAGTTGCAGT
7543-7565	AAACCAAGGCCACAGTTGCAGTG
7544-7566	AACCAAGGCCACAGTTGCAGTGT
7545-7567	ACCAAGGCCACAGTTGCAGTGTA
7546-7568	CCAAGGCCACAGTTGCAGTGTAT
7547-7569	CAAGGCCACAGTTGCAGTGTATC
7548-7570	AAGGCCACAGTTGCAGTGTATCT
7549-7571	AGGCCACAGTTGCAGTGTATCTG
7550-7572	GGCCACAGTTGCAGTGTATCTGG
7551-7573	GCCACAGTTGCAGTGTATCTGGA
7552-7574	CCACAGTTGCAGTGTATCTGGAA
7553-7575	CACAGTTGCAGTGTATCTGGAAA
7554-7576	ACAGTTGCAGTGTATCTGGAAAG
7555-7577	CAGTTGCAGTGTATCTGGAAAGC
7556-7578	AGTTGCAGTGTATCTGGAAAGCC
7557-7579	GTTGCAGTGTATCTGGAAAGCCT
7558-7580	TTGCAGTGTATCTGGAAAGCCTA
7559-7581	TGCAGTGTATCTGGAAAGCCTAC
7560-7582	GCAGTGTATCTGGAAAGCCTACA
7561-7583	CAGTGTATCTGGAAAGCCTACAG
7562-7584	AGTGTATCTGGAAAGCCTACAGG
7563-7585	GTGTATCTGGAAAGCCTACAGGA
7564-7586	TGTATCTGGAAAGCCTACAGGAC
7565-7587	GTATCTGGAAAGCCTACAGGACA
7566-7588	TATCTGGAAAGCCTACAGGACAC

Position	Sequence
7567-7589	ATCTGGAAAGCCTACAGGACACC
7568-7590	TCTGGAAAGCCTACAGGACACCA
7569-7591	CTGGAAAGCCTACAGGACACCAA
7570-7592	TGGAAAGCCTACAGGACACCAAA
7571-7593	GGAAAGCCTACAGGACACCAAAA
7572-7594	GAAAGCCTACAGGACACCAAAAT
7573-7595	AAAGCCTACAGGACACCAAAATA
7574-7596	AAGCCTACAGGACACCAAAATAA
7575-7597	AGCCTACAGGACACCAAAATAAC
7576-7598	GCCTACAGGACACCAAAATAACC
7577-7599	CCTACAGGACACCAAAATAACCT
7578-7600	CTACAGGACACCAAAATAACCTT
7579-7601	TACAGGACACCAAAATAACCTTA
7580-7602	ACAGGACACCAAAATAACCTTAA
7581-7603	CAGGACACCAAAATAACCTTAAT
7582-7604	AGGACACCAAAATAACCTTAATC
7583-7605	GGACACCAAAATAACCTTAATCA
7584-7606	GACACCAAAATAACCTTAATCAT
7585-7607	ACACCAAAATAACCTTAATCATC
7586-7608	CACCAAAATAACCTTAATCATCA
7587-7609	ACCAAAATAACCTTAATCATCAA
7588-7610	CCAAATAACCTTAATCATCAAT
7589-7611	CAAAATAACCTTAATCATCAATT
7590-7612	AAAATAACCTTAATCATCAATTG
7591-7613	AAATAACCTTAATCATCAATTGG
7592-7614	AATAACCTTAATCATCAATTGGT
7593-7615	ATAACCTTAATCATCAATTGGTT
7594-7616	TAACCTTAATCATCAATTGGTTA
7595-7617	AACCTTAATCATCAATTGGTTAC
7596-7618	ACCTTAATCATCAATTGGTTACA
7597-7619	CCTTAATCATCAATTGGTTACAG
7598-7620	CTTAATCATCAATTGGTTACAGG
7599-7621	TTAATCATCAATTGGTTACAGGA
7600-7622	TAATCATCAATTGGTTACAGGAG
7601-7623	AATCATCAATTGGTTACAGGAGG
7602-7624	ATCATCAATTGGTTACAGGAGGC
7603-7625	TCATCAATTGGTTACAGGAGGCT
7604-7626	CATCAATTGGTTACAGGAGGCTT
7605-7627	ATCAATTGGTTACAGGAGGCTTT
7606-7628	TCAATTGGTTACAGGAGGCTTTA
7607-7629	CAATTGGTTACAGGAGGCTTTAA
7608-7630	AATTGGTTACAGGAGGCTTTAAG
7609-7631	ATTGGTTACAGGAGGCTTTAAGT
7610-7632	TTGGTTACAGGAGGCTTTAAGTT
7611-7633	TGGTTACAGGAGGCTTTAAGTTC
7612-7634	GTTACAGGAGGCTTTAAGTTCA
7613-7635	GTTACAGGAGGCTTTAAGTTCAG
7614-7636	TTACAGGAGGCTTTAAGTTCAGC
7615-7637	TACAGGAGGCTTTAAGTTCAGCA
7616-7638	ACAGGAGGCTTTAAGTTCAGCAT
7617-7639	CAGGAGGCTTTAAGTTCAGCATC
7618-7640	AGGAGGCTTTAAGTTCAGCATCT
7619-7641	GGAGGCTTTAAGTTCAGCATCTT
7620-7642	GAGGCTTTAAGTTCAGCATCTTT
7621-7643	AGGCTTTAAGTTCAGCATCTTTG
7622-7644	GGCTTTAAGTTCAGCATCTTTGG
7623-7645	GCTTTAAGTTCAGCATCTTTGGC
7624-7646	CTTTAAGTTCAGCATCTTTGGCT
7625-7647	TTAAGTTCAGCATCTTTGGCTC
7626-7648	TTAAGTTCAGCATCTTTGGCTCA
7627-7649	TAAGTTCAGCATCTTTGGCTCAC
7628-7650	AAGTTCAGCATCTTTGGCTCACA
7629-7651	AGTTCAGCATCTTTGGCTCACAT
7630-7652	GTCAGCATCTTTGGCTCACATG
7631-7653	TCAGCATCTTTGGCTCACATGA
7632-7654	TCAGCATCTTTGGCTCACATGAA

Position	Sequence
7633-7655	CAGCATCTTTGGCTCACATGAAG
7634-7656	AGCATCTTTGGCTCACATGAAGG
7635-7657	GCATCTTTGGCTCACATGAAGGC
7636-7658	CATCTTTGGCTCACATGAAGGCC
7637-7659	ATCTTTGGCTCACATGAAGGCCA
7638-7660	TCTTTGGCTCACATGAAGGCCAA
7639-7661	CTTTGGCTCACATGAAGGCCAAA
7640-7662	TTTGGCTCACATGAAGGCCAAAT
7641-7663	TTGGCTCACATGAAGGCCAAATT
7642-7664	TGGCTCACATGAAGGCCAAATTC
7643-7665	GGCTCACATGAAGGCCAAATTC
7644-7666	GCTCACATGAAGGCCAAATTCG
7645-7667	CTCACATGAAGGCCAAATTCGGA
7646-7668	TCACATGAAGGCCAAATTCGAG
7647-7669	CACATGAAGGCCAAATTCGAGA
7648-7670	ACATGAAGGCCAAATTCGAGAG
7649-7671	CATGAAGGCCAAATTCGAGAGA
7650-7672	ATGAAGGCCAAATTCGAGAGAC
7651-7673	TGAAGGCCAAATTCGAGAGACT
7652-7674	GAAGGCCAAATTCGAGAGACTC
7653-7675	AAGGCCAAATTCGAGAGACTCT
7654-7676	AGGCCAAATTCGAGAGACTCTA
7655-7677	GGCCAAATTCGAGAGACTCTAG
7656-7678	GCCAAATTCGAGAGACTCTAGA
7657-7679	CCAAATTCGAGAGACTCTAGAA
7658-7680	CAAATTCGAGAGACTCTAGAAG
7659-7681	AAATTCGAGAGACTCTAGAAGA
7660-7682	AATTCGAGAGACTCTAGAAGAT
7661-7683	ATTCCGAGAGACTCTAGAAGATA
7662-7684	TTCCGAGAGACTCTAGAAGATAC
7663-7685	TCCGAGAGACTCTAGAAGATACA
7664-7686	CCGAGAGACTCTAGAAGATACAC
7665-7687	CGAGAGACTCTAGAAGATACACG
7666-7688	GAGAGACTCTAGAAGATACACGA
7667-7689	AGAGACTCTAGAAGATACACGAG
7668-7690	GAGACTCTAGAAGATACACGAGA
7669-7691	AGACTCTAGAAGATACACGAGAC
7670-7692	GACTCTAGAAGATACACGAGACC
7671-7693	ACTCTAGAAGATACACGAGACCG
7672-7694	CTCTAGAAGATACACGAGACCGA
7673-7695	TCTAGAAGATACACGAGACCGAA
7674-7696	CTAGAAGATACACGAGACCGAAT
7675-7697	TAGAAGATACACGAGACCGAATG
7676-7698	AGAAGATACACGAGACCGAATGT
7677-7699	GAAGATACACGAGACCGAATGTA
7678-7700	AAGATACACGAGACCGAATGTAT
7679-7701	AGATACACGAGACCGAATGTATC
7680-7702	GATACACGAGACCGAATGTATCA
7681-7703	ATACACGAGACCGAATGTATCAA
7682-7704	TACACGAGACCGAATGTATCAAA
7683-7705	ACACGAGACCGAATGTATCAAAT
7684-7706	CACGAGACCGAATGTATCAAATG
7685-7707	ACGAGACCGAATGTATCAAATGG
7686-7708	CGAGACCGAATGTATCAAATGGA
7687-7709	GAGACCGAATGTATCAAATGGAC
7688-7710	AGACCGAATGTATCAAATGGACA
7689-7711	GACCGAATGTATCAAATGGACAT
7690-7712	ACCGAATGTATCAAATGGACATT
7691-7713	CCGAATGTATCAAATGGACATTC
7692-7714	CGAATGTATCAAATGGACATTCA
7693-7715	GAATGTATCAAATGGACATTCCAG
7694-7716	AATGTATCAAATGGACATTCCAGC
7695-7717	ATGTATCAAATGGACATTCCAGCA
7696-7718	TGTATCAAATGGACATTCCAGCAG
7697-7719	GTATCAAATGGACATTCCAGCAGG
7698-7720	TATCAAATGGACATTCCAGCAGGA

Position	Sequence
7699-7721	ATCAAATGGACATT CAGCAGGAA
7700-7722	TCAAATGGACATT CAGCAGGAAC
7701-7723	CAAATGGACATT CAGCAGGAACT
7702-7724	AAATGGACATT CAGCAGGAACTT
7703-7725	AATGGACATT CAGCAGGAAC TTC
7704-7726	ATGGACATT CAGCAGGAAC TTC A
7705-7727	TGGACATT CAGCAGGAACT TCA A
7706-7728	GGACATT CAGCAGGAACT TCA A C
7707-7729	GACATT CAGCAGGAACT TCA A C G
7708-7730	ACATT CAGCAGGAACT TCA A C G A
7709-7731	CATT CAGCAGGAACT TCA A C G A T
7710-7732	ATTCAGCAGGAACT TCA A C G A T A
7711-7733	TTCAGCAGGAACT TCA A C G A T A C
7712-7734	TCAGCAGGAACT TCA A C G A T A C C
7713-7735	CAGCAGGAACT TCA A C G A T A C C T
7714-7736	AGCAGGAACT TCA A C G A T A C C T G
7715-7737	GCAGGAACT TCA A C G A T A C C T G T
7716-7738	CAGGAACT TCA A C G A T A C C T G T C
7717-7739	AGGAACT TCA A C G A T A C C T G T C T
7718-7740	GGAAC TCA A C G A T A C C T G T C T C
7719-7741	GAAC TCA A C G A T A C C T G T C T C T
7720-7742	AACT TCA A C G A T A C C T G T C T C T G
7721-7743	ACT TCA A C G A T A C C T G T C T C T G G
7722-7744	CT TCA A C G A T A C C T G T C T C T G G T
7723-7745	T TCA A C G A T A C C T G T C T C T G G T A
7724-7746	TCA A C G A T A C C T G T C T C T G G T A G
7725-7747	CA A C G A T A C C T G T C T C T G G T A G G
7726-7748	A A C G A T A C C T G T C T C T G G T A G G C
7727-7749	A C G A T A C C T G T C T C T G G T A G G C C
7728-7750	C G A T A C C T G T C T C T G G T A G G C C A
7729-7751	G A T A C C T G T C T C T G G T A G G C C A G
7730-7752	A T A C C T G T C T C T G G T A G G C C A G G
7731-7753	T A C C T G T C T C T G G T A G G C C A G G T
7732-7754	A C C T G T C T C T G G T A G G C C A G G T T
7733-7755	C C T G T C T C T G G T A G G C C A G G T T T
7734-7756	C T G T C T C T G G T A G G C C A G G T T T A
7735-7757	T G T C T C T G G T A G G C C A G G T T T A T
7736-7758	G T C T C T G G T A G G C C A G G T T T A T A
7737-7759	T C T C T G G T A G G C C A G G T T T A T A G
7738-7760	C T C T G G T A G G C C A G G T T T A T A G C
7739-7761	T C T G G T A G G C C A G G T T T A T A G C A
7740-7762	C T G G T A G G C C A G G T T T A T A G C A C
7741-7763	T G G T A G G C C A G G T T T A T A G C A C A
7742-7764	G G T A G G C C A G G T T T A T A G C A C A C
7743-7765	G T A G G C C A G G T T T A T A G C A C A C T
7744-7766	T A G G C C A G G T T T A T A G C A C A C T T
7745-7767	A G G C C A G G T T T A T A G C A C A C T T G
7746-7768	G G C C A G G T T T A T A G C A C A C T T G T
7747-7769	G C C A G G T T T A T A G C A C A C T T G T C
7748-7770	C C A G G T T T A T A G C A C A C T T G T C A
7749-7771	C A G G T T T A T A G C A C A C T T G T C A C
7750-7772	A G G T T T A T A G C A C A C T T G T C A C C
7751-7773	G G T T T A T A G C A C A C T T G T C A C C T
7752-7774	G T T T A T A G C A C A C T T G T C A C C T A
7753-7775	T T T A T A G C A C A C T T G T C A C C T A C
7754-7776	T T A T A G C A C A C T T G T C A C C T A C A
7755-7777	T A T A G C A C A C T T G T C A C C T A C A T
7756-7778	A T A G C A C A C T T G T C A C C T A C A T T
7757-7779	T A G C A C A C T T G T C A C C T A C A T T T
7758-7780	A G C A C A C T T G T C A C C T A C A T T T C
7759-7781	G C A C A C T T G T C A C C T A C A T T T C T
7760-7782	C A C A C T T G T C A C C T A C A T T T C T G
7761-7783	A C A C T T G T C A C C T A C A T T T C T G A
7762-7784	C A C T T G T C A C C T A C A T T T C T G A T
7763-7785	A C T T G T C A C C T A C A T T T C T G A T T
7764-7786	C T T G T C A C C T A C A T T T C T G A T T G

Position	Sequence
7765-7787	TGTCACCTACATTCTGATTGG
7766-7788	TGTCACCTACATTCTGATTGGT
7767-7789	GTCACCTACATTCTGATTGGTG
7768-7790	TCACCTACATTTCTGATTGGTGG
7769-7791	CACCTACATTTCTGATTGGTGGGA
7770-7792	ACCTACATTTCTGATTGGTGGAC
7771-7793	CCTACATTTCTGATTGGTGGACT
7772-7794	CTACATTTCTGATTGGTGGACTC
7773-7795	TACATTTCTGATTGGTGGACTCT
7774-7796	ACATTTCTGATTGGTGGACTCTT
7775-7797	CATTTCTGATTGGTGGACTCTTG
7776-7798	ATTTCTGATTGGTGGACTCTTGC
7777-7799	TTTCTGATTGGTGGACTCTTGCT
7778-7800	TTCTGATTGGTGGACTCTTGCTG
7779-7801	TCTGATTGGTGGACTCTTGCTGC
7780-7802	CTGATTGGTGGACTCTTGCTGCT
7781-7803	TGATTGGTGGACTCTTGCTGCTA
7782-7804	GATTGGTGGACTCTTGCTGCTAA
7783-7805	ATGGTGGACTCTTGCTGCTAAG
7784-7806	TGGTGGACTCTTGCTGCTAAGA
7785-7807	TGGTGGACTCTTGCTGCTAAGAA
7786-7808	GGTGGACTCTTGCTGCTAAGAAC
7787-7809	GPGACTCTTGCTGCTAAGAACC
7788-7810	TGGACTCTTGCTGCTAAGAACCCT
7789-7811	GGACTCTTGCTGCTAAGAACCCTT
7790-7812	GACTCTTGCTGCTAAGAACCCTTA
7791-7813	ACTCTTGCTGCTAAGAACCCTTAC
7792-7814	CTCTTGCTGCTAAGAACCCTTACT
7793-7815	TCTTGCTGCTAAGAACCCTTACTG
7794-7816	CTTGCTGCTAAGAACCCTTACTGA
7795-7817	TTGCTGCTAAGAACCCTTACTGAC
7796-7818	TGCTGCTAAGAACCCTTACTGACT
7797-7819	GCTGCTAAGAACCCTTACTGACTT
7798-7820	CTGCTAAGAACCCTTACTGACTTT
7799-7821	TGCTAAGAACCCTTACTGACTTTG
7800-7822	GCTAAGAACCCTTACTGACTTTGC
7801-7823	CTAAGAACCCTTACTGACTTTGCA
7802-7824	TAAGAACCCTTACTGACTTTGCAG
7803-7825	AAGAACCCTTACTGACTTTGCAGA
7804-7826	AGAACCCTTACTGACTTTGCAGAG
7805-7827	GAACCCTTACTGACTTTGCAGAGC
7806-7828	AACCCTTACTGACTTTGCAGAGCA
7807-7829	ACCTTACTGACTTTGCAGAGCAA
7808-7830	CCTTACTGACTTTGCAGAGCAAT
7809-7831	CTTACTGACTTTGCAGAGCAATA
7810-7832	TTACTGACTTTGCAGAGCAATAT
7811-7833	TACTGACTTTGCAGAGCAATATT
7812-7834	ACTGACTTTGCAGAGCAATATTC
7813-7835	CTGACTTTGCAGAGCAATATTCT
7814-7836	TGACTTTGCAGAGCAATATTCTA
7815-7837	GACTTTGCAGAGCAATATTCTAT
7816-7838	ACTTTGCAGAGCAATATTCTATC
7817-7839	CTTTGCAGAGCAATATTCTATCC
7818-7840	TTTGCAGAGCAATATTCTATCCA
7819-7841	TTGCAGAGCAATATTCTATCCAA
7820-7842	TGCAGAGCAATATTCTATCCAAG
7821-7843	GCAGAGCAATATTCTATCCAAGA
7822-7844	CAGAGCAATATTCTATCCAAGAT
7823-7845	AGAGCAATATTCTATCCAAGATT
7824-7846	GAGCAATATTCTATCCAAGATTG
7825-7847	AGCAATATTCTATCCAAGATTGG
7826-7848	GCAATATTCTATCCAAGATTGGG
7827-7849	CAATATTCTATCCAAGATTGGGC
7828-7850	AATATTCTATCCAAGATTGGGCT
7829-7851	ATATTCTATCCAAGATTGGGCTA
7830-7852	TATTCTATCCAAGATTGGGCTAA

Position	Sequence
7831-7853	ATTCTATCCAAGATTGGGCTAAA
7832-7854	TTCTATCCAAGATTGGGCTAAAC
7833-7855	TCTATCCAAGATTGGGCTAAACG
7834-7856	CTATCCAAGATTGGGCTAAACGT
7835-7857	TATCCAAGATTGGGCTAAACGTA
7836-7858	ATCCAAGATTGGGCTAAACGTAT
7837-7859	TCCAAGATTGGGCTAAACGTATG
7838-7860	CCAAGATTGGGCTAAACGTATGA
7839-7861	CAAGATTGGGCTAAACGTATGAA
7840-7862	AAGATTGGGCTAAACGTATGAAA
7841-7863	AGATTGGGCTAAACGTATGAAAG
7842-7864	GATTGGGCTAAACGTATGAAAGC
7843-7865	ATTGGGCTAAACGTATGAAAGCA
7844-7866	TTGGGCTAAACGTATGAAAGCAT
7845-7867	TGGGCTAAACGTATGAAAGCATT
7846-7868	GGGCTAAACGTATGAAAGCATTG
7847-7869	GGCTAAACGTATGAAAGCATTGG
7848-7870	GCTAAACGTATGAAAGCATTGGT
7849-7871	CTAAACGTATGAAAGCATTGGTA
7850-7872	TAAACGTATGAAAGCATTGGTAG
7851-7873	AAACGTATGAAAGCATTGGTAGA
7852-7874	AACGTATGAAAGCATTGGTAGAG
7853-7875	ACGTATGAAAGCATTGGTAGAGC
7854-7876	CGTATGAAAGCATTGGTAGAGCA
7855-7877	GTATGAAAGCATTGGTAGAGCAA
7856-7878	TATGAAAGCATTGGTAGAGCAAG
7857-7879	ATGAAAGCATTGGTAGAGCAAGG
7858-7880	TGAAAGCATTGGTAGAGCAAGGG
7859-7881	GAAAGCATTGGTAGAGCAAGGGT
7860-7882	AAAGCATTGGTAGAGCAAGGGTT
7861-7883	AAGCATTGGTAGAGCAAGGGTTC
7862-7884	AGCATTGGTAGAGCAAGGGTTCA
7863-7885	GCATTGGTAGAGCAAGGGTTCAC
7864-7886	CATTGGTAGAGCAAGGGTTCACT
7865-7887	ATTGGTAGAGCAAGGGTTCACTG
7866-7888	TTGGTAGAGCAAGGGTTCACTGT
7867-7889	TGGTAGAGCAAGGGTTCACTGTT
7868-7890	GGTAGAGCAAGGGTTCACTGTTC
7869-7891	GTAGAGCAAGGGTTCACTGTTC
7870-7892	TAGAGCAAGGGTTCACTGTTCCT
7871-7893	AGAGCAAGGGTTCACTGTTCCTG
7872-7894	GAGCAAGGGTTCACTGTTCCTGA
7873-7895	AGCAAGGGTTCACTGTTCCTGAA
7874-7896	GCAAGGGTTCACTGTTCCTGAAA
7875-7897	CAAGGGTTCACTGTTCCTGAAAT
7876-7898	AAGGGTTCACTGTTCCTGAAATC
7877-7899	AGGGTTCACTGTTCCTGAAATCA
7878-7900	GGTTCACTGTTCCTGAAATCAA
7879-7901	GGTTCACTGTTCCTGAAATCAAG
7880-7902	GTTCACTGTTCCTGAAATCAAGA
7881-7903	TTCCTGTTCCTGAAATCAAGAC
7882-7904	TCCTGTTCCTGAAATCAAGACC
7883-7905	CACTGTTCCTGAAATCAAGACCA
7884-7906	ACTGTTCCTGAAATCAAGACCAT
7885-7907	CTGTTCCTGAAATCAAGACCATC
7886-7908	TGTTCCTGAAATCAAGACCATCC
7887-7909	GTTTCCTGAAATCAAGACCATCCT
7888-7910	TTTCCTGAAATCAAGACCATCCTT
7889-7911	TCCTGAAATCAAGACCATCCTTG
7890-7912	CCTGAAATCAAGACCATCCTTGG
7891-7913	CTGAAATCAAGACCATCCTTGGG
7892-7914	TGAAATCAAGACCATCCTTGGGA
7893-7915	GAAATCAAGACCATCCTTGGGAC
7894-7916	AAATCAAGACCATCCTTGGGACC
7895-7917	AATCAAGACCATCCTTGGGACCA
7896-7918	ATCAAGACCATCCTTGGGACCAT

Position	Sequence
7897-7919	TCAAGACCATCCTTGGGACCATG
7898-7920	CAAGACCATCCTTGGGACCATGC
7899-7921	AAGACCATCCTTGGGACCATGCC
7900-7922	AGACCATCCTTGGGACCATGCCT
7901-7923	GACCATCCTTGGGACCATGCCTG
7902-7924	ACCATCCTTGGGACCATGCCTGC
7903-7925	CCATCCTTGGGACCATGCCTGCC
7904-7926	CATCCTTGGGACCATGCCTGCCT
7905-7927	ATCCTTGGGACCATGCCTGCCTT
7906-7928	TCCTTGGGACCATGCCTGCCTTT
7907-7929	CCTTGGGACCATGCCTGCCTTTG
7908-7930	CTTGGGACCATGCCTGCCTTTGA
7909-7931	TTGGGACCATGCCTGCCTTTGAA
7910-7932	TGGGACCATGCCTGCCTTTGAAG
7911-7933	GGGACCATGCCTGCCTTTGAAGT
7912-7934	GGACCATGCCTGCCTTTGAAGTC
7913-7935	GACCATGCCTGCCTTTGAAGTCA
7914-7936	ACCATGCCTGCCTTTGAAGTCAG
7915-7937	CCATGCCTGCCTTTGAAGTCAGT
7916-7938	CATGCCTGCCTTTGAAGTCAGTC
7917-7939	ATGCCTGCCTTTGAAGTCAGTCT
7918-7940	TGCCTGCCTTTGAAGTCAGTCTT
7919-7941	GCCTGCCTTTGAAGTCAGTCTTC
7920-7942	CCTGCCTTTGAAGTCAGTCTTCA
7921-7943	CTGCCTTTGAAGTCAGTCTTCAG
7922-7944	TGCCTTTGAAGTCAGTCTTCAGG
7923-7945	GCCTTTGAAGTCAGTCTTCAGGC
7924-7946	CCTTTGAAGTCAGTCTTCAGGCT
7925-7947	CTTTGAAGTCAGTCTTCAGGCTC
7926-7948	TTTGAAGTCAGTCTTCAGGCTCT
7927-7949	TTGAAGTCAGTCTTCAGGCTCTT
7928-7950	TGAAGTCAGTCTTCAGGCTCTTC
7929-7951	GAAGTCAGTCTTCAGGCTCTTCA
7930-7952	AAGTCAGTCTTCAGGCTCTTCAG
7931-7953	AGTCAGTCTTCAGGCTCTTCAGA
7932-7954	GTCAGTCTTCAGGCTCTTCAGAA
7933-7955	TCAGTCTTCAGGCTCTTCAGAAA
7934-7956	CAGTCTTCAGGCTCTTCAGAAAAG
7935-7957	AGTCTTCAGGCTCTTCAGAAAAGC
7936-7958	GTCTTCAGGCTCTTCAGAAAAGCT
7937-7959	TCTTCAGGCTCTTCAGAAAAGCTA
7938-7960	CTTCAGGCTCTTCAGAAAAGCTAC
7939-7961	TTCAGGCTCTTCAGAAAAGCTACC
7940-7962	TCAGGCTCTTCAGAAAAGCTACCT
7941-7963	CAGGCTCTTCAGAAAAGCTACCTT
7942-7964	AGGCTCTTCAGAAAAGCTACCTTC
7943-7965	GGCTCTTCAGAAAAGCTACCTTCC
7944-7966	GCTCTTCAGAAAAGCTACCTTCCA
7945-7967	CTCTTCAGAAAAGCTACCTTCCAG
7946-7968	TCTTCAGAAAAGCTACCTTCCAGA
7947-7969	CTTCAGAAAAGCTACCTTCCAGAC
7948-7970	TTCAGAAAAGCTACCTTCCAGACA
7949-7971	TCAGAAAAGCTACCTTCCAGACAC
7950-7972	CAGAAAAGCTACCTTCCAGACACC
7951-7973	AGAAAAGCTACCTTCCAGACACCT
7952-7974	GAAAAGCTACCTTCCAGACACCTG
7953-7975	AAAGCTACCTTCCAGACACCTGA
7954-7976	AAGCTACCTTCCAGACACCTGAT
7955-7977	AGCTACCTTCCAGACACCTGATT
7956-7978	GCTACCTTCCAGACACCTGATTT
7957-7979	CTACCTTCCAGACACCTGATTTT
7958-7980	TACCTTCCAGACACCTGATTTTA
7959-7981	ACCTTCCAGACACCTGATTTTAT
7960-7982	CCTTCCAGACACCTGATTTTATA
7961-7983	CTTCCAGACACCTGATTTTATAG
7962-7984	TTCCAGACACCTGATTTTATAGT

Position	Sequence
7963-7985	TCCAGACACCTGATTTTATAGTC
7964-7986	CCAGACACCTGATTTTATAGTCC
7965-7987	CAGACACCTGATTTTATAGTCCC
7966-7988	AGACACCTGATTTTATAGTCCCC
7967-7989	GACACCTGATTTTATAGTCCCCC
7968-7990	ACACCTGATTTTATAGTCCCCCT
7969-7991	CACCTGATTTTATAGTCCCCCTA
7970-7992	ACCTGATTTTATAGTCCCCCTAA
7971-7993	CCTGATTTTATAGTCCCCCTAAC
7972-7994	CTGATTTTATAGTCCCCCTAACA
7973-7995	TGATTTTATAGTCCCCCTAACAG
7974-7996	GATTTTATAGTCCCCCTAACAGA
7975-7997	ATTTTATAGTCCCCCTAACAGAT
7976-7998	TTTATAGTCCCCCTAACAGATT
7977-7999	TTTATAGTCCCCCTAACAGATTT
7978-8000	TTATAGTCCCCCTAACAGATTG
7979-8001	TATAGTCCCCCTAACAGATTGA
7980-8002	ATAGTCCCCCTAACAGATTGAG
7981-8003	TAGTCCCCCTAACAGATTGAGG
7982-8004	AGTCCCCCTAACAGATTGAGGA
7983-8005	GTCCCCCTAACAGATTGAGGAT
7984-8006	TCCCCCTAACAGATTGAGGATT
7985-8007	CCCCCTAACAGATTGAGGATTC
7986-8008	CCCCTAACAGATTGAGGATTCC
7987-8009	CCCTAACAGATTGAGGATTCCA
7988-8010	CCTAACAGATTGAGGATTCCAT
7989-8011	CTAACAGATTGAGGATTCCATC
7990-8012	TAACAGATTGAGGATTCCATCA
7991-8013	AACAGATTGAGGATTCCATCAG
7992-8014	ACAGATTGAGGATTCCATCAGT
7993-8015	CAGATTGAGGATTCCATCAGTT
7994-8016	AGATTGAGGATTCCATCAGTTC
7995-8017	GATTGAGGATTCCATCAGTTCA
7996-8018	ATTTGAGGATTCCATCAGTTCAG
7997-8019	TTTGAGGATTCCATCAGTTCAGA
7998-8020	TTGAGGATTCCATCAGTTCAGAT
7999-8021	TGAGGATTCCATCAGTTCAGATA
8000-8022	GAGGATTCCATCAGTTCAGATAA
8001-8023	AGGATTCCATCAGTTCAGATAAA
8002-8024	GGATTCCATCAGTTCAGATAAAC
8003-8025	GATTCCATCAGTTCAGATAAACT
8004-8026	ATTCATCAGTTCAGATAAACTT
8005-8027	TTCCATCAGTTCAGATAAACTTC
8006-8028	TCCATCAGTTCAGATAAACTTCA
8007-8029	CCATCAGTTCAGATAAACTTCAA
8008-8030	CATCAGTTCAGATAAACTTCAAA
8009-8031	ATCAGTTCAGATAAACTTCAAAG
8010-8032	TCAGTTCAGATAAACTTCAAAGA
8011-8033	CAGTTCAGATAAACTTCAAAGAC
8012-8034	AGTTCAGATAAACTTCAAAGACT
8013-8035	GTTTCAGATAAACTTCAAAGACTT
8014-8036	TTCAGATAAACTTCAAAGACTTA
8015-8037	TCAGATAAACTTCAAAGACTTAA
8016-8038	CAGATAAACTTCAAAGACTTAAA
8017-8039	AGATAAACTTCAAAGACTTAAAA
8018-8040	GATAAACTTCAAAGACTTAAAAA
8019-8041	ATAAACTTCAAAGACTTAAAAAA
8020-8042	TAAACTTCAAAGACTTAAAAAAT
8021-8043	AAACTTCAAAGACTTAAAAAATA
8022-8044	AACTTCAAAGACTTAAAAATAT
8023-8045	ACTTCAAAGACTTAAAAATATA
8024-8046	CTTCAAAGACTTAAAAATATAA
8025-8047	TTCAAAGACTTAAAAATATAAA
8026-8048	TCAAAGACTTAAAAATATAAAA
8027-8049	CAAAGACTTAAAAATATAAAAA
8028-8050	AAAGACTTAAAAATATAAAAAAT

Position	Sequence
8029-8051	AAGACTTAAAAAATATAAAAAATC
8030-8052	AGACTTAAAAAATATAAAAAATCC
8031-8053	GACTTAAAAAATATAAAAAATCCC
8032-8054	ACTTAAAAAATATAAAAAATCCCA
8033-8055	CTTAAAAAATATAAAAAATCCCAT
8034-8056	TTAAAAAATATAAAAAATCCCATC
8035-8057	TAAAAAATATAAAAAATCCCATCC
8036-8058	AAAAAATATAAAAAATCCCATCCA
8037-8059	AAAAATATAAAAAATCCCATCCAG
8038-8060	AAAATATAAAAAATCCCATCCAGG
8039-8061	AAATATAAAAAATCCCATCCAGGT
8040-8062	AATATAAAAAATCCCATCCAGGTT
8041-8063	ATATAAAAAATCCCATCCAGGTTT
8042-8064	TATAAAAAATCCCATCCAGGTTTT
8043-8065	ATAAAAAATCCCATCCAGGTTTTC
8044-8066	TAAAAATCCCATCCAGGTTTTC
8045-8067	AAAAATCCCATCCAGGTTTTC
8046-8068	AAAATCCCATCCAGGTTTTC
8047-8069	AAATCCCATCCAGGTTTTC
8048-8070	AATCCCATCCAGGTTTTC
8049-8071	ATCCCATCCAGGTTTTC
8050-8072	TCCCATCCAGGTTTTC
8051-8073	CCCATCCAGGTTTTC
8052-8074	CCATCCAGGTTTTC
8053-8075	CATCCAGGTTTTC
8054-8076	ATCCAGGTTTTC
8055-8077	TCCAGGTTTTC
8056-8078	CCAGGTTTTC
8057-8079	CAGGTTTTC
8058-8080	AGGTTTTC
8059-8081	GTTTTC
8060-8082	GTTTTC
8061-8083	TTTTCC
8062-8084	TTCC
8063-8085	TCC
8064-8086	TCC
8065-8087	CC
8066-8088	CAC
8067-8089	AC
8068-8090	CAC
8069-8091	ACC
8070-8092	CC
8071-8093	CAG
8072-8094	AGA
8073-8095	GA
8074-8096	AAT
8075-8097	ATT
8076-8098	TT
8077-8099	T
8078-8100	T
8079-8101	ACC
8080-8102	CC
8081-8103	CAT
8082-8104	AT
8083-8105	TC
8084-8106	C
8085-8107	CT
8086-8108	TT
8087-8109	TA
8088-8110	AA
8089-8111	AC
8090-8112	CA
8091-8113	AC
8092-8114	CT
8093-8115	CT
8094-8116	TT

Position	Sequence
8095-8117	TCCACATTCCTTCCTTACAATT
8096-8118	CCACATTCCTTCCTTACAATTG
8097-8119	CACATTCCTTCCTTACAATTGA
8098-8120	ACATTCCTTCCTTACAATTGAC
8099-8121	CATTCCTTCCTTACAATTGACT
8100-8122	ATTCCTTCCTTACAATTGACTT
8101-8123	TTCTTCCTTACAATTGACTTT
8102-8124	TCCTTCCTTACAATTGACTTTG
8103-8125	CCTTCCTTACAATTGACTTTGT
8104-8126	CTTCCTTACAATTGACTTTGTC
8105-8127	TTCTTACAATTGACTTTGTGCG
8106-8128	TCCTTACAATTGACTTTGTGCGA
8107-8129	CCTTACAATTGACTTTGTGCGAA
8108-8130	CTTACAATTGACTTTGTGCGAAA
8109-8131	TTACAATTGACTTTGTGCGAAAT
8110-8132	TTACAATTGACTTTGTGCGAAATG
8111-8133	TACAATTGACTTTGTGCGAAATGA
8112-8134	ACAATTGACTTTGTGCGAAATGAA
8113-8135	CAATTGACTTTGTGCGAAATGAAA
8114-8136	AATTGACTTTGTGCGAAATGAAAG
8115-8137	ATTGACTTTGTGCGAAATGAAAGT
8116-8138	TTGACTTTGTGCGAAATGAAAGTA
8117-8139	TGACTTTGTGCGAAATGAAAGTAA
8118-8140	GACTTTGTGCGAAATGAAAGTAAA
8119-8141	ACTTTGTGCGAAATGAAAGTAAAG
8120-8142	CTTTGTGCGAAATGAAAGTAAAGA
8121-8143	TTTGTGCGAAATGAAAGTAAAGAT
8122-8144	TTGTGCGAAATGAAAGTAAAGATC
8123-8145	TGTGCGAAATGAAAGTAAAGATCA
8124-8146	GTCGAAATGAAAGTAAAGATCAT
8125-8147	TCGAAATGAAAGTAAAGATCATC
8126-8148	CGAAATGAAAGTAAAGATCATCA
8127-8149	GAAATGAAAGTAAAGATCATCAG
8128-8150	AAATGAAAGTAAAGATCATCAGA
8129-8151	AATGAAAGTAAAGATCATCAGAA
8130-8152	ATGAAAGTAAAGATCATCAGAAC
8131-8153	TGAAAGTAAAGATCATCAGAACC
8132-8154	GAAAGTAAAGATCATCAGAACCA
8133-8155	AAAGTAAAGATCATCAGAACCAT
8134-8156	AAGTAAAGATCATCAGAACCATT
8135-8157	AGTAAAGATCATCAGAACCATTG
8136-8158	GTAAGATCATCAGAACCATTGA
8137-8159	TAAAGATCATCAGAACCATTGAC
8138-8160	AAAGATCATCAGAACCATTGACC
8139-8161	AAGATCATCAGAACCATTGACCA
8140-8162	AGATCATCAGAACCATTGACCAG
8141-8163	GATCATCAGAACCATTGACCAGA
8142-8164	ATCATCAGAACCATTGACCAGAT
8143-8165	TCATCAGAACCATTGACCAGATG
8144-8166	CATCAGAACCATTGACCAGATGC
8145-8167	ATCAGAACCATTGACCAGATGCA
8146-8168	TCAGAACCATTGACCAGATGCAG
8147-8169	CAGAACCATTGACCAGATGCAGA
8148-8170	AGAACCATTGACCAGATGCAGAA
8149-8171	GAACCATTGACCAGATGCAGAAC
8150-8172	AACCATTGACCAGATGCAGAAC
8151-8173	ACCATTGACCAGATGCAGAACAG
8152-8174	CCATTGACCAGATGCAGAACAGT
8153-8175	CATTGACCAGATGCAGAACAGTG
8154-8176	ATTGACCAGATGCAGAACAGTGA
8155-8177	TTGACCAGATGCAGAACAGTGAG
8156-8178	TGACCAGATGCAGAACAGTGAGC
8157-8179	GACCAGATGCAGAACAGTGAGCT
8158-8180	ACCAGATGCAGAACAGTGAGCTG
8159-8181	CCAGATGCAGAACAGTGAGCTGC
8160-8182	CAGATGCAGAACAGTGAGCTGCA

Position	Sequence
8161-8183	AGATGCAGAACAGTGAGCTGCAG
8162-8184	GATGCAGAACAGTGAGCTGCAGT
8163-8185	ATGCAGAACAGTGAGCTGCAGTG
8164-8186	TGCAGAACAGTGAGCTGCAGTGG
8165-8187	GCAGAACAGTGAGCTGCAGTGGC
8166-8188	CAGAACAGTGAGCTGCAGTGGCC
8167-8189	AGAACAGTGAGCTGCAGTGGCCC
8168-8190	GAACAGTGAGCTGCAGTGGCCCG
8169-8191	AACAGTGAGCTGCAGTGGCCCGT
8170-8192	ACAGTGAGCTGCAGTGGCCCGTT
8171-8193	CAGTGAGCTGCAGTGGCCCGTTC
8172-8194	AGTGAGCTGCAGTGGCCCGTTC
8173-8195	GTGAGCTGCAGTGGCCCGTTC
8174-8196	TGAGCTGCAGTGGCCCGTTC
8175-8197	GAGCTGCAGTGGCCCGTTC
8176-8198	AGCTGCAGTGGCCCGTTC
8177-8199	GCTGCAGTGGCCCGTTC
8178-8200	CTGCAGTGGCCCGTTC
8179-8201	TGCAGTGGCCCGTTC
8180-8202	GCAGTGGCCCGTTC
8181-8203	CAGTGGCCCGTTC
8182-8204	AGTGGCCCGTTC
8183-8205	GTGGCCCGTTC
8184-8206	TGGCCCGTTC
8185-8207	GGCCCGTTC
8186-8208	GCCCGTTC
8187-8209	CCCGTTC
8188-8210	CCGTTC
8189-8211	CGTTC
8190-8212	GTTCC
8191-8213	TTC
8192-8214	TCC
8193-8215	CC
8194-8216	CAG
8195-8217	AG
8196-8218	GAT
8197-8219	AT
8198-8220	TAT
8199-8221	AT
8200-8222	TAT
8201-8223	AT
8202-8224	TAT
8203-8225	AT
8204-8226	TCT
8205-8227	CT
8206-8228	TC
8207-8229	CAG
8208-8230	AGG
8209-8231	GG
8210-8232	GAT
8211-8233	GAT
8212-8234	AT
8213-8235	TCT
8214-8236	CT
8215-8237	TGA
8216-8238	GA
8217-8239	AAG
8218-8240	AGG
8219-8241	GG
8220-8242	GT
8221-8243	TG
8222-8244	GG
8223-8245	GAG
8224-8246	AG
8225-8247	GG
8226-8248	GAC

Position	Sequence
8227-8249	ACATTCCTCTAGCGAGAATCACC
8228-8250	CATTCCTCTAGCGAGAATCACCC
8229-8251	ATTCCCTCTAGCGAGAATCACCCCT
8230-8252	TTCCCTCTAGCGAGAATCACCCCTG
8231-8253	TCCTCTAGCGAGAATCACCCCTGC
8232-8254	CCTCTAGCGAGAATCACCCCTGCC
8233-8255	CTCTAGCGAGAATCACCCCTGCCA
8234-8256	TCTAGCGAGAATCACCCCTGCCAG
8235-8257	CTAGCGAGAATCACCCCTGCCAGA
8236-8258	TAGCGAGAATCACCCCTGCCAGAC
8237-8259	AGCGAGAATCACCCCTGCCAGACT
8238-8260	GCGAGAATCACCCCTGCCAGACTT
8239-8261	CGAGAATCACCCCTGCCAGACTTC
8240-8262	GAGAATCACCCCTGCCAGACTTCC
8241-8263	AGAATCACCCCTGCCAGACTTCCG
8242-8264	GAATCACCCCTGCCAGACTTCCGT
8243-8265	AATCACCCCTGCCAGACTTCCGTT
8244-8266	ATCACCCCTGCCAGACTTCCGTTT
8245-8267	TCACCCTGCCAGACTTCCGTTTA
8246-8268	CACCCTGCCAGACTTCCGTTTAC
8247-8269	ACCCTGCCAGACTTCCGTTTACC
8248-8270	CCCTGCCAGACTTCCGTTTACCA
8249-8271	CCTGCCAGACTTCCGTTTACCAG
8250-8272	CTGCCAGACTTCCGTTTACCAGA
8251-8273	TGCCAGACTTCCGTTTACCAGAA
8252-8274	GCCAGACTTCCGTTTACCAGAAA
8253-8275	CCAGACTTCCGTTTACCAGAAAT
8254-8276	CAGACTTCCGTTTACCAGAAATC
8255-8277	AGACTTCCGTTTACCAGAAATCG
8256-8278	GACTTCCGTTTACCAGAAATCGC
8257-8279	ACTTCCGTTTACCAGAAATCGCA
8258-8280	CTTCCGTTTACCAGAAATCGCAA
8259-8281	TTCCGTTTACCAGAAATCGCAAT
8260-8282	TCCGTTTACCAGAAATCGCAATF
8261-8283	CCGTTTACCAGAAATCGCAATTC
8262-8284	CGTTTACCAGAAATCGCAATTC
8263-8285	GTTTACCAGAAATCGCAATTC
8264-8286	TTTACCAGAAATCGCAATTC
8265-8287	TTACCAGAAATCGCAATTC
8266-8288	TACCAGAAATCGCAATTC
8267-8289	ACCAGAAATCGCAATTC
8268-8290	CCAGAAATCGCAATTC
8269-8291	CAGAAATCGCAATTC
8270-8292	AGAAATCGCAATTC
8271-8293	GAAATCGCAATTC
8272-8294	AAATCGCAATTC
8273-8295	AATCGCAATTC
8274-8296	ATCGCAATTC
8275-8297	TCGCAATTC
8276-8298	CGCAATTC
8277-8299	GCAATTC
8278-8300	CAATTC
8279-8301	AATTC
8280-8302	ATTCC
8281-8303	TCCAG
8282-8304	TCCAG
8283-8305	CCAG
8284-8306	CAG
8285-8307	AG
8286-8308	GA
8287-8309	A
8288-8310	AT
8289-8311	TT
8290-8312	TC
8291-8313	CA
8292-8314	ATA

Position	Sequence
8293-8315	TAATCCCAACTCTCAACCTTAAT
8294-8316	AATCCCAACTCTCAACCTTAATG
8295-8317	ATCCCAACTCTCAACCTTAATGA
8296-8318	TCCCAACTCTCAACCTTAATGAT
8297-8319	CCCAACTCTCAACCTTAATGATT
8298-8320	CCAACTCTCAACCTTAATGATTT
8299-8321	CAACTCTCAACCTTAATGATTTT
8300-8322	AACTCTCAACCTTAATGATTTTC
8301-8323	ACTCTCAACCTTAATGATTTTCA
8302-8324	CTCTCAACCTTAATGATTTTCAA
8303-8325	TCTCAACCTTAATGATTTTCAAG
8304-8326	CTCAACCTTAATGATTTTCAAGT
8305-8327	TCAACCTTAATGATTTTCAAGTT
8306-8328	CAACCTTAATGATTTTCAAGTTC
8307-8329	AACCTTAATGATTTTCAAGTTCC
8308-8330	ACCTTAATGATTTTCAAGTTCCCT
8309-8331	CCTTAATGATTTTCAAGTTCCCTG
8310-8332	CTTAATGATTTTCAAGTTCCCTGA
8311-8333	TTAATGATTTTCAAGTTCCCTGAC
8312-8334	TAATGATTTTCAAGTTCCCTGACC
8313-8335	AATGATTTTCAAGTTCCCTGACCT
8314-8336	ATGATTTTCAAGTTCCCTGACCTT
8315-8337	TGATTTTCAAGTTCCCTGACCTTC
8316-8338	GATTTTCAAGTTCCCTGACCTTCA
8317-8339	ATTTTCAAGTTCCCTGACCTTCA
8318-8340	TTTTCAAGTTCCCTGACCTTCA
8319-8341	TTCAAGTTCCCTGACCTTCA
8320-8342	TCAAGTTCCCTGACCTTCA
8321-8343	TCAAGTTCCCTGACCTTCA
8322-8344	CAAGTTCCCTGACCTTCA
8323-8345	AAGTTCCCTGACCTTCA
8324-8346	AGTTCCCTGACCTTCA
8325-8347	GTTCCCTGACCTTCA
8326-8348	TTCCCTGACCTTCA
8327-8349	TCCCTGACCTTCA
8328-8350	CCTGACCTTCA
8329-8351	CTGACCTTCA
8330-8352	TGACCTTCA
8331-8353	GACCTTCA
8332-8354	ACCTTCA
8333-8355	CCTTCA
8334-8356	CTTCA
8335-8357	TTCA
8336-8358	TCACATACCAGAATCCAGCTT
8337-8359	CACATACCAGAATCCAGCTTCC
8338-8360	ACATACCAGAATCCAGCTTCCC
8339-8361	CATACCAGAATCCAGCTTCCCC
8340-8362	ATACCAGAATCCAGCTTCCCCA
8341-8363	TACCAGAATCCAGCTTCCCCAC
8342-8364	ACCAGAATCCAGCTTCCCCACA
8343-8365	CCAGAATCCAGCTTCCCCACAT
8344-8366	CAGAATCCAGCTTCCCCACATC
8345-8367	AGAATCCAGCTTCCCCACATCT
8346-8368	GAATCCAGCTTCCCCACATCTC
8347-8369	AATCCAGCTTCCCCACATCTCA
8348-8370	ATCCAGCTTCCCCACATCTCAC
8349-8371	TCCAGCTTCCCCACATCTCACA
8350-8372	TCCAGCTTCCCCACATCTCACAC
8351-8373	CCAGCTTCCCCACATCTCACACA
8352-8374	CAGCTTCCCCACATCTCACACAC
8353-8375	AGCTTCCCCACATCTCACACACA
8354-8376	GCTTCCCCACATCTCACACACAA
8355-8377	CTCCCCACATCTCACACACAAT
8356-8378	TTCCCCACATCTCACACACAATT
8357-8379	TCCCCACATCTCACACACAATTG
8358-8380	CCCCACATCTCACACACAATTGA

Position	Sequence
8359-8381	CCCACATCTCACACACAATTGAA
8360-8382	CCACATCTCACACACAATTGAAG
8361-8383	CACATCTCACACACAATTGAAGT
8362-8384	ACATCTCACACACAATTGAAGTA
8363-8385	CATCTCACACACAATTGAAGTAC
8364-8386	ATCTCACACACAATTGAAGTACC
8365-8387	TCTCACACACAATTGAAGTACCT
8366-8388	CTCACACACAATTGAAGTACCTA
8367-8389	TCACACACAATTGAAGTACCTAC
8368-8390	CACACACAATTGAAGTACCTACT
8369-8391	ACACACAATTGAAGTACCTACTT
8370-8392	CACACAATTGAAGTACCTACTTT
8371-8393	ACACAATTGAAGTACCTACTTTT
8372-8394	CACAATTGAAGTACCTACTTTTG
8373-8395	ACAATTGAAGTACCTACTTTTGG
8374-8396	CAATTGAAGTACCTACTTTTGGC
8375-8397	AATTGAAGTACCTACTTTTGGCA
8376-8398	ATTGAAGTACCTACTTTTGGCAA
8377-8399	TTGAAGTACCTACTTTTGGCAAG
8378-8400	TGAAGTACCTACTTTTGGCAAGC
8379-8401	GAAGTACCTACTTTTGGCAAGCT
8380-8402	AAGTACCTACTTTTGGCAAGCTA
8381-8403	AGTACCTACTTTTGGCAAGCTAT
8382-8404	GTACCTACTTTTGGCAAGCTATA
8383-8405	TACCTACTTTTGGCAAGCTATAC
8384-8406	ACCTACTTTTGGCAAGCTATACA
8385-8407	CCTACTTTTGGCAAGCTATACAG
8386-8408	CTACTTTTGGCAAGCTATACAGT
8387-8409	TACTTTTGGCAAGCTATACAGTA
8388-8410	ACTTTTGGCAAGCTATACAGTAT
8389-8411	CTTTTGGCAAGCTATACAGTATT
8390-8412	TTTTGGCAAGCTATACAGTATTC
8391-8413	TTTGGCAAGCTATACAGTATTCT
8392-8414	TTGGCAAGCTATACAGTATTCTG
8393-8415	TGGCAAGCTATACAGTATTCTGA
8394-8416	GGCAAGCTATACAGTATTCTGAA
8395-8417	GCAAGCTATACAGTATTCTGAAA
8396-8418	CAAGCTATACAGTATTCTGAAAA
8397-8419	AAGCTATACAGTATTCTGAAAAAT
8398-8420	AGCTATACAGTATTCTGAAAAATC
8399-8421	GCTATACAGTATTCTGAAAAATCC
8400-8422	CTATACAGTATTCTGAAAAATCCA
8401-8423	TATACAGTATTCTGAAAAATCCAA
8402-8424	ATACAGTATTCTGAAAAATCCAAT
8403-8425	TACAGTATTCTGAAAAATCCAATC
8404-8426	ACAGTATTCTGAAAAATCCAATCT
8405-8427	CAGTATTCTGAAAAATCCAATCTC
8406-8428	AGTATTCTGAAAAATCCAATCTCC
8407-8429	GTATTCTGAAAAATCCAATCTCCT
8408-8430	TATTCTGAAAAATCCAATCTCCTC
8409-8431	ATTCTGAAAAATCCAATCTCCTCT
8410-8432	TTCTGAAAAATCCAATCTCCTCTT
8411-8433	TCTGAAAAATCCAATCTCCTCTTT
8412-8434	CTGAAAAATCCAATCTCCTCTTTT
8413-8435	TGAAAAATCCAATCTCCTCTTTTC
8414-8436	GAAAAATCCAATCTCCTCTTTTCA
8415-8437	AAAAATCCAATCTCCTCTTTTCAC
8416-8438	AAATCCAATCTCCTCTTTTCACA
8417-8439	AATCCAATCTCCTCTTTTCACAT
8418-8440	ATCCAATCTCCTCTTTTCACATT
8419-8441	TCCAATCTCCTCTTTTCACATTA
8420-8442	CCAATCTCCTCTTTTCACATTAG
8421-8443	CAATCTCCTCTTTTCACATTAGA
8422-8444	AATCTCCTCTTTTCACATTAGAT
8423-8445	ATCTCCTCTTTTCACATTAGATG
8424-8446	TCTCCTCTTTTCACATTAGATGC

Position	Sequence
8425-8447	CTCCTCTTTTCACATTAGATGCA
8426-8448	TCCTCTTTTCACATTAGATGCAA
8427-8449	CCTCTTTTCACATTAGATGCAAA
8428-8450	CTCTTTTCACATTAGATGCAAAT
8429-8451	TCTTTTCACATTAGATGCAAATG
8430-8452	CTTTTCACATTAGATGCAAATGC
8431-8453	TTTTCACATTAGATGCAAATGCT
8432-8454	TTTCACATTAGATGCAAATGCTG
8433-8455	TTCACATTAGATGCAAATGCTGA
8434-8456	TCACATTAGATGCAAATGCTGAC
8435-8457	CACATTAGATGCAAATGCTGACA
8436-8458	ACATTAGATGCAAATGCTGACAT
8437-8459	CATTAGATGCAAATGCTGACATA
8438-8460	ATTAGATGCAAATGCTGACATAG
8439-8461	TTAGATGCAAATGCTGACATAGG
8440-8462	TAGATGCAAATGCTGACATAGGG
8441-8463	AGATGCAAATGCTGACATAGGGA
8442-8464	GATGCAAATGCTGACATAGGGAA
8443-8465	ATGCAAATGCTGACATAGGGAAT
8444-8466	TGCAAATGCTGACATAGGGAATG
8445-8467	GCAAATGCTGACATAGGGAATGG
8446-8468	CAAATGCTGACATAGGGAATGGA
8447-8469	AAATGCTGACATAGGGAATGGAA
8448-8470	AATGCTGACATAGGGAATGGAAC
8449-8471	ATGCTGACATAGGGAATGGAAAC
8450-8472	TGCTGACATAGGGAATGGAAACCA
8451-8473	GCTGACATAGGGAATGGAAACCAC
8452-8474	CTGACATAGGGAATGGAAACCACC
8453-8475	TGACATAGGGAATGGAAACCACCT
8454-8476	GACATAGGGAATGGAAACCACCTC
8455-8477	ACATAGGGAATGGAAACCACCTCA
8456-8478	CATAGGGAATGGAAACCACCTCAG
8457-8479	ATAGGGAATGGAAACCACCTCAGC
8458-8480	TAGGGAATGGAAACCACCTCAGCA
8459-8481	AGGGAATGGAAACCACCTCAGCAA
8460-8482	GGGAATGGAAACCACCTCAGCAAA
8461-8483	GGAATGGAAACCACCTCAGCAAAC
8462-8484	GAATGGAAACCACCTCAGCAAACG
8463-8485	AATGGAAACCACCTCAGCAAACGA
8464-8486	ATGGAAACCACCTCAGCAAACGAA
8465-8487	TGGAAACCACCTCAGCAAACGAAG
8466-8488	GGAACCACCTCAGCAAACGAAGC
8467-8489	GAACCACCTCAGCAAACGAAGCA
8468-8490	AACCACCTCAGCAAACGAAGCAG
8469-8491	ACCACCTCAGCAAACGAAGCAGG
8470-8492	CCACCTCAGCAAACGAAGCAGGT
8471-8493	CACCTCAGCAAACGAAGCAGGTA
8472-8494	ACCTCAGCAAACGAAGCAGGTAT
8473-8495	CCTCAGCAAACGAAGCAGGTATC
8474-8496	CTCAGCAAACGAAGCAGGTATCG
8475-8497	TCAGCAAACGAAGCAGGTATCGC
8476-8498	CAGCAAACGAAGCAGGTATCGCA
8477-8499	AGCAAACGAAGCAGGTATCGCAG
8478-8500	GCAAACGAAGCAGGTATCGCAGC
8479-8501	CAAACGAAGCAGGTATCGCAGCT
8480-8502	AAACGAAGCAGGTATCGCAGCTT
8481-8503	AACGAAGCAGGTATCGCAGCTTC
8482-8504	ACGAAGCAGGTATCGCAGCTTCC
8483-8505	CGAAGCAGGTATCGCAGCTTCCA
8484-8506	GAAGCAGGTATCGCAGCTTCCAT
8485-8507	AAGCAGGTATCGCAGCTTCCATC
8486-8508	AGCAGGTATCGCAGCTTCCATCA
8487-8509	GCAGGTATCGCAGCTTCCATCAC
8488-8510	CAGGTATCGCAGCTTCCATCACT
8489-8511	AGGTATCGCAGCTTCCATCACTG
8490-8512	GGTATCGCAGCTTCCATCACTGC

Position	Sequence
8491-8513	GTATCGCAGCTTCCATCACTGCC
8492-8514	TATCGCAGCTTCCATCACTGCCA
8493-8515	ATCGCAGCTTCCATCACTGCCAA
8494-8516	TCGCAGCTTCCATCACTGCCAAA
8495-8517	CGCAGCTTCCATCACTGCCAAAG
8496-8518	GCAGCTTCCATCACTGCCAAAGG
8497-8519	CAGCTTCCATCACTGCCAAAGGA
8498-8520	AGCTTCCATCACTGCCAAAGGAG
8499-8521	GCTTCCATCACTGCCAAAGGAGA
8500-8522	CTTCCATCACTGCCAAAGGAGAG
8501-8523	TTCCATCACTGCCAAAGGAGAGT
8502-8524	TCCATCACTGCCAAAGGAGAGTTC
8503-8525	CCATCACTGCCAAAGGAGAGTCC
8504-8526	CATCACTGCCAAAGGAGAGTCCA
8505-8527	ATCACTGCCAAAGGAGAGTCCAA
8506-8528	TCACTGCCAAAGGAGAGTCCAAA
8507-8529	CACTGCCAAAGGAGAGTCCAAAT
8508-8530	ACTGCCAAAGGAGAGTCCAAATT
8509-8531	CTGCCAAAGGAGAGTCCAAATTA
8510-8532	TGCCAAAGGAGAGTCCAAATTAG
8511-8533	GCCAAAGGAGAGTCCAAATTAGA
8512-8534	CCAAAGGAGAGTCCAAATTAGAA
8513-8535	CAAAGGAGAGTCCAAATTAGAAG
8514-8536	AAAGGAGAGTCCAAATTAGAAGT
8515-8537	AAGGAGAGTCCAAATTAGAAGTT
8516-8538	AGGAGAGTCCAAATTAGAAGTTC
8517-8539	GGAGAGTCCAAATTAGAAGTTCT
8518-8540	GAGAGTCCAAATTAGAAGTTCTC
8519-8541	AGAGTCCAAATTAGAAGTTCTCA
8520-8542	GAGTCCAAATTAGAAGTTCTCAA
8521-8543	AGTCCAAATTAGAAGTTCTCAAT
8522-8544	GTCCAAATTAGAAGTTCTCAATT
8523-8545	TCCAAATTAGAAGTTCTCAATTT
8524-8546	CCAAATTAGAAGTTCTCAATTTT
8525-8547	CAAATTAGAAGTTCTCAATTTTG
8526-8548	AAATTAGAAGTTCTCAATTTTGA
8527-8549	AATTAGAAGTTCTCAATTTTGAT
8528-8550	ATTAGAAGTTCTCAATTTTGATT
8529-8551	TTAGAAGTTCTCAATTTTGATTT
8530-8552	TAGAAGTTCTCAATTTTGATTTT
8531-8553	AGAAGTTCTCAATTTTGATTTTC
8532-8554	GAAGTTCTCAATTTTGATTTTCA
8533-8555	AAGTTCTCAATTTTGATTTTCAA
8534-8556	AGTTCTCAATTTTGATTTTCAAG
8535-8557	GTTCTCAATTTTGATTTTCAAGC
8536-8558	TTCTCAATTTTGATTTTCAAGCA
8537-8559	TCTCAATTTTGATTTTCAAGCAA
8538-8560	CTCAATTTTGATTTTCAAGCAAA
8539-8561	TCAATTTTGATTTTCAAGCAAAT
8540-8562	CAATTTTGATTTTCAAGCAAATG
8541-8563	AATTTTGATTTTCAAGCAAATGC
8542-8564	ATTTTGATTTTCAAGCAAATGCA
8543-8565	TTTGATTTTCAAGCAAATGCAC
8544-8566	TTTGATTTTCAAGCAAATGCACA
8545-8567	TTGATTTTCAAGCAAATGCACAA
8546-8568	TGATTTTCAAGCAAATGCACAAC
8547-8569	GATTTTCAAGCAAATGCACAAC
8548-8570	ATTTTCAAGCAAATGCACAAC
8549-8571	TTTCAAGCAAATGCACAAC
8550-8572	TTTCAAGCAAATGCACAAC
8551-8573	TCAAGCAAATGCACAAC
8552-8574	TCAAGCAAATGCACAAC
8553-8575	CAAGCAAATGCACAAC
8554-8576	AAGCAAATGCACAAC
8555-8577	AGCAAATGCACAAC
8556-8578	GCAAATGCACAAC

Position	Sequence
8557-8579	CAAATGCACAACCTCTCAAACCCCT
8558-8580	AAATGCACAACCTCTCAAACCCCTA
8559-8581	AATGCACAACCTCTCAAACCCCTAA
8560-8582	ATGCACAACCTCTCAAACCCCTAAG
8561-8583	TGCACAACCTCTCAAACCCCTAAGA
8562-8584	GCACAACCTCTCAAACCCCTAAGAT
8563-8585	CACAACCTCTCAAACCCCTAAGATT
8564-8586	ACAACCTCTCAAACCCCTAAGATTA
8565-8587	CAACTCTCAAACCCCTAAGATTAA
8566-8588	AACTCTCAAACCCCTAAGATTAAT
8567-8589	ACTCTCAAACCCCTAAGATTAATC
8568-8590	CTCTCAAACCCCTAAGATTAATCC
8569-8591	TCTCAAACCCCTAAGATTAATCCG
8570-8592	CTCAAACCCCTAAGATTAATCCGC
8571-8593	TCAAACCCCTAAGATTAATCCGCT
8572-8594	CAAACCCCTAAGATTAATCCGCTG
8573-8595	AAACCCCTAAGATTAATCCGCTGG
8574-8596	AACCCCTAAGATTAATCCGCTGGC
8575-8597	ACCCTAAGATTAATCCGCTGGCT
8576-8598	CCCTAAGATTAATCCGCTGGCTC
8577-8599	CCTAAGATTAATCCGCTGGCTCT
8578-8600	CTAAGATTAATCCGCTGGCTCTG
8579-8601	TAAGATTAATCCGCTGGCTCTGA
8580-8602	AAGATTAATCCGCTGGCTCTGAA
8581-8603	AGATTAATCCGCTGGCTCTGAAG
8582-8604	GATTAATCCGCTGGCTCTGAAGG
8583-8605	ATTAATCCGCTGGCTCTGAAGGA
8584-8606	TTAATCCGCTGGCTCTGAAGGAG
8585-8607	TAATCCGCTGGCTCTGAAGGAGT
8586-8608	AATCCGCTGGCTCTGAAGGAGTC
8587-8609	ATCCGCTGGCTCTGAAGGAGTCA
8588-8610	TCCGCTGGCTCTGAAGGAGTCAG
8589-8611	CCGCTGGCTCTGAAGGAGTCAGT
8590-8612	CGCTGGCTCTGAAGGAGTCAGTG
8591-8613	GCTGGCTCTGAAGGAGTCAGTGA
8592-8614	CTGGCTCTGAAGGAGTCAGTGAA
8593-8615	TGGCTCTGAAGGAGTCAGTGAA
8594-8616	GGCTCTGAAGGAGTCAGTGAAGT
8595-8617	GCTCTGAAGGAGTCAGTGAAGTT
8596-8618	CTCTGAAGGAGTCAGTGAAGTTC
8597-8619	TCTGAAGGAGTCAGTGAAGTTCT
8598-8620	CTGAAGGAGTCAGTGAAGTTCTC
8599-8621	TGAAGGAGTCAGTGAAGTTCTCC
8600-8622	GAAGGAGTCAGTGAAGTTCTCCA
8601-8623	AAGGAGTCAGTGAAGTTCTCCAG
8602-8624	AGGAGTCAGTGAAGTTCTCCAGC
8603-8625	GGAGTCAGTGAAGTTCTCCAGCA
8604-8626	GAGTCAGTGAAGTTCTCCAGCAA
8605-8627	AGTCAGTGAAGTTCTCCAGCAAG
8606-8628	GTCAGTGAAGTTCTCCAGCAAGT
8607-8629	TCAGTGAAGTTCTCCAGCAAGTA
8608-8630	CAGTGAAGTTCTCCAGCAAGTAC
8609-8631	AGTGAAGTTCTCCAGCAAGTACC
8610-8632	GTGAAGTTCTCCAGCAAGTACCT
8611-8633	TGAAGTTCTCCAGCAAGTACCTG
8612-8634	GAAGTTCTCCAGCAAGTACCTGA
8613-8635	AAGTTCTCCAGCAAGTACCTGAG
8614-8636	AGTTCTCCAGCAAGTACCTGAGA
8615-8637	GTTCTCCAGCAAGTACCTGAGAA
8616-8638	TTCTCCAGCAAGTACCTGAGAAC
8617-8639	TCTCCAGCAAGTACCTGAGAACG
8618-8640	CTCCAGCAAGTACCTGAGAACGG
8619-8641	TCCAGCAAGTACCTGAGAACGGA
8620-8642	CCAGCAAGTACCTGAGAACGGAG
8621-8643	CAGCAAGTACCTGAGAACGGAGC
8622-8644	AGCAAGTACCTGAGAACGGAGCA

Position	Sequence
8623-8645	GCAAGTACCTGAGAACGGAGCAT
8624-8646	CAAGTACCTGAGAACGGAGCATG
8625-8647	AAGTACCTGAGAACGGAGCATGG
8626-8648	AGTACCTGAGAACGGAGCATGGG
8627-8649	GTACCTGAGAACGGAGCATGGGA
8628-8650	TACCTGAGAACGGAGCATGGGAG
8629-8651	ACCTGAGAACGGAGCATGGGAGT
8630-8652	CCTGAGAACGGAGCATGGGAGTG
8631-8653	CTGAGAACGGAGCATGGGAGTGA
8632-8654	TGAGAACGGAGCATGGGAGTGAA
8633-8655	GAGAACGGAGCATGGGAGTGAAA
8634-8656	AGAACGGAGCATGGGAGTGAAAT
8635-8657	GAACGGAGCATGGGAGTGAAATG
8636-8658	AACGGAGCATGGGAGTGAAATGC
8637-8659	ACGGAGCATGGGAGTGAAATGCT
8638-8660	CGGAGCATGGGAGTGAAATGCTG
8639-8661	GGAGCATGGGAGTGAAATGCTGT
8640-8662	GAGCATGGGAGTGAAATGCTGTT
8641-8663	AGCATGGGAGTGAAATGCTGTTT
8642-8664	GCATGGGAGTGAAATGCTGTTTT
8643-8665	CATGGGAGTGAAATGCTGTTTTT
8644-8666	ATGGGAGTGAAATGCTGTTTTTT
8645-8667	TGGGAGTGAAATGCTGTTTTTTG
8646-8668	GGGAGTGAAATGCTGTTTTTTGG
8647-8669	GGAGTGAAATGCTGTTTTTTGGG
8648-8670	GAGTGAAATGCTGTTTTTTGGGA
8649-8671	AGTGAAATGCTGTTTTTTGGGAA
8650-8672	GTGAAATGCTGTTTTTTGGGAAAT
8651-8673	TGAAATGCTGTTTTTTGGGAAATG
8652-8674	GAAATGCTGTTTTTTGGGAAATGC
8653-8675	AAATGCTGTTTTTTGGGAAATGCT
8654-8676	AATGCTGTTTTTTGGGAAATGCTA
8655-8677	ATGCTGTTTTTTGGGAAATGCTAT
8656-8678	TGCTGTTTTTTGGGAAATGCTATT
8657-8679	GCTGTTTTTTGGGAAATGCTATTG
8658-8680	CTGTTTTTTGGGAAATGCTATTGA
8659-8681	TGTTTTTGGGAAATGCTATTGAG
8660-8682	GTTTTTGGGAAATGCTATTGAGG
8661-8683	TTTTTGGGAAATGCTATTGAGGG
8662-8684	TTTTTGGGAAATGCTATTGAGGGA
8663-8685	TTTTGGGAAATGCTATTGAGGGAA
8664-8686	TTTGGGAAATGCTATTGAGGGAAA
8665-8687	TTGGGAAATGCTATTGAGGGAAAA
8666-8688	TGGGAAATGCTATTGAGGGAAAAAT
8667-8689	GGGAAATGCTATTGAGGGAAAAATC
8668-8690	GAAATGCTATTGAGGGAAAAATCA
8669-8691	AAATGCTATTGAGGGAAAAATCAA
8670-8692	AATGCTATTGAGGGAAAAATCAAA
8671-8693	ATGCTATTGAGGGAAAAATCAAAC
8672-8694	TGCTATTGAGGGAAAAATCAAACA
8673-8695	GCTATTGAGGGAAAAATCAAACAC
8674-8696	CTATTGAGGGAAAAATCAAACACA
8675-8697	TATTGAGGGAAAAATCAAACACAG
8676-8698	ATTGAGGGAAAAATCAAACACAGT
8677-8699	TTGAGGGAAAAATCAAACACAGTG
8678-8700	TGAGGGAAAAATCAAACACAGTGG
8679-8701	GAGGGAAAAATCAAACACAGTGGC
8680-8702	AGGGAAAAATCAAACACAGTGGCA
8681-8703	GGGAAAAATCAAACACAGTGGCAA
8682-8704	GGAAAAATCAAACACAGTGGCAAG
8683-8705	GAAAAATCAAACACAGTGGCAAGT
8684-8706	AAAAATCAAACACAGTGGCAAGTT
8685-8707	AAATCAAACACAGTGGCAAGTTT
8686-8708	AATCAAACACAGTGGCAAGTTTA
8687-8709	ATCAAACACAGTGGCAAGTTTAC
8688-8710	TCAAACACAGTGGCAAGTTTACA

Position	Sequence
8689-8711	CAAACACAGTGGCAAGTTTACAC
8690-8712	AAACACAGTGGCAAGTTTACACA
8691-8713	AACACAGTGGCAAGTTTACACAC
8692-8714	ACACAGTGGCAAGTTTACACACA
8693-8715	CACAGTGGCAAGTTTACACACAG
8694-8716	ACAGTGGCAAGTTTACACACAGA
8695-8717	CAGTGGCAAGTTTACACACAGAA
8696-8718	AGTGGCAAGTTTACACACAGAAA
8697-8719	GTGGCAAGTTTACACACAGAAAA
8698-8720	TGGCAAGTTTACACACAGAAAAA
8699-8721	GGCAAGTTTACACACAGAAAAAA
8700-8722	GCAAGTTTACACACAGAAAAAAA
8701-8723	CAAGTTTACACACAGAAAAAAAT
8702-8724	AAGTTTACACACAGAAAAAAATA
8703-8725	AGTTTACACACAGAAAAAAATAC
8704-8726	GTTTACACACAGAAAAAAATACA
8705-8727	TTTACACACAGAAAAAAATACAC
8706-8728	TTACACACAGAAAAAAATACACT
8707-8729	TACACACAGAAAAAAATACACTG
8708-8730	ACACACAGAAAAAAATACACTGG
8709-8731	CACACAGAAAAAAATACACTGGA
8710-8732	ACACAGAAAAAAATACACTGGAG
8711-8733	CACAGAAAAAAATACACTGGAGC
8712-8734	ACAGAAAAAAATACACTGGAGCT
8713-8735	CAGAAAAAAATACACTGGAGCTT
8714-8736	AGAAAAAAATACACTGGAGCTTA
8715-8737	GAAAAAAATACACTGGAGCTTAG
8716-8738	AAAAAAATACACTGGAGCTTAGT
8717-8739	AAAAAATACACTGGAGCTTAGTA
8718-8740	AAAAATACACTGGAGCTTAGTAA
8719-8741	AAAATACACTGGAGCTTAGTAAT
8720-8742	AAATACACTGGAGCTTAGTAATG
8721-8743	AATACACTGGAGCTTAGTAATGG
8722-8744	ATACACTGGAGCTTAGTAATGGA
8723-8745	TACACTGGAGCTTAGTAATGGAG
8724-8746	ACACTGGAGCTTAGTAATGGAGT
8725-8747	CACTGGAGCTTAGTAATGGAGTG
8726-8748	ACTGGAGCTTAGTAATGGAGTGA
8727-8749	CTGGAGCTTAGTAATGGAGTGAT
8728-8750	TGGAGCTTAGTAATGGAGTGATT
8729-8751	GGAGCTTAGTAATGGAGTGATTG
8730-8752	GAGCTTAGTAATGGAGTGATTGT
8731-8753	AGCTTAGTAATGGAGTGATTGTC
8732-8754	GCTTAGTAATGGAGTGATTGTCA
8733-8755	CTTAGTAATGGAGTGATTGTCAA
8734-8756	TTAGTAATGGAGTGATTGTCAAG
8735-8757	TAGTAATGGAGTGATTGTCAAGA
8736-8758	AGTAATGGAGTGATTGTCAAGAT
8737-8759	GTAATGGAGTGATTGTCAAGATA
8738-8760	TAATGGAGTGATTGTCAAGATAA
8739-8761	AATGGAGTGATTGTCAAGATAAA
8740-8762	ATGGAGTGATTGTCAAGATAAAC
8741-8763	TGGAGTGATTGTCAAGATAAAACA
8742-8764	GGAGTGATTGTCAAGATAAAACAA
8743-8765	GAGTGATTGTCAAGATAAAACAAT
8744-8766	AGTGATTGTCAAGATAAAACAATC
8745-8767	GTGATTGTCAAGATAAAACAATCA
8746-8768	TGATTGTCAAGATAAAACAATCAG
8747-8769	GATTGTCAAGATAAAACAATCAGC
8748-8770	ATTGTCAAGATAAAACAATCAGCT
8749-8771	TTGTCAAGATAAAACAATCAGCTT
8750-8772	TGTCAAGATAAAACAATCAGCTTA
8751-8773	GTCAGATAAAACAATCAGCTTAC
8752-8774	TCAAGATAAAACAATCAGCTTACC
8753-8775	CAAGATAAAACAATCAGCTTACCC
8754-8776	AAGATAAAACAATCAGCTTACCC

Position	Sequence
8755-8777	AGATAACAATCAGCTTACCCTG
8756-8778	GATAACAATCAGCTTACCCTGG
8757-8779	ATAACAATCAGCTTACCCTGGA
8758-8780	TAAACAATCAGCTTACCCTGGAT
8759-8781	AAACAATCAGCTTACCCTGGATA
8760-8782	AACAATCAGCTTACCCTGGATAG
8761-8783	ACAATCAGCTTACCCTGGATAGC
8762-8784	CAATCAGCTTACCCTGGATAGCA
8763-8785	AATCAGCTTACCCTGGATAGCAA
8764-8786	ATCAGCTTACCCTGGATAGCAAC
8765-8787	TCAGCTTACCCTGGATAGCAACA
8766-8788	CAGCTTACCCTGGATAGCAACAC
8767-8789	AGCTTACCCTGGATAGCAACACT
8768-8790	GCTTACCCTGGATAGCAACACTA
8769-8791	CTTACCCTGGATAGCAACACTAA
8770-8792	TTACCCTGGATAGCAACACTAAA
8771-8793	TACCCTGGATAGCAACACTAAAT
8772-8794	ACCCTGGATAGCAACACTAAATA
8773-8795	CCCTGGATAGCAACACTAAATAC
8774-8796	CCTGGATAGCAACACTAAATACT
8775-8797	CTGGATAGCAACACTAAATACTT
8776-8798	TGGATAGCAACACTAAATACTTC
8777-8799	GGATAGCAACACTAAATACTTCC
8778-8800	GATAGCAACACTAAATACTTCCA
8779-8801	ATAGCAACACTAAATACTTCCAC
8780-8802	TAGCAACACTAAATACTTCCACA
8781-8803	AGCAACACTAAATACTTCCACAA
8782-8804	GCAACACTAAATACTTCCACAAA
8783-8805	CAACACTAAATACTTCCACAAAT
8784-8806	AACACTAAATACTTCCACAAATF
8785-8807	ACACTAAATACTTCCACAAATG
8786-8808	CACTAAATACTTCCACAAATTGA
8787-8809	ACTAAATACTTCCACAAATTGAA
8788-8810	CTAAATACTTCCACAAATTGAAC
8789-8811	TAAATACTTCCACAAATTGAACA
8790-8812	AAATACTTCCACAAATTGAACAT
8791-8813	AATACTTCCACAAATTGAACATC
8792-8814	ATACTTCCACAAATTGAACATCC
8793-8815	TACTTCCACAAATTGAACATCCC
8794-8816	ACTTCCACAAATTGAACATCCCC
8795-8817	CTTCCACAAATTGAACATCCCCA
8796-8818	TTCCACAAATTGAACATCCCCAA
8797-8819	TCCACAAATTGAACATCCCCAAA
8798-8820	CCACAAATTGAACATCCCCAAAC
8799-8821	CACAAATTGAACATCCCCAAACT
8800-8822	ACAAATTGAACATCCCCAAACTG
8801-8823	CAAATTGAACATCCCCAAACTGG
8802-8824	AAATTGAACATCCCCAAACTGGA
8803-8825	AATTGAACATCCCCAAACTGGAC
8804-8826	ATTGAACATCCCCAAACTGGACT
8805-8827	TTGAACATCCCCAAACTGGACTT
8806-8828	TGAACATCCCCAAACTGGACTTC
8807-8829	GAACATCCCCAAACTGGACTTCT
8808-8830	AACATCCCCAAACTGGACTTCTC
8809-8831	ACATCCCCAAACTGGACTTCTCT
8810-8832	CATCCCCAAACTGGACTTCTCTA
8811-8833	ATCCCCAAACTGGACTTCTCTAG
8812-8834	TCCCCAAACTGGACTTCTCTAGT
8813-8835	CCCCAAACTGGACTTCTCTAGTC
8814-8836	CCCAACTGGACTTCTCTAGTCA
8815-8837	CCAAACTGGACTTCTCTAGTCAG
8816-8838	CAACTGGACTTCTCTAGTCAGG
8817-8839	AAACTGGACTTCTCTAGTCAGGC
8818-8840	AACTGGACTTCTCTAGTCAGGCT
8819-8841	ACTGGACTTCTCTAGTCAGGCTG
8820-8842	CTGGACTTCTCTAGTCAGGCTGA

