

# SEQUENCES OF PROTEINS OF IMMUNOLOGICAL INTEREST

FIFTH EDITION

Tabulation and Analysis of  
Amino Acid and Nucleic Acid Sequences of Precursors,  
V-Regions, C-Regions, J-Chain, T-Cell Receptors for Antigen,  
T-Cell Surface Antigens,  $\beta_2$ -Microglobulins,  
Major Histocompatibility Antigens, Thy-1, Complement,  
C-Reactive Protein, Thymopoietin, Integrins, Post-gamma Globulin,  
 $\alpha_2$ -Macroglobulins, and Other Related Proteins

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	'CL	'CL	'CL	'CL	'CL	'CL	'CL	'CL	'CL	'CL	'CL	'CL	'CL	'CL	'CL	'CL	'CL	'CL	'CL	'CL	'CL	'CL	'CL	'CL	'CL
0																									
1	ASP	ASP	ASP	ala	ASP	ASP	ala	val	ASX	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP
2	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE
3	GLN	GLN	GLN	GLN	GLN	GLN	arg	trp	GLX	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN
4	LEU	MET	MET	MET	MET	LEU	met	met	met	met	met	met	met	met	met	met	met	met	met	met	met	met	met	met	met
5	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
6	GLN	GLN	GLN	GLN	GLN	GLN	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
7	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
8	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO
9	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
10	phe	ser	ser	ser	ser	ser	ser	leu	ser	thr	ser	ser	ser	ser	ser	pro	ser	ser	ser	ser	thr	thr	thr	thr	thr
11	LEU	LEU	LEU	LEU	LEU	LEU	phe	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
12	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
13	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA
14	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
15	VAL	VAL	VAL	VAL	VAL	VAL	thr	thr	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
16	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
17	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP
18	THR	arg	arg	arg	arg	arg	arg	arg	arg	arg	arg	arg	arg	arg	arg	arg	arg	arg	arg	arg	arg	arg	arg	arg	arg
19	val	val	val	val	val	val	val	val	val	val	val	val	val	val	val	val	val	val	val	val	val	val	val	val	val
20	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
21	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE
22	THR	THR	THR	THR	THR	THR	THR	ser	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
23	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS
24	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	gln	gln	gln	gln	lys	gln	gln	ARG	gln	gln
25	ALA	ALA	ALA	ALA	ALA	ALA	ALA	met	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA
26	SER	SER	arg	SER	SER	SER	SER	SER	gln	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
27	GLN	GLN	arg	GLN	GLN	GLN	GLN	GLN	GLN	GLN	his	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLX	GLN
27A	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
27B	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
27C	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
27D	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
27E	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
27F	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
28	gly	ser	gly	gly	gly	ser	gly	gly	ser	ser	ser	gly	gly	asp	asp	asp	asp	asn	asp	asp	ser	thr	asn	asn	ser
29	ILE	ILE	ILE	ILE	ILE	val	ILE	ILE	val	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE
30	ser	ser	ser	ser	ser	tyr	ser	ser	asn	ser	gln	ser	asn	lys	ser	arg	asp	asn	arg	asp	lys	val	asn	asn	asn
31	asn	asn	asn	asn	asn	asn	asn	asn	asn	asn	asn	asn	asn	asn	asn	asn	asn	asn	asn	asn	asn	asn	asn	asn	asn
32	tyr	tyr	TRP	ala	asn	tyr	tyr	tyr	tyr	TRP	ser	gln	asn	tyr	tyr	phe	ser	tyr	tyr	his	tyr	tyr	tyr	tyr	phe
33	LEU	LEU	LEU	LEU	LEU	val	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
34	ALA	asn	ALA	ALA	asn	ALA	ALA	ALA	asn	ALA	asn	ser	asn	asn	asn	asn	ile	asn	asn	asn	asn	asn	asn	ALA	ALA
35	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP
36	tyr	tyr	tyr	tyr	tyr	tyr	tyr	tyr	tyr	tyr	tyr	tyr	tyr	tyr	tyr	tyr	tyr	tyr	tyr	tyr	tyr	tyr	tyr	tyr	tyr
37	GLN	GLN	GLN	GLN	GLN	gln	gln	gln	gln	his	gln	gln	gln	gln	gln	gln	gln	gln	gln	gln	gln	gln	gln	gln	gln
38	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN
39	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	thr	lys	lys	lys	lys	#	lys	lys	lys	lys	lys	lys
40	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO
41	GLY	GLY	gln	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	#	GLY	GLY	GLY	GLY	GLY	GLY
42	ALA	ALA	ALA	ALA	thr	ALA	ALA	ALA	ALA	ALA	ALA	ALA	thr	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA
43	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO
44	LEU	lys	lys	lys	lys	lys	lys	gln	lys	asn	thr	lys	lys	lys	lys	lys	lys	lys	arg	lys	lys	lys	gln	lys	lys
45	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
46	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE
47	THR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	phe	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR
48	ALA	ala	ala	asp	ala	asp	ala	ala	ala	gln	gln	ala	ala	ala	ala	ala	ala	ala	ala	ala	ala	ala	ala	ala	ala
49	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA
50	ALA	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
51	thr	ser	ser	ser	ser	thr	thr	thr	thr	ile	ser	ser	ser	ser	ser	ser	asn	asn	asn	lys	asn	asn	thr	thr	asn
52	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
53	gln	gln	gln	gln	gln	gln	gln	gln	gln	gln	gln	gln	gln	gln	gln	gln	gln	gln	gln	gln	gln	gln	gln	gln	gln
54	ser	ser	ser	ser	ser	ser	ser	ser	ser	ser	ser	ser	ser	ser	ser	ser	ser	ser	ser	ser	ser	ser	ser	ser	ser
55	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
56	val	val	val	val	val	val	val	val	val	val	val	val	val	val	val	val	val	val	val	val	val	val	val	val	val
57	PRO	thr	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO
58	SER	ARG	ARG	ARG	ARG	asn	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG
59	ARG	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE
60	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
61	GLY	GLY	GLY	GLY	asp	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
62	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
63	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
64	THR	THR	THR	THR	ala	THR																			











## HUMAN KAPPA LIGHT CHAINS SUBGROUP I (cont'd)

	125 AMYLOID	126 HBJ 6	127 AMYLOID MS #	128 PEN	# OF SEQUENCES	# OF AMINO ACIDS	OCCURRENCES OF MOST COMMON AMINO ACID	VARIABILITY
					1	1	1 (PCA)	
0					125	3, 4	122 (ASP), 118 (ASP)	3, 1, 4, 2
1	ASP	ASP	ASP	ASP	123	2	120 (ILE)	2
2	ILE	ILE	ILE	ILE	123	7	116 (GLN), 112 (GLN)	7, 4, 7, 7
3	glu	GLN	GLN	GLN	123	4	109 (MET)	4, 6
4	MET	MET	MET	MET	124	3	122 (THR)	3
5	pro	THR	THR		124	1, 2	123 (GLN), 116 (GLN)	1, 2, 2, 1
6	GLN	GLN			123	2	120 (SER)	2
7	SER				121	2	120 (PRO)	2
8	PRO				121	4	117 (SER)	4, 1
9	SER				121	4	117 (SER)	4, 1
FR 1					120	5	89 (SER)	6, 7
11	ser	LEU			119	4	111 (LEU)	4, 3
12					118	3	115 (SER)	3, 1
13					117	4	107 (ALA)	4, 4
14					113	6	106 (SER)	6, 4
15					113	3	109 (VAL)	3, 1
16					109	2	108 (GLY)	2
17					109	3, 4	106 (ASP), 98 (ASP)	3, 1, 4, 4
18					106	6	97 (ARG)	6, 6
19					107	3	101 (VAL)	3, 2
20					106	4	102 (THR)	4, 2
21					104	4	99 (ILE)	4, 2
22					104	6	95 (THR)	6, 6
23					96	1	96 (CYS)	1
24					88	6	57 (ARG)	9, 3
25					88	6	82 (ALA)	6, 4
26					85	4	79 (SER)	4, 3
27					84	4	79 (GLN), 66 (GLN)	4, 3, 5, 1
27A					3	2	2 (SER)	
27B					3	2	2 (LEU)	
27C					3	2	2 (VAL)	
27D					3	2	1 ( + )	
27E					3	2	1 ( + )	
27F					2	2	1 ( + )	
CDR 1					84	7	29 (SER)	20
28					83	5	72 (ILE)	5, 8
29					81	11	41 (SER)	22
30					79	11	27 (ASN), 24 (SER)	35, 39
31					79	9	34 (TYR)	21
32					77	4	73 (LEU)	4, 2
33					77	4	73 (LEU)	4, 2
34					73	7, 8	30 (ALA)	17, 19
35					76	1	76 (TRP)	1
36					74	2	66 (TYR)	2, 2
37					73	4	68 (GLN), 61 (GLN)	4, 3, 4, 8
38					71	4	68 (GLN), 63 (GLN)	4, 2, 4, 5
39					68	4	62 (LYS)	4, 4
40					70	3	68 (PRO)	3, 1
41					58	3	54 (GLY)	3, 2
42					60	6	49 (LYS)	7, 3
43					61	4	57 (ALA)	4, 3
44					61	1	61 (PRO)	1
45					61	7, 8	46 (LYS)	9, 3, 11
46					60	7	42 (LEU)	10
47					59	2	58 (LEU)	2
48					57	2	56 (ILE)	2
49					59	4	55 (TYR)	4, 3
CDR 2					59	9	19 (ALA)	28
50					59	5	50 (ALA)	5, 9
51					58	6	53 (SER)	6, 6
52					57	6, 7	26 (SER)	13, 15
53					58	2	56 (LEU)	2, 1
54					58	8, 9	25 (GLU)	19, 21
55					56	8	34 (SER)	13
56					57	1	57 (GLY)	1
57					58	3	50 (VAL)	3, 5
58					57	4	54 (PRO)	4, 2
59					57	1	57 (SER)	1
60					58	3	56 (ARG)	3, 1
61					57	3	55 (PHE)	3, 1
62					57	3	55 (PHE)	3, 1
63					57	6	50 (SER)	6, 8
64					57	2	55 (GLY)	2, 1
65					56	5	51 (SER)	2, 5
66					57	4	54 (GLY)	4, 2
67					55	3	51 (SER)	3, 2
68					55	3	52 (GLY)	3, 2
69					55	2	51 (THR)	2, 2
70					55	5, 6	33 (ASP), 31 (ASP)	8, 3, 11
71					54	4	49 (PHE)	4, 4
72					54	4	50 (THR)	5, 4
73					54	3	43 (LEU)	3, 8
74					54	4	51 (THR)	4, 2
75					54	3	47 (ILE)	3, 4
76					53	5	43 (SER)	6, 2
77					54	6	40 (SER)	8, 1
78					54	2	53 (LEU)	2
79					54	3, 4	52 (GLN), 48 (GLN)	3, 2, 4, 5
80					54	2	46 (PRO)	2, 3
81					54	3, 5	37 (GLU), 34 (GLU)	4, 4, 7, 9
82					54	2	53 (ASP), 50 (ASP)	2, 2, 2
83					54	4	40 (PHE)	5, 4
84					54	2	53 (ALA)	2
85					54	6	48 (THR)	6, 7
86					56	2	55 (TYR)	2
87					55	2	52 (TYR)	2, 1
88					56	1	56 (CYS)	1
89					57	4, 5	46 (GLN), 43 (GLN)	5, 6, 6
90					57	2, 3	51 (GLN), 46 (GLN)	2, 2, 3, 7
91					59	11, 12	28 (TYR)	23, 25
92					60	9	20 (ASN), 19 ( + )	27, 28
93					60	9	29 (SER)	19
CDR 3					60	12	15 (LEU)	48
94					56	4	44 (PRO)	5, 1
95					1	1	1 (GLU)	
95A								
95B								
95C								
95D								
95E								
95F								
96					44	12	10 (TRP)	53
97					43	4	39 (THR)	4, 4
98					46	3	44 (PHE)	3, 1
99					46	1	46 (GLY)	1
100					46	4, 5	28 (GLN), 27 (GLN)	6, 6, 8, 5
101					46	1	46 (GLY)	1
102					46	2	45 (THR)	2
103					46	4	38 (LYS)	4, 8
104					45	2	36 (VAL)	2, 5
105					45	4, 5	29 (GLU), 28 (GLU)	6, 2, 8
106					46	7	30 (ILE)	11
106A								
107					45	3	42 (LYS)	3, 2
108					33	2	31 (ARG)	2, 1
109					22	1	22 (THR)	1



## ANTIBODY SPECIFICITIES: HUMAN KAPPA LIGHT CHAINS SUBGROUP I

- 7) 3D6'CL: ANTI-HIV gp41
- 15) HF2-1/17: PLATE-BINDING ANTI-DNA AUTOANTIBODY
- 20) WEA: ANTI-3,4-PYRUVYLATED GALACTOSE MONOCLONAL
- 42) HuVHCAMP'CL: ANTI-HUMAN LYMPHOCYTE HYBRIDOMA
- 47) LAY: ANTI-HUMAN GAMMA G1 AND G3 GLOBULINS; PO IDIOTYPE
- 51) HuRSV19VK: ANTI-HUMAN RESPIRATORY SYNCYTIAL VIRUS
- 72) DAV: ANTI-HUMAN GAMMA G GLOBULIN
- 73) FIN: ANTI-HUMAN GAMMA G GLOBULIN
- 81) LOW: COLD AGGLUTININ WITH ANTI-BLOOD GROUP I ACTIVITY
- 101) H-G2b: ANTI-Haemophilus influenzae TYPE b CAPSULAR POLYSACCHARIDE
- 102) K-G2: ANTI-Haemophilus influenzae TYPE b CAPSULAR POLYSACCHARIDE
- 105) HEI: COLD AGGLUTININ WITH ANTI-GD (MEMBRANE-GLYCOLIPID-DEPENDENT) ACTIVITY
- 107) H-G2a: ANTI-Haemophilus influenzae TYPE b CAPSULAR POLYSACCHARIDE
- 110) WAG: ANTI-DINITROPHENYL
- 123) MAR: ANTI-LIPOPROTEIN LIPASE

## ALLOTYPE: HUMAN KAPPA LIGHT CHAINS SUBGROUP I

- 14) KUZ: INV(2)

## CLASS: HUMAN KAPPA LIGHT CHAINS SUBGROUP I

- 1) 2C12'CL: IGM-KAPPA
- 2) 1B11'CL: IGM-KAPPA
- 3) 1H1'CL: IGM-KAPPA
- 4) 2A12'CL: IGM-KAPPA
- 7) 3D6'CL: IGG1-KAPPA
- 15) HF2-1/17: IGM-KAPPA
- 20) WEA: IGM-KAPPA
- 42) HuVHCAMP'CL: IGG1-KAPPA
- 67) G1'CL: IGM-KAPPA
- 74) FW: IGG1-KAPPA
- 79) RI: IGG1-KAPPA
- 89) F-GUI: IGG3-KAPPA
- 90) S-GUI: IGG3-KAPPA

