

	U		G	
560	GAGAAGCCAUUAUCUGCA A	68	UUGCAGAUAAUGGCUUCU C	69
614	CUAUCAUCAUAGGUCGUC A	70	UGACGACCUAUGAUGAUA G	71
618	CAUCAUAGGUCGUCAUGC U	72	AGCAUGACGACCUAUGAU G	73
621	CAUAGGUCGUCAUGCUIA U	74	AUAAGCAUGACGACCUIA G	75
691	GAGUAACCUACACACCA A	76	UUGGUGUGUAGGUUAUCU C	77
735	CCUGGUACAUACUUUGA A	78	UUCAAGUUUUGUACCAG G	79
747	CUUUGAAGAAGGUGGUGG U	80	ACCACCACCUUCUUCAAA G	81
775	GGGAUGUAUAUCAAGAU A	82	UAUCUUGAUUAUCAUCC C	83
811	GCACACAGUCCUUCCAA A	84	UUUGGAAGGAACUGUGUG C	85
818	GUCCUUCCAAUUGGCUC U	86	AGAGCCAUUUGGAAGGAA C	87
844	GGUUGGCCUUUGUAUCUG A	88	UCAGAUACAAAGGCCAAC C	89
851	CUUUGUAUCUGAGCACCA A	90	UUGGUGCUCAGAUACAAA G	91
882	GAAGAAAUAUGAUGGGCG U	92	ACGCCCAUCAUAUUUCUU C	93
942	GUCCAGUUUGAAGCUCA A	94	UUGAGCUUCAACUGGGA C	95
968	GGUAUGAGCAUAGGCUCA U	96	AUGAGCCUAGCUCUAC C	97
998	GGCCCAAGCUAUGAAAUC A	98	UGAUUUCUAGCUUGGGC C	99
1001	CCCAAGCUAUGAAAUCAG A	100	UCUGAUUUCUAGCUUGG G	101
1127	CAGAUGGCAAGACAGUAG A	102	UCUACUGUCUUGCCAUCU G	103
1133	GCAAGACAGUAGAAGCAG A	104	UCUGCUUCUACUGUCUUG C	105
1184	GCAUGUACCAGAAAGGAC A	106	UGUCCUUUCUGGUACAUG C	107
1214	CCAAUCCAUUGCUUCCA U	108	AUGGAAGCAAUGGGAUUG G	109
1257	CCACAGAGCAAAGCUUGA U	110	AUCAAGCUUUGCUCUGUG G	111
1258	CACAGAGCAAAGCUUGAU A	112	UAUCAAGCUUUGCUCUGU G	113
1262	GAGCAAAGCUUGAUACA A	114	UUGUUAUCAAGCUUUGCU C	115
1285	GAGCUUGCCUUCUUUGCA A	116	UUGCAAAGAAGGCAAGCU C	117
1296	CUUUGCAAUUGCUUUGGA A	118	UUCAAGCAUUUGCAA G	119
1301	CAAUUGCUUUGGAAGAAG U	120	ACUUCUCCAAAGCAUUU G	121
1307	CUUUGGAAGAAGUCUCUA U	122	AUAGAGACUUCUCCAAA G	123
1312	GAAGAAGUCUCUAUUGAG A	124	UCUCAUAGAGACUUCUU C	125