Position	Sequence
8821-8843	TGGACTTCTCTAGTCAGGCTGAC
8822-8844	GGACTTCTCTAGTCAGGCTGACC
8823-8845	GACTTCTCTAGTCAGGCTGACCT
8824-8846	ACTTCTCTAGTCAGGCTGACCTG
8825-8847	CTTCTCTAGTCAGGCTGACCTGC
8826-8848	TTCTCTAGTCAGGCTGACCTGCG
8827-8849	TCTCTAGTCAGGCTGACCTGCGC
8828-8850	CTCTAGTCAGGCTGACCTGCGCA
8829-8851	TCTAGTCAGGCTGACCTGCGCAA
8830-8852	CTAGTCAGGCTGACCTGCGCAAC
8831-8853	TAGTCAGGCTGACCTGCGCAACG
8832-8854	AGTCAGGCTGACCTGCGCAACGA
8833-8855	GTCAGGCTGACCTGCGCAACGAG
8834-8856	TCAGGCTGACCTGCGCAACGAGA
8835-8857	CAGGCTGACCTGCGCAACGAGAT
8836-8858	AGGCTGACCTGCGCAACGAGATC
8837-8859	GGCTGACCTGCGCAACGAGATCA
8838-8860	GCTGACCTGCGCAACGAGATCAA
8839-8861	CTGACCTGCGCAACGAGATCAAG
8840-8862	TGACCTGCGCAACGAGATCAAGA
8841-8863	GACCTGCGCAACGAGATCAAGAC
8842-8864	ACCTGCGCAACGAGATCAAGACA
8843-8865	CCTGCGCAACGAGATCAAGACAC
8844-8866	CTGCGCAACGAGATCAAGACACT
8845-8867	TGCGCAACGAGATCAAGACACTG
8846-8868	GCGCAACGAGATCAAGACACTGT
8847-8869	CGCAACGAGATCAAGACACTGTT
8848-8870	GCAACGAGATCAAGACACTGTTG
8849-8871	CAACGAGATCAAGACACTGTTGA
8850-8872	AACGAGATCAAGACACTGTTGAA
8851-8873	ACGAGATCAAGACACTGTTGAAA
8852-8874	CGAGATCAAGACACTGTTGAAAG
8853-8875	GAGATCAAGACACTGTTGAAAGC
8854-8876	AGATCAAGACACTGTTGAAAGCT
8855-8877	GATCAAGACACTGTTGAAAGCTG
8856-8878	ATCAAGACACTGTTGAAAGCTGG
8857-8879	TCAAGACACTGTTGAAAGCTGGC
8858-8880	CAAGACACTGTTGAAAGCTGGCC
8859-8881	AAGACACTGTTGAAAGCTGGCCA
8860-8882	AGACACTGTTGAAAGCTGGCCAC
8861-8883	GACACTGTTGAAAGCTGGCCACA
8862-8884	ACACTGTTGAAAGCTGGCCACAT
8863-8885	CACTGTTGAAAGCTGGCCACATA
8864-8886	ACTGTTGAAAGCTGGCCACATAG
8865-8887	CTGTTGAAAGCTGGCCACATAGC
8866-8888	TGTTGAAAGCTGGCCACATAGCA
8867-8889	GTTGAAAGCTGGCCACATAGCAT
8868-8890	TTGAAAGCTGGCCACATAGCATG
8869-8891	TGAAAGCTGGCCACATAGCATGG
8870-8892	GAAAGCTGGCCACATAGCATGGA
8871-8893	AAAGCTGGCCACATAGCATGGAC
8872-8894	AAGCTGGCCACATAGCATGGACT
8873-8895	AGCTGGCCACATAGCATGGACTT
8874-8896	GCTGGCCACATAGCATGGACTTC
8875-8897	CTGGCCACATAGCATGGACTTCT
8876-8898	TGGCCACATAGCATGGACTTCTT
8877-8899	GGCCACATAGCATGGACTTCTTC
8878-8900	GCCACATAGCATGGACTTCTTCT
8879-8901	CCACATAGCATGGACTTCTTCTG
8880-8902	CACATAGCATGGACTTCTTCTGG
8881-8903	ACATAGCATGGACTTCTTCTGGA
8882-8904	CATAGCATGGACTTCTTCTGGAA
8883-8905	ATAGCATGGACTTCTTCTGGAAA
8884-8906	TAGCATGGACTTCTTCTGGAAAA
8885-8907	AGCATGGACTTCTTCTGGAAAAG
8886-8908	GCATGGACTTCTTCTGGAAAAGG

Position	Sequence
8887-8909	CATGGACTTCTTCTGGAAAAGGG
8888-8910	ATGGACTTCTTCTGGAAAAGGGT
8889-8911	TGGACTTCTTCTGGAAAAGGGTC
8890-8912	GGACTTCTTCTGGAAAAGGGTCA
8891-8913	GACTTCTTCTGGAAAAGGGTCAT
8892-8914	ACTTCTTCTGGAAAAGGGTCATG
8893-8915	CTTCTTCTGGAAAAGGGTCATGG
8894-8916	TTCTTCTGGAAAAGGGTCATGGA
8895-8917	TCTTCTGGAAAAGGGTCATGGAA
8896-8918	CTTCTGGAAAAGGGTCATGGAAA
8897-8919	TTCTGGAAAAGGGTCATGGAAAT
8898-8920	TCTGGAAAAGGGTCATGGAAATG
8899-8921	CTGGAAAAGGGTCATGGAAATGG
8900-8922	TGGAAAAGGGTCATGGAAATGGG
8901-8923	GGAAAAGGGTCATGGAAATGGGC
8902-8924	GAAAAGGGTCATGGAAATGGGCC
8903-8925	AAAAGGGTCATGGAAATGGGCCT
8904-8926	AAAGGGTCATGGAAATGGGCCTG
8905-8927	AAGGGTCATGGAAATGGGCCTGC
8906-8928	AGGGTCATGGAAATGGGCCTGCC
8907-8929	GGGTCATGGAAATGGGCCTGCCC
8908-8930	GGTCATGGAAATGGGCCTGCCCC
8909-8931	GTCATGGAAATGGGCCTGCCCCA
8910-8932	TCATGGAAATGGGCCTGCCCCAG
8911-8933	CATGGAAATGGGCCTGCCCCAGA
8912-8934	ATGGAAATGGGCCTGCCCCAGAT
8913-8935	TGGAAATGGGCCTGCCCCAGATT
8914-8936	GGAAATGGGCCTGCCCCAGATTC
8915-8937	GAAATGGGCCTGCCCCAGATTCT
8916-8938	AAATGGGCCTGCCCCAGATTCTC
8917-8939	AATGGGCCTGCCCCAGATTCTCA
8918-8940	ATGGGCCTGCCCCAGATTCTCAG
8919-8941	TGGGCCTGCCCCAGATTCTCAGA
8920-8942	GGGCCTGCCCCAGATTCTCAGAT
8921-8943	GGCCTGCCCCAGATTCTCAGATG
8922-8944	GCCTGCCCCAGATTCTCAGATGA
8923-8945	CCTGCCCCAGATTCTCAGATGAG
8924-8946	CTGCCCCAGATTCTCAGATGAGG
8925-8947	TGCCCCAGATTCTCAGATGAGGG
8926-8948	GCCCCAGATTCTCAGATGAGGGA
8927-8949	CCCCAGATTCTCAGATGAGGGAA
8928-8950	CCCAGATTCTCAGATGAGGGAAC
8929-8951	CCAGATTCTCAGATGAGGGAAACA
8930-8952	CAGATTCTCAGATGAGGGAACAC
8931-8953	AGATTCTCAGATGAGGGAACACA
8932-8954	GATTCTCAGATGAGGGAACACAT
8933-8955	ATTCTCAGATGAGGGAACACATG
8934-8956	TTCTCAGATGAGGGAACACATGA
8935-8957	TCTCAGATGAGGGAACACATGAA
8936-8958	CTCAGATGAGGGAACACATGAAT
8937-8959	TCAGATGAGGGAACACATGAATC
8938-8960	CAGATGAGGGAACACATGAATCA
8939-8961	AGATGAGGGAACACATGAATCAC
8940-8962	GATGAGGGAACACATGAATCACA
8941-8963	ATGAGGGAACACATGAATCACAA
8942-8964	TGAGGGAACACATGAATCACAAA
8943-8965	GAGGGAACACATGAATCACAAAT
8944-8966	AGGGAACACATGAATCACAAATT
8945-8967	GGGAACACATGAATCACAAATTA
8946-8968	GGAACACATGAATCACAAATTAG
8947-8969	GAACACATGAATCACAAATTAGT
8948-8970	AACACATGAATCACAAATTAGTT
8949-8971	ACACATGAATCACAAATTAGTTT
8950-8972	CACATGAATCACAAATTAGTTTC
8951-8973	ACATGAATCACAAATTAGTTTCA
8952-8974	CATGAATCACAAATTAGTTTCC

Position	Sequence
8953-8975	ATGAATCACAAATTAGTTTCACC
8954-8976	TGAATCACAAATTAGTTTCACCA
8955-8977	GAATCACAAATTAGTTTCACCAT
8956-8978	AATCACAAATTAGTTTCACCATA
8957-8979	ATCACAAATTAGTTTCACCATAG
8958-8980	TCACAAATTAGTTTCACCATAGA
8959-8981	CACAAATTAGTTTCACCATAGAA
8960-8982	ACAAATTAGTTTCACCATAGAAG
8961-8983	CAAATTAGTTTCACCATAGAAGG
8962-8984	AAATTAGTTTCACCATAGAAGGA
8963-8985	AATTAGTTTCACCATAGAAGGAC
8964-8986	ATTAGTTTCACCATAGAAGGACC
8965-8987	TTAGTTTCACCATAGAAGGACCC
8966-8988	TAGTTTCACCATAGAAGGACCCC
8967-8989	AGTTTCACCATAGAAGGACCCCT
8968-8990	GTTTCACCATAGAAGGACCCCTC
8969-8991	TTCACCATAGAAGGACCCCTCA
8970-8992	TCACCATAGAAGGACCCCTCAC
8971-8993	TCACCATAGAAGGACCCCTCACT
8972-8994	CACCATAGAAGGACCCCTCACTT
8973-8995	ACCATAGAAGGACCCCTCACTTC
8974-8996	CCATAGAAGGACCCCTCACTTCC
8975-8997	CATAGAAGGACCCCTCACTTCCT
8976-8998	ATAGAAGGACCCCTCACTTCCTT
8977-8999	TAGAAGGACCCCTCACTTCCTTT
8978-9000	AGAAGGACCCCTCACTTCCTTTG
8979-9001	GAAGGACCCCTCACTTCCTTTGG
8980-9002	AAGGACCCCTCACTTCCTTTGGA
8981-9003	AGGACCCCTCACTTCCTTTGGAC
8982-9004	GGACCCCTCACTTCCTTTGGACT
8983-9005	GACCCCTCACTTCCTTTGGACTG
8984-9006	ACCCCTCACTTCCTTTGGACTGT
8985-9007	CCCTCACTTCCTTTGGACTGTC
8986-9008	CCCTCACTTCCTTTGGACTGTCC
8987-9009	CCTCACTTCCTTTGGACTGTCCA
8988-9010	CTCACTTCCTTTGGACTGTCCAA
8989-9011	TCACTTCCTTTGGACTGTCCAAT
8990-9012	CACTTCCTTTGGACTGTCCAATA
8991-9013	ACTTCCTTTGGACTGTCCAATAA
8992-9014	CTTCCTTTGGACTGTCCAATAAG
8993-9015	TTCCTTTGGACTGTCCAATAAGA
8994-9016	TCCTTTGGACTGTCCAATAAGAT
8995-9017	CCTTTGGACTGTCCAATAAGATC
8996-9018	CTTTGGACTGTCCAATAAGATCA
8997-9019	TTGGACTGTCCAATAAGATCAA
8998-9020	TTGGACTGTCCAATAAGATCAAT
8999-9021	TGGACTGTCCAATAAGATCAATA
9000-9022	GGACTGTCCAATAAGATCAATAG
9001-9023	GACTGTCCAATAAGATCAATAGC
9002-9024	ACTGTCCAATAAGATCAATAGCA
9003-9025	CTGTCCAATAAGATCAATAGCAA
9004-9026	TGTCCAATAAGATCAATAGCAAA
9005-9027	GTCCAATAAGATCAATAGCAAAC
9006-9028	TCCAATAAGATCAATAGCAAACA
9007-9029	CCAATAAGATCAATAGCAAACAC
9008-9030	CAATAAGATCAATAGCAAACACC
9009-9031	AATAAGATCAATAGCAAACACCT
9010-9032	ATAAGATCAATAGCAAACACCTA
9011-9033	TAAGATCAATAGCAAACACCTAA
9012-9034	AAGATCAATAGCAAACACCTAAG
9013-9035	AGATCAATAGCAAACACCTAAGA
9014-9036	GATCAATAGCAAACACCTAAGAG
9015-9037	ATCAATAGCAAACACCTAAGAGT
9016-9038	TCAATAGCAAACACCTAAGAGTA
9017-9039	CAATAGCAAACACCTAAGAGTAA
9018-9040	AATAGCAAACACCTAAGAGTAAA

Position	Sequence
9019-9041	ATAGCAAACACCTAAGAGTAAAC
9020-9042	TAGCAAACACCTAAGAGTAAACC
9021-9043	AGCAAACACCTAAGAGTAAACCA
9022-9044	GCAAACACCTAAGAGTAAACCAA
9023-9045	CAAACACCTAAGAGTAAACCAA
9024-9046	AAACACCTAAGAGTAAACCAAAA
9025-9047	AACACCTAAGAGTAAACCAAAAC
9026-9048	ACACCTAAGAGTAAACCAAAACT
9027-9049	CACCTAAGAGTAAACCAAAACTT
9028-9050	ACCTAAGAGTAAACCAAAACTTG
9029-9051	CCTAAGAGTAAACCAAAACTTGG
9030-9052	CTAAGAGTAAACCAAAACTTGGT
9031-9053	TAAGAGTAAACCAAAACTTGGTT
9032-9054	AAGAGTAAACCAAAACTTGGTTT
9033-9055	AGAGTAAACCAAAACTTGGTTTA
9034-9056	GAGTAAACCAAAACTTGGTTTAT
9035-9057	AGTAAACCAAAACTTGGTTTATG
9036-9058	GTAACCAAAACTTGGTTTATGA
9037-9059	TAAACCAAAACTTGGTTTATGAA
9038-9060	AAACCAAAACTTGGTTTATGAAT
9039-9061	AACCAAAACTTGGTTTATGAATC
9040-9062	ACCAAAACTTGGTTTATGAATCT
9041-9063	CCAAACTTGGTTTATGAATCTG
9042-9064	CAAAACTTGGTTTATGAATCTGG
9043-9065	AAAACCTGGTTTATGAATCTGGC
9044-9066	AAACTGGTTTATGAATCTGGCT
9045-9067	AACTGGTTTATGAATCTGGCTC
9046-9068	ACTTGGTTTATGAATCTGGCTCC
9047-9069	CTTGGTTTATGAATCTGGCTCCC
9048-9070	TGGTTTATGAATCTGGCTCCCT
9049-9071	TGGTTTATGAATCTGGCTCCCTC
9050-9072	GGTTTATGAATCTGGCTCCCTCA
9051-9073	GTTTATGAATCTGGCTCCCTCAA
9052-9074	TTTATGAATCTGGCTCCCTCAAC
9053-9075	TTATGAATCTGGCTCCCTCAACT
9054-9076	TATGAATCTGGCTCCCTCAACTT
9055-9077	ATGAATCTGGCTCCCTCAACTTT
9056-9078	TGAATCTGGCTCCCTCAACTTTT
9057-9079	GAATCTGGCTCCCTCAACTTTTC
9058-9080	AATCTGGCTCCCTCAACTTTTCT
9059-9081	ATCTGGCTCCCTCAACTTTTCTA
9060-9082	TCTGGCTCCCTCAACTTTTCTAA
9061-9083	CTGGCTCCCTCAACTTTTCTAAA
9062-9084	TGGCTCCCTCAACTTTTCTAAAC
9063-9085	GGCTCCCTCAACTTTTCTAAACT
9064-9086	GCTCCCTCAACTTTTCTAAACTT
9065-9087	CTCCCTCAACTTTTCTAAACTTG
9066-9088	TCCCTCAACTTTTCTAAACTTGA
9067-9089	CCCTCAACTTTTCTAAACTTGAA
9068-9090	CCTCAACTTTTCTAAACTTGAAA
9069-9091	CTCAACTTTTCTAAACTTGAAAT
9070-9092	TCAACTTTTCTAAACTTGAAATT
9071-9093	CAACTTTTCTAAACTTGAAATTC
9072-9094	AACTTTTCTAAACTTGAAATTC
9073-9095	ACTTTTCTAAACTTGAAATTC
9074-9096	CTTTTCTAAACTTGAAATTC
9075-9097	TTTCTAAACTTGAAATTC
9076-9098	TTTCTAAACTTGAAATTC
9077-9099	TTCTAAACTTGAAATTC
9078-9100	TCTAAACTTGAAATTC
9079-9101	CTAAACTTGAAATTC
9080-9102	TAAACTTGAAATTC
9081-9103	AAACTTGAAATTC
9082-9104	AACTTGAAATTC
9083-9105	ACTTGAAATTC
9084-9106	CTTGAAATTC

Position	Sequence
9085-9107	TTGAAATTC AATCACAAGTCGAT
9086-9108	TGAAATTC AATCACAAGTCGATT
9087-9109	GAAATTC AATCACAAGTCGATTC
9088-9110	AAATTC AATCACAAGTCGATTCC
9089-9111	AATTC AATCACAAGTCGATTCCC
9090-9112	ATTCAATC AACAAGTCGATTCCCA
9091-9113	TTCAATC AACAAGTCGATTCCAG
9092-9114	TCAATC AACAAGTCGATTCCAGC
9093-9115	CAATC AACAAGTCGATTCCAGCA
9094-9116	AATC AACAAGTCGATTCCAGCAT
9095-9117	ATCACAAGTCGATTCCAGCATG
9096-9118	TCACAAGTCGATTCCAGCATGT
9097-9119	CACAAGTCGATTCCAGCATGTG
9098-9120	ACAAGTCGATTCCAGCATGTGG
9099-9121	CAAGTCGATTCCAGCATGTGGG
9100-9122	AAGTCGATTCCAGCATGTGGGC
9101-9123	AGTCGATTCCAGCATGTGGGCC
9102-9124	GTCGATTCCAGCATGTGGGCCA
9103-9125	TCGATTCCAGCATGTGGGCCAC
9104-9126	CGATTCCAGCATGTGGGCCACA
9105-9127	GATTCCAGCATGTGGGCCACAG
9106-9128	ATCCAGCATGTGGGCCACAGT
9107-9129	TTCCAGCATGTGGGCCACAGTG
9108-9130	TCCAGCATGTGGGCCACAGTGT
9109-9131	CCCAGCATGTGGGCCACAGTGT
9110-9132	CCAGCATGTGGGCCACAGTGTTC
9111-9133	CAGCATGTGGGCCACAGTGTCT
9112-9134	AGCATGTGGGCCACAGTGTCTA
9113-9135	GCATGTGGGCCACAGTGTCTAA
9114-9136	CATGTGGGCCACAGTGTCTAAC
9115-9137	ATGTGGGCCACAGTGTCTAACT
9116-9138	TGTGGGCCACAGTGTCTAACTG
9117-9139	GTGGGCCACAGTGTCTAACTGC
9118-9140	TGGGCCACAGTGTCTAACTGCT
9119-9141	GGGCCACAGTGTCTAACTGCTA
9120-9142	GGCCACAGTGTCTAACTGCTAA
9121-9143	GCCACAGTGTCTAACTGCTAAA
9122-9144	CCACAGTGTCTAACTGCTAAAG
9123-9145	CACAGTGTCTAACTGCTAAAGG
9124-9146	ACAGTGTCTAACTGCTAAAGGC
9125-9147	CAGTGTCTAACTGCTAAAGGCA
9126-9148	AGTGTCTAACTGCTAAAGGCAT
9127-9149	GTGTCTAACTGCTAAAGGCATG
9128-9150	TGTTCTAACTGCTAAAGGCATGG
9129-9151	GTTCTAACTGCTAAAGGCATGGC
9130-9152	TTCTAACTGCTAAAGGCATGGCA
9131-9153	TCTAACTGCTAAAGGCATGGCAC
9132-9154	CTAACTGCTAAAGGCATGGCACT
9133-9155	TAACTGCTAAAGGCATGGCACTG
9134-9156	AACTGCTAAAGGCATGGCACTGT
9135-9157	ACTGCTAAAGGCATGGCACTGTT
9136-9158	CTGCTAAAGGCATGGCACTGTTT
9137-9159	TGCTAAAGGCATGGCACTGTTTG
9138-9160	GCTAAAGGCATGGCACTGTTTGG
9139-9161	CTAAAGGCATGGCACTGTTTGGGA
9140-9162	TAAAGGCATGGCACTGTTTGGGAG
9141-9163	AAAGGCATGGCACTGTTTGGGAGA
9142-9164	AAGGCATGGCACTGTTTGGAGAAA
9143-9165	AGGCATGGCACTGTTTGGAGAAAG
9144-9166	GGCATGGCACTGTTTGGAGAAAGG
9145-9167	GCATGGCACTGTTTGGAGAAAGGG
9146-9168	CATGGCACTGTTTGGAGAAAGGGA
9147-9169	ATGGCACTGTTTGGAGAAAGGGAA
9148-9170	TGGCACTGTTTGGAGAAAGGGAAAG
9149-9171	GGCACTGTTTGGAGAAAGGGAAAGG
9150-9172	GCACTGTTTGGAGAAAGGGAAAGGC

Position	Sequence
9151-9173	CACTGTTTGGAGAAGGGAAGGCA
9152-9174	ACTGTTTGGAGAAGGGAAGGCAG
9153-9175	CTGTTTGGAGAAGGGAAGGCAGA
9154-9176	TGTTTGGAGAAGGGAAGGCAGAG
9155-9177	GTTTGGAGAAGGGAAGGCAGAGT
9156-9178	TTTGGAGAAGGGAAGGCAGAGTT
9157-9179	TTGGAGAAGGGAAGGCAGAGTTT
9158-9180	TGGAGAAGGGAAGGCAGAGTTTA
9159-9181	GGAGAAGGGAAGGCAGAGTTTAC
9160-9182	GAGAAGGGAAGGCAGAGTTTACT
9161-9183	AGAAGGGAAGGCAGAGTTTACTG
9162-9184	GAAGGGAAGGCAGAGTTTACTGG
9163-9185	AAGGGAAGGCAGAGTTTACTGGG
9164-9186	AGGGAAGGCAGAGTTTACTGGGA
9165-9187	GGGAAGGCAGAGTTTACTGGGAG
9166-9188	GGAAGGCAGAGTTTACTGGGAGG
9167-9189	GAAGGCAGAGTTTACTGGGAGGC
9168-9190	AAGGCAGAGTTTACTGGGAGGCA
9169-9191	AGGCAGAGTTTACTGGGAGGCAT
9170-9192	GGCAGAGTTTACTGGGAGGCATG
9171-9193	GCAGAGTTTACTGGGAGGCATGA
9172-9194	CAGAGTTTACTGGGAGGCATGAT
9173-9195	AGAGTTTACTGGGAGGCATGATG
9174-9196	GAGTTTACTGGGAGGCATGATGC
9175-9197	AGTTTACTGGGAGGCATGATGCT
9176-9198	GTTTACTGGGAGGCATGATGCTC
9177-9199	TTTACTGGGAGGCATGATGCTCA
9178-9200	TTACTGGGAGGCATGATGCTCAT
9179-9201	TACTGGGAGGCATGATGCTCATT
9180-9202	ACTGGGAGGCATGATGCTCATT
9181-9203	CTGGGAGGCATGATGCTCATTTA
9182-9204	TGGGAGGCATGATGCTCATTTAA
9183-9205	GGGAGGCATGATGCTCATTTAAA
9184-9206	GGAGGCATGATGCTCATTTAAAT
9185-9207	GAGGCATGATGCTCATTTAAATG
9186-9208	AGGCATGATGCTCATTTAAATGG
9187-9209	GGCATGATGCTCATTTAAATGGA
9188-9210	GCATGATGCTCATTTAAATGGAA
9189-9211	CATGATGCTCATTTAAATGGAAA
9190-9212	ATGATGCTCATTTAAATGGAAAG
9191-9213	TGATGCTCATTTAAATGGAAAGG
9192-9214	GATGCTCATTTAAATGGAAAGGT
9193-9215	ATGCTCATTTAAATGGAAAGGTT
9194-9216	TGCTCATTTAAATGGAAAGGTTA
9195-9217	GCTCATTTAAATGGAAAGGTTAT
9196-9218	CTCATTTAAATGGAAAGGTTATT
9197-9219	TCATTTAAATGGAAAGGTTATTG
9198-9220	CATTTAAATGGAAAGGTTATTGG
9199-9221	ATTTAAATGGAAAGGTTATTGGA
9200-9222	TTTAAATGGAAAGGTTATTGGAA
9201-9223	TTAAATGGAAAGGTTATTGGAAC
9202-9224	TAAATGGAAAGGTTATTGGAAC
9203-9225	AAATGGAAAGGTTATTGGAAC
9204-9226	AATGGAAAGGTTATTGGAAC
9205-9227	ATGGAAAGGTTATTGGAAC
9206-9228	TGGAAAGGTTATTGGAAC
9207-9229	GGAAAGGTTATTGGAAC
9208-9230	GAAAGGTTATTGGAAC
9209-9231	AAAGGTTATTGGAAC
9210-9232	AAGGTTATTGGAAC
9211-9233	AGGTTATTGGAAC
9212-9234	GGTTATTGGAAC
9213-9235	GTTATTGGAAC
9214-9236	TTATTGGAAC
9215-9237	TATTGGAAC
9216-9238	ATTGGAAC

Position	Sequence
9217-9239	TTGGAACCTTGAAAAATTCCTT
9218-9240	TGGAACCTTGAAAAATTCCTT
9219-9241	GGAACCTTGAAAAATTCCTTTT
9220-9242	GAACCTTGAAAAATTCCTTTTC
9221-9243	AACTTGAAAAATTCCTTTTCT
9222-9244	ACTTGAAAAATTCCTTTTCTT
9223-9245	CTTGAAAAATTCCTTTTCTTT
9224-9246	TTGAAAAATTCCTTTTCTTTT
9225-9247	TTGAAAAATTCCTTTTCTTTTC
9226-9248	TGAAAAATTCCTTTTCTTTTCA
9227-9249	GAAAAATTCCTTTTCTTTTCAG
9228-9250	AAAAATTCCTTTTCTTTTCAGC
9229-9251	AAAATTCCTTTTCTTTTCAGCC
9230-9252	AAATTCCTTTTCTTTTCAGCCC
9231-9253	AATTCCTTTTCTTTTCAGCCCA
9232-9254	ATTCTTTTCTTTTCAGCCAG
9233-9255	TTCTTTTCTTTTCAGCCAGC
9234-9256	TCTTTTCTTTTCAGCCAGCC
9235-9257	CTTTTCTTTTCAGCCAGCCA
9236-9258	TCTTTCTTTTCAGCCAGCCAT
9237-9259	CTTTTCTTTTCAGCCAGCCATT
9238-9260	TTTCTTTTCAGCCAGCCATTT
9239-9261	TTTCTTTTCAGCCAGCCATTTG
9240-9262	TTCTTTTCAGCCAGCCATTTGA
9241-9263	TCTTTTCAGCCAGCCATTTGAG
9242-9264	CTTTTCAGCCAGCCATTTGAGA
9243-9265	TTTTCAGCCAGCCATTTGAGAT
9244-9266	TTTCAGCCAGCCATTTGAGATC
9245-9267	TTCAGCCAGCCATTTGAGATCA
9246-9268	TCAGCCAGCCATTTGAGATCAC
9247-9269	CAGCCAGCCATTTGAGATCAG
9248-9270	AGCCAGCCATTTGAGATCACGG
9249-9271	GCCAGCCATTTGAGATCACGGC
9250-9272	CCCAGCCATTTGAGATCACGGCA
9251-9273	CCAGCCATTTGAGATCACGGCAT
9252-9274	CAGCCATTTGAGATCACGGCATC
9253-9275	AGCCATTTGAGATCACGGCATCC
9254-9276	GCCATTTGAGATCACGGCATCCA
9255-9277	CCATTTGAGATCACGGCATCCAC
9256-9278	CATTTGAGATCACGGCATCCACA
9257-9279	ATTTGAGATCACGGCATCCACAA
9258-9280	TTTGAGATCACGGCATCCACAAA
9259-9281	TTGAGATCACGGCATCCACAAAC
9260-9282	TGAGATCACGGCATCCACAAACA
9261-9283	GAGATCACGGCATCCACAAACAA
9262-9284	AGATCACGGCATCCACAAACAAT
9263-9285	GATCACGGCATCCACAAACAATG
9264-9286	ATCACGGCATCCACAAACAATGA
9265-9287	TCACGGCATCCACAAACAATGAA
9266-9288	CACGGCATCCACAAACAATGAAG
9267-9289	ACGGCATCCACAAACAATGAAGG
9268-9290	CGGCATCCACAAACAATGAAGGG
9269-9291	GGCATCCACAAACAATGAAGGGA
9270-9292	GCATCCACAAACAATGAAGGGAA
9271-9293	CATCCACAAACAATGAAGGGAAT
9272-9294	ATCCACAAACAATGAAGGGAATT
9273-9295	TCCACAAACAATGAAGGGAATTT
9274-9296	CCACAAACAATGAAGGGAATTTG
9275-9297	CACAAACAATGAAGGGAATTTGA
9276-9298	ACAAACAATGAAGGGAATTTGAA
9277-9299	CAAACAATGAAGGGAATTTGAAA
9278-9300	AAACAATGAAGGGAATTTGAAAG
9279-9301	AACAATGAAGGGAATTTGAAAGT
9280-9302	ACAATGAAGGGAATTTGAAAGTT
9281-9303	CAATGAAGGGAATTTGAAAGTTC
9282-9304	AATGAAGGGAATTTGAAAGTTCC

Position	Sequence
9283-9305	ATGAAGGGAATTTGAAAGTTCGT
9284-9306	TGAAGGGAATTTGAAAGTTCGTT
9285-9307	GAAGGGAATTTGAAAGTTCGTTT
9286-9308	AAGGGAATTTGAAAGTTCGTTT
9287-9309	AGGGAATTTGAAAGTTCGTTTTC
9288-9310	GGGAATTTGAAAGTTCGTTTTC
9289-9311	GGAAATTTGAAAGTTCGTTTTC
9290-9312	GAATTTGAAAGTTCGTTTTC
9291-9313	AATTTGAAAGTTCGTTTTC
9292-9314	ATTTGAAAGTTCGTTTTC
9293-9315	TTTGAAAGTTCGTTTTC
9294-9316	TTGAAAGTTCGTTTTC
9295-9317	TGAAAGTTCGTTTTC
9296-9318	GAAAGTTCGTTTTC
9297-9319	AAAGTTCGTTTTC
9298-9320	AAGTTCGTTTTC
9299-9321	AGTTCGTTTTC
9300-9322	GTTTCGTTTTC
9301-9323	TTCGTTTTC
9302-9324	TCGTTTTC
9303-9325	CGTTTTC
9304-9326	GTTTTC
9305-9327	TTTTC
9306-9328	TTTC
9307-9329	TTTC
9308-9330	TTC
9309-9331	CC
9310-9332	C
9311-9333	AT
9312-9334	TT
9313-9335	TA
9314-9336	AAG
9315-9337	AGG
9316-9338	GGT
9317-9339	GTT
9318-9340	TTA
9319-9341	TAAC
9320-9342	AAC
9321-9343	AC
9322-9344	CAG
9323-9345	AGG
9324-9346	GGG
9325-9347	GGA
9326-9348	GA
9327-9349	AAG
9328-9350	AG
9329-9351	GAT
9330-9352	AT
9331-9353	TAG
9332-9354	AG
9333-9355	GACT
9334-9356	ACT
9335-9357	CT
9336-9358	TT
9337-9359	CT
9338-9360	CCT
9339-9361	CT
9340-9362	TGA
9341-9363	GA
9342-9364	AAT
9343-9365	ATA
9344-9366	TAA
9345-9367	AA
9346-9368	ACT
9347-9369	CT
9348-9370	TAT

Position	Sequence
9349-9371	ATGCACTGTTTCTGAGTCCCAGT
9350-9372	TGCACTGTTTCTGAGTCCCAGTG
9351-9373	GCACTGTTTCTGAGTCCCAGTGC
9352-9374	CACTGTTTCTGAGTCCCAGTGCC
9353-9375	ACTGTTTCTGAGTCCCAGTGCCC
9354-9376	CTGTTTCTGAGTCCCAGTGCCCA
9355-9377	TGTTTCTGAGTCCCAGTGCCAG
9356-9378	GTTTCTGAGTCCCAGTGCCAGC
9357-9379	TTTCTGAGTCCCAGTGCCAGCA
9358-9380	TTCTGAGTCCCAGTGCCAGCAA
9359-9381	TCTGAGTCCCAGTGCCAGCAAG
9360-9382	CTGAGTCCCAGTGCCAGCAAGC
9361-9383	TGAGTCCCAGTGCCAGCAAGCA
9362-9384	GAGTCCCAGTGCCAGCAAGCAA
9363-9385	AGTCCCAGTGCCAGCAAGCAAG
9364-9386	GTCCCAGTGCCAGCAAGCAAGT
9365-9387	TCCCAGTGCCAGCAAGCAAGTT
9366-9388	CCCAGTGCCAGCAAGCAAGTTG
9367-9389	CCAGTGCCAGCAAGCAAGTTGG
9368-9390	CAGTGCCAGCAAGCAAGTTGGC
9369-9391	AGTGCCAGCAAGCAAGTTGGCA
9370-9392	GTGCCAGCAAGCAAGTTGGCAA
9371-9393	TGCCAGCAAGCAAGTTGGCAAG
9372-9394	GCCAGCAAGCAAGTTGGCAAGT
9373-9395	CCCAGCAAGCAAGTTGGCAAGTA
9374-9396	CCAGCAAGCAAGTTGGCAAGTAA
9375-9397	CAGCAAGCAAGTTGGCAAGTAAG
9376-9398	AGCAAGCAAGTTGGCAAGTAAGT
9377-9399	GCAAGCAAGTTGGCAAGTAAGTG
9378-9400	CAAGCAAGTTGGCAAGTAAGTGC
9379-9401	AAGCAAGTTGGCAAGTAAGTGCT
9380-9402	AGCAAGTTGGCAAGTAAGTGCTA
9381-9403	GCAAGTTGGCAAGTAAGTGCTAG
9382-9404	CAAGTTGGCAAGTAAGTGCTAGG
9383-9405	AAGTTGGCAAGTAAGTGCTAGGT
9384-9406	AGTTGGCAAGTAAGTGCTAGGTT
9385-9407	GTTGGCAAGTAAGTGCTAGGTTT
9386-9408	TTGGCAAGTAAGTGCTAGGTTCA
9387-9409	TGGCAAGTAAGTGCTAGGTTCAA
9388-9410	GGCAAGTAAGTGCTAGGTTCAAT
9389-9411	GCAAGTAAGTGCTAGGTTCAATC
9390-9412	CAAGTAAGTGCTAGGTTCAATCA
9391-9413	AAGTAAGTGCTAGGTTCAATCAG
9392-9414	AGTAAGTGCTAGGTTCAATCAGT
9393-9415	GTAAGTGCTAGGTTCAATCAGTA
9394-9416	TAAGTGCTAGGTTCAATCAGTAT
9395-9417	AAGTGCTAGGTTCAATCAGTATA
9396-9418	AGTGCTAGGTTCAATCAGTATAA
9397-9419	GTGCTAGGTTCAATCAGTATAAG
9398-9420	TGCTAGGTTCAATCAGTATAAGT
9399-9421	GCTAGGTTCAATCAGTATAAGTA
9400-9422	CTAGGTTCAATCAGTATAAGTAC
9401-9423	TAGGTTCAATCAGTATAAGTACA
9402-9424	AGGTTCAATCAGTATAAGTACAA
9403-9425	GGTTCAATCAGTATAAGTACAAC
9404-9426	GTTCAATCAGTATAAGTACAACC
9405-9427	TTCAATCAGTATAAGTACAACCA
9406-9428	TCAATCAGTATAAGTACAACCAA
9407-9429	CAATCAGTATAAGTACAACCAAA
9408-9430	AATCAGTATAAGTACAACCAAAA
9409-9431	ATCAGTATAAGTACAACCAAAAT
9410-9432	TCAGTATAAGTACAACCAAAATT
9411-9433	CAGTATAAGTACAACCAAAATTT
9412-9434	AGTATAAGTACAACCAAAATTTT
9413-9435	GTATAAGTACAACCAAAATTTCT
9414-9436	TATAAGTACAACCAAAATTTCTC

Position	Sequence
9415-9437	ATAAGTACAACCAAATTTCTCT
9416-9438	TAAGTACAACCAAATTTCTCTG
9417-9439	AAGTACAACCAAATTTCTCTGC
9418-9440	AGTACAACCAAATTTCTCTGCT
9419-9441	GTACAACCAAATTTCTCTGCTG
9420-9442	TACAACCAAATTTCTCTGCTGG
9421-9443	ACAACCAAATTTCTCTGCTGGA
9422-9444	CAACCAAATTTCTCTGCTGGAA
9423-9445	AACCAAATTTCTCTGCTGGAAA
9424-9446	ACCAAATTTCTCTGCTGGAAAC
9425-9447	CCAAATTTCTCTGCTGGAAACA
9426-9448	CAAAATTTCTCTGCTGGAAACAA
9427-9449	AAAATTTCTCTGCTGGAAACAAC
9428-9450	AAATTTCTCTGCTGGAAACAACG
9429-9451	AATTTCTCTGCTGGAAACAACGA
9430-9452	ATTTCTCTGCTGGAAACAACGAG
9431-9453	TTTCTCTGCTGGAAACAACGAGA
9432-9454	TTCTCTGCTGGAAACAACGAGAA
9433-9455	TCTCTGCTGGAAACAACGAGAAC
9434-9456	CTCTGCTGGAAACAACGAGAACA
9435-9457	TCTGCTGGAAACAACGAGAACAT
9436-9458	CTGCTGGAAACAACGAGAACATT
9437-9459	TGCTGGAAACAACGAGAACATTA
9438-9460	GCTGGAAACAACGAGAACATTAT
9439-9461	CTGGAAACAACGAGAACATTATG
9440-9462	TGGAAACAACGAGAACATTATGG
9441-9463	GGAAACAACGAGAACATTATGGA
9442-9464	GAAACAACGAGAACATTATGGAG
9443-9465	AAACAACGAGAACATTATGGAGG
9444-9466	AACAACGAGAACATTATGGAGGC
9445-9467	ACAACGAGAACATTATGGAGGCC
9446-9468	CAACGAGAACATTATGGAGGCCC
9447-9469	AACGAGAACATTATGGAGGCCCA
9448-9470	ACGAGAACATTATGGAGGCCCAT
9449-9471	CGAGAACATTATGGAGGCCCATG
9450-9472	GAGAACATTATGGAGGCCCATGT
9451-9473	AGAACATTATGGAGGCCCATGTA
9452-9474	GAACATTATGGAGGCCCATGTAG
9453-9475	AACATTATGGAGGCCCATGTAGG
9454-9476	ACATTATGGAGGCCCATGTAGGA
9455-9477	CATTATGGAGGCCCATGTAGGAA
9456-9478	ATTATGGAGGCCCATGTAGGAAT
9457-9479	TTATGGAGGCCCATGTAGGAATA
9458-9480	TATGGAGGCCCATGTAGGAATAA
9459-9481	ATGGAGGCCCATGTAGGAATAAA
9460-9482	TGGAGGCCCATGTAGGAATAAAT
9461-9483	GGAGGCCCATGTAGGAATAAATG
9462-9484	GAGGCCCATGTAGGAATAAATGG
9463-9485	AGGCCCATGTAGGAATAAATGGA
9464-9486	GGCCCATGTAGGAATAAATGGAG
9465-9487	GCCCATGTAGGAATAAATGGAGA
9466-9488	CCCATGTAGGAATAAATGGAGAA
9467-9489	CCATGTAGGAATAAATGGAGAAG
9468-9490	CATGTAGGAATAAATGGAGAAGC
9469-9491	ATGTAGGAATAAATGGAGAAGCA
9470-9492	TGTAGGAATAAATGGAGAAGCAA
9471-9493	GTAGGAATAAATGGAGAAGCAAA
9472-9494	TAGGAATAAATGGAGAAGCAAAT
9473-9495	AGGAATAAATGGAGAAGCAAATC
9474-9496	GCAATAAATGGAGAAGCAAATCT
9475-9497	GAATAAATGGAGAAGCAAATCTG
9476-9498	AATAAATGGAGAAGCAAATCTGG
9477-9499	ATAAATGGAGAAGCAAATCTGGA
9478-9500	TAAATGGAGAAGCAAATCTGGAT
9479-9501	AAATGGAGAAGCAAATCTGGATT
9480-9502	AATGGAGAAGCAAATCTGGATTT

Position	Sequence
9481-9503	ATGGAGAAGCAAATCTGGATTTC
9482-9504	TGAGAAGCAAATCTGGATTCT
9483-9505	GGAGAAGCAAATCTGGATTCTT
9484-9506	GAGAAGCAAATCTGGATTCTTA
9485-9507	AGAAGCAAATCTGGATTCTTAA
9486-9508	GAAGCAAATCTGGATTCTTAAA
9487-9509	AAGCAAATCTGGATTCTTAAAC
9488-9510	AGCAAATCTGGATTCTTAAACA
9489-9511	GCAAATCTGGATTCTTAAACAT
9490-9512	CAAATCTGGATTCTTAAACATT
9491-9513	AAATCTGGATTCTTAAACATTC
9492-9514	AATCTGGATTCTTAAACATTCC
9493-9515	ATCTGGATTCTTAAACATTCCCT
9494-9516	TCTGGATTCTTAAACATTCCCTT
9495-9517	CTGGATTCTTAAACATTCCCTTT
9496-9518	TGGATTCTTAAACATTCCCTTTA
9497-9519	GGATTCTTAAACATTCCCTTTAA
9498-9520	GATTCTTAAACATTCCCTTTAAC
9499-9521	ATTCTTAAACATTCCCTTTAACA
9500-9522	TTCTTAAACATTCCCTTTAACAA
9501-9523	TTCTTAAACATTCCCTTTAACAA
9502-9524	TCTTAAACATTCCCTTTAACAA
9503-9525	CTTAAACATTCCCTTTAACAA
9504-9526	TTAAACATTCCCTTTAACAA
9505-9527	TAAACATTCCCTTTAACAA
9506-9528	AAACATTCCCTTTAACAA
9507-9529	AACATTCCCTTTAACAA
9508-9530	ACATTCCCTTTAACAA
9509-9531	CATTCCCTTTAACAA
9510-9532	ATCCTTTAACAA
9511-9533	TTCTTTAACAA
9512-9534	TCCTTTAACAA
9513-9535	CCTTTAACAA
9514-9536	CTTTAACAA
9515-9537	TTAACAA
9516-9538	TTAACAA
9517-9539	TAACAA
9518-9540	AACAAT
9519-9541	ACAAT
9520-9542	CAAT
9521-9543	AAT
9522-9544	AT
9523-9545	TT
9524-9546	T
9525-9547	C
9526-9548	CT
9527-9549	TG
9528-9550	GAA
9529-9551	AAAT
9530-9552	AATG
9531-9553	ATGCG
9532-9554	TGCG
9533-9555	GCG
9534-9556	CG
9535-9557	GT
9536-9558	T
9537-9559	CT
9538-9560	TAC
9539-9561	AC
9540-9562	C
9541-9563	CT
9542-9564	TT
9543-9565	TAC
9544-9566	AC
9545-9567	CAC
9546-9568	ACA

Position	Sequence
9547-9569	CAATAATCACAACCTCTCCACTG
9548-9570	AATAATCACAACCTCTCCACTGA
9549-9571	ATAATCACAACCTCTCCACTGAA
9550-9572	TAATCACAACCTCTCCACTGAAA
9551-9573	AATCACAACCTCTCCACTGAAAG
9552-9574	ATCACAACCTCTCCACTGAAAGA
9553-9575	TCACAACCTCTCCACTGAAAGAT
9554-9576	CACAACCTCTCCACTGAAAGATT
9555-9577	ACAACCTCTCCACTGAAAGATTT
9556-9578	CAACTCTCTCCACTGAAAGATTTC
9557-9579	AACTCTCTCCACTGAAAGATTCT
9558-9580	ACTCTCTCCACTGAAAGATTCTC
9559-9581	CTCTCTCCACTGAAAGATTCTCT
9560-9582	TCCTCTCCACTGAAAGATTCTCTC
9561-9583	CCTCTCTCCACTGAAAGATTCTCT
9562-9584	CTCCTCTCCACTGAAAGATTCTCTA
9563-9585	TCCCTCTCCACTGAAAGATTCTCTAT
9564-9586	CCCTCTCTCCACTGAAAGATTCTCTATG
9565-9587	CACTCTCTCCACTGAAAGATTCTCTATGG
9566-9588	ACTCTCTCTCCACTGAAAGATTCTCTATGGG
9567-9589	CTGAAAGATTCTCTCTATGGGA
9568-9590	TGAAAGATTCTCTCTATGGGAA
9569-9591	GAAAGATTCTCTCTATGGGAAA
9570-9592	AAAGATTCTCTCTATGGGAAAA
9571-9593	AAGATTCTCTCTATGGGAAAAA
9572-9594	AGATTCTCTCTATGGGAAAAAA
9573-9595	GATTCTCTCTATGGGAAAAAAC
9574-9596	ATTTCTCTCTATGGGAAAAACA
9575-9597	TTTCTCTCTATGGGAAAAACAG
9576-9598	TTCTCTCTATGGGAAAAACAGG
9577-9599	TCTCTCTATGGGAAAAACAGGC
9578-9600	CTCTCTATGGGAAAAACAGGCT
9579-9601	TCTCTATGGGAAAAACAGGCTT
9580-9602	CTCTATGGGAAAAACAGGCTTG
9581-9603	TCTATGGGAAAAACAGGCTTGA
9582-9604	CTATGGGAAAAACAGGCTTGAA
9583-9605	TATGGGAAAAACAGGCTTGAAG
9584-9606	ATGGGAAAAACAGGCTTGAAGG
9585-9607	TGGGAAAAACAGGCTTGAAGGA
9586-9608	GGGAAAAACAGGCTTGAAGGAA
9587-9609	GGAAAAACAGGCTTGAAGGAAT
9588-9610	GAAAAACAGGCTTGAAGGAATT
9589-9611	AAAAACAGGCTTGAAGGAATTC
9590-9612	AAAAACAGGCTTGAAGGAATTCT
9591-9613	AAAACAGGCTTGAAGGAATTCTT
9592-9614	AAACAGGCTTGAAGGAATTCTTG
9593-9615	AACAGGCTTGAAGGAATTCTTGA
9594-9616	ACAGGCTTGAAGGAATTCTTGAA
9595-9617	CAGGCTTGAAGGAATTCTTGAAA
9596-9618	AGGCTTGAAGGAATTCTTGAAAA
9597-9619	GGCTTGAAGGAATTCTTGAAAAC
9598-9620	GCTTGAAGGAATTCTTGAAAACG
9599-9621	CTTGAAGGAATTCTTGAAAACGA
9600-9622	TTGAAGGAATTCTTGAAAACGAC
9601-9623	TGAAGGAATTCTTGAAAACGACA
9602-9624	GAAGGAATTCTTGAAAACGACAA
9603-9625	AAGGAATTCTTGAAAACGACAAA
9604-9626	AGGAATTCTTGAAAACGACAAAAG
9605-9627	GGAATTCTTGAAAACGACAAAAGC
9606-9628	GAATTCTTGAAAACGACAAAAGCA
9607-9629	AATTCTTGAAAACGACAAAAGCAA
9608-9630	ATTCTTGAAAACGACAAAAGCAAT
9609-9631	TTCTTGAAAACGACAAAAGCAATC
9610-9632	TCTTGAAAACGACAAAAGCAATCA
9611-9633	CTTGAAAACGACAAAAGCAATCAT
9612-9634	TTGAAAACGACAAAAGCAATCATT

Position	Sequence
9613-9635	TGAAAACGCAAAGCAATCATT
9614-9636	GAAAACGCAAAGCAATCATTG
9615-9637	AAAACGCAAAGCAATCATTGA
9616-9638	AAACGCAAAGCAATCATTGAT
9617-9639	AACGCAAAGCAATCATTGATT
9618-9640	ACGCAAAGCAATCATTGATTT
9619-9641	CGCAAAGCAATCATTGATTTA
9620-9642	GACAAAGCAATCATTGATTAA
9621-9643	ACAAAGCAATCATTGATTTAAG
9622-9644	CAAAGCAATCATTGATTTAAGT
9623-9645	AAAGCAATCATTGATTTAAGTG
9624-9646	AAGCAATCATTGATTTAAGTGT
9625-9647	AGCAATCATTGATTTAAGTGTA
9626-9648	GCAATCATTGATTTAAGTGTA
9627-9649	CAATCATTGATTTAAGTGTA
9628-9650	AATCATTGATTTAAGTGTA
9629-9651	ATCATTGATTTAAGTGTA
9630-9652	TCATTGATTTAAGTGTA
9631-9653	CATTGATTTAAGTGTA
9632-9654	ATTTGATTTAAGTGTA
9633-9655	TTTGATTTAAGTGTA
9634-9656	TTGATTTAAGTGTA
9635-9657	TGATTTAAGTGTA
9636-9658	GATTTAAGTGTA
9637-9659	ATTTAAGTGTA
9638-9660	TTTAAGTGTA
9639-9661	TTAAGTGTA
9640-9662	TAAGTGTA
9641-9663	AAGTGTA
9642-9664	AGTGTA
9643-9665	GTGTA
9644-9666	TGTA
9645-9667	GTA
9646-9668	TAA
9647-9669	AAA
9648-9670	AAAG
9649-9671	AAGCT
9650-9672	AGCT
9651-9673	GCT
9652-9674	CT
9653-9675	TC
9654-9676	CAG
9655-9677	AGT
9656-9678	GT
9657-9679	T
9658-9680	ATA
9659-9681	TA
9660-9682	AAG
9661-9683	AG
9662-9684	GAA
9663-9685	AAAA
9664-9686	AAAA
9665-9687	AAAA
9666-9688	AAAA
9667-9689	AAAA
9668-9690	AAAA
9669-9691	AAAA
9670-9692	AAAA
9671-9693	AAAA
9672-9694	AAAA
9673-9695	AAAA
9674-9696	AAAA
9675-9697	AAAA
9676-9698	AAAA
9677-9699	AAAA
9678-9700	AAAA

Position	Sequence
9679-9701	ATTCCATCACAAATCCTTTGGCT
9680-9702	TTCCATCACAAATCCTTTGGCTG
9681-9703	TCCATCACAAATCCTTTGGCTGT
9682-9704	CCATCACAAATCCTTTGGCTGTG
9683-9705	CATCACAAATCCTTTGGCTGTGC
9684-9706	ATCACAAATCCTTTGGCTGTGCT
9685-9707	TCACAAATCCTTTGGCTGTGCTT
9686-9708	CACAAATCCTTTGGCTGTGCTTT
9687-9709	ACAAATCCTTTGGCTGTGCTTTG
9688-9710	CAAATCCTTTGGCTGTGCTTTGT
9689-9711	AAATCCTTTGGCTGTGCTTTGTG
9690-9712	AATCCTTTGGCTGTGCTTTGTGA
9691-9713	ATCCTTTGGCTGTGCTTTGTGAG
9692-9714	TCCTTTGGCTGTGCTTTGTGAGT
9693-9715	CCTTTGGCTGTGCTTTGTGAGTT
9694-9716	CTTTGGCTGTGCTTTGTGAGTTT
9695-9717	TTGGCTGTGCTTTGTGAGTTTA
9696-9718	TTGGCTGTGCTTTGTGAGTTTAT
9697-9719	TGGCTGTGCTTTGTGAGTTTATC
9698-9720	GGCTGTGCTTTGTGAGTTTATCA
9699-9721	GCTGTGCTTTGTGAGTTTATCAG
9700-9722	CTGTGCTTTGTGAGTTTATCAGT
9701-9723	TGTGCTTTGTGAGTTTATCAGTC
9702-9724	GTGCTTTGTGAGTTTATCAGTCA
9703-9725	TGCTTTGTGAGTTTATCAGTCAG
9704-9726	GCTTTGTGAGTTTATCAGTCAGA
9705-9727	CTTTGTGAGTTTATCAGTCAGAG
9706-9728	TTGTGAGTTTATCAGTCAGAGC
9707-9729	TTGTGAGTTTATCAGTCAGAGCA
9708-9730	TGTGAGTTTATCAGTCAGAGCAT
9709-9731	GTGAGTTTATCAGTCAGAGCATC
9710-9732	TGAGTTTATCAGTCAGAGCATCA
9711-9733	GAGTTTATCAGTCAGAGCATCAA
9712-9734	AGTTTATCAGTCAGAGCATCAAA
9713-9735	GTTTATCAGTCAGAGCATCAAAT
9714-9736	TTTATCAGTCAGAGCATCAAATC
9715-9737	TTATCAGTCAGAGCATCAAATCC
9716-9738	TATCAGTCAGAGCATCAAATCCT
9717-9739	ATCAGTCAGAGCATCAAATCCTT
9718-9740	TCAGTCAGAGCATCAAATCCTTT
9719-9741	CAGTCAGAGCATCAAATCCTTTG
9720-9742	AGTCAGAGCATCAAATCCTTTGA
9721-9743	GTCAGAGCATCAAATCCTTTGAC
9722-9744	TCAGAGCATCAAATCCTTTGACA
9723-9745	CAGAGCATCAAATCCTTTGACAG
9724-9746	AGAGCATCAAATCCTTTGACAGG
9725-9747	GAGCATCAAATCCTTTGACAGGC
9726-9748	AGCATCAAATCCTTTGACAGGCA
9727-9749	GCATCAAATCCTTTGACAGGCAT
9728-9750	CATCAAATCCTTTGACAGGCATT
9729-9751	ATCAAATCCTTTGACAGGCATTT
9730-9752	TCAAATCCTTTGACAGGCATTTT
9731-9753	CAAATCCTTTGACAGGCATTTTG
9732-9754	AAATCCTTTGACAGGCATTTTGA
9733-9755	AATCCTTTGACAGGCATTTTGAA
9734-9756	ATCCTTTGACAGGCATTTTGAAA
9735-9757	TCCTTTGACAGGCATTTTGAAAA
9736-9758	CCTTTGACAGGCATTTTGAAAAA
9737-9759	CTTTGACAGGCATTTTGAAAAAA
9738-9760	TTTGACAGGCATTTTGAAAAAAA
9739-9761	TTGACAGGCATTTTGAAAAAAAC
9740-9762	TGACAGGCATTTTGAAAAAAACA
9741-9763	GACAGGCATTTTGAAAAAAACAG
9742-9764	ACAGGCATTTTGAAAAAAACAGA
9743-9765	CAGGCATTTTGAAAAAAACAGAA
9744-9766	AGGCATTTTGAAAAAAACAGAAA

Position	Sequence
9745-9767	GGCATTGAAAAAACAGAAAC
9746-9768	GCATTGAAAAAACAGAAACA
9747-9769	CATTGAAAAAACAGAAACAA
9748-9770	ATTTGAAAAAACAGAAACAAT
9749-9771	TTTGAAAAAACAGAAACAATG
9750-9772	TTGAAAAAACAGAAACAATGC
9751-9773	TTGAAAAAACAGAAACAATGCA
9752-9774	TGAAAAAACAGAAACAATGCAT
9753-9775	GAAAAAACAGAAACAATGCATT
9754-9776	AAAAAACAGAAACAATGCATTA
9755-9777	AAAAACAGAAACAATGCATTAG
9756-9778	AAAAACAGAAACAATGCATTAGA
9757-9779	AAACAGAAACAATGCATTAGAT
9758-9780	AAACAGAAACAATGCATTAGATT
9759-9781	AACAGAAACAATGCATTAGATTT
9760-9782	ACAGAAACAATGCATTAGATTTT
9761-9783	CAGAAACAATGCATTAGATTTTG
9762-9784	AGAAACAATGCATTAGATTTTGT
9763-9785	GAAACAATGCATTAGATTTTGTC
9764-9786	AAACAATGCATTAGATTTTGTCAC
9765-9787	AACAATGCATTAGATTTTGTCACC
9766-9788	ACAATGCATTAGATTTTGTCACCA
9767-9789	CAATGCATTAGATTTTGTCACCAA
9768-9790	AATGCATTAGATTTTGTCACCAA
9769-9791	ATGCATTAGATTTTGTCACCAA
9770-9792	TGCATTAGATTTTGTCACCAAAT
9771-9793	GCATTAGATTTTGTCACCAAATC
9772-9794	CATTAGATTTTGTCACCAAATCC
9773-9795	ATTAGATTTTGTCACCAAATCCT
9774-9796	TTAGATTTTGTCACCAAATCCTA
9775-9797	TAGATTTTGTCACCAAATCCTAT
9776-9798	AGATTTTGTCACCAAATCCTATA
9777-9799	GATTTTGTCACCAAATCCTATAA
9778-9800	ATTTTGTCACCAAATCCTATAAAT
9779-9801	TTTTTGTCACCAAATCCTATAATG
9780-9802	TTTGTCACCAAATCCTATAATGA
9781-9803	TTGTCACCAAATCCTATAATGAA
9782-9804	TGTCACCAAATCCTATAATGAAA
9783-9805	GTCACCAAATCCTATAATGAAAC
9784-9806	TCACCAAATCCTATAATGAAACA
9785-9807	CACCAAATCCTATAATGAAACAA
9786-9808	ACCAAATCCTATAATGAAACAAA
9787-9809	CCAAATCCTATAATGAAACAAAA
9788-9810	CAAATCCTATAATGAAACAAAAA
9789-9811	AAATCCTATAATGAAACAAAAAT
9790-9812	AATCCTATAATGAAACAAAAATT
9791-9813	ATCCTATAATGAAACAAAAATTA
9792-9814	TCCTATAATGAAACAAAAATTAA
9793-9815	CCTATAATGAAACAAAAATTAAAG
9794-9816	CTATAATGAAACAAAAATTAAAGT
9795-9817	TATAATGAAACAAAAATTAAAGTT
9796-9818	ATAATGAAACAAAAATTAAAGTTT
9797-9819	TAATGAAACAAAAATTAAAGTTTG
9798-9820	AATGAAACAAAAATTAAAGTTTGA
9799-9821	ATGAAACAAAAATTAAAGTTTGAT
9800-9822	TGAAACAAAAATTAAAGTTTGATA
9801-9823	GAAACAAAAATTAAAGTTTGATAA
9802-9824	AAACAAAAATTAAAGTTTGATAAG
9803-9825	AACAAAAATTAAAGTTTGATAAGT
9804-9826	ACAAAAATTAAAGTTTGATAAGTA
9805-9827	CAAAAAATTAAAGTTTGATAAGTAC
9806-9828	AAAAATTAAAGTTTGATAAGTACA
9807-9829	AAAATTAAAGTTTGATAAGTACAA
9808-9830	AAATTAAAGTTTGATAAGTACAAA
9809-9831	AATTAAAGTTTGATAAGTACAAAG
9810-9832	ATTAAGTTTGATAAGTACAAAGC

Position	Sequence
9811-9833	TTAAGTTGATAAGTACAAAGCT
9812-9834	TAAGTTGATAAGTACAAAGCTG
9813-9835	AAGTTTGTATAAGTACAAAGCTGA
9814-9836	AGTTTGTATAAGTACAAAGCTGAA
9815-9837	GTTTGTATAAGTACAAAGCTGAAA
9816-9838	TTGTATAAGTACAAAGCTGAAAA
9817-9839	TTGTATAAGTACAAAGCTGAAAAA
9818-9840	TGTATAAGTACAAAGCTGAAAAAT
9819-9841	GATAAGTACAAAGCTGAAAAATC
9820-9842	ATAAGTACAAAGCTGAAAAATCT
9821-9843	TAAGTACAAAGCTGAAAAATCTC
9822-9844	AAGTACAAAGCTGAAAAATCTCA
9823-9845	AGTACAAAGCTGAAAAATCTCAC
9824-9846	GTACAAAGCTGAAAAATCTCACG
9825-9847	TACAAAGCTGAAAAATCTCACGA
9826-9848	ACAAAGCTGAAAAATCTCACGAC
9827-9849	CAAAGCTGAAAAATCTCACGACG
9828-9850	AAAGCTGAAAAATCTCACGACGA
9829-9851	AAGCTGAAAAATCTCACGACGAG
9830-9852	AGCTGAAAAATCTCACGACGAGC
9831-9853	GCTGAAAAATCTCACGACGAGCT
9832-9854	CTGAAAAATCTCACGACGAGCTC
9833-9855	TGAAAAATCTCACGACGAGCTCC
9834-9856	GAAAAATCTCACGACGAGCTCCC
9835-9857	AAAAATCTCACGACGAGCTCCCC
9836-9858	AAAATCTCACGACGAGCTCCCCA
9837-9859	AAATCTCACGACGAGCTCCCCAG
9838-9860	AATCTCACGACGAGCTCCCCAGG
9839-9861	ATCTCACGACGAGCTCCCCAGGA
9840-9862	TCTCACGACGAGCTCCCCAGGAC
9841-9863	CTCACGACGAGCTCCCCAGGACC
9842-9864	TCACGACGAGCTCCCCAGGACCT
9843-9865	CACGACGAGCTCCCCAGGACCTT
9844-9866	ACGACGAGCTCCCCAGGACCTTT
9845-9867	CGACGAGCTCCCCAGGACCTTTC
9846-9868	GACGAGCTCCCCAGGACCTTTCA
9847-9869	ACGAGCTCCCCAGGACCTTTCAA
9848-9870	CGAGCTCCCCAGGACCTTTCAA
9849-9871	GAGCTCCCCAGGACCTTTCAAAT
9850-9872	AGCTCCCCAGGACCTTTCAAATT
9851-9873	GCTCCCCAGGACCTTTCAAATTC
9852-9874	CTCCCCAGGACCTTTCAAATTC
9853-9875	TCCCCAGGACCTTTCAAATTCCT
9854-9876	CCCAGGACCTTTCAAATTCCTG
9855-9877	CCAGGACCTTTCAAATTCCTGG
9856-9878	CCAGGACCTTTCAAATTCCTGGA
9857-9879	CAGGACCTTTCAAATTCCTGGAT
9858-9880	AGGACCTTTCAAATTCCTGGATA
9859-9881	GGACCTTTCAAATTCCTGGATAC
9860-9882	GACCTTTCAAATTCCTGGATACA
9861-9883	ACCTTTCAAATTCCTGGATACAC
9862-9884	CCTTTCAAATTCCTGGATACACT
9863-9885	CTTTCAAATTCCTGGATACACTG
9864-9886	TTCAAATTCCTGGATACACTGT
9865-9887	TCAAATTCCTGGATACACTGTT
9866-9888	TCAAATTCCTGGATACACTGTTC
9867-9889	CAAATTCCTGGATACACTGTTC
9868-9890	AAATTCCTGGATACACTGTTC
9869-9891	AATTCCTGGATACACTGTTCAG
9870-9892	ATTCCTGGATACACTGTTCAGT
9871-9893	TTTCCTGGATACACTGTTCAGTT
9872-9894	TTCCTGGATACACTGTTCAGTTG
9873-9895	CCTGGATACACTGTTCAGTTGT
9874-9896	CTGGATACACTGTTCAGTTGTC
9875-9897	TGGATACACTGTTCAGTTGTCA
9876-9898	GGATACACTGTTCAGTTGTCAA

Position	Sequence
9877-9899	GATACACTGTCCAGTTGTCAAT
9878-9900	ATACACTGTCCAGTTGTCAATG
9879-9901	TACACTGTCCAGTTGTCAATGT
9880-9902	ACACTGTCCAGTTGTCAATGTT
9881-9903	CACTGTCCAGTTGTCAATGTTG
9882-9904	ACTGTCCAGTTGTCAATGTTGA
9883-9905	CTGTCCAGTTGTCAATGTTGAA
9884-9906	TGTCCAGTTGTCAATGTTGAAG
9885-9907	GTTCCAGTTGTCAATGTTGAAGT
9886-9908	TTCCAGTTGTCAATGTTGAAGTG
9887-9909	TCCAGTTGTCAATGTTGAAGTGT
9888-9910	CCAGTTGTCAATGTTGAAGTGTC
9889-9911	CAGTTGTCAATGTTGAAGTGCT
9890-9912	AGTTGTCAATGTTGAAGTGCTC
9891-9913	GTTGTCAATGTTGAAGTGCTCC
9892-9914	TTGTCAATGTTGAAGTGCTCCA
9893-9915	TGTCAATGTTGAAGTGCTCCAT
9894-9916	GTCATGTTGAAGTGCTCCATT
9895-9917	TCAATGTTGAAGTGCTCCATTC
9896-9918	CAATGTTGAAGTGCTCCATTCA
9897-9919	AATGTTGAAGTGCTCCATTAC
9898-9920	ATGTTGAAGTGCTCCATTACCC
9899-9921	TGTTGAAGTGCTCCATTACCCA
9900-9922	GTTGAAGTGCTCCATTACCCAT
9901-9923	TTGAAGTGCTCCATTACCATA
9902-9924	TGAAGTGCTCCATTACCATAG
9903-9925	GAAGTGCTCCATTACCATAGA
9904-9926	AAGTGCTCCATTACCATAGAG
9905-9927	AGTGCTCCATTACCATAGAGA
9906-9928	GTGCTCCATTACCATAGAGAT
9907-9929	TGCTCCATTACCATAGAGATG
9908-9930	GTCTCCATTACCATAGAGATGT
9909-9931	TCTCCATTACCATAGAGATGTC
9910-9932	CTCCATTACCATAGAGATGTCG
9911-9933	TCCATTACCATAGAGATGTCGG
9912-9934	CCATTACCATAGAGATGTCGGC
9913-9935	CATTACCATAGAGATGTCGGCA
9914-9936	ATTACCATAGAGATGTCGGCAT
9915-9937	TTCACCATAGAGATGTCGGCATT
9916-9938	TCACCATAGAGATGTCGGCATT
9917-9939	CACCATAGAGATGTCGGCATTCG
9918-9940	ACCATAGAGATGTCGGCATTCGG
9919-9941	CCATAGAGATGTCGGCATTCGGC
9920-9942	CATAGAGATGTCGGCATTCGGCT
9921-9943	ATAGAGATGTCGGCATTCGGCTA
9922-9944	TAGAGATGTCGGCATTCGGCTAT
9923-9945	AGAGATGTCGGCATTCGGCTATG
9924-9946	GAGATGTCGGCATTCGGCTATGT
9925-9947	AGATGTCGGCATTCGGCTATGTG
9926-9948	GATGTCGGCATTCGGCTATGTGT
9927-9949	ATGTCGGCATTCGGCTATGTGTT
9928-9950	TGTCGGCATTCGGCTATGTGTTT
9929-9951	GTCGGCATTCGGCTATGTGTTCC
9930-9952	TCCGGCATTCGGCTATGTGTTCCC
9931-9953	CGGCATTCGGCTATGTGTTCCCA
9932-9954	GGCATTCGGCTATGTGTTCCCAA
9933-9955	GCATTCGGCTATGTGTTCCCAA
9934-9956	CATTCGGCTATGTGTTCCCAAAA
9935-9957	ATTCGGCTATGTGTTCCCAAAAG
9936-9958	TTCGGCTATGTGTTCCCAAAAGC
9937-9959	TCGGCTATGTGTTCCCAAAAGCA
9938-9960	CGGCTATGTGTTCCCAAAAGCAG
9939-9961	GGCTATGTGTTCCCAAAAGCAGT
9940-9962	GCTATGTGTTCCCAAAAGCAGTC
9941-9963	CTATGTGTTCCCAAAAGCAGTCA
9942-9964	TATGTGTTCCCAAAAGCAGTCAG

Position	Sequence
9943-9965	ATGTGTTCCCAAAGCAGTCAGC
9944-9966	TGTGTTCCCAAAGCAGTCAGCA
9945-9967	GTGTTCCCAAAGCAGTCAGCAT
9946-9968	TGTTCCAAAGCAGTCAGCATG
9947-9969	GTTCCCAAAGCAGTCAGCATGC
9948-9970	TTCCAAAGCAGTCAGCATGCC
9949-9971	TCCCAAAGCAGTCAGCATGCCT
9950-9972	CCCAAAGCAGTCAGCATGCCTA
9951-9973	CCAAAAGCAGTCAGCATGCCTAG
9952-9974	CAAAAAGCAGTCAGCATGCCTAGT
9953-9975	AAAAGCAGTCAGCATGCCTAGTT
9954-9976	AAAGCAGTCAGCATGCCTAGTTT
9955-9977	AAGCAGTCAGCATGCCTAGTTTC
9956-9978	AGCAGTCAGCATGCCTAGTTTCT
9957-9979	GCAGTCAGCATGCCTAGTTTCTC
9958-9980	CAGTCAGCATGCCTAGTTTCTCC
9959-9981	AGTCAGCATGCCTAGTTTCTCCA
9960-9982	GTCAGCATGCCTAGTTTCTCCAT
9961-9983	TCAGCATGCCTAGTTTCTCCATC
9962-9984	CAGCATGCCTAGTTTCTCCATCC
9963-9985	AGCATGCCTAGTTTCTCCATCCT
9964-9986	GCATGCCTAGTTTCTCCATCCTA
9965-9987	CATGCCTAGTTTCTCCATCCTAG
9966-9988	ATGCCTAGTTTCTCCATCCTAGG
9967-9989	TGCCTAGTTTCTCCATCCTAGGT
9968-9990	GCCTAGTTTCTCCATCCTAGGTT
9969-9991	CCTAGTTTCTCCATCCTAGGTTT
9970-9992	CTAGTTTCTCCATCCTAGGTTCT
9971-9993	TAGTTTCTCCATCCTAGGTTCTG
9972-9994	AGTTTCTCCATCCTAGGTTCTGA
9973-9995	GTTTCTCCATCCTAGGTTCTGAC
9974-9996	TTTCTCCATCCTAGGTTCTGACG
9975-9997	TTCTCCATCCTAGGTTCTGACGT
9976-9998	TCTCCATCCTAGGTTCTGACGTC
9977-9999	CTCCATCCTAGGTTCTGACGTCC
9978-10000	TCCATCCTAGGTTCTGACGTCCG
9979-10001	CCATCCTAGGTTCTGACGTCCGT
9980-10002	CATCCTAGGTTCTGACGTCCGTG
9981-10003	ATCCTAGGTTCTGACGTCCGTGT
9982-10004	TCCTAGGTTCTGACGTCCGTGTG
9983-10005	CCTAGGTTCTGACGTCCGTGTGC
9984-10006	CTAGGTTCTGACGTCCGTGTGCC
9985-10007	TAGGTTCTGACGTCCGTGTGCCCT
9986-10008	AGGTTCTGACGTCCGTGTGCCCTT
9987-10009	GGTTCTGACGTCCGTGTGCCCTTC
9988-10010	GTTCTGACGTCCGTGTGCCCTTCA
9989-10011	TTCTGACGTCCGTGTGCCCTTCAT
9990-10012	TCTGACGTCCGTGTGCCCTTCATA
9991-10013	CTGACGTCCGTGTGCCCTTCATAC
9992-10014	TGACGTCCGTGTGCCCTTCATACA
9993-10015	GACGTCCGTGTGCCCTTCATACAC
9994-10016	ACGTCCGTGTGCCCTTCATACACA
9995-10017	CGTCCGTGTGCCCTTCATACACAT
9996-10018	GTCCGTGTGCCCTTCATACACATT
9997-10019	TCCGTGTGCCCTTCATACACATTA
9998-10020	CCGTGTGCCCTTCATACACATTAA
9999-10021	CGTGTGCCCTTCATACACATTAAT
10000-10022	GTGTGCCCTTCATACACATTAATC
10001-10023	TGTGCCCTTCATACACATTAATCC
10002-10024	GTGCCCTTCATACACATTAATCCT
10003-10025	TGCCCTTCATACACATTAATCCTG
10004-10026	GCCTTCATACACATTAATCCTGC
10005-10027	CCTTCATACACATTAATCCTGCC
10006-10028	CTTCATACACATTAATCCTGCCA
10007-10029	TTCATACACATTAATCCTGCCAT
10008-10030	TCATACACATTAATCCTGCCATC

Position	Sequence
10009-10031	CATACACATTAATCCTGCCATCA
10010-10032	ATACACATTAATCCTGCCATCAT
10011-10033	TACACATTAATCCTGCCATCATT
10012-10034	ACACATTAATCCTGCCATCATT
10013-10035	CACATTAATCCTGCCATCATTAG
10014-10036	ACATTAATCCTGCCATCATTAGA
10015-10037	CATTAATCCTGCCATCATTAGAG
10016-10038	ATTAATCCTGCCATCATTAGAGC
10017-10039	TTAATCCTGCCATCATTAGAGCT
10018-10040	TAATCCTGCCATCATTAGAGCTG
10019-10041	AATCCTGCCATCATTAGAGCTGC
10020-10042	ATCCTGCCATCATTAGAGCTGCC
10021-10043	TCCTGCCATCATTAGAGCTGCCA
10022-10044	CCTGCCATCATTAGAGCTGCCAG
10023-10045	CTGCCATCATTAGAGCTGCCAGT
10024-10046	TGCCATCATTAGAGCTGCCAGTC
10025-10047	GCCATCATTAGAGCTGCCAGTCC
10026-10048	CCATCATTAGAGCTGCCAGTCCCT
10027-10049	CATCATTAGAGCTGCCAGTCCCTT
10028-10050	ATCATTAGAGCTGCCAGTCCCTTC
10029-10051	TCATTAGAGCTGCCAGTCCCTTCA
10030-10052	CATTAGAGCTGCCAGTCCCTTCAT
10031-10053	ATTAGAGCTGCCAGTCCCTTCATG
10032-10054	TTAGAGCTGCCAGTCCCTTCATGT
10033-10055	TAGAGCTGCCAGTCCCTTCATGTC
10034-10056	AGAGCTGCCAGTCCCTTCATGTCC
10035-10057	GAGCTGCCAGTCCCTTCATGTCCC
10036-10058	AGCTGCCAGTCCCTTCATGTCCCT
10037-10059	GCTGCCAGTCCCTTCATGTCCCTA
10038-10060	CTGCCAGTCCCTTCATGTCCCTAG
10039-10061	TGCCAGTCCCTTCATGTCCCTAGA
10040-10062	GCCAGTCCCTTCATGTCCCTAGAA
10041-10063	CCAGTCCCTTCATGTCCCTAGAAA
10042-10064	CAGTCCCTTCATGTCCCTAGAAAT
10043-10065	AGTCCCTTCATGTCCCTAGAAATC
10044-10066	GTCCTTCATGTCCCTAGAAATCT
10045-10067	TCCTTCATGTCCCTAGAAATCTC
10046-10068	CCTTCATGTCCCTAGAAATCTCA
10047-10069	CTTCATGTCCCTAGAAATCTCAA
10048-10070	TTCATGTCCCTAGAAATCTCAAG
10049-10071	TCATGTCCCTAGAAATCTCAAGC
10050-10072	CATGTCCCTAGAAATCTCAAGCT
10051-10073	ATGTCCCTAGAAATCTCAAGCTT
10052-10074	TGTCCCTAGAAATCTCAAGCTTT
10053-10075	GTCCCTAGAAATCTCAAGCTTTC
10054-10076	TCCCTAGAAATCTCAAGCTTTCT
10055-10077	CCCTAGAAATCTCAAGCTTTCTC
10056-10078	CCTAGAAATCTCAAGCTTTCTCT
10057-10079	CTAGAAATCTCAAGCTTTCTCTT
10058-10080	TAGAAATCTCAAGCTTTCTCTTC
10059-10081	AGAAATCTCAAGCTTTCTCTTCC
10060-10082	GAAATCTCAAGCTTTCTCTTCCA
10061-10083	AAATCTCAAGCTTTCTCTTCCAC
10062-10084	AATCTCAAGCTTTCTCTTCCACA
10063-10085	ATCTCAAGCTTTCTCTTCCACAT
10064-10086	TCTCAAGCTTTCTCTTCCACATT
10065-10087	CTCAAGCTTTCTCTTCCACATTT
10066-10088	TCAAGCTTTCTCTTCCACATTTT
10067-10089	CAAGCTTTCTCTTCCACATTTTCA
10068-10090	AAGCTTTCTCTTCCACATTTTCAA
10069-10091	AGCTTTCTCTTCCACATTTTCAAG
10070-10092	GCTTTCTCTTCCACATTTTCAAGG
10071-10093	CTTTCTCTTCCACATTTTCAAGGA
10072-10094	TTTCTCTTCCACATTTTCAAGGAA
10073-10095	TTCTCTTCCACATTTTCAAGGAAT
10074-10096	TCTCTTCCACATTTTCAAGGAATT

Position	Sequence
10075-10097	CTCTCCACATTCAAGGAATTG
10076-10098	TCTTCCACATTCAAGGAATTGT
10077-10099	CTTCCACATTTCAAGGAATTGTG
10078-10100	TTCCACATTTCAAGGAATTGTGT
10079-10101	TCCACATTTCAAGGAATTGTGTA
10080-10102	CCACATTTCAAGGAATTGTGTAC
10081-10103	CACATTTCAAGGAATTGTGTACC
10082-10104	ACATTTCAAGGAATTGTGTACCA
10083-10105	CATTTCAAGGAATTGTGTACCAT
10084-10106	ATTTCAAGGAATTGTGTACCATA
10085-10107	TTTCAAGGAATTGTGTACCATAA
10086-10108	TCAAGGAATTGTGTACCATAAG
10087-10109	TCAAGGAATTGTGTACCATAAGC
10088-10110	CAAGGAATTGTGTACCATAAGCC
10089-10111	AAGGAATTGTGTACCATAAGCCA
10090-10112	AGGAATTGTGTACCATAAGCCAT
10091-10113	GGAATTGTGTACCATAAGCCATA
10092-10114	GAATTGTGTACCATAAGCCATAT
10093-10115	AATTGTGTACCATAAGCCATATT
10094-10116	ATTGTGTACCATAAGCCATATTT
10095-10117	TTGTGTACCATAAGCCATATTTT
10096-10118	TGTGTACCATAAGCCATATTTT
10097-10119	GTGTACCATAAGCCATATTTT
10098-10120	TGTACCATAAGCCATATTTTAT
10099-10121	GTACCATAAGCCATATTTTATT
10100-10122	TACCATAAGCCATATTTTATT
10101-10123	ACCATAAGCCATATTTTATTCC
10102-10124	CCATAAGCCATATTTTATTCCCT
10103-10125	CATAAGCCATATTTTATTCTCG
10104-10126	ATAAGCCATATTTTATTCTCGC
10105-10127	TAAGCCATATTTTATTCTCGCC
10106-10128	AAGCCATATTTTATTCTCGCCA
10107-10129	AGCCATATTTTATTCTCGCCAT
10108-10130	GCCATATTTTATTCTCGCCATG
10109-10131	CCATATTTTATTCTCGCCATGG
10110-10132	CATATTTTATTCTCGCCATGGG
10111-10133	ATATTTTATTCTCGCCATGGGC
10112-10134	TATTTTATTCTCGCCATGGGCA
10113-10135	ATTTTATTCTCGCCATGGGCAA
10114-10136	TTTTTATTCTCGCCATGGGCAAT
10115-10137	TTTATTCTCGCCATGGGCAATA
10116-10138	TTATTCTCGCCATGGGCAATAT
10117-10139	TTATTCTCGCCATGGGCAATATT
10118-10140	TATTCTCGCCATGGGCAATATTA
10119-10141	ATCTCGCCATGGGCAATATTAC
10120-10142	TTCTCGCCATGGGCAATATTACC
10121-10143	TCCTGCCATGGGCAATATTACCT
10122-10144	CCTGCCATGGGCAATATTACCTA
10123-10145	CTGCCATGGGCAATATTACCTAT
10124-10146	TGCCATGGGCAATATTACCTATG
10125-10147	GCCATGGGCAATATTACCTATGA
10126-10148	CCATGGGCAATATTACCTATGAT
10127-10149	CATGGGCAATATTACCTATGATT
10128-10150	ATGGGCAATATTACCTATGATTT
10129-10151	TGGGCAATATTACCTATGATTT
10130-10152	GGGCAATATTACCTATGATTTCT
10131-10153	GGCAATATTACCTATGATTTCTC
10132-10154	GCAATATTACCTATGATTTCTCC
10133-10155	CAATATTACCTATGATTTCTCCT
10134-10156	AATATTACCTATGATTTCTCCTT
10135-10157	ATATTACCTATGATTTCTCCTTT
10136-10158	TATTACCTATGATTTCTCCTTTA
10137-10159	ATTACCTATGATTTCTCCTTTAA
10138-10160	TTACCTATGATTTCTCCTTTAAA
10139-10161	TACCTATGATTTCTCCTTTAAAT
10140-10162	ACCTATGATTTCTCCTTTAAATC