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- 3) 1H1'CL: LEVY, S., MENDEL, E., KON, S., AVNUR, Z. & LEVY, R. (1988) J. EXP. MED., 168, 475-489.
- 4) 2A12'CL: LEVY, S., MENDEL, E., KON, S., AVNUR, Z. & LEVY, R. (1988) J. EXP. MED., 168, 475-489.
- 5) BR: KIM, H.S. & DEUTSCH, H.F. (1988) IMMUNOL., 64, 573-579.
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- 7) 3D6'CL: FELGENHAUER, M., KOHL, J. & RUKER, F. (1990) NUCL. ACIDS RES., 18, 4927.
- 8) HK102'CL: BENTLEY, D.L. & RABBITTS, T.H. (1980) NATURE, 288, 730-733. (CHECKED BY AUTHOR 11/30/82)
- 9) EU: GOTTILIEB, P.D., CUNNINGHAM, B.A., RUTISHAUSER, U. & EDELMAN, G.M. (1970) BIOCHEMISTRY, 9, 3155-3161. (CHECKED BY AUTHOR)
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- 15) HF2-1/17: ATKINSON, P.M., LAMPMAN, G.W., FURIE, B.C., NAPARSTEK, Y., SCHWARTZ, R.S., STOLLAR, B.D. & FURIE, B. (1985) J. CLIN. INVEST., 75, 1138-1143. (CHECKED BY AUTHOR 08/21/85); LAMPMAN, G.W., FURIE, B., SCHWARTZ, R.S., STOLLAR, B.D. & FURIE, B.C. (1989) BLOOD, 74, 262-269.
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- 19) OUI(IOC): KOHLER, H., SHIMIZU, A., PAUL, C. & PUTNAM, F.W. (1970) SCIENCE, 169, 56-59. (KAPLAN, A.P. & METZGER, H. (1969) BIOCHEMISTRY, 8, 3944-3951.) (CHECKED BY AUTHOR 06/15/83)
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- 23) DAUD'CL: KLOBECK, H.G., COMBRIATO, G. & ZACHAU, H.G. (1984) NUC. ACIDS RES., 12, 18, 6995-7006.
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- 53) **BJ26**: ALESCIO-ZONTA, L. & BAGLIONI, C. (1970) EUR. J. BIOCHEM., 15, 450-463. (CHECKED BY AUTHOR)
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- 55) **RF2**: SMITHIES, O., GIBSON, D., FANNING, E.M., GOODFLIESH, R.M., GILMAN, J.G. & BALLANTYNE, D.L. (1971) BIOCHEMISTRY, 10, 4912-4921. (CHECKED BY AUTHOR)
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- 59) **JBL**: SEON, B.K. (1982) MOL. IMMUNOL., 19, 83-86. (CHECKED BY AUTHOR 05/23/83)
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- 64) **HF2-1/13B**: ATKINSON, P.M., LAMPMAN, G.W., FURIE, B.C., NAPARSTEK, Y., SCHWARTZ, R.S., STOLLAR, B.D. & FURIE, B. (1985) J. CLIN. INVEST., 75, 1138-1143. (CHECKED BY AUTHOR 08/21/85)
- 65) **HF2-18/2**: ATKINSON, P.M., LAMPMAN, G.W., FURIE, B.C., NAPARSTEK, Y., SCHWARTZ, R.S., STOLLAR, B.D. & FURIE, B. (1985) J. CLIN. INVEST., 75, 1138-1143. (CHECKED BY AUTHOR 08/21/85)
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- 82) **AMYLOID ES30S**: WESTERMARK, P., SLETTEN, K. & NATVIG, J.B. (1981) ACTA PATH. MICROBIOL. SCAND., C89, 199-203. (CHECKED BY AUTHOR 11/09/81)
- 83) **OCO**: WANG, A.C., WELLS, J.V., FUDENBERG, H.H. & GERGELY, J. (1974) IMMUNOCHEM., 11, 341-345. (CHECKED BY AUTHOR)
- 84) **BOL**: WANG, A.C., WELLS, J.V., FUDENBERG, H.H. & GERGELY, J. (1974) IMMUNOCHEM., 11, 341-345. (CHECKED BY AUTHOR)
- 85) **AMYLOID M**: GLENNER, G.G., TERRY, W., HERADA, M., ISERSKY, C. & PAGE, D. (1971) SCIENCE, 172, 1150-1151. (CHECKED BY AUTHOR 09/22/78)
- 86) **SAC**: SMITHIES, O., GIBSON, O.M., FANNING, E.M., PERCY, M.E., PARR, D.M. & CONNELL, G.E. (1971) SCIENCE, 172, 574-577. (CHECKED BY AUTHOR)
- 87) **BJ**: MILSTEIN, C. (1966) BIOCHEM. J., 101, 352-368. (CHECKED BY AUTHOR)
- 88) **GO**: WANG, A.C., FUDENBERG, H.H. & CREYSSEL, R. (1974) EUR. J. IMMUNOL., 4, 446-448. (CHECKED BY AUTHOR)
- 89) **F-GUI**: WANG, A.C., FUDENBERG, H.H. & CREYSSEL, R. (1982) ACTA HAEMAT., 68, 187-195. (CHECKED BY AUTHOR 05/26/83)
- 90) **S-GUI**: WANG, A.C., FUDENBERG, H.H. & CREYSSEL, R. (1982) ACTA HAEMAT., 68, 187-195. (CHECKED BY AUTHOR 05/26/83)
- 91) **HF6-21/28**: ATKINSON, P.M., LAMPMAN, G.W., FURIE, B.C., NAPARSTEK, Y., SCHWARTZ, R.S., STOLLAR, B.D. & FURIE, B. (1985) J. CLIN. INVEST., 75, 1138-1143. (CHECKED BY AUTHOR 08/21/85)
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- 94) **TEI**: CAPRA, J.D. & KUNDEL, H.G. (1970) PROC. NAT. ACAD. SCI. USA, 67, 87-92. (CHECKED BY AUTHOR)
- 95) **MON**: NIAL, H.D. & EDMAN, P. (1967) NATURE, 216, 262-263. (CHECKED BY AUTHOR 07/25/79)
- 96) **ALE**: MILSTEIN, C., MILSTEIN, C.P. & FEINSTEIN, A. (1969) NATURE, 221, 151-154. (CHECKED BY AUTHOR)
- 97) **JOB**: CAPRA, J.D. & KUNDEL, H.G. (1970) PROC. NAT. ACAD. SCI. USA, 67, 87-92. (CHECKED BY AUTHOR)
- 98) **POT**: CAPRA, J.D. & KUNDEL, H.G. (1970) PROC. NAT. ACAD. SCI. USA, 67, 87-92. (CHECKED BY AUTHOR WHO CORRECTED RESIDUE 9 AS GIVEN IN TABLE)
- 99) **CON**: NIAL, H.D. & EDMAN, P. (1967) NATURE, 216, 262-263. (CHECKED BY AUTHOR 07/25/79)
- 100) **TRA**: NIAL, H.D. & EDMAN, P. (1967) NATURE, 216, 262-263. (CHECKED BY AUTHOR 07/25/79)
- 101) **H-G2b**: SCOTT, M.G., TARRAND, J.J., CRIMMINS, D.L., MCCOURT, D.W., SIEGEL, N.R., SMITH, C.E. AND NAHM, M.H. (1989) J. IMMUNOL., 143, 293-298.
- 102) **K-G2**: SCOTT, M.G., TARRAND, J.J., CRIMMINS, D.L., MCCOURT, D.W., SIEGEL, N.R., SMITH, C.E. AND NAHM, M.H. (1989) J. IMMUNOL., 143, 293-298.
- 103) **BRA**: WANG, A.C., WELLS, J.V., FUDENBERG, H.H. & GERGELY, J. (1974) IMMUNOCHEM., 11, 341-345. (CHECKED BY AUTHOR)
- 104) **LUX**: NIAL, H.D. & EDMAN, P. (1967) NATURE, 216, 262-263. (CHECKED BY AUTHOR 07/25/79)
- 105) **HEI**: RIESEN, W.F., MAJANIEMI, I., HUSER, H., BRAUN, D.G. & ROELCKE, D. (1978) SCAND. J. IMMUNOL., 8, 145-148. (CHECKED BY AUTHOR 10/10/79)
- 106) **PAP**: NIAL, H.D. & EDMAN, P. (1967) NATURE, 216, 262-263. (CHECKED BY AUTHOR 07/25/79)
- 107) **H-G2a**: SCOTT, M.G., TARRAND, J.J., CRIMMINS, D.L., MCCOURT, D.W., SIEGEL, N.R., SMITH, C.E. AND NAHM, M.H. (1989) J. IMMUNOL., 143, 293-298.
- 108) **CRA**: NIAL, H.D. & EDMAN, P. (1967) NATURE, 216, 262-263. (CHECKED BY AUTHOR 07/25/79)
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- 110) **WAG**: KAPLAN, A.P. & METZGER, H. (1969) BIOCHEMISTRY, 8, 3944-3951. (CHECKED BY AUTHOR)
- 111) **ROE**: JOHNSTON, S.L., ABRAHAM, G.N. & WELCH, E.H. (1975) BIOCHEM. BIOPHYS. RES. COMMUN., 66, 842-847. (CHECKED BY AUTHOR 10/17/77)
- 112) **HBJ1**: HOOD, L., GRAY, W.R., SANDERS, B.G. & DREYER, W.J. (1967) COLD SPRING HARBOR SYMP. QUANTITATIVE BIOL., 32, 133-145.
- 113) **AMYLOID 547**: WESTERMARK, P., SLETTEN, K. & NATVIG, J.B. (1981) ACTA PATH. MICROBIOL. SCAND., C89, 199-203. (CHECKED BY AUTHOR 11/09/81)
- 114) **WES**: JOHNSTON, S.L., ABRAHAM, G.N. & WELCH, E.H. (1975) BIOCHEM. BIOPHYS. RES. COMMUN., 66, 842-847. (CHECKED BY AUTHOR 10/17/77)
- 115) **HBJ10**: HOOD, L., GRAY, W.R., SANDERS, B.G. & DREYER, W.J. (1967) COLD SPRING HARBOR SYMP. QUANTITATIVE BIOL., 32, 133-145.
- 116) **LOD**: JOHNSTON, S.L., ABRAHAM, G.N. & WELCH, E.H. (1975) BIOCHEM. BIOPHYS. RES. COMMUN., 66, 842-847. (CHECKED BY AUTHOR 10/17/77)
- 117) **BEN**: CAPRA, J.D., KEHOE, J.M., WILLIAMS, R.C., JR., FEIZI, T. & KUNDEL, H.G. (1972) PROC. NAT. ACAD. SCI. USA, 69, 40-43. (CHECKED BY AUTHOR)
- 118) **MAA**: CAPRA, J.D., KEHOE, J.M., WILLIAMS, R.C., JR., FEIZI, T. & KUNDEL, H.G. (1972) PROC. NAT. ACAD. SCI. USA, 69, 40-43. (CHECKED BY AUTHOR)
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- 122) **AMYLOID 594**: WESTERMARK, P., SLETTEN, K. & NATVIG, J.B. (1981) ACTA PATH. MICROBIOL. SCAND., C89, 199-203. (CHECKED BY AUTHOR 11/09/81)
- 123) **MAR**: KAPLAN, A.P. & METZGER, H. (1969) BIOCHEMISTRY, 8, 3944-3951. (CHECKED BY AUTHOR)
- 124) **CL**: SOLOMON, A., MCLAUGHLIN, C.L. & CAPRA, J.D. (1975) J. CLINICAL INVESTIGATION, 55, 579-586. (CHECKED BY AUTHOR)
- 125) **AMYLOID**: COHEN, A.S., SHIRAHAMA, T., SKINNER, M., BENSON, M.D. & CATHCART, E.S. (1973) PROTIDES BIOL. FLUIDS, 20, 73-80.
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- 127) **AMYLOID MS**: PICK, A.I., SCHREIBMAN, S., LAVIE, G. & FROHLICHMAN, R. (1973) PROTIDES BIOL. FLUIDS, 20, 63-72.
- 128) **FEN**: MOULIN, A. & FOUGEREAU, M. (1973) NATURE NEW BIOLOGY, 246, 176-178.



## GENERAL NOTES: HUMAN KAPPA LIGHT CHAINS SUBGROUP I

## IDENTICAL SETS OF FRAMEWORK SEGMENTS:

**FR1:** SET 1: 2C12'CL[1],1B11'CL[2],1H1'CL[3],2A12'CL[4]. (4 IDENTICAL)  
 SET 2: DEN[6],3D6'CL[7],HK102'CL[8],EU[9],PA[11],WIL(=)[21],HBJ4[52],PAU[57],FRA[61],GR'[66],PAUL[78],MON[95]. (12 IDENTICAL)  
 SET 3: HK137'CL[12],HAU[13],HF2-1/17[15],OU(IOC)[19],WEA[20],DAUDI'CL[23],HK134'CL[24],WALKER'CL[26],HK101'CL[27],VKI-Chr1'CL[29],DEE[53],AND[35],REI[38],AU[39],ROY[40],HuVHCAMP'CL[42],AG[43],SCW[44],RZ[50],BU26[53],RFZ[55],HA[56],FSM[58],BJ48[62],HF3-16/6[63],HF2-1/13B[64],HF2-18/2[65],HOM[68],ESM IGG[70],ESM IGM[71],AMYLOID VII1-B[77],WAL[80],LOW[81],F-GUI[89],DIE[92],CAR A[93],TEI[94],CON[99],TRA[100],H-G2b[101],K-G2[102]. (41 IDENTICAL)  
 SET 4: Vb'CL[16],Vb''CL[17],WES[22]. (3 IDENTICAL)  
 SET 5: Vd'CL[25],LUX[104]. (2 IDENTICAL)  
 SET 6: AMYLOID BAN[30],BEL[48],HuRSV19VK[51],BJ19[54]. (4 IDENTICAL)  
 SET 7: DAV[72],FIN[73]. (2 IDENTICAL)

**FR2:** SET 1: 2C12'CL[1],1B11'CL[2],1H1'CL[3],2A12'CL[4]. (4 IDENTICAL)  
 SET 2: HK102'CL[8],Vb'CL[16],Vb''CL[17],Vd'CL[25],WALKER'CL[26],Va''CL[28],Ve'CL[31],AU[39],ROY[40],HuVHCAMP'CL[42],KA[46],HuRSV19VK[51]. (12 IDENTICAL)  
 SET 3: PA[11],PAU[57]. (2 IDENTICAL)  
 SET 4: HK137'CL[12],AMYLOID BAN[30]. (2 IDENTICAL)  
 SET 5: WIL(=)[21],V13'CL[32]. (2 IDENTICAL)  
 SET 6: HK134'CL[24],HK101'CL[27]. (2 IDENTICAL)  
 SET 7: VKI-Chr1'CL[29],VKI-ZI'CL[37]. (2 IDENTICAL)  
 SET 8: OU(IOC)[19],WIL(-)[34]. (2 IDENTICAL)  
 SET 9: RZ[50],RFZ[55]. (2 IDENTICAL)

**FR3:** SET 1: 2C12'CL[1],1B11'CL[2],1H1'CL[3],2A12'CL[4]. (4 IDENTICAL)  
 SET 2: 3D6'CL[7],HK102'CL[8],PA[11]. (3 IDENTICAL)  
 SET 3: HK137'CL[12],HAU[13],Vb'CL[16],Vb''CL[17],HK134'CL[24],HK101'CL[27],Va''CL[28]. (7 IDENTICAL)  
 SET 4: HF2-1/17[15],Vd'CL[25]. (2 IDENTICAL)  
 SET 5: Ve'CL[31],V13'CL[32]. (2 IDENTICAL)  
 SET 6: HuVHCAMP'CL[42],LAY[47],HuRSV19VK[51]. (3 IDENTICAL)

**FR4:** SET 1: 2C12'CL[1],1B11'CL[2],1H1'CL[3],2A12'CL[4],G1'CL[67]. (5 IDENTICAL)  
 SET 2: BR[5],GAL(I)[18],AU[39],HuVHCAMP'CL[42],CL\* [124]. (5 IDENTICAL HUMAN V-KAPPA-I; ALSO 6 HUMAN V-KAPPA-II: GM 60'CL[1],RMI6410'CL[11],A-G1[14],C-G1[15],B-G1[16],E-G1[19]; 23 HUMAN V-KAPPA-III: PIE[2],GLO[4],CUR[5],HAH 14.1'CL[7],HAH 14.2'CL[8],HAH 16.1'CL[9],NOV'CL[10],HIC (R)'CL[11],PAY[15],BOR'[17],HEW'CL[18],ROB'CL[19],BRA'CL[21],HAH'CL[22],HIC'CL[24],WOL[31],EVI-15'CL[32],GOL[33],Taykv322'CL[34],GF4/1.1'CL[54],REE[56],HAH (R)'CL[73],VKAPPA3'CL[85]; AND 2 HUMAN V-KAPPA-IV: FK-001'CL[1],PB1IV'CL[5].)  
 SET 3: DEN[6],WIL(=)[21],WIL(-)[34],BI[41],AG[43]. (5 IDENTICAL HUMAN V-KAPPA-I; ALSO 3 HUMAN V-KAPPA-II: NIM[4],FR[9],H-G2a[15]; 10 HUMAN V-KAPPA-III: GAR[1],FLO[3],TH3'CL[13],GOT[16],WEU[26],IARC/BL41'CL[46],FR4[47],Taykv312'CL[58],Taykv308'CL[66],TH9'CL[90]; AND 1 HUMAN V-KAPPA-IV: LEN[3].)  
 SET 4: 3D6'CL[7],CAR[10]. (2 IDENTICAL)  
 SET 5: EU[9],WEA[20],LAY[47],BJ48[62]. (4 IDENTICAL)  
 SET 6: PA[11]. (IDENTICAL TO 1 HUMAN V-KAPPA-III: BRO'CL[20].)  
 SET 7: HAU[13]. (IDENTICAL TO 2 HUMAN V-KAPPA-III: POM[48],CLL'CL[50].)  
 SET 8: HF2-1/17[15],RZ[50]. (2 IDENTICAL HUMAN V-KAPPA-I; ALSO 13 HUMAN V-KAPPA-III: SON[14],KAS[28],SIC'CL[30],Taykv310'CL[55],Taykv320'CL[56],LS1'CL[39],LS2'CL[40],LS4'CL[41],LS5'CL[42],LS6'CL[43],LS7'CL[44],LS8'CL[45],Taykv306'CL[59]; 2 HUMAN V-KAPPA-IV: VJ1'CL[4],Ly66r'CL[12]; 4 MOUSE V-KAPPA-V: SE20.2'CL[29],NVH65-212'CL[47],DNA9'CL[127],DNA2'CL[128]; AND 2 MOUSE V-KAPPA-MISC: DNA2'CL[1],DNA9'CL[2].)  
 SET 9: WES[22],MEV[45]. (2 IDENTICAL)  
 SET 10: OU(IOC)[19],WALKER'CL[26]. (2 IDENTICAL HUMAN V-KAPPA-I; ALSO 1 HUMAN V-KAPPA-II: TEW[5]; AND 2 HUMAN V-KAPPA-III: 8E10'CL[12],GER[53].)

## IDENTICAL SETS OF COMPLEMENTARITY DETERMINING REGIONS:

**CDR1:** SET 1: 2C12'CL[1],1B11'CL[2],1H1'CL[3],2A12'CL[4]. (4 IDENTICAL)  
 SET 2: PA[11],PAU[57]. (2 IDENTICAL)  
 SET 3: HF2-1/17[15],HF3-16/6[63],HF2-1/13B[64],HF2-18/2[65]. (4 IDENTICAL)  
 SET 4: Vb'CL[16],Vb''CL[17],HK134'CL[24]. (3 IDENTICAL)  
 SET 5: GAL(I)[18],WEA[20]. (2 IDENTICAL)  
 SET 6: Vd'CL[25],Ve'CL[31]. (2 IDENTICAL)  
 SET 7: VKI-Chr1'CL[29],VKI-ZI'CL[37]. (2 IDENTICAL)  
 SET 8: AU[39],NE[60],SHE[75]. (3 IDENTICAL)  
 SET 9: HuVHCAMP'CL[42]. (IDENTICAL TO 1 RAT V-KAPPA: YTH 34.5HL'CL[1].)  
 SET 10: RZ[50],RFZ[55]. (2 IDENTICAL)  
 SET 11: HuRSV19VK[51]. (IDENTICAL TO 1 MOUSE V-KAPPA-II: MuRSV19VL'CL[116].)

**CDR2:** SET 1: 2C12'CL[1],1B11'CL[2],1H1'CL[3]. (3 IDENTICAL)  
 SET 2: BR[5]. (IDENTICAL TO 1 RABBIT V-KAPPA: BS-5[20].)  
 SET 3: 3D6'CL[7],EU[9]. (2 IDENTICAL)  
 SET 4: HK102'CL[8],Va''CL[28]. (2 IDENTICAL)  
 SET 5: HK137'CL[12],HF2-1/17[15],Vb'CL[16],Vb''CL[17],HK134'CL[24],WALKER'CL[26],HK101'CL[27],VKI-Chr1'CL[29],V108'CL[36],VKI-ZI'CL[37]. (10 IDENTICAL)  
 SET 6: Vd'CL[25],Ve'CL[31],V13'CL[32]. (3 IDENTICAL)  
 SET 7: AU[39],RZ[50]. (2 IDENTICAL)  
 SET 8: HuVHCAMP'CL[42]. (IDENTICAL TO 1 RAT V-KAPPA: YTH 34.5HL'CL[1].)  
 SET 9: AG[43],NI[49]. (2 IDENTICAL)  
 SET 10: HuRSV19VK[51]. (IDENTICAL TO 13 MOUSE V-KAPPA-II: PC2205(NZB)[46],vk1-B'CL[51],PC2567(NZB)[55],G8 CA 1.7[56],L XIX 27'CL[67],G5 BB 2.2[68],G6 BD 2.6[69],G7 AB 2.9[70],JV3'CL[82],CM4'CL[84],K18.1'CL[88],F17.170.2'CL[95],MuRSV19VL'CL[116].)

**CDR3:** SET 1: 2C12'CL[1],1B11'CL[2]. (2 IDENTICAL)  
 SET 2: 1H1'CL[3],G1'CL[67]. (2 IDENTICAL)  
 SET 3: Vb'CL[16],Vb''CL[17]. (2 IDENTICAL)  
 SET 4: HK134'CL[24],HK101'CL[27]. (2 IDENTICAL)  
 SET 5: AMYLOID BAN[30]. (IDENTICAL TO 2 MOUSE V-KAPPA-V: mA8 A'CL[184],BV17-45'CL[189].)  
 SET 6: HuVHCAMP'CL[42]. (IDENTICAL TO 1 RAT V-KAPPA: YTH 34.5HL'CL[1].)  
 SET 7: LAY[47]. (IDENTICAL TO 1 HUMAN V-KAPPA-III: POM[48].)  
 SET 8: HuRSV19VK[51]. (IDENTICAL TO 1 MOUSE V-KAPPA-II: MuRSV19VL'CL[116].)