1315	GAAGUCUCUAUUGAGACA A	126	UUGUCUCAUAGAGACUU C	127
1356	GGACUUGGCUGCUUGCAU U	128	AAUGCAAGCAGCCAAGUC C	129
1359	CUUGGCUGCUUGCAUUA A	130	UUUAAUGCAAGCAGCCAA G	131
1371	CAUUAAGGUUUACCCAA U	132	AUUGGGUAAACCUUUAAU G	133
1385	CCAAUGUGCAACGUUCUG A	134	UCAGAACGUUGCACAUG G	135
1390	GUGCAACGUUCUGACUAC U	136	AGUAGUCAGAACGUUGCA C	137
1396	CGUUCUGACUACUUGAAU A	138	UAUUCAAGUAGUCAGAAC G	139
1415	CAUUUGAGUUCAUGGAUA A	140	UUAUCCAUGAACUCAAAU G	141
1422	GUUCAUGGAUAAACUUGG A	142	UCCAAGUUUAUCCAUGAA C	143
1425	CAUGGAUAAACUUGGAGA A	144	UUCUCCAAGUUUAUCCA G	145
1455	CAAACUAGCUCAGGCCAA A	146	UUUGGCCUGAGCUAGUUU G	147
1487	CCUGAGCUAAGAAGGAUA A	148	UUAUCCUUCUAGCUCAG G	149
1493	CUAAGAAGGAUAAUUGUC U	150	AGACAAUUAUCCUUCUUA G	151
1544	CUGUGUUACACUCAAGGA U	152	AUCCUUGAGUGUAACACA G	153
1546	GUGUACACUCAAGGAUA A	154	UUAUCCUUGAGUGUAACA C	155
1552	CACUCAAGGAUAAAGGCA A	156	UUGCCUUUAUCCUUGAGU G	157
1581	GUAUUUUGUUAGAAGCC A	158	UGGCUUCUAAACAAAUA C	159
1646	GUUAUUGCCACCUUUGUG A	160	UCACAAAGGUGGCAAUAA C	161
1711	CAGCCUAGGAAUUCGGUU A	162	UAACCGAAUCCUAGGCU G	163
1713	GCCUAGGAAUUCGGUUAG U	164	ACUAACCGAAUCCUAGG C	165
1714	CCUAGGAAUUCGGUUAGU A	166	UACUAACCGAAUCCUAG G	167
1718	GGAAUUCGGUUAGUACUC A	168	UGAGUACUAACCGAAUUC C	169
1719	GAAUUCGGUUAGUACUCA U	170	AUGAGUACUAACCGAAU C	171
1725	GGUUAGUACUCAUUUGUA U	172	AUACAAAUGAGUACUAAC C	173
1730	GUACUCAUUUGUAUUCAC U	174	AGUGAAUACAAAUGAGUA C	175
1804	GGUAAAUGAUAGCCACAG U	176	ACUGUGGCUAUCAUUUAC C	177
1805	GUAAAUGAUAGCCACAGU A	178	UACUGUGGCUAUCAUUUA C	179
1816	CCACAGUAUUGCUCUUUA A	180	UUAGGGAGCAAUACUGUG G	181
1892	GGGAAGUUCUGGUGUCAU A	182	UAUGACACCAGAACUCC C	183
1897	GUUCUGGUGUCAUAGUA A	184	AUAUCAUGACACCAGAA A	185