Position	Sequence
10141-10163	CCTATGATTTCTCCTTAAATCA
10142-10164	CTATGATTTCTCCTTAAATCAA
10143-10165	TATGATTTCTCCTTAAATCAAG
10144-10166	ATGATTTCTCCTTAAATCAAGT
10145-10167	TGATTTCTCCTTAAATCAAGTG
10146-10168	GATTTCTCCTTAAATCAAGTGT
10147-10169	ATTTCTCCTTAAATCAAGTGTC
10148-10170	TTTCTCCTTAAATCAAGTGTC
10149-10171	TTCTCCTTAAATCAAGTGTCAT
10150-10172	TCTCCTTAAATCAAGTGTCATC
10151-10173	CTCCTTAAATCAAGTGTCATCA
10152-10174	TCCTTAAATCAAGTGTCATCAC
10153-10175	CCTTAAATCAAGTGTCATCACA
10154-10176	CTTAAATCAAGTGTCATCACAC
10155-10177	TTAAATCAAGTGTCATCACACT
10156-10178	TAAATCAAGTGTCATCACACTG
10157-10179	TAAATCAAGTGTCATCACACTGA
10158-10180	AAATCAAGTGTCATCACACTGAA
10159-10181	AATCAAGTGTCATCACACTGAAT
10160-10182	ATCAAGTGTCATCACACTGAATA
10161-10183	TCAAGTGTCATCACACTGAATAC
10162-10184	CAAGTGTCATCACACTGAATACC
10163-10185	AAGTGTCATCACACTGAATACCA
10164-10186	AGTGTCATCACACTGAATACCAA
10165-10187	GTGTCATCACACTGAATACCAAT
10166-10188	TGTCATCACACTGAATACCAATG
10167-10189	GTCATCACACTGAATACCAATGC
10168-10190	TCATCACACTGAATACCAATGCT
10169-10191	CATCACACTGAATACCAATGCTG
10170-10192	ATCACACTGAATACCAATGCTGA
10171-10193	TCACACTGAATACCAATGCTGAA
10172-10194	CACACTGAATACCAATGCTGAAC
10173-10195	ACACTGAATACCAATGCTGAACT
10174-10196	CACTGAATACCAATGCTGAACTT
10175-10197	ACTGAATACCAATGCTGAACTTT
10176-10198	CTGAATACCAATGCTGAACTTTT
10177-10199	TGAATACCAATGCTGAACTTTTT
10178-10200	GAATACCAATGCTGAACTTTTTA
10179-10201	AATACCAATGCTGAACTTTTTAA
10180-10202	ATACCAATGCTGAACTTTTTAAC
10181-10203	TACCAATGCTGAACTTTTTAACC
10182-10204	ACCAATGCTGAACTTTTTAACCA
10183-10205	CCAATGCTGAACTTTTTAACCAG
10184-10206	CAATGCTGAACTTTTTAACCAGT
10185-10207	AATGCTGAACTTTTTAACCAGTC
10186-10208	ATGCTGAACTTTTTAACCAGTCA
10187-10209	TGCTGAACTTTTTAACCAGTCAG
10188-10210	GCTGAACTTTTTAACCAGTCAGA
10189-10211	CTGAACTTTTTAACCAGTCAGAT
10190-10212	TGAACTTTTTAACCAGTCAGATA
10191-10213	GAACTTTTTAACCAGTCAGATAT
10192-10214	AACTTTTTAACCAGTCAGATATT
10193-10215	ACTTTTTAACCAGTCAGATATTG
10194-10216	CTTTTTAACCAGTCAGATATTGT
10195-10217	TTTTTAACCAGTCAGATATTGTT
10196-10218	TTTTAACCAGTCAGATATTGTTG
10197-10219	TTTAACCAGTCAGATATTGTTGC
10198-10220	TTAACCAGTCAGATATTGTTGCT
10199-10221	TAACCAGTCAGATATTGTTGCTC
10200-10222	AACCAGTCAGATATTGTTGCTCA
10201-10223	ACCAGTCAGATATTGTTGCTCAT
10202-10224	CCAGTCAGATATTGTTGCTCATC
10203-10225	CAGTCAGATATTGTTGCTCATCT
10204-10226	AGTCAGATATTGTTGCTCATCTC
10205-10227	GTCAGATATTGTTGCTCATCTCC
10206-10228	TCAGATATTGTTGCTCATCTCCT

Position	Sequence
10207-10229	CAGATATGTTGCTCATCTCCTT
10208-10230	AGATATTGTTGCTCATCTCCTTT
10209-10231	GATATTGTTGCTCATCTCCTTTC
10210-10232	ATATTGTTGCTCATCTCCTTTCT
10211-10233	TATTGTTGCTCATCTCCTTTCTT
10212-10234	ATTGTTGCTCATCTCCTTTCTTC
10213-10235	TTGTTGCTCATCTCCTTTCTTCA
10214-10236	TGTTGCTCATCTCCTTTCTTCAT
10215-10237	GTTGCTCATCTCCTTTCTTCATC
10216-10238	TTGCTCATCTCCTTTCTTCATCT
10217-10239	TGCTCATCTCCTTTCTTCATCTT
10218-10240	GCTCATCTCCTTTCTTCATCTTC
10219-10241	CTCATCTCCTTTCTTCATCTTCA
10220-10242	TCATCTCCTTTCTTCATCTTCAT
10221-10243	CATCTCCTTTCTTCATCTTCATC
10222-10244	ATCTCCTTTCTTCATCTTCATCT
10223-10245	TCTCCTTTCTTCATCTTCATCTG
10224-10246	CTCCTTTCTTCATCTTCATCTGT
10225-10247	TCCTTTCTTCATCTTCATCTGTC
10226-10248	CCTTTCTTCATCTTCATCTGTCA
10227-10249	CTTTCTTCATCTTCATCTGTCAF
10228-10250	TTTCTTCATCTTCATCTGTCAAT
10229-10251	TTCTTCATCTTCATCTGTCAATG
10230-10252	TCTTCATCTTCATCTGTCAATGA
10231-10253	CTTCATCTTCATCTGTCAATGAT
10232-10254	TTTCATCTTCATCTGTCAATGATG
10233-10255	TCATCTTCATCTGTCAATGATGC
10234-10256	CATCTTCATCTGTCAATGATGCA
10235-10257	ATCTTCATCTGTCAATGATGCAC
10236-10258	TCTTCATCTGTCAATGATGCACT
10237-10259	CCTTCATCTGTCAATGATGCACTG
10238-10260	TTTCATCTGTCAATGATGCACTGC
10239-10261	TCATCTGTCAATGATGCACTGCAG
10240-10262	CATCTGTCAATGATGCACTGCAGT
10241-10263	ATCTGTCAATGATGCACTGCAGTA
10242-10264	TCTGTCAATGATGCACTGCAGTAC
10243-10265	CTGTCAATGATGCACTGCAGTACA
10244-10266	TGTCATGATGCACTGCAGTACAA
10245-10267	GTCATGATGCACTGCAGTACAAA
10246-10268	TCATGATGCACTGCAGTACAAAT
10247-10269	CATTGATGCACTGCAGTACAAATT
10248-10270	ATTGATGCACTGCAGTACAAATTA
10249-10271	TTGATGCACTGCAGTACAAATTAG
10250-10272	TGATGCACTGCAGTACAAATTAGA
10251-10273	GATGCACTGCAGTACAAATTAGAG
10252-10274	ATGCACTGCAGTACAAATTAGAGG
10253-10275	TGCACTGCAGTACAAATTAGAGGG
10254-10276	GCACTGCAGTACAAATTAGAGGGG
10255-10277	CACTGCAGTACAAATTAGAGGGGC
10256-10278	ACTGCAGTACAAATTAGAGGGGCA
10257-10279	CTGCAGTACAAATTAGAGGGGCAC
10258-10280	TGCAGTACAAATTAGAGGGGCACC
10259-10281	GCAGTACAAATTAGAGGGGCACCA
10260-10282	CAGTACAAATTAGAGGGGCACCAC
10261-10283	AGTACAAATTAGAGGGGCACCACA
10262-10284	GTACAAATTAGAGGGGCACCACAA
10263-10285	TACAAATTAGAGGGGCACCACAAG
10264-10286	ACAAATTAGAGGGGCACCACAAGA
10265-10287	CAAATTAGAGGGGCACCACAAGAT
10266-10288	AAATTAGAGGGGCACCACAAGATT
10267-10289	AATTAGAGGGGCACCACAAGATTG
10268-10290	ATTAGAGGGGCACCACAAGATTGA
10269-10291	TTAGAGGGGCACCACAAGATTGAC
10270-10292	TAGAGGGGCACCACAAGATTGACA
10271-10293	AGAGGGGCACCACAAGATTGACAA
10272-10294	GAGGGGCACCACAAGATTGACAAG

Position	Sequence
10273-10295	AGGGCACCACAAGATTGACAAGA
10274-10296	GGCACCACAAGATTGACAAGAA
10275-10297	GGCACCACAAGATTGACAAGAAA
10276-10298	GCACCACAAGATTGACAAGAAAA
10277-10299	CACCACAAGATTGACAAGAAAAA
10278-10300	ACCACAAGATTGACAAGAAAAAG
10279-10301	CCACAAGATTGACAAGAAAAAGG
10280-10302	CACAAGATTGACAAGAAAAAGGG
10281-10303	ACAAGATTGACAAGAAAAAGGGG
10282-10304	CAAGATTGACAAGAAAAAGGGGA
10283-10305	AAGATTGACAAGAAAAAGGGGAT
10284-10306	AGATTGACAAGAAAAAGGGGATT
10285-10307	GATTGACAAGAAAAAGGGGATTG
10286-10308	ATTGACAAGAAAAAGGGGATTGA
10287-10309	TTGACAAGAAAAAGGGGATTGAA
10288-10310	TGACAAGAAAAAGGGGATTGAAG
10289-10311	GACAAGAAAAAGGGGATTGAAGT
10290-10312	ACAAGAAAAAGGGGATTGAAGTT
10291-10313	CAAGAAAAAGGGGATTGAAGTTA
10292-10314	AAGAAAAAGGGGATTGAAGTTAG
10293-10315	AGAAAAAGGGGATTGAAGTTAGC
10294-10316	GAAAAAGGGGATTGAAGTTAGCC
10295-10317	AAAAAGGGGATTGAAGTTAGCCA
10296-10318	AAAAGGGGATTGAAGTTAGCCAC
10297-10319	AAAGGGGATTGAAGTTAGCCACA
10298-10320	AAGGGGATTGAAGTTAGCCACAG
10299-10321	AGGGGATTGAAGTTAGCCACAGC
10300-10322	GGGGATTGAAGTTAGCCACAGCT
10301-10323	GGGATTGAAGTTAGCCACAGCTC
10302-10324	GGATTGAAGTTAGCCACAGCTCT
10303-10325	GATTGAAGTTAGCCACAGCTCTG
10304-10326	ATTGAAGTTAGCCACAGCTCTGT
10305-10327	TTGAAGTTAGCCACAGCTCTGTC
10306-10328	TGAAGTTAGCCACAGCTCTGTCT
10307-10329	GAAGTTAGCCACAGCTCTGTCTC
10308-10330	AAGTTAGCCACAGCTCTGTCTCT
10309-10331	AGTTAGCCACAGCTCTGTCTCTG
10310-10332	GTTAGCCACAGCTCTGTCTCTGA
10311-10333	TTAGCCACAGCTCTGTCTCTGAG
10312-10334	TAGCCACAGCTCTGTCTCTGAGC
10313-10335	AGCCACAGCTCTGTCTCTGAGCA
10314-10336	GCCACAGCTCTGTCTCTGAGCAA
10315-10337	CCACAGCTCTGTCTCTGAGCAAC
10316-10338	CACAGCTCTGTCTCTGAGCAACA
10317-10339	ACAGCTCTGTCTCTGAGCAACAA
10318-10340	CAGCTCTGTCTCTGAGCAACAAA
10319-10341	AGCTCTGTCTCTGAGCAACAAAT
10320-10342	GCTCTGTCTCTGAGCAACAAATT
10321-10343	CTCTGTCTCTGAGCAACAAATTT
10322-10344	TCTGTCTCTGAGCAACAAATTTG
10323-10345	CTGTCTCTGAGCAACAAATTTGT
10324-10346	TGTCTCTGAGCAACAAATTTGTG
10325-10347	GTCTCTGAGCAACAAATTTGTGG
10326-10348	TCTCTGAGCAACAAATTTGTGGA
10327-10349	CTCTGAGCAACAAATTTGTGGAG
10328-10350	TCTGAGCAACAAATTTGTGGAGG
10329-10351	CTGAGCAACAAATTTGTGGAGGG
10330-10352	TGAGCAACAAATTTGTGGAGGGT
10331-10353	GAGCAACAAATTTGTGGAGGGTA
10332-10354	AGCAACAAATTTGTGGAGGGTAG
10333-10355	GCAACAAATTTGTGGAGGGTAGT
10334-10356	CAACAAATTTGTGGAGGGTAGTC
10335-10357	AACAAATTTGTGGAGGGTAGTCA
10336-10358	ACAAATTTGTGGAGGGTAGTCAT
10337-10359	CAAATTTGTGGAGGGTAGTCATA
10338-10360	AAATTTGTGGAGGGTAGTCATAA

Position	Sequence
10339-10361	AATTTGTGGAGGGTAGTCATAAC
10340-10362	ATTTGTGGAGGGTAGTCATAACA
10341-10363	TTTGTGGAGGGTAGTCATAACAG
10342-10364	TTGTGGAGGGTAGTCATAACAGT
10343-10365	TGTGGAGGGTAGTCATAACAGTA
10344-10366	GTGGAGGGTAGTCATAACAGTAC
10345-10367	TGGAGGGTAGTCATAACAGTACT
10346-10368	GGAGGGTAGTCATAACAGTACTG
10347-10369	GAGGGTAGTCATAACAGTACTGT
10348-10370	AGGGTAGTCATAACAGTACTGTG
10349-10371	GGGTAGTCATAACAGTACTGTGA
10350-10372	GGTAGTCATAACAGTACTGTGAG
10351-10373	GTAGTCATAACAGTACTGTGAGC
10352-10374	TAGTCATAACAGTACTGTGAGCT
10353-10375	AGTCATAACAGTACTGTGAGCTT
10354-10376	GTCATAACAGTACTGTGAGCTTA
10355-10377	TCATAACAGTACTGTGAGCTTAA
10356-10378	CATAACAGTACTGTGAGCTTAAC
10357-10379	ATAACAGTACTGTGAGCTTAACC
10358-10380	TAACAGTACTGTGAGCTTAACCA
10359-10381	AACAGTACTGTGAGCTTAACCAC
10360-10382	ACAGTACTGTGAGCTTAACCACG
10361-10383	CAGTACTGTGAGCTTAACCACGA
10362-10384	AGTACTGTGAGCTTAACCACGAA
10363-10385	GTACTGTGAGCTTAACCACGAAA
10364-10386	TACTGTGAGCTTAACCACGAAAA
10365-10387	ACTGTGAGCTTAACCACGAAAAA
10366-10388	CTGTGAGCTTAACCACGAAAAAT
10367-10389	TGTGAGCTTAACCACGAAAAATA
10368-10390	GTGAGCTTAACCACGAAAAATAT
10369-10391	TGAGCTTAACCACGAAAAATATG
10370-10392	GAGCTTAACCACGAAAAATATGG
10371-10393	AGCTTAACCACGAAAAATATGGA
10372-10394	GCTTAACCACGAAAAATATGGAA
10373-10395	CTTAACCACGAAAAATATGGAA
10374-10396	TTAACCACGAAAAATATGGAAAGT
10375-10397	TAACCACGAAAAATATGGAAAGTG
10376-10398	AACCACGAAAAATATGGAAAGTGT
10377-10399	ACCACGAAAAATATGGAAAGTGTC
10378-10400	CCACGAAAAATATGGAAAGTGTC
10379-10401	CACGAAAAATATGGAAAGTGTCAG
10380-10402	ACGAAAAATATGGAAAGTGTCAGT
10381-10403	CGAAAAATATGGAAAGTGTCAGTG
10382-10404	GAAAAATATGGAAAGTGTCAGTGG
10383-10405	AAAAATATGGAAAGTGTCAGTGGC
10384-10406	AAAATATGGAAAGTGTCAGTGGCA
10385-10407	AAATATGGAAAGTGTCAGTGGCAA
10386-10408	AATATGGAAAGTGTCAGTGGCAAA
10387-10409	ATATGGAAAGTGTCAGTGGCAAAA
10388-10410	TATGGAAAGTGTCAGTGGCAAAAA
10389-10411	ATGGAAAGTGTCAGTGGCAAAAAC
10390-10412	TGGAAAGTGTCAGTGGCAAAAACC
10391-10413	GGAAGTGTCAGTGGCAAAAACCA
10392-10414	GAAGTGTCAGTGGCAAAAACCAC
10393-10415	AAGTGTCAGTGGCAAAAACCACA
10394-10416	AGTGTCAGTGGCAAAAACCACAA
10395-10417	GTGTCAGTGGCAAAAACCACAAA
10396-10418	TGTCAGTGGCAAAAACCACAAAA
10397-10419	GTCAGTGGCAAAAACCACAAAAG
10398-10420	TCAGTGGCAAAAACCACAAAAGC
10399-10421	CAGTGGCAAAAACCACAAAAGCC
10400-10422	AGTGGCAAAAACCACAAAAGCCG
10401-10423	GTGGCAAAAACCACAAAAGCCGA
10402-10424	TGGCAAAAACCACAAAAGCCGAA
10403-10425	GGCAAAAACCACAAAAGCCGAAA
10404-10426	GCAAAAACCACAAAAGCCGAAAT

Position	Sequence
10405-10427	CAAAAACCACAAAAGCCGAAATT
10406-10428	AAAAACCACAAAAGCCGAAATTC
10407-10429	AAAACCACAAAAGCCGAAATTC
10408-10430	AAACCACAAAAGCCGAAATCCA
10409-10431	AACCACAAAAGCCGAAATCCAA
10410-10432	ACCACAAAAGCCGAAATCCAAT
10411-10433	CCACAAAAGCCGAAATCCAATT
10412-10434	CACAAAAGCCGAAATCCAATTT
10413-10435	ACAAAAGCCGAAATCCAATTTT
10414-10436	CAAAAGCCGAAATCCAATTTTG
10415-10437	AAAAGCCGAAATCCAATTTTGA
10416-10438	AAAGCCGAAATCCAATTTTGAG
10417-10439	AAGCCGAAATCCAATTTTGAGA
10418-10440	AGCCGAAATCCAATTTTGAGAA
10419-10441	GCCGAAATCCAATTTTGAGAAT
10420-10442	CCGAAATCCAATTTTGAGAATG
10421-10443	CGAAATCCAATTTTGAGAATGA
10422-10444	GAAATCCAATTTTGAGAATGAA
10423-10445	AAATCCAATTTTGAGAATGAAT
10424-10446	AATCCAATTTTGAGAATGAATT
10425-10447	ATCCAATTTTGAGAATGAATTT
10426-10448	TTCCAATTTTGAGAATGAATTC
10427-10449	TCCAATTTTGAGAATGAATTTCA
10428-10450	CCAATTTTGAGAATGAATTTCAA
10429-10451	CAATTTTGAGAATGAATTTCAAG
10430-10452	AATTTTGAGAATGAATTTCAAGC
10431-10453	ATTTTGAGAATGAATTTCAAGCA
10432-10454	TTTTGAGAATGAATTTCAAGCAA
10433-10455	TTTGAGAATGAATTTCAAGCAAG
10434-10456	TTGAGAATGAATTTCAAGCAAGA
10435-10457	TGAGAATGAATTTCAAGCAAGAA
10436-10458	GAGAATGAATTTCAAGCAAGAAC
10437-10459	AGAATGAATTTCAAGCAAGAACT
10438-10460	GAATGAATTTCAAGCAAGAACTT
10439-10461	AATGAATTTCAAGCAAGAACTTA
10440-10462	ATGAATTTCAAGCAAGAACTTAA
10441-10463	TGAATTTCAAGCAAGAACTTAAT
10442-10464	GAATTTCAAGCAAGAACTTAATG
10443-10465	AATTTCAAGCAAGAACTTAATGG
10444-10466	ATTTCAAGCAAGAACTTAATGGA
10445-10467	TTCAAGCAAGAACTTAATGGAA
10446-10468	TTCAAGCAAGAACTTAATGGAAA
10447-10469	TCAAGCAAGAACTTAATGGAAAT
10448-10470	CAAGCAAGAACTTAATGGAAATA
10449-10471	AAGCAAGAACTTAATGGAAATAC
10450-10472	AGCAAGAACTTAATGGAAATACC
10451-10473	GCAAGAACTTAATGGAAATACCA
10452-10474	CAAGAACTTAATGGAAATACCAA
10453-10475	AAGAACTTAATGGAAATACCAAG
10454-10476	AGAACTTAATGGAAATACCAAGT
10455-10477	GAACTTAATGGAAATACCAAGTC
10456-10478	AACTTAATGGAAATACCAAGTCA
10457-10479	ACTTAATGGAAATACCAAGTCAA
10458-10480	CTTAATGGAAATACCAAGTCAAAA
10459-10481	TTAATGGAAATACCAAGTCAAAA
10460-10482	TAATGGAAATACCAAGTCAAAAAC
10461-10483	AATGGAAATACCAAGTCAAAAACC
10462-10484	ATGGAAATACCAAGTCAAAAACCT
10463-10485	TGGAAATACCAAGTCAAAAACCTA
10464-10486	GAAATACCAAGTCAAAAACCTAC
10465-10487	GAAATACCAAGTCAAAAACCTACT
10466-10488	AAATACCAAGTCAAAAACCTACTG
10467-10489	AATACCAAGTCAAAAACCTACTGT
10468-10490	ATACCAAGTCAAAAACCTACTGTCT
10469-10491	TACCAAGTCAAAAACCTACTGTCT
10470-10492	ACCAAGTCAAAAACCTACTGTCTC

Position	Sequence
10471-10493	CCAAGTCAAACCTACTGTCTCT
10472-10494	CAAGTCAAACCTACTGTCTCTT
10473-10495	AAGTCAAACCTACTGTCTCTTC
10474-10496	AGTCAAACCTACTGTCTCTTCC
10475-10497	GTCAAACCTACTGTCTCTTCCT
10476-10498	TCAAACCTACTGTCTCTTCCTC
10477-10499	CAAACCTACTGTCTCTTCCTCC
10478-10500	AAAACCTACTGTCTCTTCCTCCA
10479-10501	AAACCTACTGTCTCTTCCTCCAT
10480-10502	AACCTACTGTCTCTTCCTCCATG
10481-10503	ACCTACTGTCTCTTCCTCCATGG
10482-10504	CCTACTGTCTCTTCCTCCATGGA
10483-10505	CTACTGTCTCTTCCTCCATGGAA
10484-10506	TACTGTCTCTTCCTCCATGGAAT
10485-10507	ACTGTCTCTTCCTCCATGGAATT
10486-10508	CTGTCTCTTCCTCCATGGAATTT
10487-10509	TGTCTCTTCCTCCATGGAATTTA
10488-10510	GTCTCTTCCTCCATGGAATTTAA
10489-10511	TCTCTTCCTCCATGGAATTTAAG
10490-10512	CTCTTCCTCCATGGAATTTAAGT
10491-10513	TCTTCCTCCATGGAATTTAAGTA
10492-10514	CTTCCTCCATGGAATTTAAGTAT
10493-10515	TTTCCTCCATGGAATTTAAGTATG
10494-10516	TCCTCCATGGAATTTAAGTATGA
10495-10517	CCTCCATGGAATTTAAGTATGAT
10496-10518	CTCCATGGAATTTAAGTATGATT
10497-10519	TCCATGGAATTTAAGTATGATTT
10498-10520	CCATGGAATTTAAGTATGATTTT
10499-10521	CATGGAATTTAAGTATGATTTCA
10500-10522	ATGGAATTTAAGTATGATTTCAA
10501-10523	TGGAATTTAAGTATGATTTCAAT
10502-10524	GGAATTTAAGTATGATTTCAATT
10503-10525	GAATTTAAGTATGATTTCAATTC
10504-10526	AATTTAAGTATGATTTCAATTC
10505-10527	ATTTAAGTATGATTTCAATTC
10506-10528	TTTAAGTATGATTTCAATTC
10507-10529	TTAAGTATGATTTCAATTC
10508-10530	TAAGTATGATTTCAATTC
10509-10531	AAGTATGATTTCAATTC
10510-10532	AGTATGATTTCAATTC
10511-10533	GTATGATTTCAATTC
10512-10534	TATGATTTCAATTC
10513-10535	ATGATTTCAATTC
10514-10536	TGATTTCAATTC
10515-10537	GATTTCAATTC
10516-10538	ATTTCAATTC
10517-10539	TTTCAATTC
10518-10540	TTCATTC
10519-10541	TCAATTC
10520-10542	CAATTC
10521-10543	AATTC
10522-10544	ATTTC
10523-10545	TTTTC
10524-10546	TCTTC
10525-10547	CTTTC
10526-10548	TTCAATGCTGACTCTACCGCTA
10527-10549	TCAATGCTGACTCTACCGCTAA
10528-10550	CAATGCTGACTCTACCGCTAAA
10529-10551	AATGCTGACTCTACCGCTAAAG
10530-10552	ATGCTGACTCTACCGCTAAAGG
10531-10553	TGCTGACTCTACCGCTAAAGGA
10532-10554	GCTGACTCTACCGCTAAAGGAG
10533-10555	CTGACTCTACCGCTAAAGGAGC
10534-10556	TGTACTCTACCGCTAAAGGAGCA
10535-10557	GTACTCTACCGCTAAAGGAGCAG
10536-10558	TACTCTACCGCTAAAGGAGCAGT

Position	Sequence
10537-10559	ACTCTACCGCTAAAGGAGCAGTT
10538-10560	CTCTACCGCTAAAGGAGCAGTTG
10539-10561	TCTACCGCTAAAGGAGCAGTTGA
10540-10562	CTACCGCTAAAGGAGCAGTTGAC
10541-10563	TACCGCTAAAGGAGCAGTTGACC
10542-10564	ACCGCTAAAGGAGCAGTTGACCA
10543-10565	CCGCTAAAGGAGCAGTTGACCAC
10544-10566	CGCTAAAGGAGCAGTTGACCACA
10545-10567	GCTAAAGGAGCAGTTGACCACAA
10546-10568	CTAAAGGAGCAGTTGACCACAAG
10547-10569	TAAAGGAGCAGTTGACCACAAGC
10548-10570	AAAGGAGCAGTTGACCACAAGCT
10549-10571	AAGGAGCAGTTGACCACAAGCTT
10550-10572	AGGAGCAGTTGACCACAAGCTTA
10551-10573	GGAGCAGTTGACCACAAGCTTAG
10552-10574	GAGCAGTTGACCACAAGCTTAGC
10553-10575	AGCAGTTGACCACAAGCTTAGCT
10554-10576	GCAGTTGACCACAAGCTTAGCTT
10555-10577	CAGTTGACCACAAGCTTAGCTTG
10556-10578	AGTTGACCACAAGCTTAGCTTGG
10557-10579	GTTGACCACAAGCTTAGCTTGGA
10558-10580	TTGACCACAAGCTTAGCTTGAA
10559-10581	TGACCACAAGCTTAGCTTGAAA
10560-10582	GACCACAAGCTTAGCTTGAAAAG
10561-10583	ACCACAAGCTTAGCTTGAAAAGC
10562-10584	CCACAAGCTTAGCTTGAAAAGCC
10563-10585	CACAAGCTTAGCTTGAAAAGCCT
10564-10586	ACAAGCTTAGCTTGAAAAGCCTC
10565-10587	CAAGCTTAGCTTGAAAAGCCTCA
10566-10588	AAGCTTAGCTTGAAAAGCCTCAC
10567-10589	AGCTTAGCTTGAAAAGCCTCACC
10568-10590	GCTTAGCTTGAAAAGCCTCACCT
10569-10591	CTTAGCTTGAAAAGCCTCACCTC
10570-10592	TTAGCTTGAAAAGCCTCACCTCT
10571-10593	TAGCTTGAAAAGCCTCACCTCTT
10572-10594	AGCTTGAAAAGCCTCACCTCTTA
10573-10595	GCTTGAAAAGCCTCACCTCTTAC
10574-10596	CTTGAAAAGCCTCACCTCTTACT
10575-10597	TTGAAAAGCCTCACCTCTTACTT
10576-10598	TGAAAAGCCTCACCTCTTACTTT
10577-10599	GGAAAAGCCTCACCTCTTACTTTT
10578-10600	GAAAAGCCTCACCTCTTACTTTTC
10579-10601	AAAGCCTCACCTCTTACTTTTCC
10580-10602	AAGCCTCACCTCTTACTTTTCCA
10581-10603	AGCCTCACCTCTTACTTTTCCAT
10582-10604	GCCTCACCTCTTACTTTTCCATT
10583-10605	CCTCACCTCTTACTTTTCCATTG
10584-10606	CTCACCTCTTACTTTTCCATTGA
10585-10607	TCACCTCTTACTTTTCCATTGAG
10586-10608	CACCTCTTACTTTTCCATTGAGT
10587-10609	ACCTCTTACTTTTCCATTGAGTC
10588-10610	CCTCTTACTTTTCCATTGAGTCA
10589-10611	CTCTTACTTTTCCATTGAGTCAT
10590-10612	TCTTACTTTTCCATTGAGTCATC
10591-10613	CTTACTTTTCCATTGAGTCATCT
10592-10614	TTACTTTTCCATTGAGTCATCTA
10593-10615	TACTTTTCCATTGAGTCATCTAC
10594-10616	ACTTTTCCATTGAGTCATCTACC
10595-10617	CTTTTCCATTGAGTCATCTACCA
10596-10618	TTTTTCCATTGAGTCATCTACCAA
10597-10619	TTTCCATTGAGTCATCTACCAAA
10598-10620	TTCCATTGAGTCATCTACCAAAG
10599-10621	TCCATTGAGTCATCTACCAAAGG
10600-10622	CCATTGAGTCATCTACCAAAGGA
10601-10623	CATTGAGTCATCTACCAAAGGAG
10602-10624	ATTGAGTCATCTACCAAAGGAGA

Position	Sequence
10603-10625	TTGAGTCATCTACCAAAGGAGAT
10604-10626	TGAGTCATCTACCAAAGGAGATG
10605-10627	GAGTCATCTACCAAAGGAGATGT
10606-10628	AGTCATCTACCAAAGGAGATGTC
10607-10629	GTCATCTACCAAAGGAGATGTCA
10608-10630	TCATCTACCAAAGGAGATGTCAA
10609-10631	CATCTACCAAAGGAGATGTCAAG
10610-10632	ATCTACCAAAGGAGATGTCAAGG
10611-10633	TCTACCAAAGGAGATGTCAAGGG
10612-10634	CTACCAAAGGAGATGTCAAGGGT
10613-10635	TACCAAAGGAGATGTCAAGGGTT
10614-10636	ACCAAAGGAGATGTCAAGGGTTC
10615-10637	CCAAAGGAGATGTCAAGGGTTCG
10616-10638	CAAAGGAGATGTCAAGGGTTCGG
10617-10639	AAAGGAGATGTCAAGGGTTCGGT
10618-10640	AAGGAGATGTCAAGGGTTCGGTT
10619-10641	AGGAGATGTCAAGGGTTCGGTTC
10620-10642	GGAGATGTCAAGGGTTCGGTTCT
10621-10643	GAGATGTCAAGGGTTCGGTTCTT
10622-10644	AGATGTCAAGGGTTCGGTTCTTT
10623-10645	GATGTCAAGGGTTCGGTTCTTTC
10624-10646	ATGTCAAGGGTTCGGTTCTTTTCT
10625-10647	TGTCAAGGGTTCGGTTCTTTCTC
10626-10648	GTCAGGGTTCGGTTCTTTCTCG
10627-10649	TCAAGGGTTCGGTTCTTTCTCGG
10628-10650	CAAGGGTTCGGTTCTTTCTCGGG
10629-10651	AAGGGTTCGGTTCTTTCTCGGGA
10630-10652	AGGGTTCGGTTCTTTCTCGGGAA
10631-10653	GGTTCGGTTCTTTCTCGGGAAT
10632-10654	GGTTCGGTTCTTTCTCGGGAATA
10633-10655	GTCGGTTCTTTCTCGGGAATAT
10634-10656	TCGGTTCTTTCTCGGGAATAT
10635-10657	TCGGTTCTTTCTCGGGAATATTC
10636-10658	CGGTCTTTCTCGGGAATATTC
10637-10659	GGTCTTTCTCGGGAATATTCAG
10638-10660	GTCTTTCTCGGGAATATTCAGG
10639-10661	TTCTTTCTCGGGAATATTCAGGA
10640-10662	TCTTTCTCGGGAATATTCAGGAA
10641-10663	CTTTCTCGGGAATATTCAGGAAC
10642-10664	TTTCTCGGGAATATTCAGGAACT
10643-10665	TTCTCGGGAATATTCAGGAACTA
10644-10666	TCTCGGGAATATTCAGGAACTAT
10645-10667	CTCGGGAATATTCAGGAACTATT
10646-10668	TCGGGAATATTCAGGAACTATTG
10647-10669	CGGGAATATTCAGGAACTATTGC
10648-10670	GGAATATTCAGGAACTATTGCT
10649-10671	GGAATATTCAGGAACTATTGCTA
10650-10672	GAATATTCAGGAACTATTGCTAG
10651-10673	AATATTCAGGAACTATTGCTAGT
10652-10674	ATATTCAGGAACTATTGCTAGTG
10653-10675	TATTCAGGAACTATTGCTAGTGA
10654-10676	ATTCAGGAACTATTGCTAGTGAG
10655-10677	TTCAGGAACTATTGCTAGTGAGG
10656-10678	TCAGGAACTATTGCTAGTGAGGC
10657-10679	CAGGAACTATTGCTAGTGAGGCC
10658-10680	AGGAACTATTGCTAGTGAGGCCA
10659-10681	GGAACATTGCTAGTGAGGCCAA
10660-10682	GAACATTGCTAGTGAGGCCAAC
10661-10683	AACTATTGCTAGTGAGGCCAAC
10662-10684	ACTATTGCTAGTGAGGCCAACAC
10663-10685	CTATTGCTAGTGAGGCCAACACT
10664-10686	TATTGCTAGTGAGGCCAACACTT
10665-10687	ATTGCTAGTGAGGCCAACACTTA
10666-10688	TTGCTAGTGAGGCCAACACTTAC
10667-10689	TGCTAGTGAGGCCAACACTTACT
10668-10690	GCTAGTGAGGCCAACACTTACTT

Position	Sequence
10669-10691	CTAGTGAGGCCAACACTTACTTG
10670-10692	TAGTGAGGCCAACACTTACTTGA
10671-10693	AGTGAGGCCAACACTTACTTGAA
10672-10694	GTGAGGCCAACACTTACTTGAAT
10673-10695	TGAGGCCAACACTTACTTGAATT
10674-10696	GAGGCCAACACTTACTTGAATTC
10675-10697	AGGCCAACACTTACTTGAATTCC
10676-10698	GGCCAACACTTACTTGAATTCCA
10677-10699	GCCAACACTTACTTGAATTCCAA
10678-10700	CCAACACTTACTTGAATTCCAAG
10679-10701	CAACACTTACTTGAATTCCAAGA
10680-10702	AACACTTACTTGAATTCCAAGAG
10681-10703	ACACTTACTTGAATTCCAAGAGC
10682-10704	CACTTACTTGAATTCCAAGAGCA
10683-10705	ACTTACTTGAATTCCAAGAGCAC
10684-10706	CTTACTTGAATTCCAAGAGCACA
10685-10707	TTACTTGAATTCCAAGAGCACAC
10686-10708	TACTTGAATTCCAAGAGCACACG
10687-10709	ACTTGAATTCCAAGAGCACACGG
10688-10710	CTTGAATTCCAAGAGCACACGGT
10689-10711	TTGAATTCCAAGAGCACACGGTC
10690-10712	TGAATTCCAAGAGCACACGGTCT
10691-10713	GAATTCCAAGAGCACACGGTCTT
10692-10714	AATTCCAAGAGCACACGGTCTTC
10693-10715	ATTCCAAGAGCACACGGTCTTCA
10694-10716	TTCCAAGAGCACACGGTCTTCAG
10695-10717	TCCAAGAGCACACGGTCTTCAGT
10696-10718	CCAAGAGCACACGGTCTTCAGTG
10697-10719	CAAGAGCACACGGTCTTCAGTGA
10698-10720	AAGAGCACACGGTCTTCAGTGAA
10699-10721	AGAGCACACGGTCTTCAGTGAAG
10700-10722	GAGCACACGGTCTTCAGTGAAGC
10701-10723	AGCACACGGTCTTCAGTGAAGCT
10702-10724	GCACACGGTCTTCAGTGAAGCTG
10703-10725	CACACGGTCTTCAGTGAAGCTGC
10704-10726	ACACGGTCTTCAGTGAAGCTGCA
10705-10727	CACGGTCTTCAGTGAAGCTGCAG
10706-10728	ACGGTCTTCAGTGAAGCTGCAGG
10707-10729	CGGTCTTCAGTGAAGCTGCAGGG
10708-10730	GGTCTTCAGTGAAGCTGCAGGGC
10709-10731	GCTTCAGTGAAGCTGCAGGGCA
10710-10732	TCTTCAGTGAAGCTGCAGGGCAC
10711-10733	CTTCAGTGAAGCTGCAGGGCACT
10712-10734	TTCAGTGAAGCTGCAGGGCACTT
10713-10735	TCAGTGAAGCTGCAGGGCACTTC
10714-10736	CAGTGAAGCTGCAGGGCACTTCC
10715-10737	AGTGAAGCTGCAGGGCACTCCA
10716-10738	GTGAAGCTGCAGGGCACTTCCAA
10717-10739	TGAAGCTGCAGGGCACTTCCAAA
10718-10740	GAAGCTGCAGGGCACTTCCAAA
10719-10741	AAGCTGCAGGGCACTTCCAAAAT
10720-10742	AGCTGCAGGGCACTTCCAAAATT
10721-10743	GCTGCAGGGCACTTCCAAAATTG
10722-10744	CTGCAGGGCACTTCCAAAATTGA
10723-10745	TGCAGGGCACTTCCAAAATTGAT
10724-10746	GCAGGGCACTTCCAAAATTGATG
10725-10747	CAGGGCACTTCCAAAATTGATGA
10726-10748	AGGGCACTTCCAAAATTGATGAT
10727-10749	GGGCACTTCCAAAATTGATGATA
10728-10750	GGCACTTCCAAAATTGATGATAT
10729-10751	GCACTTCCAAAATTGATGATATC
10730-10752	CACTTCCAAAATTGATGATATCT
10731-10753	ACTTCCAAAATTGATGATATCTG
10732-10754	CTTCCAAAATTGATGATATCTGG
10733-10755	TTCCAAAATTGATGATATCTGGA
10734-10756	TCCAAAATTGATGATATCTGGAA

Position	Sequence
10735-10757	CCAAAATTGATGATATCTGGAAC
10736-10758	CAAAATTGATGATATCTGGAACC
10737-10759	AAAATTGATGATATCTGGAACCT
10738-10760	AAATTGATGATATCTGGAACCTT
10739-10761	AATTGATGATATCTGGAACCTTG
10740-10762	ATTGATGATATCTGGAACCTTGA
10741-10763	TTGATGATATCTGGAACCTTGAA
10742-10764	TGATGATATCTGGAACCTTGAAG
10743-10765	GATGATATCTGGAACCTTGAAGT
10744-10766	ATGATATCTGGAACCTTGAAGTA
10745-10767	TGATATCTGGAACCTTGAAGTAA
10746-10768	GATATCTGGAACCTTGAAGTAAA
10747-10769	ATATCTGGAACCTTGAAGTAAAA
10748-10770	TATCTGGAACCTTGAAGTAAAAG
10749-10771	ATCTGGAACCTTGAAGTAAAAGA
10750-10772	TCTGGAACCTTGAAGTAAAAGAA
10751-10773	CTGGAACCTTGAAGTAAAAGAAA
10752-10774	TGGAACCTTGAAGTAAAAGAAAA
10753-10775	GGAACCTTGAAGTAAAAGAAAAT
10754-10776	GAACCTTGAAGTAAAAGAAAATT
10755-10777	AACCTTGAAGTAAAAGAAAATTT
10756-10778	ACCTTGAAGTAAAAGAAAATTTT
10757-10779	CCTTGAAGTAAAAGAAAATTTTG
10758-10780	CTTGAAGTAAAAGAAAATTTTGC
10759-10781	TTGAAGTAAAAGAAAATTTTGCT
10760-10782	TGAAGTAAAAGAAAATTTTGCTG
10761-10783	GAAGTAAAAGAAAATTTTGCTGG
10762-10784	AAGTAAAAGAAAATTTTGCTGGG
10763-10785	AGTAAAAGAAAATTTTGCTGGGAG
10764-10786	GTAAGAAAATTTTGCTGGGAGA
10765-10787	TAAAAGAAAATTTTGCTGGGAGAA
10766-10788	AAAAGAAAATTTTGCTGGGAGAG
10767-10789	AAAGAAAATTTTGCTGGGAGAGC
10768-10790	AAGAAAATTTTGCTGGGAGAGCC
10769-10791	AGAAAATTTTGCTGGGAGAGCCA
10770-10792	GAAAATTTTGCTGGGAGAGCCAC
10771-10793	AAAATTTTGCTGGGAGAGCCACA
10772-10794	AAATTTTGCTGGGAGAGCCACAC
10773-10795	AATTTTGCTGGGAGAGCCACACT
10774-10796	ATTTTGCTGGGAGAGCCACACTC
10775-10797	TTTTGCTGGGAGAGCCACACTCC
10776-10798	TTTGCTGGGAGAGCCACACTCCA
10777-10799	TTGCTGGGAGAGCCACACTCCAA
10778-10800	TGCTGGGAGAGCCACACTCCAAC
10779-10801	GCTGGGAGAGCCACACTCCAACG
10780-10802	CTGGGAGAGCCACACTCCAACGC
10781-10803	TGGGAGAGCCACACTCCAACGCA
10782-10804	GGGAGAGCCACACTCCAACGCAT
10783-10805	GAGAGAGCCACACTCCAACGCATA
10784-10806	AGAAGCCACACTCCAACGCATAT
10785-10807	GAAGCCACACTCCAACGCATATA
10786-10808	AAGCCACACTCCAACGCATATAT
10787-10809	AGCCACACTCCAACGCATATATT
10788-10810	GCCACACTCCAACGCATATATTC
10789-10811	CCACACTCCAACGCATATATTCC
10790-10812	CACACTCCAACGCATATATTCCC
10791-10813	ACACTCCAACGCATATATTCCCT
10792-10814	CACTCCAACGCATATATTCCCTC
10793-10815	ACTCCAACGCATATATTCCCTCT
10794-10816	CTCCAACGCATATATTCCCTCTG
10795-10817	TCCAACGCATATATTCCCTCTGG
10796-10818	CCAACGCATATATTCCCTCTGGG
10797-10819	CAACGCATATATTCCCTCTGGGA
10798-10820	AACGCATATATTCCCTCTGGGAG
10799-10821	ACGCATATATTCCCTCTGGGAGC
10800-10822	CGCATATATTCCCTCTGGGAGCA

Position	Sequence
10801-10823	GCATATATTCCTCTGGGAGCAC
10802-10824	CATATATTCCTCTGGGAGCACA
10803-10825	ATATATTCCTCTGGGAGCACAG
10804-10826	TATATTCCTCTGGGAGCACAGT
10805-10827	ATATTCCTCTGGGAGCACAGTA
10806-10828	TATTCCTCTGGGAGCACAGTAC
10807-10829	ATTCCCTCTGGGAGCACAGTACG
10808-10830	TTCCTCTGGGAGCACAGTACGA
10809-10831	TCCCTCTGGGAGCACAGTACGAA
10810-10832	CCCTCTGGGAGCACAGTACGAAA
10811-10833	CCTCTGGGAGCACAGTACGAAAA
10812-10834	CTCTGGGAGCACAGTACGAAAAA
10813-10835	TCTGGGAGCACAGTACGAAAAAC
10814-10836	CTGGGAGCACAGTACGAAAAACC
10815-10837	TGGGAGCACAGTACGAAAAACCA
10816-10838	GGGAGCACAGTACGAAAAACCAC
10817-10839	GGAGCACAGTACGAAAAACCACT
10818-10840	GAGCACAGTACGAAAAACCACTT
10819-10841	AGCACAGTACGAAAAACCACTTA
10820-10842	GCACAGTACGAAAAACCACTTAC
10821-10843	CACAGTACGAAAAACCACTTACA
10822-10844	ACAGTACGAAAAACCACTTACAG
10823-10845	CAGTACGAAAAACCACTTACAGC
10824-10846	AGTACGAAAAACCACTTACAGCT
10825-10847	GTACGAAAAACCACTTACAGCTA
10826-10848	TACGAAAAACCACTTACAGCTAG
10827-10849	ACGAAAAACCACTTACAGCTAGA
10828-10850	CGAAAAACCACTTACAGCTAGAG
10829-10851	GAAAAACCACTTACAGCTAGAGG
10830-10852	AAAAACCACTTACAGCTAGAGGG
10831-10853	AAAACCACTTACAGCTAGAGGGC
10832-10854	AAACCACTTACAGCTAGAGGGCC
10833-10855	AACCACTTACAGCTAGAGGGCCT
10834-10856	ACCCTTACAGCTAGAGGGCCTC
10835-10857	CCACTTACAGCTAGAGGGCCTCT
10836-10858	CACTTACAGCTAGAGGGCCTCTT
10837-10859	ACTTACAGCTAGAGGGCCTCTTT
10838-10860	CTTACAGCTAGAGGGCCTCTTTT
10839-10861	TTACAGCTAGAGGGCCTCTTTT
10840-10862	TACAGCTAGAGGGCCTCTTTTTC
10841-10863	ACAGCTAGAGGGCCTCTTTTTC
10842-10864	CAGCTAGAGGGCCTCTTTTTCAC
10843-10865	AGCTAGAGGGCCTCTTTTTCACC
10844-10866	GCTAGAGGGCCTCTTTTTCACCA
10845-10867	CTAGAGGGCCTCTTTTTCACCAA
10846-10868	TAGAGGGCCTCTTTTTCACCAAC
10847-10869	AGAGGGCCTCTTTTTCACCAACG
10848-10870	GAGGGCCTCTTTTTCACCAACGG
10849-10871	AGGGCCTCTTTTTCACCAACGGA
10850-10872	GGGCCTCTTTTTCACCAACGGAG
10851-10873	GGCCTCTTTTTCACCAACGGAGA
10852-10874	GCCTCTTTTTCACCAACGGAGAA
10853-10875	CCTCTTTTTCACCAACGGAGAAC
10854-10876	CTCTTTTTCACCAACGGAGAAC
10855-10877	TCTTTTTCACCAACGGAGAACAT
10856-10878	CTTTTTCACCAACGGAGAACATA
10857-10879	TTTTTTCACCAACGGAGAACATAC
10858-10880	TTTTTTCACCAACGGAGAACATACA
10859-10881	TTTTCACCAACGGAGAACATACAA
10860-10882	TTTTCACCAACGGAGAACATACAAG
10861-10883	TTTTCACCAACGGAGAACATACAAGC
10862-10884	TTTTCACCAACGGAGAACATACAAGCA
10863-10885	TTTTCACCAACGGAGAACATACAAGCAA
10864-10886	TTTTCACCAACGGAGAACATACAAGCAA
10865-10887	TTTTCACCAACGGAGAACATACAAGCAAAG
10866-10888	TTTTCACCAACGGAGAACATACAAGCAAAGC

Position	Sequence
10867-10889	ACGGAGAACATACAAGCAAAGCC
10868-10890	CGGAGAACATACAAGCAAAGCCA
10869-10891	GGAGAACATACAAGCAAAGCCAC
10870-10892	GAGAACATACAAGCAAAGCCACC
10871-10893	AGAACATACAAGCAAAGCCACCC
10872-10894	GAACATACAAGCAAAGCCACCCT
10873-10895	AACATACAAGCAAAGCCACCCTG
10874-10896	ACATACAAGCAAAGCCACCCTGG
10875-10897	CATACAAGCAAAGCCACCCTGGA
10876-10898	ATACAAGCAAAGCCACCCTGGAA
10877-10899	TACAAGCAAAGCCACCCTGGAAC
10878-10900	ACAAGCAAAGCCACCCTGGAACT
10879-10901	CAAGCAAAGCCACCCTGGAACTC
10880-10902	AAGCAAAGCCACCCTGGAACTCT
10881-10903	AGCAAAGCCACCCTGGAACTCTC
10882-10904	GCAAAGCCACCCTGGAACTCTCT
10883-10905	CAAAGCCACCCTGGAACTCTCTC
10884-10906	AAAGCCACCCTGGAACTCTCTCC
10885-10907	AAGCCACCCTGGAACTCTCTCCA
10886-10908	AGCCACCCTGGAACTCTCTCCAT
10887-10909	GCCACCCTGGAACTCTCTCCATG
10888-10910	CCACCCTGGAACTCTCTCCATGG
10889-10911	CACCCTGGAACTCTCTCCATGGC
10890-10912	ACCCTGGAACTCTCTCCATGGCA
10891-10913	CCCTGGAACTCTCTCCATGGCAA
10892-10914	CCTGGAACTCTCTCCATGGCAAA
10893-10915	CTGGAACTCTCTCCATGGCAAAT
10894-10916	TGGAACTCTCTCCATGGCAAATG
10895-10917	GGAACTCTCTCCATGGCAAATGT
10896-10918	GAACTCTCTCCATGGCAAATGTC
10897-10919	AACTCTCTCCATGGCAAATGTCA
10898-10920	ACTCTCTCCATGGCAAATGTCAG
10899-10921	CTCTCTCCATGGCAAATGTCAGC
10900-10922	TCTCTCCATGGCAAATGTCAGCT
10901-10923	CTCTCCATGGCAAATGTCAGCTC
10902-10924	TCTCCATGGCAAATGTCAGCTCT
10903-10925	CTCCATGGCAAATGTCAGCTCTT
10904-10926	TCCATGGCAAATGTCAGCTCTTG
10905-10927	CCATGGCAAATGTCAGCTCTTGT
10906-10928	CATGGCAAATGTCAGCTCTTGTT
10907-10929	ATGGCAAATGTCAGCTCTTGTTT
10908-10930	TGGCAAATGTCAGCTCTTGTTCA
10909-10931	GGCAAATGTCAGCTCTTGTTTCAG
10910-10932	GCAAATGTCAGCTCTTGTTTCAGG
10911-10933	CAAATGTCAGCTCTTGTTTCAGGT
10912-10934	AAATGTCAGCTCTTGTTTCAGGTC
10913-10935	AATGTCAGCTCTTGTTTCAGGTCC
10914-10936	ATGTCAGCTCTTGTTTCAGGTCCA
10915-10937	TGTCAGCTCTTGTTTCAGGTCCAT
10916-10938	GTCAGCTCTTGTTTCAGGTCCATG
10917-10939	TCAGCTCTTGTTTCAGGTCCATGC
10918-10940	CAGCTCTTGTTTCAGGTCCATGCA
10919-10941	AGCTCTTGTTTCAGGTCCATGCAA
10920-10942	GCTCTTGTTTCAGGTCCATGCAAG
10921-10943	CTCTTGTTTCAGGTCCATGCAAGT
10922-10944	TCTTGTTTCAGGTCCATGCAAGTC
10923-10945	CTTGTTTCAGGTCCATGCAAGTCA
10924-10946	TTTGTTTCAGGTCCATGCAAGTCAG
10925-10947	TGTTCAGGTCCATGCAAGTCAGC
10926-10948	GTTTCAGGTCCATGCAAGTCAGCC
10927-10949	TTCAGGTCCATGCAAGTCAGCCC
10928-10950	TCAGGTCCATGCAAGTCAGCCCA
10929-10951	CAGGTCCATGCAAGTCAGCCCAG
10930-10952	AGGTCCATGCAAGTCAGCCCAGT
10931-10953	GGTCCATGCAAGTCAGCCCAGTT
10932-10954	GTCCATGCAAGTCAGCCCAGTTC

Position	Sequence
10933-10955	TCCATGCAAGTCAGCCCAGTTCC
10934-10956	CCATGCAAGTCAGCCCAGTTCCCT
10935-10957	CATGCAAGTCAGCCCAGTTCCCTT
10936-10958	ATGCAAGTCAGCCCAGTTCCCTTC
10937-10959	TGCAAGTCAGCCCAGTTCCCTTCC
10938-10960	GCAAGTCAGCCCAGTTCCCTTCCA
10939-10961	CAAGTCAGCCCAGTTCCCTTCCAT
10940-10962	AAGTCAGCCCAGTTCCCTTCCATG
10941-10963	AGTCAGCCCAGTTCCCTTCCATGA
10942-10964	GTCAGCCCAGTTCCCTTCCATGAT
10943-10965	TCAGCCCAGTTCCCTTCCATGATT
10944-10966	CAGCCCAGTTCCCTTCCATGATTT
10945-10967	AGCCCAGTTCCCTTCCATGATTTT
10946-10968	GCCCAGTTCCCTTCCATGATTTCC
10947-10969	CCCAGTTCCCTTCCATGATTTCCC
10948-10970	CCAGTTCCCTTCCATGATTTCCCT
10949-10971	CAGTTCCCTTCCATGATTTCCCTG
10950-10972	AGTTCCCTTCCATGATTTCCCTGA
10951-10973	GTTCCCTTCCATGATTTCCCTGAC
10952-10974	TTCCTTCCATGATTTCCCTGACC
10953-10975	TCCTTCCATGATTTCCCTGACCT
10954-10976	CCTTCCATGATTTCCCTGACCTT
10955-10977	CTTCCATGATTTCCCTGACCTTG
10956-10978	TTCCATGATTTCCCTGACCTTGG
10957-10979	TCCATGATTTCCCTGACCTTGGC
10958-10980	CCATGATTTCCCTGACCTTGGCC
10959-10981	CATGATTTCCCTGACCTTGGCCA
10960-10982	ATGATTTCCCTGACCTTGGCCAG
10961-10983	TGATTTCCCTGACCTTGGCCAGG
10962-10984	GATTTCCCTGACCTTGGCCAGGA
10963-10985	ATTTCCCTGACCTTGGCCAGGAA
10964-10986	TTCCCTGACCTTGGCCAGGAAG
10965-10987	TTCCCTGACCTTGGCCAGGAAGT
10966-10988	TCCCTGACCTTGGCCAGGAAGTG
10967-10989	CCCTGACCTTGGCCAGGAAGTGG
10968-10990	CCTGACCTTGGCCAGGAAGTGGC
10969-10991	CTGACCTTGGCCAGGAAGTGGCC
10970-10992	TGACCTTGGCCAGGAAGTGGCCC
10971-10993	GACCTTGGCCAGGAAGTGGCCCT
10972-10994	ACCTTGGCCAGGAAGTGGCCCTG
10973-10995	CCTTGGCCAGGAAGTGGCCCTGA
10974-10996	CTTGGCCAGGAAGTGGCCCTGAA
10975-10997	TTGGCCAGGAAGTGGCCCTGAAT
10976-10998	TGGCCAGGAAGTGGCCCTGAATG
10977-10999	GGCCAGGAAGTGGCCCTGAATGC
10978-11000	GCCAGGAAGTGGCCCTGAATGCT
10979-11001	CCAGGAAGTGGCCCTGAATGCTA
10980-11002	CAGGAAGTGGCCCTGAATGCTAA
10981-11003	AGGAAGTGGCCCTGAATGCTAAC
10982-11004	GGAAGTGGCCCTGAATGCTAAC
10983-11005	GAAGTGGCCCTGAATGCTAACAC
10984-11006	AAGTGGCCCTGAATGCTAACACT
10985-11007	AGTGGCCCTGAATGCTAACACTA
10986-11008	GTGGCCCTGAATGCTAACACTAA
10987-11009	TGGCCCTGAATGCTAACACTAAG
10988-11010	GGCCCTGAATGCTAACACTAAGA
10989-11011	GCCCTGAATGCTAACACTAAGAA
10990-11012	CCCTGAATGCTAACACTAAGAAC
10991-11013	CCTGAATGCTAACACTAAGAACC
10992-11014	CTGAATGCTAACACTAAGAACCA
10993-11015	TGAATGCTAACACTAAGAACCCAG
10994-11016	GAATGCTAACACTAAGAACCAGA
10995-11017	AATGCTAACACTAAGAACCAGAA
10996-11018	ATGCTAACACTAAGAACCAGAAG
10997-11019	TGCTAACACTAAGAACCAGAAGA
10998-11020	GCTAACACTAAGAACCAGAAGAT

Position	Sequence
10999-11021	CTAACACTAAGAACCAGAAGATC
11000-11022	TAAACACTAAGAACCAGAAGATCA
11001-11023	AACACTAAGAACCAGAAGATCAG
11002-11024	ACACTAAGAACCAGAAGATCAGA
11003-11025	CACTAAGAACCAGAAGATCAGAT
11004-11026	ACTAAGAACCAGAAGATCAGATG
11005-11027	CTAAGAACCAGAAGATCAGATGG
11006-11028	TAAGAACCAGAAGATCAGATGGA
11007-11029	AAGAACCAGAAGATCAGATGGAA
11008-11030	AGAACCAGAAGATCAGATGGAAA
11009-11031	GAACCAGAAGATCAGATGGAAAA
11010-11032	AACCAGAAGATCAGATGGAAAAA
11011-11033	ACCAGAAGATCAGATGGAAAAAT
11012-11034	CCAGAAGATCAGATGGAAAAATG
11013-11035	CAGAAGATCAGATGGAAAAATGA
11014-11036	AGAAGATCAGATGGAAAAATGAA
11015-11037	GAAGATCAGATGGAAAAATGAAG
11016-11038	AAGATCAGATGGAAAAATGAAGT
11017-11039	AGATCAGATGGAAAAATGAAGTC
11018-11040	GATCAGATGGAAAAATGAAGTCC
11019-11041	ATCAGATGGAAAAATGAAGTCCG
11020-11042	TCAGATGGAAAAATGAAGTCCGG
11021-11043	CAGATGGAAAAATGAAGTCCGGA
11022-11044	AGATGGAAAAATGAAGTCCGGAT
11023-11045	GATGGAAAAATGAAGTCCGGATT
11024-11046	ATGGAAAAATGAAGTCCGGATTC
11025-11047	TGGAAAAATGAAGTCCGGATTCA
11026-11048	GGAAAAATGAAGTCCGGATT CAT
11027-11049	GAAAAATGAAGTCCGGATT CATT
11028-11050	AAAAATGAAGTCCGGATT CATT C
11029-11051	AAATGAAGTCCGGATT CATT CT
11030-11052	AAATGAAGTCCGGATT CATT CTG
11031-11053	AATGAAGTCCGGATT CATT CTGG
11032-11054	ATGAAGTCCGGATT CATT CTGGG
11033-11055	TGAAGTCCGGATT CATT CTGGGT
11034-11056	GAAGTCCGGATT CATT CTGGGTC
11035-11057	AAGTCCGGATT CATT CTGGGTCT
11036-11058	AGTCCGGATT CATT CTGGGTCTT
11037-11059	GTCGGATT CATT CTGGGTCTTT
11038-11060	TCCGGATT CATT CTGGGTCTTTC
11039-11061	CCGGATT CATT CTGGGTCTTTCC
11040-11062	CGGATT CATT CTGGGTCTTTCCA
11041-11063	GGATT CATT CTGGGTCTTTCCAG
11042-11064	GATT CATT CTGGGTCTTTCCAGA
11043-11065	ATT CATT CTGGGTCTTTCCAGAG
11044-11066	TT CATT CTGGGTCTTTCCAGAGC
11045-11067	TCATT CTGGGTCTTTCCAGAGCC
11046-11068	CATT CTGGGTCTTTCCAGAGCCA
11047-11069	ATT CTGGGTCTTTCCAGAGCCAG
11048-11070	TT CTGGGTCTTTCCAGAGCCAGG
11049-11071	TCTGGGTCTTTCCAGAGCCAGGT
11050-11072	CTGGGTCTTTCCAGAGCCAGGTC
11051-11073	TGGGTCTTTCCAGAGCCAGGTCG
11052-11074	GGGTCTTTCCAGAGCCAGGTCGA
11053-11075	GGTCTTTCCAGAGCCAGGTCGAG
11054-11076	GTCCTTTCCAGAGCCAGGTCGAGC
11055-11077	TCTTTCCAGAGCCAGGTCGAGCT
11056-11078	CTTTCCAGAGCCAGGTCGAGCTT
11057-11079	TTTCCAGAGCCAGGTCGAGCTTT
11058-11080	TTCCAGAGCCAGGTCGAGCTTTC
11059-11081	TCCAGAGCCAGGTCGAGCTTTC
11060-11082	CCAGAGCCAGGTCGAGCTTTCCA
11061-11083	CAGAGCCAGGTCGAGCTTTCCAA
11062-11084	AGAGCCAGGTCGAGCTTTCCAAT
11063-11085	GAGCCAGGTCGAGCTTTCCAATG
11064-11086	AGCCAGGTCGAGCTTTCCAATGA

Position	Sequence
11065-11087	GCCAGGTCGAGCTTCCAATGAC
11066-11088	CCAGGTCGAGCTTCCAATGACC
11067-11089	CAGGTCGAGCTTCCAATGACCA
11068-11090	AGGTCGAGCTTCCAATGACCAA
11069-11091	GGTCGAGCTTCCAATGACCAAG
11070-11092	GTCGAGCTTCCAATGACCAAGA
11071-11093	TCGAGCTTCCAATGACCAAGAA
11072-11094	CGAGCTTCCAATGACCAAGAAA
11073-11095	GAGCTTCCAATGACCAAGAAA
11074-11096	AGCTTCCAATGACCAAGAAAAG
11075-11097	GCTTCCAATGACCAAGAAAAGG
11076-11098	CTTCCAATGACCAAGAAAAGGC
11077-11099	TTCCAATGACCAAGAAAAGGCA
11078-11100	TTCCAATGACCAAGAAAAGGCAC
11079-11101	TCCAATGACCAAGAAAAGGCACA
11080-11102	CCAATGACCAAGAAAAGGCACAC
11081-11103	CAATGACCAAGAAAAGGCACACC
11082-11104	AATGACCAAGAAAAGGCACACCT
11083-11105	ATGACCAAGAAAAGGCACACCTT
11084-11106	TGACCAAGAAAAGGCACACCTTG
11085-11107	GACCAAGAAAAGGCACACCTTGA
11086-11108	ACCAAGAAAAGGCACACCTTGAC
11087-11109	CCAAGAAAAGGCACACCTTGACA
11088-11110	CAAGAAAAGGCACACCTTGACAT
11089-11111	AAGAAAAGGCACACCTTGACATT
11090-11112	AGAAAAGGCACACCTTGACATTG
11091-11113	GAAAAGGCACACCTTGACATTGC
11092-11114	AAAAGGCACACCTTGACATTGCA
11093-11115	AAAGGCACACCTTGACATTGCAG
11094-11116	AAGGCACACCTTGACATTGCAGG
11095-11117	AGGCACACCTTGACATTGCAGGA
11096-11118	GGCACACCTTGACATTGCAGGAT
11097-11119	GCACACCTTGACATTGCAGGATC
11098-11120	CACACCTTGACATTGCAGGATCC
11099-11121	ACACCTTGACATTGCAGGATCCT
11100-11122	CACCTTGACATTGCAGGATCCTT
11101-11123	ACCTTGACATTGCAGGATCCTTA
11102-11124	CCTTGACATTGCAGGATCCTTAG
11103-11125	CTTGACATTGCAGGATCCTTAGA
11104-11126	TTGACATTGCAGGATCCTTAGAA
11105-11127	TGACATTGCAGGATCCTTAGAAG
11106-11128	GACATTGCAGGATCCTTAGAAGG
11107-11129	ACATTGCAGGATCCTTAGAAGGA
11108-11130	CATTGCAGGATCCTTAGAAGGAC
11109-11131	ATTGCAGGATCCTTAGAAGGACA
11110-11132	TTGCAGGATCCTTAGAAGGACAC
11111-11133	TGCAGGATCCTTAGAAGGACACC
11112-11134	GCAGGATCCTTAGAAGGACACCT
11113-11135	CAGGATCCTTAGAAGGACACCTA
11114-11136	AGGATCCTTAGAAGGACACCTAA
11115-11137	GGATCCTTAGAAGGACACCTAAG
11116-11138	GATCCTTAGAAGGACACCTAAGG
11117-11139	ATCCTTAGAAGGACACCTAAGGT
11118-11140	TCCTTAGAAGGACACCTAAGGTT
11119-11141	CCTTAGAAGGACACCTAAGGTTC
11120-11142	CTTAGAAGGACACCTAAGGTTC
11121-11143	TTAGAAGGACACCTAAGGTTCCT
11122-11144	TAGAAGGACACCTAAGGTTCCTC
11123-11145	AGAAGGACACCTAAGGTTCCTCA
11124-11146	GAAGGACACCTAAGGTTCCTCAA
11125-11147	AAGGACACCTAAGGTTCCTCAAA
11126-11148	AGGACACCTAAGGTTCCTCAAAA
11127-11149	GGACACCTAAGGTTCCTCAAAA
11128-11150	GACACCTAAGGTTCCTCAAAAAT
11129-11151	ACACCTAAGGTTCCTCAAAAATA
11130-11152	CACCTAAGGTTCCTCAAAAATAT

Position	Sequence
11131-11153	ACCTAAGGTTCTCAAAAATATC
11132-11154	CCTAAGGTTCTCAAAAATATCA
11133-11155	CTAAGGTTCTCAAAAATATCAT
11134-11156	TAAGGTTCTCAAAAATATCATC
11135-11157	AAGGTTCTCAAAAATATCATCC
11136-11158	AGGTTCTCAAAAATATCATCCT
11137-11159	GGTTCCTCAAAAATATCATCCTA
11138-11160	GTTTCCTCAAAAATATCATCCTAC
11139-11161	TTCTCAAAAATATCATCCTACC
11140-11162	TCCTCAAAAATATCATCCTACCA
11141-11163	CCTCAAAAATATCATCCTACCAG
11142-11164	CTCAAAAATATCATCCTACCAGT
11143-11165	TCAAAAATATCATCCTACCAGTC
11144-11166	CAAAAATATCATCCTACCAGTCT
11145-11167	AAAAATATCATCCTACCAGTCTA
11146-11168	AAAATATCATCCTACCAGTCTAT
11147-11169	AAATATCATCCTACCAGTCTATG
11148-11170	AATATCATCCTACCAGTCTATGA
11149-11171	ATATCATCCTACCAGTCTATGAC
11150-11172	TATCATCCTACCAGTCTATGACA
11151-11173	ATCATCCTACCAGTCTATGACAA
11152-11174	TCATCCTACCAGTCTATGACAAG
11153-11175	CATCCTACCAGTCTATGACAAGA
11154-11176	ATCCTACCAGTCTATGACAAGAG
11155-11177	TCCTACCAGTCTATGACAAGAGC
11156-11178	CCTACCAGTCTATGACAAGAGCT
11157-11179	CTACCAGTCTATGACAAGAGCTT
11158-11180	TACCAGTCTATGACAAGAGCTTA
11159-11181	ACCAGTCTATGACAAGAGCTTAT
11160-11182	CCAGTCTATGACAAGAGCTTATG
11161-11183	CAGTCTATGACAAGAGCTTATGG
11162-11184	AGTCTATGACAAGAGCTTATGGG
11163-11185	GTCCTATGACAAGAGCTTATGGGA
11164-11186	TCTATGACAAGAGCTTATGGGAT
11165-11187	CTATGACAAGAGCTTATGGGATT
11166-11188	TATGACAAGAGCTTATGGGATTT
11167-11189	ATGACAAGAGCTTATGGGATTTT
11168-11190	TGACAAGAGCTTATGGGATTTCC
11169-11191	GACAAGAGCTTATGGGATTTCCCT
11170-11192	ACAAGAGCTTATGGGATTTCCCTA
11171-11193	CAAGAGCTTATGGGATTTCCCTAA
11172-11194	AAGAGCTTATGGGATTTCCCTAAA
11173-11195	AGAGCTTATGGGATTTCCCTAAAG
11174-11196	GAGCTTATGGGATTTCCCTAAAGC
11175-11197	AGCTTATGGGATTTCCCTAAAGCT
11176-11198	GCTTATGGGATTTCCCTAAAGCTG
11177-11199	CTTATGGGATTTCCCTAAAGCTGG
11178-11200	TTATGGGATTTCCCTAAAGCTGGA
11179-11201	TATGGGATTTCCCTAAAGCTGGAT
11180-11202	ATGGGATTTCCCTAAAGCTGGATG
11181-11203	TGGGATTTCCCTAAAGCTGGATGT
11182-11204	GGGATTTCCCTAAAGCTGGATGTA
11183-11205	GGATTTCCCTAAAGCTGGATGTAA
11184-11206	GATTTCCCTAAAGCTGGATGTAAC
11185-11207	ATTTCCCTAAAGCTGGATGTAACC
11186-11208	TTTCCCTAAAGCTGGATGTAACCA
11187-11209	TTCCCTAAAGCTGGATGTAACCAC
11188-11210	TCCTAAAGCTGGATGTAACCACC
11189-11211	CCTAAAGCTGGATGTAACCACCA
11190-11212	CTAAAGCTGGATGTAACCACCAG
11191-11213	TAAAGCTGGATGTAACCACCAGC
11192-11214	AAAGCTGGATGTAACCACCAGCA
11193-11215	AAGCTGGATGTAACCACCAGCAT
11194-11216	AGCTGGATGTAACCACCAGCATT
11195-11217	GCTGGATGTAACCACCAGCATTG
11196-11218	CTGGATGTAACCACCAGCATTGG

Position	Sequence
11197-11219	TGGATGTAACCACCAGCATTGGT
11198-11220	GGATGTAACCACCAGCATTGGTA
11199-11221	GATGTAACCACCAGCATTGGTAG
11200-11222	ATGTAACCACCAGCATTGGTAGG
11201-11223	TGTAACCACCAGCATTGGTAGGA
11202-11224	GTAACCACCAGCATTGGTAGGAG
11203-11225	TAACCACCAGCATTGGTAGGAGA
11204-11226	AACCACCAGCATTGGTAGGAGAC
11205-11227	ACCACCAGCATTGGTAGGAGACA
11206-11228	CCACCAGCATTGGTAGGAGACAG
11207-11229	CACCAGCATTGGTAGGAGACAGC
11208-11230	ACCAGCATTGGTAGGAGACAGCA
11209-11231	CCAGCATTGGTAGGAGACAGCAT
11210-11232	CAGCATTGGTAGGAGACAGCATC
11211-11233	AGCATTGGTAGGAGACAGCATCT
11212-11234	GCATTGGTAGGAGACAGCATCTT
11213-11235	CATTGGTAGGAGACAGCATCTTC
11214-11236	ATTGGTAGGAGACAGCATCTTCG
11215-11237	TTGGTAGGAGACAGCATCTTCGT
11216-11238	TGGTAGGAGACAGCATCTTCGTG
11217-11239	GGTAGGAGACAGCATCTTCGTGT
11218-11240	GTAGGAGACAGCATCTTCGTGTT
11219-11241	TAGGAGACAGCATCTTCGTGTTT
11220-11242	AGGAGACAGCATCTTCGTGTTTC
11221-11243	GGAGACAGCATCTTCGTGTTTCA
11222-11244	GAGACAGCATCTTCGTGTTTCAA
11223-11245	AGACAGCATCTTCGTGTTTCAAC
11224-11246	GACAGCATCTTCGTGTTTCAACT
11225-11247	ACAGCATCTTCGTGTTTCAACTG
11226-11248	CAGCATCTTCGTGTTTCAACTGC
11227-11249	AGCATCTTCGTGTTTCAACTGCC
11228-11250	GCATCTTCGTGTTTCAACTGCCT
11229-11251	CATCTTCGTGTTTCAACTGCCTT
11230-11252	ATCTTCGTGTTTCAACTGCCTTT
11231-11253	TCTTCGTGTTTCAACTGCCTTTG
11232-11254	CTTCGTGTTTCAACTGCCTTTGT
11233-11255	TTCGTGTTTCAACTGCCTTTGTG
11234-11256	TCGTGTTTCAACTGCCTTTGTGT
11235-11257	CGTGTTTCAACTGCCTTTGTGTA
11236-11258	GTGTTTCAACTGCCTTTGTGTAC
11237-11259	TGTTTCAACTGCCTTTGTGTACA
11238-11260	GTTTCAACTGCCTTTGTGTACAC
11239-11261	TTTCAACTGCCTTTGTGTACACC
11240-11262	TTC AACTGCCTTTGTGTACACCA
11241-11263	TCAACTGCCTTTGTGTACACCAA
11242-11264	CAACTGCCTTTGTGTACACCAAA
11243-11265	AACTGCCTTTGTGTACACCAAAA
11244-11266	ACTGCCTTTGTGTACACCAAAAA
11245-11267	CTGCCTTTGTGTACACCAAAAAAC
11246-11268	TGCCTTTGTGTACACCAAAAAACC
11247-11269	GCCTTTGTGTACACCAAAAAACCC
11248-11270	CCTTTGTGTACACCAAAAAACCCC
11249-11271	CTTTGTGTACACCAAAAAACCCCA
11250-11272	TTTGTGTACACCAAAAAACCCCAA
11251-11273	TTGTGTACACCAAAAAACCCCAAT
11252-11274	TGTGTACACCAAAAAACCCCAATG
11253-11275	GTGTACACCAAAAAACCCCAATGG
11254-11276	TGTACACCAAAAAACCCCAATGGC
11255-11277	GTACACCAAAAAACCCCAATGGCT
11256-11278	TACACCAAAAAACCCCAATGGCTA
11257-11279	ACACCAAAAAACCCCAATGGCTAT
11258-11280	CACCAAAAAACCCCAATGGCTATT
11259-11281	ACCAAAAAACCCCAATGGCTATTTC
11260-11282	CCA AAAAAACCCCAATGGCTATTCA
11261-11283	CAAAAAACCCCAATGGCTATTTCAT
11262-11284	AAAAACCCCAATGGCTATTTCATT

Position	Sequence
11263-11285	AAAACCCCAATGGCTATTCATTC
11264-11286	AAACCCCAATGGCTATTCATTC
11265-11287	AACCCCAATGGCTATTCATTC
11266-11288	ACCCCAATGGCTATTCATTC
11267-11289	CCCCAATGGCTATTCATTC
11268-11290	CCCAATGGCTATTCATTC
11269-11291	CCAATGGCTATTCATTC
11270-11292	CAATGGCTATTCATTC
11271-11293	AATGGCTATTCATTC
11272-11294	ATGGCTATTCATTC
11273-11295	TGGCTATTCATTC
11274-11296	GGCTATTCATTC
11275-11297	GCTATTCATTC
11276-11298	CTATTCATTC
11277-11299	TATTCATTC
11278-11300	ATTCATTC
11279-11301	TTCATTC
11280-11302	TCATTC
11281-11303	CATTC
11282-11304	ATTC
11283-11305	TTCTCCATCCCTGTAAAAGTTT
11284-11306	TCTCCATCCCTGTAAAAGTTT
11285-11307	CTCCATCCCTGTAAAAGTTT
11286-11308	TCCATCCCTGTAAAAGTTT
11287-11309	CCATCCCTGTAAAAGTTT
11288-11310	CATCCCTGTAAAAGTTT
11289-11311	ATCCCTGTAAAAGTTT
11290-11312	TCCCTGTAAAAGTTT
11291-11313	CCCTGTAAAAGTTT
11292-11314	CCTGTAAAAGTTT
11293-11315	CTGTAAAAGTTT
11294-11316	TGTAAAAGTTT
11295-11317	GTAAGTTT
11296-11318	TAAAGTTT
11297-11319	AAAAGTTT
11298-11320	AAAGTTT
11299-11321	AAGTTT
11300-11322	AGTTT
11301-11323	GTTTGGCTGATAAATTCATTAC
11302-11324	TTTGGCTGATAAATTCATTACT
11303-11325	FTTGGCTGATAAATTCATTACTC
11304-11326	TTGGCTGATAAATTCATTACTCC
11305-11327	TGGCTGATAAATTCATTACTCCT
11306-11328	GGCTGATAAATTCATTACTCCTG
11307-11329	GCTGATAAATTCATTACTCCTGG
11308-11330	CTGATAAATTCATTACTCCTGGG
11309-11331	TGATAAATTCATTACTCCTGGGC
11310-11332	GATAAATTCATTACTCCTGGGCT
11311-11333	ATAAATTCATTACTCCTGGGCTG
11312-11334	TAAATTCATTACTCCTGGGCTGA
11313-11335	AAATTCATTACTCCTGGGCTGAA
11314-11336	AATTCATTACTCCTGGGCTGAAA
11315-11337	ATTCATTACTCCTGGGCTGAAAC
11316-11338	TTCATTACTCCTGGGCTGAAACT
11317-11339	TCATTACTCCTGGGCTGAAACTA
11318-11340	CATTACTCCTGGGCTGAAACTAA
11319-11341	ATTACTCCTGGGCTGAAACTAAA
11320-11342	TTACTCCTGGGCTGAAACTAAAT
11321-11343	TACTCCTGGGCTGAAACTAAATG
11322-11344	ACTCCTGGGCTGAAACTAAATGA
11323-11345	CTCCTGGGCTGAAACTAAATGAT
11324-11346	TCCTGGGCTGAAACTAAATGATC
11325-11347	CCTGGGCTGAAACTAAATGATCT
11326-11348	CTGGGCTGAAACTAAATGATCTA
11327-11349	TGGGCTGAAACTAAATGATCTAA
11328-11350	GGGCTGAAACTAAATGATCTAAA