## IDENTICAL SETS OF J-MINIGENES:

SET 1: 2C12'CL[1],1B11'CL[2],1H1'CL[3],2A12'CL[4],G1'CL[67]. (5 IDENTICAL)  
 SET 2: BR[5],AU[39]. (2 IDENTICAL HUMAN V-KAPPA-I; ALSO 1 HUMAN V-KAPPA-II: RPMI6410'CL[11]; 6 HUMAN V-KAPPA-III: PIE[2],HIC (R)'CL[11],ROB'CL[19],HIC'CL[24],GF4/1.1'CL[54],VKAPPA3'CL[85]; AND 1 HUMAN V-KAPPA-IV: PB1IV'CL[5].)  
 SET 3: DEN[6],BI[41]. (2 IDENTICAL HUMAN V-KAPPA-I; ALSO 1 HUMAN V-KAPPA-II: FR[9]; AND 5 HUMAN V-KAPPA-III: GAR[1],FLO[3],IARC/BL41'CL[46],Taykv312'CL[58],Taykv308'CL[66].)  
 SET 4: HF2-1/17[15],RZ[50]. (2 IDENTICAL HUMAN V-KAPPA-I; ALSO 7 HUMAN V-KAPPA-III: LS1'CL[39],LS2'CL[40],LS4'CL[41],LS5'CL[42],LS6'CL[43],LS7'CL[44],LS8'CL[45].)  
 SET 5: GAL(I)[18]. (IDENTICAL TO 1 HUMAN V-KAPPA-III: GOL[33].)  
 SET 6: WIL(=)[21],WIL(-)[34]. (2 IDENTICAL)  
 SET 7: WALKER'CL[26]. (IDENTICAL TO 1 HUMAN V-KAPPA-II: TEW[5]; AND 2 HUMAN V-KAPPA-III: 8E10'CL[12],GER[53].)  
 SET 8: HuVHCAMP'CL[42]. (IDENTICAL TO 8 HUMAN V-KAPPA-III: CUR[5],HAH 14.1'CL[7],HAH 14.2'CL[8],HAH 16.1'CL[9],HAH'CL[22],WOL[31],EVI-15'CL[32],HAH (R)'CL[73]; AND 1 HUMAN V-KAPPA-IV: FK-001'CL[1].)  
 SET 9: AG[43]. (IDENTICAL TO 1 HUMAN V-KAPPA-III: GOT[16].)

# SEE SIGNAL PEPTIDE TABLE IF # OCCURS AT POSITION 0.



## SPECIFIC NOTES: HUMAN KAPPA LIGHT CHAINS SUBGROUP I

- 1) **2C12'CL**: HETEROHYBRIDOMA FORMED BY FUSING CELLS FROM LYMPH NODES OR SPLEEN FROM A PATIENT SUFFERING FROM FOLLICULAR SMALL CLEAVED CELL LYMPHOMA AND CELL LINE K6H6-B5.
- 2) **1B11'CL**: HETEROHYBRIDOMA FORMED BY FUSING CELLS FROM LYMPH NODES OR SPLEEN FROM A PATIENT SUFFERING FROM FOLLICULAR SMALL CLEAVED CELL LYMPHOMA AND CELL LINE K6H6-B5.
- 3) **1H1'CL**: HETEROHYBRIDOMA WAS FORMED BY FUSING CELLS FROM LYMPH NODES OR SPLEEN FROM A PATIENT SUFFERING FROM FOLLICULAR SMALL CLEAVED CELL LYMPHOMA AND CELL LINE K6H6-B5.
- 4) **2A12'CL**: HETEROHYBRIDOMA WAS FORMED BY FUSING CELLS FROM LYMPH NODES OR SPLEEN FROM A PATIENT SUFFERING FROM FOLLICULAR SMALL CLEAVED CELL LYMPHOMA AND CELL LINE K6H6-B5.
- 8) **HK102'CL**: THE SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF HUMAN FETAL LIVER DNA.
- 12) **HK137'CL**: THE AMINO ACID SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF HUMAN FETAL DNA.
- 21) **WIL(=)**: WIL(-) AND WIL(=) ARE PRODUCED BY THE SAME PATIENT WITH MULTIPLE MYELOMA.
- 24) **HK134'CL**: THE AMINO ACID SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF HUMAN FETAL DNA.
- 27) **HK101'CL**: THE SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF HUMAN FETAL LIVER DNA.
- 30) **AMYLOID BAN**: AMINO ACID RESIDUE ASN AT POSITION 61 IS LINKED TO CARBOHYDRATE. AMINO ACID RESIDUES FOUND AT POSITIONS 104 AND 105 ARE VAL, LEU AND GLN, GLU RESPECTIVELY.
- 34) **WIL(-)**: WIL(-) AND WIL(=) ARE PRODUCED BY THE SAME PATIENT WITH MULTIPLE MYELOMA.
- 35) **AND**: IT IS ISOLATED FROM THE AMYLOID FIBRILS FROM THE SPLEEN OF THE PATIENT.
- 36) **V108'CL**: HUMAN IMMUNOGLOBULIN KAPPA ORPHON GENE LOCATED ON CHROMOSOME 2 IN THE REGION 2q12-14.
- 43) **AG**: THE AMINO ACID RESIDUES AT POSITIONS 39 AND 41 WERE REPORTED BY THE AUTHORS AS GLY AND LYS RESPECTIVELY; HOWEVER, THE PROOF WAS NOT ABSOLUTE. THUS, THEY ARE OMITTED.
- 51) **HuRSV19VK**: THIS SEQUENCE CONTAINS THE FR'S OF REI WITH SOME MODIFICATIONS, AND CDR'S OF HuRSV19VL. WHEN HuRSV19VK IS COMBINED WITH HuRSV19VH, FV DOES NOT BIND VIRUS; BUT WHEN COMBINED WITH HuRSV19VHFN5, FV BINDS VIRUS.
- 53) **BJ26**: ACID RESIDUES AT POSITIONS 39 AND 41 OF BJ26 WERE REPORTED BY THE AUTHORS AS GLY AND LYS RESPECTIVELY. SINCE THIS PROTEIN WAS SEQUENCED BEFORE THE SEQUENCES OF MANY OTHER PROTEINS WERE KNOWN AT THESE TWO POSITIONS, WE HAVE OMITTED THEM.
- 54) **BJ19**: THE AMINO ACID RESIDUES AT POSITIONS 39 AND 41 WERE REPORTED BY THE AUTHORS AS GLY AND LYS RESPECTIVELY. SINCE THIS PROTEIN WAS SEQUENCED BEFORE THE SEQUENCES OF MANY OTHER PROTEINS WERE KNOWN AT THESE TWO POSITIONS, WE HAVE OMITTED THEM.
- 59) **JBL**: THE AMINO ACID RESIDUE FOUND AT POSITION 34 WAS ALA OR SER.
- 67) **G1'CL**: HETEROHYBRIDOMA WAS FORMED BY FUSING CELLS FROM LYMPH NODES OR SPLEEN FROM A PATIENT SUFFERING FROM FOLLICULAR SMALL CLEAVED CELL LYMPHOMA AND CELL LINE K6H6-B5.
- 74) **PW**: THE SEQUENCE WAS FROM A PATIENT WITH TRANSITIONAL CELL CARCINOMA OF THE URINARY BLADDER.
- 79) **RI**: THE SEQUENCE WAS FROM A PATIENT WITH TRANSITIONAL CELL CARCINOMA OF THE URINARY BLADDER.
- 82) **AMYLOID ES305**: THE AMINO ACID RESIDUES AT POSITIONS 21 AND 29 WERE ILE OR LEU.
- 89) **F-GUI**: THE SEQUENCES OF F-GUI AND S-GUI WERE FROM THE SAME PATIENT.
- 90) **S-GUI**: THE SEQUENCES OF F-GUI AND S-GUI WERE FROM THE SAME PATIENT.
- 121) **GM131'CL**: FROM AN EPSTEIN-BARR VIRUS-TRANSFORMED HUMAN LYMPHOID CELL LINE
- 127) **AMYLOID MS**: THE AMINO ACID RESIDUE AT POSITION 2 MS WAS ILE OR LEU.

\* THE FOLLOWING WERE EQUALLY AND MOST FREQUENTLY OCCURRING:

AT POSITION	RESIDUES
27D	(TRP, HIS, GLU)
27E	(THR, SER)
92	(ASP, ASN)











HUMAN HEAVY CHAINS SUBGROUP I (cont'd)

	73	74	75	76	77	78	79	# OF	# OF	OCCURRENCES	VARIABILITY
	DUN	SAW	ADA	NOR	LEA	HAR	RIC	SEQUENCES	AMINO ACIDS	OF MOST COMMON AMINO ACID	
0											
1	pca							68	5	32 (GLN)	11.
2	VAL	pca						68	9	59 (VAL)	10.
3	GLN	glu						67	6	59 (GLN)	6.8
4	LEU	LEU			pca	pca	leu	63	2	62 (LEU)	2.
5								53	4	49 (VAL)	4.3
6								53	3	43 (GLN)	3.7
7								53	2	53 (SER)	1.
8								54	2	53 (GLY)	2.
9								54	5	47 (ALA)	5.7
10								54	3	51 (GLU)	3.2
11								54	2	50 (VAL)	2.2
12								55	6	41 (LYS)	8.
13								54	2	53 (LYS)	2.
14								54	2	53 (PRO)	2.
15								54	3	52 (GLY)	3.1
16								52	5	23 (ALA)	11.
17								50	2	49 (SER)	2.
18								51	5	37 (VAL)	6.9
19								53	3	44 (LYS)	3.6
20								52	4	36 (VAL)	5.8
21								51	3	48 (SER)	3.2
22								49	4	48 (CYS)	2.
23								51	4	47 (LYS)	4.3
24								51	5	34 (ALA)	7.5
25								50	3	48 (SER)	3.1
26								50	2	48 (GLY)	2.1
27								51	6	32 (TYR)	9.6
28								49	3	55 (THR)	7.
29								49	3	47 (PHE)	3.1
30								49	9	22 (THR)	20.
31								49	8	33 (SER)	12.
32								49	5	40 (TYR)	6.1
33								49	7	18 (ALA)	19.
34								49	7	33 (ILE)	10.
35								49	10	21 (SER)	23.
35A											
35B											
36								49	2	48 (TRP)	2.
37								49	4	44 (VAL)	4.5
38								49	2	48 (ARG)	2.
39								49	2	48 (GLN)	2.
40								49	4	37 (ALA)	5.3
41								49	4	46 (PRO)	4.3
42								49	2	48 (GLY)	2.
43								48	4	33 (GLN)	5.8
44								48	2	43 (GLY)	2.2
45								48	2	47 (LEU)	2.
46								48	1	48 (GLU)	1.
47								48	2	47 (TRP)	2.
48								48	4	41 (MET)	4.7
49								48	2	47 (GLY)	2.
50								48	10	18 (TRP)	27.
51								48	4	45 (ILE)	4.3
52								48	10	13 (ASN)	37.
52A								47	7	30 (PRO)	
52B								1	1	1 (TYR)	
52C											
53								48	10	14 (GLY)	34.
54								48	8	12 (ASN)	32.
55								48	5	34 (GLY)	7.1
56								48	11	16 (ASP)	33.
57								48	5	35 (THR)	6.9
58								48	10	24 (ASN)	20.
59								48	5	43 (TYR)	5.6
60								47	6	30 (ALA)	9.4
61								48	4	32 (GLN)	6.
62								48	8	24 (LYS)	16.
63								48	4	36 (PHE)	5.3
64								49	6	44 (GLN)	6.7
65								49	6	41 (GLY)	7.2
66								49	3	39 (ARG)	3.8
67								48	3	45 (VAL)	3.2
68								48	4	45 (THR)	4.3
69								49	7	26 (ILE)	13.
70								49	2	35 (THR)	2.8
71								49	5	19 (ALA)	13.
72								49	3	46 (ASP)	3.2
73								49	9	21 (THR)	19.
74								50	1	50 (SER)	1.
75								50	7	26 (THR)	13.
76								50	5	39 (SER)	6.4
77								50	5	45 (THR)	5.6
78								50	3	43 (ALA)	3.5
79								50	4	45 (TYR)	4.4
80								50	2	36 (MET)	2.8
81								50	2	35 (GLU)	7.1
82								51	5	37 (LEU)	6.9
82A								51	7	31 (SER)	
82B								51	6	37 (SER)	
82C								51	2	49 (LEU)	
83								51	5	33 (ARG)	7.7
84								51	5	34 (SER)	7.5
85								51	4, 5	24 (GLU), 23 (GLU)	8.5, 11.
86								51	1, 2	51 (ASP), 50 (ASP)	1., 2.
87								51	3	48 (THR)	3.2
88								51	3	48 (ALA)	3.2
89								51	5	34 (VAL)	7.5
90								51	2	50 (TYR)	2.
91								51	2	48 (TYR)	2.1
92								51	1	51 (CYS)	1.
93								51	3	49 (ALA)	3.1
94								51	5	43 (ARG)	5.9
95								38	11, 12	10 (ALA)	42., 46.
96								39	15	10 (PRO)	58.
97								39	14	12 (GLY)	45.
98								37	14	10 (TYR)	52.
99								37	15	11 (GLY)	50.
100								37	14	10 (SER)	52.
100A								36	13	13 (GLY)	
100B								35	15	9 (GLY)	
100C								32	11	9 (GLY)	
100D								26	13	6 (CYS)	
100E								21	8	9 (TYR)	
100F								20	11	6 (ARG)	
100G								16	7	7 (GLY)	
100H								16	7	8 (ASP)	
100I								9	5	4 (TYR)	
100J								14	8	3 (+)	
100K								20	4	13 (PHE)	
101								38	6	30 (ASP), 29 (ASP)	7.6, 7.9
102								39	9, 10	18 (TYR)	19., 22.
103								39	2, 3	37 (TRP)	2.1, 3.2
104								39	4	36 (GLY)	4.3
105								39	6, 7	32 (GLN), 31 (GLN)	7.3, 8.8
106								39	1	39 (GLY)	1.
107								40	5	34 (THR)	5.9
108								39	4	25 (LEU)	6.2
109								39	3	37 (VAL)	3.2
110								40	3	37 (THR)	3.2
111								40	1	40 (VAL)	1.
112								42	2	40 (SER)	2.1
113								41	1	41 (SER)	1.

## ANTIBODY SPECIFICITIES: HUMAN HEAVY CHAINS SUBGROUP I

- 1) LS2'CL: ANTI-Pr2 RBC AUTOANTIBODY
- 2) LS5'CL: ANTI-Pr2 RBC AUTOANTIBODY
- 3) LS6'CL: ANTI-Pr2 RBC AUTOANTIBODY
- 4) LS1'CL: ANTI-Pr2 RBC AUTOANTIBODY
- 5) LS4'CL: ANTI-Pr2 RBC AUTOANTIBODY
- 6) LS8'CL: ANTI-Pr2 RBC AUTOANTIBODY
- 21/28'CL: ANTI-DNA AUTOANTIBODY HYBRIDOMA
- 11) 8E10'CL: ANTI-DNA AUTOANTIBODY HYBRIDOMA
- 25) EV1-15'CL: ANTI-CYTOMEGALOVIRUS HYBRIDOMA
- 26) KAS: ANTI-HUMAN GAMMA G GLOBULIN; WA IDIOTYPE
- 27) BOR': ANTI-HUMAN GAMMA G GLOBULIN; WA IDIOTYPE
- 28) RF-TS1'CL: ANTI-IGG RHEUMATOID FACTOR
- 29) LS7'CL: ANTI-Pr2 RBC AUTOANTIBODY
- 33) RF-TS3'CL: ANTI-IGG1, IGG2, IGG4 RHEUMATOID FACTOR
- 41) Ab2022'CL: ANTI-INSULIN AUTOANTIBODY
- 42) SIE: ANTI-HUMAN GAMMA G GLOBULIN; WA IDIOTYPE
- 45) WOL: ANTI-HUMAN GAMMA G GLOBULIN; WA IDIOTYPE
- 53) STE: COLD AGGLUTININ WITH ANTI-BLOOD GROUP I ACTIVITY
- 55) TH3'CL: ANTI-ssDNA, IgG HYBRIDOMA
- 67) KOH: ANTI-HUMAN GAMMA G GLOBULIN
- 68) MAR: ANTI-LIPOPROTEIN LIPASE

## CLASS: HUMAN HEAVY CHAINS SUBGROUP I

- 7) 1B9/F2'CL: IGM-LAMBDA
- 10) 21/28'CL: IGM-
- 11) 8E10'CL: IGM-
- 14) 51P1'CL: IGM-
- 15) AND'CL: IGM-
- 16) NEI'CL: IGM-
- 22) X17115'CL: IGM-
- 23) TH9'CL: IGM-KAPPA
- 24) WIL2'CL: IGM-
- 25) EV1-15'CL: IGM-KAPPA
- 26) KAS: IGM-KAPPA
- 27) BOR': IGM-KAPPA
- 28) RF-TS1'CL: IGM-KAPPA
- 30) ND'CL: IGE-
- 32) EU: IGG1-KAPPA
- 33) RF-TS3'CL: IGM-KAPPA
- 39) MOT: IGG-
- 41) Ab2022'CL: IGM-KAPPA
- 42) SIE: IGM-KAPPA
- 43) lambda IGD-1'CL: IGD-
- 45) WOL: IGM-KAPPA
- 48) DI: IGM-
- 49) 60P1'CL: IGM-
- 50) CA: IGG1-
- 51) BRO' IGG: IGG-KAPPA
- 53) STE: IGG1-
- 54) ZUC: IGG3-
- 55) TH3'CL: IGM-KAPPA
- 56) HUS: IGG3-
- 57) OMM'CL: IGG3-
- 58) BOT: IGM-
- 59) BEN(I): IGG3-
- 60) ZUC': IGG3-
- 61) WIS: IGG3-
- 62) VAU: IGG1-
- 63) LEB: IGG1-
- 64) SAC: IGG1-KAPPA
- 67) KOH: IGM-LAMBDA
- 68) MAR: IGM-
- 71) WAR: IGG1-
- 72) VIL: IGG3-LAMBDA
- 73) DON: IGG4-
- 74) SAW: IGG2-
- 75) ADA: IGA-
- 76) NOR: IGA-
- 79) RIC: IGG3-