	U		C	
1934	GCUGUGCAUUAAACUUGC A	186	UGCAAGUUUAAUGCACAG C	187
1937	GUGCAUUAAACUUGCACA U	188	AUGUGCAAGUUUAAUGCA C	189
1939	GCAUUAAACUUGCACAUG A	190	UCAUGUGCAAGUUUAAUG C	191
1953	CAUGACUGGAACGAAGUA U	192	AUACUUCGUUCCAGUCAU G	193
1960	GGAACGAAGUAUGAGUGC A	194	UGCACUCAUACUUCGUUC C	195
1961	GAACGAAGUAUGAGUGCA A	196	UUGCACUCAUACUUCGUU C	197
1972	GAGUGCAACUCAAAUGUG U	198	ACACAUUUGAGUUGCACU C	199
1976	GCAACUCAAAUGUGUUGA A	200	UUCAACACAUUUGAGUUG C	201
1982	CAAUGUGUUGAAGAUAC U	202	AGUAUCUUCAACACAUUU G	203
1987	GUGUUGAAGAUACUGCAG U	204	ACUGCAGUAUCUUCAACA C	205
1989	GUUGAAGAUACUGCAGUC A	206	UGACUGCAGUAUCUUCAA C	207
2020	CCUUGCUGAAUGUUUCCA A	208	UUGGAAACAUUCAGCAAG G	209
2021	CUUGCUGAAUGUUUCCAA U	210	AUUGGAAACAUUCAGCAA G	211
2024	GCUGAAUGUUUCCAAUAG A	212	UCUAUUGGAAACAUUCAG C	213
2035	CCAAUAGACUAAAUACUG U	214	ACAGUAUUUAGUCUAUUG G	215
2067	GAGUUUGGAAUCCGGAAU A	216	UAUUCGGAAUCCAAACU C	217
2073	GGAAUCCGGAAUAAAUAC U	218	AGUAUUUUAUUCGGAUUC C	219
2074	GAAUCCGGAAUAAAUACU A	220	UAGUAUUUAUUCGGAAU C	221
2080	GGAAUAAAUACUACCUGG A	222	UCCAGGUAGUAUUUAUUC C	223
2133	GGCCUGGCCUGAAUUAUUA U	224	AUAAUAUUCAGGCCAGGC C	225
2134	GCCUGAAUUAUUAUCUAC U	226	AGUAGUAUAAUUAUUCAGG C	227
2136	CUGGCCUGAAUUAUUAUC U	228	AGUAUAAUUAUUCAGGCCA G	229
2166	CAUAAUUCAUCCAAGUGC A	230	UGCACUUGGAUGAAUAU G	231
2180	GUGCAAUAAUGUAAGCUG A	232	UCAGCUUACAUUAUUGCA C	233
2182	GCAUAAUGUAAGCUGAA U	234	AUUCAGCUUACAUUAUUG C	235
2272	CACUAUCUUAUCUUCUCC U	236	AGGAGAAGAUAAAGAUAGU G	237
2283	CUUCUCCUGAACUGUUGA U	238	AUCAACAGUUCAGGAGAA G	239

**Table 8. siRNAs targeting wildtype IDH1**

Position on mRNA (FIG. 21B)	sense (5' to 3')	SEQ ID NO:	antisense (5' to 3')	SEQ ID NO:
611	AACCUAUCAUCAUAGGUC G	240	CGACCUAUGAUGAUAGGU U	241
612	ACCUAUCAUCAUAGGUCG U	242	ACGACCUAUGAUGAUAGG U	243
613	CCUAUCAUCAUAGGUCGU C	244	GACGACCUAUGAUGAUAG G	245
614	CUAUCAUCAUAGGUCGUC A	246	UGACGACCUAUGAUGAUA G	247
615	UAUCAUCAUAGGUCGUCA U	248	AUGACGACCUAUGAUGAU A	249
616	AUCAUCAUAGGUCGUCAU G	250	CAUGACGACCUAUGAUGA U	251
617	UCAUCAUAGGUCGUCAUG C	252	GCAUGACGACCUAUGAUG A	253
618	CAUCAUAGGUCGUCAUGC U	254	AGCAUGACGACCUAUGAU G	255
619	AUCAUAGGUCGUCAUGC U	256	AAGCAUGACGACCUAUGA U	257
620	UCAUAGGUCGUCAUGC A	258	UAAGCAUGACGACCUAUG A	259
621	CAUAGGUCGUCAUGC U	260	AUAAGCAUGACGACCUAU G	261
622	AUAGGUCGUCAUGC G	262	CAUAAGCAUGACGACCUA U	263
623	UAGGUCGUCAUGC G	264	CCAUAAGCAUGACGACCU A	265
624	AGGUCGUCAUGC G	266	CCCAUAAGCAUGACGACC U	267
625	GGUCGUCAUGC G	268	CCCCAUAAGCAUGACGAC C	269
626	GUCGUCAUGC A	270	UCCCAUAAGCAUGACGAC C	271
627	UCGUCAUGC U	272	AUCCCAUAAGCAUGACGA C	273

**Table 9. siRNAs targeting G395A mutant IDH1 (SEQ ID NO:5) (equivalent to G629A of SEQ ID NO:9 (FIG. 21B))**

Position on mRNA (FIG. 21B)	sense (5' to 3')	SEQ ID NO:	antisense (5' to 3')	SEQ ID NO:
611	AACCUAUCAUCAUAGGUCA	274	UGACCUAUGAUGAUAGGUU	275
612	ACCUAUCAUCAUAGGUCAU	276	AUGACCUAUGAUGAUAGGU	277
613	CCUAUCAUCAUAGGUCAUC	278	GAUGACCUAUGAUGAUAGG	279
614	CUAUCAUCAUAGGUCAUCA	280	UGAUGACCUAUGAUGAUAG	281
615	UAUCAUCAUAGGUCAUCAU	282	AUGAUGACCUAUGAUGAUA	283