Position	Sequence
11329-11351	GGCTGAACTAAATGATCTAAAT
11330-11352	GCTGAACTAAATGATCTAAATT
11331-11353	CTGAACTAAATGATCTAAATTC
11332-11354	TGAACTAAATGATCTAAATTCA
11333-11355	GAACTAAATGATCTAAATTCAG
11334-11356	AACTAAATGATCTAAATTCAGT
11335-11357	AACTAAATGATCTAAATTCAGTT
11336-11358	ACTAAATGATCTAAATTCAGTTC
11337-11359	CTAAATGATCTAAATTCAGTTCT
11338-11360	TAAATGATCTAAATTCAGTTCTT
11339-11361	AAATGATCTAAATTCAGTTCTTG
11340-11362	AATGATCTAAATTCAGTTCTTGT
11341-11363	ATGATCTAAATTCAGTTCTTGTC
11342-11364	TGATCTAAATTCAGTTCTTGTC
11343-11365	GATCTAAATTCAGTTCTTGTCAT
11344-11366	ATCTAAATTCAGTTCTTGTCATG
11345-11367	TCTAAATTCAGTTCTTGTCATGC
11346-11368	CTAAATTCAGTTCTTGTCATGCC
11347-11369	TAAATTCAGTTCTTGTCATGCCT
11348-11370	AAATTCAGTTCTTGTCATGCCTA
11349-11371	AATTCAGTTCTTGTCATGCCTAC
11350-11372	ATTCAGTTCTTGTCATGCCTACG
11351-11373	TTCAGTTCTTGTCATGCCTACGT
11352-11374	TCAGTTCTTGTCATGCCTACGTT
11353-11375	CAGTTCTTGTCATGCCTACGTTT
11354-11376	AGTTCTTGTCATGCCTACGTTCC
11355-11377	GTTCTTGTCATGCCTACGTTCCA
11356-11378	TTCTTGTCATGCCTACGTTCCAT
11357-11379	TCTTGTCATGCCTACGTTCCATG
11358-11380	CTTGTCATGCCTACGTTCCATGT
11359-11381	TTGTCATGCCTACGTTCCATGTC
11360-11382	TGTCATGCCTACGTTCCATGTCC
11361-11383	GTCATGCCTACGTTCCATGTCCC
11362-11384	TCATGCCTACGTTCCATGTCCCA
11363-11385	CATGCCTACGTTCCATGTCCCAT
11364-11386	ATGCCTACGTTCCATGTCCCATT
11365-11387	TGCCTACGTTCCATGTCCCATTT
11366-11388	GCCTACGTTCCATGTCCCATTTA
11367-11389	CCTACGTTCCATGTCCCATTTAC
11368-11390	CTACGTTCCATGTCCCATTTACA
11369-11391	TACGTTCCATGTCCCATTTACAG
11370-11392	ACGTTCCATGTCCCATTTACAGA
11371-11393	CGTTCCATGTCCCATTTACAGAT
11372-11394	GTTCATGTCCCATTTACAGATC
11373-11395	TTCCATGTCCCATTTACAGATCT
11374-11396	TCCATGTCCCATTTACAGATCTT
11375-11397	CCATGTCCCATTTACAGATCTTC
11376-11398	CATGTCCCATTTACAGATCTTCA
11377-11399	ATGTCCCATTTACAGATCTTCAG
11378-11400	TGTCCCATTTACAGATCTTCAGG
11379-11401	GTCCCATTTACAGATCTTCAGGT
11380-11402	TCCATTTACAGATCTTCAGGTT
11381-11403	CCATTTACAGATCTTCAGGTTT
11382-11404	CCATTTACAGATCTTCAGGTTCC
11383-11405	CATTTACAGATCTTCAGGTTCCA
11384-11406	ATTTACAGATCTTCAGGTTCCAT
11385-11407	TTTACAGATCTTCAGGTTCCATC
11386-11408	TTACAGATCTTCAGGTTCCATCG
11387-11409	TACAGATCTTCAGGTTCCATCGT
11388-11410	ACAGATCTTCAGGTTCCATCGTG
11389-11411	CAGATCTTCAGGTTCCATCGTGC
11390-11412	AGATCTTCAGGTTCCATCGTGCA
11391-11413	GATCTTCAGGTTCCATCGTGCAA
11392-11414	ATCTTCAGGTTCCATCGTGCAAA
11393-11415	TCTTCAGGTTCCATCGTGCAAAC
11394-11416	CTTCAGGTTCCATCGTGCAAAC

Position	Sequence
11395-11417	TTCAGGTTCCATCGTGCAAACCTT
11396-11418	TCAGGTTCCATCGTGCAAACCTTG
11397-11419	CAGGTTCCATCGTGCAAACCTTGA
11398-11420	AGGTCCATCGTGCAAACCTTGAC
11399-11421	GGTCCATCGTGCAAACCTTGACT
11400-11422	GTTCCATCGTGCAAACCTTGACTT
11401-11423	TTCCATCGTGCAAACCTTGACTTC
11402-11424	TCCATCGTGCAAACCTTGACTTCA
11403-11425	CCATCGTGCAAACCTTGACTTCAG
11404-11426	CATCGTGCAAACCTTGACTTCAGA
11405-11427	ATCGTGCAAACCTTGACTTCAGAG
11406-11428	TCGTGCAAACCTTGACTTCAGAGA
11407-11429	CGTGCAAACCTTGACTTCAGAGAA
11408-11430	GTGCAAACCTTGACTTCAGAGAAA
11409-11431	TGCAAACCTTGACTTCAGAGAAAT
11410-11432	GCAAACCTTGACTTCAGAGAAATA
11411-11433	CAAACCTTGACTTCAGAGAAATAC
11412-11434	AAACCTTGACTTCAGAGAAATACA
11413-11435	AACTTGACTTCAGAGAAATACAA
11414-11436	ACTTGACTTCAGAGAAATACAAA
11415-11437	CTTGACTTCAGAGAAATACAAAT
11416-11438	TTGACTTCAGAGAAATACAAATC
11417-11439	TGACTTCAGAGAAATACAAATCT
11418-11440	GACTTCAGAGAAATACAAATCTA
11419-11441	ACTTCAGAGAAATACAAATCTAT
11420-11442	CTTCAGAGAAATACAAATCTATA
11421-11443	TTCAGAGAAATACAAATCTATAA
11422-11444	TCAGAGAAATACAAATCTATAAG
11423-11445	CAGAGAAATACAAATCTATAAGA
11424-11446	AGAGAAATACAAATCTATAAGAA
11425-11447	GAGAAATACAAATCTATAAGAAG
11426-11448	AGAAATACAAATCTATAAGAAGC
11427-11449	GAAATACAAATCTATAAGAAGCT
11428-11450	AAATACAAATCTATAAGAAGCTG
11429-11451	AATACAAATCTATAAGAAGCTGA
11430-11452	ATACAAATCTATAAGAAGCTGAG
11431-11453	TACAAATCTATAAGAAGCTGAGA
11432-11454	ACAAATCTATAAGAAGCTGAGAA
11433-11455	CAAATCTATAAGAAGCTGAGAAC
11434-11456	AAATCTATAAGAAGCTGAGAACT
11435-11457	AATCTATAAGAAGCTGAGAACTT
11436-11458	ATCTATAAGAAGCTGAGAACTTC
11437-11459	TCTATAAGAAGCTGAGAACTTCA
11438-11460	CTATAAGAAGCTGAGAACTTCAT
11439-11461	TATAAGAAGCTGAGAACTTCATC
11440-11462	ATAAGAAGCTGAGAACTTCATCA
11441-11463	TAAGAAGCTGAGAACTTCATCAT
11442-11464	AAGAAGCTGAGAACTTCATCATT
11443-11465	AGAAGCTGAGAACTTCATCATTT
11444-11466	GAAGCTGAGAACTTCATCATTTG
11445-11467	AAGCTGAGAACTTCATCATTTGC
11446-11468	AGCTGAGAACTTCATCATTTGCC
11447-11469	GCTGAGAACTTCATCATTTGCCC
11448-11470	CTGAGAACTTCATCATTTGCCCT
11449-11471	TGAGAACTTCATCATTTGCCCTC
11450-11472	GAGAACTTCATCATTTGCCCTCA
11451-11473	AGAACTTCATCATTTGCCCTCAA
11452-11474	GAACTTCATCATTTGCCCTCAAC
11453-11475	AACTTCATCATTTGCCCTCAACC
11454-11476	ACTTCATCATTTGCCCTCAACCT
11455-11477	CTTCATCATTTGCCCTCAACCTA
11456-11478	TTCATCATTTGCCCTCAACCTAC
11457-11479	TCATCATTTGCCCTCAACCTACC
11458-11480	CATCATTTGCCCTCAACCTACCA
11459-11481	ATCATTTGCCCTCAACCTACCAA
11460-11482	TCATTTGCCCTCAACCTACCAAC

Position	Sequence
11461-11483	CATTTGCCCTCAACCTACCAACA
11462-11484	ATTTGCCCTCAACCTACCAACAC
11463-11485	TTTGCCCTCAACCTACCAACACT
11464-11486	TGCCCTCAACCTACCAACACTC
11465-11487	TGCCCTCAACCTACCAACACTCC
11466-11488	GCCCTCAACCTACCAACACTCCC
11467-11489	CCCTCAACCTACCAACACTCCCC
11468-11490	CCTCAACCTACCAACACTCCCGG
11469-11491	CTCAACCTACCAACACTCCCCGA
11470-11492	TCAACCTACCAACACTCCCGAG
11471-11493	CAACCTACCAACACTCCCGAGG
11472-11494	AACCTACCAACACTCCCGAGGT
11473-11495	ACCTACCAACACTCCCGAGGTA
11474-11496	CCTACCAACACTCCCGAGGTAA
11475-11497	CTACCAACACTCCCGAGGTAAA
11476-11498	TACCAACACTCCCGAGGTAAAA
11477-11499	ACCAACACTCCCGAGGTAAAAAT
11478-11500	CCAACACTCCCGAGGTAAAAATT
11479-11501	CAACACTCCCGAGGTAAAAATTC
11480-11502	AACACTCCCGAGGTAAAAATTC
11481-11503	ACACTCCCGAGGTAAAAATTC
11482-11504	CACTCCCGAGGTAAAAATTCCT
11483-11505	ACTCCCGAGGTAAAAATTCCTG
11484-11506	CTCCCGAGGTAAAAATTCCTGA
11485-11507	TCCCGAGGTAAAAATTCCTGAA
11486-11508	CCCGAGGTAAAAATTCCTGAAG
11487-11509	CCGAGGTAAAAATTCCTGAAGT
11488-11510	CCGAGGTAAAAATTCCTGAAGTT
11489-11511	CGAGGTAAAAATTCCTGAAGTTG
11490-11512	GAGGTAAAAATTCCTGAAGTTGA
11491-11513	AGGTAAAAATTCCTGAAGTTGAT
11492-11514	GGTAAAAATTCCTGAAGTTGATG
11493-11515	GTAATAATTCCTGAAGTTGATGT
11494-11516	TAAATAATTCCTGAAGTTGATGTG
11495-11517	AAAATAATTCCTGAAGTTGATGTGT
11496-11518	AAATAATTCCTGAAGTTGATGTGT
11497-11519	AATAATTCCTGAAGTTGATGTGT
11498-11520	ATTCCTGAAGTTGATGTGT
11499-11521	TTCCTGAAGTTGATGTGT
11500-11522	TCCCTGAAGTTGATGTGT
11501-11523	CCCTGAAGTTGATGTGT
11502-11524	CCTGAAGTTGATGTGT
11503-11525	CTGAAGTTGATGTGT
11504-11526	TGAAGTTGATGTGT
11505-11527	GAAGTTGATGTGT
11506-11528	AAGTTGATGTGT
11507-11529	AGTTGATGTGT
11508-11530	GTTGATGTGT
11509-11531	TTGATGTGT
11510-11532	TGATGTGT
11511-11533	GATGTGT
11512-11534	ATGTGT
11513-11535	TGTGT
11514-11536	GTGT
11515-11537	TGT
11516-11538	GTT
11517-11539	TTA
11518-11540	TAACA
11519-11541	AACAA
11520-11542	ACAAA
11521-11543	CAAAA
11522-11544	AAAA
11523-11545	AAAT
11524-11546	AAT
11525-11547	AT
11526-11548	T

Position	Sequence
11527-11549	ATTCTCAACCAGAAGACTCCTTG
11528-11550	TTCTCAACCAGAAGACTCCTTGA
11529-11551	TCTCAACCAGAAGACTCCTTGAT
11530-11552	CTCAACCAGAAGACTCCTTGATT
11531-11553	TCAACCAGAAGACTCCTTGATTC
11532-11554	CAACCAGAAGACTCCTTGATTCC
11533-11555	AACCAGAAGACTCCTTGATTCCC
11534-11556	ACCAGAAGACTCCTTGATTCCCT
11535-11557	CCAGAAGACTCCTTGATTCCCTT
11536-11558	CAGAAGACTCCTTGATTCCCTTT
11537-11559	AGAAGACTCCTTGATTCCCTTTT
11538-11560	GAAGACTCCTTGATTCCCTTTTT
11539-11561	AAGACTCCTTGATTCCCTTTTTT
11540-11562	AGACTCCTTGATTCCCTTTTTTG
11541-11563	GACTCCTTGATTCCCTTTTTTGA
11542-11564	ACTCCTTGATTCCCTTTTTTGAG
11543-11565	CTCCTTGATTCCCTTTTTTGAGA
11544-11566	TCCTTGATTCCCTTTTTTGAGAT
11545-11567	CCTTGATTCCCTTTTTTGAGATA
11546-11568	CTTGATTCCCTTTTTTGAGATAA
11547-11569	TTGATTCCCTTTTTTGAGATAAC
11548-11570	TGATTCCCTTTTTTGAGATAACC
11549-11571	GATTCCCTTTTTTGAGATAACCG
11550-11572	ATTCCCTTTTTTGAGATAACCGT
11551-11573	TTCCCTTTTTTGAGATAACCGTG
11552-11574	TCCCTTTTTTGAGATAACCGTGC
11553-11575	CCCTTTTTTGAGATAACCGTGCC
11554-11576	CCTTTTTTGAGATAACCGTGCC
11555-11577	CTTTTTTGAGATAACCGTGCCG
11556-11578	TTTTTGAGATAACCGTGCCGTA
11557-11579	TTTTTGAGATAACCGTGCCGTA
11558-11580	TTTTTGAGATAACCGTGCCGTA
11559-11581	TTTGAGATAACCGTGCCGTAATC
11560-11582	TTGAGATAACCGTGCCGTAATCT
11561-11583	TGAGATAACCGTGCCGTAATCTC
11562-11584	GAGATAACCGTGCCGTAATCTCA
11563-11585	AGATAACCGTGCCGTAATCTCAG
11564-11586	GATAACCGTGCCGTAATCTCAGT
11565-11587	ATAACCGTGCCGTAATCTCAGTT
11566-11588	TAACCGTGCCGTAATCTCAGTTA
11567-11589	AACCGTGCCGTAATCTCAGTTAA
11568-11590	ACCGTGCCGTAATCTCAGTTAAC
11569-11591	CCGTGCCTGAATCTCAGTTAACT
11570-11592	CGTGCCTGAATCTCAGTTAACTG
11571-11593	GTGCCTGAATCTCAGTTAACTGT
11572-11594	TGCCTGAATCTCAGTTAACTGTG
11573-11595	GCCTGAATCTCAGTTAACTGTGT
11574-11596	CCTGAATCTCAGTTAACTGTGTG
11575-11597	CTGAATCTCAGTTAACTGTGTGCC
11576-11598	TGAATCTCAGTTAACTGTGTGCC
11577-11599	GAATCTCAGTTAACTGTGTGCCA
11578-11600	AATCTCAGTTAACTGTGTGCCCAG
11579-11601	ATCTCAGTTAACTGTGTGCCCAGT
11580-11602	TCTCAGTTAACTGTGTGCCCAGTT
11581-11603	CTCAGTTAACTGTGTGCCCAGTTC
11582-11604	TCAGTTAACTGTGTGCCCAGTTCA
11583-11605	CAGTTAACTGTGTGCCCAGTTCAC
11584-11606	AGTTAACTGTGTGCCCAGTTCACG
11585-11607	GTTAACTGTGTGCCCAGTTCACGC
11586-11608	TTAACTGTGTGCCCAGTTCACGCT
11587-11609	TAACTGTGTGCCCAGTTCACGCTT
11588-11610	AACTGTGTGCCCAGTTCACGCTTC
11589-11611	ACTGTGTGCCCAGTTCACGCTTCC
11590-11612	CTGTGTGCCCAGTTCACGCTTCCA
11591-11613	TGTGTGCCCAGTTCACGCTTCCAA
11592-11614	GTGTGCCCAGTTCACGCTTCCAAA

Position	Sequence
11593-11615	TGTCCAGTTCACGCTTCCAAAA
11594-11616	GTCCAGTTCACGCTTCCAAAA
11595-11617	TCCAGTTCACGCTTCCAAAAAG
11596-11618	CCCAGTTCACGCTTCCAAAAAGT
11597-11619	CCAGTTCACGCTTCCAAAAAGTG
11598-11620	CAGTTCACGCTTCCAAAAAGTGT
11599-11621	AGTTCACGCTTCCAAAAAGTGT
11600-11622	GTTACAGCTTCCAAAAAGTGT
11601-11623	TTCACGCTTCCAAAAAGTGTTC
11602-11624	TCACGCTTCCAAAAAGTGTTC
11603-11625	CACGCTTCCAAAAAGTGTTCAG
11604-11626	ACGCTTCCAAAAAGTGTTCAGA
11605-11627	CGCTTCCAAAAAGTGTTCAGAT
11606-11628	GCTTCCAAAAAGTGTTCAGATG
11607-11629	CTTCCAAAAAGTGTTCAGATGG
11608-11630	TTCCAAAAAGTGTTCAGATGGC
11609-11631	TCCAAAAAGTGTTCAGATGGCA
11610-11632	CCAAAAAGTGTTCAGATGGCAT
11611-11633	CAAAAAAGTGTTCAGATGGCATT
11612-11634	AAAAAGTGTTCAGATGGCATTG
11613-11635	AAAAGTGTTCAGATGGCATTGC
11614-11636	AAAGTGTTCAGATGGCATTGCT
11615-11637	AAGTGTTCAGATGGCATTGCTG
11616-11638	AGTGTTCAGATGGCATTGCTGC
11617-11639	GTGTTCAGATGGCATTGCTGCT
11618-11640	TGTTTCAGATGGCATTGCTGCTT
11619-11641	GTTTCAGATGGCATTGCTGCTTT
11620-11642	TTTCAGATGGCATTGCTGCTTTG
11621-11643	TTCAGATGGCATTGCTGCTTTGG
11622-11644	TCAGATGGCATTGCTGCTTTGGA
11623-11645	CAGATGGCATTGCTGCTTTGGAT
11624-11646	AGATGGCATTGCTGCTTTGGATC
11625-11647	GATGGCATTGCTGCTTTGGATCT
11626-11648	ATGGCATTGCTGCTTTGGATCTA
11627-11649	TGGCATTGCTGCTTTGGATCTAA
11628-11650	GGCATTGCTGCTTTGGATCTAAA
11629-11651	GCATTGCTGCTTTGGATCTAAAT
11630-11652	CATTGCTGCTTTGGATCTAAATG
11631-11653	ATTGCTGCTTTGGATCTAAATGC
11632-11654	TTGCTGCTTTGGATCTAAATGCA
11633-11655	TGCTGCTTTGGATCTAAATGCAG
11634-11656	GCTGCTTTGGATCTAAATGCAGT
11635-11657	CTGCTTTGGATCTAAATGCAGTA
11636-11658	TGCTTTGGATCTAAATGCAGTAG
11637-11659	GCTTTGGATCTAAATGCAGTAGC
11638-11660	CTTTGGATCTAAATGCAGTAGCC
11639-11661	TTTGGATCTAAATGCAGTAGCCA
11640-11662	TTGGATCTAAATGCAGTAGCCAA
11641-11663	TGGATCTAAATGCAGTAGCCAAC
11642-11664	GGATCTAAATGCAGTAGCCAACA
11643-11665	GATCTAAATGCAGTAGCCAACAA
11644-11666	ATCTAAATGCAGTAGCCAACAAG
11645-11667	TCTAAATGCAGTAGCCAACAAGA
11646-11668	CTAAATGCAGTAGCCAACAAGAT
11647-11669	TAAATGCAGTAGCCAACAAGATC
11648-11670	AAATGCAGTAGCCAACAAGATCG
11649-11671	AATGCAGTAGCCAACAAGATCGC
11650-11672	ATGCAGTAGCCAACAAGATCGCA
11651-11673	TGCAGTAGCCAACAAGATCGCAG
11652-11674	GCAGTAGCCAACAAGATCGCAGA
11653-11675	CAGTAGCCAACAAGATCGCAGAC
11654-11676	AGTAGCCAACAAGATCGCAGACT
11655-11677	GTAGCCAACAAGATCGCAGACTT
11656-11678	TAGCCAACAAGATCGCAGACTTT
11657-11679	AGCCAACAAGATCGCAGACTTTG
11658-11680	GCCAACAAGATCGCAGACTTTGA

Position	Sequence
11659-11681	CCAACAAGATCGCAGACTTTGAG
11660-11682	CAACAAGATCGCAGACTTTGAGT
11661-11683	AACAAGATCGCAGACTTTGAGTT
11662-11684	ACAAGATCGCAGACTTTGAGTTG
11663-11685	CAAGATCGCAGACTTTGAGTTGC
11664-11686	AAGATCGCAGACTTTGAGTTGCC
11665-11687	AGATCGCAGACTTTGAGTTGCC
11666-11688	GATCGCAGACTTTGAGTTGCCCA
11667-11689	ATCGCAGACTTTGAGTTGCCCAC
11668-11690	TCGCAGACTTTGAGTTGCCACC
11669-11691	CGCAGACTTTGAGTTGCCACCA
11670-11692	GCAGACTTTGAGTTGCCACCAT
11671-11693	CAGACTTTGAGTTGCCACCATC
11672-11694	AGACTTTGAGTTGCCACCATCA
11673-11695	GACTTTGAGTTGCCACCATCAT
11674-11696	ACTTTGAGTTGCCACCATCATC
11675-11697	CTTTGAGTTGCCACCATCATCG
11676-11698	TTTGTGAGTTGCCACCATCATCGT
11677-11699	TTGAGTTGCCACCATCATCGTG
11678-11700	TGAGTTGCCACCATCATCGTGC
11679-11701	GAGTTGCCACCATCATCGTGCC
11680-11702	AGTTGCCACCATCATCGTGCC
11681-11703	GTGCCACCATCATCGTGCC
11682-11704	TGCCACCATCATCGTGCC
11683-11705	TGCCACCATCATCGTGCC
11684-11706	GCCACCATCATCGTGCC
11685-11707	CCCACCATCATCGTGCC
11686-11708	CCACCATCATCGTGCC
11687-11709	CACCATCATCGTGCC
11688-11710	ACCATCATCGTGCC
11689-11711	CCATCATCGTGCC
11690-11712	CATCATCGTGCC
11691-11713	ATCATCGTGCC
11692-11714	TCATCGTGCC
11693-11715	CATCGTGCC
11694-11716	ATCGTGCC
11695-11717	TCGTGCCTGAGCAGACCATTGAG
11696-11718	CGTGCCTGAGCAGACCATTGAGA
11697-11719	GTGCCTGAGCAGACCATTGAGAT
11698-11720	TGCCTGAGCAGACCATTGAGATT
11699-11721	GCCTGAGCAGACCATTGAGATTC
11700-11722	CCTGAGCAGACCATTGAGATTCC
11701-11723	CTGAGCAGACCATTGAGATTCCC
11702-11724	TGAGCAGACCATTGAGATTCCCT
11703-11725	GAGCAGACCATTGAGATTCCCTC
11704-11726	AGCAGACCATTGAGATTCCCTCC
11705-11727	GCAGACCATTGAGATTCCCTCCA
11706-11728	CAGACCATTGAGATTCCCTCCAT
11707-11729	AGACCATTGAGATTCCCTCCATT
11708-11730	GACCATTGAGATTCCCTCCATTA
11709-11731	ACCATTGAGATTCCCTCCATTAA
11710-11732	CCATTGAGATTCCCTCCATTAAAG
11711-11733	CATTGAGATTCCCTCCATTAAAGT
11712-11734	ATTGAGATTCCCTCCATTAAAGTT
11713-11735	TTGAGATTCCCTCCATTAAAGTTC
11714-11736	TGAGATTCCCTCCATTAAAGTTCT
11715-11737	GAGATTCCCTCCATTAAAGTTCTC
11716-11738	AGATTCCCTCCATTAAAGTTCTCT
11717-11739	GATTCCCTCCATTAAAGTTCTCTG
11718-11740	ATTCCCTCCATTAAAGTTCTCTGT
11719-11741	TTCCCTCCATTAAAGTTCTCTGTA
11720-11742	TCCCTCCATTAAAGTTCTCTGTAC
11721-11743	CCCTCCATTAAAGTTCTCTGTACC
11722-11744	CCTCCATTAAAGTTCTCTGTACCT
11723-11745	CTCCATTAAAGTTCTCTGTACCTG
11724-11746	TCCATTAAAGTTCTCTGTACCTGC

Position	Sequence
11725-11747	CCATTAAGTTCTCTGTACCTGCT
11726-11748	CATTAAGTTCTCTGTACCTGCTG
11727-11749	ATTAAGTTCTCTGTACCTGCTGG
11728-11750	TTAAGTTCTCTGTACCTGCTGGA
11729-11751	TAAGTTCTCTGTACCTGCTGGAA
11730-11752	AAGTTCTCTGTACCTGCTGGAA
11731-11753	AGTTCTCTGTACCTGCTGGAA
11732-11754	GTTCTCTGTACCTGCTGGAA
11733-11755	TTCTCTGTACCTGCTGGAA
11734-11756	TCTCTGTACCTGCTGGAA
11735-11757	CTCTGTACCTGCTGGAA
11736-11758	TCTGTACCTGCTGGAA
11737-11759	CTGTACCTGCTGGAA
11738-11760	TGTACCTGCTGGAA
11739-11761	GTACCTGCTGGAA
11740-11762	TACCTGCTGGAA
11741-11763	ACCTGCTGGAA
11742-11764	CCTGCTGGAA
11743-11765	CTGCTGGAA
11744-11766	TGCTGGAA
11745-11767	GCTGGAA
11746-11768	CTGGAA
11747-11769	TGGAA
11748-11770	GGAATGTCATTCCCTTCA
11749-11771	GAATGTCATTCCCTTCA
11750-11772	AATGTCATTCCCTTCAAG
11751-11773	ATTGTCATTCCCTTCAAGC
11752-11774	TTGTCATTCCCTTCAAGCA
11753-11775	TGTCATTCCCTTCAAGCAC
11754-11776	GTCATTCCCTTCAAGCACT
11755-11777	TCATTCCCTTCAAGCACTG
11756-11778	CATTCCTTCCCTTCAAGCACTGA
11757-11779	ATTCCTTCCCTTCAAGCACTGAC
11758-11780	TTCCTTCCCTTCAAGCACTGACT
11759-11781	TCCTTCCCTTCAAGCACTGACTG
11760-11782	CCTTCCCTTCAAGCACTGACTGC
11761-11783	CTTCCCTTCAAGCACTGACTGCA
11762-11784	TTCCCTTCAAGCACTGACTGCAC
11763-11785	TCCTTCAAGCACTGACTGCACG
11764-11786	CCTTCAAGCACTGACTGCACGC
11765-11787	CTTCAAGCACTGACTGCACGCT
11766-11788	TTCAAGCACTGACTGCACGCTT
11767-11789	TCAAGCACTGACTGCACGCTTT
11768-11790	TCAAGCACTGACTGCACGCTTTG
11769-11791	CAAGCACTGACTGCACGCTTTGA
11770-11792	AAGCACTGACTGCACGCTTTGAG
11771-11793	AGCACTGACTGCACGCTTTGAGG
11772-11794	GCACTGACTGCACGCTTTGAGGT
11773-11795	CACTGACTGCACGCTTTGAGGTA
11774-11796	ACTGACTGCACGCTTTGAGGTAG
11775-11797	CTGACTGCACGCTTTGAGGTAGA
11776-11798	TGACTGCACGCTTTGAGGTAGAC
11777-11799	GACTGCACGCTTTGAGGTAGACT
11778-11800	ACTGCACGCTTTGAGGTAGACTC
11779-11801	CTGCACGCTTTGAGGTAGACTCT
11780-11802	TGCACGCTTTGAGGTAGACTCTC
11781-11803	GCACGCTTTGAGGTAGACTCTCC
11782-11804	CACGCTTTGAGGTAGACTCTCCC
11783-11805	ACGCTTTGAGGTAGACTCTCCCG
11784-11806	CGCTTTGAGGTAGACTCTCCCGT
11785-11807	GCTTTGAGGTAGACTCTCCCGTG
11786-11808	CTTTGAGGTAGACTCTCCCGTGT
11787-11809	TTTGAGGTAGACTCTCCCGTGTA
11788-11810	TGAGGTAGACTCTCCCGTGATA
11789-11811	TGAGGTAGACTCTCCCGTGATA
11790-11812	GAGGTAGACTCTCCCGTGATAA

Position	Sequence
11791-11813	AGGTAGACTCTCCCGTGATAAT
11792-11814	GGTAGACTCTCCCGTGATAATG
11793-11815	GTAGACTCTCCCGTGATAATGC
11794-11816	TAGACTCTCCCGTGATAATGCC
11795-11817	AGACTCTCCCGTGATAATGCCA
11796-11818	GACTCTCCCGTGATAATGCCAC
11797-11819	ACTCTCCCGTGATAATGCCACT
11798-11820	CTCTCCCGTGATAATGCCACTT
11799-11821	TCTCCCGTGATAATGCCACTTG
11800-11822	CTCCCGTGATAATGCCACTTGG
11801-11823	TCCCGTGATAATGCCACTTGGA
11802-11824	CCCGTGATAATGCCACTTGGAG
11803-11825	CCGTGTATAATGCCACTTGGAGT
11804-11826	CGTGTATAATGCCACTTGGAGTG
11805-11827	GTGTATAATGCCACTTGGAGTGC
11806-11828	TGTATAATGCCACTTGGAGTGCC
11807-11829	GTATAATGCCACTTGGAGTGCCA
11808-11830	TATAATGCCACTTGGAGTGCCAG
11809-11831	ATAATGCCACTTGGAGTGCCAGT
11810-11832	TAATGCCACTTGGAGTGCCAGTT
11811-11833	AATGCCACTTGGAGTGCCAGTTT
11812-11834	ATGCCACTTGGAGTGCCAGTTTG
11813-11835	TGCCACTTGGAGTGCCAGTTTGA
11814-11836	GCCACTTGGAGTGCCAGTTTGAA
11815-11837	CCACTTGGAGTGCCAGTTTGAAA
11816-11838	CACTTGGAGTGCCAGTTTGAAAA
11817-11839	ACTTGGAGTGCCAGTTTGAAAAA
11818-11840	CTTGGAGTGCCAGTTTGAAAAAC
11819-11841	TTGGAGTGCCAGTTTGAAAAACA
11820-11842	TGGAGTGCCAGTTTGAAAAACAA
11821-11843	GGAGTGCCAGTTTGAAAAACAAA
11822-11844	GAGTGCCAGTTTGAAAAACAAG
11823-11845	AGTGCCAGTTTGAAAAACAAGC
11824-11846	GTGCCAGTTTGAAAAACAAGCA
11825-11847	TGCCAGTTTGAAAAACAAGCAG
11826-11848	GCCAGTTTGAAAAACAAGCAGA
11827-11849	CCAGTTTGAAAAACAAGCAGAT
11828-11850	CAGTTTGAAAAACAAGCAGATT
11829-11851	AGTTTGAAAAACAAGCAGATTA
11830-11852	GTTTGAAAAACAAGCAGATTAT
11831-11853	TTTGAAAAACAAGCAGATTATG
11832-11854	TTGAAAAACAAGCAGATTATGT
11833-11855	TGAAAAACAAGCAGATTATGTT
11834-11856	GAAAAACAAGCAGATTATGTTG
11835-11857	AAAAACAAGCAGATTATGTTGA
11836-11858	AAAAACAAGCAGATTATGTTGAA
11837-11859	AAACAAGCAGATTATGTTGAAA
11838-11860	AACAAGCAGATTATGTTGAAAC
11839-11861	ACAAGCAGATTATGTTGAAACA
11840-11862	CAAAGCAGATTATGTTGAAACAG
11841-11863	AAAGCAGATTATGTTGAAACAGT
11842-11864	AAGCAGATTATGTTGAAACAGTC
11843-11865	AGCAGATTATGTTGAAACAGTCC
11844-11866	GCAGATTATGTTGAAACAGTCCCT
11845-11867	CAGATTATGTTGAAACAGTCCCTG
11846-11868	AGATTATGTTGAAACAGTCCCTGG
11847-11869	GATTATGTTGAAACAGTCCCTGGA
11848-11870	ATTATGTTGAAACAGTCCCTGGAT
11849-11871	TTATGTTGAAACAGTCCCTGGATT
11850-11872	TATGTTGAAACAGTCCCTGGATTC
11851-11873	ATGTTGAAACAGTCCCTGGATTCC
11852-11874	TGTTGAAACAGTCCCTGGATTCCA
11853-11875	GTTGAAACAGTCCCTGGATTCCAC
11854-11876	TTGAAACAGTCCCTGGATTCCACA
11855-11877	TGAAACAGTCCCTGGATTCCACAT
11856-11878	GAAACAGTCCCTGGATTCCACATG

Position	Sequence
11857-11879	AAACAGTCTGGATTCCACATGC
11858-11880	AACAGTCTGGATTCCACATGCA
11859-11881	ACAGTCTGGATTCCACATGCAG
11860-11882	CAGTCTGGATTCCACATGCAGC
11861-11883	AGTCTGGATTCCACATGCAGCT
11862-11884	GTCTGGATTCCACATGCAGCTC
11863-11885	TCCTGGATTCCACATGCAGCTCA
11864-11886	CCTGGATTCCACATGCAGCTCAA
11865-11887	CTGGATTCCACATGCAGCTCAAC
11866-11888	TGGATTCCACATGCAGCTCAACC
11867-11889	GGATTCCACATGCAGCTCAACCG
11868-11890	GATTCCACATGCAGCTCAACCGT
11869-11891	ATTCCACATGCAGCTCAACCGTA
11870-11892	TTCCACATGCAGCTCAACCGTAC
11871-11893	TCCACATGCAGCTCAACCGTACA
11872-11894	CCACATGCAGCTCAACCGTACAG
11873-11895	CACATGCAGCTCAACCGTACAGT
11874-11896	ACATGCAGCTCAACCGTACAGTT
11875-11897	CATGCAGCTCAACCGTACAGTTC
11876-11898	ATGCAGCTCAACCGTACAGTTCC
11877-11899	TGCAGCTCAACCGTACAGTTCTCT
11878-11900	GCAGCTCAACCGTACAGTTCTCTA
11879-11901	CAGCTCAACCGTACAGTTCTCTAG
11880-11902	AGCTCAACCGTACAGTTCTCTAGA
11881-11903	GCTCAACCGTACAGTTCTCTAGAA
11882-11904	CTCAACCGTACAGTTCTCTAGAAT
11883-11905	TCAACCGTACAGTTCTCTAGAATA
11884-11906	CAACCGTACAGTTCTCTAGAATAT
11885-11907	AACCGTACAGTTCTCTAGAATATG
11886-11908	ACCGTACAGTTCTCTAGAATATGA
11887-11909	CCGTACAGTTCTCTAGAATATGAA
11888-11910	CGTACAGTTCTCTAGAATATGAAC
11889-11911	GTACAGTTCTCTAGAATATGAACT
11890-11912	TACAGTTCTCTAGAATATGAACTA
11891-11913	ACAGTTCTCTAGAATATGAACTAA
11892-11914	CAGTTCTCTAGAATATGAACTAAA
11893-11915	AGTTCTCTAGAATATGAACTAAAT
11894-11916	GTTCTCTAGAATATGAACTAAATG
11895-11917	TTCTCTAGAATATGAACTAAATGT
11896-11918	TCCTAGAATATGAACTAAATGTT
11897-11919	CCTAGAATATGAACTAAATGTTT
11898-11920	CTAGAATATGAACTAAATGTTTT
11899-11921	TAGAATATGAACTAAATGTTTTG
11900-11922	AGAATATGAACTAAATGTTTTGG
11901-11923	GAATATGAACTAAATGTTTTGGG
11902-11924	AATATGAACTAAATGTTTTGGGA
11903-11925	ATATGAACTAAATGTTTTGGGAA
11904-11926	TATGAACTAAATGTTTTGGGAAC
11905-11927	ATGAACTAAATGTTTTGGGAACA
11906-11928	TGAACTAAATGTTTTGGGAACAC
11907-11929	GAACTAAATGTTTTGGGAACACA
11908-11930	AACTAAATGTTTTGGGAACACAC
11909-11931	ACTAAATGTTTTGGGAACACACA
11910-11932	CTAAATGTTTTGGGAACACACAA
11911-11933	TAAATGTTTTGGGAACACACAAA
11912-11934	AAATGTTTTGGGAACACACAAAA
11913-11935	AATGTTTTGGGAACACACAAAAT
11914-11936	ATGTTTTGGGAACACACAAAATC
11915-11937	TGTTTTGGGAACACACAAAATCG
11916-11938	GTTTTGGGAACACACAAAATCGA
11917-11939	TTTTGGGAACACACAAAATCGAA
11918-11940	TTTGGGAACACACAAAATCGAAG
11919-11941	TTGGGAACACACAAAATCGAAGA
11920-11942	TGGGAACACACAAAATCGAAGAT
11921-11943	GGGAACACACAAAATCGAAGATG
11922-11944	GGAACACACAAAATCGAAGATGG

Position	Sequence
11923-11945	GAACACACAAAATCGAAGATGGT
11924-11946	AACACACAAAATCGAAGATGGTA
11925-11947	ACACACAAAATCGAAGATGGTAC
11926-11948	CACACAAAATCGAAGATGGTACG
11927-11949	ACACAAAATCGAAGATGGTACGT
11928-11950	CACAAAATCGAAGATGGTACGTT
11929-11951	ACAAAATCGAAGATGGTACGTTA
11930-11952	CAAAAATCGAAGATGGTACGTTAG
11931-11953	AAAATCGAAGATGGTACGTTAGC
11932-11954	AAATCGAAGATGGTACGTTAGCC
11933-11955	AATCGAAGATGGTACGTTAGCCT
11934-11956	ATCGAAGATGGTACGTTAGCCTC
11935-11957	TCGAAGATGGTACGTTAGCCTCT
11936-11958	CGAAGATGGTACGTTAGCCTCTA
11937-11959	GAAGATGGTACGTTAGCCTCTAA
11938-11960	AAGATGGTACGTTAGCCTCTAAG
11939-11961	AGATGGTACGTTAGCCTCTAAGA
11940-11962	GATGGTACGTTAGCCTCTAAGAC
11941-11963	ATGGTACGTTAGCCTCTAAGACT
11942-11964	TGGTACGTTAGCCTCTAAGACTA
11943-11965	GGTACGTTAGCCTCTAAGACTAA
11944-11966	GTACGTTAGCCTCTAAGACTAAA
11945-11967	TACGTTAGCCTCTAAGACTAAAG
11946-11968	ACGTTAGCCTCTAAGACTAAAGG
11947-11969	CGTTAGCCTCTAAGACTAAAGGA
11948-11970	GTTAGCCTCTAAGACTAAAGGAA
11949-11971	TTAGCCTCTAAGACTAAAGGAAC
11950-11972	TAGCCTCTAAGACTAAAGGAACA
11951-11973	AGCCTCTAAGACTAAAGGAACAC
11952-11974	GCCTCTAAGACTAAAGGAACACT
11953-11975	CCTCTAAGACTAAAGGAACACTT
11954-11976	CTCTAAGACTAAAGGAACACTTG
11955-11977	TCTAAGACTAAAGGAACACTTGC
11956-11978	CTAAGACTAAAGGAACACTTGCA
11957-11979	TAAGACTAAAGGAACACTTGCAC
11958-11980	AAGACTAAAGGAACACTTGACACA
11959-11981	AGACTAAAGGAACACTTGACACAC
11960-11982	GACTAAAGGAACACTTGACACACC
11961-11983	ACTAAAGGAACACTTGACACACCG
11962-11984	CTAAAGGAACACTTGACACACCGT
11963-11985	TAAAGGAACACTTGACACACCGTG
11964-11986	AAAGGAACACTTGACACACCGTGA
11965-11987	AAGGAACACTTGACACACCGTGAC
11966-11988	AGGAACACTTGACACACCGTGACT
11967-11989	GGAACACTTGACACACCGTGACTT
11968-11990	GAACACTTGACACACCGTGACTTC
11969-11991	AACACTTGACACACCGTGACTTCA
11970-11992	ACACTTGACACACCGTGACTTCAG
11971-11993	CACTTGACACACCGTGACTTCAGT
11972-11994	ACTTGACACACCGTGACTTCAGTG
11973-11995	CTTGACACACCGTGACTTCAGTGC
11974-11996	TTGACACACCGTGACTTCAGTGCA
11975-11997	TGACACACCGTGACTTCAGTGCA
11976-11998	GCACACCGTGACTTCAGTGCA
11977-11999	CACACCGTGACTTCAGTGCA
11978-12000	ACACCGTGACTTCAGTGCA
11979-12001	CACCGTGACTTCAGTGCA
11980-12002	ACCGTGACTTCAGTGCA
11981-12003	CCGTGACTTCAGTGCA
11982-12004	CGTGACTTCAGTGCA
11983-12005	GTGACTTCAGTGCA
11984-12006	TGACTTCAGTGCA
11985-12007	GACTTCAGTGCA
11986-12008	ACTTCAGTGCA
11987-12009	CTTCAGTGCA
11988-12010	TTCAGTGCA

Position	Sequence
11989-12011	TCAGTGCAGAATATGAAGAAGAT
11990-12012	CAGTGCAGAATATGAAGAAGATG
11991-12013	AGTGCAGAATATGAAGAAGATGG
11992-12014	GTGCAGAATATGAAGAAGATGGC
11993-12015	TGCAGAATATGAAGAAGATGGCA
11994-12016	GCAGAATATGAAGAAGATGGCAA
11995-12017	CAGAATATGAAGAAGATGGCAAA
11996-12018	AGAATATGAAGAAGATGGCAAAT
11997-12019	GAATATGAAGAAGATGGCAAATT
11998-12020	AATATGAAGAAGATGGCAAATTT
11999-12021	ATATGAAGAAGATGGCAAATTTG
12000-12022	TATGAAGAAGATGGCAAATTTGA
12001-12023	ATGAAGAAGATGGCAAATTTGAA
12002-12024	TGAAGAAGATGGCAAATTTGAAG
12003-12025	GAAGAAGATGGCAAATTTGAAGG
12004-12026	AAGAAGATGGCAAATTTGAAGGA
12005-12027	AGAAGATGGCAAATTTGAAGGAC
12006-12028	GAAGATGGCAAATTTGAAGGACT
12007-12029	AAGATGGCAAATTTGAAGGACTT
12008-12030	AGATGGCAAATTTGAAGGACTTC
12009-12031	GATGGCAAATTTGAAGGACTTCA
12010-12032	ATGGCAAATTTGAAGGACTTCAG
12011-12033	TGGCAAATTTGAAGGACTTCAGG
12012-12034	GGCAAATTTGAAGGACTTCAGGA
12013-12035	GCAAATTTGAAGGACTTCAGGAA
12014-12036	CAAATTTGAAGGACTTCAGGAAT
12015-12037	AAATTTGAAGGACTTCAGGAATG
12016-12038	AATTTGAAGGACTTCAGGAATGG
12017-12039	ATTTGAAGGACTTCAGGAATGGG
12018-12040	TTTGAAGGACTTCAGGAATGGGA
12019-12041	TTGAAGGACTTCAGGAATGGGAA
12020-12042	TGAAGGACTTCAGGAATGGGAAG
12021-12043	GAAGGACTTCAGGAATGGGAAGG
12022-12044	AAGGACTTCAGGAATGGGAAGGA
12023-12045	AGGACTTCAGGAATGGGAAGGAA
12024-12046	GGACTTCAGGAATGGGAAGGAAA
12025-12047	GACTTCAGGAATGGGAAGGAAAA
12026-12048	ACTTCAGGAATGGGAAGGAAAAAG
12027-12049	CTTCAGGAATGGGAAGGAAAAAGC
12028-12050	TTCAGGAATGGGAAGGAAAAAGCG
12029-12051	TCAGGAATGGGAAGGAAAAAGCGC
12030-12052	CAGGAATGGGAAGGAAAAAGCGCA
12031-12053	AGGAATGGGAAGGAAAAAGCGCAC
12032-12054	GGAATGGGAAGGAAAAAGCGCAC
12033-12055	GAATGGGAAGGAAAAAGCGCACCT
12034-12056	AATGGGAAGGAAAAAGCGCACCTC
12035-12057	ATGGGAAGGAAAAAGCGCACCTCA
12036-12058	TGGGAAGGAAAAAGCGCACCTCAA
12037-12059	GGGAAGGAAAAAGCGCACCTCAAT
12038-12060	GGAAGGAAAAAGCGCACCTCAATA
12039-12061	GAAGGAAAAAGCGCACCTCAATAT
12040-12062	AAGGAAAAAGCGCACCTCAATATC
12041-12063	AGGAAAAAGCGCACCTCAATATCA
12042-12064	GGAAAAAGCGCACCTCAATATCAA
12043-12065	GAAAAAGCGCACCTCAATATCAAAA
12044-12066	AAAAGCGCACCTCAATATCAAAAA
12045-12067	AAAGCGCACCTCAATATCAAAAAG
12046-12068	AAGCGCACCTCAATATCAAAAAGC
12047-12069	AGCGCACCTCAATATCAAAAAGCC
12048-12070	GCGCACCTCAATATCAAAAAGCCC
12049-12071	CGCACCTCAATATCAAAAAGCCCA
12050-12072	GCACCTCAATATCAAAAAGCCCAG
12051-12073	CACCTCAATATCAAAAAGCCCAGC
12052-12074	ACCTCAATATCAAAAAGCCCAGCG
12053-12075	CCTCAATATCAAAAAGCCCAGCGT
12054-12076	CTCAATATCAAAAAGCCCAGCGTT

Position	Sequence
12055-12077	TCAATATCAAAGCCAGCGTTC
12056-12078	CAATATCAAAGCCAGCGTTC
12057-12079	AATATCAAAGCCAGCGTTCAC
12058-12080	ATATCAAAGCCAGCGTTCACC
12059-12081	TATCAAAGCCAGCGTTCACCG
12060-12082	ATCAAAGCCAGCGTTCACCGA
12061-12083	TCAAAGCCAGCGTTCACCGAT
12062-12084	CAAAGCCAGCGTTCACCGATC
12063-12085	AAAAGCCAGCGTTCACCGATCT
12064-12086	AAAGCCAGCGTTCACCGATCTC
12065-12087	AAGCCAGCGTTCACCGATCTCC
12066-12088	AGCCAGCGTTCACCGATCTCCA
12067-12089	GCCAGCGTTCACCGATCTCCAT
12068-12090	CCCAGCGTTCACCGATCTCCATC
12069-12091	CCAGCGTTCACCGATCTCCATCT
12070-12092	CAGCGTTCACCGATCTCCATCTG
12071-12093	AGCGTTCACCGATCTCCATCTGC
12072-12094	GCGTTCACCGATCTCCATCTGCG
12073-12095	CGTTCACCGATCTCCATCTGCGC
12074-12096	GTTACCGATCTCCATCTGCGCT
12075-12097	TTCACCGATCTCCATCTGCGCTA
12076-12098	TCACCGATCTCCATCTGCGCTAC
12077-12099	CACCGATCTCCATCTGCGCTACC
12078-12100	ACCGATCTCCATCTGCGCTACCA
12079-12101	CCGATCTCCATCTGCGCTACCAG
12080-12102	CGATCTCCATCTGCGCTACCAGA
12081-12103	GATCTCCATCTGCGCTACCAGAA
12082-12104	ATCTCCATCTGCGCTACCAGAAA
12083-12105	TCTCCATCTGCGCTACCAGAAAAG
12084-12106	CTCCATCTGCGCTACCAGAAAAGA
12085-12107	TCCATCTGCGCTACCAGAAAAGAC
12086-12108	CCATCTGCGCTACCAGAAAAGACA
12087-12109	CATCTGCGCTACCAGAAAAGACAA
12088-12110	ATCTGCGCTACCAGAAAAGACAAG
12089-12111	TCTGCGCTACCAGAAAAGACAAGA
12090-12112	CTGCGCTACCAGAAAAGACAAGAA
12091-12113	TGCGCTACCAGAAAAGACAAGAAA
12092-12114	GCGCTACCAGAAAAGACAAGAAAAG
12093-12115	CGCTACCAGAAAAGACAAGAAAAGG
12094-12116	GCTACCAGAAAAGACAAGAAAAGGC
12095-12117	CTACCAGAAAAGACAAGAAAAGGCA
12096-12118	TACCAGAAAAGACAAGAAAAGGCAT
12097-12119	ACCAGAAAAGACAAGAAAAGGCATC
12098-12120	CCAGAAAAGACAAGAAAAGGCATCT
12099-12121	CAGAAAAGACAAGAAAAGGCATCTC
12100-12122	AGAAAAGACAAGAAAAGGCATCTCC
12101-12123	GAAAAGACAAGAAAAGGCATCTCCA
12102-12124	AAAGACAAGAAAAGGCATCTCCAC
12103-12125	AAGACAAGAAAAGGCATCTCCACC
12104-12126	AGACAAGAAAAGGCATCTCCACCT
12105-12127	GACAAGAAAAGGCATCTCCACCTC
12106-12128	ACAAGAAAAGGCATCTCCACCTCA
12107-12129	CAAGAAAAGGCATCTCCACCTCAG
12108-12130	AAGAAAAGGCATCTCCACCTCAGC
12109-12131	AGAAAAGGCATCTCCACCTCAGCA
12110-12132	GAAAAGGCATCTCCACCTCAGCAG
12111-12133	AAAGGCATCTCCACCTCAGCAGC
12112-12134	AAGGCATCTCCACCTCAGCAGCC
12113-12135	AGGCATCTCCACCTCAGCAGCCT
12114-12136	GGCATCTCCACCTCAGCAGCCTC
12115-12137	GCATCTCCACCTCAGCAGCCTCC
12116-12138	CATCTCCACCTCAGCAGCCTCCC
12117-12139	ATCTCCACCTCAGCAGCCTCCCC
12118-12140	TCTCCACCTCAGCAGCCTCCCCA
12119-12141	CTCCACCTCAGCAGCCTCCCCAG
12120-12142	TCCACCTCAGCAGCCTCCCCAGC

Position	Sequence
12121-12143	CCACCTCAGCAGCCTCCCCAGCC
12122-12144	CACCTCAGCAGCCTCCCCAGCCG
12123-12145	ACCTCAGCAGCCTCCCCAGCCGT
12124-12146	CCTCAGCAGCCTCCCCAGCCGTA
12125-12147	CTCAGCAGCCTCCCCAGCCGTAG
12126-12148	TCAGCAGCCTCCCCAGCCGTAGG
12127-12149	CAGCAGCCTCCCCAGCCGTAGGC
12128-12150	AGCAGCCTCCCCAGCCGTAGGCA
12129-12151	GCAGCCTCCCCAGCCGTAGGCAC
12130-12152	CAGCCTCCCCAGCCGTAGGCACC
12131-12153	AGCCTCCCCAGCCGTAGGCACCG
12132-12154	GCCTCCCCAGCCGTAGGCACCGT
12133-12155	CCTCCCCAGCCGTAGGCACCGTG
12134-12156	CTCCCCAGCCGTAGGCACCGTGG
12135-12157	TCCCCAGCCGTAGGCACCGTGGG
12136-12158	CCCAGCCGTAGGCACCGTGGGC
12137-12159	CCCAGCCGTAGGCACCGTGGGCA
12138-12160	CCAGCCGTAGGCACCGTGGGCAT
12139-12161	CAGCCGTAGGCACCGTGGGCATG
12140-12162	AGCCGTAGGCACCGTGGGCATGG
12141-12163	GCCGTAGGCACCGTGGGCATGGA
12142-12164	CCGTAGGCACCGTGGGCATGGAT
12143-12165	CGTAGGCACCGTGGGCATGGATA
12144-12166	GTAGGCACCGTGGGCATGGATAT
12145-12167	TAGGCACCGTGGGCATGGATATG
12146-12168	AGGCACCGTGGGCATGGATATGG
12147-12169	GGCACCGTGGGCATGGATATGGA
12148-12170	GCACCGTGGGCATGGATATGGAT
12149-12171	CACCGTGGGCATGGATATGGATG
12150-12172	ACCGTGGGCATGGATATGGATGA
12151-12173	CCGTGGGCATGGATATGGATGAA
12152-12174	CGTGGGCATGGATATGGATGAAG
12153-12175	GTGGGCATGGATATGGATGAAGA
12154-12176	TGGGCATGGATATGGATGAAGAT
12155-12177	GGGCATGGATATGGATGAAGATG
12156-12178	GGCATGGATATGGATGAAGATGA
12157-12179	GCATGGATATGGATGAAGATGAC
12158-12180	CATGGATATGGATGAAGATGACG
12159-12181	ATGGATATGGATGAAGATGACGA
12160-12182	TGGATATGGATGAAGATGACGAC
12161-12183	GGATATGGATGAAGATGACGACT
12162-12184	GATATGGATGAAGATGACGACTT
12163-12185	ATATGGATGAAGATGACGACTTT
12164-12186	TATGGATGAAGATGACGACTTTT
12165-12187	ATGGATGAAGATGACGACTTTTC
12166-12188	TGGATGAAGATGACGACTTTTCT
12167-12189	GGATGAAGATGACGACTTTTCTA
12168-12190	GATGAAGATGACGACTTTTCTAA
12169-12191	ATGAAGATGACGACTTTTCTAAA
12170-12192	TGAAGATGACGACTTTTCTAAAT
12171-12193	GAAGATGACGACTTTTCTAAATG
12172-12194	AAGATGACGACTTTTCTAAATGG
12173-12195	AGATGACGACTTTTCTAAATGGA
12174-12196	GATGACGACTTTTCTAAATGGAA
12175-12197	ATGACGACTTTTCTAAATGGAAC
12176-12198	TGACGACTTTTCTAAATGGAACT
12177-12199	GACGACTTTTCTAAATGGAACTT
12178-12200	ACGACTTTTCTAAATGGAACTTC
12179-12201	CGACTTTTCTAAATGGAACTTCT
12180-12202	GACTTTTCTAAATGGAACTTCTA
12181-12203	ACTTTTCTAAATGGAACTTCTAC
12182-12204	CTTTTCTAAATGGAACTTCTACT
12183-12205	TTTTTCTAAATGGAACTTCTACTA
12184-12206	TTTCTAAATGGAACTTCTACTAC
12185-12207	TTCTAAATGGAACTTCTACTACA
12186-12208	TCTAAATGGAACTTCTACTACAG

Position	Sequence
12187-12209	CTAAATGGAAGTTCTACTACAGC
12188-12210	TAAATGGAAGTTCTACTACAGCC
12189-12211	AAATGGAAGTTCTACTACAGCCC
12190-12212	AATGGAAGTTCTACTACAGCCCT
12191-12213	ATGGAAGTTCTACTACAGCCCTC
12192-12214	TGGAAGTTCTACTACAGCCCTCA
12193-12215	GGAAGTTCTACTACAGCCCTCAG
12194-12216	GAAAGTTCTACTACAGCCCTCAGT
12195-12217	AAAGTTCTACTACAGCCCTCAGTC
12196-12218	ACTTCTACTACAGCCCTCAGTCC
12197-12219	CTTCTACTACAGCCCTCAGTCCCT
12198-12220	TTCTACTACAGCCCTCAGTCCCTC
12199-12221	TCTACTACAGCCCTCAGTCCCTCT
12200-12222	CTACTACAGCCCTCAGTCCCTCTC
12201-12223	TACTACAGCCCTCAGTCCCTCTCC
12202-12224	ACTACAGCCCTCAGTCCCTCTCCA
12203-12225	CTACAGCCCTCAGTCCCTCTCCAG
12204-12226	TACAGCCCTCAGTCCCTCTCCAGA
12205-12227	ACAGCCCTCAGTCCCTCTCCAGAT
12206-12228	CAGCCCTCAGTCCCTCTCCAGATA
12207-12229	AGCCCTCAGTCCCTCTCCAGATAA
12208-12230	GCCCTCAGTCCCTCTCCAGATAAA
12209-12231	CCCTCAGTCCCTCTCCAGATAAAA
12210-12232	CCTCAGTCCCTCTCCAGATAAAAA
12211-12233	CTCAGTCCCTCTCCAGATAAAAAA
12212-12234	TCAGTCCCTCTCCAGATAAAAAAAC
12213-12235	CAGTCCCTCTCCAGATAAAAAAAT
12214-12236	AGTCCCTCTCCAGATAAAAAAATC
12215-12237	GTCCTCTCCAGATAAAAAAATCA
12216-12238	TCCTCTCCAGATAAAAAAATCAC
12217-12239	CCTCTCCAGATAAAAAAATCACCC
12218-12240	CTCTCCAGATAAAAAAATCACCA
12219-12241	TCTCCAGATAAAAAAATCACCAT
12220-12242	CTCCAGATAAAAAAATCACCATATA
12221-12243	TCCAGATAAAAAAATCACCATAT
12222-12244	CCAGATAAAAAAATCACCATATTT
12223-12245	CAGATAAAAAAATCACCATATTTT
12224-12246	AGATAAAAAAATCACCATATTTCA
12225-12247	GATAAAAAAATCACCATATTTCAA
12226-12248	ATAAAAAAATCACCATATTTCAAA
12227-12249	TAAAAAATCACCATATTTCAAAA
12228-12250	AAAAAATCACCATATTTCAAAAC
12229-12251	AAAAATCACCATATTTCAAAACT
12230-12252	AAAAATCACCATATTTCAAAACTG
12231-12253	AAACTCACCATATTTCAAAACTGA
12232-12254	AACTCACCATATTTCAAAACTGAG
12233-12255	ACTCACCATATTTCAAAACTGAGT
12234-12256	CTCACCATATTTCAAAACTGAGTT
12235-12257	TCACCATATTTCAAAACTGAGTTG
12236-12258	CACCATATTTCAAAACTGAGTTGA
12237-12259	ACCATATTTCAAAACTGAGTTGAG
12238-12260	CCATATTTCAAAACTGAGTTGAGG
12239-12261	CATATTTCAAAACTGAGTTGAGGG
12240-12262	ATATTTCAAAACTGAGTTGAGGGT
12241-12263	TATTTCAAAACTGAGTTGAGGGTC
12242-12264	ATTTCAAAACTGAGTTGAGGGTCC
12243-12265	TTCAAAACTGAGTTGAGGGTCCG
12244-12266	TCAAAACTGAGTTGAGGGTCCGG
12245-12267	CAAAACTGAGTTGAGGGTCCGGG
12246-12268	AAAACTGAGTTGAGGGTCCGGGA
12247-12269	AAACTGAGTTGAGGGTCCGGGAA
12248-12270	AACTGAGTTGAGGGTCCGGGAAT
12249-12271	ACTGAGTTGAGGGTCCGGGAATC
12250-12272	CTGAGTTGAGGGTCCGGGAATCT
12251-12273	TGAGTTGAGGGTCCGGGAATCTG
12252-12274	GAGTTGAGGGTCCGGGAATCTGA

Position	Sequence
12253-12275	AGTTGAGGGTCCGGGAATCTGAT
12254-12276	GTTGAGGGTCCGGGAATCTGATG
12255-12277	TTGAGGGTCCGGGAATCTGATGA
12256-12278	TGAGGGTCCGGGAATCTGATGAG
12257-12279	GAGGGTCCGGGAATCTGATGAGG
12258-12280	AGGGTCCGGGAATCTGATGAGGA
12259-12281	GGGTCCGGGAATCTGATGAGGAA
12260-12282	GGTCCGGGAATCTGATGAGGAAA
12261-12283	GTCCGGGAATCTGATGAGGAAAC
12262-12284	TCCGGGAATCTGATGAGGAAACT
12263-12285	CCGGGAATCTGATGAGGAAACTC
12264-12286	CGGGGAATCTGATGAGGAAACTCA
12265-12287	GGGAATCTGATGAGGAAACTCAG
12266-12288	GGAATCTGATGAGGAAACTCAGA
12267-12289	GAATCTGATGAGGAAACTCAGAT
12268-12290	AATCTGATGAGGAAACTCAGATC
12269-12291	ATCTGATGAGGAAACTCAGATCA
12270-12292	TCTGATGAGGAAACTCAGATCAA
12271-12293	CTGATGAGGAAACTCAGATCAAA
12272-12294	TGATGAGGAAACTCAGATCAAAG
12273-12295	GATGAGGAAACTCAGATCAAAGT
12274-12296	ATGAGGAAACTCAGATCAAAGTT
12275-12297	TGAGGAAACTCAGATCAAAGTTA
12276-12298	GAGGAAACTCAGATCAAAGTTAA
12277-12299	AGGAAACTCAGATCAAAGTTAAT
12278-12300	GGAAACTCAGATCAAAGTTAATT
12279-12301	GAAACTCAGATCAAAGTTAATTG
12280-12302	AAACTCAGATCAAAGTTAATTGG
12281-12303	AACTCAGATCAAAGTTAATTGGG
12282-12304	ACTCAGATCAAAGTTAATTGGGA
12283-12305	CTCAGATCAAAGTTAATTGGGAA
12284-12306	TCAGATCAAAGTTAATTGGGAAG
12285-12307	CAGATCAAAGTTAATTGGGAAGA
12286-12308	AGATCAAAGTTAATTGGGAAGAA
12287-12309	GATCAAAGTTAATTGGGAAGAAG
12288-12310	ATCAAAGTTAATTGGGAAGAAGA
12289-12311	TCAAAGTTAATTGGGAAGAAGAG
12290-12312	CAAAGTTAATTGGGAAGAAGAGG
12291-12313	AAAGTTAATTGGGAAGAAGAGGC
12292-12314	AAGTTAATTGGGAAGAAGAGGCA
12293-12315	AGTTAATTGGGAAGAAGAGGCAG
12294-12316	GTTAATTGGGAAGAAGAGGCAGC
12295-12317	TTAATTGGGAAGAAGAGGCAGCT
12296-12318	TAATTGGGAAGAAGAGGCAGCTT
12297-12319	AATTGGGAAGAAGAGGCAGCTTC
12298-12320	ATTGGGAAGAAGAGGCAGCTTCT
12299-12321	TTGGGAAGAAGAGGCAGCTTCTG
12300-12322	TGGGAAGAAGAGGCAGCTTCTGG
12301-12323	GGGAAGAAGAGGCAGCTTCTGGC
12302-12324	GGAAGAAGAGGCAGCTTCTGGCT
12303-12325	GAAGAAGAGGCAGCTTCTGGCTT
12304-12326	AAGAAGAGGCAGCTTCTGGCTTG
12305-12327	AGAAGAGGCAGCTTCTGGCTTGC
12306-12328	GAAGAGGCAGCTTCTGGCTTGCT
12307-12329	AAGAGGCAGCTTCTGGCTTGCTA
12308-12330	AGAGGCAGCTTCTGGCTTGCTAA
12309-12331	GAGGCAGCTTCTGGCTTGCTAAC
12310-12332	AGGCAGCTTCTGGCTTGCTAAC
12311-12333	GGCAGCTTCTGGCTTGCTAACCT
12312-12334	GCAGCTTCTGGCTTGCTAACCTC
12313-12335	CAGCTTCTGGCTTGCTAACCTCT
12314-12336	AGCTTCTGGCTTGCTAACCTCTC
12315-12337	GCTTCTGGCTTGCTAACCTCTCT
12316-12338	CTTCTGGCTTGCTAACCTCTCTG
12317-12339	TTCTGGCTTGCTAACCTCTCTGA
12318-12340	TCTGGCTTGCTAACCTCTCTGAA

Position	Sequence
12319-12341	CTGGCTTGCTAACCTCTCTGAAA
12320-12342	TGGCTTGCTAACCTCTCTGAAAG
12321-12343	GGCTTGCTAACCTCTCTGAAAGA
12322-12344	GCTTGCTAACCTCTCTGAAAGAC
12323-12345	CTTGCTAACCTCTCTGAAAGACA
12324-12346	TTGCTAACCTCTCTGAAAGACAA
12325-12347	TGCTAACCTCTCTGAAAGACAAC
12326-12348	GCTAACCTCTCTGAAAGACAACG
12327-12349	CTAACCTCTCTGAAAGACAACGT
12328-12350	TAACTCTCTGAAAGACAACGTG
12329-12351	AACCTCTCTGAAAGACAACGTGC
12330-12352	ACCTCTCTGAAAGACAACGTGCC
12331-12353	CCTCTCTGAAAGACAACGTGCC
12332-12354	CTCTCTGAAAGACAACGTGCCCA
12333-12355	TCTCTGAAAGACAACGTGCCCAA
12334-12356	CTCTGAAAGACAACGTGCCCAAG
12335-12357	TCTGAAAGACAACGTGCCCAAGG
12336-12358	CTGAAAGACAACGTGCCCAAGGC
12337-12359	TGAAAGACAACGTGCCCAAGGCC
12338-12360	GAAAGACAACGTGCCCAAGGCCA
12339-12361	AAAGACAACGTGCCCAAGGCCAC
12340-12362	AAGACAACGTGCCCAAGGCCACA
12341-12363	AGACAACGTGCCCAAGGCCACAG
12342-12364	GACAACGTGCCCAAGGCCACAGG
12343-12365	ACAACGTGCCCAAGGCCACAGGG
12344-12366	CAACGTGCCCAAGGCCACAGGGG
12345-12367	AACGTGCCCAAGGCCACAGGGGT
12346-12368	ACGTGCCCAAGGCCACAGGGGTC
12347-12369	CGTGCCCAAGGCCACAGGGGTCC
12348-12370	GTGCCCAAGGCCACAGGGGTCTT
12349-12371	TGCCCAAGGCCACAGGGGTCTTT
12350-12372	GCCCAAGGCCACAGGGGTCTTTT
12351-12373	CCCAAGGCCACAGGGGTCTTTTA
12352-12374	CCAAGGCCACAGGGGTCTTTTAT
12353-12375	CAAGGCCACAGGGGTCTTTATG
12354-12376	AAGGCCACAGGGGTCTTTATGA
12355-12377	AGGCCACAGGGGTCTTTATGAT
12356-12378	GGCCACAGGGGTCTTTATGATT
12357-12379	GCCACAGGGGTCTTTATGATTA
12358-12380	CCACAGGGGTCTTTATGATTAT
12359-12381	CACAGGGGTCTTTATGATTATG
12360-12382	ACAGGGGTCTTTATGATTATGT
12361-12383	CAGGGGTCTTTATGATTATGTC
12362-12384	AGGGGTCTTTATGATTATGTCA
12363-12385	GGGTCTTTATGATTATGTCAA
12364-12386	GGTCTTTATGATTATGTCAAC
12365-12387	GGTCTTTATGATTATGTCAACA
12366-12388	GTCCTTTATGATTATGTCAACAA
12367-12389	TCCTTTATGATTATGTCAACAAG
12368-12390	CCTTTATGATTATGTCAACAAGT
12369-12391	CTTTATGATTATGTCAACAAGTA
12370-12392	TTTATGATTATGTCAACAAGTAC
12371-12393	TTATGATTATGTCAACAAGTACC
12372-12394	TATGATTATGTCAACAAGTACCA
12373-12395	ATGATTATGTCAACAAGTACCAC
12374-12396	TGATTATGTCAACAAGTACCACT
12375-12397	GATTATGTCAACAAGTACCACTG
12376-12398	ATTATGTCAACAAGTACCACTGG
12377-12399	TTATGTCAACAAGTACCACTGGG
12378-12400	TATGTCAACAAGTACCACTGGGA
12379-12401	ATGTCAACAAGTACCACTGGGAA
12380-12402	TGTCAACAAGTACCACTGGGAAC
12381-12403	GTCAACAAGTACCACTGGGAACA
12382-12404	TCAACAAGTACCACTGGGAACAC
12383-12405	CAACAAGTACCACTGGGAACACA
12384-12406	AACAAGTACCACTGGGAACACAC

Position	Sequence
12385-12407	ACAAGTACCACTGGGAACACACA
12386-12408	CAAGTACCACTGGGAACACACAG
12387-12409	AAGTACCACTGGGAACACACAGG
12388-12410	AGTACCACTGGGAACACACAGGG
12389-12411	GTACCACTGGGAACACACAGGGC
12390-12412	TACCACTGGGAACACACAGGGCT
12391-12413	ACCAC TGGGAACACACAGGGCTC
12392-12414	CCACTGGGAACACACAGGGCTCA
12393-12415	CACTGGGAACACACAGGGCTCAC
12394-12416	ACTGGGAACACACAGGGCTCACC
12395-12417	CTGGGAACACACAGGGCTCACCC
12396-12418	TGGGAACACACAGGGCTCACCCCT
12397-12419	GGGAACACACAGGGCTCACCCCTG
12398-12420	GGAACACACAGGGCTCACCCCTGA
12399-12421	GAACACACAGGGCTCACCCCTGAG
12400-12422	AACACACAGGGCTCACCCCTGAGA
12401-12423	ACACACAGGGCTCACCCCTGAGAG
12402-12424	CACACAGGGCTCACCCCTGAGAGA
12403-12425	ACACAGGGCTCACCCCTGAGAGAA
12404-12426	CACAGGGCTCACCCCTGAGAGAAG
12405-12427	ACAGGGCTCACCCCTGAGAGAAGT
12406-12428	CAGGGCTCACCCCTGAGAGAAGTG
12407-12429	AGGGCTCACCCCTGAGAGAAGTGT
12408-12430	GGGCTCACCCCTGAGAGAAGTGTC
12409-12431	GGCTCACCCCTGAGAGAAGTGCTT
12410-12432	GCTCACCCCTGAGAGAAGTGCTTT
12411-12433	CTCACCCCTGAGAGAAGTGCTTTC
12412-12434	TCACCCCTGAGAGAAGTGCTTTCA
12413-12435	CACCCCTGAGAGAAGTGCTTTCAA
12414-12436	ACCCTGAGAGAAGTGCTTTCAAA
12415-12437	CCCTGAGAGAAGTGCTTTCAAAG
12416-12438	CCTGAGAGAAGTGCTTTCAAAGC
12417-12439	CTGAGAGAAGTGCTTTCAAAGCT
12418-12440	TGAGAGAAGTGCTTTCAAAGCTG
12419-12441	GAGAGAAGTGCTTTCAAAGCTGA
12420-12442	AGAGAAGTGCTTTCAAAGCTGAG
12421-12443	GAGAAGTGCTTTCAAAGCTGAGA
12422-12444	AGAAGTGCTTTCAAAGCTGAGAA
12423-12445	GAAGTGCTTTCAAAGCTGAGAAG
12424-12446	AAGTGCTTTCAAAGCTGAGAAGA
12425-12447	AGTGCTTTCAAAGCTGAGAAGAA
12426-12448	GTGCTTTCAAAGCTGAGAAGAAA
12427-12449	TGCTTTCAAAGCTGAGAAGAAAT
12428-12450	GCTTTCAAAGCTGAGAAGAAATC
12429-12451	TCTTTCAAAGCTGAGAAGAAATCT
12430-12452	CTTTCAAAGCTGAGAAGAAATCTG
12431-12453	TTC AAAGCTGAGAAGAAATCTGC
12432-12454	TCAAAGCTGAGAAGAAATCTGCA
12433-12455	CAAAGCTGAGAAGAAATCTGCAG
12434-12456	AAAGCTGAGAAGAAATCTGCAGA
12435-12457	AAGCTGAGAAGAAATCTGCAGAA
12436-12458	AGCTGAGAAGAAATCTGCAGAAC
12437-12459	GCTGAGAAGAAATCTGCAGAACAA
12438-12460	CTGAGAAGAAATCTGCAGAACAAA
12439-12461	TGAGAAGAAATCTGCAGAACAAAT
12440-12462	GAGAAGAAATCTGCAGAACAAATG
12441-12463	AGAAGAAATCTGCAGAACAAATGC
12442-12464	GAAGAAATCTGCAGAACAAATGCT
12443-12465	AAGAAATCTGCAGAACAAATGCTG
12444-12466	AGAAATCTGCAGAACAAATGCTGA
12445-12467	GAAATCTGCAGAACAAATGCTGAG
12446-12468	AAATCTGCAGAACAAATGCTGAGT
12447-12469	AATCTGCAGAACAAATGCTGAGTG
12448-12470	ATCTGCAGAACAAATGCTGAGTGG
12449-12471	TCTGCAGAACAAATGCTGAGTGGG
12450-12472	CTGCAGAACAAATGCTGAGTGGGT

Position	Sequence
12451-12473	TGCAGAACAATGCTGAGTGGGTT
12452-12474	GCAGAACAATGCTGAGTGGGTTT
12453-12475	CAGAACAATGCTGAGTGGGTTTA
12454-12476	AGAACAATGCTGAGTGGGTTTAT
12455-12477	GAACAATGCTGAGTGGGTTTATC
12456-12478	AACAATGCTGAGTGGGTTTATCA
12457-12479	ACAATGCTGAGTGGGTTTATCAA
12458-12480	CAATGCTGAGTGGGTTTATCAAG
12459-12481	AATGCTGAGTGGGTTTATCAAGG
12460-12482	ATGCTGAGTGGGTTTATCAAGGG
12461-12483	TGCTGAGTGGGTTTATCAAGGGG
12462-12484	GCTGAGTGGGTTTATCAAGGGGC
12463-12485	CTGAGTGGGTTTATCAAGGGGCC
12464-12486	TGAGTGGGTTTATCAAGGGGCCA
12465-12487	GAGTGGGTTTATCAAGGGGCCAT
12466-12488	AGTGGGTTTATCAAGGGGCCATT
12467-12489	GTGGGTTTATCAAGGGGCCATTA
12468-12490	TGGGTTTATCAAGGGGCCATTAG
12469-12491	GGGTTTATCAAGGGGCCATTAGG
12470-12492	GGTTTATCAAGGGGCCATTAGGC
12471-12493	GTTTATCAAGGGGCCATTAGGCA
12472-12494	TTTATCAAGGGGCCATTAGGCAA
12473-12495	TTATCAAGGGGCCATTAGGCAAA
12474-12496	TATCAAGGGGCCATTAGGCAAAT
12475-12497	ATCAAGGGGCCATTAGGCAAATT
12476-12498	TCAAGGGGCCATTAGGCAAATTG
12477-12499	CAAGGGGCCATTAGGCAAATTGA
12478-12500	AAGGGGCCATTAGGCAAATTGAT
12479-12501	AGGGGCCATTAGGCAAATTGATG
12480-12502	GGGGCCATTAGGCAAATTGATGA
12481-12503	GGGCCATTAGGCAAATTGATGAT
12482-12504	GGCCATTAGGCAAATTGATGATA
12483-12505	GCCATTAGGCAAATTGATGATAT
12484-12506	CCATTAGGCAAATTGATGATATC
12485-12507	CATTAGGCAAATTGATGATATCG
12486-12508	ATTAGGCAAATTGATGATATCGA
12487-12509	TTAGGCAAATTGATGATATCGAC
12488-12510	TAGGCAAATTGATGATATCGACG
12489-12511	AGGCAAATTGATGATATCGACGT
12490-12512	GGCAAATTGATGATATCGACGTG
12491-12513	GCAAATTGATGATATCGACGTGA
12492-12514	CAAATTGATGATATCGACGTGAG
12493-12515	AAATTGATGATATCGACGTGAGG
12494-12516	AATTGATGATATCGACGTGAGGT
12495-12517	ATTGATGATATCGACGTGAGGTT
12496-12518	TTGATGATATCGACGTGAGGTTT
12497-12519	TGATGATATCGACGTGAGGTTCC
12498-12520	GATGATATCGACGTGAGGTTCCA
12499-12521	ATGATATCGACGTGAGGTTCCAG
12500-12522	TGATATCGACGTGAGGTTCCAGA
12501-12523	GATATCGACGTGAGGTTCCAGAA
12502-12524	ATATCGACGTGAGGTTCCAGAAA
12503-12525	TATCGACGTGAGGTTCCAGAAAG
12504-12526	ATCGACGTGAGGTTCCAGAAAGC
12505-12527	TCGACGTGAGGTTCCAGAAAGCA
12506-12528	CGACGTGAGGTTCCAGAAAGCAG
12507-12529	GACGTGAGGTTCCAGAAAGCAGC
12508-12530	ACGTGAGGTTCCAGAAAGCAGCC
12509-12531	CGTGAGGTTCCAGAAAGCAGCCA
12510-12532	GTGAGGTTCCAGAAAGCAGCCAG
12511-12533	TGAGGTTCCAGAAAGCAGCCAGT
12512-12534	GAGGTTCCAGAAAGCAGCCAGTG
12513-12535	AGGTTCCAGAAAGCAGCCAGTGG
12514-12536	GGTTCAGAAAGCAGCCAGTGGC
12515-12537	GTTCCAGAAAGCAGCCAGTGGCA
12516-12538	TTCCAGAAAGCAGCCAGTGGCAC

Position	Sequence
12517-12539	TCCAGAAAGCAGCCAGTGGCACC
12518-12540	CCAGAAAGCAGCCAGTGGCACCA
12519-12541	CAGAAAGCAGCCAGTGGCACCAC
12520-12542	AGAAAGCAGCCAGTGGCACCCT
12521-12543	GAAAGCAGCCAGTGGCACCCTG
12522-12544	AAAGCAGCCAGTGGCACCCTGG
12523-12545	AAGCAGCCAGTGGCACCCTGGG
12524-12546	AGCAGCCAGTGGCACCCTGGGA
12525-12547	GCAGCCAGTGGCACCCTGGGAC
12526-12548	CAGCCAGTGGCACCCTGGGACC
12527-12549	AGCCAGTGGCACCCTGGGACCT
12528-12550	GCCAGTGGCACCCTGGGACCTA
12529-12551	CCAGTGGCACCCTGGGACCTAC
12530-12552	CAGTGGCACCCTGGGACCTACC
12531-12553	AGTGGCACCCTGGGACCTACCA
12532-12554	GTGGCACCCTGGGACCTACCAA
12533-12555	TGGCACCCTGGGACCTACCAAG
12534-12556	GGCACCCTGGGACCTACCAAGA
12535-12557	GCACCCTGGGACCTACCAAGAG
12536-12558	CACCCTGGGACCTACCAAGAGT
12537-12559	ACCACTGGGACCTACCAAGAGTG
12538-12560	CCACTGGGACCTACCAAGAGTGG
12539-12561	CACTGGGACCTACCAAGAGTGG
12540-12562	ACTGGGACCTACCAAGAGTGGAA
12541-12563	CTGGGACCTACCAAGAGTGGAA
12542-12564	TGGGACCTACCAAGAGTGGAAAG
12543-12565	GGGACCTACCAAGAGTGGAAAGG
12544-12566	GGACCTACCAAGAGTGGAAAGG
12545-12567	GACCTACCAAGAGTGGAAAGGACA
12546-12568	ACCTACCAAGAGTGGAAAGGACAA
12547-12569	CCTACCAAGAGTGGAAAGGACAAG
12548-12570	CTACCAAGAGTGGAAAGGACAAGG
12549-12571	TACCAAGAGTGGAAAGGACAAGGC
12550-12572	ACCAAGAGTGGAAAGGACAAGGCC
12551-12573	CCAAGAGTGGAAAGGACAAGGCC
12552-12574	CAAGAGTGGAAAGGACAAGGCCCA
12553-12575	AAGAGTGGAAAGGACAAGGCCCAG
12554-12576	AGAGTGGAAAGGACAAGGCCCAGA
12555-12577	GAGTGGAAAGGACAAGGCCCAGAA
12556-12578	AGTGGAAAGGACAAGGCCCAGAAT
12557-12579	GTGGAAAGGACAAGGCCCAGAATC
12558-12580	TGGAAGGACAAGGCCCAGAATCT
12559-12581	GGAAGGACAAGGCCCAGAATCTG
12560-12582	GAAGGACAAGGCCCAGAATCTGT
12561-12583	AAGGACAAGGCCCAGAATCTGTA
12562-12584	AGGACAAGGCCCAGAATCTGTAC
12563-12585	GGACAAGGCCCAGAATCTGTACC
12564-12586	GACAAGGCCCAGAATCTGTACCA
12565-12587	ACAAGGCCCAGAATCTGTACCAG
12566-12588	CAAGGCCCAGAATCTGTACCAGG
12567-12589	AAGGCCCAGAATCTGTACCAGGA
12568-12590	AGGCCCAGAATCTGTACCAGGAA
12569-12591	GGCCCAGAATCTGTACCAGGAAC
12570-12592	GCCCAGAATCTGTACCAGGAACT
12571-12593	CCCAGAATCTGTACCAGGAACTG
12572-12594	CCAGAATCTGTACCAGGAACTGT
12573-12595	CAGAATCTGTACCAGGAACTGTT
12574-12596	AGAATCTGTACCAGGAACTGTTG
12575-12597	GAATCTGTACCAGGAACTGTTGA
12576-12598	AATCTGTACCAGGAACTGTTGAC
12577-12599	ATCTGTACCAGGAACTGTTGACT
12578-12600	TCTGTACCAGGAACTGTTGACTC
12579-12601	CTGTACCAGGAACTGTTGACTCA
12580-12602	TGTACCAGGAACTGTTGACTCAG
12581-12603	GTACCAGGAACTGTTGACTCAGG
12582-12604	TACCAGGAACTGTTGACTCAGGA