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- 6) LS8'CL: SILBERSTEIN, L.E., LITWIN, S. & CARMACK, C.E. (1989) J. EXP. MED., 169, 1631-1643.
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- 8) 21-2'CL: BERMAN, J.E., MELLIS, S.J., POLLOCK, R., SMITH, C.L., SUH, H., HEINKE, B., KOWAL, C., SURTI, U., CHESS, L., CANTOR, C.R. & ALT, F.W. (1988) EMBO J., 7, 727-738.
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- 13) V35'CL: MATSUDA, F., LEE, K.H., NAKAI, S., SATO, T., KODAIRA, M., ZONG, S.Q., OHNO, H., FUKUHARA, S. & HONJO, T. (1988) EMBO J., 7, 1047-1051.
- 14) 51P1'CL: SCHROEDER, H.W., JR., HILLSON, J.L. & PERLMUTTER, R.M. (1987) SCIENCE, 238, 791-793; CHEN, P.P., LIU, M.-F., GLASS, C.A., SINHA, S., KIPPS, T.J. & CARSON, D.A. (1989) ARTHRITIS & RHEUMATISM, 32, 72-76.
- 15) AND'CL: KIPPS, T.J., TOMHAVE, E., PRATT, L.F., DUFFY, S., CHEN, P.P. & CARSON, D.A. (1989) PROC. NATL. ACAD. SCI. USA, 86, 5913-5917.
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- 19) 1-92'CL: BERMAN, J.E., MELLIS, S.J., POLLOCK, R., SMITH, C.L., SUH, H., HEINKE, B., KOWAL, C., SURTI, U., CHESS, L., CANTOR, C.R. & ALT, F.W. (1988) EMBO J., 7, 727-738.
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- 27) **BOR'**: NEWKIRK, M.M., MAGEED, R.A., JEFFERIS, R., CHEN, P.P. & CAPRA, J.D. (1987) J.EXP.MED., 166, 550-564.
- 28) **RF-TS1'CL**: PASCUAL, V., RANDEN, I., THOMPSON, K., SIOUD, M.FORRE, O., NATVIG, J. & CAPRA, J.D. (1990) J.CLIN.INVEST., 86, 1320-1328.
- 29) **LS2'CL**: SILBERSTEIN, L.E., LITWIN, S. & CARMACK, E. (1989) J.EXP.MED., 169, 1631-1643.
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- 32) **EU**: CUNNINGHAM, B.A., RUTISHAUSER, U., GALL, W.E., GOTTLIEB, P.D., WAKDAL, M.J. & EDELMAN, G.M. (1970) BIOCHEMISTRY, 9, 3161-3170. (CHECKED BY AUTHOR)
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- 34) **5-1R1'CL**: BERMAN, J.E., MELLIS, S.J., POLLOCK, R., SMITH, C.L., SUH, H., HEINKE, B., KOWAL, C., SURTI, U., CHESS, L., CANTOR, C.R. & ALT, F.W. (1988) EMBO J., 7, 727-738.
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- 41) **Ab2022'CL**: SANZ, I., CASALI, P., THOMAS, J.W., NOTKINS, A.L. & CAPRA, J.D. (1989) J.IMMUNOL., 142, 4054-4061.
- 42) **81E**: ANDREWS, D.W. & CAPRA, J.D. (1981) PROC.NATL.ACAD.SCI.USA, 78, 3799-3803; ANDREWS, D.W. & CAPRA, J.D. (1981) BIOCHEMISTRY, 20, 5816-5822. (CHECKED BY AUTHOR 11/15/82); ANDREWS, D.W. & CAPRA, J.D. (1981) BIOCHEMISTRY, 20, 5822-5830.
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## IDENTICAL SETS OF FRAMEWORK SEGMENTS:

- FR1**: SET 1: LS2'CL[1], LS5'CL[2], LS6'CL[3], LS1'CL[4], LS4'CL[5]. (5 IDENTICAL)  
 SET 2: 21-2'CL[8], 3-1'CL[9], 21/28'CL[10], 8E10'CL[11], V35'CL[13], 1-92'CL[19]. (6 IDENTICAL)  
 SET 3: 51P1'CL[14], AND'CL[15], NEI'CL[16], hv1263'CL[20], 783c'CL[21], X17115'CL[22], EV1-15'CL[25], RF-TS1'CL[28]. (8 IDENTICAL)  
 SET 4: 5-1R1'CL[34], VhAU'CL[35], VH251'CL[37]. (3 IDENTICAL)  
 SET 5: WS1'CL[40], Ab2022'CL[41], Ab2'CL[44], Vh383ex'CL[46]. (4 IDENTICAL)  
 SET 6: VAU[62], LEB[63]. (2 IDENTICAL)
- FR2**: SET 1: LS2'CL[1], LS5'CL[2], LS6'CL[3], LS1'CL[4], LS4'CL[5], LS8'CL[6], 1B9/F2'CL[7], 21-2'CL[8], 3-1'CL[9], HG3'CL[12], V35'CL[13], 51P1'CL[14], AND'CL[15], NEI'CL[16], hv1263'CL[20], 783c'CL[21], X17115'CL[22], EV1-15'CL[25], KAS[26], BOR'[27], LS7'CL[29], EU[32], RF-TS3'CL[33], lambda IGD-1'CL[43]. (25 IDENTICAL)  
 SET 2: 21/28'CL[10], 8E10'CL[11], E3-10'CL[18], 1-92'CL[19]. (4 IDENTICAL)  
 SET 3: 5-1R1'CL[34], VhAU'CL[35], 5-2R1'CL[36], VH251'CL[37], 83P2'CL[38], Ab2022'CL[41], M61'CL[47]. (7 IDENTICAL)  
 SET 4: Ab2'CL[44], Vh383ex'CL[46]. (2 IDENTICAL)  
 SET 5: WOL[45]. (IDENTICAL TO 7 HUMAN V-H-III: TIL[33], 4B4'CL[48], M26'CL[49], 9-1'CL[50], TEI[54], 12-2'CL[55], 20F1'CL[82].)
- FR3**: SET 1: LS2'CL[1], LS5'CL[2], LS6'CL[3], LS1'CL[4], LS4'CL[5], LS8'CL[6], LS7'CL[29]. (7 IDENTICAL)  
 SET 2: 21-2'CL[8], 3-1'CL[9], HG3'CL[12]. (3 IDENTICAL)  
 SET 3: 21/28'CL[10], 8E10'CL[11], E3-10'CL[18]. (3 IDENTICAL)  
 SET 4: 51P1'CL[14], AND'CL[15], NEI'CL[16]. (3 IDENTICAL)  
 SET 5: 783c'CL[21], X17115'CL[22]. (2 IDENTICAL)  
 SET 6: ND'CL[30]. (IDENTICAL TO 1 HUMAN V-H-III: U266'CL[136].)  
 SET 7: 5-1R1'CL[34], VhAU'CL[35], VH251'CL[37], 83P2'CL[38], M61'CL[47]. (5 IDENTICAL)
- FR4**: SET 1: LS2'CL[1], LS5'CL[2], LS6'CL[3], LS1'CL[4], LS8'CL[6], 1B9/F2'CL[7], 21/28'CL[10], NEI'CL[16], TH9'CL[23], WIL2'CL[24], KAS[26], BOR'[27], LS7'CL[29], WOL[45]. (14 IDENTICAL HUMAN V-H-I; ALSO 7 HUMAN V-H-II: 15P1'CL[1], MLI'CL[3], MCE[46], DR12910-28'CL[48], Ab17'CL[49], 444'CL[52], NZU[55]; 34 HUMAN V-H-III: 18/2'CL[1], 18/17'CL[1], 18/29'CL[3], 1/17'CL[4], 30P1'CL[5], M49'CL[6], HP2-4[7], Ab25'CL[12], Vh38C1.10'CL[15], Vh38C1.8'CL[16], Vh38C1.9'CL[17], 60P2'CL[18], 63P1'CL[19], GF4/1.1'CL[20], Vh38C1.4'CL[21], Vh38C1.5'CL[22], 56P1'CL[25], 2P1'CL[26], M74'CL[28], TIL[33], HN.14'CL[41], WEA[47], 4B4'CL[48], M26'CL[49], NIE[60], DOB[62], VHL0.7'CL[63], K686'CL[68], 4K88'CL[69], K588'CL[70], K5C7'CL[71], K6G5'CL[72], K6G5'CL[73], 20F1'CL[82]; 1 MOUSE V-H-IIB: PING20066'CL[29]; 1 MOUSE V-H-IIIA: MOPC47A[110]; AND 1 MOUSE V-H-IIID: B3'40'CL[25].)  
 SET 2: 8E10'CL[11], TH3'CL[55]. (2 IDENTICAL HUMAN V-H-I; ALSO 1 HUMAN V-H-III: TIL[33]; AND 1 MOUSE V-H-IIIA: MOPC47A[110].)  
 SET 3: 51P1'CL[14], RF-TS1'CL[28], Ab2022'CL[41], M61'CL[47], 60P1'CL[49], AF2'CL[65]. (6 IDENTICAL HUMAN V-H-I; ALSO 6 HUMAN V-H-II: L16'CL[2], M71'CL[4], C6B2'CL[14], 58P2'CL[16], CE-1'CL[41], 37P1'CL[47]; AND 3 HUMAN V-H-III: 38P1'CL[36], 3D6'CL[43], 13P1'CL[97].)  
 SET 4: AND'CL[15]. (IDENTICAL TO 1 HUMAN V-H-II: Paq-1'CL[22]; AND 2 HUMAN V-H-III: RF-SJ2'CL[31], RF-SJ1'CL[46].)  
 SET 5: 783c'CL[21], X17115'CL[22], EV1-15'CL[25], ND'CL[30], Ab2'CL[44]. (5 IDENTICAL HUMAN V-H-I; ALSO 6 HUMAN V-H-II: FK-801'CL[1], HIG[24], Ab44'CL[29], Eog-8'CL[30], MuRSV19VH[36], MuRSV19CFHFS[38]; 6 HUMAN V-H-III: 4G12'CL[10], Ab2'CL[24], M72'CL[24], KIM46H'CL[29], U266'CL[136], 70P1'CL[183]; 2 MOUSE V-H-IIA: HDEX12[15], MB1'CL[160]; AND 1 MOUSE V-H-IIC: MuRSV19VH'CL[37].)



## GENERAL NOTES: HUMAN HEAVY CHAINS SUBGROUP I (cont'd)

SET 6: 83P2'CL[38]. (IDENTICAL TO 2 HUMAN V-H-II: Ab26'CL[18],M60'CL[42]; AND 5 HUMAN V-H-III: Ab18'CL[11],  
RF-KL1'CL[13],1B11'CL[74],1R1'CL[75],2C12'CL[80].)

SET 7: ZUC[54],ZUC'[60]. (2 IDENTICAL)

## IDENTICAL SETS OF COMPLEMENTARITY DETERMINING REGIONS:

**CDR1:** SET 1: LS2'CL[1],LS5'CL[2],LS6'CL[3],LS1'CL[4],LS4'CL[5],LS8'CL[6],LS7'CL[29]. (7 IDENTICAL HUMAN V-H-I; ALSO 1  
MOUSE V-H-IIB: BXW-14'CL[173].)

SET 2: 21-2'CL[8],3-1'CL[9],HG3'CL[12]. (3 IDENTICAL)

SET 3: 21/28'CL[10],8E10'CL[11],E3-10'CL[18]. (3 IDENTICAL HUMAN V-H-I; ALSO 6 HUMAN V-H-III: 56P1'CL[25],  
2P1'CL[26],M72'CL[27],M74'CL[28],RF-SJ2'CL[31],v65-2'CL[84]; AND 1 SHARK V-H: Re107'CL[3].)

SET 4: V35'CL[13]. (IDENTICAL TO 2 MOUSE V-H-IIA: H26-1'CL[50],H26-6'CL[113].)

SET 5: 51P1'CL[14],AND'CL[15],NEI'CL[16],hv1263'CL[20],783c'CL[21],X17115'CL[22],KAS[26]. (7 IDENTICAL HUMAN  
V-H-I; ALSO 3 RABBIT V-H: 5C3'CL[1],5.5'CL[2],4K'CL[3].)

SET 6: 5-1R1'CL[34],VhAU'CL[35],83P2'CL[38],Ab2022'CL[41],M61'CL[47]. (5 IDENTICAL)

**CDR2:** SET 1: LS2'CL[1],LS5'CL[2],LS6'CL[3],LS1'CL[4],LS4'CL[5],LS8'CL[6],LS7'CL[29]. (7 IDENTICAL)

SET 2: 21-2'CL[8],3-1'CL[9],HG3'CL[12]. (3 IDENTICAL)

SET 3: 21/28'CL[10],8E10'CL[11],E3-10'CL[18]. (3 IDENTICAL)

SET 4: 51P1'CL[14],AND'CL[15],NEI'CL[16],783c'CL[21],X17115'CL[22]. (5 IDENTICAL)

SET 5: 5-1R1'CL[34],VhAU'CL[35],Vh251'CL[37],83P2'CL[38],M61'CL[47]. (5 IDENTICAL)

SET 6: Ab2'CL[44],Vh383ex'CL[46]. (2 IDENTICAL)

**CDR3:** SET 1: LS2'CL[1],LS5'CL[2],LS6'CL[3],LS1'CL[4],LS8'CL[6],LS7'CL[29]. (6 IDENTICAL)

SET 2: HG3'CL[12]. (IDENTICAL TO 1 HUMAN V-H-III: LAMBDA-VH26'CL[9]; 1 MOUSE V-H-IB: PJ14'CL[33]; AND 5 MOUSE  
V-H-IIB: 186-2'CL[6],186-1'CL[12],23'CL[28],102'CL[51],102'CL[72].)

SET 3: ND'CL[30]. (IDENTICAL TO 1 HUMAN V-H-III: U266'CL[136].)

## IDENTICAL SETS OF J-MINIGENES:

SET 1: LS2'CL[1],LS5'CL[2],LS6'CL[3],LS1'CL[4],LS8'CL[6],NEI'CL[16],WIL2'CL[24],BOR'[27],LS7'CL[29]. (9 IDENTICAL  
HUMAN V-H-I; ALSO 4 HUMAN V-H-II: ML1'CL[3],DRI2910-2P8'CL[48],Ab17'CL[49],M44'CL[52]; 17 HUMAN V-H-III:  
30P1'CL[5],Ab25'CL[12],60P2'CL[18],63P1'CL[9],56P1'CL[25],M74'CL[28],TIL[33],HN-14'CL[41],W26'CL[49],  
VH10-7'CL[63],K6H6'CL[68],K4BB'CL[69],K5BB'CL[70],K5C'CL[71],K5G5'CL[72],K6F5'CL[73],20P1'CL[82]; AND 1  
MOUSE V-H-IIIB: H37-40'CL[25].)

SET 2: 1B9/F2'CL[7]. (IDENTICAL TO 1 MOUSE V-H-IIB: pING2006E'CL[29]; AND 1 MOUSE V-H-IIIA: MOPC47A[110].)

SET 3: 21/28'CL[10]. (IDENTICAL TO 1 HUMAN V-H-III: TIL[33].)

SET 4: 51P1'CL[14],RF-TS1'CL[28],M61'CL[47],60P1'CL[49],AF2'CL[65]. (5 IDENTICAL HUMAN V-H-I; ALSO 6 HUMAN V-H-II:  
L16'CL[2],M71'CL[4],C6B2'CL[14],58P2'CL[16],CE-1'CL[41],37P1'CL[47]; AND 3 HUMAN V-H-III: 38P1'CL[36],  
3D6'CL[43],13P1'CL[97].)

SET 5: AND'CL[15]. (IDENTICAL TO 1 HUMAN V-H-II: Pag-1'CL[22]; AND 2 HUMAN V-H-III: RF-SJ2'CL[31],RF-SJ1'CL[46].)

SET 6: 783c'CL[21],X17115'CL[22],EV1-15'CL[25],ND'CL[30],Ab2'CL[44]. (5 IDENTICAL HUMAN V-H-I; ALSO 3 HUMAN  
V-H-II: FK-001'CL[11],H1G1'CL[24],Ab44'CL[29]; AND 6 HUMAN V-H-III: 4G12'CL[10],Ab21'CL[24],M72'CL[27],  
KIM46H'CL[29],U266'CL[136],70B1'CL[183].)

SET 7: TH9'CL[23]. (IDENTICAL TO 1 HUMAN V-H-III: DOB[62].)

SET 8: 83P2'CL[38]. (IDENTICAL TO 2 HUMAN V-H-II: Ab26'CL[18],M60'CL[42]; AND 1 HUMAN V-H-III: Ab18'CL[11].)

SET 9: ZUC[54],ZUC'[60]. (2 IDENTICAL)

SET 10: TH3'CL[55]. (IDENTICAL TO 1 HUMAN V-H-III: TIL[33].)

## SPECIFIC NOTES: HUMAN HEAVY CHAINS SUBGROUP I

- 7) 1B9/F2'CL: FROM A PATIENT WITH B CELL ACUTE LYMPHOCYTIC LEUKEMIA WITH CHARACTERISTIC t(8;14) CYTOGENETIC TRANSLOCATION AT DIAGNOSIS.
- 10) 21/28'CL: FROM SPLEEN CELLS OF A SYSTEMIC LUPUS ERYTHEMATOSUS PATIENT.
- 11) 8E10'CL: FROM PERIPHERAL BLOOD LYMPHOCYTES OF A SYSTEMIC LUPUS ERYTHEMATOSUS PATIENT.
- 12) HG3'CL: THE AMINO ACID SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF HUMAN FETAL LIVER GENOMIC DNA.
- 14) 51P1'CL: FROM HUMAN FETUS AT 130 DAYS OF GESTATION.
- 16) NEI'CL: FOR ALIGNMENT, TWO RESIDUES, SER GLU, ARE PLACED AT POSITION 116G.
- 21) 783c'CL: ALSO KNOWN AS 783'CL. FOR ALIGNMENT, EIGHT RESIDUES, TRP TYR PRO ASN SER ASP TYR TYR, ARE PLACED AT POSITION 116G.
- 22) X17115'CL: IT IS AN IGM MEMBRANE BOUND FORM. FOR ALIGNMENT, SIX RESIDUES: TRP TYR PRO ASN SER ASP, ARE PLACED AT POSITIONS 100E.
- 23) TH9'CL: THIS HYBRIDOMA WAS GENERATED BY FUSION OF PERIPHERAL BLOOD CELLS OF A PATIENT WITH LEPROSY AND THE HUMAN MYELOBLASTOID CELL LINE GM4672. TERMINATION AT POSITION 107. TH9 MIGHT BE A PSEUDOGENE.
- 25) EV1-15'CL: THE HYBRIDOMA WAS PRODUCED BY FUSING HUMAN B LYMPHOCYTES WITH THE SPAZ CELL LINE. THE THIRD CDR IS VERY LONG REQUIRING TO PLACE FIVE AMINO ACID RESIDUES AT POSITION 100K: PHE TYR ASP GLY MET.
- 26) KAS: IT IS A HUMAN MONOCLONAL RHEUMATOID FACTOR FROM THE PLASMA OF PATIENT WITH MIXED CRYOGLOBULINEMIA
- 27) BOR': IT IS A HUMAN MONOCLONAL RHEUMATOID FACTOR FROM THE PLASMA OF PATIENT WITH MIXED CRYOGLOBULINEMIA
- 30) ND'CL: THE AMINO ACID SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF MOUSE CDNA. IT CORRESPONDS TO THE AMINO ACID SEQUENCE DETERMINED EARLIER EXCEPT THAT THE AMINO ACID SEQUENCE DETERMINATION GAVE PCA AT POSITION 1, VAL AT 2, VAL AT 34, GLY AT 35, ILE AT 48 AND HIS AT 49.
- 33) RF-TS3'CL: ASP OCCURS AT POSITION 104 INSTEAD OF THE USUAL GLY.
- 39) MOT: PAPAIN CLEAVES BETWEEN ARG 56 AND THR 57, AND BETWEEN ARG 62 AND SER 63.
- 43) lambda IGD-1'CL: CLASS SWITCH FROM IGM TO IGD IS PROBABLY DUE TO HOMOLOGOUS RECOMBINATION BETWEEN sigma/mu AND SIGMA/mu. RESIDUE 52C IS PHE, WITH ANOTHER RESIDUE GLN BETWEEN 52C AND 53. RESIDUE 100J IS LYS, WITH TWO MORE RESIDUES LEU AND ALA BETWEEN 100J AND 100K.
- 49) 60P1'CL: FROM HUMAN FETUS AT 130 DAYS OF GESTATION.
- 54) ZUC: IT WAS FROM A CASE OF HEAVY CHAIN DISEASE.
- 55) TH3'CL: THIS HYBRIDOMA WAS GENERATED BY FUSION OF PERIPHERAL BLOOD CELLS OF A PATIENT WITH LEPROSY AND THE HUMAN MYELOBLASTOID CELL LINE GM4672.
- 57) OMN'CL: THE AMINO ACID SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF HUMAN CELL LINE CDNA. IT WAS FROM A CASE OF HEAVY CHAIN DISEASE.
- 58) BOT: IT WAS FROM A CASE OF IGM HEAVY CHAIN DISEASE.
- 60) ZUC': IT WAS OBTAINED FROM THE SAME PATIENT AS ZUC, AND EXISTED IN A MONOMER FORM.
- 61) WIS: IT WAS FROM A CASE OF HEAVY CHAIN DISEASE. ITS RESIDUES AT POSITIONS 108 AND 109 ARE ASN AND CYS RESPECTIVELY, WHICH DO NOT CORRESPOND TO THE USUAL RESIDUES FOUND AT THESE POSITIONS IN HUMAN HEAVY CHAIN SUBGROUP I.
- 62) VAU: IT WAS FROM A CASE OF HEAVY CHAIN DISEASE.
- 63) LEB: IT WAS FROM A CASE OF HEAVY CHAIN DISEASE.
- 64) SAC: IT WAS FROM A CASE OF HEAVY CHAIN DISEASE.
- 65) AF2'CL: THIS D-J SEGMENT WAS FROM AN EPSTEIN-BARR VIRUS TRANSFORMED HUMAN B-CELL LINE AF2. THE D-SEGMENT SHOWED 65% HOMOLOGUITY TO MOUSE DFL16 MINIGENE AND WAS THUS DESIGNATED AS DHFL16.