616	AUCAUCAUAGGUCAUCAUG	284	CAUGAUGACCUAUGAUGAU	285
617	UCAUCAUAGGUCAUCAUGC	286	GCAUGAUGACCUAUGAUGA	287
618	CAUCAUAGGUCAUCAUGCU	288	AGCAUGAUGACCUAUGAUG	289
619	AUCAUAGGUCAUCAUGCUU	290	AAGCAUGAUGACCUAUGAU	291
620	UCAUAGGUCAUCAUGCUUA	292	UAAGCAUGAUGACCUAUGA	293
621	CAUAGGUCAUCAUGCUUAU	294	AUAAGCAUGAUGACCUAUG	295
622	AUAGGUCAUCAUGCUUAUG	296	CAUAAGCAUGAUGACCUAU	297
623	UAGGUCAUCAUGCUUAUGG	298	CCAUAAGCAUGAUGACCUA	299
624	AGGUCAUCAUGCUUAUGGG	300	CCCAUAAGCAUGAUGACCU	301
625	GGUCAUCAUGCUUAUGGGG	302	CCCCAUAAGCAUGAUGACC	303
626	GUUCAUCAUGCUUAUGGGGA	304	UCCCCAUAAGCAUGAUGAC	305
627	UCAUCAUGCUUAUGGGGAU	306	AUCCCCAUAAGCAUGAUGA	307

**Table 10.** siRNAs targeting C394A mutant IDH1 (SEQ ID NO:5) (equivalent to C628A of SEQ ID NO:9 (FIG. 21B)) (Arg132Ser (SEQ ID NO:8))

Position on mRNA (FIG. 21B)	sense (5' to 3')	SEQ ID NO:	antisense (5' to 3')	SEQ ID NO:
611	AACCUAUCAUCAUAGGUAG	308	CUACCUAUGAUGAUAGGUU	309
612	ACCUAUCAUCAUAGGUAGU	310	ACUACCUAUGAUGAUAGGU	311
613	CCUAUCAUCAUAGGUAGUC	312	GACUACCUAUGAUGAUAGG	313
614	CUAUCAUCAUAGGUAGUCA	314	UGACUACCUAUGAUGAUAG	315
615	UAUCAUCAUAGGUAGUCAU	316	AUGACUACCUAUGAUGAUA	317
616	AUCAUCAUAGGUAGUCAUG	318	CAUGACUACCUAUGAUGAU	319
617	UCAUCAUAGGUAGUCAUGC	320	GCAUGACUACCUAUGAUGA	321
618	CAUCAUAGGUAGUCAUGCU	322	AGCAUGACUACCUAUGAUG	323
619	AUCAUAGGUAGUCAUGCUU	324	AAGCAUGACUACCUAUGAU	325
620	UCAUAGGUAGUCAUGCUUA	326	UAAGCAUGACUACCUAUGA	327
621	CAUAGGUAGUCAUGCUUAU	328	AUAAGCAUGACUACCUAUG	329
622	AUAGGUAGUCAUGCUUAUG	330	CAUAAGCAUGACUACCUAU	331
623	UAGGUAGUCAUGCUUAUGG	332	CCAUAAGCAUGACUACCUA	333
624	AGGUAGUCAUGCUUAUGGG	334	CCCAUAAGCAUGACUACCU	335
625	GGUAGUCAUGCUUAUGGGG	336	CCCCAUAAGCAUGACUACC	337
626	GUAGUCAUGCUUAUGGGGA	338	UCCCCAUAAGCAUGACUAC	339
627	UAGUCAUGCUUAUGGGGAU	340	AUCCCCAUAAGCAUGACUA	341

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