Position	Sequence
12583-12605	ACCAGGAAC TGTGACTCAGGAA
12584-12606	CCAGGAAC TGTGACTCAGGAAG
12585-12607	CAGGAAC TGTGACTCAGGAAGG
12586-12608	AGGAAC TGTGACTCAGGAAGGC
12587-12609	GGAAC TGTGACTCAGGAAGGCC
12588-12610	GAACTGTGACTCAGGAAGGCCA
12589-12611	AACTGTGACTCAGGAAGGCCAA
12590-12612	ACTGTGACTCAGGAAGGCCAAG
12591-12613	CTGTGACTCAGGAAGGCCAAGC
12592-12614	TGTTGACTCAGGAAGGCCAAGCC
12593-12615	GTTGACTCAGGAAGGCCAAGCCA
12594-12616	TTGACTCAGGAAGGCCAAGCCAG
12595-12617	TGACTCAGGAAGGCCAAGCCAGT
12596-12618	GACTCAGGAAGGCCAAGCCAGTT
12597-12619	ACTCAGGAAGGCCAAGCCAGTTT
12598-12620	CTCAGGAAGGCCAAGCCAGTTTC
12599-12621	TCAGGAAGGCCAAGCCAGTTTCC
12600-12622	CAGGAAGGCCAAGCCAGTTTCCA
12601-12623	AGGAAGGCCAAGCCAGTTTCCAG
12602-12624	GGAAGGCCAAGCCAGTTTCCAGG
12603-12625	GAAGGCCAAGCCAGTTTCCAGGG
12604-12626	AAGGCCAAGCCAGTTTCCAGGGA
12605-12627	AGGCCAAGCCAGTTTCCAGGGAC
12606-12628	GGCCAAGCCAGTTTCCAGGGACT
12607-12629	GCCAAGCCAGTTTCCAGGGACTC
12608-12630	CCAAGCCAGTTTCCAGGGACTCA
12609-12631	CAAGCCAGTTTCCAGGGACTCAA
12610-12632	AAGCCAGTTTCCAGGGACTCAAG
12611-12633	AGCCAGTTTCCAGGGACTCAAGG
12612-12634	GCCAGTTTCCAGGGACTCAAGGA
12613-12635	CCAGTTTCCAGGGACTCAAGGAT
12614-12636	CAGTTTCCAGGGACTCAAGGATA
12615-12637	AGTTTCCAGGGACTCAAGGATAA
12616-12638	GTTTCCAGGGACTCAAGGATAAC
12617-12639	TTTCCAGGGACTCAAGGATAACG
12618-12640	TTCCAGGGACTCAAGGATAACGT
12619-12641	TCCAGGGACTCAAGGATAACGTG
12620-12642	CCAGGGACTCAAGGATAACGTGT
12621-12643	CAGGGACTCAAGGATAACGTGTT
12622-12644	AGGGACTCAAGGATAACGTGTTT
12623-12645	GGGACTCAAGGATAACGTGTTTG
12624-12646	GGACTCAAGGATAACGTGTTTGA
12625-12647	GACTCAAGGATAACGTGTTTGAT
12626-12648	ACTCAAGGATAACGTGTTTGATG
12627-12649	CTCAAGGATAACGTGTTTGATGG
12628-12650	TCAAGGATAACGTGTTTGATGGC
12629-12651	CAAGGATAACGTGTTTGATGGCT
12630-12652	AAGGATAACGTGTTTGATGGCTT
12631-12653	AGGATAACGTGTTTGATGGCTTG
12632-12654	GGATAACGTGTTTGATGGCTTGG
12633-12655	GATAACGTGTTTGATGGCTTGGT
12634-12656	ATAACGTGTTTGATGGCTTGGTA
12635-12657	TAACTGTTTGATGGCTTGGTAC
12636-12658	AACGTGTTTGATGGCTTGGTACG
12637-12659	ACGTGTTTGATGGCTTGGTACGA
12638-12660	CGTGTTTGATGGCTTGGTACGAG
12639-12661	GTGTTTGATGGCTTGGTACGAGT
12640-12662	TGTTTGATGGCTTGGTACGAGTT
12641-12663	GTTTGATGGCTTGGTACGAGTTA
12642-12664	TTTGATGGCTTGGTACGAGTTAC
12643-12665	TTGATGGCTTGGTACGAGTTACT
12644-12666	TGATGGCTTGGTACGAGTTACTC
12645-12667	GATGGCTTGGTACGAGTTACTCA
12646-12668	ATGGCTTGGTACGAGTTACTCAA
12647-12669	TGGCTTGGTACGAGTTACTCAAA
12648-12670	GGCTTGGTACGAGTTACTCAAAA

Position	Sequence
12649-12671	GCTTGGTACGAGTTACTCAAAAA
12650-12672	CTTGGTACGAGTTACTCAAAAAAT
12651-12673	TTGGTACGAGTTACTCAAAAAATT
12652-12674	TGGTACGAGTTACTCAAAAAATTC
12653-12675	GGTACGAGTTACTCAAAAAATTCC
12654-12676	GTACGAGTTACTCAAAAAATTCCA
12655-12677	TACGAGTTACTCAAAAAATTCCAT
12656-12678	ACGAGTTACTCAAAAAATTCCATA
12657-12679	CGAGTTACTCAAAAAATTCCATAT
12658-12680	GAGTTACTCAAAAAATTCCATATG
12659-12681	AGTTACTCAAAAAATTCCATATGA
12660-12682	GTTACTCAAAAAATTCCATATGAA
12661-12683	TTACTCAAAAAATTCCATATGAAA
12662-12684	TACTCAAAAAATTCCATATGAAAG
12663-12685	ACTCAAAAAATTCCATATGAAAGT
12664-12686	CTCAAAAAATTCCATATGAAAGTC
12665-12687	TCAAAAAATTCCATATGAAAGTCA
12666-12688	CAAAAAATTCCATATGAAAGTCAA
12667-12689	AAAAATTCCATATGAAAGTCAAG
12668-12690	AAATTCCATATGAAAGTCAAGC
12669-12691	AAATTCCATATGAAAGTCAAGCA
12670-12692	AATTCCATATGAAAGTCAAGCAT
12671-12693	ATCCATATGAAAGTCAAGCATC
12672-12694	TTCCATATGAAAGTCAAGCATCT
12673-12695	TCCATATGAAAGTCAAGCATCTG
12674-12696	CCATATGAAAGTCAAGCATCTGA
12675-12697	CATATGAAAGTCAAGCATCTGAT
12676-12698	ATATGAAAGTCAAGCATCTGATT
12677-12699	TATGAAAGTCAAGCATCTGATTG
12678-12700	ATGAAAGTCAAGCATCTGATTGA
12679-12701	TGAAAGTCAAGCATCTGATTGAC
12680-12702	GAAAGTCAAGCATCTGATTGACT
12681-12703	AAAGTCAAGCATCTGATTGACTC
12682-12704	AAGTCAAGCATCTGATTGACTCA
12683-12705	AGTCAAGCATCTGATTGACTCAC
12684-12706	GTCAGCATCTGATTGACTCACT
12685-12707	TCAAGCATCTGATTGACTCACTC
12686-12708	CAAGCATCTGATTGACTCACTCA
12687-12709	AAGCATCTGATTGACTCACTCAT
12688-12710	AGCATCTGATTGACTCACTCATT
12689-12711	GCATCTGATTGACTCACTCATTG
12690-12712	CATCTGATTGACTCACTCATTGA
12691-12713	ATCTGATTGACTCACTCATTGAT
12692-12714	TCTGATTGACTCACTCATTGATT
12693-12715	CTGATTGACTCACTCATTGATTT
12694-12716	TGATTGACTCACTCATTGATTTT
12695-12717	GATTGACTCACTCATTGATTTTC
12696-12718	ATTGACTCACTCATTGATTTTCT
12697-12719	TTGACTCACTCATTGATTTTCTG
12698-12720	TGACTCACTCATTGATTTTCTGA
12699-12721	GACTCACTCATTGATTTTCTGAA
12700-12722	ACTCACTCATTGATTTTCTGAAC
12701-12723	CTCACTCATTGATTTTCTGAACT
12702-12724	TCACTCATTGATTTTCTGAACTT
12703-12725	CACTCATTGATTTTCTGAACTTC
12704-12726	ACTCATTGATTTTCTGAACTTCC
12705-12727	CTCATTGATTTTCTGAACTTCCC
12706-12728	TCATTGATTTTCTGAACTTCCCC
12707-12729	CATTGATTTTCTGAACTTCCCCA
12708-12730	ATGATTTTCTGAACTTCCCCAG
12709-12731	TTGATTTTCTGAACTTCCCCAGA
12710-12732	TGATTTTCTGAACTTCCCCAGAT
12711-12733	GATTTTCTGAACTTCCCCAGATT
12712-12734	ATTTTCTGAACTTCCCCAGATTCC
12713-12735	TTTCTGAACTTCCCCAGATTCCC
12714-12736	TTTCTGAACTTCCCCAGATTCCCA

Position	Sequence
12715-12737	TTCTGAACTTCCCAGATTCCAG
12716-12738	TCTGAACTTCCCAGATTCCAGT
12717-12739	CTGAACTTCCCAGATTCCAGTT
12718-12740	TGAACTTCCCAGATTCCAGTTT
12719-12741	GAACTTCCCAGATTCCAGTTTC
12720-12742	AACTTCCCAGATTCCAGTTTCC
12721-12743	ACTTCCCAGATTCCAGTTTCCG
12722-12744	CTTCCCAGATTCCAGTTTCCGG
12723-12745	TTCCCAGATTCCAGTTTCCGGG
12724-12746	TCCCAGATTCCAGTTTCCGGGG
12725-12747	CCCCAGATTCCAGTTTCCGGGGA
12726-12748	CCCAGATTCCAGTTTCCGGGGAA
12727-12749	CCAGATTCCAGTTTCCGGGGAAA
12728-12750	CAGATTCCAGTTTCCGGGGAAAC
12729-12751	AGATTCCAGTTTCCGGGGAAACC
12730-12752	GATTCCAGTTTCCGGGGAAACCT
12731-12753	ATTCCAGTTTCCGGGGAAACCTG
12732-12754	TTCCAGTTTCCGGGGAAACCTGG
12733-12755	TCCAGTTTCCGGGGAAACCTGGG
12734-12756	CCAGTTTCCGGGGAAACCTGGGA
12735-12757	CAGTTTCCGGGGAAACCTGGGAT
12736-12758	AGTTTCCGGGGAAACCTGGGATA
12737-12759	GTTTCCGGGGAAACCTGGGATAT
12738-12760	TTTCCGGGGAAACCTGGGATATA
12739-12761	TTCCGGGGAAACCTGGGATATAC
12740-12762	TCCGGGGAAACCTGGGATATACA
12741-12763	CCGGGGAAACCTGGGATATACAC
12742-12764	CGGGGAAACCTGGGATATACACT
12743-12765	GGGGAAACCTGGGATATACACTA
12744-12766	GGGAAACCTGGGATATACACTAG
12745-12767	GAAACCTGGGATATACACTAGG
12746-12768	GAAACCTGGGATATACACTAGGG
12747-12769	AAACCTGGGATATACACTAGGGA
12748-12770	AACCTGGGATATACACTAGGGAG
12749-12771	ACCTGGGATATACACTAGGGAGG
12750-12772	CCTGGGATATACACTAGGGAGGA
12751-12773	CTGGGATATACACTAGGGAGGAA
12752-12774	TGGGATATACACTAGGGAGGAAC
12753-12775	GGGATATACACTAGGGAGGAACT
12754-12776	GGATATACACTAGGGAGGAACTT
12755-12777	GATATACACTAGGGAGGAACTTT
12756-12778	ATATACACTAGGGAGGAACTTTG
12757-12779	TATACACTAGGGAGGAACTTTGC
12758-12780	ATACACTAGGGAGGAACTTTGCA
12759-12781	TACACTAGGGAGGAACTTTGCAC
12760-12782	ACACTAGGGAGGAACTTTGCACT
12761-12783	CACTAGGGAGGAACTTTGCACTA
12762-12784	ACTAGGGAGGAACTTTGCACTAT
12763-12785	CTAGGGAGGAACTTTGCACTATG
12764-12786	TAGGGAGGAACTTTGCACTATGT
12765-12787	AGGGAGGAACTTTGCACTATGTT
12766-12788	GGGAGGAACTTTGCACTATGTTT
12767-12789	GGAGGAACTTTGCACTATGTTCA
12768-12790	GAGGAACTTTGCACTATGTTTCA
12769-12791	AGGAACTTTGCACTATGTTTCA
12770-12792	GAACTTTGCACTATGTTTCA
12771-12793	GAACTTTGCACTATGTTTCA
12772-12794	AACTTTGCACTATGTTTCA
12773-12795	ACTTTGCACTATGTTTCA
12774-12796	CTTTGCACTATGTTTCA
12775-12797	TTTGCATATGTTTCA
12776-12798	TTGCATATGTTTCA
12777-12799	TGCATATGTTTCA
12778-12800	GCATATGTTTCA
12779-12801	CACTATGTTTCA
12780-12802	ACTATGTTTCA

Position	Sequence
12781-12803	CTATGTTTCATAAGGGAGGTAGGG
12782-12804	TATGTTTCATAAGGGAGGTAGGGA
12783-12805	ATGTTTCATAAGGGAGGTAGGGAC
12784-12806	TGTTTCATAAGGGAGGTAGGGACG
12785-12807	GTTTCATAAGGGAGGTAGGGACGG
12786-12808	TTCATAAGGGAGGTAGGGACGGT
12787-12809	TCATAAGGGAGGTAGGGACGGTA
12788-12810	CATAAGGGAGGTAGGGACGGTAC
12789-12811	ATAAGGGAGGTAGGGACGGTACT
12790-12812	TAAGGGAGGTAGGGACGGTACTG
12791-12813	AAGGGAGGTAGGGACGGTACTGT
12792-12814	AGGGAGGTAGGGACGGTACTGTC
12793-12815	GGGAGGTAGGGACGGTACTGTCC
12794-12816	GGAGGTAGGGACGGTACTGTCCC
12795-12817	GAGGTAGGGACGGTACTGTCCCA
12796-12818	AGGTAGGGACGGTACTGTCCCAG
12797-12819	GGTAGGGACGGTACTGTCCCAGG
12798-12820	GTAGGGACGGTACTGTCCCAGGT
12799-12821	TAGGGACGGTACTGTCCCAGGTA
12800-12822	AGGGACGGTACTGTCCCAGGTAT
12801-12823	GGGACGGTACTGTCCCAGGTATA
12802-12824	GGACGGTACTGTCCCAGGTATAT
12803-12825	GACGGTACTGTCCCAGGTATATT
12804-12826	ACGGTACTGTCCCAGGTATATTC
12805-12827	CGGTACTGTCCCAGGTATATTCG
12806-12828	GGTACTGTCCCAGGTATATTCGA
12807-12829	GTACTGTCCCAGGTATATTCGAA
12808-12830	TACTGTCCCAGGTATATTCGAAA
12809-12831	ACTGTCCCAGGTATATTCGAAAG
12810-12832	CTGTCCCAGGTATATTCGAAAGT
12811-12833	TGTCCCAGGTATATTCGAAAGTC
12812-12834	GTCCCAGGTATATTCGAAAGTCC
12813-12835	TCCCAGGTATATTCGAAAGTCCA
12814-12836	CCCAGGTATATTCGAAAGTCCAT
12815-12837	CCAGGTATATTCGAAAGTCCATA
12816-12838	CAGGTATATTCGAAAGTCCATAA
12817-12839	AGGTATATTCGAAAGTCCATAAT
12818-12840	GGTATATTCGAAAGTCCATAATG
12819-12841	GTATATTCGAAAGTCCATAATGG
12820-12842	TATATTCGAAAGTCCATAATGGT
12821-12843	ATATTCGAAAGTCCATAATGGTT
12822-12844	TATTCGAAAGTCCATAATGGTTC
12823-12845	ATTCGAAAGTCCATAATGGTTCA
12824-12846	TTCGAAAGTCCATAATGGTTTCAG
12825-12847	TCGAAAGTCCATAATGGTTTCAGA
12826-12848	CGAAAGTCCATAATGGTTTCAGAA
12827-12849	GAAAGTCCATAATGGTTTCAGAAA
12828-12850	AAAGTCCATAATGGTTTCAGAAAT
12829-12851	AAGTCCATAATGGTTTCAGAAATA
12830-12852	AGTCCATAATGGTTTCAGAAATAC
12831-12853	GTCATAATGGTTTCAGAAATACT
12832-12854	TCCATAATGGTTTCAGAAATACTG
12833-12855	CCATAATGGTTTCAGAAATACTGT
12834-12856	CATAATGGTTTCAGAAATACTGTT
12835-12857	ATAATGGTTTCAGAAATACTGTTT
12836-12858	TAATGGTTTCAGAAATACTGTTTT
12837-12859	AATGGTTTCAGAAATACTGTTTTC
12838-12860	ATGGTTTCAGAAATACTGTTTTCC
12839-12861	TGGTTTCAGAAATACTGTTTTCCT
12840-12862	GGTTCAGAAATACTGTTTTCCTA
12841-12863	GTTTCAGAAATACTGTTTTCCTAT
12842-12864	TTCAGAAATACTGTTTTCCTATT
12843-12865	TCAGAAATACTGTTTTCCTATTT
12844-12866	CAGAAATACTGTTTTCCTATTTT
12845-12867	AGAAATACTGTTTTCCTATTTCC
12846-12868	GAAATACTGTTTTCCTATTTCCA

Position	Sequence
12847-12869	AAATACTGTTTCCTATTTCCAA
12848-12870	AATACTGTTTCCTATTTCCAAG
12849-12871	ATACTGTTTCCTATTTCCAAGA
12850-12872	TACTGTTTCCTATTTCCAAGAC
12851-12873	ACTGTTTCCTATTTCCAAGACC
12852-12874	CTGTTTCCTATTTCCAAGACCT
12853-12875	TGTTTCCTATTTCCAAGACCTA
12854-12876	GTTTCCTATTTCCAAGACCTAG
12855-12877	TTTCCTATTTCCAAGACCTAGT
12856-12878	TTTCCTATTTCCAAGACCTAGTG
12857-12879	TCCTATTTCCAAGACCTAGTGA
12858-12880	TCCTATTTCCAAGACCTAGTGAT
12859-12881	CCTATTTCCAAGACCTAGTGATT
12860-12882	CTATTTCCAAGACCTAGTGATTA
12861-12883	TATTTCCAAGACCTAGTGATTAC
12862-12884	ATTTCCAAGACCTAGTGATTACA
12863-12885	TTCCAAGACCTAGTGATTACAC
12864-12886	TTCCAAGACCTAGTGATTACACT
12865-12887	TCCAAGACCTAGTGATTACACTT
12866-12888	CCAAGACCTAGTGATTACACTTC
12867-12889	CAAGACCTAGTGATTACACTTCC
12868-12890	AAGACCTAGTGATTACACTTCCT
12869-12891	AGACCTAGTGATTACACTTCCTT
12870-12892	GACCTAGTGATTACACTTCCTTT
12871-12893	ACCTAGTGATTACACTTCCTTTC
12872-12894	CCTAGTGATTACACTTCCTTTCG
12873-12895	CTAGTGATTACACTTCCTTTCGA
12874-12896	TAGTGATTACACTTCCTTTCGAG
12875-12897	AGTGATTACACTTCCTTTCGAGT
12876-12898	GTGATTACACTTCCTTTCGAGTT
12877-12899	TGATTACACTTCCTTTCGAGTTA
12878-12900	GATTACACTTCCTTTCGAGTTAA
12879-12901	ATTACACTTCCTTTCGAGTTAAG
12880-12902	TTACACTTCCTTTCGAGTTAAGG
12881-12903	TACACTTCCTTTCGAGTTAAGGA
12882-12904	ACACTTCCTTTCGAGTTAAGGAA
12883-12905	CACTTCCTTTCGAGTTAAGGAAA
12884-12906	ACTTCCTTTCGAGTTAAGGAAAC
12885-12907	CTTCCTTTCGAGTTAAGGAAACA
12886-12908	TTCTTTCGAGTTAAGGAAACAT
12887-12909	TCCTTTCGAGTTAAGGAAACATA
12888-12910	CCTTTCGAGTTAAGGAAACATAA
12889-12911	CTTTCGAGTTAAGGAAACATAAA
12890-12912	TTCGAGTTAAGGAAACATAAAC
12891-12913	TTCGAGTTAAGGAAACATAAACT
12892-12914	TCGAGTTAAGGAAACATAAACTA
12893-12915	CGAGTTAAGGAAACATAAACTAA
12894-12916	GAGTTAAGGAAACATAAACTAAT
12895-12917	AGTTAAGGAAACATAAACTAATA
12896-12918	GTTAAGGAAACATAAACTAATAG
12897-12919	TTAAGGAAACATAAACTAATAGA
12898-12920	TAAGGAAACATAAACTAATAGAT
12899-12921	AAGGAAACATAAACTAATAGATG
12900-12922	AGGAAACATAAACTAATAGATGT
12901-12923	GGAAACATAAACTAATAGATGTA
12902-12924	GAAACATAAACTAATAGATGTAA
12903-12925	AAACATAAACTAATAGATGTAAT
12904-12926	AACATAAACTAATAGATGTAATC
12905-12927	ACATAAACTAATAGATGTAATCT
12906-12928	CATAAACTAATAGATGTAATCTC
12907-12929	ATAAACTAATAGATGTAATCTCG
12908-12930	TAAACTAATAGATGTAATCTCGA
12909-12931	AAACTAATAGATGTAATCTCGAT
12910-12932	AACTAATAGATGTAATCTCGATG
12911-12933	ACTAATAGATGTAATCTCGATGT
12912-12934	CTAATAGATGTAATCTCGATGTA

Position	Sequence
12913-12935	TAATAGATGTAATCTCGATGTAT
12914-12936	AATAGATGTAATCTCGATGTATA
12915-12937	ATAGATGTAATCTCGATGTATAG
12916-12938	TAGATGTAATCTCGATGTATAGG
12917-12939	AGATGTAATCTCGATGTATAGGG
12918-12940	GATGTAATCTCGATGTATAGGGA
12919-12941	ATGTAATCTCGATGTATAGGGAA
12920-12942	TGTAATCTCGATGTATAGGGAAC
12921-12943	GTAATCTCGATGTATAGGGAACT
12922-12944	TAATCTCGATGTATAGGGAACTG
12923-12945	AATCTCGATGTATAGGGAACTGT
12924-12946	ATCTCGATGTATAGGGAACTGTT
12925-12947	TCTCGATGTATAGGGAACTGTTG
12926-12948	CTCGATGTATAGGGAACTGTTGA
12927-12949	TCGATGTATAGGGAACTGTTGAA
12928-12950	CGATGTATAGGGAACTGTTGAAA
12929-12951	GATGTATAGGGAACTGTTGAAAG
12930-12952	ATGTATAGGGAACTGTTGAAAGA
12931-12953	TGTATAGGGAACTGTTGAAAGAT
12932-12954	GTATAGGGAACTGTTGAAAGATT
12933-12955	TATAGGGAACTGTTGAAAGATT
12934-12956	ATAGGGAACTGTTGAAAGATTTA
12935-12957	TAGGGAACTGTTGAAAGATTTAT
12936-12958	AGGGAACTGTTGAAAGATTTATC
12937-12959	GGGAACTGTTGAAAGATTTATCA
12938-12960	GGAACCTGTTGAAAGATTTATCAA
12939-12961	GAACCTGTTGAAAGATTTATCAAA
12940-12962	AACTGTTGAAAGATTTATCAAAA
12941-12963	ACTGTTGAAAGATTTATCAAAAG
12942-12964	CTGTTGAAAGATTTATCAAAAGA
12943-12965	TGTTGAAAGATTTATCAAAAGAA
12944-12966	GTTGAAAGATTTATCAAAAGAAG
12945-12967	TTGAAAGATTTATCAAAAGAAGC
12946-12968	TGAAAGATTTATCAAAAGAAGCC
12947-12969	GAAAGATTTATCAAAAGAAGCCC
12948-12970	AAAGATTTATCAAAAGAAGCCCA
12949-12971	AAGATTTATCAAAAGAAGCCCAA
12950-12972	AGATTTATCAAAAGAAGCCCAAG
12951-12973	GATTTATCAAAAGAAGCCCAAGA
12952-12974	ATTTATCAAAAGAAGCCCAAGAG
12953-12975	TTTATCAAAAGAAGCCCAAGAGG
12954-12976	TTATCAAAAGAAGCCCAAGAGGT
12955-12977	TATCAAAAGAAGCCCAAGAGGTA
12956-12978	ATCAAAAGAAGCCCAAGAGGTAT
12957-12979	TCAAAAGAAGCCCAAGAGGTATT
12958-12980	CAAAAGAAGCCCAAGAGGTATTT
12959-12981	AAAAGAAGCCCAAGAGGTATTTA
12960-12982	AAAGAAGCCCAAGAGGTATTTAA
12961-12983	AAGAAGCCCAAGAGGTATTTAAA
12962-12984	AGAAGCCCAAGAGGTATTTAAAG
12963-12985	GAAGCCCAAGAGGTATTTAAAGC
12964-12986	AAGCCCAAGAGGTATTTAAAGCC
12965-12987	AGCCCAAGAGGTATTTAAAGCCA
12966-12988	GCCCAAGAGGTATTTAAAGCCAT
12967-12989	CCCAAGAGGTATTTAAAGCCATT
12968-12990	CCAAGAGGTATTTAAAGCCATTC
12969-12991	CAAGAGGTATTTAAAGCCATTCA
12970-12992	AAGAGGTATTTAAAGCCATTCAG
12971-12993	AGAGGTATTTAAAGCCATTCAGT
12972-12994	GAGGTATTTAAAGCCATTCAGTC
12973-12995	AGGTATTTAAAGCCATTCAGTCT
12974-12996	GGTATTTAAAGCCATTCAGTCTC
12975-12997	GTATTTAAAGCCATTCAGTCTCT
12976-12998	TATTTAAAGCCATTCAGTCTCTC
12977-12999	ATTTAAAGCCATTCAGTCTCTCA
12978-13000	TTTAAAGCCATTCAGTCTCTCAA

Position	Sequence
12979-13001	TTAAAGCCATTTCAGTCTCTCAAG
12980-13002	TAAAGCCATTTCAGTCTCTCAAGA
12981-13003	AAAGCCATTTCAGTCTCTCAAGAC
12982-13004	AAGCCATTTCAGTCTCTCAAGACC
12983-13005	AGCCATTTCAGTCTCTCAAGACCA
12984-13006	GCCATTTCAGTCTCTCAAGACCAC
12985-13007	CCATTTCAGTCTCTCAAGACCACA
12986-13008	CATTTCAGTCTCTCAAGACCACAG
12987-13009	ATTTCAGTCTCTCAAGACCACAGA
12988-13010	TTCAGTCTCTCAAGACCACAGAG
12989-13011	TCAGTCTCTCAAGACCACAGAGG
12990-13012	CAGTCTCTCAAGACCACAGAGGT
12991-13013	AGTCTCTCAAGACCACAGAGGTG
12992-13014	GTCTCTCAAGACCACAGAGGTGC
12993-13015	TCTCTCAAGACCACAGAGGTGCT
12994-13016	CTCTCAAGACCACAGAGGTGCTA
12995-13017	TCTCAAGACCACAGAGGTGCTAC
12996-13018	CTCAAGACCACAGAGGTGCTACG
12997-13019	TCAAGACCACAGAGGTGCTACGT
12998-13020	CAAGACCACAGAGGTGCTACGTA
12999-13021	AAGACCACAGAGGTGCTACGTAA
13000-13022	AGACCACAGAGGTGCTACGTAAT
13001-13023	GACCACAGAGGTGCTACGTAATC
13002-13024	ACCACAGAGGTGCTACGTAATCT
13003-13025	CCACAGAGGTGCTACGTAATCTT
13004-13026	CACAGAGGTGCTACGTAATCTTC
13005-13027	ACAGAGGTGCTACGTAATCTTCA
13006-13028	CAGAGGTGCTACGTAATCTTCAG
13007-13029	AGAGGTGCTACGTAATCTTCAGG
13008-13030	GAGGTGCTACGTAATCTTCAGGA
13009-13031	AGGTGCTACGTAATCTTCAGGAC
13010-13032	GGTGCTACGTAATCTTCAGGACC
13011-13033	GTGCTACGTAATCTTCAGGACCT
13012-13034	TGCTACGTAATCTTCAGGACCTT
13013-13035	GCTACGTAATCTTCAGGACCTTT
13014-13036	CTACGTAATCTTCAGGACCTTTT
13015-13037	TACGTAATCTTCAGGACCTTTTA
13016-13038	ACGTAATCTTCAGGACCTTTTAC
13017-13039	CGTAATCTTCAGGACCTTTTACA
13018-13040	GTAATCTTCAGGACCTTTTACAA
13019-13041	TAATCTTCAGGACCTTTTACAAT
13020-13042	AATCTTCAGGACCTTTTACAATT
13021-13043	ATCTTCAGGACCTTTTACAATTC
13022-13044	TCTTCAGGACCTTTTACAATTC
13023-13045	CTTCAGGACCTTTTACAATTCAT
13024-13046	TTTCAGGACCTTTTACAATTCATT
13025-13047	TCAGGACCTTTTACAATTCATTT
13026-13048	CAGGACCTTTTACAATTCATTTT
13027-13049	AGGACCTTTTACAATTCATTTTC
13028-13050	GGACCTTTTACAATTCATTTTCC
13029-13051	GACCTTTTACAATTCATTTTCCA
13030-13052	ACCTTTTACAATTCATTTTCCAA
13031-13053	CCTTTTACAATTCATTTTCCAAC
13032-13054	CTTTTACAATTCATTTTCCAAC
13033-13055	TTTACAATTCATTTTCCAAC
13034-13056	TTTACAATTCATTTTCCAAC
13035-13057	TTACAATTCATTTTCCAAC
13036-13058	TACAATTCATTTTCCAAC
13037-13059	ACAATTCATTTTCCAAC
13038-13060	CAATTCATTTTCCAAC
13039-13061	AATTCATTTTCCAAC
13040-13062	ATTCATTTTCCAAC
13041-13063	TTCATTTTCCAAC
13042-13064	TCATTTTCCAAC
13043-13065	CATTTTCCAAC
13044-13066	ATTTTCCAAC

Position	Sequence
13045-13067	TTTCCAACTAATAGAAGATAAC
13046-13068	TTTCCAACTAATAGAAGATAACA
13047-13069	TTCCAACTAATAGAAGATAACAT
13048-13070	TCCAACTAATAGAAGATAACATT
13049-13071	CCAACCTAATAGAAGATAACATTA
13050-13072	CAACTAATAGAAGATAACATTAA
13051-13073	AACTAATAGAAGATAACATTAAA
13052-13074	ACTAATAGAAGATAACATTAAAC
13053-13075	CTAATAGAAGATAACATTAAACA
13054-13076	TAATAGAAGATAACATTAAACAG
13055-13077	AATAGAAGATAACATTAAACAGC
13056-13078	ATAGAAGATAACATTAAACAGCT
13057-13079	TAGAAGATAACATTAAACAGCTG
13058-13080	AGAAGATAACATTAAACAGCTGA
13059-13081	GAAGATAACATTAAACAGCTGAA
13060-13082	AAGATAACATTAAACAGCTGAAA
13061-13083	AGATAACATTAAACAGCTGAAAG
13062-13084	GATAACATTAAACAGCTGAAAGA
13063-13085	ATAACATTAAACAGCTGAAAGAG
13064-13086	TAACATTAAACAGCTGAAAGAGA
13065-13087	AACATTAAACAGCTGAAAGAGAT
13066-13088	ACATTAAACAGCTGAAAGAGATG
13067-13089	CATTAAACAGCTGAAAGAGATGA
13068-13090	ATTAACAGCTGAAAGAGATGAA
13069-13091	TTAACAGCTGAAAGAGATGAAA
13070-13092	TAAACAGCTGAAAGAGATGAAAT
13071-13093	AAACAGCTGAAAGAGATGAAATT
13072-13094	AACAGCTGAAAGAGATGAAATTT
13073-13095	ACAGCTGAAAGAGATGAAATTTA
13074-13096	CAGCTGAAAGAGATGAAATTTAC
13075-13097	AGCTGAAAGAGATGAAATTTACT
13076-13098	GCTGAAAGAGATGAAATTTACTT
13077-13099	CTGAAAGAGATGAAATTTACTTA
13078-13100	TGAAAGAGATGAAATTTACTTAT
13079-13101	GAAAGAGATGAAATTTACTTATC
13080-13102	AAAGAGATGAAATTTACTTATCT
13081-13103	AAGAGATGAAATTTACTTATCTT
13082-13104	AGAGATGAAATTTACTTATCTTA
13083-13105	GAGATGAAATTTACTTATCTTAT
13084-13106	AGATGAAATTTACTTATCTTATT
13085-13107	GATGAAATTTACTTATCTTATTA
13086-13108	ATGAAATTTACTTATCTTATTAA
13087-13109	TGAAATTTACTTATCTTATTAAAT
13088-13110	GAAATTTACTTATCTTATTAAATT
13089-13111	AAATTTACTTATCTTATTAAATTA
13090-13112	AATTTACTTATCTTATTAAATTAT
13091-13113	ATTTACTTATCTTATTAAATTATA
13092-13114	TTTACTTATCTTATTAAATTATAT
13093-13115	TTACTTATCTTATTAAATTATATC
13094-13116	TACTTATCTTATTAAATTATATCC
13095-13117	ACTTATCTTATTAAATTATATCCA
13096-13118	CTTATCTTATTAAATTATATCCAA
13097-13119	TTATCTTATTAAATTATATCCAAG
13098-13120	TATCTTATTAAATTATATCCAAGA
13099-13121	ATCTTATTAAATTATATCCAAGAT
13100-13122	TCTTATTAAATTATATCCAAGATG
13101-13123	CTTATTAAATTATATCCAAGATGA
13102-13124	TTATTAAATTATATCCAAGATGAG
13103-13125	TATTAAATTATATCCAAGATGAGA
13104-13126	ATTAATTATATCCAAGATGAGAT
13105-13127	TTAATTATATCCAAGATGAGATC
13106-13128	TAATTATATCCAAGATGAGATCA
13107-13129	AATTATATCCAAGATGAGATCAA
13108-13130	ATTATATCCAAGATGAGATCAAC
13109-13131	TTATATCCAAGATGAGATCAACA
13110-13132	TATATCCAAGATGAGATCAACAC

Position	Sequence
13111-13133	ATATCCAAGATGAGATCAACACA
13112-13134	TATCCAAGATGAGATCAACACAA
13113-13135	ATCCAAGATGAGATCAACACAAT
13114-13136	TCCAAGATGAGATCAACACAATC
13115-13137	CCAAGATGAGATCAACACAATCT
13116-13138	CAAGATGAGATCAACACAATCTT
13117-13139	AAGATGAGATCAACACAATCTTC
13118-13140	AGATGAGATCAACACAATCTTCA
13119-13141	GATGAGATCAACACAATCTTCAA
13120-13142	ATGAGATCAACACAATCTTCAAT
13121-13143	TGAGATCAACACAATCTTCAATG
13122-13144	GAGATCAACACAATCTTCAATGA
13123-13145	AGATCAACACAATCTTCAATGAT
13124-13146	GATCAACACAATCTTCAATGATT
13125-13147	ATCAACACAATCTTCAATGATTA
13126-13148	TCAACACAATCTTCAATGATTAT
13127-13149	CAACACAATCTTCAATGATTATA
13128-13150	AACACAATCTTCAATGATTATAT
13129-13151	ACACAATCTTCAATGATTATATC
13130-13152	CACAATCTTCAATGATTATATCC
13131-13153	ACAATCTTCAATGATTATATCCC
13132-13154	CAATCTTCAATGATTATATCCCA
13133-13155	AATCTTCAATGATTATATCCCAT
13134-13156	ATCTTCAATGATTATATCCCATATA
13135-13157	TCTTCAATGATTATATCCCATAT
13136-13158	CTTCAATGATTATATCCCATATG
13137-13159	TTCAATGATTATATCCCATATGT
13138-13160	TCAATGATTATATCCCATATGTT
13139-13161	CAATGATTATATCCCATATGTTT
13140-13162	AATGATTATATCCCATATGTTTT
13141-13163	ATGATTATATCCCATATGTTTTT
13142-13164	TGATTATATCCCATATGTTTTTA
13143-13165	GATTATATCCCATATGTTTTTAA
13144-13166	ATTATATCCCATATGTTTTTAAA
13145-13167	TTATATCCCATATGTTTTTAAAT
13146-13168	TATATCCCATATGTTTTTAAATT
13147-13169	ATATCCCATATGTTTTTAAATTG
13148-13170	TATCCCATATGTTTTTAAATTGT
13149-13171	ATCCCATATGTTTTTAAATTGTT
13150-13172	TCCCATATGTTTTTAAATTGTTG
13151-13173	CCCATATGTTTTTAAATTGTTGA
13152-13174	CCATATGTTTTTAAATTGTTGAA
13153-13175	CATATGTTTTTAAATTGTTGAAA
13154-13176	ATATGTTTTTAAATTGTTGAAAG
13155-13177	TATGTTTTTAAATTGTTGAAAGA
13156-13178	ATGTTTTTAAATTGTTGAAAGAA
13157-13179	TGTTTTTAAATTGTTGAAAGAAA
13158-13180	GTTTTTAAATTGTTGAAAGAAAA
13159-13181	TTTTTAAATTGTTGAAAGAAAAC
13160-13182	TTTTAAATTGTTGAAAGAAAACC
13161-13183	TTTAAATTGTTGAAAGAAAACCT
13162-13184	TTAAATTGTTGAAAGAAAACCTA
13163-13185	TAAATTGTTGAAAGAAAACCTAT
13164-13186	AAATTGTTGAAAGAAAACCTATG
13165-13187	AATTGTTGAAAGAAAACCTATGC
13166-13188	ATTGTTGAAAGAAAACCTATGCC
13167-13189	TTGTTGAAAGAAAACCTATGCCT
13168-13190	TGTTGAAAGAAAACCTATGCCTT
13169-13191	GTTGAAAGAAAACCTATGCCTTA
13170-13192	TTGAAAGAAAACCTATGCCTTAA
13171-13193	TGAAAGAAAACCTATGCCTTAAT
13172-13194	GAAAGAAAACCTATGCCTTAATC
13173-13195	AAAGAAAACCTATGCCTTAATCT
13174-13196	AAGAAAACCTATGCCTTAATCTT
13175-13197	AGAAAACCTATGCCTTAATCTTC
13176-13198	GAAAACCTATGCCTTAATCTTCA

Position	Sequence
13177-13199	AAAACCTATGCCTTAATCTTCAT
13178-13200	AAACCTATGCCTTAATCTTCATA
13179-13201	AACCTATGCCTTAATCTTCATAA
13180-13202	ACCTATGCCTTAATCTTCATAAG
13181-13203	CCTATGCCTTAATCTTCATAAGT
13182-13204	CTATGCCTTAATCTTCATAAGTT
13183-13205	TATGCCTTAATCTTCATAAGTTC
13184-13206	ATGCCTTAATCTTCATAAGTTCA
13185-13207	TGCCTTAATCTTCATAAGTTCAA
13186-13208	GCCTTAATCTTCATAAGTTCAAT
13187-13209	CCTTAATCTTCATAAGTTCAATG
13188-13210	CTTAATCTTCATAAGTTCAATGA
13189-13211	TTAATCTTCATAAGTTCAATGAA
13190-13212	TAATCTTCATAAGTTCAATGAAT
13191-13213	AATCTTCATAAGTTCAATGAATT
13192-13214	ATCTTCATAAGTTCAATGAATTT
13193-13215	TCTTCATAAGTTCAATGAATTTA
13194-13216	CTTCATAAGTTCAATGAATTTAT
13195-13217	TTCATAAGTTCAATGAATTTATT
13196-13218	TCATAAGTTCAATGAATTTATTC
13197-13219	CATAAGTTCAATGAATTTATTCA
13198-13220	ATAAGTTCAATGAATTTATTCAA
13199-13221	TAAGTTCAATGAATTTATTCAA
13200-13222	AAGTTCAATGAATTTATTCAAAA
13201-13223	AGTTCAATGAATTTATTCAAAAC
13202-13224	GTTCAATGAATTTATTCAAAACG
13203-13225	TTCATGAATTTATTCAAAACGA
13204-13226	TCAATGAATTTATTCAAAACGAG
13205-13227	CAATGAATTTATTCAAAACGAGC
13206-13228	AATGAATTTATTCAAAACGAGCT
13207-13229	ATGAATTTATTCAAAACGAGCTT
13208-13230	TGAATTTATTCAAAACGAGCTTC
13209-13231	GAATTTATTCAAAACGAGCTTCA
13210-13232	AATTTATTCAAAACGAGCTTCAG
13211-13233	ATTTATTCAAAACGAGCTTCAGG
13212-13234	TTTATTCAAAACGAGCTTCAGGA
13213-13235	TTATTCAAAACGAGCTTCAGGAA
13214-13236	TATTCAAAACGAGCTTCAGGAAG
13215-13237	ATTCAAAACGAGCTTCAGGAAGC
13216-13238	TTCAAACGAGCTTCAGGAAGCT
13217-13239	TCAAACGAGCTTCAGGAAGCTT
13218-13240	CAAACGAGCTTCAGGAAGCTTC
13219-13241	AAAACGAGCTTCAGGAAGCTTCT
13220-13242	AAACGAGCTTCAGGAAGCTTCTC
13221-13243	AACGAGCTTCAGGAAGCTTCTCA
13222-13244	ACGAGCTTCAGGAAGCTTCTCAA
13223-13245	CGAGCTTCAGGAAGCTTCTCAAG
13224-13246	GAGCTTCAGGAAGCTTCTCAAGA
13225-13247	AGCTTCAGGAAGCTTCTCAAGAG
13226-13248	GCTTCAGGAAGCTTCTCAAGAGT
13227-13249	CTTCAGGAAGCTTCTCAAGAGTT
13228-13250	FTCAGGAAGCTTCTCAAGAGTTA
13229-13251	TCAGGAAGCTTCTCAAGAGTTAC
13230-13252	CAGGAAGCTTCTCAAGAGTTACA
13231-13253	AGGAAGCTTCTCAAGAGTTACAG
13232-13254	GGAAGCTTCTCAAGAGTTACAGC
13233-13255	GAAGCTTCTCAAGAGTTACAGCA
13234-13256	AAGCTTCTCAAGAGTTACAGCAG
13235-13257	AGCTTCTCAAGAGTTACAGCAGA
13236-13258	GCTTCTCAAGAGTTACAGCAGAT
13237-13259	CTTCTCAAGAGTTACAGCAGATC
13238-13260	TTCTCAAGAGTTACAGCAGATCC
13239-13261	TCTCAAGAGTTACAGCAGATCCA
13240-13262	CTCAAGAGTTACAGCAGATCCAT
13241-13263	TCAAGAGTTACAGCAGATCCATC
13242-13264	CAAGAGTTACAGCAGATCCATCA

Position	Sequence
13243-13265	AAGAGTTACAGCAGATCCATCAA
13244-13266	AGAGTTACAGCAGATCCATCAAT
13245-13267	GAGTTACAGCAGATCCATCAATA
13246-13268	AGTTACAGCAGATCCATCAATAC
13247-13269	GTTACAGCAGATCCATCAATACA
13248-13270	TTACAGCAGATCCATCAATACAT
13249-13271	TACAGCAGATCCATCAATACATT
13250-13272	ACAGCAGATCCATCAATACATTA
13251-13273	CAGCAGATCCATCAATACATTAT
13252-13274	AGCAGATCCATCAATACATTATG
13253-13275	GCAGATCCATCAATACATTATGG
13254-13276	CAGATCCATCAATACATTATGGC
13255-13277	AGATCCATCAATACATTATGGCC
13256-13278	GATCCATCAATACATTATGGCCC
13257-13279	ATCCATCAATACATTATGGCCCT
13258-13280	TCCATCAATACATTATGGCCCTT
13259-13281	CCATCAATACATTATGGCCCTTC
13260-13282	CATCAATACATTATGGCCCTTCG
13261-13283	ATCAATACATTATGGCCCTTCGT
13262-13284	TCAATACATTATGGCCCTTCGTG
13263-13285	CAATACATTATGGCCCTTCGTGA
13264-13286	AATACATTATGGCCCTTCGTGAA
13265-13287	ATACATTATGGCCCTTCGTGAAG
13266-13288	TACATTATGGCCCTTCGTGAAGA
13267-13289	ACATTATGGCCCTTCGTGAAGAA
13268-13290	CATTATGGCCCTTCGTGAAGAAAT
13269-13291	ATTATGGCCCTTCGTGAAGAAATA
13270-13292	TTATGGCCCTTCGTGAAGAAATAT
13271-13293	TATGGCCCTTCGTGAAGAAATATT
13272-13294	ATGGCCCTTCGTGAAGAAATATTT
13273-13295	TGGCCCTTCGTGAAGAAATATTTT
13274-13296	GGCCCTTCGTGAAGAAATATTTTG
13275-13297	GCCCTTCGTGAAGAAATATTTTGA
13276-13298	CCCTTCGTGAAGAAATATTTTGAT
13277-13299	CCTTCGTGAAGAAATATTTTGATC
13278-13300	CTTCGTGAAGAAATATTTTGATCC
13279-13301	TTCGTGAAGAAATATTTTGATCCA
13280-13302	TCGTGAAGAAATATTTTGATCCAA
13281-13303	CGTGAAGAAATATTTTGATCCAAG
13282-13304	GTGAAGAAATATTTTGATCCAAGT
13283-13305	TGAAGAAATATTTTGATCCAAGTA
13284-13306	GAAGAAATATTTTGATCCAAGTAT
13285-13307	AAGAAATATTTTGATCCAAGTATA
13286-13308	AGAATATTTTGATCCAAGTATAG
13287-13309	GAATATTTTGATCCAAGTATAGT
13288-13310	AATATTTTGATCCAAGTATAGTT
13289-13311	ATATTTTGATCCAAGTATAGTTG
13290-13312	TATTTGATCCAAGTATAGTTGG
13291-13313	ATTTTGATCCAAGTATAGTTGGC
13292-13314	TTTTGATCCAAGTATAGTTGGCT
13293-13315	TTGATCCAAGTATAGTTGGCTG
13294-13316	TTGATCCAAGTATAGTTGGCTGG
13295-13317	TGATCCAAGTATAGTTGGCTGGA
13296-13318	GATCCAAGTATAGTTGGCTGGAC
13297-13319	ATCCAAGTATAGTTGGCTGGACA
13298-13320	TCCAAGTATAGTTGGCTGGACAG
13299-13321	CCAAGTATAGTTGGCTGGACAGT
13300-13322	CAAGTATAGTTGGCTGGACAGTG
13301-13323	AAGTATAGTTGGCTGGACAGTGA
13302-13324	AGTATAGTTGGCTGGACAGTGAA
13303-13325	GTATAGTTGGCTGGACAGTGAAA
13304-13326	TATAGTTGGCTGGACAGTGAAAT
13305-13327	ATAGTTGGCTGGACAGTGAAATA
13306-13328	TAGTTGGCTGGACAGTGAAATAT
13307-13329	AGTTGGCTGGACAGTGAAATATT
13308-13330	GTTGGCTGGACAGTGAAATATTA

Position	Sequence
13309-13331	TTGGCTGGACAGTGAAATATTAT
13310-13332	TGGCTGGACAGTGAAATATTATG
13311-13333	GGCTGGACAGTGAAATATTATGA
13312-13334	GCTGGACAGTGAAATATTATGAA
13313-13335	CTGGACAGTGAAATATTATGAAC
13314-13336	TGGACAGTGAAATATTATGAACT
13315-13337	GGACAGTGAAATATTATGAACTT
13316-13338	GACAGTGAAATATTATGAACTTG
13317-13339	ACAGTGAAATATTATGAACTTGA
13318-13340	CAGTGAAATATTATGAACTTGAA
13319-13341	AGTGAAATATTATGAACTTGAAG
13320-13342	GTGAAATATTATGAACTTGAAGA
13321-13343	TGAAATATTATGAACTTGAAGAA
13322-13344	GAAATATTATGAACTTGAAGAAA
13323-13345	AAATATTATGAACTTGAAGAAAA
13324-13346	AATATTATGAACTTGAAGAAAAG
13325-13347	ATATTATGAACTTGAAGAAAAGA
13326-13348	TATTATGAACTTGAAGAAAAGAT
13327-13349	ATTATGAACTTGAAGAAAAGATA
13328-13350	TTATGAACTTGAAGAAAAGATAG
13329-13351	TATGAACTTGAAGAAAAGATAGT
13330-13352	ATGAACTTGAAGAAAAGATAGTC
13331-13353	TGAACTTGAAGAAAAGATAGTCA
13332-13354	GAACTTGAAGAAAAGATAGTCAG
13333-13355	AACTTGAAGAAAAGATAGTCAGT
13334-13356	ACTTGAAGAAAAGATAGTCAGTC
13335-13357	CTTGAAGAAAAGATAGTCAGTCT
13336-13358	TTGAAGAAAAGATAGTCAGTCTG
13337-13359	TGAAGAAAAGATAGTCAGTCTGA
13338-13360	GAAGAAAAGATAGTCAGTCTGAT
13339-13361	AAGAAAAGATAGTCAGTCTGATC
13340-13362	AGAAAAGATAGTCAGTCTGATCA
13341-13363	GAAAAGATAGTCAGTCTGATCAA
13342-13364	AAAAGATAGTCAGTCTGATCAAG
13343-13365	AAAGATAGTCAGTCTGATCAAGA
13344-13366	AAGATAGTCAGTCTGATCAAGAA
13345-13367	AGATAGTCAGTCTGATCAAGAAC
13346-13368	GATAGTCAGTCTGATCAAGAACC
13347-13369	ATAGTCAGTCTGATCAAGAACCT
13348-13370	TAGTCAGTCTGATCAAGAACCTG
13349-13371	AGTCAGTCTGATCAAGAACCTGT
13350-13372	GTCAGTCTGATCAAGAACCTGTT
13351-13373	TCAGTCTGATCAAGAACCTGTTA
13352-13374	CAGTCTGATCAAGAACCTGTTAG
13353-13375	AGTCTGATCAAGAACCTGTTAGT
13354-13376	GTCGATCAAGAACCTGTTAGTT
13355-13377	TCTGATCAAGAACCTGTTAGTTG
13356-13378	CTGATCAAGAACCTGTTAGTTGC
13357-13379	TGATCAAGAACCTGTTAGTTGCT
13358-13380	GATCAAGAACCTGTTAGTTGCTC
13359-13381	ATCAAGAACCTGTTAGTTGCTCT
13360-13382	TCAAGAACCTGTTAGTTGCTCTT
13361-13383	CAAGAACCTGTTAGTTGCTCTTA
13362-13384	AAGAACCTGTTAGTTGCTCTTAA
13363-13385	AGAACCTGTTAGTTGCTCTTAAG
13364-13386	GAACCTGTTAGTTGCTCTTAAGG
13365-13387	AACCTGTTAGTTGCTCTTAAGGA
13366-13388	ACCTGTTAGTTGCTCTTAAGGAC
13367-13389	CCTGTTAGTTGCTCTTAAGGACT
13368-13390	CTGTTAGTTGCTCTTAAGGACTT
13369-13391	TGTTAGTTGCTCTTAAGGACTTC
13370-13392	GTTAGTTGCTCTTAAGGACTTCC
13371-13393	TTAGTTGCTCTTAAGGACTTCCA
13372-13394	TAGTTGCTCTTAAGGACTTCCAT
13373-13395	AGTTGCTCTTAAGGACTTCCATT
13374-13396	GTTGCTCTTAAGGACTTCCATTC

Position	Sequence
13375-13397	TTGCTCTTAAGGACTTCCATTCT
13376-13398	TGCTCTTAAGGACTTCCATTCTG
13377-13399	GCTCTTAAGGACTTCCATTCTGA
13378-13400	CTCTTAAGGACTTCCATTCTGAA
13379-13401	TCTTAAGGACTTCCATTCTGAAT
13380-13402	CCTAAGGACTTCCATTCTGAATA
13381-13403	TTAAGGACTTCCATTCTGAATAT
13382-13404	TAAGGACTTCCATTCTGAATATA
13383-13405	AAGGACTTCCATTCTGAATATAT
13384-13406	AGGACTTCCATTCTGAATATATT
13385-13407	GGACTTCCATTCTGAATATATTG
13386-13408	GACTTCCATTCTGAATATATTGT
13387-13409	ACTTCCATTCTGAATATATTGTC
13388-13410	CTTCCATTCTGAATATATTGTCA
13389-13411	TTCCATTCTGAATATATTGTCAG
13390-13412	TCCATTCTGAATATATTGTCAGT
13391-13413	CCATTCTGAATATATTGTCAGTG
13392-13414	CATTCTGAATATATTGTCAGTGC
13393-13415	ATTCTGAATATATTGTCAGTGCC
13394-13416	TTCTGAATATATTGTCAGTGCCT
13395-13417	TCTGAATATATTGTCAGTGCCTC
13396-13418	CTGAATATATTGTCAGTGCCTCT
13397-13419	TGAATATATTGTCAGTGCCTCTA
13398-13420	GAATATATTGTCAGTGCCTCTAA
13399-13421	AATATATTGTCAGTGCCTCTAAC
13400-13422	ATATATTGTCAGTGCCTCTAACT
13401-13423	TATATTGTCAGTGCCTCTAACTT
13402-13424	ATATTGTCAGTGCCTCTAACTTT
13403-13425	TATTGTCAGTGCCTCTAACTTTA
13404-13426	ATTGTCAGTGCCTCTAACTTTAC
13405-13427	TTGTCAGTGCCTCTAACTTTACT
13406-13428	TGTCAGTGCCTCTAACTTTACTT
13407-13429	GTCAGTGCCTCTAACTTTACTTC
13408-13430	TCAGTGCCTCTAACTTTACTTCC
13409-13431	CAGTGCCTCTAACTTTACTTCCC
13410-13432	AGTGCCTCTAACTTTACTTCCCA
13411-13433	GTGCCTCTAACTTTACTTCCCAA
13412-13434	TGCCTCTAACTTTACTTCCCAAC
13413-13435	GCCTCTAACTTTACTTCCCAACT
13414-13436	CCTCTAACTTTACTTCCCAACTC
13415-13437	CTCTAACTTTACTTCCCAACTCT
13416-13438	TCTAACTTTACTTCCCAACTCTC
13417-13439	CTAACTTTACTTCCCAACTCTCA
13418-13440	TAACCTTTACTTCCCAACTCTCAA
13419-13441	AACTTTACTTCCCAACTCTCAAG
13420-13442	ACTTTACTTCCCAACTCTCAAGT
13421-13443	CTTTACTTCCCAACTCTCAAGTC
13422-13444	TTTACTTCCCAACTCTCAAGTCA
13423-13445	TTACTTCCCAACTCTCAAGTCAA
13424-13446	FACTTCCCAACTCTCAAGTCAAG
13425-13447	ACTTCCCAACTCTCAAGTCAAGT
13426-13448	CTTCCCAACTCTCAAGTCAAGTT
13427-13449	TTCCCAACTCTCAAGTCAAGTTG
13428-13450	TCCCAACTCTCAAGTCAAGTTGA
13429-13451	CCCAACTCTCAAGTCAAGTTGAG
13430-13452	CCAACTCTCAAGTCAAGTTGAGC
13431-13453	CAACTCTCAAGTCAAGTTGAGCA
13432-13454	AACTCTCAAGTCAAGTTGAGCAA
13433-13455	ACTCTCAAGTCAAGTTGAGCAAT
13434-13456	CTCTCAAGTCAAGTTGAGCAATT
13435-13457	TCTCAAGTCAAGTTGAGCAATTT
13436-13458	CTCAAGTCAAGTTGAGCAATTTCT
13437-13459	TCAAGTCAAGTTGAGCAATTTCT
13438-13460	CAAGTCAAGTTGAGCAATTTCTG
13439-13461	AAGTCAAGTTGAGCAATTTCTGC
13440-13462	AGTCAAGTTGAGCAATTTCTGCA

Position	Sequence
13441-13463	GTCAGTTGAGCAATTTCTGCAC
13442-13464	TCAAGTTGAGCAATTTCTGCACA
13443-13465	CAAGTTGAGCAATTTCTGCACAG
13444-13466	AAGTTGAGCAATTTCTGCACAGA
13445-13467	AGTTGAGCAATTTCTGCACAGAA
13446-13468	GTTGAGCAATTTCTGCACAGAAA
13447-13469	TTGAGCAATTTCTGCACAGAAAT
13448-13470	TGAGCAATTTCTGCACAGAAATA
13449-13471	GAGCAATTTCTGCACAGAAATAT
13450-13472	AGCAATTTCTGCACAGAAATATT
13451-13473	GCAATTTCTGCACAGAAATATTC
13452-13474	CAATTTCTGCACAGAAATATTCA
13453-13475	AATTTCTGCACAGAAATATTCAG
13454-13476	ATTTCTGCACAGAAATATTCAGG
13455-13477	TTTCTGCACAGAAATATTCAGGA
13456-13478	TTCTGCACAGAAATATTCAGGAA
13457-13479	TCTGCACAGAAATATTCAGGAAT
13458-13480	CTGCACAGAAATATTCAGGAATA
13459-13481	TGCACAGAAATATTCAGGAATAT
13460-13482	GCACAGAAATATTCAGGAATATC
13461-13483	CACAGAAATATTCAGGAATATCT
13462-13484	ACAGAAATATTCAGGAATATCTT
13463-13485	CAGAAATATTCAGGAATATCTTA
13464-13486	AGAAATATTCAGGAATATCTTAG
13465-13487	GAAATATTCAGGAATATCTTAGC
13466-13488	AAATATTCAGGAATATCTTAGCA
13467-13489	AATATTCAGGAATATCTTAGCAT
13468-13490	ATATTCAGGAATATCTTAGCATC
13469-13491	TATTCAGGAATATCTTAGCATCC
13470-13492	ATTCAGGAATATCTTAGCATCCT
13471-13493	TTCAGGAATATCTTAGCATCCTT
13472-13494	TCAGGAATATCTTAGCATCCTTA
13473-13495	CAGGAATATCTTAGCATCCTTAC
13474-13496	AGGAATATCTTAGCATCCTTACC
13475-13497	GGAATATCTTAGCATCCTTACCG
13476-13498	GAATATCTTAGCATCCTTACCGA
13477-13499	AATATCTTAGCATCCTTACCGAT
13478-13500	ATATCTTAGCATCCTTACCGATC
13479-13501	TATCTTAGCATCCTTACCGATCC
13480-13502	ATCTTAGCATCCTTACCGATCCA
13481-13503	TCTTAGCATCCTTACCGATCCAG
13482-13504	CTTAGCATCCTTACCGATCCAGA
13483-13505	TTAGCATCCTTACCGATCCAGAT
13484-13506	TAGCATCCTTACCGATCCAGATG
13485-13507	AGCATCCTTACCGATCCAGATGG
13486-13508	GCATCCTTACCGATCCAGATGGA
13487-13509	CATCCTTACCGATCCAGATGGAA
13488-13510	ATCCTTACCGATCCAGATGGAAA
13489-13511	TCCTTACCGATCCAGATGGAAAA
13490-13512	CCTTACCGATCCAGATGGAAAAG
13491-13513	CTTACCGATCCAGATGGAAAAGG
13492-13514	TTACCGATCCAGATGGAAAAGGG
13493-13515	TACCGATCCAGATGGAAAAGGGA
13494-13516	ACCGATCCAGATGGAAAAGGGAA
13495-13517	CCGATCCAGATGGAAAAGGGAAA
13496-13518	CGATCCAGATGGAAAAGGGAAAAG
13497-13519	GATCCAGATGGAAAAGGGAAAAGA
13498-13520	ATCCAGATGGAAAAGGGAAAAGAG
13499-13521	TCCAGATGGAAAAGGGAAAAGAGA
13500-13522	CCAGATGGAAAAGGGAAAAGAGAA
13501-13523	CAGATGGAAAAGGGAAAAGAGAAG
13502-13524	AGATGGAAAAGGGAAAAGAGAAGA
13503-13525	GATGGAAAAGGGAAAAGAGAAGAT
13504-13526	ATGGAAAAGGGAAAAGAGAAGATT
13505-13527	TGGAAAAGGGAAAAGAGAAGATTG
13506-13528	GGAAAAGGGAAAAGAGAAGATTGC

Position	Sequence
13507-13529	GAAAAGGGAAAGAGAAGATTGCA
13508-13530	AAAAGGGAAAGAGAAGATTGCAG
13509-13531	AAAGGGAAAGAGAAGATTGCAGA
13510-13532	AAGGGAAAGAGAAGATTGCAGAG
13511-13533	AGGGAAAGAGAAGATTGCAGAGC
13512-13534	GGGAAAGAGAAGATTGCAGAGCT
13513-13535	GGAAAGAGAAGATTGCAGAGCTT
13514-13536	GAAAGAGAAGATTGCAGAGCTTT
13515-13537	AAAGAGAAGATTGCAGAGCTTTC
13516-13538	AAGAGAAGATTGCAGAGCTTTCT
13517-13539	AGAGAAGATTGCAGAGCTTTCTG
13518-13540	GAGAAGATTGCAGAGCTTTCTGC
13519-13541	AGAAGATTGCAGAGCTTTCTGCC
13520-13542	GAAGATTGCAGAGCTTTCTGCCA
13521-13543	AAGATTGCAGAGCTTTCTGCCAC
13522-13544	AGATTGCAGAGCTTTCTGCCACT
13523-13545	GATTGCAGAGCTTTCTGCCACTG
13524-13546	ATTGCAGAGCTTTCTGCCACTGC
13525-13547	TTGCAGAGCTTTCTGCCACTGCT
13526-13548	TGCAGAGCTTTCTGCCACTGCTC
13527-13549	GCAGAGCTTTCTGCCACTGCTCA
13528-13550	CAGAGCTTTCTGCCACTGCTCAG
13529-13551	AGAGCTTTCTGCCACTGCTCAGG
13530-13552	GAGCTTTCTGCCACTGCTCAGGA
13531-13553	AGCTTTCTGCCACTGCTCAGGAA
13532-13554	GCTTTCTGCCACTGCTCAGGAAA
13533-13555	CTTTCTGCCACTGCTCAGGAAAT
13534-13556	TTTCTGCCACTGCTCAGGAAATA
13535-13557	TTCTGCCACTGCTCAGGAAATAA
13536-13558	TCTGCCACTGCTCAGGAAATAAT
13537-13559	CTGCCACTGCTCAGGAAATAATF
13538-13560	TGCCACTGCTCAGGAAATAATTA
13539-13561	GCCACTGCTCAGGAAATAATTAA
13540-13562	CCACTGCTCAGGAAATAATTAAA
13541-13563	CACTGCTCAGGAAATAATTAAAA
13542-13564	ACTGCTCAGGAAATAATTAAAAG
13543-13565	CTGCTCAGGAAATAATTAAAAGC
13544-13566	TGCTCAGGAAATAATTAAAAGCC
13545-13567	GCTCAGGAAATAATTAAAAGCCA
13546-13568	CTCAGGAAATAATTAAAAGCCAG
13547-13569	TCAGGAAATAATTAAAAGCCAGG
13548-13570	CAGGAAATAATTAAAAGCCAGGC
13549-13571	AGGAAATAATTAAAAGCCAGGCC
13550-13572	GGAAATAATTAAAAGCCAGGCCA
13551-13573	GAAATAATTAAAAGCCAGGCCAT
13552-13574	AAATAATTAAAAGCCAGGCCATT
13553-13575	AATAATTAAAAGCCAGGCCATTG
13554-13576	ATAATTAAAAGCCAGGCCATTGC
13555-13577	TAATTAAAAGCCAGGCCATTGCG
13556-13578	AATTAAAAGCCAGGCCATTGCGA
13557-13579	ATTAAAAGCCAGGCCATTGCGAC
13558-13580	TAAAAGCCAGGCCATTGCGACG
13559-13581	TAAAAGCCAGGCCATTGCGACGA
13560-13582	AAAAGCCAGGCCATTGCGACGAA
13561-13583	AAAGCCAGGCCATTGCGACGAAG
13562-13584	AAGCCAGGCCATTGCGACGAAGA
13563-13585	AGCCAGGCCATTGCGACGAAGAA
13564-13586	GCCAGGCCATTGCGACGAAGAAA
13565-13587	CCAGGCCATTGCGACGAAGAAAA
13566-13588	CAGGCCATTGCGACGAAGAAAAAT
13567-13589	AGGCCATTGCGACGAAGAAAAATA
13568-13590	GGCCATTGCGACGAAGAAAAATAA
13569-13591	GCCATTGCGACGAAGAAAAATAAT
13570-13592	CCATTGCGACGAAGAAAAATAATT
13571-13593	CATTGCGACGAAGAAAAATAATTT
13572-13594	ATTGCGACGAAGAAAAATAATTC

Position	Sequence
13573-13595	TTGCGACGAAGAAAATAATTTCT
13574-13596	TGCGACGAAGAAAATAATTTCTG
13575-13597	GCGACGAAGAAAATAATTTCTGA
13576-13598	CGACGAAGAAAATAATTTCTGAT
13577-13599	GACGAAGAAAATAATTTCTGATT
13578-13600	ACGAAGAAAATAATTTCTGATTA
13579-13601	CGAAGAAAATAATTTCTGATTAC
13580-13602	GAAGAAAATAATTTCTGATTACC
13581-13603	AAGAAAATAATTTCTGATTACCA
13582-13604	AGAAAATAATTTCTGATTACCAC
13583-13605	GAAAATAATTTCTGATTACCACC
13584-13606	AAAATAATTTCTGATTACCACCA
13585-13607	AAATAATTTCTGATTACCACCAG
13586-13608	AATAATTTCTGATTACCACCAGC
13587-13609	ATAATTTCTGATTACCACCAGCA
13588-13610	TAATTTCTGATTACCACCAGCAG
13589-13611	AATTTCTGATTACCACCAGCAGT
13590-13612	ATTTCTGATTACCACCAGCAGTT
13591-13613	TTTCTGATTACCACCAGCAGTTT
13592-13614	TTCTGATTACCACCAGCAGTTTA
13593-13615	TCTGATTACCACCAGCAGTTTAG
13594-13616	CTGATTACCACCAGCAGTTTAGA
13595-13617	TGATTACCACCAGCAGTTTAGAT
13596-13618	GATTACCACCAGCAGTTTAGATA
13597-13619	ATTACCACCAGCAGTTTAGATAT
13598-13620	TTACCACCAGCAGTTTAGATATA
13599-13621	TACCACCAGCAGTTTAGATATAA
13600-13622	ACCACCAGCAGTTTAGATATAAA
13601-13623	CCACCAGCAGTTTAGATATAAAC
13602-13624	CACCAGCAGTTTAGATATAAACT
13603-13625	ACCAGCAGTTTAGATATAAACTG
13604-13626	CCAGCAGTTTAGATATAAACTGC
13605-13627	CAGCAGTTTAGATATAAACTGCA
13606-13628	AGCAGTTTAGATATAAACTGCAA
13607-13629	GCAGTTTAGATATAAACTGCAAG
13608-13630	CAGTTTAGATATAAACTGCAAGA
13609-13631	AGTTTAGATATAAACTGCAAGAT
13610-13632	GTTTAGATATAAACTGCAAGATT
13611-13633	TTTAGATATAAACTGCAAGATTT
13612-13634	TTAGATATAAACTGCAAGATTTT
13613-13635	TAGATATAAACTGCAAGATTTTT
13614-13636	AGATATAAACTGCAAGATTTTTC
13615-13637	GATATAAACTGCAAGATTTTTCA
13616-13638	ATATAAACTGCAAGATTTTTCAG
13617-13639	TATAAACTGCAAGATTTTTCAGA
13618-13640	ATAAACTGCAAGATTTTTCAGAC
13619-13641	TAAACTGCAAGATTTTTCAGACC
13620-13642	AAACTGCAAGATTTTTCAGACCA
13621-13643	AACTGCAAGATTTTTCAGACCAA
13622-13644	ACTGCAAGATTTTTCAGACCAAC
13623-13645	CTGCAAGATTTTTCAGACCAACT
13624-13646	TGCAAGATTTTTCAGACCAACTC
13625-13647	GCAAGATTTTTCAGACCAACTCT
13626-13648	CAAGATTTTTCAGACCAACTCTC
13627-13649	AAGATTTTTCAGACCAACTCTCT
13628-13650	AGATTTTTCAGACCAACTCTCTG
13629-13651	GATTTTTCAGACCAACTCTCTGA
13630-13652	ATTTTTCAGACCAACTCTCTGAT
13631-13653	TTTTTCAGACCAACTCTCTGATT
13632-13654	TTTTCAGACCAACTCTCTGATTA
13633-13655	TTTCAGACCAACTCTCTGATTAC
13634-13656	TTCAGACCAACTCTCTGATTACT
13635-13657	TCAGACCAACTCTCTGATTACTA
13636-13658	CAGACCAACTCTCTGATTACTAT
13637-13659	AGACCAACTCTCTGATTACTATG
13638-13660	GACCAACTCTCTGATTACTATGA

Position	Sequence
13639-13661	ACCAACTCTCTGATTACTATGAA
13640-13662	CCAACTCTCTGATTACTATGAAA
13641-13663	CAACTCTCTGATTACTATGAAAA
13642-13664	AACTCTCTGATTACTATGAAAAA
13643-13665	ACTCTCTGATTACTATGAAAAAT
13644-13666	CTCTCTGATTACTATGAAAAATT
13645-13667	TCTCTGATTACTATGAAAAATTT
13646-13668	CTCTGATTACTATGAAAAATTTA
13647-13669	TCGATTACTATGAAAAATTTAT
13648-13670	CTGATTACTATGAAAAATTTATT
13649-13671	TGATTACTATGAAAAATTTATTG
13650-13672	GATTACTATGAAAAATTTATTGC
13651-13673	ATTACTATGAAAAATTTATTGCT
13652-13674	TTACTATGAAAAATTTATTGCTG
13653-13675	TACTATGAAAAATTTATTGCTGA
13654-13676	ACTATGAAAAATTTATTGCTGAA
13655-13677	CTATGAAAAATTTATTGCTGAAT
13656-13678	TATGAAAAATTTATTGCTGAATC
13657-13679	ATGAAAAATTTATTGCTGAATCC
13658-13680	TGAAAAATTTATTGCTGAATCCA
13659-13681	GAAAAATTTATTGCTGAATCCAA
13660-13682	AAAAATTTATTGCTGAATCCAAA
13661-13683	AAAATTTATTGCTGAATCCAAA
13662-13684	AAATTTATTGCTGAATCCAAAAG
13663-13685	AATTTATTGCTGAATCCAAAAGA
13664-13686	ATTTATTGCTGAATCCAAAAGAT
13665-13687	TTTATTGCTGAATCCAAAAGATT
13666-13688	TTATTGCTGAATCCAAAAGATTG
13667-13689	TATTGCTGAATCCAAAAGATTGA
13668-13690	ATTGCTGAATCCAAAAGATTGAT
13669-13691	TTGCTGAATCCAAAAGATTGATT
13670-13692	TGCTGAATCCAAAAGATTGATTG
13671-13693	GCTGAATCCAAAAGATTGATTGA
13672-13694	CTGAATCCAAAAGATTGATTGAC
13673-13695	TGAATCCAAAAGATTGATTGACC
13674-13696	GAATCCAAAAGATTGATTGACCT
13675-13697	AATCCAAAAGATTGATTGACCTG
13676-13698	ATCCAAAAGATTGATTGACCTGT
13677-13699	TCCAAAAGATTGATTGACCTGTC
13678-13700	CCAAAAGATTGATTGACCTGTCC
13679-13701	CAAAGATTGATTGACCTGTCCA
13680-13702	AAAAGATTGATTGACCTGTCCAT
13681-13703	AAAGATTGATTGACCTGTCCATT
13682-13704	AAGATTGATTGACCTGTCCATT
13683-13705	AGATTGATTGACCTGTCCATTCA
13684-13706	GATTGATTGACCTGTCCATTCAA
13685-13707	ATTGATTGACCTGTCCATTCAAA
13686-13708	TTGATTGACCTGTCCATTCAAAA
13687-13709	TGATTGACCTGTCCATTCAAAAC
13688-13710	GATTGACCTGTCCATTCAAACCT
13689-13711	ATTGACCTGTCCATTCAAACCTA
13690-13712	TTGACCTGTCCATTCAAACCTAC
13691-13713	TGACCTGTCCATTCAAACCTACC
13692-13714	GACCTGTCCATTCAAACCTACCA
13693-13715	ACCTGTCCATTCAAACCTACCAC
13694-13716	CCTGTCCATTCAAACCTACCACA
13695-13717	CTGTCCATTCAAACCTACCACAC
13696-13718	TGTCCATTCAAACCTACCACACA
13697-13719	GTCCATTCAAACCTACCACACAT
13698-13720	TCCATTCAAACCTACCACACATT
13699-13721	CCATTCAAACCTACCACACATTT
13700-13722	CATTCAAACCTACCACACATTT
13701-13723	ATTCAAACCTACCACACATTTCT
13702-13724	TTCAAACCTACCACACATTTCTG
13703-13725	TCAAACCTACCACACATTTCTGA
13704-13726	CAAACCTACCACACATTTCTGAT

Position	Sequence
13705-13727	AAACTACCACACATTTCTGATA
13706-13728	AAACTACCACACATTTCTGATAT
13707-13729	AACTACCACACATTTCTGATATA
13708-13730	ACTACCACACATTTCTGATATAC
13709-13731	CTACCACACATTTCTGATATACA
13710-13732	TACCACACATTTCTGATATACAT
13711-13733	ACCACACATTTCTGATATACATC
13712-13734	CCACACATTTCTGATATACATCA
13713-13735	CACACATTTCTGATATACATCAC
13714-13736	ACACATTTCTGATATACATCACC
13715-13737	CACATTTCTGATATACATCACGG
13716-13738	ACATTTCTGATATACATCACGGA
13717-13739	CATTTCTGATATACATCACGGAG
13718-13740	ATTTCTGATATACATCACGGAGT
13719-13741	TTTCTGATATACATCACGGAGTT
13720-13742	TTCTGATATACATCACGGAGTTA
13721-13743	TCTGATATACATCACGGAGTTAC
13722-13744	CTGATATACATCACGGAGTTACT
13723-13745	TGATATACATCACGGAGTTACTG
13724-13746	GATATACATCACGGAGTTACTGA
13725-13747	ATATACATCACGGAGTTACTGAA
13726-13748	TATACATCACGGAGTTACTGAAA
13727-13749	ATACATCACGGAGTTACTGAAAA
13728-13750	TACATCACGGAGTTACTGAAAA
13729-13751	ACATCACGGAGTTACTGAAAAAG
13730-13752	CATCACGGAGTTACTGAAAAAGC
13731-13753	ATCACGGAGTTACTGAAAAAGCT
13732-13754	TCACGGAGTTACTGAAAAAGCTG
13733-13755	CACGGAGTTACTGAAAAAGCTGC
13734-13756	ACGGAGTTACTGAAAAAGCTGCA
13735-13757	CGGAGTTACTGAAAAAGCTGCAA
13736-13758	GGAGTTACTGAAAAAGCTGCAAT
13737-13759	GAGTTACTGAAAAAGCTGCAATC
13738-13760	AGTTACTGAAAAAGCTGCAATCA
13739-13761	GTTACTGAAAAAGCTGCAATCAA
13740-13762	TTACTGAAAAAGCTGCAATCAAC
13741-13763	TACTGAAAAAGCTGCAATCAACC
13742-13764	ACTGAAAAAGCTGCAATCAACCA
13743-13765	CTGAAAAAGCTGCAATCAACCAC
13744-13766	TGAAAAAGCTGCAATCAACCACA
13745-13767	GAAAAAGCTGCAATCAACCACAG
13746-13768	AAAAGCTGCAATCAACCACAGT
13747-13769	AAAAGCTGCAATCAACCACAGTC
13748-13770	AAAGCTGCAATCAACCACAGTCA
13749-13771	AAGCTGCAATCAACCACAGTCAT
13750-13772	AGCTGCAATCAACCACAGTCATG
13751-13773	GCTGCAATCAACCACAGTCATGA
13752-13774	CTGCAATCAACCACAGTCATGAA
13753-13775	TGCAATCAACCACAGTCATGAAC
13754-13776	GCAATCAACCACAGTCATGAACC
13755-13777	CAATCAACCACAGTCATGAACCC
13756-13778	AATCAACCACAGTCATGAACCCC
13757-13779	ATCAACCACAGTCATGAACCCCT
13758-13780	TCAACCACAGTCATGAACCCCTA
13759-13781	CAACCACAGTCATGAACCCCTAC
13760-13782	AACCACAGTCATGAACCCCTACA
13761-13783	ACCACAGTCATGAACCCCTACAT
13762-13784	CCACAGTCATGAACCCCTACATG
13763-13785	CACAGTCATGAACCCCTACATGA
13764-13786	ACAGTCATGAACCCCTACATGAA
13765-13787	CAGTCATGAACCCCTACATGAAG
13766-13788	AGTCATGAACCCCTACATGAAGC
13767-13789	GTCATGAACCCCTACATGAAGCT
13768-13790	TCATGAACCCCTACATGAAGCTT
13769-13791	CATGAACCCCTACATGAAGCTTG
13770-13792	ATGAACCCCTACATGAAGCTTGC

Position	Sequence
13771-13793	TGAACCCCTACATGAAGCTTGCT
13772-13794	GAACCCCTACATGAAGCTTGCTC
13773-13795	AACCCCTACATGAAGCTTGCTCC
13774-13796	ACCCCTACATGAAGCTTGCTCCA
13775-13797	CCCCTACATGAAGCTTGCTCCAG
13776-13798	CCCTACATGAAGCTTGCTCCAGG
13777-13799	CCTACATGAAGCTTGCTCCAGGA
13778-13800	CTACATGAAGCTTGCTCCAGGAG
13779-13801	TACATGAAGCTTGCTCCAGGAGA
13780-13802	ACATGAAGCTTGCTCCAGGAGAA
13781-13803	CATGAAGCTTGCTCCAGGAGAAC
13782-13804	ATGAAGCTTGCTCCAGGAGAACT
13783-13805	TGAAGCTTGCTCCAGGAGAACTT
13784-13806	GAAGCTTGCTCCAGGAGAACTTA
13785-13807	AAGCTTGCTCCAGGAGAACTTAC
13786-13808	AGCTTGCTCCAGGAGAACTTACT
13787-13809	GCTTGCTCCAGGAGAACTTACTA
13788-13810	CTTGCTCCAGGAGAACTTACTAT
13789-13811	TTGCTCCAGGAGAACTTACTATC
13790-13812	TGCTCCAGGAGAACTTACTATCA
13791-13813	GCTCCAGGAGAACTTACTATCAT
13792-13814	CTCCAGGAGAACTTACTATCATC
13793-13815	TCCAGGAGAACTTACTATCATCC
13794-13816	CCAGGAGAACTTACTATCATCCT
13795-13817	CAGGAGAACTTACTATCATCCTC
13796-13818	AGGAGAACTTACTATCATCCTCT
13797-13819	GGAGAACTTACTATCATCCTCTA
13821-13843	TTTTTAAAAGAAATCTTCATTT
13822-13844	TTTTTAAAAGAAATCTTCATTTA
13823-13845	TTTTTAAAAGAAATCTTCATTTAT
13824-13846	TTTAAAAGAAATCTTCATTTATT
13825-13847	TTAAAAGAAATCTTCATTTATTC
13826-13848	TAAAAGAAATCTTCATTTATTCT
13827-13849	AAAAGAAATCTTCATTTATTCTT
13828-13850	AAAGAAATCTTCATTTATTCTTC
13829-13851	AAGAAATCTTCATTTATTCTTCT
13830-13852	AGAAATCTTCATTTATTCTTCTT
13831-13853	GAAATCTTCATTTATTCTTCTTT
13832-13854	AAATCTTCATTTATTCTTCTTTT
13833-13855	AATCTTCATTTATTCTTCTTTTTC
13834-13856	ATCTTCATTTATTCTTCTTTTCC
13835-13857	TCTTCATTTATTCTTCTTTTCCA
13836-13858	CTTCATTTATTCTTCTTTTCCAA
13837-13859	TTCATTTATTCTTCTTTTCCAAT
13838-13860	TCATTTATTCTTCTTTTCCAATF
13839-13861	CATTTATTCTTCTTTTCCAATFG
13840-13862	ATTTATTCTTCTTTTCCAATTGA
13841-13863	TTATTCTTCTTTTCCAATTGAA
13842-13864	TTATTCTTCTTTTCCAATTGAAC
13843-13865	TATTCTTCTTTTCCAATTGAACT
13844-13866	ATTCTTCTTTTCCAATTGAACTF
13845-13867	TTCTTCTTTTCCAATTGAACTTF
13846-13868	TCTTCTTTTCCAATTGAACTTTC
13847-13869	CTTCTTTTCCAATTGAACTTTCA
13848-13870	TTCTTTTCCAATTGAACTTTCAC
13849-13871	TCTTTTCCAATTGAACTTTCACA
13850-13872	CTTTTCCAATTGAACTTTCACAT
13851-13873	TTTCCAATTGAACTTTCACATA
13852-13874	TTCCAATTGAACTTTCACATAG
13853-13875	TTCCAATTGAACTTTCACATAGC
13854-13876	TCCAATTGAACTTTCACATAGCA
13855-13877	CCAATTGAACTTTCACATAGCAC
13856-13878	CAATTGAACTTTCACATAGCACA
13857-13879	AATTGAACTTTCACATAGCACAG
13858-13880	ATTGAACTTTCACATAGCACAGA
13859-13881	TTGAACTTTCACATAGCACAGAA