+ THE FOLLOWING WERE EQUALLY AND MOST FREQUENTLY OCCURRING:

AT POSITION	RESIDUES
100J	(TYR,ALA)











HUMAN HEAVY CHAINS SUBGROUP II (cont'd)

	46 MCE' #	47 37R1 CL #	48* DR 12910 -2F8 CL #	49* Ab17 CL #	50* LES-B CL #	51* LES-A CL #	52 M44 CL #	53 LV66 CL #	54 JBL2 CL #	55 NZU #	56 SA	57 CAR	58 SPA #	59 IO	60 64P1 CL #	61* ERI #	# OF SEQUENCES	# OF AMINO ACIDS	OCCURRENCES OF MOST COMMON AMINO ACID
	0	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	1	pca	GLN	---	---	---	GLN	GLN	---	---	---	pca	pca	---	---	51	4	39 (GLN), 38 (GLN)	
	2	ile	---	---	---	---	VAL	leu	---	---	---	glu	VAL	---	---	51	4	43 (VAL)	
	3	thr	thr	---	---	---	GLN	GLN	---	---	---	glu	thr	---	---	51	4	39 (GLN)	
	4	leu	---	---	---	---	leu	leu	---	---	---	leu	leu	---	---	51	6	50 (LEU)	
	5	lys	lys	---	---	---	arg	pro	---	---	---	arg	---	---	---	50	6	38 (GLN), 37 (GLN)	
	6	glu	glu	---	---	---	glu	glu	---	---	---	glu	---	---	---	50	2	33 (GLU), 32 (GLU)	
	7	SER	SER	---	---	---	SER	SER	---	---	---	SER	---	---	---	50	3	44 (SER)	
	8	GLY	GLY	---	---	---	ser	GLY	---	---	---	---	---	---	---	49	2	48 (GLY)	
	9	PRO	PRO	---	---	---	PRO	PRO	---	---	---	---	---	---	---	49	3	43 (PRO)	
	10	thr	thr	---	---	---	GLY	GLY	---	---	---	---	---	---	---	49	3	41 (GLY)	
	11	leu	leu	---	---	---	leu	leu	---	---	---	---	---	---	---	49	1	49 (LEU)	
	12	VAL	VAL	---	---	---	VAL	VAL	---	---	---	---	---	---	---	49	2	45 (VAL)	
	13	LYS	LYS	---	---	---	LYS	arg	---	---	---	---	---	---	---	49	2	41 (LYS)	
	14	PRO	PRO	---	---	---	PRO	PRO	---	---	---	---	---	---	---	49	2	48 (PRO)	
	15	thr	thr	---	---	---	SER	pro	---	---	---	---	---	---	---	49	4	38 (SER)	
	16	glu	GLN	---	---	---	asp	---	---	---	---	---	---	---	---	48	5	26 (GLN)	
	17	THR	THR	---	---	---	THR	---	---	---	---	---	---	---	---	48	3	46 (THR)	
	18	leu	leu	---	---	---	leu	leu	---	---	---	---	---	---	---	48	3	47 (LEU)	
	19	thr	thr	---	---	---	SER	ala	---	---	---	---	---	---	---	49	3	39 (SER)	
	20	leu	leu	---	---	---	leu	leu	---	---	---	leu	---	---	---	50	2	49 (LEU)	
	21	THR	THR	---	---	---	ile	ile	---	---	THR	THR	---	---	---	51	2	49 (THR)	
	22	CYS	CYS	---	---	---	CYS	CYS	---	---	CYS	CYS	---	---	---	51	1	51 (CYS)	
	23	thr	thr	---	---	ALA	asn	thr	---	---	thr	thr	---	---	---	52	1	25 (THR)	
	24	phe	phe	---	---	---	val	gly	---	---	val	val	---	---	---	52	5	31 (VAL)	
	25	SER	SER	tyr	---	---	SER	SER	---	---	SER	SER	---	---	---	52	3	45 (SER)	
	26	GLN	GLN	---	---	---	GLY	GLY	---	---	GLY	GLY	---	---	---	51	2	50 (GLN)	
	27	phe	phe	gly	---	---	ASP	---	---	---	gly	---	---	---	---	50	6	19 (GLY)	
	28	SER	SER	SER	---	---	ile	---	---	---	SER	---	---	---	---	50	4	41 (SER)	
	29	leu	ile	leu	leu	---	leu	---	---	---	leu	---	---	---	---	50	4	18 (VAL)	
	30	SER	SER	SER	SER	---	SER	---	---	---	---	---	---	---	---	50	4	46 (SER)	
	31	thr	SER	thr	asn	---	leu	---	---	---	---	---	---	---	---	50	8	28 (SER)	
	32	ser	tyr	gly	tyr	---	leu	---	---	---	---	---	---	---	---	50	13	13 (TYR)	
	33	gly	tyr	gly	cys	---	cys	---	---	---	---	---	---	---	---	50	9	15 (+)	
	34	val	val	trp	trp	---	pro	---	---	---	---	---	---	---	---	50	7	14 (TRP)	
	35	gly	ser	gly	ser	---	asp	---	---	---	---	---	---	---	---	50	12	13 (SER)	
	35A	val	val	val	asn	---	asn	---	---	---	---	---	---	---	---	33	5	18 (TRP)	
	35B	gly	---	gly	arg	---	arg	---	---	---	---	---	---	---	---	27	5	12 (ASN)	
	36	TRP	TRP	TRP	TRP	---	thr	---	---	---	---	---	---	---	---	52	2	51 (TRP)	
	37	ILE	ILE	ILE	ILE	---	gly	---	---	---	---	---	---	---	---	52	4	40 (ILE)	
	38	ARG	ARG	ARG	ARG	---	---	---	---	---	---	---	---	---	---	51	1	51 (ARG)	
	39	GLN	GLN	GLN	GLN	---	---	---	---	---	---	---	---	---	---	51	3	49 (GLN)	
	40	arg	pro	pro	pro	---	---	---	---	---	---	---	---	---	---	51	2	36 (PRO)	
	41	PRO	PRO	PRO	PRO	---	---	---	---	---	---	---	---	---	---	51	2	50 (PRO)	
	42	gly	gly	gly	gly	---	gly	---	---	---	---	---	---	---	---	51	2	39 (GLY)	
	43	lys	lys	lys	lys	---	lys	---	---	---	---	---	---	---	---	51	3	30 (LYS)	
	44	ala	GLY	ala	GLY	---	GLY	---	---	---	---	---	---	---	---	51	2	44 (GLY)	
	45	leu	leu	leu	leu	---	leu	---	---	---	---	---	---	---	---	51	2	49 (LEU)	
	46	GLU	GLU	GLU	GLU	---	GLU	---	---	---	---	---	---	---	---	51	1	51 (GLU)	
	47	TRP	TRP	ser	TRP	---	TRP	---	---	---	---	---	---	---	---	51	2	50 (TRP)	
	48	leu	ile	val	ile	---	ile	---	---	---	---	---	---	---	---	51	3	31 (ILE)	
	49	ala	GLY	ala	GLY	---	ala	---	---	---	---	---	---	---	---	51	2	43 (GLY)	
	50	phe	tyr	leu	glu	---	glu	---	---	---	---	---	---	---	---	51	9	18 (ARG)	
	51	ile	ile	ile	thr	---	ile	---	---	---	---	---	---	---	---	51	5	34 (ILE)	
	52	asn	TYR	TYR	asn	asn	asn	---	---	---	---	---	---	---	---	51	8	29 (TYR)	
	52A	---	---	---	---	---	---	---	---	---	---	---	---	---	---	17	3	13 (TYR)	
	52B	---	---	---	---	---	---	---	---	---	---	---	---	---	---	13	2	11 (ARG)	
	52C	---	---	---	---	---	---	---	---	---	---	---	---	---	---	1	1	1 (ALA)	
	53	trp	tyr	trp	tyr	---	his	---	---	---	---	---	---	---	---	51	10, 11	14 (TYR)	
	54	asp	ser	arg	ser	---	ser	---	---	---	---	---	---	---	---	51	8	23 (SER)	
	55	asp	gly	asp	gly	---	gly	---	---	---	---	---	---	---	---	51	4	28 (GLY)	
	56	asp	ser	asp	ser	---	arg	---	---	---	---	---	---	---	---	51	8	19 (SER)	
	57	ASN	thr	lys	val	---	thr	---	---	---	---	---	---	---	---	51	8	26 (THR)	
	58	arg	asn	leu	lys	---	thr	---	---	---	---	---	---	---	---	51	10	13 (+)	
	59	TYR	TYR	TYR	TYR	---	TYR	---	---	---	---	---	---	---	---	51	6	45 (TYR)	
	60	ser	asn	ser	asn	asn	asn	---	---	---	---	---	---	---	---	51	6, 7	27 (ASN), 26 (ASN)	
	61	pro	pro	pro	pro	---	pro	---	---	---	---	---	---	---	---	51	6	30 (PRO)	
	62	SER	SER	SER	SER	---	SER	---	---	---	---	---	---	---	---	51	4	46 (SER)	
	63	leu	leu	leu	leu	---	leu	---	---	---	---	---	---	---	---	52	3	36 (LEU)	
	64	arg	LYS	LYS	glu	---	thr	---	---	---	---	---	---	---	---	52	5	37 (LYS)	
	65	SER	SER	SER	SER	---	SER	---	---	---	---	---	---	---	---	52	3	43 (SER)	
	66	ARG	ARG	ARG	ARG	---	ARG	---	---	---	---	---	---	---	---	52	1	52 (ARG)	
	67	leu	val	leu	val	---	val	---	---	---	---	---	---	---	---	52	4	30 (VAL)	
	68	THR	THR	THR	THR	---	THR	---	---	---	---	---	---	---	---	52	3	49 (THR)	
	69	gly	ILE	ILE	ILE	---	ILE	---	---	---	---	---	---	---	---	52	5	38 (ILE)	
	70	thr	ser	thr	ser	---	ser	---	---	---	---	---	---	---	---	52	4	30 (SER)	
	71	lys	val	lys	val	---	lys	---	---	---	---	---	---	---	---	52	1	28 (VAL)	
	72	ASP	ASP	ASP	ASP	---	ASP	---	---	---	---	---	---	---	---	52	2	51 (ASP)	
	73	THR	THR	THR	ser	---	THR	---	---	---	---	---	---	---	---	52	5	47 (THR)	
	74	SER	SER	SER	SER	---	SER	---	---	---	---	---	---	---	---	52	2	51 (SER)	
	75	arg	LYS	LYS	LYS	---	LYS	---	---	---	---	---	---	---	---	52	3	48 (LYS)	
	76	ASN	ASN	ASN	ASN	---	ASN	---	---	---	---	---	---	---	---	52	1	52 (ASN)	
	77	GLN	GLN	GLN	GLN	---	GLN	---	---	---	---	---	---	---	---	52	4	49 (GLN)	
	78	val	PHE	val	PHE	---	PHE	---	---	---	---	---	---	---	---	52	2	43 (PHE)	
	79	val	SER	val	phe	---	SER	---	---	---	---	---	---	---	---	52	4	41 (SER)	
	80	leu	leu	leu	leu	---	leu	---	---	---	---	---	---	---	---	52	1	52 (LEU)	
	81	thr	lys	thr	lys	---	lys	---	---	---	---	---	---	---	---	52	8	22 (LYS)	
	82	ile	leu	met	met	---	leu	---	---	---	---	---	---	---	---	52	4	42 (LEU)	
	82A	thr	ser	thr	ser	---	thr	---	---	---	---	---	---	---	---	52	1	22 (SER)	
	82B	asn	SER	asn	SER	---	SER	---	---	---	---	---	---	---	---	50	3	42 (SER)	
	82C	met	VAL	met	VAL	---	ala	---	---	---	met	---	---	---	---	52	3	43 (VAL)	
	83	asp	THR	asp	THR	---	THR	---	---	---	asp	---	---	---	---	53	5	42 (THR)	
	84	PRO	ala	PRO	ala	---	ala	---	---	---	PRO	---	---	---	---	53	3	30 (ALA)	
	85	val	ala	val	ala	---	ala	---	---	---	val	---	---	---	---	53	4	30 (ALA)	
	86	ASP	ASP	thr	ASP	---	ASP	---	---	---	ASP	---	---	---	---	53	2	52 (ASP)	
	87	ser	THR	glu	THR	---	THR	---	---	---	ser	---	---	---	---	53	3	49 (THR)	
	88	gly	ALA	pro	ALA	---	ALA	---	---	---	gly	---	---	---	---	53	5	50 (ALA)	
	89	chr	VAL	ile	VAL	---	thr	---	---	---	thr	---	---	---	---	53	5	41 (VAL)	
	90	TYR	TYR	ile	TYR	---	TYR	---	---	---	TYR	---	---	---	---	53	2	52 (TYR)	
	91	phe	TYR	thr	TYR	---	phe	---	---	---	phe	---	---	---	---	53	4	46 (TYR)	
	92	CYS	CYS	met	CYS	---	CYS	---	---	---	CYS	---	---	---	---	53	2	52 (CYS)	
	93	ALA	ALA	his	ALA	---	ALA	---	---	---	ALA	---	---	---	---	53	5	48 (ALA)	
	94	his	ARG	thr	ARG	---	ARG	---	---	---	his	---	---	---	---	52	4	45 (ARG)	
	95	ARG	GLU	ASP	CYS	---	GLY	---	---	---	THR</								



HUMAN HEAVY CHAINS SUBGROUP II (cont'd)

VARIABILITY

	0	
	1	5.2, 5.4
	2	4.8
	3	2.2
	4	
	5	7.9, 8.1
	6	3.3, 3.1
	7	3.4
	8	2.2
	9	3.4
	10	3.6
	11	1.1
	12	2.2
	13	2.4
	14	2.2
FR 1	15	5.2
	16	9.2
	17	3.1
	18	3.8
	19	
	20	2.2
	21	2.1
	22	1.1
	23	15.1
	24	8.4
	25	3.5
	26	2.2
	27	16.1
	28	4.9
	29	11.1
	30	4.3
CDR 1	31	14.1
	32	30.1
	33	30.1
	34	25.1
	35	46.1
	35A	
	35B	
	36	2.2
	37	5.2
FR 2	38	1.1
	39	3.1
	40	2.1
	41	2.2
	42	2.6
	43	5.1
	44	3.3
	45	2.1
	46	2.2
	47	2.2
	48	4.9
	49	2.4
	50	25.1
	51	7.5
	52	14.1
CDR 2	52A	
	52B	
	52C	
	53	36.1, 40.1
	54	18.1
	55	7.3
	56	21.1
	57	16.1
	58	39.1
	59	6.8
	60	11.1, 14.1
	61	10.1
	62	4.4
	63	4.3
	64	7.1
	65	3.6
	66	1.1
	67	6.9
	68	2.2
	69	6.8
	70	6.9
	71	11.1
	72	2.2
	73	5.5
	74	2.2
	75	3.2
	76	1.1
	77	4.2
	78	2.4
	79	5.1
FR 3	80	1.1
	81	19.1
	82	5.1
	82A	
	82B	
	82C	
	83	6.3
	84	5.3
	85	7.1
	86	2.2
	87	3.2
	88	3.2
	89	6.5
	90	2.2
	91	4.6
	92	2.2
	93	5.5
	94	4.6
	95	70.1
	96	88.1
	97	110.1
	98	76.1
	99	57.1
	100	87.1
	100A	
CDR 3	100B	
	100C	
	100D	
	100E	
	100F	
	100G	
	100H	
	100I	
	100J	
	100K	
	101	6.5
	102	19.1
	103	3.2
	104	1.1
	105	6.5
FR 4	106	1.1
	107	3.5
	108	15.1
	109	2.1
	110	4.4
	111	2.1
	112	2.1
	113	3.3

## ANTIBODY SPECIFICITIES: HUMAN HEAVY CHAINS SUBGROUP II

- 2) L16'CL: ANTI-POLYdT, CARDIOLIPIN, AND ssDNA
- 3) ML1'CL: ANTI-POLYdT, AND ssDNA
- 5) F19L16'CL: ANTI-ssDNA, CARDIOLIPIN, POLY-dT
- 6) F19ML1'CL: ANTI-ssDNA, POLY-dT
- 10) A10'CL: ANTI-ssDNA, dsDNA, CARDIOLIPIN, POLY-dT, HEN EGG LYSOZYME
- 11) FK-001'CL: ANTI-Pseudomonas aeruginosa EXOTOXIN A HYBRIDOMA
- 12) A431'CL: ANTI-ssDNA, dsDNA, CARDIOLIPIN, POLY-dT, PIGEON CYTOCHROME C
- 14) C6B2'CL: ANTI-DNA HYBRIDOMA
- 18) Ab26'CL: POLYREACTIVE AUTOANTIBODY
- 22) Pag-1'CL: ANTI-D ANTIGEN OF THE Rh-BLOOD-GROUP SYSTEM
- 25) HuVNP'CL: ANTI-4-HYDROXY-3-NITROPHENACETYL CAPROIC ACID (BINDING CONSTANT = 1.9X10EXP6)
- 27) HuVHLYS'CL: ANTI-LYSOZYME HYBRIDOMA
- 29) Ab4'CL: POLYREACTIVE AUTOANTIBODY
- 30) Fog-B'CL: ANTI-D ANTIGEN OF THE Rh-BLOOD-GROUP SYSTEM
- 32) HuVHCAMP'CL: ANTI-HUMAN LYMPHOCYTE HYBRIDOMA
- 33) 6H-3C4'CL: HUMAN SPERM-IMMOBILIZING ANTIBODY
- 34) NEMM: ANTI-3-(3'-HYDROXY-3',7',11',15',TETRAMETHYL HEXADECYL) 2-METHYL 1,4 NAPHTHOQUINONE (VIT. K10H)
- 35) GER: MONOCLONAL CRYOIMMUNOGLOBULIN
- 38) HuRSV19CHFN5: ANTI-HUMAN RESPIRATORY SYNCYTIAL VIRUS
- 39) LES-C'CL: RHEUMATOID FACTOR
- 48) DR12910-2F8'CL: ANTI-DR 1,2,9,10 HYBRIDOMA
- 49) Ab17'CL: POLYREACTIVE AUTOANTIBODY
- 50) LES-B'CL: RHEUMATOID FACTOR
- 51) LES-A'CL: RHEUMATOID FACTOR
- 61) ERI: ANTI-4-HYDROXY-3-NITROPHENACETYL CAPROIC ACID (BINDING CONSTANT = 1.9X10EXP6)

## CLASS: HUMAN HEAVY CHAINS SUBGROUP II

- 1) 15P1'CL: IGM-
- 2) L16'CL: IGM-LAMBDA
- 3) ML1'CL: IGM-KAPPA
- 5) F19L16'CL: IGM-LAMBDA
- 6) F19ML1'CL: IGM-KAPPA
- 10) A10'CL: IGM-KAPPA
- 11) FK-001'CL: IGM-KAPPA
- 12) A431'CL: IGM-LAMBDA
- 14) C6B2'CL: IGM-KAPPA
- 16) 58P2'CL: IGM-
- 18) Ab26'CL: IGM-LAMBDA
- 22) Pag-1'CL: IGG1-LAMBDA
- 25) HuVNP'CL: IGE-
- 27) HuVHLYS'CL: IGG2-KAPPA
- 29) Ab4'CL: IGA-LAMBDA
- 30) Fog-B'CL: IGG1-LAMBDA
- 32) HuVHCAMP'CL: IGG1-KAPPA
- 34) NEMM: IGG1-LAMBDA
- 35) GER: IGG-KAPPA
- 37) WAH: IGD-LAMBDA
- 39) LES-C'CL: IGM-
- 40) COR: IGG1-
- 43) DAM: IGG1-LAMBDA
- 44) HE: IGG1-
- 45) OU: IGM-KAPPA
- 46) MCE'CL: IGM-KAPPA
- 47) 37P1'CL: IGM-
- 48) DR12910-2F8'CL: IGM-
- 49) Ab17'CL: IGG3-KAPPA
- 50) LES-B'CL: IGM-
- 51) LES-A'CL: IGM-
- 55) NZU: IGM-
- 56) SA: IGG2-LAMBDA
- 60) 64P1'CL: IGM-
- 61) ERI: IGD-

## REFERENCE: HUMAN HEAVY CHAINS SUBGROUP II

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- 2) L16'CL: LOGTENBERG, T., YOUNG, F.M., VAN ES, J.H., GMELIG-MEYLING, F.H.J. & ALT, F.W. (1989) J.EXP.MED., 170, 1347-1355.
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- 5) F19L16'CL: LOGTENBERG, T., YOUNG, F.M., VAN ES, J., GMELIG-MEYLING, F.H.J., BERMAN, J.E. & ALT, F.W. (1989) J.AUTOIMMUNITY, 2, 203-213.
- 6) F19ML1'CL: LOGTENBERG, T., YOUNG, F.M., VAN ES, J., GMELIG-MEYLING, F.H.J., BERMAN, J.E. & ALT, F.W. (1989) J.AUTOIMMUNITY, 2, 203-213.
- 7) 6-IG1'CL: BERMAN, J.E., MELLIS, S.J., POLLOCK, R., SMITH, C.L., SUH, H., HEINKE, B., KOWAL, C., SURTI, U., CHESS, L., CANTOR, C.R. & ALT, F.W. (1988) EMBO J., 7, 727-738.
- 8) VHV1'CL: BULUWELA, L. & RABBITTS, T.H. (1988) EUR. J. IMMUNOL., 18, 1843-1845.
- 9) VHV6'CL: SCHROEDER, H.W., JR., WALTER, M.A., HOFKER, M.H., EBENS, A., VAN DIJK, K.W., LIAO, L.C., COX, D.W., MILNER, E.C.B. & PERLMUTTER, R.M. (1988) PROC.NATL.ACAD.SCI.USA, 85, 8196-8200.
- 10) A10'CL: LOGTENBERG, T., YOUNG, F.M., VAN ES, J., GMELIG-MEYLING, F.H.J., BERMAN, J.E. & ALT, F.W. (1989) J.AUTOIMMUNITY, 2, 203-213.
- 11) FK-001'CL: LEHMAN, D.W. & PUTNAM, F.W. (1980) PROC.NATL.ACAD.SCI.USA, 77, 3239-3243. (CHECKED BY AUTHOR 05/01/80)
- 12) A431'CL: LOGTENBERG, T., YOUNG, F.M., VAN ES, J., GMELIG-MEYLING, F.H.J., BERMAN, J.E. & ALT, F.W. (1989) J.AUTOIMMUNITY, 2, 203-213.
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## IDENTICAL SETS OF FRAMEWORK SEGMENTS:

- FR1:** SET 1: 15P1'CL[1], L16'CL[2], ML1'CL[3], M71'CL[4], F19L16'CL[5], F19ML1'CL[6], 6-1G1'CL[7], VHVI'CL[8], VH6'CL[9], A10'CL[10], FK-001'CL[11], A431'CL[12]. (12 IDENTICAL)
- SET 2: 71-2'CL[13], 71-4'CL[15]. (2 IDENTICAL)
- SET 3: 1-9I1'CL[19], 12G-1'CL[20]. (2 IDENTICAL)
- SET 4: HuVNP'CL[25], HuVHLYS'CL[27], HuVHCAMP'CL[32]. (3 IDENTICAL)
- SET 5: HuRSV19VH[36], HuRSV19CHFNS[38]. (2 IDENTICAL)
- FR2:** SET 1: 15P1'CL[1], L16'CL[2], ML1'CL[3], M71'CL[4], F19L16'CL[5], F19ML1'CL[6], 6-1G1'CL[7], VHVI'CL[8], VH6'CL[9], A10'CL[10], FK-001'CL[11], A431'CL[12]. (12 IDENTICAL)
- SET 2: 71-2'CL[13], C6B2'CL[14], 71-4'CL[15], 58P2'CL[16], SUP-T1 VH-JA'CL[17], 1-9I1'CL[19], 12G-1'CL[20], 2-1'CL[21], 58'CL[28], 6H-3C4'CL[33], GER[35], WAH[37], 37P1'CL[47], Ab17'CL[49], LES-B'CL[50], LES-A'CL[51]. (16 IDENTICAL HUMAN V-H-I; ALSO MISCELLANEOUS V-H: LG2, J111'CL[18], LL2.8(11)'CL[32], XENOPUS LAEVIS 11'CL[38], XENOPUS LAEVIS C14(11)'CL[55], XENOPUS LAEVIS C40(11)'CL[57].)
- SET 3: 11'CL[23], 79'CL[26], Fog-B'CL[30]. (3 IDENTICAL)
- SET 4: HuVNP'CL[25], HuVHLYS'CL[27], HuVHCAMP'CL[32], NEWM[34], HuRSV19VH[36], HuRSV19CHFNS[38]. (6 IDENTICAL)
- SET 5: CE-1'CL[41], M60'CL[42]. (2 IDENTICAL)
- FR3:** SET 1: 15P1'CL[1], L16'CL[2], ML1'CL[3], M71'CL[4], F19L16'CL[5], F19ML1'CL[6], 6-1G1'CL[7], VHVI'CL[8], VH6'CL[9], A10'CL[10]. (10 IDENTICAL)
- SET 2: 71-2'CL[13], C6B2'CL[14], 71-4'CL[15], 58P2'CL[16], SUP-T1 VH-JA'CL[17], Ab44'CL[29], 37P1'CL[47]. (7 IDENTICAL)
- SET 3: 1-9I1'CL[19], 12G-1'CL[20]. (2 IDENTICAL)
- SET 4: HuVNP'CL[25], HuVHLYS'CL[27], HuVHCAMP'CL[32], NEWM[34], HuRSV19VH[36]. (5 IDENTICAL)
- FR4:** SET 1: 15P1'CL[1], ML1'CL[3], MCE'[46], DR12910-2F8'CL[48], Ab17'CL[49], M44'CL[52], NZU[55]. (7 IDENTICAL HUMAN V-H-II; ALSO 14 HUMAN V-H-I: LS2'CL[11], LS5'CL[21], LS6'CL[3], LS1'CL[4], LS8'CL[6], 1B9/P2'CL[7], 21/28'CL[10], NET'CL[16], TH'CL[23], WL2'CL[24], KAS[26], BOR[27], H3'CL[29], WOL[45]. 4 HUMAN V-H-III: 1B9'CL[11], 18/17'CL[12], 18/9'CL[17], 1/17'CL[41], 30P1'CL[42], M43'CL[46], HP2-1'CL[77], Ab25'CL[12], Vh38C1.1'CL[15], Vh38C1.3'CL[16], Vh38C1.5'CL[17], 60P2'CL[18], 63P1'CL[19], GF4/1.1'CL[20], Vh38C1.4'CL[21], Vh38C1.5'CL[22], 56P1'CL[25], 2P1'CL[26], M74'CL[28], TIL[33], HN.14'CL[41], WEA[47], 4B4'CL[48], M26'CL[49], NIE[60], DOB[62], VH10.7'CL[63], K6B8'CL[68], K4B8'CL[69], K5B8'CL[70], K5C7'CL[71], K5C5'CL[72], K6F5'CL[73], 20P1'CL[82]. 1 MOUSE V-H-IIB: DING2005E'CL[29]. 1 MOUSE V-H-IIIA: MOPC47A[101]. AND 1 MOUSE V-H-IID: H37-40'CL[25].)
- SET 2: L16'CL[2], M71'CL[4], C6B2'CL[14], 58P2'CL[16], CE-1'CL[41], 37P1'CL[47]. (6 IDENTICAL HUMAN V-H-II; ALSO 6 HUMAN V-H-I: 51P1'CL[14], RF-TS1'CL[28], Ab2022'CL[41], M61'CL[47], 60P1'CL[49], AF2'CL[65]; AND 3 HUMAN V-H-III: 38P1'CL[36], 3D6'CL[43], 13P1'CL[97].)
- SET 3: Pag-1'CL[22]. (IDENTICAL TO 1 HUMAN V-H-I: AND'CL[15]; AND 2 HUMAN V-H-III: RF-SJ2'CL[31], RF-SJ1'CL[46].)
- SET 4: FK-001'CL[11], HIG1'CL[24], Ab44'CL[29], Fog-B'CL[30], HuRSV19VH[36], HuRSV19CHFNS[38]. (6 IDENTICAL HUMAN V-H-II; ALSO 5 HUMAN V-H-I: 783C'CL[21], K17115'CL[22], EV1-15'CL[25], ND'CL[30], Ab2'CL[44]; 6 HUMAN V-H-III: 4G12'CL[13], Ab21'CL[24], KIM4'CL[29], KIM4'CL[29], 0266'CL[136], 70P1'CL[183]; 2 MOUSE V-H-IIA: HDX12[15], MB1'CL[160]. AND 1 MOUSE V-H-IIC: MuRSV19VH'CL[37].)
- SET 5: Ab26'CL[18], M60'CL[42]. (2 IDENTICAL HUMAN V-H-II; ALSO 1 HUMAN V-H-I: 83P2'CL[38]; AND 5 HUMAN V-H-III: Ab18'CL[11], RF-KL1'CL[13], 1B11'CL[74], 1H1'CL[75], 2C12'CL[80].)
- SET 6: HuVNP'CL[25], HuVHLYS'CL[27], HuVHCAMP'CL[32], NEWM[34]. (4 IDENTICAL)

## IDENTICAL SETS OF COMPLEMENTARITY DETERMINING REGIONS:

- CDR1:** SET 1: 15P1'CL[1], L16'CL[2], ML1'CL[3], M71'CL[4], F19L16'CL[5], F19ML1'CL[6], 6-1G1'CL[7], VHVI'CL[8], VH6'CL[9]. (9 IDENTICAL)
- SET 2: 71-4'CL[15], 58P2'CL[16], 37P1'CL[47]. (3 IDENTICAL)
- SET 3: 1-9I1'CL[19], 12G-1'CL[20]. (2 IDENTICAL)
- SET 4: 11'CL[23], 79'CL[26]. (2 IDENTICAL)
- SET 5: HIG1'CL[24], 58'CL[28], Ab44'CL[29], 6H-3C4'CL[33], LES-C'CL[39]. (5 IDENTICAL)
- SET 6: HuVNP'CL[25]. (IDENTICAL TO 1 HUMAN V-H-III: H11'CL[23]; 9 MOUSE V-H-IIA: 4m4 GL'CL[94], 5D3'CL[112], SE3'CL[119], AM9'CL[120], AM10'CL[130], AM12'CL[131], 706'CL[142], 2.9 GL'CL[169], 4238'CL[206]; AND 69 MOUSE V-H-IIB: B1-H'CL[1], B1-8.DELTA1V3[2], B1-48'CL[3], N-HYB'CL[4], 18C10'CL[5], 186-2'CL[6], B1-8.VA'CL[7], S2D8'CL[8], 6P6'CL[9], S2E9'CL[10], P17.170.2[11], 186-1'CL[12], B4'CL[13], S2H5'CL[14], SIF12'CL[15], ANTI-TGAL 17'CL[16], H1-9'CL[18], CH12'CL[19], 4m5 GL'CL[24], 22.5'CL[27], 23'CL[28], DING2006E'CL[29], B1-8.VI/V2[30], B1-8.VI/V2[31], N12'CL[32], 124'CL[33], 124'CL[34], 564'CL[35], 503'CL[36], 567'CL[37], 569'CL[38], 132.16'CL[39], N1G9'CL[40], 102'CL[51], 33'CL[52], CH-51'CL[55], DB1-514.3'CL[56], DF4-12.6'CL[57], H1-45'CL[59], SIF2'CL[60], C1R4 GL'CL[64], CH10'CL[68], CH-55'CL[74], CH31'CL[76], H1-29'CL[79], DBF1-608.1'CL[89], AC38.15.3[93], H1-59'CL[94], 104B'CL[101], 20.119.2[104], 4B9P'CL[106], MYA4'CL[109], 167.1'CL[113], 219.7'CL[114], 5D68'CL[122], 167.2'CL[127], CH12'CL[129], P1.59.2'CL[137], VcD15 GL'CL[138], 19.13'CL[141], 6C7S'CL[144], 3B15'CL[145], 3B15'CL[146], 4A88'CL[164], NQ22.87.1'CL[165], AC38.251.5[168], 4m10 GL'CL[174], AC38.262.2[175], 4F55'CL[178], 10H12S'CL[180], VNP'CL[185].)
- SET 7: HuVHLYS'CL[27]. (IDENTICAL TO 6 MOUSE V-H-IIB: PJ14'CL[33], D1.3[38], MOPC141'CL[56], G2b-4'CL[61], 56-1'CL[73], G3-3'CL[86].)
- RS1:** SET 8: HuVHCAMP'CL[32]. (IDENTICAL TO 2 MOUSE V-H-IIA: 26-10VH'CL[74], 26-10[188]; 4 MOUSE V-H-IIIA: CBA/J V3'CL[91], VB4.4'CL[99], C57BL/10 V3'CL[100], C57BL V3'CL[101]; AND 1 RAT V-H: YTH 34.5HL'CL[1].)
- SET 9: HuRSV19VH[36], HuRSV19CHFNS[38]. (2 IDENTICAL HUMAN V-H-II; ALSO 1 MOUSE V-H-IIA: L13'CL[173]; 5 MOUSE V-H-IIC: Vp38 GL'CL[20], F4.16.25'CL[25], H4a-3'CL[28], H2b-3'CL[32], MuRSV19VH'CL[37]; AND 1 MISCELLANEOUS V-H: XENOPUS LAEVIS V'CL[42].)
- CDR2:** SET 1: 15P1'CL[1], L16'CL[2], ML1'CL[3], M71'CL[4], F19L16'CL[5], F19ML1'CL[6], 6-1G1'CL[7], VHVI'CL[8], VH6'CL[9]. (9 IDENTICAL)
- SET 2: 71-2'CL[13], 71-4'CL[15], 58P2'CL[16], 37P1'CL[47]. (4 IDENTICAL)
- SET 3: Ab26'CL[18], 1-9I1'CL[19], 12G-1'CL[20]. (3 IDENTICAL)
- SET 4: HuVNP'CL[25]. (IDENTICAL TO 19 MOUSE V-H-IIB: B1-8'CL[11], B1-8.DELTA1V3[2], B1-48'CL[3], N-HYB'CL[4], 18C10'CL[5], 186-2'CL[6], S2D8'CL[8], 6P6'CL[9], S2E9'CL[10], 186-1'CL[12], ANTI-TGAL 17'CL[16], H1-9'CL[18], H1-31G9'CL[21], H1-39'CL[43], 3C52'CL[46], N1G9'CL[40], 20.119.25'CL[104], 219.7'CL[114], 167.2'CL[127].)
- SET 5: HuVHLYS'CL[27]. (IDENTICAL TO 1 MOUSE V-H-IB: D1.3[38].)
- SET 6: HuVHCAMP'CL[32]. (IDENTICAL TO 1 RAT V-H: YTH 34.5HL'CL[1].)
- SET 7: HuRSV19VH[36], HuRSV19CHFNS[38]. (2 IDENTICAL HUMAN V-H-II; ALSO 1 MOUSE V-H-IIC: MuRSV19VH'CL[37].)



**GENERAL NOTES: HUMAN HEAVY CHAINS SUBGROUP II (cont'd)**

SET 8: LES-C'CL[39],LES-B'CL[50],LES-A'CL[51]. (3 IDENTICAL)

**CDR3:** SET 1: HuVHLYS'CL[27]. (IDENTICAL TO 1 MOUSE V-H-IB: D1.3[38].)

SET 2: HuVHCAMP'CL[32]. (IDENTICAL TO 1 RAT V-H: YTH 34.5HL'CL[1].)

SET 3: HuRSV19VH[36],HuRSV19CHFNS[38]. (2 IDENTICAL HUMAN V-H-II; ALSO 1 MOUSE V-H-IIC: MuRSV19VH'CL[37].)

SET 4: LES-C'CL[39],LES-B'CL[50],LES-A'CL[51]. (3 IDENTICAL)

**IDENTICAL SETS OF J-MINIGENES:**

SET 1: ML1'CL[3],DR12910-2F8'CL[48],Ab17'CL[49],M44'CL[52]. (4 IDENTICAL HUMAN V-H-II; ALSO 9 HUMAN V-H-I: LS2'CL[1],LS5'CL[2],LS6'CL[3],LS1'CL[4],LS8'CL[6],NE'CL[16],HL2'CL[24],BOR'CL[27],LS7'CL[29],17 HUMAN V-H-III: 50P1'CL[5],Ab25'CL[15],60P2'CL[18],63P1'CL[19],56P1'CL[25],M74'CL[28],T1L[33],HN.14'CL[41],M26'CL[49],VH10.7'CL[63],K6H6'CL[68],K4B8'CL[69],K5B8'CL[70],K5C7'CL[71],K5G5'CL[72],K6F5'CL[73],20P1'CL[82]; AND 1 MOUSE V-H-IIID: H37-40'CL[25].)

SET 2: L16'CL[2],M71'CL[4],C6B2'CL[14],58P2'CL[16],CE-1'CL[41],37P1'CL[47]. (6 IDENTICAL HUMAN V-H-II; ALSO 5 HUMAN V-H-I: 51P1'CL[14],RF-TS[1],CL[28],M61'CL[47],60P1'CL[49],AF2'CL[65]; AND 3 HUMAN V-H-III: 38P1'CL[36],3D6'CL[43],13P1'CL[9].)