Position	Sequence
13860-13882	TGAACTTTCACATAGCACAGAAA
13861-13883	GAACTTTCACATAGCACAGAAA
13862-13884	AACTTTCACATAGCACAGAAA
13863-13885	ACTTTCACATAGCACAGAAA
13864-13886	CTTTCACATAGCACAGAAAAT
13865-13887	TTTCACATAGCACAGAAAAT
13866-13888	TTCACATAGCACAGAAAATTC
13867-13889	TCACATAGCACAGAAAATTC
13868-13890	CACATAGCACAGAAAATTC
13869-13891	ACATAGCACAGAAAATTC
13870-13892	CATAGCACAGAAAATTC
13871-13893	ATAGCACAGAAAATTC
13872-13894	TAGCACAGAAAATTC
13873-13895	AGCACAGAAAATTC
13874-13896	GCACAGAAAATTC
13875-13897	CACAGAAAATTC
13876-13898	ACAGAAAATTC
13877-13899	CAGAAAATTC
13878-13900	AGAAAATTC
13879-13901	GAAAATTC
13880-13902	AAAAATTC
13881-13903	AAAATTC
13882-13904	AAATTC
13883-13905	AAATTC
13884-13906	AATTC
13885-13907	ATTTC
13886-13908	TTTC
13887-13909	TTC
13888-13910	TC
13889-13911	AACTGCCTATATTGATAAAACC
13890-13912	AACTGCCTATATTGATAAAACCA
13891-13913	ACTGCCTATATTGATAAAACCAT
13892-13914	CTGCCTATATTGATAAAACCATA
13893-13915	TGCCTATATTGATAAAACCATAC
13894-13916	GCCTATATTGATAAAACCATACA
13895-13917	CCTATATTGATAAAACCATACAG
13896-13918	CTATATTGATAAAACCATACAGT
13897-13919	TATATTGATAAAACCATACAGTG
13898-13920	ATATTGATAAAACCATACAGTGA
13899-13921	TATTGATAAAACCATACAGTGAG
13900-13922	ATTGATAAAACCATACAGTGAGC
13901-13923	TTGATAAAACCATACAGTGAGCC
13902-13924	TGATAAAACCATACAGTGAGCCA
13903-13925	GATAAAACCATACAGTGAGCCAG
13904-13926	ATAAAACCATACAGTGAGCCAGC
13905-13927	TAAAACCATACAGTGAGCCAGCC
13906-13928	AAAACCATACAGTGAGCCAGCCT
13907-13929	AAACCATACAGTGAGCCAGCCTT
13908-13930	AACCATACAGTGAGCCAGCCTTG
13909-13931	ACCATACAGTGAGCCAGCCTTGC
13910-13932	CCATACAGTGAGCCAGCCTTGCA
13911-13933	CATACAGTGAGCCAGCCTTGCA
13912-13934	ATACAGTGAGCCAGCCTTGCA
13913-13935	TACAGTGAGCCAGCCTTGCA
13914-13936	ACAGTGAGCCAGCCTTGCA
13915-13937	CAGTGAGCCAGCCTTGCA
13916-13938	AGTGAGCCAGCCTTGCA
13917-13939	GTGAGCCAGCCTTGCA
13918-13940	TGAGCCAGCCTTGCA
13919-13941	GAGCCAGCCTTGCA
13920-13942	AGCCAGCCTTGCA
13921-13943	GCCAGCCTTGCA
13922-13944	CCAGCCTTGCA
13923-13945	CAGCCTTGCA
13924-13946	AGCCTTGCA
13925-13947	GCCTTGCA

Position	Sequence
13926-13948	CCTTGCACTAGGCAGTAGACTAT
13927-13949	CTTGCACTAGGCAGTAGACTATA
13928-13950	TTGCAGTAGGCAGTAGACTATAA
13929-13951	TGCAGTAGGCAGTAGACTATAAG
13930-13952	GCAGTAGGCAGTAGACTATAAGC
13931-13953	CAGTAGGCAGTAGACTATAAGCA
13932-13954	AGTAGGCAGTAGACTATAAGCAG
13933-13955	GTAGGCAGTAGACTATAAGCAGA
13934-13956	TAGGCAGTAGACTATAAGCAGAA
13935-13957	AGGCAGTAGACTATAAGCAGAAG
13936-13958	GGCAGTAGACTATAAGCAGAAGC
13937-13959	GCAGTAGACTATAAGCAGAAGCA
13938-13960	CAGTAGACTATAAGCAGAAGCAC
13939-13961	AGTAGACTATAAGCAGAAGCACA
13940-13962	GTAGACTATAAGCAGAAGCACAT
13941-13963	TAGACTATAAGCAGAAGCACATA
13942-13964	AGACTATAAGCAGAAGCACATAT
13943-13965	GACTATAAGCAGAAGCACATATG
13944-13966	ACTATAAGCAGAAGCACATATGA
13945-13967	CTATAAGCAGAAGCACATATGAA
13946-13968	TATAAGCAGAAGCACATATGAAC
13947-13969	ATAAGCAGAAGCACATATGAACT
13948-13970	TAAGCAGAAGCACATATGAACTG
13949-13971	AAGCAGAAGCACATATGAACTGG
13950-13972	AGCAGAAGCACATATGAACTGGA
13951-13973	GCAGAAGCACATATGAACTGGAC
13952-13974	CAGAAGCACATATGAACTGGACC
13953-13975	AGAAGCACATATGAACTGGACCT
13954-13976	GAAGCACATATGAACTGGACCTG
13955-13977	AAGCACATATGAACTGGACCTGC
13956-13978	AGCACATATGAACTGGACCTGCA
13957-13979	GCACATATGAACTGGACCTGCAC
13958-13980	CACATATGAACTGGACCTGCACC
13959-13981	ACATATGAACTGGACCTGCACCA
13960-13982	CATATGAACTGGACCTGCACCAA
13961-13983	ATATGAACTGGACCTGCACCAAA
13962-13984	TATGAACTGGACCTGCACCAAAG
13963-13985	ATGAACTGGACCTGCACCAAAGC
13964-13986	TGAACTGGACCTGCACCAAAGCT
13965-13987	GAACTGGACCTGCACCAAAGCTG
13966-13988	AACTGGACCTGCACCAAAGCTGG
13967-13989	ACTGGACCTGCACCAAAGCTGGC
13968-13990	CTGGACCTGCACCAAAGCTGGCA
13969-13991	TGGACCTGCACCAAAGCTGGCAC
13970-13992	GGACCTGCACCAAAGCTGGCACC
13971-13993	GACCTGCACCAAAGCTGGCACCA
13972-13994	ACCTGCACCAAAGCTGGCACCAG
13973-13995	CCTGCACCAAAGCTGGCACCAGG
13974-13996	CTGCACCAAAGCTGGCACCAGGG
13975-13997	TGCACCAAAGCTGGCACCAGGGC
13976-13998	GCACCAAAGCTGGCACCAGGGCT
13977-13999	CACCAAAGCTGGCACCAGGGCTC
13978-14000	ACCAAAGCTGGCACCAGGGCTCG
13979-14001	CCAAAGCTGGCACCAGGGCTCGG
13980-14002	CAAAGCTGGCACCAGGGCTCGGA
13981-14003	AAAGCTGGCACCAGGGCTCGGAA
13982-14004	AAGCTGGCACCAGGGCTCGGAAG
13983-14005	AGCTGGCACCAGGGCTCGGAAGG
13984-14006	GCTGGCACCAGGGCTCGGAAGGT
13985-14007	CTGGCACCAGGGCTCGGAAGGTC
13986-14008	TGGCACCAGGGCTCGGAAGGTCT
13987-14009	GGCACCAGGGCTCGGAAGGTCTC
13988-14010	GCACCAGGGCTCGGAAGGTCTCT
13989-14011	CACCAGGGCTCGGAAGGTCTCTG
13990-14012	ACCAGGGCTCGGAAGGTCTCTGA
13991-14013	CCAGGGCTCGGAAGGTCTCTGAA

Position	Sequence
13992-14014	CAGGGCTCGGAAGGTCTCTGAAC
13993-14015	AGGGCTCGGAAGGTCTCTGAACT
13994-14016	GGGCTCGGAAGGTCTCTGAACTC
13995-14017	GGCTCGGAAGGTCTCTGAACTCA
13996-14018	GCTCGGAAGGTCTCTGAACTCAG
13997-14019	CTCGGAAGGTCTCTGAACTCAGA
13998-14020	TCGGAAGGTCTCTGAACTCAGAA
13999-14021	CGGAAGGTCTCTGAACTCAGAAG
14000-14022	GGAAGGTCTCTGAACTCAGAAGG
14001-14023	GAAGGTCTCTGAACTCAGAAGGA
14002-14024	AAGGTCTCTGAACTCAGAAGGAT
14003-14025	AGGTCTCTGAACTCAGAAGGATG
14004-14026	GGTCTCTGAACTCAGAAGGATGG
14005-14027	GTCTCTGAACTCAGAAGGATGGC
14006-14028	TCTCTGAACTCAGAAGGATGGCA
14007-14029	CTCTGAACTCAGAAGGATGGCAT
14008-14030	TCTGAACTCAGAAGGATGGCATT
14009-14031	CTGAACTCAGAAGGATGGCATT
14010-14032	TGAACTCAGAAGGATGGCATT
14011-14033	GAACTCAGAAGGATGGCATT
14012-14034	AACTCAGAAGGATGGCATT
14013-14035	ACTCAGAAGGATGGCATT
14014-14036	CTCAGAAGGATGGCATT
14015-14037	TCAGAAGGATGGCATT
14016-14038	CAGAAGGATGGCATT
14017-14039	AGAAGGATGGCATT
14018-14040	GAAGGATGGCATT
14019-14041	AAGGATGGCATT
14020-14042	AGGATGGCATT
14021-14043	GGATGGCATT
14022-14044	GATGGCATT
14023-14045	ATGGCATT
14024-14046	TGGCATT
14025-14047	GGCATT
14026-14048	GCATT
14027-14049	CATT
14028-14050	ATT
14029-14051	T
14030-14052	
14031-14053	
14032-14054	
14033-14055	
14034-14056	
14035-14057	
14036-14058	
14037-14059	
14038-14060	
14039-14061	
14040-14062	
14041-14063	
14042-14064	
14043-14065	
14044-14066	
14045-14067	
14046-14068	
14047-14069	
14048-14070	
14049-14071	
14050-14072	
14051-14073	
14052-14074	
14053-14075	
14054-14076	
14055-14077	
14056-14078	
14057-14079	

Position	Sequence
14058-14080	TGAGTTATTTGCTAAACTTGGG
14059-14081	GAGTTATTTGCTAAACTTGGGG
14060-14082	AGTTATTTGCTAAACTTGGGGG
14061-14083	GTTATTTGCTAAACTTGGGGGA
14062-14084	TTATTTGCTAAACTTGGGGGAG
14063-14085	TATTTGCTAAACTTGGGGGAGG
14064-14086	ATTTGCTAAACTTGGGGGAGGA
14065-14087	TTTGCTAAACTTGGGGGAGGAG
14066-14088	TTTGCTAAACTTGGGGGAGGAGG
14067-14089	TTGCTAAACTTGGGGGAGGAGGA
14068-14090	TGCTAAACTTGGGGGAGGAGGAA
14069-14091	GCTAAACTTGGGGGAGGAGGAAC
14070-14092	CTAAACTTGGGGGAGGAGGAACA
14071-14093	TAAACTTGGGGGAGGAGGAACAA
14072-14094	AAACTTGGGGGAGGAGGAACAAA
14073-14095	AACTTGGGGGAGGAGGAACAAAT
14074-14096	ACTTGGGGGAGGAGGAACAAATA
14075-14097	CTTGGGGGAGGAGGAACAAATAA
14076-14098	TTGGGGGAGGAGGAACAAATAAA
14077-14099	TGGGGGAGGAGGAACAAATAAAT
14078-14100	GGGGGAGGAGGAACAAATAAATG
14079-14101	GGGGAGGAGGAACAAATAAATGG
14080-14102	GGGAGGAGGAACAAATAAATGGA
14081-14103	GGAGGAGGAACAAATAAATGGAG
14082-14104	GAGGAGGAACAAATAAATGGAGT
14083-14105	AGGAGGAACAAATAAATGGAGTC
14084-14106	GGAGGAACAAATAAATGGAGTCT
14085-14107	GAGGAACAAATAAATGGAGTCTT
14086-14108	AGGAACAAATAAATGGAGTCTTT
14087-14109	GGAACAAATAAATGGAGTCTTTA
14088-14110	GAACAAATAAATGGAGTCTTTAT
14089-14111	AACAAATAAATGGAGTCTTTATT
14090-14112	ACAAATAAATGGAGTCTTTATTG
14091-14113	CAAATAAATGGAGTCTTTATTGT
14092-14114	AAATAAATGGAGTCTTTATTGTG
14093-14115	AATAAATGGAGTCTTTATTGTGT
14094-14116	ATAAATGGAGTCTTTATTGTGTA
14095-14117	TAAATGGAGTCTTTATTGTGTAT
14096-14118	AAATGGAGTCTTTATTGTGTATC
14097-14119	AATGGAGTCTTTATTGTGTATCA
14098-14120	ATGGAGTCTTTATTGTGTATCAT
14099-14121	TGGAGTCTTTATTGTGTATCATA

SIRNA SILENCING OF APOLIPOPROTEIN B**CROSS-REFERENCES TO RELATED APPLICATIONS**

[0001] This application claims the benefit of U.S. Provisional Patent Applications Nos. 60/703,226, filed Jul. 27, 2005 and 60/629,808 filed Nov. 17, 2004, the disclosures of each of which are hereby incorporated by reference in their entirety for all purposes.

BACKGROUND OF THE INVENTION

[0002] Apolipoprotein B (also known as ApoB, apolipoprotein B-100; ApoB-100, apolipoprotein B-48; ApoB-48 and Ag(x) antigen), is a large glycoprotein that serves an indispensable role in the assembly and secretion of lipids and in the transport and receptor-mediated uptake and delivery of distinct classes of lipoproteins. Apolipoprotein B was cloned (Law et al., *PNAS USA* 82:8340-8344 (1985)) and mapped to chromosome 2p23-2p24 in 1986 (Deeb et al., *PNAS USA* 83, 419-422 (1986)). ApoB has a variety of functions, from the absorption and processing of dietary lipids to the regulation of circulating lipoprotein levels (Davidson and Shelness, *Annu. Rev. Nutr.*, 20:169-193 (2000)). Two forms of ApoB have been characterized: ApoB-100 and ApoB-48. ApoB-100 is the major protein component of LDL, contains the domain required for interaction of this lipoprotein species with the LDL receptor, and participates in the transport and delivery of endogenous plasma cholesterol (Davidson and Shelness, 2000, *supra*). ApoB-48 circulates in association with chylomicrons and chylomicron remnants which are cleared the LDL-receptor-related protein (Davidson and Shelness, 2000, *supra*). ApoB-48 plays a role in the delivery of dietary lipid from the small intestine to the liver.

[0003] Susceptibility to atherosclerosis is highly correlated with the ambient concentration of apolipoprotein B-containing lipoproteins (Davidson and Shelness, 2000, *supra*). Elevated plasma levels of the ApoB-100-containing lipoprotein Lp(a) are associated with increased risk for atherosclerosis and its manifestations, which may include hypercholesterolemia (Seed et al., *N. Engl. J. Med.* 322:1494-1499 (1990), myocardial infarction (Sandkamp et al., *Clin. Chem.* 36:20-23 (1990), and thrombosis (Nowak-Gottl et al., *Pediatrics*, 99:E11 (1997)).

[0004] Apolipoprotein B knockout mice (bearing disruptions of both ApoB-100 and ApoB-48) have been generated which are protected from developing hypercholesterolemia when fed a high-fat diet (Farese et al., *PNAS USA*. 92:1774-1778 (1995) and Kim and Young, *J. Lipid Res.*, 39:703-723 (1998)). The incidence of atherosclerosis has been investigated in mice expressing exclusively ApoB-100 or ApoB-48 and susceptibility to atherosclerosis was found to be dependent on total cholesterol levels.

[0005] Methods for modulating serum cholesterol using antibodies that specifically bind to ApoB are set forth in U.S. Pat. Nos. 6,156,315; 6,309,844; and 6,096,516 and WO 99/18986. Small molecules that lower plasma concentrations of apolipoprotein B or apolipoprotein B-containing lipoproteins by stimulating a pathway for apolipoprotein B degradation are set forth in WO 01/30354. However, these compositions must be administered continuously to effectively modulate serum cholesterol (i.e., by modulating

ApoB). None of the compositions or methods described can specifically modulate serum cholesterol on a long term basis.

[0006] Thus, there is a need for compositions and methods for specifically modulating apolipoprotein B expression. The present invention addresses these and other needs.

SUMMARY OF THE INVENTION

[0007] The present invention provides compositions comprising siRNA molecules that target ApoB expression and methods of using such compositions to silence ApoB gene expression. In some embodiments, the compositions can also be used to modulate (i.e., enhance or decrease) an immune response.

[0008] One embodiment of the present invention provides a nucleic acid-lipid particle that targets ApoB expression. The nucleic acid-lipid particle comprises an siRNA molecule that silences Apolipoprotein B (ApoB) expression; a cationic lipid; and a non-cationic lipid. The nucleic acid-lipid particle can further comprise a conjugated lipid that inhibits aggregation of particles. The nucleic acid-lipid particles comprise an siRNA molecule comprising a sequence set forth in Table 1, rows A-F of Table 2, Table 3, and Table 4. In some embodiments, the nucleic acid-lipid particles comprise at least 2, 3, 4, 5, or 6 or more siRNA molecules comprising the sequences set forth in Table 1, rows A-F of Table 2, and Tables 3-7.

[0009] The cationic lipid may be, e.g., N,N-dioleoyl-N,N-dimethylammonium chloride (DODAC), N,N-distearoyl-N,N-dimethylammonium bromide (DDAB), N-(1-(2,3-dioleoyloxy)propyl)-N,N,N-trimethylammonium chloride (DOTAP), N-(1-(2,3-dioleoyloxy)propyl)-N,N,N-trimethylammonium chloride (DOTMA), and N,N-dimethyl-2,3-dioleoyloxypropylamine (DODMA), 1,2-DiLinoleoyloxy-N,N-dimethylaminopropane (DLinDMA), and 1,2-Dilinolenyloxy-N,N-dimethylaminopropane (DLendMA), or mixtures thereof. The cationic lipid may comprise from about 2 mol % to about 60 mol %, about 5 % mol % to about 45 mol %, about 5 mol % to about 15 mol %, about 30 mol % to about 50 mol % or about 40 mol % to about 50 mol % of the total lipid present in the particle.

[0010] The non-cationic lipid may be an anionic lipid or a neutral lipid including, but not limited to, dioleoylphosphatidylethanolamine (DOPE), palmitoyloleoylphosphatidylcholine (POPC), egg phosphatidylcholine (EPC), distearoylphosphatidylcholine (DSPC), palmitoyloleoylphosphatidylglycerol (POPG), dipalmitoyl phosphatidyl ethanolamine (DPPE), dimyristoylphosphoethanolamine (DMPE), distearoyl-phosphatidyl-ethanolamine (DSPE), 16-O-monomethyl PE, 16-O-dimethyl PE, 18-1-trans PE, palmitoyloleoylphosphatidylethanolamine (POPE), 1-stearoyl-2-oleoyl-phosphatidylethanolamine (SOPE), 1,2-dielaidoyl-sn-glycero-3-phosphoethanolamine (transDOPE), cholesterol, or mixtures thereof. The non-cationic lipid comprises from about 5 mol % to about 90 mol % or about 20 mol % to about 85 mol % of the total lipid present in the particle.

[0011] The conjugated lipid that inhibits aggregation of particles may be a polyethyleneglycol (PEG)-lipid conjugate, a polyamide (ATTA)-lipid conjugate, a cationic-polymer-lipid conjugates (CPLs), or mixtures thereof. In one

preferred embodiment, the nucleic acid-lipid particules comprise either a PEG-lipid conjugate or an ATTA-lipid conjugate together with a CPL. The conjugated lipid that inhibits aggregation of particles may comprise a polyethyleneglycol-lipid including, e.g., a PEG-diacylglycerol (DAG), a PEG dialkylxypropyl (DAA), a PEG-phospholipid, a PEG-ceramide (Cer), or mixtures thereof. The PEG-DAA conjugate may be PEG-dilauryloxypropyl (C12), a PEG-dimyristyloxypropyl (C14), a PEG-dipalmitoyloxypropyl (C16), and a PEG-distearoyloxypropyl (C18). In some embodiments, the conjugated lipid that inhibits aggregation of particles has the formula: A-W-Y, wherein: A is a lipid moiety; W is a hydrophilic polymer; and Y is a polycationic moiety. W may be a polymer selected from the group consisting of polyethyleneglycol (PEG), polyamide, polylactic acid, polyglycolic acid, polylactic acid/polyglycolic acid copolymers or combinations thereof, said polymer having a molecular weight of about 250 to about 7000 daltons. In some embodiments, Y has at least 4 positive charges at a selected pH. In some embodiments, Y may be lysine, arginine, asparagine, glutamine, derivatives thereof and combinations thereof. The conjugated lipid that prevents aggregation of particles may comprise from about 0 mol % to about 20 mol %, about 0.5 mol % to about 20 mol %, about 1 mol % to about 15 mol %, about 4 mol % to about 10 mol %, or about about 2 mol % of the total lipid present in said particle.

[0012] In some embodiments, the nucleic acid-lipid particle further comprises cholesterol at, e.g., about 0 mol % to about 10 mol %, about 2 mol % to about 10 mol %, about 10 mol % to about 60 mol % or about 20 mol % to about 45 mol % of the total lipid present in said particle.

[0013] In some embodiments, the siRNA in the nucleic acid-lipid particle is not substantially degraded after exposure of the particle to a nuclease at 37° C. for at least 20, 30, 45, or 60 minutes; or after incubation of the particle in serum at 37° C. for at least 30, 45, or 60 minutes.

[0014] In some embodiments, the siRNA is fully encapsulated in the nucleic acid-lipid particle. In some embodiments, the siRNA is complexed to the lipid portion of the particle.

[0015] The present invention further provides pharmaceutical compositions comprising the nucleic acid-lipid particles described herein and a pharmaceutically acceptable carrier.

[0016] The nucleic acid-lipid particles of the present invention are useful for the therapeutic delivery of nucleic acids comprising an interfering RNA sequence (i.e., an siRNA sequence that targets ApoB expression). In particular, it is an object of this invention to provide in vitro and in vivo methods for treatment of a disease in a mammal by down-regulating or silencing the transcription and translation of a target nucleic acid sequence of interest. In these methods, an interfering RNA is formulated into a nucleic acid-lipid particle, and the particles are administered to patients requiring such treatment. Alternatively, cells are removed from a patient, the interfering RNA delivered in vitro, and re-injected into the patient. In one embodiment, the present invention provides for a method of introducing a nucleic acid into a cell by contacting a cell with a nucleic acid-lipid particle comprised of a cationic lipid, a non-cationic lipid, and an interfering RNA. The nucleic acid-lipid particle may further comprise a conjugated lipid that inhibits aggregation of the particles.

[0017] In one embodiment, at least 1%, 2%, 4%, 6%, 8%, or 10% of the total injected dose of the nucleic acid-lipid particles is present in plasma about 1, 2, 4, 6, 8, 12, 16, 18, or 24 hours after injection. In other embodiments, more than about 20%, 30%, 40% and as much as 60%, 70% or 80% of the total injected dose of the nucleic acid-lipid particles is present in plasma about 1, 4, 6, 8, 10, 12, 20, or 24 hours after injection. In one embodiment, the effect of an interfering RNA (e.g., downregulation of the target sequence) at a site proximal or distal to the site of administration is detectable at about 12, 24, 48, 72, or 96 hours, or about 6, 8, 10, 12, 14, 16, 18, 19, 20, 22, 24, 26, or 28 days after administration of the nucleic acid-lipid particles. In one embodiment, downregulation of expression of the target sequence is detectable at about 12, 24, 48, 72, or 96 hours, or about 6, 8, 10, 12, 14, 16, 18, 19, 20, 22, 24, 26, or 28 days after administration. In some embodiments, downregulation of expression of an ApoB sequence is detected by measuring ApoB mRNA levels in a biological sample from the mammal. In some embodiments, downregulation of expression of an ApoB sequence is detected by measuring ApoB protein levels in a biological sample from the mammal. In some embodiments, downregulation of expression of an ApoB sequence is measured by measuring cholesterol levels in a biological sample from the mammal.

[0018] The particles are suitable for use in intravenous nucleic acid transfer as they are stable in circulation, of a size required for pharmacodynamic behavior resulting in access to extravascular sites and target cell populations. The particles are also suitable for subcutaneous and intraperitoneal administration. The invention also provides for pharmaceutically acceptable compositions comprising a nucleic acid-lipid particle.

[0019] Another embodiment of the present invention provides methods for in vivo delivery of interfering RNA (e.g., an siRNA that silences expression of Apolipoprotein B). A nucleic acid-lipid particle comprising a cationic lipid, a non-cationic lipid, an interfering RNA, and optionally a conjugated lipid that inhibits aggregation of particles, and is administered (e.g., intravenously, intraperitoneally, intramuscularly, or subcutaneously) to a subject (e.g., a mammal such as a human or a rodent).

[0020] A further embodiment of the present invention provides a method of treating a disease or disorder in a mammalian subject. A therapeutically effective amount of a nucleic acid-lipid particle comprising a cationic lipid, a non-cationic lipid, a conjugated lipid that inhibits aggregation of particles, and interfering RNA (e.g., an siRNA that silences expression of Apolipoprotein B) is administered to the mammalian subject (e.g., a rodent such as a mouse, a primate such as a human or a monkey). In some embodiments, the disease or disorder is a in which ApoB is expressed or overexpressed and expression of ApoB is silenced by the siRNA. In some embodiments, the disease or disorder is atherosclerosis, angina pectoris, high blood pressure, diabetes, or hypothyroidism. In some embodiments, the disease or disorder involves hypercholesterolemia (e.g., atherosclerosis, angina pectoris, or high blood pressure) and serum cholesterol levels are lowered when expression of ApoB is silenced by said siRNA.

[0021] One embodiment of the invention provides a modified siRNA that is capable of silencing expression of a target

sequence (i.e., an ApoB sequence), comprising a double-stranded region of about 15 to about 30 nucleotides in length and a non-immunostimulatory mismatch motif consisting of a 5'-XX'-3' dinucleotide corresponding to a 5'-GU-3' dinucleotide in an unmodified siRNA sequence that is capable of silencing expression of the target sequence, wherein X and X' are independently selected from the group consisting of A, U, C, and G, with the proviso that if X is G, X' is not U and if X' is U, X is not G. The modified siRNA is less immunogenic than an siRNA that does not comprise the non-immunostimulatory mismatch motif. In some embodiments, the siRNA comprises one, two, three, or more additional immunostimulatory mismatch motifs relative to the target sequence. The immunostimulatory mismatch motifs may be adjacent to each other or, alternatively, they may be separated by 1, 2, 4, 6, 8, 10, or 12 or more nucleotides.

[0022] Another embodiment of the invention provides a modified siRNA that is capable of silencing expression of a target sequence (i.e., an ApoB sequence) comprising a double stranded sequence of about 15 to about 30 nucleotides in length and an immunostimulatory mismatch motif consisting of a 5'-GU-3' dinucleotide corresponding to a 5'-XX'-3' dinucleotide motif in an unmodified siRNA that is capable of silencing expression of a target sequence, wherein X and X' are independently selected from the group consisting of A, U, C, and G, with the proviso that if X is G, X' is not U and if X' is U, X is not G. The modified siRNA is more immunogenic than an siRNA that does not comprise the immunostimulatory mismatch motif. In some embodiments, the siRNA comprises one, two, three, or more additional immunostimulatory mismatch motifs relative to the target sequence. The immunostimulatory mismatch motifs may be adjacent to each other or, alternatively, they may be separated by 1, 2, 4, 6, 8, 10, or 12 or more nucleotides.

[0023] In some embodiments, the siRNA described herein are used in methods of silencing expression of a target sequence and/or in methods of modulating (i.e., enhancing or reducing) immune responses associated with the siRNA. An effective amount of the siRNA is administered to a mammalian subject, thereby silencing expression of a target sequence (i.e., an ApoB sequence) or modulating an immune response associated with the siRNA.

[0024] The invention also provides pharmaceutical compositions comprising the siRNA molecules (i.e., the siRNA sequences that target ApoB) described herein.

[0025] Yet another embodiment of the invention provides a method of identifying and modifying an siRNA having immunostimulatory properties. The method comprises (a) contacting an unmodified siRNA sequence with a mammalian responder cell under conditions suitable for the responder cell to produce a detectable immune response; (b) identifying the unmodified siRNA sequence as an immunostimulatory siRNA by the presence of a detectable immune response in the responder cell; and (c) modifying the immunostimulatory siRNA by substituting at least one nucleotide with a modified nucleotide, thereby generating a modified siRNA sequence that is less immunostimulatory than the unmodified siRNA sequence.

[0026] In some embodiments, the modified siRNA comprises the modified siRNA contains at least one 2'-O-methyl

(2'OMe) purine or pyrimidine nucleotide such as a 2'OMe-guanosine, 2'OMe-uridine, 2'OMe-adenosine nucleotide, and/or 2'OMe-cytosine nucleotide. In certain instances, the unmodified siRNA sequence comprises a 5'-GU-3' motif and at least one nucleotide in the 5'-GU-3' motif is substituted with a modified nucleotide. In one embodiment, the mammalian responder cell is a peripheral blood mononuclear cell (PBMC). In another embodiment, the detectable immune response comprises production of a cytokine or growth factor such as, for example, TNF- α , TNF- β , IFN- α , IFN- γ , IL-6, IL-12, or a combination thereof.

[0027] In another embodiment, the present invention provides isolated nucleic acid molecules comprising an siRNA sequence set forth in Table 1, rows A-F of Table 2, and Tables 3-7. The siRNA sequence can be modified or unmodified and can further include its complementary strand, thereby generating an siRNA duplex.

[0028] Other features, objects, and advantages of the invention and its preferred embodiments will become apparent from the detailed description, examples, and claims that follow.

BRIEF DESCRIPTION OF THE DRAWINGS

[0029] FIG. 1 illustrates data showing plasma IFN- α levels six hours following administration of SNALP encapsulating siRNA targeting ApoB.

[0030] FIG. 2 illustrates data showing IFN- α levels produced by human PBMC 24 hours following contacting the PBMC with SNALP encapsulating siRNA targeting ApoB.

[0031] FIG. 3 illustrates data showing in vitro silencing of ApoB in AML12 cells 40 hours after transfection with SNALP encapsulating siRNA targeting ApoB.

[0032] FIG. 4 illustrates data showing in vivo silencing of ApoB in mice 48 hours following three once daily treatments of siRNA targeting ApoB (2.5 mg/kg).

[0033] FIG. 5 illustrates data showing ApoB silencing from multiple-dose IV administration of SNALP. Values describe measured ApoB:GAPDH mRNA ratios as a percentage of the ratio found in control PBS-treated liver. "Mismatch" is a shortform name of the siRNA apob-1-mismatch. Indicated dosages refer to siRNA amount per body weight. Indicated time points refer to time after the third and last daily SNALP injection. Each column represents the mean of 5 animals and error bars denote the standard error of the mean (SEM).

[0034] FIG. 6 illustrates data showing an extended time course of ApoB silencing from multiple-dose IV administration of SNALP. Values describe measured plasma ApoB protein as a percentage of the concentration found in control PBS-treated blood. "Mismatch" is a shortform name of the siRNA apob-1-mismatch. Arrows indicate the three consecutive days of SNALP injection at a dosage of 5 mg siRNA per kg body weight. Each data point represents the mean of 5 animals and error bars denote SEM.

[0035] FIG. 7 illustrates data showing ApoB silencing from multiple-dose IV administration of SNALP prepared via a Stepwise Dilution process. Values describe measured ApoB:GAPDH mRNA ratios as a percentage of the ratio found in control PBS-treated liver. Samples were collected 2 days after administration the third and last daily admin-

istration of SNALP at 5 mg siRNA per kg body weight. Each column represents the mean of 5 animals and error bars denote the standard error of the mean (SEM).

[0036] **FIG. 8** illustrates data showing ApoB silencing from multiple-dose IV administration of SNALP containing different cationic lipids. Values describe measured ApoB:GAPDH mRNA ratios as a percentage of the ratio found in control PBS-treated liver. "Mismatch" is a shortform name of the siRNA apob-1-mismatch. Samples were collected 2 days after administration the third and last daily administration of SNALP at 5 mg siRNA per kg body weight. Each column represents the mean of 5 animals and error bars denote the standard error of the mean (SEM).

[0037] **FIG. 9** illustrates data showing ApoB silencing from multiple-dose IV administration of SNALP containing different phospholipids. Values describe measured ApoB:GAPDH mRNA ratios as a percentage of the ratio found in control PBS-treated liver. "Mismatch" is a shortform name of the siRNA apob-1-mismatch. Samples were collected 1 day after administration the third and last daily administration of SNALP at 3.5 mg siRNA per kg body weight. Each column represents the mean of 4 (for apob-1 SNALP, PBS) or 3 (for mismatch SNALP) animals and error bars denote the standard error of the mean (SEM).

[0038] **FIG. 10** illustrates data showing a time course of ApoB silencing from single-dose IV administration of SNALP. Values describe measured plasma ApoB protein as a percentage of the concentration found in control PBS-treated blood. "Mismatch" is a shortform name of the siRNA apob-1-mismatch. On Study Day 0, animals were administered one SNALP injection at a dosage of 5 mg siRNA per kg body weight. Each data point represents the mean of 4 animals and error bars denote SEM.

[0039] **FIG. 11** illustrates data showing a time course of ApoB silencing from single-dose IV administration of SNALP. Values describe measured plasma ApoB protein as a percentage of the concentration found in control PBS-treated blood. "Mismatch" is a shortform name of the siRNA apob-1-mismatch. On Study Day 0, animals were administered one SNALP injection at a dosage of 5 mg siRNA per kg body weight. Each data point represents the mean of 4 animals and error bars denote SEM.

[0040] **FIG. 12** illustrates data showing the efficacy of anti-ApoB SNALP treatment in a hypercholesterolemia model. Total cholesterol concentration in female C57BL/6 mice was monitored in blood collected via tail nick. The red arrow indicates the day of IV SNALP administration at a dosage of 5 mg siRNA per kg body weight. Each data point between Day 0 and 32 (inclusive) represents the mean of 4 animals. Each data point from Day 35 onwards represents the mean of 2 animals. Error bars denote the standard error of the mean (SEM).

[0041] **FIG. 13** illustrates data showing ApoB silencing from single-dose IV administration of SNALP. Values describe measured ApoB:GAPDH mRNA ratios as a percentage of the ratio found in control PBS-treated liver. "Mismatch" is a shortform name of the siRNA apob-1-mismatch. Samples were collected four days after administration of SNALP at 2 mg siRNA per kg body weight. Each column represents the mean of 4 animals (except n=3 for mismatch) and error bars denote the standard error of the mean (SEM).

[0042] **FIG. 14** depicts data demonstrating in vivo silencing of ApoB expression following multi-dose intraperitoneal administration of SNALP encapsulating ApoB siRNA. 'Liver mRNA' values describe measured ApoB:GAPDH mRNA ratios as a percentage of the ratio found in control PBS-treated liver. 'Plasma protein' values describe ApoB protein as a percentage of the concentration found in control PBS-treated plasma. SNALP were administered to animals at 2 mg siRNA per kg body weight per injection, with injections on three consecutive days. Samples were collected 48 hours after the last administration of SNALP. Each column represents the mean of 4 animals (except 3 animals for mismatch SNALP) and error bars denote the standard error of the mean (SEM).

[0043] **FIG. 15** depicts data demonstrating in vivo silencing of ApoB gene expression following single-dose subcutaneous administration of SNALP encapsulating ApoB siRNA. Values describe measured ApoB:GAPDH mRNA ratios as a percentage of the ratio found in control PBS-treated liver. "mismatch" is a shortform name of the siRNA apob-1-mismatch. Samples were collected 48 hours after administration of SNALP at 1, 3 or 10 mg siRNA per kg body weight. Each column represents the mean of 4 animals and error bars denote the standard deviation (SD) of the mean.

[0044] **FIG. 16** depicts data demonstrating in vivo silencing of ApoB gene expression following single-dose IV administration of a panel of SNALP encapsulating ApoB siRNA. Values describe measured ApoB:GAPDH mRNA ratios as a percentage of the ratio found in control PBS-treated liver. Each column represents the mean of 4 animals and error bars denote the standard deviation.

[0045] **FIG. 17** depicts data demonstrating in vivo silencing of ApoB gene expression following single-dose IV administration of a panel of SNALP encapsulating ApoB siRNA. Values describe measured apolipoprotein B protein levels in plasma a percentage of the apoB levels found in control PBS-treated plasma. Each column represents the mean of 4 animals and error bars denote the propagated standard deviation.

[0046] **FIG. 18** depicts data reflecting plasma interferon- α levels following single-dose IV administration of a panel of SNALP encapsulating ApoB siRNA. Values describe measured interferon-alpha levels in plasma at 6 h after dosing. Each column represents the mean of 4 animals and error bars denote the standard deviation.

[0047] **FIG. 19** depicts data demonstrating in vivo silencing of ApoB gene expression following single-dose IV administration of a panel of SNALP encapsulating ApoB siRNA. Relative ApoB silencing from 100 nM dosage of apoB siRNA. Values describe measured apolipoprotein B protein levels in HepG2 cell supernatants as a percentage of the apoB levels found in untreated cell supernatants. Each column represents the mean of 3 replicates normalized to total protein levels in cell lysates, and error bars denote the propagated standard deviation.

[0048] **FIG. 20** is Table 5 which sets forth siRNA sequences that target human ApoB and are derived from GenBank Accession No. NM_000384. The potential immunostimulatory activity of each siRNA is indicated.

[0049] **FIG. 21** is Table 6 which sets forth siRNA sequences that target murine ApoB and are derived from

GenBank Accession No. XM_137955. The potential immunostimulatory activity of each siRNA is indicated.

[0050] FIG. 22 is Table 7 which sets forth additional siRNA sequences that target human ApoB and are derived from GenBank Accession No. NM_000384.

DETAILED DESCRIPTION OF THE INVENTION

I. Introduction

[0051] The present invention provides nucleic acid-lipid particles that target ApoB expression comprising an siRNA that silences ApoB expression; a cationic lipid and a non-cationic lipid. In certain instances, the nucleic acid-lipid particle can further comprise a conjugated lipid that inhibits aggregation of particles. The siRNA sequence can be modified or unmodified.

[0052] In certain embodiments, the nucleic acid-lipid particles described herein are particularly useful for silencing ApoB expression to treat diseases or disorders associated with expression or overexpression of ApoB. Such diseases include, e.g., atherosclerosis, angina pectoris, high blood pressure, diabetes, hypothyroidism, and hypercholesterolemia. For example, administration of nucleic acid-lipid particles comprising the siRNA sequences described herein can be used to lower serum cholesterol levels.

[0053] One embodiment of the present invention is based on the surprising discovery that siRNA molecules have immunostimulatory effects that can be modulated.

[0054] Without being bound to any particular theory, it is postulated that the siRNA molecules' immunostimulatory activity is mediated by Toll-Like Receptor mediated signaling. These findings have significant implications for the clinical development of RNAi as a novel therapeutic approach and in the interpretation of specific gene silencing effects using siRNA. For example, immunostimulatory siRNA can be modified to disrupt a GU-rich (e.g., a 5'-GU-3', 5'-UGU-3', 5'-GUGU-3', or a 5'-UGUGU-3' motif), thus reducing their immunostimulatory properties while retaining their ability to silence a target gene (i.e., ApoB). The GU-rich motif may be disrupted by substitution of a nucleotide in the motif or by chemically modifying a nucleotide in the motif. Alternatively, the immunostimulatory siRNA can be used to generate controlled, transient cytokine production; activated T cell and NK cell proliferation, tumor-specific CTL responses, non-gene specific tumor regression, and B cell activation (i.e., antibody production). In addition, non-immunostimulatory siRNA can be modified to comprise a GU-rich motif, thus enhancing their immunostimulatory properties while retaining their ability to silence a target gene (i.e., ApoB).

II. Definitions

[0055] The term "Apolipoprotein B" or "ApoB" refers to the main apolipoprotein of chylomicrons and low density lipoproteins (LDL). Mutations in ApoB are associated with hypercholesterolemia. ApoB occurs in the plasma in 2 main forms: apoB48 and apoB100 which are synthesized in the intestine and liver, respectively, due to an organ-specific stop codon. ApoB48 contains 2,152 residues compared to 4,535 residues in apoB100. Cloning and characterization of ApoB is described by e.g., Glickman et al., *PNAS USA* 83:5296-

5300 (1986); Chen et al., *J. Biol. Chem.* 261: 2918-12921 (1986); and Hospattankar et al., *J. Biol. Chem.* 261:9102-9104 (1986). ApoB sequences are set forth in, e.g., Genbank Accession Nos. NM_000384 and BC051278. siRNA sequences that target ApoB are set forth in Tables 1-7 and in Soutschek et al., *Nature* 432:173-178 (2004).

[0056] The term "interfering RNA" or "RNAi" or "interfering RNA sequence" refers to double-stranded RNA (i.e., duplex RNA) that targets (i.e., silences, reduces, or inhibits) expression of a target gene (i.e., by mediating the degradation of mRNAs which are complementary to the sequence of the interfering RNA) when the interfering RNA is in the same cell as the target gene. Interfering RNA thus refers to the double stranded RNA formed by two complementary strands or by a single, self-complementary strand. Interfering RNA typically has substantial or complete identity to the target gene. The sequence of the interfering RNA can correspond to the full length target gene, or a subsequence thereof.

[0057] Interfering RNA includes small-interfering RNA" or "siRNA," i.e., interfering RNA of about 15-60, 15-50, 15-50, or 15-40 (duplex) nucleotides in length, more typically about, 15-30, 15-25 or 19-25 (duplex) nucleotides in length, and is preferably about 20-24 or about 21-22 or 21-23 (duplex) nucleotides in length (e.g., each complementary sequence of the double stranded siRNA is 15-60, 15-50, 15-50, 15-40, 15-30, 15-25 or 19-25 nucleotides in length, preferably about 20-24 or about 21-22 or 21-23 nucleotides in length, and the double stranded siRNA is about 15-60, 15-50, 15-50, 15-40, 15-30, 15-25 or 19-25 preferably about 20-24 or about 21-22 or 21-23 base pairs in length). siRNA duplexes may comprise 3' overhangs of about 1 to about 4 nucleotides, preferably of about 2 to about 3 nucleotides and 5' phosphate termini. In some embodiments, the siRNA lacks a terminal phosphate. Examples of siRNA include, without limitation, a double-stranded polynucleotide molecule assembled from two separate oligonucleotides, wherein one strand is the sense strand and the other is the complementary antisense strand; a double-stranded polynucleotide molecule assembled from a single oligonucleotide, where the sense and antisense regions are linked by a nucleic acid-based or non-nucleic acid-based linker; a double-stranded polynucleotide molecule with a hairpin secondary structure having self-complementary sense and antisense regions; and a circular single-stranded polynucleotide molecule with two or more loop structures and a stem having self-complementary sense and antisense regions, where the circular polynucleotide can be processed in vivo or in vitro to generate an active double-stranded siRNA molecule.

[0058] The siRNA can be chemically synthesized or may be encoded by a plasmid (e.g., transcribed as sequences that automatically fold into duplexes with hairpin loops). siRNA can also be generated by cleavage of longer dsRNA (e.g., dsRNA greater than about 25 nucleotides in length) with the *E. coli* RNase III or Dicer. These enzymes process the dsRNA into biologically active siRNA (see, e.g., Yang et al., *PNAS USA* 99: 9942-7 (2002); Calegari et al., *PNAS USA* 99: 14236 (2002); Byrom et al., *Ambion TechNotes* 10(1): 4-6 (2003); Kawasaki et al., *Nucleic Acids Res.* 31: 981-7 (2003); Knight and Bass, *Science* 293: 2269-71 (2001); and Robertson et al., *J. Biol. Chem.* 243: 82 (1968)). Preferably, dsRNA are at least 50 nucleotides to about 100, 200, 300,

400 or 500 nucleotides in length. A dsRNA may be as long as 1000, 1500, 2000, 5000 nucleotides in length, or longer. The dsRNA can encode for an entire gene transcript or a partial gene transcript.

[0059] "Substantial identity" refers to a sequence that hybridizes to a reference sequence under stringent conditions, or to a sequence that has a specified percent identity over a specified region of a reference sequence.

[0060] The phrase "stringent hybridization conditions" refers to conditions under which a probe will hybridize to its target subsequence, typically in a complex mixture of nucleic acids, but to no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in Tijssen, *Techniques in Biochemistry and Molecular Biology—Hybridization with Nucleic Probes*, "Overview of principles of hybridization and the strategy of nucleic acid assays" (1993). Generally, stringent conditions are selected to be about 5-10° C. lower than the the melting point (T_m) for the specific sequence at a defined ionic strength pH. The T_m is the temperature (under defined ionic strength, pH, and nucleic concentration) at which 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at T_m , 50% of the probes are occupied at equilibrium). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. For selective or specific hybridization, a positive signal is at least two times background, preferably 10 times background hybridization.

[0061] Exemplary stringent hybridization conditions can be as following: 50% formamide, 5×SSC, and 1% SDS, incubating at 42° C., or, 5×SSC, 1% SDS, incubating at 65° C., with wash in 0.2×SSC, and 0.1% SDS at 65° C. For PCR, a temperature of about 36° C. is typical for low stringency amplification, although annealing temperatures may vary between about 32° C. and 48° C. depending on primer length. For high stringency PCR amplification, a temperature of about 62° C. is typical, although high stringency annealing temperatures can range from about 50° C. to about 65° C., depending on the primer length and specificity. Typical cycle conditions for both high and low stringency amplifications include a denaturation phase of 90° C.-95° C. for 30 sec.-2 min., an annealing phase lasting 30 sec.-2 min., and an extension phase of about 72° C. for 1-2 min. Protocols and guidelines for low and high stringency amplification reactions are provided, e.g., in Innis et al. (1990) *PCR Protocols, A Guide to Methods and Applications*, Academic Press, Inc. N.Y.).

[0062] Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides which they encode are substantially identical. This occurs, for example, when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. In such cases, the nucleic acids typically hybridize under moderately stringent hybridization conditions. Exemplary "moderately stringent hybridization conditions" include a hybridization in a buffer of 40% formamide, 1 M NaCl, 1% SDS at 37° C., and a wash in 1×SSC at 45° C. A positive hybridization is at least twice background. Those of ordinary skill will readily recognize that

alternative hybridization and wash conditions can be utilized to provide conditions of similar stringency. Additional guidelines for determining hybridization parameters are provided in numerous reference, e.g., and Current Protocols in Molecular Biology, ed. Ausubel, et al.

[0063] The terms "substantially identical" or "substantial identity," in the context of two or more nucleic acids, refer to two or more sequences or subsequences that are the same or have a specified percentage of nucleotides that are the same (i.e., at least about 60%, preferably 65%, 70%, 75%, preferably 80%, 85%, 90%, or 95% identity over a specified region), when compared and aligned for maximum correspondence over a comparison window, or designated region as measured using one of the following sequence comparison algorithms or by manual alignment and visual inspection. This definition, when the context indicates, also refers analogously to the complement of a sequence. Preferably, the substantial identity exists over a region that is at least about 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 75, or 100 nucleotides in length.

[0064] For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Default program parameters can be used, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

[0065] A "comparison window", as used herein, includes reference to a segment of any one of the number of contiguous positions selected from the group consisting of from 20 to 600, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well-known in the art. Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith & Waterman, *Adv. Appl. Math.* 2:482 (1981), by the homology alignment algorithm of Needleman & Wunsch, *J. Mol. Biol.* 48:443 (1970), by the search for similarity method of Pearson & Lipman, *PNAS USA* 85:2444 (1988), by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, Wis.), or by manual alignment and visual inspection (see, e.g., *Current Protocols in Molecular Biology* (Ausubel et al., eds. 1995 supplement)).

[0066] A preferred example of algorithm that is suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul et al., *Nuc. Acids Res.* 25:3389-3402 (1997) and Altschul et al., *J. Mol. Biol.* 215:403-410 (1990), respectively. BLAST and BLAST 2.0 are used, with the parameters described herein, to determine percent sequence identity for the nucleic acids and proteins of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotech-

nology Information (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul et al., supra). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always >0) and N (penalty score for mismatching residues; always <0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W , T , and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) or 10, $M=5$, $N=-4$ and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff & Henikoff, *PNAS USA* 89:10915 (1989)) alignments (B) of 50, expectation (E) of 10, $M=5$, $N=-4$, and a comparison of both strands.

[0067] The BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, e.g., Karlin & Altschul, *PNAS USA* 90:5873-5787 (1993)). One measure of similarity provided by the BLAST algorithm is the smallest sum probability ($P(N)$), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.2, more preferably less than about 0.01, and most preferably less than about 0.001.

[0068] The phrase "inhibiting expression of a target gene" refers to the ability of a siRNA of the invention to silence, reduce, or inhibit expression of a target gene (e.g., ApoB). To examine the extent of gene silencing, a test sample (e.g., a biological sample from organism of interest expressing the target gene or a sample of cells in culture expressing the target gene) is contacted with an siRNA that silences, reduces, or inhibits expression of the target gene. Expression of the target gene in the test sample is compared to expression of the target gene in a control sample (e.g., a biological sample from organism of interest expressing the target gene or a sample of cells in culture expressing the target gene) that is not contacted with the siRNA. Control samples (i.e., samples expressing the target gene) are assigned a value of 100%. Silencing, inhibition, or reduction of expression of a target gene is achieved when the value of test the test sample relative to the control sample is about 95%, 90%, 85%, 80%, 75%, 70%, 65%, 60%, 55%, 50%, 45%, 40%, 35%, 30%, 25%, 20%, or 10%. Suitable assays include, e.g., examination of protein or mRNA levels using techniques known to

those of skill in the art such as dot blots, northern blots, in situ hybridization, ELISA, immunoprecipitation, enzyme function, as well as phenotypic assays known to those of skill in the art.

[0069] An "effective amount" or "therapeutically effective amount" of an siRNA is an amount sufficient to produce the desired effect, e.g., inhibition of expression of a target sequence in comparison to the normal expression level detected in the absence of the siRNA. Inhibition of expression of a target gene or target sequence is achieved when the value obtained with the siRNA relative to the control is about 90%, 80%, 70%, 60%, 50%, 40%, 30%, 25%, 20%, 15%, 10%, 5%, or 0%.

[0070] By "enhance," "enhancement," or "enhancing" of an immune response by a siRNA is intended to mean a detectable enhancement of an immune response, typically measured by an increase in cytokine production (e.g., IFN γ , IFN α , TNF α , IL-6, or IL-12) by a responder cell in vitro or an increase in cytokine production in the sera of a mammalian subject after administration of the siRNA. The amount of increase is determined relative to the normal level that is detected in the absence of the siRNA or other nucleic acid sequence. A detectable increase can be as small as about 5% or 10%, or as great as about 80%, 90% or 100%. More typically, a detectable increase is about 20%, 30%, 40%, 50%, 60%, or 70%.

[0071] By "decrease" or "decreasing" of an immune response by a siRNA is intended to mean a detectable decrease of an immune response, typically measured by a decrease in cytokine production (e.g., IFN γ , IFN α , TNF α , IL-6, or IL-12) by a responder cell in vitro or a decrease in cytokine production in the sera of a mammalian subject after administration of the siRNA. The amount of decrease is determined relative to the normal level that is detected in the absence of the siRNA or other nucleic acid sequence. A detectable decrease can be as small as about 5% or 10%, or as great as about 80%, 90% or 100%. More typically, a detectable decrease is about 20%, 30%, 40%, 50%, 60%, or 70%.

[0072] As used herein, the term "responder cell" refers to a cell, preferably a mammalian cell that produces a detectable immune response when contacted with an immunostimulatory double stranded RNA. Exemplary responder cells include, e.g., dendritic cells, macrophages, peripheral blood mononuclear cells ("PBMC"), splenocytes, and the like. Detectable immune responses include, e.g., production of cytokines such as IFN- α , IFN- γ , TNF- α , IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-10, IL-12, IL-13, and TGF.

[0073] The term "lipid" refers to a group of organic compounds that include, but are not limited to, esters of fatty acids and are characterized by being insoluble in water, but soluble in many organic solvents. They are usually divided into at least three classes: (1) "simple lipids" which include fats and oils as well as waxes; (2) "compound lipids" which include phospholipids and glycolipids; and (3) "derived lipids" such as steroids.

[0074] "Lipid vesicle" refers to any lipid composition that can be used to deliver a compound including, but not limited to, liposomes, wherein an aqueous volume is encapsulated by an amphipathic lipid bilayer; or wherein the lipids coat an interior comprising a large molecular component, such as a

plasmid comprising an interfering RNA sequence, with a reduced aqueous interior; or lipid aggregates or micelles, wherein the encapsulated component is contained within a relatively disordered lipid mixture.

[0075] As used herein, "lipid encapsulated" can refer to a lipid formulation that provides a compound with full encapsulation, partial encapsulation, or both. In some embodiments, the nucleic acid is fully encapsulated in the lipid formulation (e.g., to form an SPLP, pSPLP, SNALP, or other nucleic acid-lipid particle).

[0076] The nucleic acid-lipid particles of the present invention typically have a mean diameter of less than about 150 nm and are substantially nontoxic. In addition, the nucleic acids when present in the nucleic acid-lipid particles of the present invention are resistant in aqueous solution to degradation with a nuclease. Nucleic acid-lipid particles and their method of preparation are disclosed in U.S. Pat. Nos. 5,976,567 and 5,981,501 and PCT Patent Publication No. WO 96/40964.

[0077] Various suitable cationic lipids may be used in the present invention, either alone or in combination with one or more other cationic lipid species or non-cationic lipid species.

[0078] The cationic lipids of Formula I and Formula II described herein typically carry a net positive charge at a selected pH, such as physiological pH. It has been surprisingly found that cationic lipids comprising alkyl chains with multiple sites of unsaturation, e.g., at least two or three sites of unsaturation, are particularly useful for forming lipid-nucleic acid particles with increased membrane fluidity. A number of cationic lipids and related analogs, which are also useful in the present invention, have been described in co-pending U.S. Ser. No. 08/316,399; U.S. Pat. Nos. 5,208,036, 5,264,618, 5,279,833 and 5,283,185, and WO 96/10390.

[0079] The non-cationic lipids used in the present invention can be any of a variety of neutral uncharged, zwitterionic or anionic lipids capable of producing a stable complex. They are preferably neutral, although they can alternatively be positively or negatively charged. Examples of non-cationic lipids useful in the present invention include: phospholipid-related materials, such as lecithin, phosphatidylethanolamine, lysolecithin, lysophosphatidylethanolamine, phosphatidylserine, phosphatidylinositol, sphingomyelin, cephalin, cardiolipin, phosphatidic acid, cerebrosides, dicytlylphosphate, distearoylphosphatidylcholine (DSPC), dioleoylphosphatidylcholine (DOPC), dipalmitoylphosphatidylcholine (DPPC), dioleoylphosphatidylglycerol (DOPG), dipalmitoylphosphatidylglycerol (DPPG), dioleoyl-phosphatidylethanolamine (DOPE), palmitoyloleoylphosphatidylcholine (POPC), palmitoyloleoyl-phosphatidylethanolamine (POPE) and dioleoyl-phosphatidylethanolamine 4-(N-maleimidomethyl)-cyclohexane-1-carboxylate (DOPE-mal). Non-cationic lipids or sterols such as cholesterol may be present. Additional nonphosphorous containing lipids are, e.g., stearylamine, dodecylamine, hexadecylamine, acetyl palmitate, glycerolricinoleate, hexadecyl stearate, isopropyl myristate, amphoteric acrylic polymers, triethanolamine-lauryl sulfate, alkyl-aryl sulfate polyethyloxylated fatty acid amides, dioctadecyldimethyl ammonium bromide and the like, diacylphosphatidylcholine, diacylphosphatidylethanolamine, ceramide, sphingomyelin, cephalin, and

cerebrosides. Other lipids such as lysophosphatidylcholine and lysophosphatidylethanolamine may be present. Non-cationic lipids also include polyethylene glycol-based polymers such as PEG 2000, PEG 5000 and polyethylene glycol conjugated to phospholipids or to ceramides (referred to as PEG-Cer), as described in co-pending U.S. Ser. No. 08/316,429, incorporated herein by reference.

[0080] In preferred embodiments, the non-cationic lipids are diacylphosphatidylcholine (e.g., distearoylphosphatidylcholine, dioleoylphosphatidylcholine, dipalmitoylphosphatidylcholine and dilinoleoylphosphatidylcholine), diacylphosphatidylethanolamine (e.g., dioleoylphosphatidylethanolamine and palmitoyloleoylphosphatidylethanolamine), ceramide or sphingomyelin. The acyl groups in these lipids are preferably acyl groups derived from fatty acids having C₁₀-C₂₄ carbon chains. More preferably the acyl groups are lauroyl, myristoyl, palmitoyl, stearoyl or oleoyl. In particularly preferred embodiments, the non-cationic lipid can be cholesterol, 1,2-sn-dioleoylphosphatidylethanolamine, or egg sphingomyelin (ESM).

[0081] In addition to cationic and non-cationic lipids, the nucleic acid-lipid particles (e.g., SPLPs and SNALPs of the present invention can further comprise a bilayer stabilizing component (BSC) such as an ATTA-lipid or a PEG-lipid, such as PEG coupled to dialkylxypropyls (PEG-DAA) (see, U.S. Patent Publication No. 2005017682), PEG coupled to diacylglycerol (PEG-DAG) (see, U.S. Patent Publication No. 2003077829), PEG coupled to phosphatidylethanolamine (PE) (PEG-PE), or PEG conjugated to ceramides, or a mixture thereof (see, U.S. Pat. No. 5,885,613). In one preferred embodiment, the BSC is a conjugated lipid that inhibits aggregation of the nucleic acid-lipid particles. Suitable conjugated lipids include, but are not limited to PEG-lipid conjugates, ATTA-lipid conjugates, cationic-polymer-lipid conjugates (CPLs) or mixtures thereof. In one preferred embodiment, the nucleic acid-lipid particles comprise either a PEG-lipid conjugate or an ATTA-lipid conjugate together with a CPL.

[0082] PEG is a polyethylene glycol, a linear, water-soluble polymer of ethylene PEG repeating units with two terminal hydroxyl groups. PEGs are classified by their molecular weights; for example, PEG 2000 has an average molecular weight of about 2,000 daltons, and PEG 5000 has an average molecular weight of about 5,000 daltons. PEGs are commercially available from Sigma Chemical Co. and other companies and include, for example, the following: monomethoxypolyethylene glycol (MePEG-OH), monomethoxypolyethylene glycol-succinate (MePEG-S), monomethoxypolyethylene glycol-succinimidyl succinate (MePEG-S-NHS), monomethoxypolyethylene glycol-amine (MePEG-NH₂), monomethoxypolyethylene glycol-tresylate (MePEG-TRES), and monomethoxypolyethylene glycol-imidazolyl-carbonyl (MePEG-IM). In addition, monomethoxypolyethyleneglycol-acetic acid (MePEG-CH₂COOH), is particularly useful for preparing the PEG-lipid conjugates including, e.g., PEG-DAA conjugates.

[0083] In some embodiments, the PEG has an average molecular weight of from about 1000 to about 5000 daltons, more preferably, from about 1,000 to about 3,000 daltons and, even more preferably, of about 2,000 daltons. The PEG can be optionally substituted by an alkyl, alkoxy, acyl or aryl

group. PEG can be conjugated directly to the lipid or may be linked to the lipid via a linker moiety. Any linker moiety suitable for coupling the PEG to a lipid can be used including, e.g., non-ester containing linker moieties and ester-containing linker moieties.

[0084] As used herein, the term “non-ester containing linker moiety” refers to a linker moiety that does not contain a carboxylic ester bond ($-\text{OC}(\text{O})-$). Suitable non-ester containing linker moieties include, but are not limited to, amido ($-\text{C}(\text{O})\text{NH}-$), amino ($-\text{NR}-$), carbonyl ($-\text{C}(\text{O})-$), carbamate ($-\text{NHC}(\text{O})\text{O}-$), urea ($-\text{NH}-\text{C}(\text{O})\text{NH}-$), disulphide ($-\text{S}-\text{S}-$), ether ($-\text{O}-$), succinyl ($-(\text{O})\text{CCH}_2\text{CH}_2\text{C}(\text{O})-$), succinamidyl ($-\text{NHC}(\text{O})\text{CH}_2\text{CH}_2\text{C}(\text{O})\text{NH}-$), ether, disulphide, etc. as well as combinations thereof (such as a linker containing both a carbamate linker moiety and an amido linker moiety). In some embodiments, a carbamate linker is used to couple the PEG to the lipid.

[0085] In other embodiments, an ester containing linker moiety is used to couple the PEG to the lipid. Suitable ester containing linker moieties include, e.g., carbonate ($-\text{OC}(\text{O})\text{O}-$), succinoyl, phosphate esters ($-\text{O}-\text{O}-\text{POH}-\text{O}-$), sulfonate esters, and combinations thereof.

[0086] As used herein, the term “SNALP” refers to a stable nucleic acid lipid particle, including SPLP. A SNALP represents a vesicle of lipids coating a reduced aqueous interior comprising a nucleic acid (e.g., ssDNA, dsDNA, ssRNA, dsRNA, siRNA, or a plasmid, including plasmids from which an interfering RNA is transcribed). As used herein, the term “SPLP” refers to a nucleic acid lipid particle comprising a nucleic acid (e.g., a plasmid) encapsulated within a lipid vesicle. SNALPs and SPLPs typically contain a cationic lipid, a non-cationic lipid, and a lipid that prevents aggregation of the particle (e.g., a PEG-lipid conjugate). SNALPs and SPLPs have systemic application as they exhibit extended circulation lifetimes following intravenous (i.v.) injection, accumulate at distal sites (e.g., sites physically separated from the administration site and can mediate expression of the transfected gene at these distal sites. SPLPs include “pSPLP” which comprise an encapsulated condensing agent-nucleic acid complex as set forth in WO 00/03683.

[0087] The term “vesicle-forming lipid” is intended to include any amphipathic lipid having a hydrophobic moiety and a polar head group, and which by itself can form spontaneously into bilayer vesicles in water, as exemplified by most phospholipids.

[0088] The term “vesicle-adopting lipid” is intended to include any amphipathic lipid that is stably incorporated into lipid bilayers in combination with other amphipathic lipids, with its hydrophobic moiety in contact with the interior, hydrophobic region of the bilayer membrane, and its polar head group moiety oriented toward the exterior, polar surface of the membrane. Vesicle-adopting lipids include lipids that on their own tend to adopt a nonlamellar phase, yet which are capable of assuming a bilayer structure in the presence of a bilayer-stabilizing component. A typical example is DOPE (dioleoylphosphatidylethanolamine). Bilayer stabilizing components include, but are not limited to, conjugated lipids that inhibit aggregation of the SNALPs, polyamide oligomers (e.g., ATTA-lipid derivatives), peptides, proteins, detergents, lipid-derivatives, PEG-lipid

derivatives such as PEG coupled to dialkyloxypropyls, PEG coupled to diacylglycerols, PEG coupled to phosphatidylethanolamines, and PEG conjugated to ceramides (see, U.S. Pat. No. 5,885,613).

[0089] The term “amphipathic lipid” refers, in part, to any suitable material wherein the hydrophobic portion of the lipid material orients into a hydrophobic phase, while the hydrophilic portion orients toward the aqueous phase. Amphipathic lipids are usually the major component of a lipid vesicle. Hydrophilic characteristics derive from the presence of polar or charged groups such as carbohydrates, phosphate, carboxylic, sulfato, amino, sulfhydryl, nitro, hydroxyl and other like groups. Hydrophobicity can be conferred by the inclusion of apolar groups that include, but are not limited to, long chain saturated and unsaturated aliphatic hydrocarbon groups and such groups substituted by one or more aromatic, cycloaliphatic or heterocyclic group(s). Examples of amphipathic compounds include, but are not limited to, phospholipids, aminolipids and sphingolipids. Representative examples of phospholipids include, but are not limited to, phosphatidylcholine, phosphatidylethanolamine, phosphatidylserine, phosphatidylinositol, phosphatidic acid, palmitoyloleoyl phosphatidylcholine, lysophosphatidylcholine, lysophosphatidylethanolamine, dipalmitoylphosphatidylcholine, dioleoylphosphatidylcholine, distearoylphosphatidylcholine and dinoleoylphosphatidylcholine. Other compounds lacking in phosphorus, such as sphingolipid, glycosphingolipid families, diacylglycerols and β -acyloxyacids, are also within the group designated as amphipathic lipids. Additionally, the amphipathic lipid described above can be mixed with other lipids including triglycerides and sterols.

[0090] The term “neutral lipid” refers to any of a number of lipid species that exist either in an uncharged or neutral zwitterionic form at a selected pH. At physiological pH, such lipids include, for example, diacylphosphatidylcholine, diacylphosphatidylethanolamine, ceramide, sphingomyelin, cephalin, cholesterol, cerebroside and diacylglycerols.

[0091] The term “non-cationic lipid” refers to any neutral lipid as described above as well as anionic lipids.

[0092] The term “anionic lipid” refers to any lipid that is negatively charged at physiological pH. These lipids include, but are not limited to, phosphatidylglycerol, cardiolipin, diacylphosphatidylserine, diacylphosphatidic acid, N-dodecanoyl phosphatidylethanolamines, N-succinyl phosphatidylethanolamines, N-glutarylphosphatidylethanolamines, lysylphosphatidylglycerols, palmitoyloleoylphosphatidylglycerol (POPG), and other anionic modifying groups joined to neutral lipids.

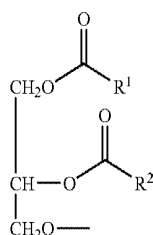
[0093] The term “cationic lipid” refers to any of a number of lipid species that carry a net positive charge at a selected pH, such as physiological pH (e.g., pH of about 7.0). As used herein, physiological pH refers to the pH of a biological fluid such as blood or lymph as well as the pH of a cellular compartment such as an endosome, an acidic endosome, or a lysosome). Such lipids include, but are not limited to, N,N-dioleoyl-N,N-dimethylammonium chloride (“DODAC”); N-(1-(2,3-dioleoyloxy)propyl)-N,N,N-trimethylammonium chloride (“DOTMA”); N,N-dimethyl-(2,3-dioleoyloxy)propylamine (“DODMA”); N,N-distearyl-N,N-dimethylammonium bromide (“DDAB”); N-(2,3-dioleoyloxy)propyl)-N,N,N-trimethylammonium chloride

("DOTAP"); 3-(N-(N',N'-dimethylaminoethane)-carbamoyl)cholesterol ("DC-Chol"); N-(1,2-dimyristyloxyprop-3-yl)-N,N-dimethyl-N-hydroxyethyl ammonium bromide ("DMRIE"); 1,2-Dilinoleyloxy-N,N-dimethylaminopropane (DLinDMA); and 1,2-Dilinolenyloxy-N,N-dimethylaminopropane (DLenDMA). The following lipids are cationic and have a positive charge at below physiological pH: DODAP, DODMA, DMDMA and the like.

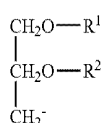
[0094] The term "hydrophobic lipid" refers to compounds having apolar groups that include, but are not limited to, long chain saturated and unsaturated aliphatic hydrocarbon groups and such groups optionally substituted by one or more aromatic, cycloaliphatic or heterocyclic group(s). Suitable examples include, but are not limited to, diacylglycerol, dialkylglycerol, N-N-dialkylamino, 1,2-diacyloxy-3-aminopropane and 1,2-dialkyl-3-aminopropane.

[0095] The term "fusogenic" refers to the ability of a liposome, an SNALP or other drug delivery system to fuse with membranes of a cell. The membranes can be either the plasma membrane or membranes surrounding organelles, e.g., endosome, nucleus, etc.

[0096] The term "diacylglycerol" refers to a compound having 2-fatty acyl chains, R¹ and R², both of which have independently between 2 and 30 carbons bonded to the 1- and 2-position of glycerol by ester linkages. The acyl groups can be saturated or have varying degrees of unsaturation. Diacylglycerols have the following general formula:

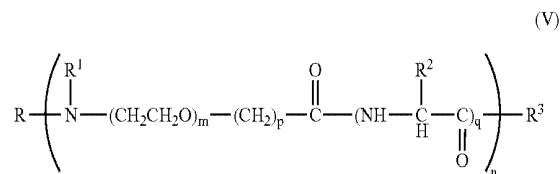


[0097] The term "dialkylxypropyl" refers to a compound having 2-alkyl chains, R¹ and R², both of which have independently between 2 and 30 carbons. The alkyl groups can be saturated or have varying degrees of unsaturation. Dialkylxypropyls have the following general formula:



[0098] The term "ATTA" or "polyamide" refers to, but is not limited to, compounds disclosed in U.S. Pat. Nos. 6,320,017 and 6,586,559, both of which are incorporated

herein by reference. These compounds include a compound having the formula



wherein: R is a member selected from the group consisting of hydrogen, alkyl and acyl; R¹ is a member selected from the group consisting of hydrogen and alkyl; or optionally, R and R¹ and the nitrogen to which they are bound form an azido moiety; R² is a member of the group selected from hydrogen, optionally substituted alkyl, optionally substituted aryl and a side chain of an amino acid; R³ is a member selected from the group consisting of hydrogen, halogen, hydroxy, alkoxy, mercapto, hydrazino, amino and NR⁴R⁵, wherein R⁴ and R⁵ are independently hydrogen or alkyl; n is 4 to 80; m is 2 to 6; p is 1 to 4; and q is 0 or 1. It will be apparent to those of skill in the art that other polyamides can be used in the compounds of the present invention.

[0099] The term "nucleic acid" or "polynucleotide" refers to a polymer containing at least two deoxyribonucleotides or ribonucleotides in either single- or double-stranded form. Unless specifically limited, the terms encompass nucleic acids containing known analogs of natural nucleotides that have similar binding properties as the reference nucleic acid and are metabolized in a manner similar to naturally occurring nucleotides. Examples of such analogs include, without limitation phosphorothioates, phosphoramidates, methyl phosphonates, chiral-methyl phosphonates, 2'-methyl ribonucleotides, and peptide nucleic acids (PNA's). Unless otherwise indicated, a particular nucleic acid sequence also implicitly encompasses conservatively modified variants thereof (e.g., degenerate codon substitutions), alleles, orthologs, SNPs, and complementary sequences as well as the sequence explicitly indicated. Specifically, degenerate codon substitutions may be achieved by generating sequences in which the third position of one or more selected (or all) codons is substituted with mixed-base and/or deoxyinosine residues (Batzer et al., *Nucleic Acid Res.* 19:5081 (1991); Ohtsuka et al., *J. Biol. Chem.* 260:2605-2608 (1985); and Cassol et al. (1992); Rossolini et al., *Mol. Cell. Probes* 8:91-98 (1994)). "Nucleotides" contain a sugar deoxyribose (DNA) or ribose (RNA), a base, and a phosphate group. Nucleotides are linked together through the phosphate groups. "Bases" include purines and pyrimidines, which further include natural compounds adenine, thymine, guanine, cytosine, uracil, inosine, and natural analogs, and synthetic derivatives of purines and pyrimidines, which include, but are not limited to, modifications which place new reactive groups such as, but not limited to, amines, alcohols, thiols, carboxylates, and alkylhalides. DNA may be in the form of antisense, plasmid DNA, parts of a plasmid DNA, pre-condensed DNA, product of a polymerase chain reaction (PCR), vectors (PI, PAC, BAC, YAC, artificial chromosomes), expression cassettes, chimeric sequences, chromosomal DNA, or derivatives of these groups. The term

nucleic acid is used interchangeably with gene, cDNA, mRNA encoded by a gene, and an interfering RNA molecule.

[0100] The term “gene” refers to a nucleic acid (e.g., DNA or RNA) sequence that comprises partial length or entire length coding sequences necessary for the production of a polypeptide or precursor (e.g., ApoB).

[0101] “Gene product,” as used herein, refers to a product of a gene such as an RNA transcript.

[0102] As used herein, the term “aqueous solution” refers to a composition comprising in whole, or in part, water.

[0103] As used herein, the term “organic lipid solution” refers to a composition comprising in whole, or in part, an organic solvent having a lipid.

[0104] “Distal site,” as used herein, refers to a physically separated site, which is not limited to an adjacent capillary bed, but includes sites broadly distributed throughout an organism.

[0105] “Serum-stable” in relation to nucleic acid-lipid particles means that the particle is not significantly degraded after exposure to a serum or nuclease assay that would significantly degrade free DNA. Suitable assays include, for example, a standard serum assay or a DNase assay such as those described in the Examples below.

[0106] “Systemic delivery,” as used herein, refers to delivery that leads to a broad biodistribution of a compound within an organism. Some techniques of administration can lead to the systemic delivery of certain compounds, but not others. Systemic delivery means that a useful, preferably therapeutic, amount of a compound is exposed to most parts of the body. To obtain broad biodistribution generally requires a blood lifetime such that the compound is not rapidly degraded or cleared (such as by first pass organs (liver, lung, etc.) or by rapid, nonspecific cell binding) before reaching a disease site distal to the site of administration. Systemic delivery of nucleic acid-lipid particles can be by any means known in the art including, for example, intravenous, subcutaneous, intraperitoneal. In some embodiments, systemic delivery of nucleic acid-lipid particles is by intravenous delivery.

[0107] “Local delivery” as used herein refers to delivery of a compound directly to a target site within an organism. For example, a compound can be locally delivered by direct injection into a disease site such as a tumor or other target site such as a site of inflammation or a target organ such as the liver, heart, pancreas, kidney, and the like.

III. siRNAs

[0108] The nucleic acid component of the nucleic acid-lipid particles of the present invention comprises an interfering RNA that silences (e.g., partially or completely inhibits) expression of a gene of interest (i.e., ApoB). An interfering RNA can be provided in several forms. For example, an interfering RNA can be provided as one or more isolated small-interfering RNA (siRNA) duplexes, longer double-stranded RNA (dsRNA), or as siRNA or dsRNA transcribed from a transcriptional cassette in a DNA plasmid. The interfering RNA may also be chemically synthesized. The interfering RNA can be administered alone or co-administered (i.e., concurrently or consecutively) with

conventional agents used to treat, e.g., a disease or disorder involving hypercholesterolemia. Such agents include statins such as, e.g., Lipitor®, Mevacor®, Zocor®, Lescol®, Crestor®, and Advicor®).

[0109] In preferred embodiments, the interfering RNA is an siRNA molecule that is capable of silencing expression of a target gene (i.e., ApoB). The siRNA is typically from about 15 to about 30 nucleotides in length. The synthesized or transcribed siRNA can have 3' overhangs of about 1-4 nucleotides, preferably of about 2-3 nucleotides, and 5' phosphate termini. In some embodiments, the siRNA lacks terminal phosphates. For example, siRNA targeting the sequences set forth in Tables 1-5 can be used to silence ApoB expression.

[0110] In some embodiments, the siRNA molecules described herein comprise at least one region of mismatch with its target sequence. As used herein, the term “region of mismatch” refers to a region of an siRNA that does not have 100% complementarity to its target sequence. An siRNA may have at least one, two, or three regions of mismatch. The regions of mismatch may be contiguous or may be separated by one or more nucleotides. The regions of mismatch may comprise a single nucleotide or may comprise two, three, four, or more nucleotides.

[0111] A. Selection of siRNA Sequences

[0112] Suitable siRNA sequences that target a gene of interest (i.e., ApoB) can be identified using any means known in the art. Typically, the methods described in Elbashir et al., *Nature* 411:494-498 (2001) and Elbashir et al., *EMBO J* 20: 6877-6888 (2001) are combined with rational design rules set forth in Reynolds et al., *Nature Biotech.* 22:326-330 (2004).

[0113] Typically, the sequence within about 50 to about 100 nucleotide 3' of the AUG start codon of a transcript from the target gene of interest is scanned for dinucleotide sequences (e.g., AA, CC, GG, or UU) (see, e.g., Elbashir, et al., *EMBO J* 20: 6877-6888 (2001)). The nucleotides immediately 3' to the dinucleotide sequences are identified as potential siRNA target sequences. Typically, the 19, 21, 23, 25, 27, 29, 31, 33, 35, or more nucleotides immediately 3' to the dinucleotide sequences are identified as potential siRNA target sites. In some embodiments, the dinucleotide sequence is an AA sequence and the 19 nucleotides immediately 3' to the AA dinucleotide are identified as a potential siRNA target site. Typically, siRNA target sites are spaced at different positions along the length of the target gene. To further enhance silencing efficiency of the siRNA sequences, potential siRNA target sites may be further analyzed to identify sites that do not contain regions of homology to other coding sequences. For example, a suitable siRNA target site of about 21 base pairs typically will not have more than 16-17 contiguous base pairs of homology to other coding sequences. If the siRNA sequences are to be expressed from an RNA Pol III promoter, siRNA target sequences lacking more than 4 contiguous A's or T's are selected.

[0114] Once a potential siRNA sequence has been identified, the sequence can be analyzed using a variety of criteria known in the art. For example, to enhance their silencing efficiency, the siRNA sequences may be analyzed by a rational design algorithm to identify sequences that have one

or more of the following features: (1) G/C content of about 25% to about 60% G/C; (2) at least 3 A/Us at positions 15-19 of the sense strand; (3) no internal repeats; (4) an A at position 19 of the sense strand; (5) an A at position 3 of the sense strand; (6) a U at position 10 of the sense strand; (7) no G/C at position 19 of the sense strand; and (8) no G at position 13 of the sense strand. siRNA design tools that incorporate algorithms that assign suitable values of each of these features and are useful for selection of siRNA can be found at, e.g., <http://boz094.ust.hk/RNAi/siRNA>. One of skill in the art will appreciate that sequences with one or more of the foregoing characteristics may be selected for further analysis and testing as potential siRNA sequences. siRNA sequences complementary to the siRNA target sites may also be designed.

[0115] Additionally, potential siRNA target sequences with one or more of the following criteria can often be eliminated as siRNA: (1) sequences comprising a stretch of 4 or more of the same base in a row; (2) sequences comprising homopolymers of Gs (i.e., to reduce possible non-specific effects due to structural characteristics of these polymers); (3) sequences comprising triple base motifs (e.g., GGG, CCC, AAA, or TTT); (4) sequences comprising stretches of 7 or more G/Cs in a row; and (5) sequence comprising direct repeats of 4 or more bases within the candidates resulting in internal fold-back structures. However, one of skill in the art will appreciate that sequences with one or more of the foregoing characteristics may still be selected for further analysis and testing as potential siRNA sequences.