SET 3: Pag-1'CL[22]. (IDENTICAL TO 1 HUMAN V-H-I: AND'CL[15]; AND 2 HUMAN V-H-III: RF-SJ2'CL[31],RF-SJ1'CL[46].)

SET 4: FK-001'CL[11],HIG1'CL[24],Ab44'CL[29]. (3 IDENTICAL HUMAN V-H-II; ALSO 5 HUMAN V-H-I: 783c'CL[21],X17115'CL[22],EVI-15'CL[25],ND'CL[30],Ab2'CL[44]; AND 6 HUMAN V-H-III: 4G12'CL[10],Ab21'CL[24],M72'CL[27],KIM46H'CL[29],U266'CL[136],70P1'CL[183].)

SET 5: Ab26'CL[18],M60'CL[42]. (2 IDENTICAL HUMAN V-H-II; ALSO 1 HUMAN V-H-I: 83P2'CL[38]; AND 1 HUMAN V-H-III: Ab18'CL[11].)

SET 6: 15P1'CL[1]. (IDENTICAL TO 7 HUMAN V-H-III: 18/2'CL[1],18/17'CL[2],18/9'CL[3],1/17'CL[4],M43'CL[6],HF2-1/17[1],2P1'CL[26].)

SET 7: HuVHLYS'CL[27],HuVHCAMP'CL[32]. (2 IDENTICAL)

SET 8: HuRSV19VH[36],HuRSV19CHFNS[38]. (2 IDENTICAL HUMAN V-H-II; ALSO 1 MOUSE V-H-IIC: MuRSV19VH'CL[37].)

**SPECIFIC NOTES: HUMAN HEAVY CHAINS SUBGROUP II**

- 1) 15P1'CL: FROM HUMAN FETUS AT 130 DAYS OF GESTATION.
- 11) FK-001'CL: IT CAN BE EXPRESSED FUNCTIONALLY IN MOUSE MYELOMA CELLS.
- 14) C6B2'CL: DERIVED FROM SPLENIC LYMPHOCYTES OF SIX MONTH OLD CHILD WITH SICKLE CELL ANEMIA.
- 16) 58P2'CL: FROM HUMAN FETUS AT 130 DAYS OF GESTATION.
- 17) SUP-T1 VH-JA'CL: FROM A PATIENT SUFFERING FROM CHILDHOOD T-CELL LYMPHOMA WITH inv(14)(q11.2;q32.2). THE INVERSION ON CHROMOSOME 14 BRINGS THE VH GENE AND JA MINIGENE TOGETHER, GIVING RISE TO A HYBRID MOLECULE CONTAINING PART OF THE IMMUNOGLOBULIN GENE AND PART OF THE T-LYMPHOCYTE RECEPTOR FOR ANTIGEN GENE.
- 22) Pag-1'CL: THREE-DIMENSIONAL MODEL HAS BEEN CONSTRUCTED FOR THIS ANTIBODY.
- 25) HuVNP'CL: A HYBRID HEAVY CHAIN CONSISTING OF FR'S FROM NEMM AND CDR'S FROM B1-8'CL, AN ANTI-4-HYDROXY-3-NITROPHENACETYL CAPROIC ACID MOUSE ANTIBODY; B1-8'CL HEAVY CHAIN HAS A BINDING CONSTANT OF 1.2X10EXP6, AND THIS HYBRID HEAVY CHAIN HAS A BINDING CONSTANT OF 1.9X10EXP6.
- 27) HuVHLYS'CL: MADE OF FR'S OF HUMAN NEMM AND CDR'S OF MOUSE D1.3.
- 30) Fog-B'CL: THREE-DIMENSIONAL MODEL HAS BEEN CONSTRUCTED FOR THIS ANTIBODY.
- 33) 6H-3C4'CL: 6H-3C4 IS AN ESTABLISHED HUMAN-MOUSE HETEROHYBRIDOMA WHICH SECRETES A HUMAN IGM-LAMBDA ANTIBODY. THIS SEQUENCE IS OBTAINED BY LIGATING THE VH GENE WITH HUMAN IGG1 REGION. THE NEW HUMAN IGG1-LAMBDA ANTIBODY FULLY RETAINS THE ORIGINAL SPECIFICITY.
- 36) HuRSV19VH: THIS SEQUENCE CONTAINS THE FR'S OF NEMM WITH SOME MODIFICATIONS, AND CDR'S OF MuRSV19VH. WHEN COMBINED WITH HuRSV19VK, THE FV DOES NOT BIND THE VIRUS.
- 38) HuRSV19CHFNS: THIS SEQUENCE CONTAINS THE FR'S OF NEMM WITH MORE MODIFICATIONS THAN HuRSV19VH, AND CDR'S OF MuRSV19VH. WHEN COMBINED WITH HuRSV19VK, THE FV BINDS THE VIRUS.
- 39) LES-C'CL: FROM A PATIENT WITH CHRONIC LYMPHOCYTIC LEUKEMIA. FOR ALIGNMENT, IT IS REQUIRED TO PLACE THREE AMINO ACID RESIDUES, GLY ALA ARG, AT POSITION 100I.
- 41) CE-1'CL: CELL LINE CESS
- 46) MCE: IT IS A CRYOIMMUNOGLOBULIN AND IS DESIGNATED BY THE AUTHORS AS MCE. IN ORDER TO DIFFERENTIATE IT FROM ANOTHER MCE SEQUENCED BY CAPRA ET AL., IT IS DENOTED AS MCE'.
- 47) 37P1'CL: FROM HUMAN FETUS AT 130 DAYS OF GESTATION.
- 49) Ab17'CL: AUTHORS PROVIDED THIS SEQUENCE WHICH IS DIFFERENT FROM THAT IN THE REFERENCE. THE RESIDUE AT POSITION 100J IS GLU, WITH THREE ADDITIONAL RESIDUES PRO GLY ASN BETWEEN POSITIONS 100J AND 100K.
- 50) LES-B'CL: FROM A PATIENT WITH CHRONIC LYMPHOCYTIC LEUKEMIA. FOR ALIGNMENT, IT IS REQUIRED TO PLACE THREE AMINO ACID RESIDUES, GLY ALA ARG, AT POSITION 100I.
- 51) LES-A'CL: FROM A PATIENT WITH CHRONIC LYMPHOCYTIC LEUKEMIA. FOR ALIGNMENT, IT IS REQUIRED TO PLACE THREE AMINO ACID RESIDUES, GLY ALA ARG, AT POSITION 100I.
- 53) Ly66'CL: AT POSITION 40 THE SEQUENCE CONNECTS TO THE CONSTANT REGION.
- 54) JBL2'CL: FROM BURKITT'S LYMPHOMA CELL LINES WHICH PRODUCE TRUNCATED HEAVY CHAINS LACKING PART OF VARIABLE REGION
- 55) NZU: IT IS A CRYOIMMUNOGLOBULIN.
- 58) SPA: IT WAS FROM A CASE OF HEAVY CHAIN DISEASE.
- 60) 64P1'CL: FROM HUMAN FETUS AT 130 DAYS OF GESTATION.

+ THE FOLLOWING WERE EQUALLY AND MOST FREQUENTLY OCCURRING:

AT POSITION	RESIDUES
33	(TYR, SER)
36	(TYR, ASP, ASN)
100A	(ILE, PHE, CYS, ALA, SER, GLY)
100H	(ALA, ASP)
100I	(ALA, ASN)





















HUMAN HEAVY CHAINS SUBGROUP III (cont'd)

	119*	120*	121*	122*	123*	124	125	126	127*	128*	129*	130*	131*	132*	133	134	135	136	137*	138	139	140	141	
	H-G2a	A-G2b	K-G2	C-G1	K-G1	ERI	LRI	WO	HEI	KN	H-G2b	C-G2b	F-G1	L.	SMM	HI	Ly91	U266	WAG	LR	LR	LB	W2	LAMBDA
				#	(+6-)	'CL	'CL						#	TH.	-IGA		'CL	'CL			'CL	'CL	'CL	-VH52
0	GLU																							
1	VAL	VAL	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU
2	LEU	LEU	VAL	VAL	VAL	ala	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
3			GLN	GLN	GLN	GLN	his	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	lys	his	his	GLN
4			LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
5	val	val	val	val	val	val	val	val	val	val	val	val	val	val	val	val	val	val	val	val	val	val	val	val
6	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU
7	SER	SER	SER	#	SER	SER	SER	SER	SER	SER	SER	SER	SER	#	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
8	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
9	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
10	GLY	GLY	GLY	GLY	GLY	GLY	asp	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	val	asp	asp	GLY	GLY
11	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	ser
12	VAL	VAL	VAL	VAL	VAL	ile	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	ile	VAL	VAL	VAL	ile
13	GLN	GLN	GLN	GLN	GLN	GLN	lys	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLX	lys	arg	arg	arg	GLN	glu	lys	GLN	GLN
14	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO
15	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	pro
16	GLY	GLY	GLY	GLY	GLY	arg	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	glu	GLY	GLY	GLY
17	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	arg
18	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	ser
19	ARG	ARG	ARG	ARG	ARG	ARG	lys	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	gin
20	LEU	LEU	LEU	LEU	#	ile	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	arg
21						SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	pro
22						CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	ser
23	ALA	ALA	ALA	ALA	ALA	thr	glu																	tyr
24	ALA	ALA	ALA	ALA	ALA	ala	val																	thr
25	SER		SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	cys
26	GLY		GLY	GLY	GLY	GLY	glu																	ser
27						PHE	PHE																	gly
28																								ser
29							PHE																	thr
30																								ser
31																								gly
32																								asp
33																								his
34																								---
35																								---
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HUMAN HEAVY CHAINS SUBGROUP III (cont'd)

	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	# OF	# OF	OCCURRENCES	VARIABILITY
	PAV	NA	SLA	LES	ANT	GRA	ARP	HOW	CRA	GUI	JLN	BUS	RE	70P1	DOS	BAL	SEQUENCES	AMINO ACIDS	OF MOST COMMON AMINO ACID	
	0																172	7	136 (GLU)	8.9
	1	GLU	GLU	GLU	asp	GLU	VAL	leu	GLU	gly	gly	pca	pca				174	7	158 (VAL)	7.7
	2	VAL	VAL	VAL	ile	VAL	VAL	VAL	VAL	phe	VAL	ser	ser				174	8	148 (GLN), 147 (GLN)	9.3, 2.4
	3	GLN	GLN	GLU	GLN	his	arg	GLN	LEU	LEU	GLN	LEU	LEU				168	5	163 (LEU)	5.2
	4	LEU	LEU	LEU	LEU															
	5	ala	val	val	val	val	val	val	asn	arg	asn	asn	asn				172	6, 8	129 (VAL)	8.5, 11.
	6	GLU	GLU	gln	GLU				arg	thr	thr	thr	thr				164	5	149 (GLU), 146 (GLU)	5.5, 5.6
	7	SER	SER	SER	SER				thr	thr	thr	thr	thr				158	3	155 (SER)	3.1
	8	GLY	GLY	GLY	GLY				ala	thr	thr	thr	thr				163	2	162 (GLY)	2.
	9	GLY	GLY	GLY	GLY				ala	glu	glu	glu	glu				171	3	169 (GLY)	3.
	10	GLY	ala	GLY	GLY	asp	GLY	gln	glx	---	---	---	---				168	5, 6	131 (GLY)	6.4, 7.7
	11	LEU	LEU	LEU	LEU				val	---	---	---	---				167	4	131 (LEU)	5.1
	12								val	---	---	---	---				163	3	154 (VAL)	3.2
	13								GLN	---	---	---	---				144	7	106 (GLN), 101 (GLN)	9.5, 10.
	14					PRO	PRO	PRO	---	---	---	---	---				148	5	142 (PRO)	5.2
	15								---	---	---	---	---				141	3	139 (GLY)	3.
	16					GLY	ser	---	---	---	---	---	---				143	5	116 (GLY)	6.2
	17						val	---	---	---	---	---	---				136	5	131 (SER)	5.2
	18						---	---	---	---	---	---	---				145	5	141 (LEU)	5.1
	19						---	---	---	---	---	---	---				140	4	124 (ARG)	4.5
	20						val	---	---	---	---	---	---				143	4	131 (LEU)	4.4
	21						---	---	---	---	---	---	---				116	5	111 (SER)	5.2
	22						---	---	---	---	---	---	---				117	2	116 (CYS)	2.
	23					ALA	---	---	---	---	---	---	---				128	8, 9	107 (ALA)	9.6, 11.
	24					ALA	---	---	---	---	---	---	---				132	5	116 (ALA)	5.7
	25						---	---	---	---	---	---	---				124	3	122 (SER)	3.
	26						---	---	---	---	---	---	---				124	6	127 (GLY)	6.4
	27						---	---	---	---	---	---	---				112	4	109 (PHE)	4.1
	28						---	---	---	---	---	---	---				104	9	75 (THR)	12.
	29						---	---	---	---	---	---	---				108	6	97 (PHE)	6.7
	30						---	---	---	---	---	---	---				103	9, 10	90 (SER)	10., 11.
	31						---	---	---	---	---	---	---				100	11	35 (SER)	31.
	32						---	---	---	---	---	---	---				103	10	55 (TYR)	19.
	33						---	---	---	---	---	---	---				98	13	35 (ALA)	36.
	34						---	---	---	---	---	---	---				101	7	85 (MET)	8.3
	35						---	---	---	---	---	---	---				97	12	39 (SER)	30.
	35A						---	---	---	---	---	---	---							
	35B						---	---	---	---	---	---	---							
	36						---	---	---	---	---	---	---				91	1	91 (TRP)	1.
	37						---	---	---	---	---	---	---				92	3	89 (VAL)	3.1
	38						---	---	---	---	---	---	---				90	2	89 (ARG)	2.
	39						---	---	---	---	---	---	---				90	2	89 (GLN)	2.
	40						---	---	---	---	---	---	---				91	2	84 (ALA)	7.6
	41						---	---	---	---	---	---	---				87	4	75 (PRO)	4.6
	42						---	---	---	---	---	---	---				87	2	86 (GLY)	2.
	43						---	---	---	---	---	---	---				87	3	85 (LYS)	3.1
	44						---	---	---	---	---	---	---				87	3	77 (GLY)	3.4
	45						---	---	---	---	---	---	---				87	2	86 (LEU)	2.
	46						---	---	---	---	---	---	---				86	3	78 (GLU), 75 (GLU)	3.3, 3.5
	47						---	---	---	---	---	---	---				85	1	85 (TRP)	1.
	48						---	---	---	---	---	---	---				86	2	84 (VAL)	2.
	49						---	---	---	---	---	---	---				86	7	40 (SER)	15.
	50						---	---	---	---	---	---	---				86	14	21 (VAL)	57.
	51						---	---	---	---	---	---	---				86	7	73 (ILE)	8.2
	52						---	---	---	---	---	---	---				85	12, 13	38 (SER)	27., 29.
	52A						---	---	---	---	---	---	---				77	13	22 (GLY)	
	52B						---	---	---	---	---	---	---				20	2	19 (LYS)	
	52C						---	---	---	---	---	---	---				20	5	8 (THR)	
	53						---	---	---	---	---	---	---				85	12	31 (ASP), 26 (ASP)	33., 39.
	54						---	---	---	---	---	---	---				84	9	56 (GLY)	13.
	55						---	---	---	---	---	---	---				83	10	37 (GLY)	22.
	56						---	---	---	---	---	---	---				83	13	20 (SER)	54.
	57						---	---	---	---	---	---	---				85	9	46 (THR)	17.
	58						---	---	---	---	---	---	---				84	14	46 (TYR)	26.
	59						---	---	---	---	---	---	---				85	3	79 (TYR)	3.2
	60						---	---	---	---	---	---	---				85	7	62 (ALA)	9.6
	61						---	---	---	---	---	---	---				85	8	51 (ASP), 48 (ASP)	13., 14.
	62						---	---	---	---	---	---	---				86	6	71 (SER)	7.3
	63						---	---	---	---	---	---	---				86	5	82 (VAL)	5.2
	64						---	---	---	---	---	---	---				85	5	70 (LYS)	6.1
	65						---	---	---	---	---	---	---				85	3	83 (GLY)	3.1
	66						---	---	---	---	---	---	---				85	3	83 (ARG)	3.1
	67						---	---	---	---	---	---	---				86	3	84 (PHE)	3.1
	68						---	---	---	---	---	---	---				86	3	76 (THR)	5.7
	69						---	---	---	---	---	---	---				86	3	84 (ILE)	3.1
	70						---	---	---	---	---	---	---				86	3	84 (SER)	3.1
	71						---	---	---	---	---	---	---				86	3	84 (ARG)	3.1
	72						---	---	---	---	---	---	---				85	4	71 (ASP), 69 (ASP)	4.8, 4.9
	73						---	---	---	---	---	---	---				84	4	50 (ASN), 48 (ASN)	6.7, 7.
	74						---	---	---	---	---	---	---				84	2	75 (SER)	2.2
	75						---	---	---	---	---	---	---				85	6	77 (LYS)	6.6
	76						---	---	---	---	---	---	---				85	5, 6	71 (ASN), 67 (ASN)	6., 7.6
	77						---	---	---	---	---	---	---				85	6	70 (THR)	7.3
	78						---	---	---	---	---	---	---				84	8	68 (LEU)	9.9
	79						---	---	---	---	---	---	---				85	4	74 (TYR)	4.6