[0116] Once a potential siRNA sequence has been identified, the sequence can be analyzed for the presence of any immunostimulatory properties, e.g., using an in vitro cytokine assay or an in vivo animal model. Motifs in the sense and/or antisense strand of the siRNA sequence such as GU-rich motifs can also provide an indication of whether the sequence may be immunostimulatory. Once an siRNA molecule is found to be immunostimulatory, it can then be modified to decrease its immunostimulatory properties. As a non-limiting example, an siRNA sequence can be contacted with a mammalian responder cell under conditions such that the cell produces a detectable immune response to determine whether the siRNA is an immunostimulatory or a non-immunostimulatory siRNA. The mammalian responder cell may be from a naïve mammal (i.e., a mammal that has not previously been in contact with the gene product of the siRNA sequence). The mammalian responder cell may be, e.g., a peripheral blood mononuclear cell (PBMC), a macrophage, and the like. The detectable immune response may comprise production of a cytokine or growth factor such as, e.g., TNF- α , TNF- β , IFN- α , IFN- γ , IL-6, IL-12, or a combination thereof. An siRNA molecule identified as being immunostimulatory can then be modified to decrease its immunostimulatory properties by replacing at least one of the nucleotides on the sense and/or antisense strand with modified nucleotides such as 2'OMe nucleotides (e.g., 2'OMe-guanosine, 2'OMe-uridine, 2'OMe-cytosine, and/or 2'OMe-adenosine). The modified siRNA can then be contacted with a mammalian responder cell as described above to confirm that its immunostimulatory properties have been reduced or abrogated.

[0117] Suitable in vitro assays for detecting an immune response include, but are not limited to, the double mono-

clonal antibody sandwich immunoassay technique of David et al. (U.S. Pat. No. 4,376,110); monoclonal-polyclonal antibody sandwich assays (Wide et al., in Kirkham and Hunter, eds., *Radioimmunoassay Methods*, E. and S. Livingstone, Edinburgh (1970)); the "Western blot" method of Gordon et al. (U.S. Pat. No. 4,452,901); immunoprecipitation of labeled ligand (Brown et al., *J. Biol. Chem.* 255:4980-4983 (1980)); enzyme-linked immunosorbent assays (ELISA) as described, for example, by Raines et al., *J. Biol. Chem.* 257:5154-5160 (1982); immunocytochemical techniques, including the use of fluorochromes (Brooks et al., *Clin. Exp. Immunol.* 39:477 (1980)); and neutralization of activity (Bowen-Pope et al., *Proc. Natl. Acad. Sci. USA* 81:2396-2400 (1984)). In addition to the immunoassays described above, a number of other immunoassays are available, including those described in U.S. Pat. Nos. 3,817,827; 3,850,752; 3,901,654; 3,935,074; 3,984,533; 3,996,345; 4,034,074; and 4,098,876.

[0118] A non-limiting example of an in vivo model for detecting an immune response includes an in vivo mouse cytokine induction assay that can be performed as follows: (1) siRNA can be administered by standard intravenous injection in the lateral tail vein; (2) blood can be collected by cardiac puncture about 6 hours after administration and processed as plasma for cytokine analysis; and (3) cytokines can be quantified using sandwich ELISA kits according to the manufacturers' instructions (e.g., mouse and human IFN- α (PBL Biomedical; Piscataway, N.J.); human IL-6 and TNF- α (eBioscience; San Diego, Calif.); and mouse IL-6, TNF- α , and IFN- γ (BD Biosciences; San Diego, Calif.)).

[0119] Monoclonal antibodies that specifically bind cytokines and growth factors are commercially available from multiple sources and can be generated using methods known in the art (see, e.g., Kohler and Milstein, *Nature* 256:495-497 (1975) and Harlow and Lane, *ANTIBODIES, A LABORATORY MANUAL*, Cold Spring Harbor Publication, New York (1999)). Generation of monoclonal antibodies has been previously described and can be accomplished by any means known in the art (Buhring et al. in *Hybridoma*, Vol. 10, No. 1, pp. 77-78 (1991)). In some methods, the monoclonal antibody is labeled (e.g., with any composition detectable by spectroscopic, photochemical, biochemical, electrical, optical, or chemical means) to facilitate detection.

[0120] B. Generating siRNA

[0121] siRNA can be provided in several forms including, e.g. as one or more isolated siRNA duplexes, longer double-stranded RNA (dsRNA) or as siRNA or dsRNA transcribed from a transcriptional cassette in a DNA plasmid. siRNA may also be chemically synthesized. The siRNA sequences may have overhangs (e.g., 3' or 5' overhangs as described in Elbashir et al., *Genes Dev.* 15:188 (2001) or Nykänen et al., *Cell* 107:309 (2001), or may lack overhangs (i.e., to have blunt ends).

[0122] An RNA population can be used to provide long precursor RNAs, or long precursor RNAs that have substantial or complete identity to a selected target sequence can be used to make the siRNA. The RNAs can be isolated from cells or tissue, synthesized, and/or cloned according to methods well known to those of skill in the art. The RNA can be a mixed population (obtained from cells or tissue, transcribed from cDNA, subtracted, selected etc.), or can represent a single target sequence. RNA can be naturally

occurring, (e.g., isolated from tissue or cell samples), synthesized in vitro (e.g., using T7 or SP6 polymerase and PCR products or a cloned cDNA), or chemically synthesized.

[0123] To form a long dsRNA, for synthetic RNAs, the complement is also transcribed in vitro and hybridized to form a dsRNA. If a naturally occurring RNA population is used, the RNA complements are also provided (e.g., to form dsRNA for digestion by *E. coli* RNase III or Dicer), e.g., by transcribing cDNAs corresponding to the RNA population, or by using RNA polymerases. The precursor RNAs are then hybridized to form double stranded RNAs for digestion. The dsRNAs can be directly administered to a subject or can be digested in vitro prior to administration.

[0124] Alternatively, one or more DNA plasmids encoding one or more siRNA templates are used to provide siRNA. siRNA can be transcribed as sequences that automatically fold into duplexes with hairpin loops from DNA templates in plasmids having RNA polymerase III transcriptional units, for example, based on the naturally occurring transcription units for small nuclear RNA U6 or human RNase P RNA H1 (see, Brummelkamp, et al., *Science* 296:550 (2002); Donzé, et al., *Nucleic Acids Res.* 30:e46 (2002); Paddison, et al., *Genes Dev.* 16:948 (2002); Yu, et al., *PNAS USA* 99:6047 (2002); Lee, et al., *Nat. Biotech.* 20:500 (2002); Miyagishi, et al., *Nat. Biotech.* 20:497 (2002); Paul, et al., *Nat. Biotech.* 20:505 (2002); and Sui, et al., *PNAS USA* 99:5515 (2002)). Typically, a transcriptional unit or cassette will contain an RNA transcript promoter sequence, such as an H1-RNA or a U6 promoter, operably linked to a template for transcription of a desired siRNA sequence and a termination sequence, comprised of 2-3 uridine residues and a polythymidine (T5) sequence (polyadenylation signal) (Brummelkamp, *Science*, supra). The selected promoter can provide for constitutive or inducible transcription. Compositions and methods for DNA-directed transcription of RNA interference molecules is described in detail in U.S. Pat. No. 6,573,099. The transcriptional unit is incorporated into a plasmid or DNA vector from which the interfering RNA is transcribed. Plasmids suitable for in vivo delivery of genetic material for therapeutic purposes are described in detail in U.S. Pat. Nos. 5,962,428 and 5,910,488. The selected plasmid can provide for transient or stable delivery of a target cell. It will be apparent to those of skill in the art that plasmids originally designed to express desired gene sequences can be modified to contain a transcriptional unit cassette for transcription of siRNA.

[0125] Methods for isolating RNA, synthesizing RNA, hybridizing nucleic acids, making and screening cDNA libraries, and performing PCR are well known in the art (see, e.g., Gubler and Hoffman, *Gene* 25:263-269 (1983); Sambrook et al., supra; Ausubel et al., supra), as are PCR methods (see U.S. Pat. Nos. 4,683,195 and 4,683,202; *PCR Protocols: A Guide to Methods and Applications* (Innis et al., eds, 1990)). Expression libraries are also well known to those of skill in the art. Additional basic texts disclosing the general methods of use in this invention include Sambrook et al., *Molecular Cloning, A Laboratory Manual* (2nd ed. 1989); Kriegler, *Gene Transfer and Expression: A Laboratory Manual* (1990); and *Current Protocols in Molecular Biology* (Ausubel et al., eds., 1994)).

[0126] The siRNA component of the SNALP can also be chemically synthesized. The oligonucleotides that comprise

the modified siRNA molecule can be synthesized using any of a variety of techniques known in the art, such as those described in Usman et al., *J. Am. Chem. Soc.* 109:7845 (1987); Scaringe et al., *Nuc. Acids Res.* 18:5433 (1990); Wincott et al., *Nuc. Acids Res.* 23:2677-2684 (1995); and Wincott et al., *Methods Mol. Bio.* 74:59 (1997). The synthesis of oligonucleotides makes use of common nucleic acid protecting and coupling groups, such as dimethoxytrityl at the 5'-end and phosphoramidites at the 3'-end. As a non-limiting example, small scale syntheses can be conducted on an Applied Biosystems synthesizer using a 0.2 μ mol scale protocol with a 2.5 min. coupling step for 2'-O-methylated nucleotides. Alternatively, syntheses at the 0.2 μ mol scale can be performed on a 96-well plate synthesizer from Protogene (Palo Alto, Calif.). However, a larger or smaller scale of synthesis is also within the scope of the present invention. Suitable reagents for oligonucleotide synthesis, methods for RNA deprotection, and methods for RNA purification are known to those of skill in the art.

[0127] Modified siRNA molecules can also be synthesized via a tandem synthesis technique, wherein both strands are synthesized as a single continuous oligonucleotide fragment or strand separated by a cleavable linker that is subsequently cleaved to provide separate fragments or strands that hybridize to form the siRNA duplex. The linker can be a polynucleotide linker or a non-nucleotide linker. The tandem synthesis of modified siRNA can be readily adapted to both multiwell/multiplate synthesis platforms as well as large scale synthesis platforms employing batch reactors, synthesis columns, and the like. Alternatively, the modified siRNA molecule can be assembled from two distinct oligonucleotides, wherein one oligonucleotide comprises the sense strand and the other comprises the antisense strand of the siRNA. For example, each strand can be synthesized separately and joined together by hybridization or ligation following synthesis and/or deprotection. In certain other instances, the modified siRNA molecule can be synthesized as a single continuous oligonucleotide fragment, wherein the self-complementary sense and antisense regions hybridize to form an siRNA duplex having hairpin secondary structure.

[0128] C. Modifying siRNA Sequences

[0129] The anti-ApoB siRNA molecules described herein can comprise at least one modified nucleotide in the sense and/or antisense strand (see, e.g., U.S. Provisional Patent Application No. 60/711,494). Examples of modified nucleotides suitable for use in the present invention include, but are not limited to, ribonucleotides having a 2'-O-methyl (2'OMe), 2'-deoxy-2'-fluoro, 2'-deoxy, 5-C-methyl, 2'-methoxyethyl, 4'-thio, 2'-amino, or 2'-C-allyl group. Modified nucleotides having a Northern conformation such as those described in, e.g., Saenger, *Principles of Nucleic Acid Structure*, Springer-Verlag Ed. (1984), are also suitable for use in the siRNA molecules of the present invention. Such modified nucleotides include, without limitation, locked nucleic acid (LNA) nucleotides (e.g., 2'-O, 4'-C-methylene-(D-ribofuranosyl) nucleotides), 2'-methoxyethoxy (MOE) nucleotides, 2'-methyl-thio-ethyl nucleotides, 2'-deoxy-2'-fluoro nucleotides, 2'-deoxy-2'-chloro nucleotides, and 2'-azido nucleotides. In certain instances, the siRNA molecule includes one or more G-clamp nucleotides. A G-clamp nucleotide refers to a modified cytosine analog wherein the modifications confer the ability to hydrogen bond both Watson-Crick and Hoogsteen faces of a complementary

guanine nucleotide within a duplex (see, e.g., Lin et al., *J. Am. Chem. Soc.* 120:8531-8532 (1998)). In addition, nucleotides having a nucleotide base analog such as, for example, C-phenyl, C-naphthyl, other aromatic derivatives, inosine, azole carboxamides, and nitroazole derivatives such as 3-nitropyrrole, 4-nitroindole, 5-nitroindole, and 6-nitroindole (see, e.g., Loakes, *Nucl. Acids Res.* 29:2437-2447 (2001)) can be incorporated into the siRNA molecule.

[0130] In certain embodiments, the siRNA molecule can further comprise one or more chemical modifications such as terminal cap moieties, phosphate backbone modifications, and the like. Examples of terminal cap moieties include, without limitation, inverted deoxy abasic residues, glyceryl modifications, 4',5'-methylene nucleotides, 1-(β -D-erythrofuransyl) nucleotides, 4'-thio nucleotides, carbocyclic nucleotides, 1,5-anhydrohexitol nucleotides, L-nucleotides, α -nucleotides, modified base nucleotides, threo-pentofuranosyl nucleotides, acyclic 3',4'-seco nucleotides, acyclic 3,4-dihydroxybutyl nucleotides, acyclic 3,5-dihydroxypentyl nucleotides, 3'-3'-inverted nucleotide moieties, 3'-3'-inverted abasic moieties, 3'-2'-inverted nucleotide moieties, 3'-2'-inverted abasic moieties, 5'-5'-inverted nucleotide moieties, 5'-5'-inverted abasic moieties, 3'-5'-inverted deoxy abasic moieties, 5'-amino-alkyl phosphate, 1,3-diamino-2-propyl phosphate, 3-aminopropyl phosphate, 6-aminoethyl phosphate, 1,2-aminododecyl phosphate, hydroxypropyl phosphate, 1,4-butanediol phosphate, 3'-phosphoramidate, 5'-phosphoramidate, hexylphosphate, aminohexyl phosphate, 3'-phosphate, 5'-amino, 3'-phosphorothioate, 5'-phosphorothioate, phosphorodithioate, and bridging or non-bridging methylphosphonate or 5'-mercapto moieties (see, e.g., U.S. Pat. No. 5,998,203; Beaucage et al., *Tetrahedron* 49:1925 (1993)). Non-limiting examples of phosphate backbone modifications (i.e., resulting in modified internucleotide linkages) include phosphorothioate, phosphorodithioate, methylphosphonate, phosphotriester, morpholino, amidate, carbamate, carboxymethyl, acetamidate, polyamide, sulfonate, sulfonamide, sulfamate, formacetal, thioformacetal, and alkylsilyl substitutions (see, e.g., Hunziker et al., *Nucleic Acid Analogues: Synthesis and Properties*, in *Modern Synthetic Methods*, VCH, 331-417 (1995); Mesmaeker et al., *Novel Backbone Replacements for Oligonucleotides*, in *Carbohydrate Modifications in Antisense Research*, ACS, 24-39 (1994)). Such chemical modifications can occur at the 5'-end and/or 3'-end of the sense strand, antisense strand, or both strands of the siRNA.

[0131] In some embodiments, the sense and/or antisense strand can further comprise a 3'-terminal overhang having about 1 to about 4 (e.g., 1, 2, 3, or 4) 2'-deoxy ribonucleotides and/or any combination of modified and unmodified nucleotides. Additional examples of modified nucleotides and types of chemical modifications that can be introduced into the modified siRNA molecule are described, e.g., in UK Patent No. GB 2,397,818 B.

[0132] The modified siRNA molecules described herein can optionally comprise one or more non-nucleotides in one or both strands of the siRNA. As used herein, the term "non-nucleotide" refers to any group or compound that can be incorporated into a nucleic acid chain in the place of one or more nucleotide units, including sugar and/or phosphate substitutions, and allows the remaining bases to exhibit their activity. The group or compound is abasic in that it does not contain a commonly recognized nucleotide base such as

adenosine, guanine, cytosine, uracil, or thymine and therefore lacks a base at the 1'-position.

[0133] In other embodiments, chemical modification of the siRNA comprises attaching a conjugate to the chemically-modified siRNA molecule. The conjugate can be attached at the 5' and/or 3'-end of the sense and/or antisense strand of the chemically-modified siRNA via a covalent attachment such as, e.g., a biodegradable linker. The conjugate can also be attached to the chemically-modified siRNA, e.g., through a carbamate group or other linking group (see, e.g., U.S. Patent Publication Nos. 20050074771, 20050043219, and 20050158727). In certain instances, the conjugate is a molecule that facilitates the delivery of the chemically-modified siRNA into a cell. Examples of conjugate molecules suitable for attachment to a chemically-modified siRNA include, without limitation, steroids such as cholesterol, glycols such as polyethylene glycol (PEG), human serum albumin (HSA), fatty acids, carotenoids, terpenes, bile acids, folates (e.g., folic acid, folate analogs and derivatives thereof), sugars (e.g., galactose, galactosamine, N-acetyl galactosamine, glucose, mannose, fructose, fucose, etc.), phospholipids, peptides, ligands for cellular receptors capable of mediating cellular uptake, and combinations thereof (see, e.g., U.S. Patent Publication Nos. 20030130186, 20040110296, and 20040249178; U.S. Pat. No. 6,753,423). Other examples include the lipophilic moiety, vitamin, polymer, peptide, protein, nucleic acid, small molecule, oligosaccharide, carbohydrate cluster, intercalator, minor groove binder, cleaving agent, and cross-linking agent conjugate molecules described in U.S. Patent Publication Nos. 20050119470 and 20050107325. Yet other examples include the 2'-O-alkyl amine, 2'-O-alkoxyalkyl amine, polyamine, C5-cationic modified pyrimidine, cationic peptide, guanidinium group, amidinium group, cationic amino acid conjugate molecules described in U.S. Patent Publication No. 20050153337. Additional examples include the hydrophobic group, membrane active compound, cell penetrating compound, cell targeting signal, interaction modifier, and steric stabilizer conjugate molecules described in U.S. Patent Publication No. 20040167090. Further examples include the conjugate molecules described in U.S. Patent Publication No. 20050239739. The type of conjugate used and the extent of conjugation to the chemically-modified siRNA molecule can be evaluated for improved pharmacokinetic profiles, bioavailability, and/or stability of the siRNA. As such, one skilled in the art can screen chemically-modified siRNA molecules having various conjugates attached thereto to identify ones having improved properties using any of a variety of well-known in vitro cell culture or in vivo animal models.

[0134] C. In Vitro Methods Using siRNA

[0135] In addition silencing ApoB gene expression, the siRNA sequences described herein can be used in a variety of in vitro diagnostic and screening methods. For example, the siRNA sequences can be used as probes, e.g., to detect ApoB sequences. The siRNA sequences can also be used in screening assays, including high throughput assays to detect the effects of compounds that modulate lipid metabolism on ApoB expression.

[0136] In one exemplary embodiment, the siRNA sequences can be used in high density oligonucleotide array

technology (e.g., GeneChip™) to identify ApoB protein, orthologs, alleles, conservatively modified variants, and polymorphic variants in this invention. In some cases, the siRNA can be used with GeneChip™ as a diagnostic tool in detecting a disease or disorder associated with ApoB expression or overexpression (e.g., hypercholesterolemia) in a biological sample, see, e.g., Gunthand et al., *AIDS Res. Hum. Retroviruses* 14: 869-876 (1998); Kozal et al., *Nat. Med.* 2:753-759 (1996); Matson et al., *Anal. Biochem.* 224:110-106 (1995); Lockhart et al., *Nat. Biotechnol.* 14:1675-1680 (1996); Gingeras et al., *Genome Res.* 8:435-448 (1998); Hacia et al., *Nucleic Acids Res.* 26:3865-3866 (1998).

[0137] In another exemplary embodiment, the siRNA sequences can be used in an in vitro diagnostic assay to determine the effects of a potential modulator of lipid metabolism (i.e., by determining the effects of the potential modulator on ApoB expression). A liver biopsy is taken from a subject undergoing treatment with the lipid metabolism modulator (e.g., a statin such as Lipitor®, Mevacor®, Zocor®, Lescol®, Crestor®, or Advicor®) and the siRNA sequences are used to detect ApoB expression, thereby determining the effect of the modulator on ApoB expression.

[0138] In yet another exemplary embodiment, the siRNA sequences can be inserted into an expression vector and transfected into cells for use in a variety of in vitro diagnostic assays. Typically the expression vector contains a strong promoter to direct transcription and a transcription/translation terminator. Suitable bacterial promoters are well known in the art and described, e.g., in Sambrook et al., and Ausubel et al, supra. Bacterial expression systems for expressing the protein are available in, e.g., *E. coli*, *Bacillus* sp., and *Salmonella* (Palva et al., *Gene* 22:229-235 (1983); Mosbach et al., *Nature* 302:543-545 (1983). Kits for such expression systems are commercially available. Eukaryotic expression systems for mammalian cells, yeast, and insect cells are well known in the art and are also commercially available.

[0139] Selection of the promoter used to direct expression of a heterologous nucleic acid depends on the particular application. The promoter is preferably positioned about the same distance from the heterologous transcription start site as it is from the transcription start site in its natural setting. As is known in the art, however, some variation in this distance can be accommodated without loss of promoter function.

[0140] In addition to the promoter, the expression vector typically contains a transcription unit or expression cassette that contains all the additional elements required for the expression of the nucleic acid in host cells. A typical expression cassette thus contains a promoter operably linked to the nucleic acid sequence and signals required for efficient polyadenylation of the transcript, ribosome binding sites, and translation termination. Additional elements of the cassette may include enhancers.

[0141] In addition to a promoter sequence, the expression cassette should also contain a transcription termination region downstream of the structural gene to provide for efficient termination. The termination region may be obtained from the same gene as the promoter sequence or may be obtained from different genes.

[0142] The particular expression vector used to transport the genetic information into the cell is not particularly

critical. Any of the conventional vectors used for expression in eukaryotic or prokaryotic cells may be used. Standard bacterial expression vectors include plasmids such as pBR322 based plasmids, pSKF, pET23D, and fusion expression systems such as MBP, GST, and LacZ. Epitope tags can also be added to recombinant proteins to provide convenient methods of isolation, e.g., c-myc.

[0143] Expression vectors containing regulatory elements from eukaryotic viruses are typically used in eukaryotic expression vectors, e.g., SV40 vectors, papilloma virus vectors, retroviral vectors, and vectors derived from Epstein-Barr virus. Other exemplary eukaryotic vectors include pMSG, pAV009/A.sup.+, pMTO10/A.sup.+, pMAMneo-5, baculovirus pDSVE, and any other vector allowing expression of proteins under the direction of the CMV promoter, SV40 early promoter, SV40 later promoter, metallothionein promoter, murine mammary tumor virus promoter, Rous sarcoma virus promoter, polyhedrin promoter, or other promoters shown effective for expression in eukaryotic cells.

[0144] The vector may further comprise a reporter gene. The siRNA sequence is operably linked to a reporter gene such as chloramphenicol acetyltransferase, firefly luciferase, bacterial luciferase, β -galactosidase and alkaline phosphatase. The reporter construct is typically transfected into a cell. After treatment with a potential modulator, the amount of reporter gene transcription, translation, or activity is measured according to standard techniques known to those of skill in the art.

[0145] The elements that are typically included in expression vectors also include a replicon that functions in *E. coli*, a gene encoding antibiotic resistance to permit selection of bacteria that harbor recombinant plasmids, and unique restriction sites in nonessential regions of the plasmid to allow insertion of eukaryotic sequences. The particular antibiotic resistance gene chosen is not critical, any of the many resistance genes known in the art are suitable. The prokaryotic sequences are preferably chosen such that they do not interfere with the replication of the DNA in eukaryotic cells, if necessary.

[0146] Transformation of eukaryotic and prokaryotic cells are performed according to standard techniques (see, e.g., Morrison, *J. Bact.* 132:349-351 (1977); Clark-Curtiss & Curtiss, *Methods in Enzymology* 101:347-362 (Wu et al., eds, 1983). Any of the well-known procedures for introducing foreign nucleotide sequences into host cells may be used. These include the use of calcium phosphate transfection, polybrene, protoplast fusion, electroporation, biolistics, liposomes, microinjection, plasma vectors, viral vectors and any of the other well known methods for introducing cloned genomic DNA, cDNA, synthetic DNA or other foreign genetic material into a host cell (see, e.g., Sambrook et al., supra). It is only necessary that the particular genetic engineering procedure used be capable of successfully introducing at least one gene into the host cell capable of expressing the nucleotide sequence of interest. Suitable cell include for such cell based assays include both primary hepatocytes and hepatocyte cell lines, as described herein, e.g., Hep G2 cells, Hep 2 cells, HEP-3B cells, McArdle RH7777 cells, BRL3A cells, and NRL clone 9 cells.

[0147] After the expression vector is introduced into the cells, the transfected cells are cultured under conditions favoring expression of the siRNA sequence. The transfected

cells can be used in high throughput assays to identify compounds that directly modulate ApoB expression as well as compounds that modulate expression of genes upstream and downstream of ApoB, thereby mapping genes involved in lipid metabolism pathways. The transfected cells can also be used to determine the effects of silencing ApoB expression on other components of the lipid metabolism pathway. For example, following expression of the siRNA in the cells, expression of other genes (e.g., ApoE, ApoA-I, ApoE, and ApoAV) in the lipid metabolism pathway can be detected to determine the effect of silencing ApoB expression.

IV. Lipid-Based Carrier Systems Containing siRNA

[0148] In one aspect, the present invention provides stabilized nucleic acid-lipid particles (SPLPs or SNALPs) and other lipid-based carrier systems containing the siRNA described herein. Preferably, the lipid-based carrier system is a SNALP. Alternatively, the lipid-based carrier system is a liposome, micelle, virosome, nucleic acid complex, or mixtures thereof.

[0149] Non-limiting examples of alternative lipid-based carrier systems suitable for use in the present invention include polycationic polymer/nucleic acid complexes (see, e.g., U.S. Patent Publication Nos. 20050222064 and 20030185890), cyclodextrin-polymer/nucleic acid complexes (see, e.g., U.S. Patent Publication No. 20040087024), biodegradable poly(β -amino ester) polymer/nucleic acid complexes (see, e.g., U.S. Patent Publication No. 20040071654), pH-sensitive liposomes (see, e.g., U.S. Patent Publication No. 20020192274; AU 2003210303), anionic liposomes (see, e.g., U.S. Patent Publication No. 20030026831), cationic liposomes (see, e.g., U.S. Patent Publication Nos. 20030229040, 20020160038, and 20020012998; U.S. Pat. No. 5,908,635; PCT Publication No. WO 01/72283), antibody-coated liposomes (see, e.g., U.S. Patent Publication No. 20030108597; PCT Publication No. WO 00/50008), reversibly masked lipoplexes (see, e.g., U.S. Patent Publication Nos. 20030180950), cell-type specific liposomes (see, e.g., U.S. Patent Publication No. 20030198664), liposomes containing nucleic acid and peptides (see, e.g., U.S. Pat. No. 6,207,456), microparticles containing polymeric matrices (see, e.g., U.S. Patent Publication No. 20040142475), pH-sensitive lipoplexes (see, e.g., U.S. Patent Publication No. 20020192275), liposomes containing lipids derivatized with releasable hydrophilic polymers (see, e.g., U.S. Patent Publication No. 20030031704), lipid-entrapped nucleic acid (see, e.g., PCT Publication Nos. WO 03/057190 and WO 03/059322), lipid-encapsulated nucleic acid (see, e.g., U.S. Patent Publication No. 20030129221; U.S. Pat. No. 5,756,122), polycationic sterol derivative/nucleic acid complexes (see, e.g., U.S. Pat. No. 6,756,054), other liposomal compositions (see, e.g., U.S. Patent Publication Nos. 20030035829 and 20030072794; U.S. Pat. No. 6,200,599), other microparticle compositions (see, e.g., U.S. Patent Publication No. 20030157030), polyplexes (see, e.g., PCT Publication No. WO 03/066069), emulsion compositions (see, e.g., U.S. Pat. No. 6,747,014), condensed nucleic acid complexes (see, e.g., U.S. Patent Publication No. 20050123600), other polycationic/nucleic acid complexes (see, e.g., U.S. Patent Publication No. 20030125281), polyvinylether/nucleic acid complexes (see, e.g., U.S. Patent Publication No. 20040156909), polycyclic amidinium/nucleic acid complexes (see, e.g., U.S. Patent Publication No. 20030220289), nanocapsule and microcap-

sule compositions (see, e.g., AU 2002358514; PCT Publication No. WO 02/096551), stabilized mixtures of liposomes and emulsions (see, e.g., EP1304160), porphyrin/nucleic acid complexes (see, e.g., U.S. Pat. No. 6,620,805), lipid-nucleic acid complexes (see, e.g., U.S. Patent Publication No. 20030203865), nucleic acid micro-emulsions (see, e.g., U.S. Patent Publication No. 20050037086), and cationic lipid-based compositions (see, e.g., U.S. Patent Publication No. 20050234232). One skilled in the art will appreciate that the anti-ApoB siRNA of the present invention can also be delivered as a naked siRNA molecule.

V. Stable Nucleic Acid-Lipid Particles (SNALPs) and Properties Thereof

[0150] The stable nucleic acid-lipid particles or, alternatively, SNALPs typically comprise an siRNA molecule that targets ApoB expression, a cationic lipid (e.g., a cationic lipid of Formula I or II) and a non-cationic lipid. The SNALP can further comprise a bilayer stabilizing component (i.e., a conjugated lipid that inhibits aggregation of the SNALPs). Preferably the SNALP comprises an siRNA molecule that targets ApoB expression, a cationic lipid, a non-cationic lipid, and a conjugated lipid that inhibits aggregation of the SNALPs. The nucleic acid-lipid particles may comprise at least 1, 2, 3, 4, 5, or more siRNA molecules comprising the sequences set forth in Table 1, rows A-F of Table 2, and Tables 3-7. In some embodiments, the nucleic acid-lipid particles comprise an siRNA molecule that targets ApoB and an siRNA molecules that targets another gene of interest (e.g., microsomal triglyceride transfer protein (MTP), acyl-CoA cholesterol acyl transferase (ACAT), farnesoid X receptor (FXR), 5-hydroxy-3-methylglutaryl-coenzyme A reductase (HMGR)).

[0151] The SNALPs of the present invention typically have a mean diameter of about 50 nm to about 150 nm, more typically about 60 nm to about 130 nm, more typically about 70 nm to about 110 nm, most typically about 70 to about 90 nm, and are substantially nontoxic. In addition, the nucleic acids present in the SNALPs of the present invention are resistant in aqueous solution to degradation with a nuclease.

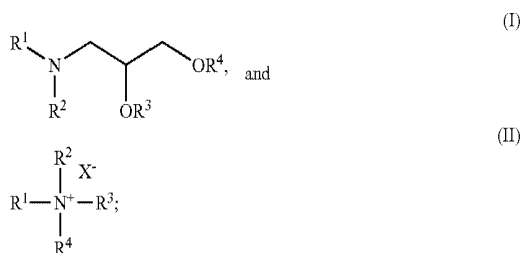
[0152] The lipid-nucleic acid particles of the present invention typically comprise a nucleic acid, a cationic lipid, a non-cationic lipid, and can further comprise a PEG-lipid conjugate. The cationic lipid typically comprises from about 2 mol % to about 60 mol %, from about 5 mol % to about 50 mol %, from about 10 mol % to about 45 mol %, from about 20 mol % to about 40 mol %, or from about 30 mol % to about 40 mol % of the total lipid present in said particle. The non-cationic lipid typically comprises from about 5 mol % to about 90 mol %, from about 10 mol % to about 85 mol %, from about 20 mol % to about 80 mol %, from about 30 mol % to about 70 mol %, from about 40 mol % to about 60 mol % or about 48 mol % of the total lipid present in said particle. The PEG-lipid conjugate typically comprises from about 0.5 mol % to about 20 mol %, from about 1.5 mol % to about 18 mol %, from about 4 mol % to about 15 mol %, from about 5 mol % to about 12 mol %, or about 2 mol % of the total lipid present in said particle. The nucleic acid-lipid particles of the present invention may further comprise cholesterol. If present, the cholesterol typically comprises from about 0 mol % to about 10 mol %, about 2 mol % to about 10 mol %, about 10 mol % to about 60 mol %, from about 12 mol % to about 58 mol %, from

about 20 mol % to about 55 mol %, or about 48 mol % of the total lipid present in said particle. It will be readily apparent to one of skill in the art that the proportions of the components of the nucleic acid-lipid particles may be varied. For example for systemic delivery, the cationic lipid may comprise from about 5 mol % to about 15 mol % of the total lipid present in said particle and for local or regional delivery, the cationic lipid may comprise from about 30 mol % to about 50 mol %, or about 40 mol % of the total lipid present in the particle.

[0153] A. Cationic Lipids

[0154] Various suitable cationic lipids may be used in the present invention, either alone or in combination with one or more other cationic lipid species or neutral lipid species.

[0155] Suitable cationic lipids include, for example, DLinDMA, DLenDMA, DODAC, DOTMA, DDAB, DOTAP, DOSPA, DOGS, DC-Chol and DMRIE, or combinations thereof. A number of these lipids and related analogs, which are also useful in the present invention, have been described in U.S. Pat. Nos. 5,208,036, 5,264,618, 5,279,833, 5,283,185, 5,753,613 and 5,785,992. Additionally, a number of commercial preparations of cationic lipids are available and can be used in the present invention. These include, for example, LIPOFECTIN® (commercially available cationic liposomes comprising DOTMA and DOPE, from GIBCO/BRL, Grand Island, N.Y., USA); LIPOFECTAMINE® (commercially available cationic liposomes comprising DOSPA and DOPE, from GIBCO/BRL); and TRANSFECTAM® (commercially available cationic liposomes comprising DOGS from Promega Corp., Madison, Wis., USA). In addition, cationic lipids of Formula I and Formula II can be used in the present invention. Cationic lipids of Formula I and II have the following structures:



wherein R¹ and R² are independently selected and are H or C₁-C₃ alkyls. R³ and R⁴ are independently selected and are alkyl groups having from about 10 to about 20 carbon atoms; at least one of R³ and R⁴ comprises at least two sites of unsaturation. In one embodiment, R³ and R⁴ are both the same, i.e., R³ and R⁴ are both linoleyl (C18), etc. In another embodiment, R³ and R⁴ are different, i.e., R³ is myristyl (C14) and R⁴ is linoleyl (C18). In some embodiments, the cationic lipids of the present invention are symmetrical, i.e., R³ and R⁴ are both the same. In another preferred embodiment, both R³ and R⁴ comprise at least two sites of unsaturation. In some embodiments, R³ and R⁴ are independently selected from dodecadienyl, tetradecadienyl, hexadecadienyl, linoleyl, and icosadienyl. In some embodiments, R³ and R⁴ are both linoleyl. In some embodiments, R³ and R⁴ comprise at least three sites of unsaturation and are independently selected from, e.g., dodecatrienyl, tetradecatrienyl, hexadecatrienyl, linolenyl, and icosatrienyl.

[0156] The cationic lipids of Formula I and Formula II described herein typically carry a net positive charge at a selected pH, such as physiological pH. It has been surprisingly found that cationic lipids comprising alkyl chains with multiple sites of unsaturation, e.g., at least two or three sites of unsaturation, are particularly useful for forming lipid-nucleic acid particles with increased membrane fluidity. A number of cationic lipids and related analogs, which are also useful in the present invention, have been described in co-pending U.S. Ser. No. 08/316,399; U.S. Pat. Nos. 5,208,036, 5,264,618, 5,279,833 and 5,283,185, and WO 96/10390.

[0157] Additional suitable cationic lipids include, e.g., dioctadecyldimethylammonium ("DODMA"), Distearoyldimethylammonium ("DSDMA"), N,N-dioleoyl-N,N-dimethylammonium chloride ("DODAC"); N-(2,3-dioleoyloxy)propyl-N,N,N-trimethylammonium chloride ("DOTMA"); N,N-distearyl-N,N-dimethylammonium bromide ("DDAB"); N-(2,3-dioleoyloxy)propyl-N,N,N-trimethylammonium chloride ("DOTAP"); 3-(N-(N',N'-dimethylaminoethane)-carbamoyl)cholesterol ("DC-Chol") and N-(1,2-dimyristyloxyprop-3-yl)-N,N-dimethyl-N-hydroxyethyl ammonium bromide ("DMRIE"). A number of these lipids and related analogs, which are also useful in the present invention, have been described in U.S. Pat. Nos. 5,208,036, 5,264,618, 5,279,833, 5,283,185, 5,753,613 and 5,785,992.

[0158] B. Non-Cationic Lipids

[0159] The non-cationic lipids used in the present invention can be any of a variety of neutral uncharged, zwitterionic or anionic lipids capable of producing a stable complex. They are preferably neutral, although they can alternatively be positively or negatively charged. Examples of non-cationic lipids useful in the present invention include: phospholipid-related materials, such as lecithin, phosphatidylethanolamine, lysolecithin, lysophosphatidylethanolamine, phosphatidylserine, phosphatidylinositol, sphingomyelin, cephalin, cardiolipin, phosphatidic acid, cerebrosides, dicytylphosphate, distearoylphosphatidylcholine (DSPC), dioleoylphosphatidylcholine (DOPC), dipalmitoylphosphatidylcholine (DPPC), dioleoylphosphatidylglycerol (DOPG), dipalmitoylphosphatidylglycerol (DPPG), dioleoyl-phosphatidylethanolamine (DOPE), palmitoyloleoylphosphatidylcholine (POPC), palmitoyloleoyl-phosphatidylethanolamine (POPE) and dioleoyl-phosphatidylethanolamine 4-(N-maleimidomethyl)-cyclohexane-1-carboxylate (DOPE-mal), dipalmitoyl phosphatidyl ethanolamine (DPPE), dimyristoylphosphoethanolamine (DMPE), distearoyl-phosphatidyl-ethanolamine (DSPE), 16-O-monomethyl PE, 16-O-dimethyl PE, 18-1-trans PE, 1-stearoyl-2-oleoyl-phosphatidylethanolamine (SOPE), and 1,2-dielaidoyl-sn-glycero-3-phosphoethanolamine (transDOPE). Non-cationic lipids or sterols such as cholesterol may be present. Additional nonphosphorous containing lipids are, e.g., stearylamine, dodecylamine, hexadecylamine, acetyl palmitate, glycerol-ceratinoleate, hexadecyl stearate, isopropyl myristate, amphoteric acrylic polymers, triethanolamine-lauryl sulfate, alkyl-aryl sulfate polyethoxylated fatty acid amides, dioctadecyldimethyl ammonium bromide and the like, diacylphosphatidylcholine, diacylphosphatidylethanolamine, ceramide, sphingomyelin, cephalin, and cerebrosides. Other lipids such as lysophosphatidylcholine and lysophosphatidylethanolamine may be present. Non-cationic lipids also

include polyethylene glycol-based polymers such as PEG 2000, PEG 5000 and polyethylene glycol conjugated to phospholipids or to ceramides (referred to as PEG-Cer), as described in co-pending U.S. Ser. No. 08/316,429.

[0160] In preferred embodiments, the non-cationic lipids are diacylphosphatidylcholine (e.g., distearoylphosphatidylcholine, dioleoylphosphatidylcholine, dipalmitoylphosphatidylcholine and dilinoleoylphosphatidylcholine), diacylphosphatidylethanolamine (e.g., dioleoylphosphatidylethanolamine and palmitoyloleoylphosphatidylethanolamine), ceramide or sphingomyelin. The acyl groups in these lipids are preferably acyl groups derived from fatty acids having C₁₀-C₂₄ carbon chains. More preferably the acyl groups are lauroyl, myristoyl, palmitoyl, stearoyl or oleoyl. In particularly preferred embodiments, the non-cationic lipid can be cholesterol, 1,2-sn-dioleoylphosphatidylethanolamine, or egg sphingomyelin (ESM).

[0161] C. Bilayer Stabilizing Component

[0162] In addition to cationic and non-cationic lipids, the nucleic acid-lipid particles (e.g., SNALPs and SPLPs) of the present invention can further comprise a bilayer stabilizing component (BSC) such as an ATTA-lipid or a PEG-lipid, such as PEG coupled to dialkylxypropyls (PEG-DAA) as described in, e.g., WO 05/026372, PEG coupled to diacylglycerol (PEG-DAG) as described in, e.g., U.S. Patent Publication Nos. 20030077829 and 2005008689, PEG coupled to phosphatidylethanolamine (PE) (PEG-PE), or PEG conjugated to ceramides, or a mixture thereof (see, U.S. Pat. No. 5,885,613). In one preferred embodiment, the BSC is a conjugated lipid that inhibits aggregation of the nucleic acid-lipid particles. Suitable conjugated lipids include, but are not limited to PEG-lipid conjugates, ATTA-lipid conjugates, cationic-polymer-lipid conjugates (CPLs) or mixtures thereof. In one preferred embodiment, the nucleic acid-lipid particles comprise either a PEG-lipid conjugate or an ATTA-lipid conjugate together with a CPL.

[0163] PEG is a polyethylene glycol, a linear, water-soluble polymer of ethylene PEG repeating units with two terminal hydroxyl groups. PEGs are classified by their molecular weights; for example, PEG 2000 has an average molecular weight of about 2,000 daltons, and PEG 5000 has an average molecular weight of about 5,000 daltons. PEGs are commercially available from Sigma Chemical Co. and other companies and include, for example, the following: monomethoxypolyethylene glycol (MePEG-OH), monomethoxypolyethylene glycol-succinate (MePEG-S), monomethoxypolyethylene glycol-succinimidyl succinate (MePEG-S-NHS), monomethoxypolyethylene glycol-amine (MePEG-NH₂), monomethoxypolyethylene glycol-tresylate (MePEG-TRES), and monomethoxypolyethylene glycol-imidazolyl-carbonyl (MePEG-IM). In addition, monomethoxypolyethyleneglycol-acetic acid (MePEG-CH₂COOH), is particularly useful for preparing the PEG-lipid conjugates including, e.g., PEG-DAA conjugates.

[0164] In some embodiments, the PEG has an average molecular weight of from about 550 daltons to about 10,000 daltons, more preferably of about 750 daltons to about 5,000 daltons, more preferably of about 1,000 daltons to about 5,000 daltons, more preferably of about 1,500 daltons to about 3,000 daltons and, even more preferably, of about 2,000 daltons, or about 750 daltons. The PEG can be

optionally substituted by an alkyl, alkoxy, acyl or aryl group. PEG can be conjugated directly to the lipid or may be linked to the lipid via a linker moiety. Any linker moiety suitable for coupling the PEG to a lipid can be used including, e.g., non-ester containing linker moieties and ester-containing linker moieties. In some embodiments, the linker moiety is a non-ester containing linker moiety. As used herein, the term "non-ester containing linker moiety" refers to a linker moiety that does not contain a carboxylic ester bond (—OC(O)—). Suitable non-ester containing linker moieties include, but are not limited to, amido (—C(O)NH—), amino (—NR—), carbonyl (—C(O)—), carbamate (—NH-C(O)O—), urea (—NHC(O)NH—), disulphide (—S—S—), ether (—O—), succinyl (—(O)CCH₂CH₂C(O)—), succinimidyl (—NHC(O)CH₂CH₂C(O)NH—), ether, disulphide, etc. as well as combinations thereof (such as a linker containing both a carbamate linker moiety and an amido linker moiety). In some embodiments, a carbamate linker is used to couple the PEG to the lipid.

[0165] In other embodiments, an ester containing linker moiety is used to couple the PEG to the lipid. Suitable ester containing linker moieties include, e.g., carbonate (—OC(O)O—), succinoyl, phosphate esters (—O—(O)POH—O—), sulfonate esters, and combinations thereof.

[0166] Phosphatidylethanolamines having a variety of acyl chain groups of varying chain lengths and degrees of saturation can be conjugated to polyethyleneglycol to form the bilayer stabilizing component. Such phosphatidylethanolamines are commercially available, or can be isolated or synthesized using conventional techniques known to those of skilled in the art. Phosphatidylethanolamines containing saturated or unsaturated fatty acids with carbon chain lengths in the range of C₁₀ to C₂₀ are preferred. Phosphatidylethanolamines with mono- or diunsaturated fatty acids and mixtures of saturated and unsaturated fatty acids can also be used. Suitable phosphatidylethanolamines include, but are not limited to, the following: dimyristoylphosphatidylethanolamine (DMPE), dipalmitoylphosphatidylethanolamine (DPPE), dioleoylphosphatidylethanolamine (DOPE) and distearoylphosphatidylethanolamine (DSPE).

[0167] In some embodiments, the PEG-lipid is a PEG-DAA conjugate has the following formula:



[0168] In Formula VI, R¹ and R² are independently selected and are alkyl groups having from about 10 to about 22 carbon atoms. The long-chain alkyl groups can be saturated or unsaturated. Suitable alkyl groups include, but are not limited to, lauryl (C₁₂), myristyl (C₁₄), palmityl (C₁₆), stearyl (C₁₈) and icosyl (C₂₀). In some embodiments, R¹ and R² are the same, i.e., R¹ and R² are both myristyl (i.e., dimyristyl), R¹ and R² are both stearyl (i.e., distearyl), etc. In some embodiments, the alkyl groups are saturated.

[0169] In Formula VI above, "PEG" is a polyethylene glycol having an average molecular weight ranging of about

550 daltons to about 10,000 daltons, about 750 daltons to about 5,000 daltons, about 1,000 daltons to about 5,000 daltons, about 1,500 daltons to about 3,000 daltons, about 2,000 daltons, or about 750 daltons. The PEG can be optionally substituted with alkyl, alkoxy, acyl or aryl. In some embodiments, the terminal hydroxyl group is substituted with a methoxy or methyl group.

[0170] In Formula VI, above, "L" is a non-ester containing linker moiety or an ester containing linker moiety. In some embodiments, L is a non-ester containing linker moiety. Suitable non-ester containing linkers include, but are not limited to, an amido linker moiety, an amino linker moiety, a carbonyl linker moiety, a carbamate linker moiety, a urea linker moiety, an ether linker moiety, a disulphide linker moiety, a succinamidyl linker moiety and combinations thereof. In some embodiments, the non-ester containing linker moiety is a carbamate linker moiety (i.e., a PEG-C-DAA conjugate), an amido linker moiety (i.e., a PEG-A-DAA conjugate), or a succinamidyl linker moiety (i.e., a PEG-S-DAA conjugate).

[0171] The PEG-DAA conjugates are synthesized using standard techniques and reagents known to those of skill in the art. It will be recognized that the PEG-DAA conjugates will contain various amide, amine, ether, thio, carbamate and urea linkages. Those of skill in the art will recognize that methods and reagents for forming these bonds are well known and readily available. See, e.g., March, *ADVANCED ORGANIC CHEMISTRY* (Wiley 1992), Larock, *COMPREHENSIVE ORGANIC TRANSFORMATIONS* (VCH 1989); and Furniss, *VOGEL'S TEXTBOOK OF PRACTICAL ORGANIC CHEMISTRY* 5th ed. (Longman 1989). It will also be appreciated that any functional groups present may require protection and deprotection at different points in the synthesis of the PEG-DAA conjugates. Those of skill in the art will recognize that such techniques are well known. See, e.g., Green and Wuts, *PROTECTIVE GROUPS IN ORGANIC SYNTHESIS* (Wiley 1991).

[0172] In some embodiments, the PEG-DAA conjugate is a dilauryloxypropyl (C12)-PEG conjugate, dimyristyloxypropyl (C14)-PEG conjugate, a dipalmitoyloxypropyl (C16)-PEG conjugate or a disteryloxypropyl (C18)-PEG conjugate. Those of skill in the art will readily appreciate that other dialkyloxypropyls can be used in the PEG-DAA conjugates of the present invention.

[0173] In addition to the foregoing, it will be readily apparent to those of skill in the art that other hydrophilic polymers can be used in place of PEG. Examples of suitable polymers that can be used in place of PEG include, but are not limited to, polyvinylpyrrolidone, polymethylloxazoline, polyethylloxazoline, polyhydroxypropyl methacrylamide, polymethacrylamide and polydimethylacrylamide, polylactic acid, polyglycolic acid, and derivatized celluloses, such as hydroxymethylcellulose or hydroxyethylcellulose.

[0174] In addition to the foregoing components, the SNALPs and SPLPs of the present invention can further comprise cationic poly(ethylene glycol) (PEG) lipids, or CPLs, that have been designed for insertion into lipid bilayers to impart a positive charge (see, Chen, et al., *Bioconj. Chem.* 11:433-437 (2000)). Suitable SPLPs and SPLP-CPLs for use in the present invention, and methods of making and using SPLPs and SPLP-CPLs, are disclosed, e.g., in U.S. Pat. No. 6,852,334 and WO 00/62813. Cationic

polymer lipids (CPLs) useful in the present invention have the following architectural features: (1) a lipid anchor, such as a hydrophobic lipid, for incorporating the CPLs into the lipid bilayer; (2) a hydrophilic spacer, such as a polyethylene glycol, for linking the lipid anchor to a cationic head group; and (3) a polycationic moiety, such as a naturally occurring amino acid, to produce a protonizable cationic head group.

[0175] Suitable CPL include compounds of Formula VII:



wherein A, W and Y are as described below.

[0176] With reference to Formula VII, "A" is a lipid moiety such as an amphipathic lipid, a neutral lipid or a hydrophobic lipid that acts as a lipid anchor. Suitable lipid examples include vesicle-forming lipids or vesicle adopting lipids and include, but are not limited to, diacylglycerols, dialkylglycerols, N-N-dialkylaminos, 1,2-diacyloxy-3-aminopropanes and 1,2-dialkyl-3-aminopropanes.

[0177] "W" is a polymer or an oligomer, such as a hydrophilic polymer or oligomer. Typically, the hydrophilic polymer is a biocompatible polymer that is nonimmunogenic or possesses low inherent immunogenicity. Alternatively, the hydrophilic polymer can be weakly antigenic if used with appropriate adjuvants. Suitable nonimmunogenic polymers include, but are not limited to, PEG, polyamides, polylactic acid, polyglycolic acid, polylactic acid/polyglycolic acid copolymers and combinations thereof. In some embodiments, the polymer has a molecular weight of from about 250 to about 7000 daltons.

[0178] "Y" is a polycationic moiety. The term polycationic moiety refers to a compound, derivative, or functional group having a positive charge, typically at least 2 positive charges at a selected pH, typically physiological pH. Suitable polycationic moieties include basic amino acids and their derivatives such as arginine, asparagine, glutamine, lysine and histidine; spermine; spermidine; cationic dendrimers; polyamines; polyamine sugars; and amino polysaccharides. The polycationic moieties can be linear, such as linear tetralysine, branched or dendrimeric in structure. Polycationic moieties have between about 2 to about 15 positive charges, between about 2 to about 12 positive charges, or between about 2 to about 8 positive charges at selected pH values. The selection of which polycationic moiety to employ may be determined by the type of liposome application which is desired.

[0179] The charges on the polycationic moieties can be either distributed around the entire liposome moiety, or alternatively, they can be a discrete concentration of charge density in one particular area of the liposome moiety e.g., a charge spike. If the charge density is distributed on the liposome, the charge density can be equally distributed or unequally distributed. All variations of charge distribution of the polycationic moiety are encompassed by the present invention.

[0180] The lipid "A," and the nonimmunogenic polymer "W," can be attached by various methods and preferably, by covalent attachment. Methods known to those of skill in the art can be used for the covalent attachment of "A" and "W." Suitable linkages include, but are not limited to, amide, amine, carboxyl, carbonate, carbamate, ester and hydrazone linkages. It will be apparent to those skilled in the art that

“A” and “W” must have complementary functional groups to effectuate the linkage. The reaction of these two groups, one on the lipid and the other on the polymer, will provide the desired linkage. For example, when the lipid is a diacylglycerol and the terminal hydroxyl is activated, for instance with NHS and DCC, to form an active ester, and is then reacted with a polymer which contains an amino group, such as with a polyamide (see, U.S. Pat. Nos. 6,320,017 and 6,586,559), an amide bond will form between the two groups.

[0181] In certain instances, the polycationic moiety can have a ligand attached, such as a targeting ligand or a chelating moiety for complexing calcium. Preferably, after the ligand is attached, the cationic moiety maintains a positive charge. In certain instances, the ligand that is attached has a positive charge. Suitable ligands include, but are not limited to, a compound or device with a reactive functional group and include lipids, amphipathic lipids, carrier compounds, bioaffinity compounds, biomaterials, biopolymers, biomedical devices, analytically detectable compounds, therapeutically active compounds, enzymes, peptides, proteins, antibodies, immune stimulators, radiolabels, fluorogens, biotin, drugs, haptens, DNA, RNA, polysaccharides, liposomes, virosomes, micelles, immunoglobulins, functional groups, other targeting moieties, or toxins.

VI. Preparation of SNALPs

[0182] The present invention provides a method of preparing serum-stable nucleic acid-lipid particles in which an interfering RNA (e.g., an anti-ApoB siRNA) is encapsulated in a lipid bilayer and is protected from degradation. The particles made by the methods of this invention typically have a size of about 50 nm to about 150 nm, about 60 nm to about 130 nm, about 70 nm to about 110 nm, or about 70 nm to about 90 nm. The particles can be formed by any method known in the art including, but not limited to: a continuous mixing method, a direct dilution process, a detergent dialysis method, or a modification of a reverse-phase method which utilizes organic solvents to provide a single phase during mixing of the components.

[0183] In preferred embodiments, the cationic lipids are lipids of Formula I and II or combinations thereof. In other preferred embodiments, the non-cationic lipids are ESM, DOPE, DOPC, DPPE, DMPE, 16:0 Monomethyl Phosphatidylethanolamine, 16:0 Dimethyl Phosphatidylethanolamine, 18:1 Trans Phosphatidylethanolamine, 18:0 18:1 Phosphatidylethanolamine (SOPE), 1,2-dielaidoyl-sn-glycero-3-phosphoethanolamine (transDOPE), 16:0 18:1 Phosphatidylethanolamine, DSPE, polyethylene glycol-based polymers (e.g., PEG 2000, PEG 5000, PEG-modified diacylglycerols, or PEG-modified dialkylxypropyls), distearoylphosphatidylcholine (DSPC), cholesterol, or combinations thereof. In still other preferred embodiments, the organic solvents are methanol, chloroform, methylene chloride, ethanol, diethyl ether or combinations thereof.

[0184] In a particularly preferred embodiment, the present invention provides for nucleic acid-lipid particles produced via a continuous mixing method, e.g., process that includes providing an aqueous solution comprising a nucleic acid such as an siRNA, in a first reservoir, and providing an organic lipid solution in a second reservoir, and mixing the aqueous solution with the organic lipid solution such that the

organic lipid solution mixes with the aqueous solution so as to substantially instantaneously produce a liposome encapsulating the nucleic acid (e.g., siRNA). This process and the apparatus for carrying this process are described in detail in U.S. Patent Publication No. 20040142025.

[0185] The action of continuously introducing lipid and buffer solutions into a mixing environment, such as in a mixing chamber, causes a continuous dilution of the lipid solution with the buffer solution, thereby producing a liposome substantially instantaneously upon mixing. As used herein, the phrase “continuously diluting a lipid solution with a buffer solution” (and variations) generally means that the lipid solution is diluted sufficiently rapidly in a hydration process with sufficient force to effectuate vesicle generation. By mixing the aqueous solution comprising a nucleic acid with the organic lipid solution, the organic lipid solution undergoes a continuous stepwise dilution in the presence of the buffer solution (i.e., aqueous solution) to produce a nucleic acid-lipid particle.

[0186] The serum-stable nucleic acid-lipid particles formed using the continuous mixing method typically have a size of from about 50 nm to about 150 nm, from about 60 nm to about 130 nm, from about 70 nm to about 110 nm, or from about 70 nm to about 90 nm. The particles thus formed do not aggregate and are optionally sized to achieve a uniform particle size.

[0187] In another embodiment, the present invention provides for nucleic acid-lipid particles produced via a direct dilution process that includes forming a liposome solution and immediately and directly introducing the liposome solution into a collection vessel containing a controlled amount of dilution buffer. In preferred aspects, the collection vessel includes one or more elements configured to stir the contents of the collection vessel to facilitate dilution. In one aspect, the amount of dilution buffer present in the collection vessel is substantially equal to the volume of liposome solution introduced thereto. As a non-limiting example, liposome solution in 45% ethanol when introduced into the collection vessel containing an equal volume of ethanol will advantageously yield smaller particles in about 22.5%, about 20%, or about 15% ethanol.

[0188] In even another embodiment, the present invention provides for nucleic acid-lipid particles produced via a direct dilution process in which a third reservoir containing dilution buffer is fluidly coupled to a second mixing region. In this embodiment, the liposome solution formed in a first mixing region is immediately and directly mixed with dilution buffer in the second mixing region. In preferred aspects, the second mixing region includes a T-connector arranged so that the liposome solution and the dilution buffer flows meet as opposing 180° flows, however, connectors providing shallower angles can be used, e.g., from about 27° to about 180°. A pump mechanism delivers a controllable flow of buffer to the second mixing region. In one aspect, the flow rate of dilution buffer provided to the second mixing region is controlled to be substantially equal to the flow rate of liposome solution introduced thereto from the first mixing region. This embodiment advantageously allows for more control of the flow of dilution buffer mixing with the liposome solution in the second mixing region, and therefore also the concentration of liposome solution in buffer throughout the second mixing process. Such control of the

dilution buffer flow rate advantageously allows for small particle size formation at reduced concentrations.

[0189] These processes and the apparatus for carrying out these direct dilution processes is described in detail in U.S. Provisional Patent Application No. 60/703,380 filed Jul. 27, 2005.

[0190] The serum-stable nucleic acid-lipid particles formed using the direct dilution process typically have a size of from about 50 nm to about 150 nm, from about 60 nm to about 130 nm, from about 70 nm to about 110 nm, or from about 70 nm to about 90 nm. The particles thus formed do not aggregate and are optionally sized to achieve a uniform particle size.

[0191] In some embodiments, the particles are formed using detergent dialysis. Without intending to be bound by any particular mechanism of formation, a plasmid or other nucleic acid (e.g., siRNA) is contacted with a detergent solution of cationic lipids to form a coated nucleic acid complex. These coated nucleic acids can aggregate and precipitate. However, the presence of a detergent reduces this aggregation and allows the coated nucleic acids to react with excess lipids (typically, non-cationic lipids) to form particles in which the plasmid or other nucleic acid is encapsulated in a lipid bilayer. Thus, serum-stable nucleic acid-lipid particles can be prepared as follows:

[0192] (a) combining a nucleic acid with cationic lipids in a detergent solution to form a coated nucleic acid-lipid complex;

[0193] (b) contacting non-cationic lipids with the coated nucleic acid-lipid complex to form a detergent solution comprising a nucleic acid-lipid complex and non-cationic lipids; and

[0194] (c) dialyzing the detergent solution of step (b) to provide a solution of serum-stable nucleic acid-lipid particles, wherein the nucleic acid is encapsulated in a lipid bilayer and the particles are serum-stable and have a size of from about 50 to about 150 nm.

[0195] An initial solution of coated nucleic acid-lipid complexes is formed by combining the nucleic acid with the cationic lipids in a detergent solution.

[0196] In these embodiments, the detergent solution is preferably an aqueous solution of a neutral detergent having a critical micelle concentration of 15-300 mM, more preferably 20-50 mM. Examples of suitable detergents include, for example, N,N'-((octanoylimino)-bis-(trimethylene))-bis-(D-gluconamide) (BIGCHAP); BRIJ 35; Deoxy-BIGCHAP; dodecylpoly(ethylene glycol) ether; Tween 20; Tween 40; Tween 60; Tween 80; Tween 85; Mega 8; Mega 9; Zwittergent® 3-08; Zwittergent® 3-10; Triton X-405; hexyl-, heptyl-, octyl- and nonyl- β -D-glucopyranoside; and heptylthiogluco-pyranoside; with octyl β -D-glucopyranoside and Tween-20 being the most preferred. The concentration of detergent in the detergent solution is typically about 100 mM to about 2 M, preferably from about 200 mM to about 1.5 M.

[0197] The cationic lipids and nucleic acids will typically be combined to produce a charge ratio (+/-) of about 1:1 to about 20:1, in a ratio of about 1:1 to about 12:1, or in a ratio of about 2:1 to about 6:1. Additionally, the overall concentration of nucleic acid in solution will typically be from

about 25 μ g/mL to about 1 mg/mL, from about 25 μ g/mL to about 200 μ g/mL, or from about 50 μ g/mL to about 100 μ g/mL. The combination of nucleic acids and cationic lipids in detergent solution is kept, typically at room temperature, for a period of time which is sufficient for the coated complexes to form. Alternatively, the nucleic acids and cationic lipids can be combined in the detergent solution and warmed to temperatures of up to about 37° C., about 50° C., about 60° C., or about 70° C. For nucleic acids which are particularly sensitive to temperature, the coated complexes can be formed at lower temperatures, typically down to about 4° C.

[0198] In some embodiments, the nucleic acid to lipid ratios (mass/mass ratios) in a formed nucleic acid-lipid particle will range from about 0.01 to about 0.2, from about 0.03 to about 0.01 or from about 0.01 to about 0.08. The ratio of the starting materials also falls within this range. In other embodiments, the nucleic acid-lipid particle preparation uses about 400 μ g nucleic acid per 10 mg total lipid or a nucleic acid to lipid ratio (mg:mg) of about 0.01 to about 0.08 and, more preferably, about 0.04, which corresponds to 1.25 mg of total lipid per 50 μ g of nucleic acid.

[0199] The detergent solution of the coated nucleic acid-lipid complexes is then contacted with non-cationic lipids to provide a detergent solution of nucleic acid-lipid complexes and non-cationic lipids. The non-cationic lipids which are useful in this step include, diacylphosphatidylcholine, diacylphosphatidylethanolamine, ceramide, sphingomyelin, cephalin, cardiolipin, and cerebrosides. In preferred embodiments, the non-cationic lipids are diacylphosphatidylcholine, diacylphosphatidylethanolamine, ceramide or sphingomyelin. The acyl groups in these lipids are preferably acyl groups derived from fatty acids having C₁₀-C₂₄ carbon chains. More preferably the acyl groups are lauroyl, myristoyl, palmitoyl, stearyl or oleoyl. In particularly preferred embodiments, the non-cationic lipid will be 1,2-sn-dioleoylphosphatidylethanolamine (DOPE), palmitoyl oleoyl phosphatidylcholine (POPC), egg phosphatidylcholine (EPC), distearoylphosphatidylcholine (DSPC), cholesterol, or a mixture thereof. In the most preferred embodiments, the nucleic acid-lipid particles will be fusogenic particles with enhanced properties in vivo and the non-cationic lipid will be DSPC or DOPE. In addition, the nucleic acid-lipid particles of the present invention may further comprise cholesterol. In other preferred embodiments, the non-cationic lipids will further comprise polyethylene glycol-based polymers such as PEG 2000, PEG 5000 and polyethylene glycol conjugated to a diacylglycerol, a ceramide or a phospholipid, as described in U.S. Pat. No. 5,820,873 and U.S. Patent Publication No. 20030077829. In further preferred embodiments, the non-cationic lipids will further comprise polyethylene glycol-based polymers such as PEG 2000, PEG 5000 and polyethylene glycol conjugated to a dialkylxypropyl.

[0200] The amount of non-cationic lipid which is used in the present methods is typically about 2 to about 20 mg of total lipids to 50 μ g of nucleic acid. Preferably, the amount of total lipid is from about 5 to about 10 mg per 50 μ g of nucleic acid.

[0201] Following formation of the detergent solution of nucleic acid-lipid complexes and non-cationic lipids, the detergent is removed, preferably by dialysis. The removal of

the detergent results in the formation of a lipid-bilayer which surrounds the nucleic acid providing serum-stable nucleic acid-lipid particles which have a size of from about 50 nm to about 150 nm, more typically about 100 nm to about 130 nm, more typically about 110 nm to about 115 nm, most typically about 65 to 95 nm. The particles thus formed do not aggregate and are optionally sized to achieve a uniform particle size.

[0202] The serum-stable nucleic acid-lipid particles can be sized by any of the methods available for sizing liposomes. The sizing may be conducted in order to achieve a desired size range and relatively narrow distribution of particle sizes.

[0203] Several techniques are available for sizing the particles to a desired size. One sizing method, used for liposomes and equally applicable to the present particles is described in U.S. Pat. No. 4,737,323. Sonicating a particle suspension either by bath or probe sonication produces a progressive size reduction down to particles of less than about 50 nm in size. Homogenization is another method which relies on shearing energy to fragment larger particles into smaller ones. In a typical homogenization procedure, particles are recirculated through a standard emulsion homogenizer until selected particle sizes, typically between about 60 and about 80 nm, are observed. In both methods, the particle size distribution can be monitored by conventional laser-beam particle size discrimination, or QELS.

[0204] Extrusion of the particles through a small-pore polycarbonate membrane or an asymmetric ceramic membrane is also an effective method for reducing particle sizes to a relatively well-defined size distribution. Typically, the suspension is cycled through the membrane one or more times until the desired particle size distribution is achieved. The particles may be extruded through successively smaller-pore membranes, to achieve a gradual reduction in size.

[0205] In another group of embodiments, the present invention provides a method for the preparation of serum-stable nucleic acid-lipid particles, comprising:

[0206] (a) preparing a mixture comprising cationic lipids and non-cationic lipids in an organic solvent;

[0207] (b) contacting an aqueous solution of nucleic acid with the mixture in step (a) to provide a clear single phase; and

[0208] (c) removing the organic solvent to provide a suspension of nucleic acid-lipid particles, wherein the nucleic acid is encapsulated in a lipid bilayer, and the particles are stable in serum and have a size of from about 50 to about 150 nm.

[0209] The nucleic acids (e.g., siRNA), cationic lipids and non-cationic lipids which are useful in this group of embodiments are as described for the detergent dialysis methods above.

[0210] The selection of an organic solvent will typically involve consideration of solvent polarity and the ease with which the solvent can be removed at the later stages of particle formation. The organic solvent, which is also used as a solubilizing agent, is in an amount sufficient to provide a clear single phase mixture of nucleic acid and lipids. Suitable solvents include, but are not limited to, chloroform, dichloromethane, diethylether, cyclohexane, cyclopentane,

benzene, toluene, methanol, or other aliphatic alcohols such as propanol, isopropanol, butanol, tert-butanol, iso-butanol, pentanol and hexanol. Combinations of two or more solvents may also be used in the present invention.

[0211] Contacting the nucleic acid with the organic solution of cationic and non-cationic lipids is accomplished by mixing together a first solution of nucleic acid, which is typically an aqueous solution, and a second organic solution of the lipids. One of skill in the art will understand that this mixing can take place by any number of methods, for example by mechanical means such as by using vortex mixers.

[0212] After the nucleic acid has been contacted with the organic solution of lipids, the organic solvent is removed, thus forming an aqueous suspension of serum-stable nucleic acid-lipid particles. The methods used to remove the organic solvent will typically involve evaporation at reduced pressures or blowing a stream of inert gas (e.g., nitrogen or argon) across the mixture.

[0213] The serum-stable nucleic acid-lipid particles thus formed will typically be sized from about 50 nm to about 150 nm, more typically about 100 nm to about 130 nm, most typically about 110 nm to about 115 nm. To achieve further size reduction or homogeneity of size in the particles, sizing can be conducted as described above.

[0214] In other embodiments, the methods will further comprise adding non-lipid polycations which are useful to effect the delivery to cells using the present compositions. Examples of suitable non-lipid polycations include, but are limited to, hexadimethrine bromide (sold under the brand name POLYBRENE®, from Aldrich Chemical Co., Milwaukee, Wis., USA) or other salts of hexadimethrine. Other suitable polycations include, for example, salts of poly-L-ornithine, poly-L-arginine, poly-L-lysine, poly-D-lysine, polyallylamine and polyethyleneimine.

[0215] In certain embodiments, the formation of the nucleic acid-lipid particles can be carried out either in a mono-phase system (e.g., a Bligh and Dyer monophasic or similar mixture of aqueous and organic solvents) or in a two-phase system with suitable mixing.

[0216] When formation of the complexes is carried out in a mono-phase system, the cationic lipids and nucleic acids are each dissolved in a volume of the mono-phase mixture. Combination of the two solutions provides a single mixture in which the complexes form. Alternatively, the complexes can form in two-phase mixtures in which the cationic lipids bind to the nucleic acid (which is present in the aqueous phase), and "pull" it into the organic phase.

[0217] In another embodiment, serum-stable nucleic acid-lipid particles can be prepared as follows:

[0218] (a) contacting nucleic acids with a solution comprising non-cationic lipids and a detergent to form a nucleic acid-lipid mixture;

[0219] (b) contacting cationic lipids with the nucleic acid-lipid mixture to neutralize a portion of the negative charge of the nucleic acids and form a charge-neutralized mixture of nucleic acids and lipids; and

[0220] (c) removing the detergent from the charge-neutralized mixture to provide the nucleic acid-lipid particles in which the nucleic acids are protected from degradation.

[0221] In one group of embodiments, the solution of non-cationic lipids and detergent is an aqueous solution. Contacting the nucleic acids with the solution of non-cationic lipids and detergent is typically accomplished by mixing together a first solution of nucleic acids and a second solution of the lipids and detergent. One of skill in the art will understand that this mixing can take place by any number of methods, for example, by mechanical means such as by using vortex mixers. Preferably, the nucleic acid solution is also a detergent solution. The amount of non-cationic lipid which is used in the present method is typically determined based on the amount of cationic lipid used, and is typically of from about 0.2 to 5 times the amount of cationic lipid, preferably from about 0.5 to about 2 times the amount of cationic lipid used.

[0222] In some embodiments, the nucleic acids are pre-condensed as described in, e.g., U.S. patent application Ser. No. 09/744,103.

[0223] The nucleic acid-lipid mixture thus formed is contacted with cationic lipids to neutralize a portion of the negative charge which is associated with the nucleic acids (or other polyanionic materials) present. The amount of cationic lipids used will typically be sufficient to neutralize at least 50% of the negative charge of the nucleic acid. Preferably, the negative charge will be at least 70% neutralized, more preferably at least 90% neutralized. Cationic lipids which are useful in the present invention, include, for example, DLinDMA and, DLenDMA. These lipids and related analogs have been described in U.S. Provisional Patent Application Nos. 60/578,075, filed Jun. 7, 2004; 60/610,746, filed Sep. 17, 2004; and 60/679,427, filed May 9, 2005.

[0224] Contacting the cationic lipids with the nucleic acid-lipid mixture can be accomplished by any of a number of techniques, preferably by mixing together a solution of the cationic lipid and a solution containing the nucleic acid-lipid mixture. Upon mixing the two solutions (or contacting in any other manner), a portion of the negative charge associated with the nucleic acid is neutralized. Nevertheless, the nucleic acid remains in an uncondensed state and acquires hydrophilic characteristics.

[0225] After the cationic lipids have been contacted with the nucleic acid-lipid mixture, the detergent (or combination of detergent and organic solvent) is removed, thus forming the nucleic acid-lipid particles. The methods used to remove the detergent will typically involve dialysis. When organic solvents are present, removal is typically accomplished by evaporation at reduced pressures or by blowing a stream of inert gas (e.g., nitrogen or argon) across the mixture.

[0226] The particles thus formed will typically be sized from about 50 nm to several microns, more typically about 50 nm to about 150 nm, even more typically about 100 nm to about 130 nm, most typically about 110 nm to about 115 nm. To achieve further size reduction or homogeneity of size in the particles, the nucleic acid-lipid particles can be sonicated, filtered or subjected to other sizing techniques which are used in liposomal formulations and are known to those of skill in the art.

[0227] In other embodiments, the methods will further comprise adding non-lipid polycations which are useful to effect the lipofection of cells using the present compositions.

Examples of suitable non-lipid polycations include, hexadimethrine bromide (sold under the brand name POLY-BRENE®, from Aldrich Chemical Co., Milwaukee, Wis., USA) or other salts of hexadimethrine. Other suitable polycations include, for example, salts of poly-L-ornithine, poly-L-arginine, poly-L-lysine, poly-D-lysine, polyallylamine and polyethyleneimine. Addition of these salts is preferably after the particles have been formed.

[0228] In another aspect, the serum-stable nucleic acid-lipid particles can be prepared as follows:

[0229] (a) contacting an amount of cationic lipids with nucleic acids in a solution; the solution comprising from about 15-35% water and about 65-85% organic solvent and the amount of cationic lipids being sufficient to produce a +/- charge ratio of from about 0.85 to about 2.0, to provide a hydrophobic nucleic acid-lipid complex;

[0230] (b) contacting the hydrophobic, nucleic acid-lipid complex in solution with non-cationic lipids, to provide a nucleic acid-lipid mixture; and

[0231] (c) removing the organic solvents from the nucleic acid-lipid mixture to provide nucleic acid-lipid particles in which the nucleic acids are protected from degradation.

[0232] The nucleic acids, non-cationic lipids, cationic lipids and organic solvents which are useful in this aspect of the invention are the same as those described for the methods above which used detergents. In one group of embodiments, the solution of step (a) is a mono-phase. In another group of embodiments, the solution of step (a) is two-phase.

[0233] In preferred embodiments, the non-cationic lipids are ESM, DOPE, DOPC, polyethylene glycol-based polymers (e.g., PEG 2000, PEG 5000, PEG-modified diacylglycerols, or PEG-modified dialkylxypropyls), distearoylphosphatidylcholine (DSPC), DPPE, DMPE, 16:0 Monomethyl Phosphatidylethanolamine, 16:0 Dimethyl Phosphatidylethanolamine, 18:1 Trans Phosphatidylethanolamine, 18:0 18:1 Phosphatidylethanolamine (SOPE), 1,2-dielaidoyl-sn-glycero-3-phosphoethanolamine (transDOPE), 16:0 18:1 Phosphatidylethanolamine, DSPE, cholesterol, or combinations thereof. In still other preferred embodiments, the organic solvents are methanol, chloroform, methylene chloride, ethanol, diethyl ether or combinations thereof.

[0234] In one embodiment, the nucleic acid an interfering RNA (i.e., and anti-ApoB siRNA); the cationic lipid is DLinDMA, DLenDMA, DODAC, DDAB, DOTMA, DOSPA, DMRIE, DOGS or combinations thereof; the non-cationic lipid is ESM, DOPE, DAG-PEGs, distearoylphosphatidylcholine (DSPC), DPPE, DMPE, 16:0 Monomethyl Phosphatidylethanolamine, 16:0 Dimethyl Phosphatidylethanolamine, 18:1 Trans Phosphatidylethanolamine, 18:0 18:1 Phosphatidylethanolamine (SOPE), 16:0 18:1 Phosphatidylethanolamine DSPE, cholesterol, or combinations thereof (e.g. DSPC and PEG-DAA); and the organic solvent is methanol, chloroform, methylene chloride, ethanol, diethyl ether or combinations thereof.

[0235] As above, contacting the nucleic acids with the cationic lipids is typically accomplished by mixing together a first solution of nucleic acids and a second solution of the

lipids, preferably by mechanical means such as by using vortex mixers. The resulting mixture contains complexes as described above. These complexes are then converted to particles by the addition of non-cationic lipids and the removal of the organic solvent. The addition of the non-cationic lipids is typically accomplished by simply adding a solution of the non-cationic lipids to the mixture containing the complexes. A reverse addition can also be used. Subsequent removal of organic solvents can be accomplished by methods known to those of skill in the art and also described above.

[0236] The amount of non-cationic lipids which is used in this aspect of the invention is typically an amount of from about 0.2 to about 15 times the amount (on a mole basis) of cationic lipids which was used to provide the charge-neutralized nucleic acid-lipid complex. Preferably, the amount is from about 0.5 to about 9 times the amount of cationic lipids used.

[0237] In yet another embodiment, the nucleic acid-lipid particles prepared by the methods described above are either net charge neutral or carry an overall charge which provides the particles with greater transfection activity. Preferably, the nucleic acid component of the particles is a nucleic acid which interferes with the production of an undesired protein. In some embodiments, the nucleic acid comprises an interfering RNA (i.e., an anti-ApoB siRNA), the non-cationic lipid is egg sphingomyelin and the cationic lipid is DLinDMA or DLenDMA. In some embodiments, the nucleic acid comprises an interfering RNA, the non-cationic lipid is a mixture of DSPC and cholesterol, and the cationic lipid is DLinDMA or DLenDMA. In other preferred embodiments, the non-cationic lipid may further comprise cholesterol.

[0238] A variety of general methods for making SNALP-CPLs (CPL-containing SNALPs) are discussed herein. Two general techniques include "post-insertion" technique, that is, insertion of a CPL into for example, a pre-formed SNALP, and the "standard" technique, wherein the CPL is included in the lipid mixture during for example, the SNALP formation steps. The post-insertion technique results in SNALPs having CPLs mainly in the external face of the SNALP bilayer membrane, whereas standard techniques provide SNALPs having CPLs on both internal and external faces. The method is especially useful for vesicles made from phospholipids (which can contain cholesterol) and also for vesicles containing PEG-lipids (such as PEG-DAAs and PEG-DAGs). Methods of making SNALP-CPL, are taught, for example, in U.S. Pat. Nos. 5,705,385, 6,586,410, 5,981,501, 6,534,484; 6,852,334; U.S. Patent Publication No. 20020072121; and WO 00/62813.

VII. Kits

[0239] The present invention also provides nucleic acid-lipid particles in kit form. The kit will typically be comprised of a one or more containers containing the compositions of the present inventions, preferably in dehydrated form, with instructions for their rehydration and administration. For example, one container of a kit may hold the dehydrated nucleic acid-lipid particles and another container of the kit may hold a buffer suitable for rehydrating the particles.

VIII. Administration of Nucleic Acid-Lipid Particles

[0240] Once formed, the serum-stable nucleic acid-lipid particles of the present invention are useful for the intro-

duction of nucleic acids (i.e., siRNA that silences expression of ApoB) into cells (e.g., a hepatocyte). Accordingly, the present invention also provides methods for introducing a nucleic acid (e.g., a plasmid or and siRNA) into a cell. The methods are carried out in vitro or in vivo by first forming the particles as described above and then contacting the particles with the cells for a period of time sufficient for delivery of the nucleic acid to the cell to occur.

[0241] The nucleic acid-lipid particles of the present invention can be adsorbed to almost any cell type with which they are mixed or contacted. Once adsorbed, the particles can either be endocytosed by a portion of the cells, exchange lipids with cell membranes, or fuse with the cells. Transfer or incorporation of the nucleic acid portion of the particle can take place via any one of these pathways. In particular, when fusion takes place, the particle membrane is integrated into the cell membrane and the contents of the particle combine with the intracellular fluid.

[0242] The nucleic acid-lipid particles of the present invention can be administered either alone or in mixture with a physiologically-acceptable carrier (such as physiological saline or phosphate buffer) selected in accordance with the route of administration and standard pharmaceutical practice. Generally, normal saline will be employed as the pharmaceutically acceptable carrier. Other suitable carriers include, e.g., water, buffered water, 0.4% saline, 0.3% glycine, and the like, including glycoproteins for enhanced stability, such as albumin, lipoprotein, globulin, etc.

[0243] The pharmaceutical carrier is generally added following particle formation. Thus, after the particle is formed, the particle can be diluted into pharmaceutically acceptable carriers such as normal saline.

[0244] The concentration of particles in the pharmaceutical formulations can vary widely, i.e., from less than about 0.05%, usually at or at least about 2-5% to as much as 10 to 30% by weight and will be selected primarily by fluid volumes, viscosities, etc., in accordance with the particular mode of administration selected. For example, the concentration may be increased to lower the fluid load associated with treatment. This may be particularly desirable in patients having atherosclerosis-associated congestive heart failure or severe hypertension. Alternatively, particles composed of irritating lipids may be diluted to low concentrations to lessen inflammation at the site of administration.

[0245] The pharmaceutical compositions of the present invention may be sterilized by conventional, well known sterilization techniques. Aqueous solutions can be packaged for use or filtered under aseptic conditions and lyophilized, the lyophilized preparation being combined with a sterile aqueous solution prior to administration. The compositions can contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions, such as pH adjusting and buffering agents, tonicity adjusting agents and the like, for example, sodium acetate, sodium lactate, sodium chloride, potassium chloride, and calcium chloride. Additionally, the particle suspension may include lipid-protective agents which protect lipids against free-radical and lipid-peroxidative damages on storage. Lipophilic free-radical quenchers, such as α -tocopherol and water-soluble iron-specific chelators, such as ferrioxamine, are suitable.

[0246] The nucleic acid-lipid particles can be incorporated into a broad range of topical dosage forms including, but not

limited to, gels, oils, emulsions, topical creams, pastes, ointments, lotions, foams, and the like.

[0247] A. In Vivo Administration

[0248] Systemic delivery for in vivo gene therapy, i.e., delivery of a therapeutic nucleic acid to a distal target cell via body systems such as the circulation, has been achieved using nucleic acid-lipid particles such as those disclosed in WO 96/40964, U.S. Pat. Nos. 5,705,385, 5,976,567, 5,981,501, and 6,410,328. This latter format provides a fully encapsulated nucleic acid-lipid particle that protects the nucleic acid from nuclease degradation in serum, is nonimmunogenic, is small in size and is suitable for repeat dosing.

[0249] For in vivo administration, administration can be in any manner known in the art, e.g., by injection, oral administration, inhalation (e.g., intranasal or intratracheal), transdermal application, or rectal administration. Administration can be accomplished via single or divided doses. The pharmaceutical compositions can be administered parenterally, i.e., intraarticularly, intravenously, intraperitoneally, subcutaneously, or intramuscularly. In some embodiments, the pharmaceutical compositions are administered intravenously or intraperitoneally by a bolus injection (see, e.g., Stadler, et al., U.S. Pat. No. 5,286,634). Intracellular nucleic acid delivery has also been discussed in Straubinger, et al., *Methods Enzymol.* Academic Press, New York. 101:512 (1983); Mannino, et al., *Biotechniques* 6:682 (1988); Nicolau, et al., *Crit. Rev. Ther. Drug Carrier Syst.* 6:239 (1989), and Behr, *Acc. Chem. Res.* 26:274 (1993). Still other methods of administering lipid based therapeutics are described in, for example, Rahman et al., U.S. Pat. No. 3,993,754; Sears, U.S. Pat. No. 4,145,410; Papahadjopoulos et al., U.S. Pat. No. 4,235,871; Schneider, U.S. Pat. No. 4,224,179; Lenk et al., U.S. Pat. No. 4,522,803; and Fountain et al., U.S. Pat. No. 4,588,578. The lipid nucleic acid particles can be administered by direct injection at the site of disease or by injection at a site distal from the site of disease (see, e.g., Culver, HUMAN GENE THERAPY, MaryAnn Liebert, Inc., Publishers, New York. pp. 70-71 (1994)).

[0250] The compositions of the present invention, either alone or in combination with other suitable components, can be made into aerosol formulations (i.e., they can be "nebulized") to be administered via inhalation (e.g., intranasally or intratracheally) (see, Brigham, et al., *Am. J. Sci.* 298(4):278 (1989)). Aerosol formulations can be placed into pressurized acceptable propellants, such as dichlorodifluoromethane, propane, nitrogen, and the like.

[0251] Formulations suitable for parenteral administration, such as, for example, by intraarticular (in the joints), intravenous, intramuscular, intradermal, intraperitoneal, and subcutaneous routes, include aqueous and non-aqueous, isotonic sterile injection solutions, which can contain antioxidants, buffers, bacteriostats, and solutes that render the formulation isotonic with the blood of the intended recipient, and aqueous and non-aqueous sterile suspensions that can include suspending agents, solubilizers, thickening agents, stabilizers, and preservatives. In the practice of this invention, compositions can be administered, for example, by intravenous infusion, orally, topically, intraperitoneally, intravesically or intrathecally.

[0252] Formulations suitable for oral administration can consist of (a) liquid solutions, such as an effective amount of

the packaged nucleic acid suspended in diluents, such as water, saline or PEG 400; (b) capsules, sachets or tablets, each containing a predetermined amount of the active ingredient, as liquids, solids, granules or gelatin; (c) suspensions in an appropriate liquid; and (d) suitable emulsions. Tablet forms can include one or more of lactose, sucrose, mannitol, sorbitol, calcium phosphates, corn starch, potato starch, microcrystalline cellulose, gelatin, colloidal silicon dioxide, talc, magnesium stearate, stearic acid, and other excipients, colorants, fillers, binders, diluents, buffering agents, moistening agents, preservatives, flavoring agents, dyes, disintegrating agents, and pharmaceutically compatible carriers. Lozenge forms can comprise the active ingredient in a flavor, e.g., sucrose, as well as pastilles comprising the active ingredient in an inert base, such as gelatin and glycerin or sucrose and acacia emulsions, gels, and the like containing, in addition to the active ingredient, carriers known in the art.

[0253] Generally, when administered intravenously, the nucleic acid-lipid formulations are formulated with a suitable pharmaceutical carrier. Many pharmaceutically acceptable carriers may be employed in the compositions and methods of the present invention. Suitable formulations for use in the present invention are found, for example, in REMINGTON'S PHARMACEUTICAL SCIENCES, Mack Publishing Company, Philadelphia, Pa., 17th ed. (1985). A variety of aqueous carriers may be used, for example, water, buffered water, 0.4% saline, 0.3% glycine, and the like, and may include glycoproteins for enhanced stability, such as albumin, lipoprotein, globulin, etc. Generally, normal buffered saline (135-150 mM NaCl) will be employed as the pharmaceutically acceptable carrier, but other suitable carriers will suffice. These compositions can be sterilized by conventional liposomal sterilization techniques, such as filtration. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions, such as pH adjusting and buffering agents, tonicity adjusting agents, wetting agents and the like, for example, sodium acetate, sodium lactate, sodium chloride, potassium chloride, calcium chloride, sorbitan monolaurate, triethanolamine oleate, etc. These compositions can be sterilized using the techniques referred to above or, alternatively, they can be produced under sterile conditions. The resulting aqueous solutions may be packaged for use or filtered under aseptic conditions and lyophilized, the lyophilized preparation being combined with a sterile aqueous solution prior to administration.

[0254] When preparing pharmaceutical preparations of the nucleic acid-lipid particles of the invention, it is preferable to use quantities of the particles which have been purified to reduce or eliminate empty particles or particles with nucleic acid associated with the external surface.

[0255] The methods of the present invention may be practiced in a variety of hosts. Preferred hosts include mammalian species, such as avian (e.g., ducks), primates (e.g., humans and chimpanzees as well as other nonhuman primates), canines, felines, equines, bovines, ovines, caprines, rodents (e.g., rats and mice), lagomorphs, and swine.

[0256] The amount of particles administered will depend upon the ratio of nucleic acid to lipid; the particular nucleic acid used, the disease state being diagnosed; the age, weight,

and condition of the patient and the judgment of the clinician; but will generally be between about 0.01 and about 50 mg per kilogram of body weight; preferably between about 0.1 and about 5 mg/kg of body weight or about 10^8 - 10^{10} particles per injection.

[0257] B. Cells for Delivery of Interfering RNA

[0258] The compositions and methods of the present invention are used to treat a wide variety of cell types, in vivo and in vitro. Suitable cells include, e.g., hematopoietic precursor (stem) cells, fibroblasts, keratinocytes, hepatocytes, endothelial cells, skeletal and smooth muscle cells, osteoblasts, neurons, quiescent lymphocytes, terminally differentiated cells, slow or noncycling primary cells, parenchymal cells, lymphoid cells, epithelial cells, bone cells, and the like.

[0259] In vivo delivery of nucleic acid lipid particles encapsulating an interfering RNA is suited for targeting cells of any type. The methods and compositions can be employed with cells of a wide variety of vertebrates, including mammals, such as, e.g. canines, felines, equines, bovines, ovines, caprines, rodents (e.g., mice, rats and guinea pigs), swine, and primates (e.g. monkeys, chimpanzees, and humans).

[0260] To the extent that tissue culture of cells may be required, it is well known in the art. Freshney (1994) (*Culture of Animal Cells, a Manual of Basic Technique*, third edition Wiley-Liss, New York), Kuchler et al. (1977) (*Biochemical Methods in Cell Culture and Virology*, Kuchler, R. J., Dowden, Hutchinson and Ross, Inc., and the references cited therein provides a general guide to the culture of cells. Cultured cell systems often will be in the form of monolayers of cells, although cell suspensions are also used.

[0261] C. Detection of SNALPs

[0262] In some embodiments, the nucleic acid-lipid particles are detectable in the subject at about 1, 2, 4, 6, 8, 12, 24, 48, 60, 72, or 96 hours, 6, 8, 10, 12, 14, 16, 18, 19, 22, 24, 25, or 28 days after administration of the particles. For example about 1, 2, 5, 10, 15, 20, 25, 30, 40, or 50% of the particles may be detectable in the subject at each of these time points. The presence of the particles can be detected in the cells, tissues, or other biological samples from the subject. The particles may be detected, e.g., by direct detection of the particles, detection of the interfering RNA sequence, detection of the target sequence of interest (i.e., by detecting expression or reduced expression of the ApoB sequence of interest), detection of a compound modulated by ApoB (e.g., serum cholesterol) or a combination thereof.

[0263] 1. Detection of Particles

[0264] Nucleic acid-lipid particles are detected herein using any methods known in the art. For example, a label can be coupled directly or indirectly to a component of the SNALP or other lipid-based carrier system using methods well known in the art. A wide variety of labels can be used, with the choice of label depending on sensitivity required, ease of conjugation with the SNALP component, stability requirements, and available instrumentation and disposal provisions. Suitable labels include, but are not limited to, spectral labels, such as fluorescent dyes (e.g., fluorescein and derivatives, such as fluorescein isothiocyanate (FITC) and Oregon Green™; rhodamine and derivatives, such

Texas red, tetrahydroisothiocyanate (TRITC), etc., digoxigenin, biotin, phycoerythrin, AMCA, CyDyes™, and the like; radiolabels, such as ^3H , ^{125}I , ^{35}S , ^{14}C , ^{32}P , ^{33}P , etc.; enzymes, such as horse radish peroxidase, alkaline phosphatase, etc.; spectral colorimetric labels, such as colloidal gold or colored glass or plastic beads, such as polystyrene, polypropylene, latex, etc. The label can be detected using any means known in the art.

[0265] 2. Detection of Nucleic Acids

[0266] Nucleic acids (i.e., siRNA that silence ApoB expression) are detected and quantified herein by any of a number of means well known to those of skill in the art. The detection of nucleic acids proceeds by well known methods such as Southern analysis, Northern analysis, gel electrophoresis, PCR, radiolabeling, scintillation counting, and affinity chromatography. Additional analytic biochemical methods such as spectrophotometry, radiography, electrophoresis, capillary electrophoresis, high performance liquid chromatography (HPLC), thin layer chromatography (TLC), hyperdiffusion chromatography, may also be employed

[0267] The selection of a nucleic acid hybridization format is not critical. A variety of nucleic acid hybridization formats are known to those skilled in the art. For example, common formats include sandwich assays and competition or displacement assays. Hybridization techniques are generally described in "Nucleic Acid Hybridization, A Practical Approach," Ed. Hames, B. D. and Higgins, S. J., IRL Press, 1985.

[0268] The sensitivity of the hybridization assays may be enhanced through use of a nucleic acid amplification system which multiplies the target nucleic acid being detected. In vitro amplification techniques suitable for amplifying sequences for use as molecular probes or for generating nucleic acid fragments for subsequent subcloning are known. Examples of techniques sufficient to direct persons of skill through such in vitro amplification methods, including the polymerase chain reaction (PCR) the ligase chain reaction (LCR), Q β -replicase amplification and other RNA polymerase mediated techniques (e.g., NASBA™) are found in Sambrook, et al., In *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, 2000, and Ausubel et al., *SHORT PROTOCOLS IN MOLECULAR BIOLOGY*, eds., Current Protocols, a joint venture between Greene Publishing Associates, Inc. and John Wiley & Sons, Inc., (2002), as well as Mullis et al. (1987), U.S. Pat. No. 4,683,202; PCR Protocols A Guide to Methods and Applications (Innis et al. eds) Academic Press Inc. San Diego, Calif. (1990) (Innis); Arnheim & Levinson (Oct. 1, 1990), *C&EN* 36; *The Journal Of NIH Research*, 3:81 (1991); (Kwoh et al., *PNAS USA* 86:1173 (1989); Guatelli et al., *PNAS USA* 87:1874 (1990); Lomell et al., *J. Clin. Chem.*, 35:1826 (1989); Landegren et al., *Science*, 241:1077 (1988); Van Brunt, *Biotechnology*, 8:291 (1990); Wu and Wallace, *Gene*, 4:560 (1989); Barringer et al., *Gene*, 89:117 (1990), and Sooknanan and Malek, *Biotechnology*, 13:563 (1995). Improved methods of cloning in vitro amplified nucleic acids are described in Wallace et al., U.S. Pat. No. 5,426, 039. Other methods described in the art are the nucleic acid sequence based amplification (NASBA™, Cangene, Mississauga, Ontario) and Q Beta Replicase systems. These systems can be used to directly identify mutants where the PCR or LCR primers are designed to be extended or ligated only

when a select sequence is present. Alternatively, the select sequences can be generally amplified using, for example, nonspecific PCR primers and the amplified target region later probed for a specific sequence indicative of a mutation.

[0269] Oligonucleotides for use as probes, e.g., in in vitro amplification methods, for use as gene probes, or as inhibitor components are typically synthesized chemically according to the solid phase phosphoramidite triester method described by Beaucage and Caruthers, *Tetrahedron Letts.*, 22(20):1859-1862 (1981), e.g., using an automated synthesizer, as described in Needham VanDevanter et al., *Nucleic Acids Res.*, 12:6159 (1984). Purification of oligonucleotides, where necessary, is typically performed by either native acrylamide gel electrophoresis or by anion exchange HPLC as described in Pearson and Regnier, *J. Chrom.*, 255:137-149 (1983). The sequence of the synthetic oligonucleotides can be verified using the chemical degradation method of Maxam and Gilbert (1980) in Grossman and Moldave (eds.) Academic Press, New York, *Methods in Enzymology*, 65:499.

[0270] An alternative means for determining the level of transcription is in situ hybridization. In situ hybridization assays are well known and are generally described in Angerer et al., *Methods Enzymol.*, 152:649 (1987). In an in situ hybridization assay cells are fixed to a solid support, typically a glass slide. If DNA is to be probed, the cells are denatured with heat or alkali. The cells are then contacted with a hybridization solution at a moderate temperature to permit annealing of specific probes that are labeled. The probes are preferably labeled with radioisotopes or fluorescent reporters.

[0271] D. Detection of an Immune Response

[0272] An immune response to induced by the siRNA (i.e., modified or unmodified siRNA that silence ApoB expression) described herein can be long-lived and can be detected long after administration of the siRNA or nucleic acid-lipid particles containing the siRNA. An immune response to the siRNA can be detected by using immunoassays that detect the presence or absence of cytokines and growth factors e.g., produced by responder cells.

[0273] Suitable immunoassays include the double monoclonal antibody sandwich immunoassay technique of David et al. (U.S. Pat. No. 4,376,110); monoclonal-polyclonal antibody sandwich assays (Wide et al., in Kirkham and Hunter, eds., *Radioimmunoassay Methods*, E. and S. Livingstone, Edinburgh (1970)); the "Western blot" method of Gordon et al. (U.S. Pat. No. 4,452,901); immunoprecipitation of labeled ligand (Brown et al. (1980) *J. Biol. Chem.* 255:4980-4983); enzyme-linked immunosorbent assays (ELISA) as described, for example, by Raines et al. (1982) *J. Biol. Chem.* 257:5154-5160; immunocytochemical techniques, including the use of fluorochromes (Brooks et al. (1980) *Clin. Exp. Immunol.* 39:477); and neutralization of activity (Bowen-Pope et al. (1984) *PNAS USA* 81:2396-2400). In addition to the immunoassays described above, a number of other immunoassays are available, including those described in U.S. Pat. Nos. 3,817,827; 3,850,752; 3,901,654; 3,935,074; 3,984,533; 3,996,345; 4,034,074; and 4,098,876.

[0274] Monoclonal antibodies that specifically bind cytokines and growth factors (e.g., IL-6, IL-12, TNF- α , IFN- α , and

IFN- γ can be generated using methods known in the art (see, e.g., Kohler and Milstein, *Nature* 256: 495-497 (1975) and Harlow and Lane, *ANTIBODIES, A LABORATORY MANUAL*, Cold Spring Harbor Publication, New York (1999)). Generation of monoclonal antibodies has been previously described and can be accomplished by any means known in the art. (Buhring et al. in *Hybridoma* 1991, Vol. 10, No. 1, pp. 77-78). For example, an animal such as a guinea pig or rat, preferably a mouse is immunized with an immunogenic polypeptide, the antibody-producing cells, preferably splenic lymphocytes, are collected and fused to a stable, immortalized cell line, preferably a myeloma cell line, to produce hybridoma cells which are then isolated and cloned. (U.S. Pat. No. 6,156,882). In some methods, the monoclonal antibody is labeled to facilitate detection.

[0275] The invention will be described in greater detail by way of specific examples. The following examples are offered for illustrative purposes, and are not intended to limit the invention in any manner. Those of skill in the art will readily recognize a variety of noncritical parameters which can be changed or modified to yield essentially the same results.

EXAMPLES

[0276] The following examples are provided to illustrate, but not to limit the claimed invention.

Example 1

Selection of Candidate ApoB siRNA

[0277] Candidate Apolipoprotein B sequences were identified by scanning and Apolipoprotein sequence to identify AA dinucleotide motifs and the 19 nucleotides 3' of the motif. The following candidate sequences were eliminated: (1) sequences comprising a stretch of 4 or more of the same base in a row; (2) sequences comprising homopolymers of Gs; (3) sequences comprising triple base motifs (GGG, CCC, AAA, or TTT); (4) sequences comprising stretches of 7 or more G/Cs in a row; and (5) sequences comprising direct repeats of 4 or more bases resulting in internal fold-back structures.

[0278] Reynold's Rational Design criteria was then applied to the remaining candidate sequences to identify sequences with:

- [0279] 1. 30%-52% GC Content;
- [0280] 2. At least 3 A/Us at positions 15-19 (sense);
- [0281] 3. Absence of internal repeats;
- [0282] 4. A at position 19 (sense);
- [0283] 5. A at position 3 (sense);
- [0284] 6. U at position 10 (sense);
- [0285] 7. No G/C at position 19 (sense); and
- [0286] 8. No G at position 13 (sense).

[0287] Next, the following criteria were removed to identify additional candidate sequences of interest: 30-52% GC

(went higher on 1 candidate); the requirement for a AA leader sequence; (no constraints chosen to get 3 candidates) triplet motifs (found in 5 candidates)

[0288] BLASTn was used to identify sequences that don't cross-hybridize in the mouse genome. Finally, the candidate sequences were scanned to avoid or reduce GUGU, polyU or GU rich sequences. The candidate sequences and their positions are shown in Table 1 below.

TABLE 1

Working Designation	Target Sequence (5'-3', sense strand only)	Selected as Immunostimulatory?
ApoB-148	GAA GAU GCA ACU CGA UUC A	No
ApoB-911	ACA GUC GCU UCU UCA GUG A	No
ApoB-1455	UGA AUG CAC GGG CAA UGA A	No
ApoB-3050	CGG GAG AAG UGG AGC AGU A	No
ApoB-3193	AGA AGC AGG ACC UUA UCU A	No
ApoB-3699	GGA CAU GGG UUC CAA AUU A	No
ApoB-10067	CCA ATG CTG GAC TTT ATA A	No
ApoB-13205	GCA TGC TTA CTG ATA TAA A	No
ApoB-309	CAA CCA GTG TAC CCT TAA A	Yes

Example 2

Production of Type I Interferons and Inflammatory Cytokines Following Administration of SNALP Encapsulating siRNA Targeting ApoB

[0289] SNALP (30:2:20:48:DLinDMA:PEG-cDMA:D-SPC:Chol) encapsulating siRNA targeting ApoB and having the sequences shown in Table 2 were administered to female Balb/C mice at 2.5 mg siRNA/kg.

TABLE 2

siRNA Identifier	Designation	Target Sequence (5'-3' sense strand)	Overhang
A	ApoB-148	GAA GAU GCA ACU CGA UUC A	dTdT
B	ApoB-911	ACA GUC GCU UCU UCA GUG A	dTdT
C	ApoB-1455	UGA AUG CAC GGG CAA UGA A	dTdT
D	ApoB-3050	CGG GAG AAG UGG AGC AGU A	dTdT
E	ApoB-3193	AGA AGC AGG ACC UUA UCU A	dTdT
F	ApoB-3699	GGA CAU GGG UUC CAA AUU A	dTdT
G	ApoB-5490	GAA UGU GGG UGG CAA CUU U	dTdT
H	ApoB-6134	UUA AUG GCU UAG AGG UAA A	dTdT

[0290] Plasma IFN- α was measured 6 hours after administration of the SNALP using methods known in the art. The results are shown in FIG. 1.

Example 3

Production of Type I Interferons and Inflammatory Cytokines Following Contact with SNALP Encapsulating siRNA Targeting ApoB

[0291] SNALP (30:2:20:48:DLinDMA:PEG-cDMA:D-SPC:Chol) encapsulating siRNA targeting ApoB and having the sequences shown in Table 1 were incubated with naïve human PBMC. siRNA was present in the culture at either 0.3

μ g/ml or 1.0 μ g/ml. IFN- α in the culture media was measured after an overnight culture using methods known in the art. The results are shown in FIG. 2.

Example 4

In Vitro Silencing of ApoB Expression

[0292] SNALP (30:2:20:48:DLinDMA:PEG-cDMA:D-SPC:Chol) encapsulating 0.93 μ g. ml siRNA targeting ApoB

and having the sequences shown in Table 2 were incubated with human AML12 cells. ApoB expression was measured 40 hours following contacting the cells with SNALP. As

shown in **FIG. 3**, siRNA of sequence A reduced ApoB expression to 59% of the control samples, siRNA of sequence B reduced ApoB expression to 69% of the control samples, siRNA of sequence C reduced ApoB expression to 66% of the control samples, siRNA of sequence D reduced ApoB expression to 56% of the control samples, siRNA of sequence E reduced ApoB expression to 42% of the control samples, siRNA of sequence F reduced ApoB expression to 67% of the control samples, siRNA of sequence G reduced ApoB expression to 73% of the control samples, siRNA of sequence H reduced ApoB expression to 87% of the control samples.

Example 5

In Vivo Silencing of ApoB Expression

[0293] SNALP (30:2:20:48:DLinDMA:PEG-cDMA:D-SPC:Chol) encapsulating siRNA targeting ApoB and having Sequences D, E, and F as shown in Table 2 were administered to female Balb/C mice at 2.5 mg siRNA (0.833 mg per siRNA sequence)/kg, once daily for 3 days. ApoB expression was measured 48 hours following administration of SNALP. As shown in **FIG. 4**, the encapsulated siRNA reduced ApoB expression by 54%.

Example 6

In Vivo Silencing of ApoB Expression Using Multiple SNALP Doses

[0294] A female Balb/c mouse model was used to demonstrate the efficacy of a SNALP formulation designed for siRNA delivery to the liver. This study demonstrated SNALP-mediated anti-ApoB activity with regards to dose response and duration of target knockdown in liver ApoB mRNA as well as biologically related parameters such as circulating ApoB protein and total cholesterol in peripheral blood.

[0295] A "2:30:20" (DSPC:Cholesterol:PEG-C-DMA:DLinDMA, 20:48:2:30% molar composition) SNALP formulation was prepared using a Direct Dilution process. SNALP containing either apob-1 or apob-1-mismatch siRNA were prepared at 0.5, 0.25 or 0.125 mg siRNA/ml for administration.

[0296] The siRNA sequences were as follows:

siRNA Duplex Name	Oligo Strands	Nucleotide Sequence ('5-3')
apob-1	sense	GUCAUCACACUGAAUACCAU
apob-1	antisense	AUUGGUAUUCAGUGAUGACAC
apob-1-mismatch	sense	GUGAUCAGACUCAAUACGAAU
apob-1-mismatch	antisense	AUUCGUAUUGAGUCUGAUCACAC

Note
apob-1-mismatch is also referred to as "mismatch".

[0297] Balb/c mice (female, 4 weeks old) were obtained from Harlan Labs. After an acclimation period (of at least 7 days), animals were administered SNALP by intravenous (IV) injection through the tail vein once daily on Study Days 0, 1 & 2 (3 doses total per animal). Dosages were 5, 2.5 or

1.25 mg siRNA per kg body weight, corresponding to 10 ml/kg (rounded to the nearest 10 microlitres). As a control, one group of animals was administered PBS vehicle.

Group	# Mice	Test Article	Day 0, 1, 2 Drug Dose	Sacrifice Time Point
1	5	PBS Vehicle	10 ml/kg	Day 4 (48 h)
2		apob-1	2:30:20	5 mg/kg
3		SNALP	2.5 mg/kg	
4			1.25 mg/kg	
5			5 mg/kg	Day 3 (24 h)
6				Day 5 (72 h)
7				Day 7 (120 h)
8		apob-1-	5 mg/kg	Day 4 (48 h)
9		mismatch	2.5 mg/kg	
10			1.25 mg/kg	
11			5 mg/kg	Day 3 (24 h)
12				Day 5 (72 h)
13				Day 7 (120 h)

[0298] Body weights were measured daily, and cageside observations of animal behaviour and/or appearance were recorded daily. Animals were sacrificed on Day 3, 4, 5 or 7 (i.e., 24-120 hours after the third and last administration of test article).

[0299] Animals were euthanized with a lethal dose of ketamine/xylazine and blood was collected via cardiac puncture prior to cervical dislocation. Blood was split in a lavender EDTA microtainer (for plasma) and a SST microtainer (for serum). The liver was removed whole, weighed, and immersed in at least 5 volumes of RNAlater. One lobe of some livers (2 animals of each group) was removed before RNAlater immersion and frozen in O.C.T. (Tissue-Tek 4583) over liquid nitrogen.

[0300] ApoB and GAPDH mRNA levels in liver were measured using a QuantiGene assay kit (Genospectra, USA) according to the manufacturer's instructions. ApoB protein levels in plasma and/or serum were measured using an ELISA method essentially as described by Zlot et al. (Journal of Lipid Research, 1999, 40:76-84). Total cholesterol in plasma and/or serum was measured using an enzymatic method according to manufacturer's instructions (Infinity Cholesterol, Thermo Electron Corp, USA). Tissue sections were prepared from frozen liver lobes and stained with haematoxylin and eosin for standard histological analysis or stained with Oil-Red-O and haematoxylin for detection of lipids.

[0301] As shown in **FIG. 5**, downregulation of ApoB mRNA in the liver was observed from a dosage level as low as 1.25 mg/kg (per injection) at 48 hours after the last injection. As shown in **FIG. 5**, treatment with the 5 mg/kg dosage led to a decrease in ApoB expression in terms of liver mRNA of as much as 88%. This silencing was observed as soon as 24 hours and continued without much lessening of effect to 120 hours after the last SNALP administration. Reductions in ApoB protein levels in plasma (up to 91% decrease) corresponded to observed patterns of reduction in liver mRNA. Silencing of ApoB was expected to have additional biological consequences and these were measured in the form of lowered serum cholesterol levels (up to 64% decrease) and occurrence of fatty liver as detected by liver weight and appearance as well as Oil-Red-O staining of liver sections for lipid deposits.

Example 7

In Vivo Silencing of ApoB Expression Using Multiple SNALP Doses

[0302] A female Balb/c mouse model was used to demonstrate the efficacy of a SNALP formulation designed for siRNA delivery to the liver. This study demonstrated SNALP-mediated anti-ApoB activity with regards to duration of target knockdown in circulating ApoB protein as well as biologically related parameters such as ApoB mRNA in liver and total cholesterol in peripheral blood.

[0303] A “2:30:20” (DSPC:Cholesterol:PEG-C-DMA:DLinDMA, 20:48:2:30% molar composition) SNALP formulation was prepared using a Direct Dilution process. SNALP containing either apob-1 or apob-1-mismatch siRNA were prepared at 0.5 mg siRNA/ml for administration. Liposomes of the same lipid formulation but not containing siRNA (also referred to as “empty particles”) were prepared at a lipid concentration equivalent to siRNA-containing SNALPs.

[0304] The “apob-1” and “apob-1-mismatch” (also referred to as “mismatch”) siRNA sequences were as described in Example 6.

[0305] Balb/c mice (female, 6 weeks old) were obtained from Harlan Labs. After an acclimation period (of at least 7 days), animals were administered SNALP by IV injection through the tail vein once daily on Study Days 0, 1 & 2 (3 doses total per animal). Dosages were 5 mg siRNA per kg body weight, corresponding to 10 ml/kg (rounded to the nearest 10 microlitres). As a control, one group of animals was administered PBS vehicle.

Group	# Mice	Test Article	Day 0, 1, & 2 Drug Dose	Sample Collection
1	5	PBS Vehicle	10 ml/kg	Tail nick on Day
2		apob-1 2:30:20 SNALP	5 mg/kg	-4, 3, 4, 5, 7, 10, 14 & 17.
3		mismatch 2:30:20 SNALP		Euth on Day 21 for liver and blood.
4		Empty particles	equiv. [lipid]	

[0306] Body weights were measured on each day of injection and each day that samples were collected, and cage-side observations of animal behaviour and/or appearance were recorded at the same time. Animals were sacrificed on Day 21, 19 days after the third and last administration of test article.

[0307] Animals were euthanized with a lethal dose of ketamine/xylazine and blood was collected via cardiac puncture prior to cervical dislocation. Blood was split in a lavender EDTA microtainer (for plasma) and a SST microtainer (for serum). The liver was removed whole, weighed, and immersed in at least 5 volumes of RNAlater. One lobe of some livers (2 animals of each group) was removed before RNAlater immersion and frozen in O.C.T. (Tissue-Tek 4583) over liquid nitrogen.

[0308] ApoB and GAPDH mRNA levels in liver were measured using a QuantiGene assay kit (Genospectra, USA) according to the manufacturer's instructions. ApoB protein

levels in plasma and/or serum were measured using an ELISA method essentially as described by Zlot et al. (Journal of Lipid Research, 1999, 40:76-84). Total cholesterol in plasma and/or serum was measured using an enzymatic method according to manufacturer's instructions (Infinity Cholesterol, Thermo Electron Corp, USA). Tissue sections were prepared from frozen liver lobes and stained with haematoxylin and eosin for standard histological analysis or stained with Oil-Red-O and haematoxylin for detection of lipids.

[0309] Serum cholesterol levels of mice given apob-1 SNALP were observed to have returned to baseline levels within 15 days of the cessation of treatment. As shown in FIG. 6, decreased ApoB protein levels in plasma were detected through to 19 days after administration of the final dose of SNALP. The small measured decrease in ApoB protein (13%) at 19 days after SNALP administration was correlated to a similar small (21%) decrease in the corresponding ApoB liver mRNA.

Example 8

In Vivo Silencing of ApoB Expression Using SNALP Prepared via a Stepwise Dilution Process

[0310] A female Balb/c mouse model was used to demonstrate the efficacy of a SNALP formulation designed for siRNA delivery to the liver. This study demonstrated SNALP-mediated anti-ApoB activity with regards to target knockdown in liver ApoB mRNA as well as biologically related parameters such as circulating ApoB protein and total cholesterol in peripheral blood.

[0311] SNALP containing apob-1 siRNA were prepared at 0.5 mg siRNA/ml for administration. A “2:30:20+10% DODAC” (DSPC:Cholesterol:PEG-C-DMA:DLinDMA:DODAC, 20:38:2:30:10% molar composition) SNALP formulation was prepared using a Stepwise Dilution process. Similarly, “5:30:20” (DSPC:Cholesterol:PEG-C-DMA:DLinDMA:DODAC, 20:45:5:30% molar composition), a “2:30:20 DODMA” (DSPC:Cholesterol:PEG-C-DMA:DODMA, 20:48:2:30% molar composition) and a “2:30:10” (DSPC:Cholesterol:PEG-C-DMA:DLinDMA, 10:58:2:30% molar composition) SNALP formulations were prepared.

[0312] The “apob-1” siRNA sequences were as described in Example 6.

[0313] Balb/c mice (female, 4 weeks old) were obtained from Harlan Labs. After an acclimation period (of at least 7 days), animals were administered SNALP by IV injection through the tail vein once daily on Study Days 0, 1 & 2 (3 doses total per animal). Dosages were 5 mg siRNA per kg body weight, corresponding to 10 ml/kg (rounded to the nearest 10 microlitres). As a control, one group of animals was administered PBS vehicle.

Group	# Mice	Test Article	Day 0, 1, & 2 Drug Dose	Sample Collection
1	5	PBS vehicle	10 ml/kg	Tail nick at
2		apob-1 2:30:20 + 10% DODAC	5 mg/kg	Hour 6. Euth at

-continued

Group	# Mice	Test Article	Day 0, 1, & 2 Drug Dose	Sample Collection
3		5:30:20		Day 4 for blood & liver.
4		2:30:20		
		DODMA		
5		2:30:10		

[0314] Body weights were measured daily, and cageside observations of animal behaviour and/or appearance were recorded at the same time. Animals were sacrificed on Day 4, 48 hours after the third and last administration of test article.

[0315] Animals were euthanized with a lethal dose of ketamine/xylazine and blood was collected via cardiac puncture prior to cervical dislocation. Blood was split in a lavender EDTA microtainer (for plasma) and a SST microtainer (for serum). The liver was removed whole, weighed, and immersed in at least 5 volumes of RNAlater.

[0316] ApoB and GAPDH mRNA levels in liver were measured using a QuantiGene assay kit (Genospectra, USA) according to the manufacturer's instructions. ApoB protein levels in plasma and/or serum were measured using an ELISA method essentially as described by Zlot et al. (Journal of Lipid Research, 1999, 40:76-84). Total cholesterol in plasma and/or serum was measured using an enzymatic method according to manufacturer's instructions (Infinity Cholesterol, Thermo Electron Corp, USA). Interferon- α in plasma and/or serum was measured using a commercially available ELISA kit (PBL Biomedical Laboratories, USA) according to the manufacturer's instructions.

[0317] As shown in FIG. 7, downregulation of ApoB mRNA in the liver was observed upon treatment with all four formulations but ranged from 99% decrease to 44% decrease. Reductions in ApoB protein levels in plasma (79, 76, 23, 75% decrease, respectively) roughly corresponded to observed patterns of reduction in liver mRNA. Silencing of ApoB was expected to have additional biological consequences and these were measured in the form of lowered serum cholesterol levels (relative difference in decrease more similar to mRNA than to pattern of protein reduction).

Example 9

In Vivo Silencing of ApoB Expression Using Multiple Doses of SNALP Comprising Different Cationic Lipids

[0318] A female Balb/c mouse model was used to demonstrate the efficacy of SNALP formulations, containing various cationic lipids, that are designed for siRNA delivery to the liver. This study demonstrated SNALP-mediated anti-ApoB activity with regards to target knockdown in liver ApoB mRNA as well as biologically related parameters such as circulating ApoB protein and total cholesterol in peripheral blood.

[0319] "2:30:20 DODMA" (DSPC:Cholesterol:PEG-C-DMA:DODMA, 20:48:2:30% molar composition) and "2:30:20 DLenDMA" (DSPC:Cholesterol:PEG-C-DMA-

:DLenDMA, 20:48:2:30% molar composition) SNALP formulations were prepared using a Direct Dilution process. SNALP containing either apob-1 or apob-1-mismatch siRNA were prepared at 0.5 mg siRNA/ml for administration.

[0320] The "apob-1" and "apob-1-mismatch" (also referred to as "mismatch") siRNA sequences were as described in Example 6.

[0321] Balb/c mice (female, 4 weeks old) were obtained from Harlan Labs. After an acclimation period (of at least 7 days), animals were administered SNALP by IV injection through the tail vein once daily on Study Days 0, 1 & 2 (3 doses total per animal). Dosages were 5 mg siRNA per kg body weight, corresponding to 10 ml/kg (rounded to the nearest 10 microlitres). As a control, one group of animals was administered PBS vehicle.

Group	# Mice	Test Article	Day 0, 1, 2 Drug Dose	Day 4 Sacrifice
1	5	PBS vehicle	10 ml/kg	Collect liver & blood.
2		apob-1	5 mg/kg	
3		DODMA		
		2:30:20		
		DLenDMA		
4		apob-1-	2:30:20	
		mismatch	DODMA	
5		2:30:20		
		DLenDMA		

[0322] Body weights were measured every day, and cageside observations of animal behaviour and/or appearance were recorded at the same time. Animals were sacrificed on Study Day 4, 48 hours after the third and last administration of test article.

[0323] Animals were euthanized with a lethal dose of ketamine/xylazine and blood was collected via cardiac puncture prior to cervical dislocation. Blood was split in a lavender EDTA microtainer (for plasma) and a SST microtainer (for serum). The liver was removed whole, weighed, and immersed in at least 5 volumes of RNAlater.

[0324] ApoB and GAPDH mRNA levels in liver were measured using a QuantiGene assay kit (Genospectra, USA) according to the manufacturer's instructions. ApoB protein levels in plasma and/or serum were measured using an ELISA method essentially as described by Zlot et al. (Journal of Lipid Research, 1999, 40:76-84). Total cholesterol in plasma and/or serum was measured using an enzymatic method according to manufacturer's instructions (Infinity Cholesterol, Thermo Electron Corp, USA).

[0325] As shown in FIG. 8, downregulation of ApoB mRNA in the liver was observed upon treatment with formulations containing either cationic lipid: 79% silencing with DODMA and 71% silencing with DLenDMA. Reductions in ApoB protein levels in plasma (72 and 52% decrease, respectively) roughly corresponded to observed patterns of reduction in liver mRNA. Silencing of ApoB was expected to have additional biological consequences and these were measured in the form of lowered serum cholesterol levels (25 and 14% decrease, respectively).

Example 10

In Vivo Silencing of ApoB Expression Using Multiple Doses of SNALP Containing Different Phospholipids

[0326] A female Balb/c mouse model was used to demonstrate the efficacy of SNALP formulations, containing various phospholipids, that are designed for siRNA delivery to the liver. This study demonstrated SNALP-mediated anti-ApoB activity with regards to target knockdown in liver ApoB mRNA as well as biologically related parameters such as circulating ApoB protein and total cholesterol in peripheral blood.

[0327] “2:30:20 DOPE” (DOPE:Cholesterol:PEG-C-DMA:DLinDMA, 20:48:2:30% molar composition), “2:30:20 DSPE” (DSPE:Cholesterol:PEG-C-DMA:DLinDMA, 20:48:2:30% molar composition) and “2:30:20 DPPE” (DPPE:Cholesterol:PEG-C-DMA:DLinDMA, 20:48:2:30% molar composition) SNALP formulations were prepared using a Direct Dilution process. SNALP containing either apob-1 or apob-1-mismatch siRNA were prepared at 0.35 mg siRNA/ml for administration.

[0328] The “apob-1” and “apob-1-mismatch” (also referred to as “mismatch”) siRNA sequences were as described in Example 6.

[0329] Balb/c mice (female, 4 weeks old) were obtained from Harlan Labs. After an acclimation period (of at least 7 days), animals were administered SNALP by IV injection through the tail vein once daily on Study Days 0, 1 & 2 (3 doses total per animal). Dosages were 3.5 mg siRNA per kg body weight, corresponding to 10 ml/kg (rounded to the nearest 10 microlitres). As a control, one group of animals was administered PBS vehicle.

Group	# Mice	Test Article	Day 0, 1, 2 Drug Dose	Day 3 Collection
1	4	PBS vehicle	10 ml/kg	Collect liver
2	4	apob-1	2:30:20 DOPE	3.5 mg/kg and blood.
3	4		2:30:20 DSPE	
4	4		2:30:20 DPPE	
5	3	apob-1- mismatch	2:30:20 DOPE	
6	3		2:30:20 DSPE	
7	3		2:30:20 DPPE	

[0330] Body weights were measured each day, and cage-side observations of animal behaviour and/or appearance were recorded at the same time. Animals were sacrificed on Study Day 3, 24 hours after the third and last administration of test article.

[0331] Animals were euthanized with a lethal dose of ketamine/xylazine and blood was collected via cardiac puncture prior to cervical dislocation. Blood from each animal

was collected into a lavender EDTA microtainer (for plasma). The spleen was removed and weighed. The liver was removed whole, weighed, and immersed in at least 5 volumes of RNAlater.

[0332] ApoB and GAPDH mRNA levels in liver were measured using a QuantiGene assay kit (Genospectra, USA) according to the manufacturer’s instructions. ApoB protein levels in plasma and/or serum were measured using an ELISA method essentially as described by Zlot et al. (Journal of Lipid Research, 1999, 40:76-84). Total cholesterol in plasma and/or serum was measured using an enzymatic method according to manufacturer’s instructions (Infinity Cholesterol, Thermo Electron Corp, USA).

[0333] As shown in FIG. 9, downregulation of ApoB mRNA in the liver was observed upon treatment with formulations containing any of the phospholipids: 94% silencing with DOPE, 87% silencing with DSPE and 90% silencing with DPPE. The considerable degree of ‘non-specific effect’, which was correlated to the SNALP dosage but not the action of the active apob-1 siRNA, was not unexpected as similar effects have been observed at this time point in other studies (see, e.g., Examples 21 and 22) and are known to be transient. Reductions in ApoB protein levels in plasma were not quantified as samples fell below the lower limit (13%) of the assay. Silencing of ApoB was expected to have additional biological consequences and these were measured in the form of lowered serum cholesterol levels (30, 31 and 40% decrease, respectively).

Example 11

In Vivo Silencing of ApoB Expression Using a Single SNALP Dose

[0334] A female Balb/c mouse model was used to demonstrate the efficacy of a SNALP formulation designed for siRNA delivery to the liver. This study demonstrated SNALP-mediated anti-ApoB activity with regards to dose response and duration of target knockdown in circulating ApoB protein as well as biologically related parameters such as ApoB mRNA in liver and total cholesterol in peripheral blood.

[0335] A “2:30:20” (DSPC:Cholesterol:PEG-C-DMA:DLinDMA, 20:48:2:30% molar composition) SNALP formulation was prepared using a Direct Dilution process. SNALP containing either apob-1 or apob-1-mismatch siRNA were prepared at 0.5 mg siRNA/ml for administration.

[0336] The apob-1 and apob-1-mismatch (also referred to as “mismatch”) siRNA sequences were as described in Example 6.

[0337] Balb/c mice (female, 4 weeks old) were obtained from Harlan Labs. After an acclimation period (of at least 7 days), animals were administered SNALP by IV injection through the tail vein once on Study Day 0 (1 dose total per animal). Dosage was 5 mg siRNA per kg body weight, corresponding to 10 ml/kg (rounded to the nearest 10 microlitres). As a control, one group of animals was administered PBS vehicle.

Example 12

In Vivo Silencing of ApoB Expression Using a Single SNALP Dose

Group	# Mice	Test Article	Day 0 Drug Dose	Sacrifice Time Point
1	4	PBS vehicle	10 ml/kg	Day 10
2		apob-1 2:30:20 SNALP	5 mg/kg	Day 1
3				Day 3
4				Day 7
5				Day 10
6		apob-1-mismatch		Day 1
7				Day 3
8				Day 7
9				Day 10

[0338] Body weights were measured on the day of injection and each day that samples were collected, and cageside observations of animal behaviour and/or appearance were recorded at the same time. Animals were sacrificed 1, 3, 7 and 10 days after test article administration.

[0339] Animals were euthanized with a lethal dose of ketamine/xylazine and blood was collected via cardiac puncture prior to cervical dislocation. Blood was split in a lavender EDTA microtainer (for plasma) and a SST microtainer (for serum). The liver was removed whole, weighed, and immersed in at least 5 volumes of RNAlater. One lobe of some livers (2 animals of each group) was removed before RNAlater immersion and frozen in O.C.T. (Tissue-Tek 4583) over liquid nitrogen.

[0340] ApoB and GAPDH mRNA levels in liver were measured using a QuantiGene assay kit (Genospectra, USA) according to the manufacturer's instructions. ApoB protein levels in plasma and/or serum were measured using an ELISA method essentially as described by Zlot et al. (Journal of Lipid Research, 1999, 40:76-84). Total cholesterol in plasma and/or serum was measured using an enzymatic method according to manufacturer's instructions (Infinity Cholesterol, Thermo Electron Corp, USA). Tissue sections were prepared from frozen liver lobes and stained with haematoxylin and eosin for standard histological analysis or stained with Oil-Red-O and haematoxylin for detection of lipids.

[0341] As shown in FIG. 10, SNALP-mediated down-regulation of ApoB protein in plasma was observed to have the greatest effect (84% decrease) at 1 day after administration. This silencing effect gradually lessened over the duration of the study period, to as low as 13% decrease at 10 days after SNALP administration. A transient 'non-specific' effect, which was correlated to the SNALP dosage but not the action of the active apob-1 siRNA, was observed at Day 1 but this was essentially abolished by Day 3, at which time the specific activity of active SNALP resulted in a 49% decrease in the plasma ApoB protein level. Reductions in ApoB liver mRNA (up to 72% decrease) corresponded to observed patterns of reduction in plasma ApoB protein. Silencing of ApoB was expected to have additional biological consequences and these were measured in the form of lowered serum cholesterol levels (up to 24% decrease at Day 3, resolved by Day 10) and occurrence of fatty liver as detected by liver weight and appearance as well as Oil-Red-O staining of liver sections for lipid deposits.

[0342] A female Balb/c mouse model was used to demonstrate the efficacy of a SNALP formulation designed for siRNA delivery to the liver. This study was performed for method development (use of tail nicks to assay silencing at multiple time points, allowing for a decrease in the number of animals utilized) and demonstrated SNALP-mediated anti-ApoB activity with regards to duration of target knock-down in circulating ApoB protein as well as biologically related parameters such as ApoB mRNA in liver and total cholesterol in peripheral blood.

[0343] A "2:30:20" (DSPC:Cholesterol:PEG-C-DMA:DLinDMA, 20:48:2:30% molar composition) SNALP formulation was prepared using a Direct Dilution process. SNALP containing either apob-1 or apob-1-mismatch siRNA were prepared at 0.5 mg siRNA/ml for administration.

[0344] The "apob-1" and "apob-1-mismatch" (also referred to as "mismatch") siRNA sequences were as described in Example 6.

[0345] Balb/c mice (female, 4 weeks old) were obtained from Harlan Labs. After an acclimation period (of at least 7 days), animals were administered SNALP by IV injection through the tail vein once on Study Day 0 (1 dose total per animal). Dosage was 5 mg siRNA per kg body weight, corresponding to 10 ml/kg (rounded to the nearest 10 microlitres). As a control, one group of animals was administered PBS vehicle.

Group	# Mice	Test Article	Day 0 Drug Dose	Sample Collection
1	4	PBS vehicle	10 ml/kg	Tail nicks
2		apob-1 2:30:20	5 mg/kg	at Hour 6, Day
3		apob-1- SNALP mismatch		1, 2 & 3. Terminal bleed on Day 4 & collect liver.

[0346] Body weights were measured on the day of injection and each day that samples were collected, and cageside observations of animal behaviour and/or appearance were recorded at the same time. Animals were sacrificed on Day 4, 96 hours after IV administration of test article.

[0347] Animals were euthanized with a lethal dose of ketamine/xylazine and blood was collected via cardiac puncture prior to cervical dislocation. Blood was split in a lavender EDTA microtainer (for plasma) and a SST microtainer (for serum). The liver was removed whole, weighed, and immersed in at least 5 volumes of RNAlater. One lobe of some livers (2 animals of each group) was removed before RNAlater immersion and frozen in O.C.T. (Tissue-Tek 4583) over liquid nitrogen.

[0348] ApoB and GAPDH mRNA levels in liver were measured using a QuantiGene assay kit (Genospectra, USA) according to the manufacturer's instructions. ApoB protein levels in plasma and/or serum were measured using an

ELISA method essentially as described by Zlot et al. (Journal of Lipid Research, 1999, 40:76-84). Total cholesterol in plasma and/or serum was measured using an enzymatic method according to manufacturer's instructions (Infinity Cholesterol, Thermo Electron Corp, USA). Tissue sections were prepared from frozen liver lobes and stained with haematoxylin and eosin for standard histological analysis or stained with Oil-Red-O and haematoxylin for detection of lipids. Interferon-alpha in plasma and/or serum was measured using a commercially available ELISA kit (PBL Biomedical Laboratories, USA) according to the manufacturer's instructions.

[0349] As shown in FIG. 11, SNALP-mediated down-regulation of ApoB protein in plasma was observed to have the greatest effect (53% decrease) at Hour 24 after administration. This silencing effect gradually lessened over the duration of the study period, to as low as 27% decrease at Hour 96 after SNALP administration. A transient 'non-specific' effect, which was correlated to the SNALP dosage but not the action of the active apob-1 siRNA, was observed at Hour 24 but this was essentially abolished by Hour 48, at which time the specific activity of active SNALP resulted in a 34% decrease in the plasma ApoB protein level. At the the sacrifice time point, 96 hours after SNALP administration, reduction in ApoB liver mRNA (30% decrease) corresponded to observed reduction in plasma ApoB protein. Silencing of ApoB was expected to have additional biological consequences and these were measured in the form of lowered serum cholesterol levels (21% silencing at Hour 96) and occurrence of fatty liver as detected by liver weight and appearance as well as Oil-Red-O staining of liver sections for lipid deposits.

Example 13

In Vivo Silencing of ApoB Expression

[0350] A diet-induced high cholesterol mouse model was used to demonstrate the efficacy of liver-targeted anti-ApoB SNALP in lowering total blood cholesterol level. This study demonstrated SNALP-mediated anti-ApoB activity with regards to the extent and duration of the effect of lowering total cholesterol in the blood. Reduction of blood cholesterol is a potentially therapeutic application of SNALP technology.

[0351] A "2:40:10" (DSPC:Cholesterol:PEG-C-DMA:DLinDMA, 10:48:2:40% molar composition) SNALP formulation was prepared using a Direct Dilution process. SNALP containing either apob-1 or apob-1-mismatch siRNA were prepared at 0.5 mg siRNA/ml for administration.

[0352] The "apob-1" and "apob-1-mismatch" (also referred to as "mismatch") siRNA sequences were as described in Example 6.

[0353] Balb/c and C57BL/6 mice (female, 4 weeks old) were obtained from Harlan Labs. After an acclimation period (of at least 7 days), and after tail nick samples are taken on Study Day 0, animals in selected cages were switched to a high fat diet (a so-called 'Western diet', Harlan Teklad # 88137: 0.2% cholesterol, 4.5 kcal/g, 43% calories derived from fat) which will be supplied ad libitum in pellet form. The normal diet was Laboratory Rodent Diet (PMI

Nutrition International), containing 12% calories derived from fat and 200 ppm cholesterol, which was supplied in the same manner.

[0354] Blood cholesterol levels in animals fed normal versus high fat diet were monitored for four weeks in order to establish a baseline for the hypercholesterolemia model.

[0355] Body weights were measured twice per week, and cageside observations of animal behaviour and/or appearance were recorded at the same time. Plasma was collected via tail nick once per week up to Study Day 28.

[0356] On Study Day 32, animals were administered SNALP by intravenous (IV) injection through the tail vein once Study Day 0 (1 dose total per animal). Dosage was 5 mg siRNA per kg body weight, corresponding to 10 ml/kg (rounded to the nearest 10 microlitres).

Cage	# Mice	Mouse Strain	IV Dose at 5 mg/kg	Sample Collection
1	2	Balb/c	apob-1	2:40:10 BW 2x/week.
	2	Normal Diet	mismatch	SNALP Tail Nick 2x/week
2	2	Balb/c	apob-1	for cholesterol,
	2	High Fat Diet	mismatch	ApoB protein.
3	2	C57BL/6	apob-1	
	2	Normal Diet	mismatch	
4	2	C57BL/6	apob-1	
	2	High Fat Diet	mismatch	

[0357] Body weights were measured twice per week, and cageside observations of animal behaviour and/or appearance were recorded at the same time. Plasma was collected via tail nick twice per week up to Study Day 39.

[0358] Total cholesterol in plasma was measured using an enzymatic method according to manufacturer's instructions (Infinity Cholesterol, Thermo Electron Corp, USA).

[0359] As shown in FIG. 22, IV administration of a single dose of anti-ApoB SNALP completely abrogated the elevated cholesterol levels previously induced by a high fat 'Western' diet in female C57BL/6 mice. Similar results were obtained using female Balb/c mice

Example 14

In Vivo Silencing of ApoB Expression

[0360] A female Balb/c mouse model was used to demonstrate the efficacy of a SNALP formulation designed for siRNA delivery to the liver. These studies demonstrated SNALP-mediated anti-ApoB activity with regards to dose response and duration of target knockdown in liver ApoB mRNA as well as biologically related parameters such as circulating ApoB protein and total cholesterol in peripheral blood

[0361] A "2:40:10" (DSPC:Cholesterol:PEG-C-DMA:DLinDMA, 10:48:2:40% molar composition) SNALP formulation was prepared using a Direct Dilution process, at a nucleic acid to lipid ratio of 0.039. SNALP containing either apob-1 or apob-1-mismatch siRNA were prepared at 0.2 mg siRNA/ml for administration.

[0362] The "apob-1" and "apob-1-mismatch" (also referred to as "mismatch") siRNA sequences were as described in Example 6.

[0363] Balb/c mice (female, 4 weeks old) were obtained from Harlan Labs. After an acclimation period (of at least 7 days), animals were administered SNALP by intravenous (IV) injection through the tail vein once on Study Day 0 (1 dose total per animal). Dosage was 2 mg siRNA per kg body weight, corresponding to 10 ml/kg (rounded to the nearest 10 microlitres). As a control, one group of animals was administered PBS vehicle.

Group	# Mice	Test Article	Day 0	
			Drug Dose	Sample Collection
1	4	PBS vehicle	10 ml/kg	Tail nick at
2	4	apob-1 2:40:10	2 mg/kg	Day 1, 2 & 3.
3	3	apob-1- mismatch SNALP		Euth at Day 4 for blood & liver.

[0364] Body weights were measured daily, and cageside observations of animal behaviour and/or appearance were recorded daily. Animals were sacrificed on Day 4, 96 hours after administration of test article.

[0365] Animals were euthanized with a lethal dose of ketamine/xylazine and blood was collected via cardiac puncture prior to cervical dislocation. Blood was split in a lavender EDTA microtainer (for plasma) and a SST microtainer (for serum). The liver was removed whole, weighed, and immersed in at least 5 volumes of RNAlater.

[0366] ApoB and GAPDH mRNA levels in liver were measured using a QuantiGene assay kit (Genospectra, USA) according to the manufacturer's instructions. ApoB protein levels in plasma and/or serum were measured using an ELISA method essentially as described by Zlot et al. (Journal of Lipid Research, 1999, 40:76-84). Total cholesterol in plasma and/or serum was measured using an enzymatic method according to manufacturer's instructions (Infinity Cholesterol, Thermo Electron Corp, USA).

[0367] As shown in FIG. 13, downregulation of ApoB mRNA in the liver was observed at 96 hours after a single injection of SNALP at a dosage of 2 mg/kg. Silencing of ApoB was expected to have additional biological consequences and these were measured in the form of lowered serum cholesterol levels (up to 59% decrease) and occurrence of fatty liver as detected by liver weight.

Example 15

In Vivo Silencing of ApoB Expression Following Intraperitoneal Administration of SNALP

[0368] A female Balb/c mouse model was used to demonstrate the efficacy of SNALP formulation administered intraperitoneally.

[0369] A "2:40:10" (DSPC:Cholesterol:PEG-C-DMA:DLinDMA, 10:48:2:40% molar composition) SNALP formulation was prepared using a Direct Dilution process, at a nucleic acid to lipid ratio of 0.0195. SNALP containing either apob-1 or apob-1-mismatch siRNA were prepared at 0.2 mg siRNA/ml for administration.

[0370] The "apob-1" and "apob-1-mismatch" (also referred to as "mismatch") siRNA sequences were as described in Example 6.

[0371] Balb/c mice (female, 4 weeks old) were obtained from Harlan Labs. After an acclimation period (of at least 7 days), animals were administered SNALP by intraperitoneal (IP) injection in the abdominal region once daily on Study Days 0, 1 & 2 (3 doses total per animal). Dosage was 2 mg siRNA per kg body weight, corresponding to 10 ml/kg (rounded to the nearest 10 microlitres). As a control, one group of animals was given an intravenous (IV) injection of PBS vehicle.

Group	# Mice	Test Article	Dose Regime	Day 4
				Sacrifice
1	4	PBS vehicle	IV Day 0	Collect
2	4	apob-1 2:40:10	IP Days 0, 1 & 2	plasma
3	3	mismatch SNALP 2 mg/kg per dose		& liver.

[0372] Body weights were measured daily, and cageside observations of animal behaviour and/or appearance were recorded daily. Animals were sacrificed on Day 4, 48 hours after the final administration of test article.

[0373] Animals were euthanized with a lethal dose of ketamine/xylazine and blood was collected via cardiac puncture prior to cervical dislocation. Blood was collected in lavender EDTA microtainer and processed for plasma. The liver was removed whole, weighed, and immersed in at least 5 volumes of RNAlater.

[0374] ApoB and GAPDH mRNA levels in liver were measured using a QuantiGene assay kit (Genospectra, USA) according to the manufacturer's instructions. ApoB protein levels in plasma and/or serum were measured using an ELISA method essentially as described by Zlot et al. (Journal of Lipid Research, 1999, 40:76-84).

[0375] As shown in FIG. 14, downregulation of ApoB mRNA in the liver was observed at 48 hours after the third injection of SNALP and this downregulation effect was observed in both ApoB mRNA and ApoB protein. The use of a negative control treatment, consisting of SNALP containing siRNA that do not target the ApoB gene, demonstrates that the observed downregulation effect is specific to a formulation that contains siRNA designed to act against the target gene.

Example 16

In Vivo Silencing of ApoB Expression Following Subcutaneous Administration of SNALP

[0376] A female Balb/c mouse model was used to demonstrate the efficacy of SNALP administered subcutaneously.

[0377] A "2:40:10" (DSPC:Cholesterol:PEG-C-DMA:DLinDMA, 10:48:2:40% molar composition) SNALP formulation was prepared using a Direct Dilution process, at a nucleic acid to lipid ratio of 0.0195. SNALP containing either apob-1 or apob-1-mismatch siRNA were prepared at either 0.1, 0.3 or 1.0 mg siRNA/ml for administration.

[0378] The “apob-1” and “apob-1-mismatch” (also referred to as “mismatch”) siRNA sequences were as described in Example 6, except that all uridine residues in each sense strand carried a 2'-O-methyl modification (referred to below as “UmodS”).

[0379] Balb/c mice (female, 4 weeks old) were obtained from Harlan Labs. After an acclimation period (of at least 7 days), animals were administered SNALP by subcutaneous (subQ) injection in the scapular region once on Study Day 0 (1 dose total per animal). Dosage was 1, 3 or 10 mg siRNA per kg body weight, corresponding to 10 ml/kg (rounded to the nearest 10 microlitres). As a control, one group of animals was given an intravenous (IV) injection of PBS vehicle.

Group	# Mice	Test Article	Day 0 Dose	Sample Collection
1	4	PBS vehicle	IV 10 mL/kg	Euthanize on Day 2.
2	5	2:40:10 Direct UmodS	subQ 1 mg/kg	Collect Liver.
3	5	Dilution apob-1 UmodS	subQ 3 mg/kg	
4	5	SNALP apob-1 UmodS	subQ 10 mg/kg	
5	5	apob-1-MM UmodS	subQ 3 mg/kg	

[0380] Body weights were measured daily, and cageside observations of animal behaviour and/or appearance were recorded daily. Animals were sacrificed on Day 2, 48 hours after administration of test article.

[0381] Animals were euthanized with a lethal dose of ketamine/xylazine and the liver was removed whole, weighed, and immersed in at least 5 volumes of RNAlater. ApoB and GAPDH mRNA levels in liver were measured using a QuantiGene assay kit (Genospectra, USA) according to the manufacturer's instructions.

[0382] As shown in FIG. 15, downregulation of ApoB mRNA in the liver was observed at 48 hours after a single injection of SNALP and this downregulation effect increased with the administration of greater dosages (up to 10 mg/kg). The use of a negative control treatment, consisting of SNALP containing siRNA that do not target the ApoB gene, demonstrates that the observed downregulation effect is specific to a formulation that contains siRNA designed to act against the target gene.

Example 17

In Vivo Silencing of ApoB Expression Using SNALP Encapsulating Anti-ApoB siRNA

[0383] A female Balb/c mouse model was used to demonstrate the relative efficacy of a panel of SNALP encapsulating anti-ApoB siRNA.

[0384] A panel of siRNA sequences was generated by scanning the murine ApoB sequence (XM 137955) using the rules described in Example 1 above. Table 3 sets forth the sequence, position, and predicted immunostimulatory activity of each identified siRNA sequence.

TABLE 3

Position	SiRNA target sequence	Immunostimulatory activity
1512	GAAGAACCAUGGAACAAGU	High
2688	GCAUCAUCAUCCAGACUU	Low
10849	CCAUCACUUUGACCAGGAA	Med
12190	GGAUACGUAUUCUUCAGAA	Med
13395	CCACAAGAUUGAUUGACCU	High

[0385] A “2:40:10” (DSPC:Cholesterol:PEG-C-DMA:DLinDMA, 10:48:2:40% molar composition) SNALP formulation was prepared using a Direct Dilution process. SNALP containing the ApoB siRNA set forth in Table 4 were prepared at 0.2 mg siRNA/ml for administration. The “apob-1” and “apob-1-mismatch” (also referred to as “mismatch”) siRNA sequences were as described in Example 6. “Protiva apob-1” and “Protiva apob-1 mismatch” have the same sequences as the siRNA sequences described in Example 6, but were produced from different manufacturing lots. UmodS was as described in Example 16 above. The notation “no phosphate” indicates that the siRNA lacks a terminal phosphate.

[0386] Balb/c mice (female, 4 weeks old) were obtained from Harlan Labs. After an acclimation period (of at least 7 days), animals were administered SNALP by intravenous (IV) injection through the tail vein once daily on Study Day 0. Dosage was 2 mg siRNA per kg body weight, corresponding to 10 ml/kg (rounded to the nearest 10 microlitres). As a control, one group of animals was administered PBS vehicle.

Group	# Mice	Test Article	Day 0 IV Drug Dose	Sample Collection	Test Article Lot No.
1	4	PBS vehicle	10 mL/kg	Hour 6 tail	N/A
2	4	apob-1 :40:10	2 mg/kg	nick for	242-072005-01
3	4	apob-1 no phosphate 1xD:L		plasma.	242-080405-06
4	4	apob-1 U-mod-sense NALP2		Hour 48	242-072505-01
5	4	apoB-1514 (i.e., 1512)		collection of	242-080405-01
6	4	apoB-2690 (i.e., 2688)		liver in	242-080405-02
7	4	apoB-10851 (i.e., 10849)		RNA later and	242-080405-03

-continued

Group	# Mice	Test Article	Day 0 IV Drug Dose	Sample Collection	Test Article Lot No.
8	4	apoB-12192 (i.e., 12190)		plasma.	242-080405-04
9	4	apoB-13397 (i.e., 13395)			242-080405-05
10	4	apob-1-mismatch			233-061505-05
11	4	Protiva apob-1			242-080405-07
12	4	Protiva apob-1 no phosphate			242-080405-08

[0387] Body weights were measured daily, and cageside observations of animal behaviour and/or appearance were recorded daily. Animals were sacrificed on Day 3, 48 h after the single dose administration.

[0388] Animals were euthanized with a lethal dose of ketamine/xylazine and blood was collected via cardiac puncture prior to cervical dislocation. Blood was collected in a lavender EDTA microtainer (for plasma). The liver was removed whole, weighed, and immersed in at least 5 volumes of RNAlater. Spleens were removed whole and weighed.

[0389] ApoB and GAPDH mRNA levels in liver were measured using a QuantiGene assay kit (Genospectra, USA) according to the manufacturer's instructions. ApoB protein levels in plasma and/or serum were measured using an ELISA method essentially as described by Zlot et al. (Journal of Lipid Research, 1999, 40:76-84). Total cholesterol in plasma and/or serum was measured using an enzymatic method according to manufacturer's instructions (Infinity Cholesterol, Thermo Electron Corp, USA). Interferon-alpha levels in plasma were measured using a sandwich ELISA method according to manufacturer's instructions (Mouse Interferon- α , PBL Biomedical, Piscataway, N.J.).

[0390] Silencing efficacy of newly designed apoB siRNA: As shown in FIGS. 16 and 17, downregulation of ApoB in the mouse was observed at the 2 mg/kg dosage at 48 hours after dosing. Downregulation of apoB by the newly designed siRNA was achieved to the greatest extent with apoB-12192 (liver mRNA—54% decrease, plasma protein—35% decrease). Silencing of ApoB was expected to have additional biological consequences and these were measured in the form of lowered serum cholesterol levels (15% decrease with apoB-12192).

[0391] Immunostimulatory activity of newly designed apoB siRNA: Scoring of the newly designed apoB siRNA for the presence or absence of putative immunostimulatory motifs indicated that an absence of any such motifs correlated with a lack of induction of interferon- α release at 6 h in mouse plasma (see, FIG. 18).

Example 18

In Vitro Silencing of ApoB Expression Using SNALP Encapsulating Anti-ApoB siRNA

[0392] A panel of apoB siRNA were screened in vitro using HepG2 cells to assess their efficacy in silencing ApoB gene expression. Downregulation of secreted apoB protein

was demonstrated with a number of these siRNA, at levels matching or exceeding that of apoB-1.

[0393] Candidate Apolipoprotein B sequences were identified using the methods set forth in Example 1 above, by scanning and mouse ApoB (XM_137955) and human ApoB (NM_000384) sequences to identify AA dinucleotide motifs and the 21 nucleotides 3' of the motif. The sequences and their positions are set forth in Table 4 below.

TABLE 4

Mouse apoB	Human apoB	Sense	23 bp target sequence
327	428	AA	AGAGGUGUAUGGCUUCAAC CC
328	429	AA	GAGGUGUAUGGCUUCAACC CU
330	431	GA	GGUGUAUGGCUUCAACCCU GA
1151	1252	CA	GCCCCAUCACUUUACAAGC CU
1157	1258	CA	UCACUUUACAAGCCUUGGU UC
1167	1268	CA	AGCCUUGGUUCAGUGUGGA CA
1989	2090	AA	AAUAGAAGGGAAUCUUUAU UU
1990	2091	AA	AUAGAAGGGAAUCUUUAU UU
1991	2092	AA	UAGAAGGGAAUCUUUAUU UG
1993	2094	UA	GAAGGGAAUCUUUAUUUUG AU
1995	2096	GA	AGGGAAUCUUUAUUUUGAU CC
1996	2097	AA	GGGAAUCUUUAUUUUGAUC CA
2727	2828	CA	GAUGAACACCAACUUCUUC CA
2732	2833	GA	ACACCAACUUCUCCACGA GU
2733	2834	AA	CACCAACUUCUCCACGAG UC
3473	3574	AA	UGGACUCAUCUGCUACAGC UU
3475	3576	AA	AUGGACUCAUCUGCUACAG CU
3998	4099	CA	AGUCUGUGGGAUCCAUUCU GC
3999	4100	AA	GUCUGUGGGAUCCAUUCU CC
4242	4343	CA	AGGAUCUGGAGAAACAUA UA
4243	4344	AA	GGAUUCUGGAGAAACAUA AU
4246	4347	GA	UCUGGAGAAACAUAUUG AC
6560	6664	GA	UACAAUUUGAUCAGUAUUA UA

TABLE 4-continued

Mouse apoB	Human apoB	Sense	23 bp target sequence
6564	6668	CA	AUUUGAUCAGUAUUAUAAA GA
6565	6669	AA	UUUGAUCAGUAUUAUAAAAG AU
9098	9217	UA	UUGGAACUUUGAAAAAUUC UC
10048	10164	CA	AGUGUCAUCACACUGAAUA CC
10049	10165	AA	GUGUCAUCACACUGAAUAC CA
10055	10171	CA	UCACACUGAAUACCAAUGC UG
10346	10462	UA	AUGGAAAUACCAAGUCAAA AC
10347	10463	AA	UGGAAAUACCAAGUCAAAA AC
10886	11002	UA	ACACUAAGAACCAGAAGAU CA
12093	12299	AA	UUGGGAAGAAGAGGCAGCU UC

[0394] HepG2 cells (human hepatocellular carcinoma) were transfected with the murine siRNA sequences using Lipofectamine 2000 (Invitrogen) at a 100 nM dosage at the following ratios: 70 pmol siRNA:1 uL lipofectamine and 20 pmol siRNA:1 uL lipofectamine. Cells were plated on day 0, transfected with complexes on day 1, media was replaced with fresh media on day 2 and supernatants and cells were harvested on day 3 (48 h after transfection).

[0395] ApoB expression was measured by assaying the supernatants of transfected HepG2 cells for secreted apoB protein using an ELISA method essentially as described by Soutschek et al. (Nature, 2004, 432:173-78). Cell lysates were assayed for total protein using the BCA assay (BCA Micro Kit, Pierce). ApoB levels in HepG2 supernatants were normalized to total protein levels.

[0396] As shown in FIG. 19, downregulation of ApoB in HepG2 cells was observed at the 100 nM dosage at both transfection ratios. Downregulation of apoB by the newly designed siRNA was achieved with a number of the newly designed siRNA at levels matching or exceeding that of apoB-1. These include apob-10048, apob-10049, apob-10346 and apob-10884.

[0397] It is to be understood that the above description is intended to be illustrative and not restrictive. Many embodiments will be apparent to those of skill in the art upon reading the above description. The scope of the invention should, therefore, be determined not with reference to the above description, but should instead be determined with reference to the appended claims, along with the full scope of equivalents to which such claims are entitled. The disclosures of all articles and references, including patent applications, patents, PCT publications, and Accession Nos. are incorporated herein by reference for all purposes.

SEQUENCE LISTING

The patent application contains a lengthy "Sequence Listing" section. A copy of the "Sequence Listing" is available in electronic form from the USPTO web site (<http://seqdata.uspto.gov/?pageRequest=docDetail&DocID=US20060134189A1>). An electronic copy of the "Sequence Listing" will also be available from the USPTO upon request and payment of the fee set forth in 37 CFR 1.19(b)(3).

What is claimed is:

1. A nucleic acid lipid particle comprising:
 - a siRNA molecule that silences Apolipoprotein B (ApoB) expression;
 - a cationic lipid; and
 - a non-cationic lipid.
2. The nucleic acid-lipid particle in accordance with claim 1, wherein said nucleic acid-lipid particle comprises an siRNA molecule comprising a sequence set forth in Table 1, rows A-F of Table 2, and Tables 3-7.
3. The nucleic acid-lipid particle in accordance with claim 1, wherein said nucleic acid-particle comprises at least two siRNA molecules, wherein each siRNA molecule comprises a sequence independently selected from the sequences set forth in Table 1, rows A-F of Table 2, and Tables 3-7.
4. The nucleic acid-lipid particle in accordance with claim 1, wherein the siRNA silences ApoB expression by at least about 2 fold more than an siRNA that is not in a nucleic acid-lipid particle.

5. The nucleic acid-lipid particle in accordance with claim 1, wherein the siRNA silences ApoB expression by at least about 5 fold more than an siRNA that is not in a nucleic acid-lipid particle.

6. The nucleic acid-lipid particle in accordance with claim 1, wherein said cationic lipid is a member selected from the group consisting of N,N-dioleoyl-N,N-dimethylammonium chloride (DODAC), N,N-distearyl-N,N-dimethylammonium bromide (DDAB), N-(1-(2,3-dioleoyloxy)propyl)-N,N,N-trimethylammonium chloride (DOTAP), N-(1-(2,3-dioleoyloxy)propyl)-N,N,N-trimethylammonium chloride (DOTMA), and N,N-dimethyl-2,3-dioleoyloxypropylamine (DODMA), 1,2-DiLinoleoyloxy-N,N-dimethylaminopropane (DLinDMA), 1,2-Dilinolenyloxy-N,N-dimethylaminopropane (DLendMA), and a mixture thereof.

7. The nucleic acid-lipid particle in accordance with claim 1, wherein said cationic lipid is DLinDMA.

8. The nucleic acid-lipid particle in accordance with claim 1, wherein said non-cationic lipid is an anionic lipid.

9. The nucleic acid-lipid particle in accordance with claim 1, wherein said non-cationic lipid is a neutral lipid.

10. The nucleic acid-lipid particle in accordance with claim 1, wherein said non-cationic lipid is a member selected from the group consisting of dioleoylphosphatidylethanolamine (DOPE), palmitoyloleoylphosphatidylcholine (POPC), egg phosphatidylcholine (EPC), distearoylphosphatidylcholine (DSPC), palmitoyloleoylphosphatidylglycerol (POPG), dipalmitoyl phosphatidyl ethanolamine (DPPE), dimyristoylphosphoethanolamine (DMPE), distearoyl-phosphatidyl-ethanolamine (DSPE), 16-O-monomethyl PE, 16-O-dimethyl PE, 18-1-trans PE, palmitoyloleoylphosphatidylethanolamine (POPE), 1-stearoyl-2-oleoyl-phosphatidylethanolamine (SOPE), cholesterol, and a mixture thereof.

11. The nucleic acid-lipid particle in accordance with claim 1, wherein said non-cationic lipid is DSPC.

12. The nucleic acid-lipid particle in accordance with claim 1, further comprising a conjugated lipid that inhibits aggregation of particles

13. The nucleic acid-lipid particle in accordance with claim 12, wherein the conjugated lipid that inhibits aggregation of particles is a member selected from the group consisting of: a polyethyleneglycol (PEG)-lipid conjugate, a polyamide (ATTA)-lipid conjugate, and a mixture thereof.

14. The nucleic acid-lipid particle in accordance with claim 13, wherein the PEG-lipid conjugate is member selected from the group consisting of: a PEG-diacylglycerol (PEG-DAG), a PEG dialkylxypropyl (PEG-DAA), a PEG-phospholipid, a PEG-ceramide (PEG-Cer), and a mixture thereof.

15. The nucleic acid-lipid particle in accordance with claim 13, wherein the conjugated lipid that inhibits aggregation of particles comprises a PEG-DAA conjugate.

16. The nucleic acid-lipid particle in accordance with claim 15, wherein the PEG-DAA conjugate is a member selected from the group consisting of a PEG-dilauryloxypropyl (C_{12}), a PEG-dimyristyloxypropyl (C_{14}), a PEG-dipalmityloxypropyl (C_{16}), and a PEG-distearoxypropyl (C_{18}).

17. The nucleic acid-lipid particle in accordance with claim 15, wherein said PEG-DAA conjugate is a PEG-dimyristyloxypropyl (C_{14}).

18. The nucleic acid-lipid particle in accordance with claim 1, wherein said cationic lipid comprises from about 5 mol % to about 15 mol % of the total lipid present in said particle.

19. The nucleic acid-lipid particle in accordance with claim 1, wherein said cationic lipid comprises from about 30 mol % to about 50 mol % of the total lipid present in said particle.

20. The nucleic acid-lipid particle in accordance with claim 1, wherein said cationic lipid comprises from about 30 mol % to about 50 mol % of the total lipid present in said particle.

21. The nucleic acid-lipid particle in accordance with claim 1, wherein said cationic lipid comprises about 40 mol % of the total lipid present in said particle.

22. The nucleic acid-lipid particle in accordance with claim 1, wherein said non-cationic lipid comprises from about 5 mol % to about 90 mol % of the total lipid present in said particle.

23. The nucleic acid-lipid particle in accordance with claim 1, wherein said non-cationic lipid comprises from about 20 mol % to about 85 mol % of the total lipid present in said particle.

24. The nucleic acid-lipid particle in accordance with claim 15, wherein said PEG-DAA conjugate comprises from 0.5 mol % to about 20 mol % of the total lipid present in said particle.

25. The nucleic acid-lipid particle in accordance with claim 15, wherein said PEG-DAA conjugate comprises from 2 mol % to about 15 mol % of the total lipid present in said particle.

26. The nucleic acid-lipid particle in accordance with claim 15, wherein said PEG-DAA conjugate comprises about 2 mol % of the total lipid present in said particle.

27. The nucleic acid-lipid particle in accordance with claim 1, further comprising cholesterol.

28. The nucleic acid-lipid particle in accordance with claim 27, wherein the cholesterol comprises from about 0 mol % to about 10 mol % of the total lipid present in said particle.

29. The nucleic acid-lipid particle in accordance with claim 27, wherein the cholesterol comprises from about 10 mol % to about 60 mol % of the total lipid present in said particle.

30. The nucleic acid-lipid particle in accordance with claim 27, wherein the cholesterol comprises from about 20 mol % to about 45 mol % of the total lipid present in said particle.

31. The nucleic acid-lipid particle in accordance with claim 1, wherein the nucleic acid in said nucleic acid-lipid particle is not substantially degraded after exposure of said particle to a nuclease at 37° C. for 20 minutes.

32. The nucleic acid-lipid particle in accordance with claim 1, wherein the nucleic acid in said nucleic acid-lipid particle is not substantially degraded after incubation of said particle in serum at 37° C. for 30 minutes.

33. The nucleic acid-lipid particle in accordance with claim 1, wherein the nucleic acid is fully encapsulated in said nucleic acid-lipid particle.

34. The nucleic acid-lipid particle in accordance with claim 1, wherein said particle has a nucleic acid:lipid ratio (mg:mg) of from about 0.01 to about 0.2.

35. The nucleic acid-lipid particle in accordance with claim 1, wherein said particle has a nucleic acid:lipid ratio (mg:mg) of from about 0.02 to about 0.1.

36. The nucleic acid-lipid particle in accordance with claim 1, wherein said particle has a nucleic acid:lipid ratio (mg:mg) of about 0.04.

37. The nucleic acid-lipid particle in accordance with claim 1, wherein said particle has a median diameter of less than about 150 nm.

38. The nucleic acid-lipid particle in accordance with claim 1, wherein said particle has a median diameter of less than about 100 nm.

39. A pharmaceutical composition comprising a nucleic acid-lipid particle in accordance with claim 1 and a pharmaceutically acceptable carrier.

40. A method of introducing an siRNA that silences ApoB expression into a cell, said method comprising contacting said cell with a nucleic acid-lipid particle comprising a cationic lipid, a non-cationic lipid, and said siRNA.

41. The method of claim 40, wherein said nucleic acid-lipid particle further comprises a conjugated lipid that inhibits aggregation of particles.

42. The method of claim 40, wherein said nucleic acid-lipid particle comprises an siRNA molecule comprising any one of the sequences set forth in Table 1, rows A-F of Table 2, and Tables 3-7.

43. The method of claim 40, wherein said nucleic acid-lipid particle comprises at least two siRNA molecules, wherein each siRNA molecule comprises a sequence independently selected from the sequences set forth in Table 1, rows A-F of Table 2, and Tables 3-7.

44. The method of claim 40, wherein said siRNA in said nucleic acid-lipid particle is resistant in aqueous solution to degradation with a nuclease.

45. The method of claim 40, wherein said cationic lipid is a member selected from the group consisting of DODAC, DDAB, DOTAP, DOTMA, DODMA, DLinDMA, DLenDMA, and a mixture thereof.

46. The method of claim 40, wherein said non-cationic lipid is a member selected from the group consisting of DOPE, POPC, EPC, DSPC, POPG, DPPE, DMPE, DSPE, 16-O-monomethyl PE, 16-O-dimethyl PE, 18-1-trans PE, POPE, SOPE, cholesterol, and a mixture thereof.

47. The method of claim 40, wherein the conjugated lipid that inhibits aggregation of particles comprises a PEG-lipid conjugate selected from the group consisting of: a PEG-DAG, a PEG-DAA, a PEG-phospholipid, a PEG-Cer, and a mixture thereof.

48. The method of claim 40, wherein said cell is in a mammal.

49. The method of claim 48, wherein said contacting comprises administering said nucleic acid-lipid particle via a route selected from the group consisting of: intravenous, subcutaneous, and intraperitoneal.

50. The method of claim 48, wherein the mammal is a human.

51. The method of claim 50, wherein said human has a disease or disorder associated with expression of a ApoB and wherein expression of ApoB is silenced by said siRNA.

52. The method of claim 50, wherein said disease or disorder is associated with overexpression of ApoB and wherein expression of ApoB is silenced by said siRNA.

53. The method of claim 50, wherein said human has a disease or disorder selected from the group consisting of: atherosclerosis, angina pectoris, high blood pressure, diabetes, and hypothyroidism.

54. The method of claim 50, wherein said human has a disease or disorder involving hypercholesterolemia and wherein serum cholesterol levels are lowered when expression of ApoB is silenced by said siRNA.

55. The method of claim 54, wherein said disease is a member selected from the group consisting of: atherosclerosis, angina pectoris, and high blood pressure.

56. An isolated nucleic acid comprising a sequence set forth in in Table 1, rows A-F of Table 2, and Tables 3-7.

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