**ANTIBODY SPECIFICITIES: HUMAN HEAVY CHAINS SUBGROUP III**

- 1) 18/2'CL: ANTI-DNA AUTOANTIBODY HYBRIDOMA
- 2) 18/17'CL: ANTI-DNA AUTOANTIBODY HYBRIDOMA
- 3) 18/9'CL: ANTI-DNA AUTOANTIBODY HYBRIDOMA
- 4) 1/17'CL: ANTI-DNA AUTOANTIBODY HYBRIDOMA
- 7) HF2-1/17: PLATE-BINDING ANTI-DNA AUTOANTIBODY
- 10) 4G12'CL: ANTI-MALIGNANT TUMOR, ESPECIALLY LUNG SQUAMOUS CELL CARCINOMA, HYBRIDOMA
- 11) Ab18'CL: POLYREACTIVE AUTOANTIBODY
- 12) Ab25'CL: ANTI-THYROGLOBULIN AUTOANTIBODY
- 13) RF-KL1'CL: ANTI-IGG1, IGG2, IGG4, IGG3m(st) RHEUMATOID FACTOR
- 20) GF4/1.1'CL: ANTI-TETANUS TOXOID
- 24) Ab21'CL: POLYREACTIVE AUTOANTIBODY
- 29) KIM46H'CL: ANTI-DNA HYBRIDOMA
- 31) RF-SJ2'CL: ANTI-IGG1, IGG2, IGG4 RHEUMATOID FACTOR
- 41) HN.14'CL: ANTI-MYELIN-ASSOCIATED GLYCOPROTEIN HYBRIDOMA
- 42) RF-TS2'CL: ANTI-IGG1, IGG2, IGG4 RHEUMATOID FACTOR
- 43) 3D6'CL: ANTI-HIV gp41
- 45) POM: ANTI-HUMAN GAMMA G1 GLOBULIN; PO IDIOTYPE
- 46) RF-SJ1'CL: ANTI-IGG RHEUMATOID FACTOR
- 47) WEA: ANTI-3,4-PYRUVYLATED GALACTOSE MONOCLONAL
- 48) 4B4'CL: ANTI-Sm AUTOANTIBODY HYBRIDOMA
- 51) LAY: ANTI-HUMAN GAMMA G1 AND G3 GLOBULINS; PO IDIOTYPE
- 59) TUR: COLD AGGLUTININ WITH ANTI-PR ACTIVITY
- 74) 1B11'CL: HETEROHYBRIDOMA ANTIBODY TO LYMPHOMA CELLS POSSESSING IDIOTOPE REACTING WITH ANTI-IDIOTYPE 7D11 AFTER TREATMENT WITH 7D11.
- 75) 1H1'CL: HETEROHYBRIDOMA ANTIBODY TO LYMPHOMA CELLS POSSESSING IDIOTOPE REACTING WITH ANTI-IDIOTYPE 7D11 BEFORE TREATMENT WITH 7D11.
- 76) 333'CL: HETEROHYBRIDOMA ANTIBODY TO LYMPHOMA CELLS POSSESSING IDIOTOPE REACTING WITH ANTI-IDIOTYPE 7D11 BEFORE TREATMENT WITH 7D11.
- 77) 112'CL: HETEROHYBRIDOMA ANTIBODY TO LYMPHOMA CELLS POSSESSING IDIOTOPE REACTING WITH ANTI-IDIOTYPE 7D11 AFTER TREATMENT WITH 7D11.
- 78) 126'CL: HETEROHYBRIDOMA ANTIBODY TO LYMPHOMA CELLS POSSESSING IDIOTOPE REACTING WITH ANTI-IDIOTYPE 7D11 AFTER TREATMENT WITH 7D11.
- 79) 115'CL: HETEROHYBRIDOMA ANTIBODY TO LYMPHOMA CELLS POSSESSING IDIOTOPE REACTING WITH ANTI-IDIOTYPE 7D11 AFTER TREATMENT WITH 7D11.
- 80) 2C12'CL: HETEROHYBRIDOMA ANTIBODY TO LYMPHOMA CELLS POSSESSING IDIOTOPE REACTING WITH ANTI-IDIOTYPE 7D11 BEFORE TREATMENT WITH 7D11.
- 81) 2A12'CL: HETEROHYBRIDOMA ANTIBODY TO LYMPHOMA CELLS POSSESSING IDIOTOPE REACTING WITH ANTI-IDIOTYPE 7D11 BEFORE TREATMENT WITH 7D11.
- 83) FR: ANTI-PHOSPHOCOLINE(BINDING CONSTANT=6.4X10EXP4)
- 111) A-G1: ANTI-Haemophilus influenzae TYPE b CAPSULAR POLYSACCHARIDE
- 113) B-G1: ANTI-Haemophilus influenzae TYPE b CAPSULAR POLYSACCHARIDE
- 114) B-G2b: ANTI-Haemophilus influenzae TYPE b CAPSULAR POLYSACCHARIDE
- 116) B-G2a: ANTI-Haemophilus influenzae TYPE b CAPSULAR POLYSACCHARIDE
- 117) C-G2a: ANTI-Haemophilus influenzae TYPE b CAPSULAR POLYSACCHARIDE
- 118) A-G2a: ANTI-Haemophilus influenzae TYPE b CAPSULAR POLYSACCHARIDE
- 119) H-G2a: ANTI-Haemophilus influenzae TYPE b CAPSULAR POLYSACCHARIDE
- 120) A-G2b: ANTI-Haemophilus influenzae TYPE b CAPSULAR POLYSACCHARIDE
- 121) K-G2: ANTI-Haemophilus influenzae TYPE b CAPSULAR POLYSACCHARIDE
- 122) C-G1: ANTI-Haemophilus influenzae TYPE b CAPSULAR POLYSACCHARIDE
- 123) K-G1(+4-): ANTI-Haemophilus influenzae TYPE b CAPSULAR POLYSACCHARIDE
- 127) HEI: COLD AGGLUTININ WITH ANTI-GD (MEMBRANE-GLYCOLIPID-DEPENDENT) ACTIVITY
- 128) KM: COLD AGGLUTININ WITH ANTI-GD (MEMBRANE-GLYCOLIPID-DEPENDENT) ACTIVITY
- 129) H-G2b: ANTI-Haemophilus influenzae TYPE b CAPSULAR POLYSACCHARIDE
- 130) C-G2b: ANTI-Haemophilus influenzae TYPE b CAPSULAR POLYSACCHARIDE
- 131) F-G1: ANTI-Haemophilus influenzae TYPE b CAPSULAR POLYSACCHARIDE
- 132) L.TH.: COLD AGGLUTININ WITH ANTI-PR2 ACTIVITY (RBC MEMBRANE ANTIGEN ON HUMAN, RAT AND GUINEA PIG ERYTHROCYTES INACTIVATED BY PROTEOLYTIC ENZYMES AND NEURAMINIDASE)
- 137) WAG: ANTI-DINITROPHENYL
- 142) R.K.: COLD AGGLUTININ WITH ANTI-PR1H ACTIVITY (RBC MEMBRANE ANTIGEN ON HUMAN ERYTHROCYTES INACTIVATED BY PROTEOLYTIC ENZYMES AND NEURAMINIDASE)
- 143) GOKII: ANTI-MEASLES VIRUS (WOODFOLK STRAIN); ANTI-SUBACUTE SCLEROSING PANENCEPHALITIS VIRUS (LEC STRAIN)

**CLASS: HUMAN HEAVY CHAINS SUBGROUP III**

- 1) 18/2'CL: IGM-
- 2) 18/17'CL: IGM-
- 3) 18/9'CL: IGM-
- 4) 1/17'CL: IGM-
- 5) 30P1'CL: IGM-
- 7) HF2-1/17: IGM-KAPPA
- 10) 4G12'CL: IGM-LAMBDA
- 11) Ab18'CL: IGM-KAPPA
- 12) Ab25'CL: IGM-LAMBDA
- 13) RF-KL1'CL: IGM-KAPPA
- 18) 60P2'CL: IGM-
- 19) 63P1'CL: IGM-
- 20) GF4/1.1'CL: IGG3-KAPPA
- 24) Ab21'CL: IGM-KAPPA
- 25) 56P1'CL: IGM-
- 26) 2P1'CL: IGM-
- 29) KIM46H'CL: IGM-LAMBDA
- 31) RF-SJ2'CL: IGM-LAMBDA
- 33) TIL: IGG2 & IGM-KAPPA
- 36) 38P1'CL: IGM-
- 38) BRO'IGM: IGM-LAMBDA
- 39) BUT: IGA2 A2M(2)-
- 40) CAM': IGM-KAPPA
- 41) HN.14'CL: IGM-
- 42) RF-TS2'CL: IGM-KAPPA
- 43) 3D6'CL: IGG1-KAPPA
- 45) POM: IGM-KAPPA
- 46) RF-SJ1'CL: IGM-LAMBDA
- 47) WEA: IGM-KAPPA
- 48) 4B4'CL: IGM-
- 51) LAY: IGM-KAPPA
- 52) BUR: IGA1-LAMBDA
- 53) KOL: IGG1-LAMBDA
- 54) TEI: IGG1-KAPPA
- 56) HIL: IGG1-LAMBDA
- 57) TRO: IGA1-LAMBDA
- 58) WAS: IGG1-
- 59) TUR: IGA1-KAPPA
- 60) NIE: IGG1-
- 61) GAL: IGM-KAPPA
- 62) DOB: IGG1 GM(1,-17)-KAPPA KM(3)
- 63) VH10.7'CL: IGD-

## CLASS: HUMAN HEAVY CHAINS SUBGROUP III (cont'd)

64) ZAP: IGA1-KAPPA  
 65) JON: IGG3-  
 66) GA: IGM-  
 68) K6H6'CL: IGM-LAMBDA  
 69) K4B8'CL: IGM-LAMBDA  
 70) K5B8'CL: IGM-LAMBDA  
 71) K5C7'CL: IGM-LAMBDA  
 72) K5G5'CL: IGM-LAMBDA  
 73) K6F5'CL: IGM-LAMBDA  
 82) 20P1'CL: IGM-  
 83) FR: IGM-KAPPA  
 85) MU: IGA-  
 86) DAU: IGM-  
 90) GR': IGG & IGA-KAPPA  
 91) VIN: IGG4-LAMBDA  
 93) GO: IGG1-  
 94) FOR: IGA2-LAMBDA  
 95) BEN(III): IGM-  
 96) PS (SHA): IGE-LAMBDA  
 97) 13P1'CL: IGM-  
 99) WAT: IGG2-LAMBDA  
 100) LOW: IGA2-KAPPA  
 101) JOR: IGA1-LAMBDA  
 102) BRO: IGA1-LAMBDA  
 103) V.N.: IGG1-KAPPA  
 105) GAA: IGG1-LAMBDA  
 107) SKI: IGA1-LAMBDA  
 108) WEI: IGG1-LAMBDA  
 109) WE: IGG-KAPPA  
 110) AVI: IGA2-KAPPA  
 112) EVA: IGM-LAMBDA  
 115) ESM: IGM-  
 125) LR1'CL: IGM-  
 126) WO: IGM-  
 132) L.TH.: IGM-KAPPA  
 133) SMM-IGA: IGA-LAMBDA  
 134) HI: IGG-  
 137) WAG: IGM-  
 138) LR: IGM-LAMBDA PYROGLOBULIN  
 139) LBW2'CL: IGM-  
 142) R.K.: IGA-KAPPA  
 144) PAL: IGG1-  
 145) POD: IGA1-  
 146) DB'CL: IGM-  
 147) LBW14'CL: IGM-  
 149) HA: IGA1-  
 150) GIT: IGM-  
 151) SEI: IGA1-KAPPA  
 152) KOO: IGA1-KAPPA  
 153) BER: IGA1-KAPPA  
 154) HIM: IGA1-KAPPA  
 155) KNI: IGA1-KAPPA  
 156) SHE: IGA1-KAPPA  
 157) LIV: IGA1-KAPPA  
 158) PUT: IGA1-LAMBDA  
 159) HER: IGA2-LAMBDA  
 160) MOY: IGA1-LAMBDA  
 161) PIT: IGA1-LAMBDA  
 162) TOL: IGA1-LAMBDA  
 163) CRI: IGA1-LAMBDA  
 164) GLU: IGA1-LAMBDA  
 165) SMM-IGG: IGG-LAMBDA  
 166) PAC: IGG1-  
 167) THA: IGA1-KAPPA  
 168) KAR: IGA1-KAPPA  
 169) PAR: IGA2-  
 170) PAV: IGG3-KAPPA  
 171) NA: IGM-  
 172) SLA: IGA1-LAMBDA  
 173) LES: IGA1-KAPPA  
 174) ANT: IGM-  
 175) GRA: IGG3-  
 176) ARP: IGA1-  
 177) HOW: IGM-  
 178) CRA: IGG1-  
 179) GUI: IGG1-LAMBDA  
 181) BUS: IGM-  
 182) RE: IGM-  
 184) DOS: IGM-  
 185) BAL: IGM-

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- 3) 18/9'CL: DERSIMONIAN, H., SCHWARTZ, R.S., BARRETT, K.J. & STOLLAR, B.D. (1987) J. IMMUNOL., 139, 2496-2501.
- 4) 1/17'CL: DERSIMONIAN, H., SCHWARTZ, R.S., BARRETT, K.J. & STOLLAR, B.D. (1987) J. IMMUNOL., 139, 2496-2501.
- 5) 30P1'CL: SCHROEDER, H.W., JR., HILLSON, J.L. & PERLMUTTER, R.M. (1987) SCIENCE, 238, 791-793; CHEN, P.P., LIU, M.-F., SINHA, S. & CARSON, D.A. (1988) ARTH. RHEUM., 31, 1429-1431.
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## REFERENCE: HUMAN HEAVY CHAINS SUBGROUP III (cont'd)

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## GENERAL NOTES: HUMAN HEAVY CHAINS SUBGROUP III

## IDENTICAL SETS OF FRAMEWORK SEGMENTS:

- FR1:** SET 1: 18/2'CL[1], 18/17'CL[2], 18/9'CL[3], 1/17'CL[4], 30P1'CL[5], M43'CL[6], HF2-1/17[7], vh26c'CL[8], LAMBDA-VH26'CL[9], 4G12'CL[10], Ab25'CL[12], RF-KL1'CL[13], TIL[33], POM[45], TUR[59]. (15 IDENTICAL)  
 SET 2: Ab18'CL[11], H11'CL[23], 38P1'CL[36], 13-2'CL[37], BRO'IGM[38], TEI[54], 12-2'CL[55], GR'V[90]. (8 IDENTICAL)  
 SET 3: Vh38C1.10'CL[15], Vh38C1.8'CL[16], Vh38C1.9'CL[17]. (3 IDENTICAL)  
 SET 4: 60P2'CL[18], 63P1'CL[19], VIN[91]. (3 IDENTICAL HUMAN V-H-III; ALSO 1 MISCELLANEOUS V-H: GOLDFISH 5A'CL[64].)  
 SET 5: 56P1'CL[25], 2P1'CL[26], M72'CL[27], M74'CL[28], KIM46H'CL[29], 1-9III'CL[30], RF-SJ2'CL[31], FL2-2'CL[34], RF-TS2'CL[42]. (9 IDENTICAL)  
 SET 6: 4B4'CL[48], M26'CL[49], 9-1'CL[50]. (3 IDENTICAL HUMAN V-H-III; ALSO 2 MOUSE V-H-IIID: H28-A2'CL[24], H37-82'CL[54].)  
 SET 7: K6H6'CL[68], K4B8'CL[69], K5B8'CL[70], K5C7'CL[71], K5G5'CL[72]. (5 IDENTICAL)  
 SET 8: 1B11'CL[74], 1H1'CL[75], 333'CL[76], 126'CL[78]. (4 IDENTICAL)  
 SET 9: H11'CL[98]. (IDENTICAL TO 2 MOUSE V-H-IIID: 36-18'CL[48], 36-15'CL[49].)  
**FR2:** SET 1: TIL[33], 4B4'CL[48], M26'CL[49], 9-1'CL[50], TEI[54], 12-2'CL[55], 20P1'CL[82]. (7 IDENTICAL HUMAN V-H-III; ALSO 1 HUMAN V-H-I: WOL[45].)  
 SET 2: 18/2'CL[1], 18/17'CL[2], 18/9'CL[3], 1/17'CL[4], 30P1'CL[5], M43'CL[6], HF2-1/17[7], vh26c'CL[8], LAMBDA-VH26'CL[9], 4G12'CL[10], Ab18'CL[11], RE-KL1'CL[13], 8-1B'CL[14], Vh38C1.10'CL[15], Vh38C1.8'CL[16], Vh38C1.9'CL[17], 60P2'CL[18], 63P1'CL[19], GF4/1.1'CL[20], Vh38C1.4'CL[21], Vh38C1.5'CL[22], AD21'CL[24], V65-4'CL[35], 3D6'CL[43], TUR[59], V65-2'CL[84]. (26 IDENTICAL HUMAN V-H-III; ALSO 1 MISCELLANEOUS V-H: GOLDFISH 3'CL[63].)  
 SET 3: 56P1'CL[25], 2P1'CL[26], M72'CL[27], M74'CL[28], KIM46H'CL[29], 1-9III'CL[30], RF-SJ2'CL[31], RF-TS2'CL[42], POM[45], LAY[51], BUR[52], KOL[53], HIL[56], WAS[58], NIE[60], GAL[61], VH10.7'CL[63], FR[83]. (18 IDENTICAL HUMAN V-H-III; ALSO 1 MOUSE V-H-IIID: BV04-01'CL[62], MRL-4'CL[64], MRL-DNA4'CL[65], H220-3'CL[70]; AND 1 CHICKEN V-H: COL-3'CL[9].)  
 SET 4: 22-2B'CL[32]. (IDENTICAL TO 1 MISCELLANEOUS V-H: RTVH431'CL[67].)  
 SET 5: 38P1'CL[36], 13-2'CL[37]. (2 IDENTICAL)  
 SET 6: WEA[47], GA[66]. (2 IDENTICAL)  
 SET 7: TIL[33], K6H6'CL[68], K4B8'CL[69], K5B8'CL[70], K5C7'CL[71], K6F5'CL[73]. (6 IDENTICAL)  
 SET 8: 1B11'CL[74], 1H1'CL[75], 333'CL[76], 112'CL[77], 126'CL[78], 115'CL[79], 2C12'CL[80], 2A12'CL[81]. (8 IDENTICAL)  
**FR3:** SET 1: U266'CL[136]. (IDENTICAL TO 1 HUMAN V-H-I: ND'CL[30].)  
 SET 2: 18/2'CL[1], 18/17'CL[2], 18/9'CL[3], 1/17'CL[4], 30P1'CL[5], M43'CL[6], HF2-1/17[7], LAMBDA-VH26'CL[9], 4G12'CL[10], Ab18'CL[11], KIM46H'CL[29], 1-9III'CL[30], FL2-2'CL[34]. (13 IDENTICAL)  
 SET 3: 8-1B'CL[14], 56P1'CL[25], M72'CL[27], M74'CL[28], CAM'40. (5 IDENTICAL HUMAN V-H-III; ALSO 1 MISCELLANEOUS V-H: GOLDFISH 5A'CL[64].)  
 SET 4: Vh38C1.10'CL[15], Vh38C1.8'CL[16], Vh38C1.9'CL[17], Vh38C1.4'CL[21], Vh38C1.5'CL[22]. (5 IDENTICAL)  
 SET 5: 60P2'CL[18], 63P1'CL[19]. (2 IDENTICAL)  
 SET 6: 38P1'CL[36], 13-2'CL[37]. (2 IDENTICAL)  
 SET 7: 4B4'CL[48], M26'CL[49], 9-1'CL[50]. (3 IDENTICAL)  
 SET 8: K6H6'CL[68], K4B8'CL[69], K5B8'CL[70], K5G5'CL[72], K6F5'CL[73]. (5 IDENTICAL)  
 SET 9: 1B11'CL[74], 2C12'CL[80], 2A12'CL[81]. (3 IDENTICAL)  
 SET 10: 1H1'CL[75], 333'CL[76]. (2 IDENTICAL)  
**FR4:** SET 1: 18/2'CL[1], 18/17'CL[2], 18/9'CL[3], 1/17'CL[4], 30P1'CL[5], M43'CL[6], HF2-1/17[7], Ab25'CL[12], Vh38C1.10'CL[15], Vh38C1.8'CL[16], Vh38C1.9'CL[17], 60P2'CL[18], 63P1'CL[19], GF4/1.1'CL[20], Vh38C1.4'CL[21], Vh38C1.5'CL[22], 56P1'CL[25], 2P1'CL[26], M74'CL[28], TIL[33], HN.14'CL[41], WEA[47], 4B4'CL[48], M26'CL[49], NIE[60], DOB[62], VH10.7'CL[63], K6H6'CL[68], K4B8'CL[69], K5B8'CL[70], K5C7'CL[71], K5G5'CL[72], K6F5'CL[73], 20P1'CL[82], 54 IDENTICAL HUMAN V-H-III; ALSO 14 HUMAN V-H-I: 152'CL[11], 135'CL[12], 158'CL[13], L51'CL[4], L58'CL[6], 159'F2'CL[7], 21/28'CL[10], NEI'CL[16], TH9'CL[23], WIL2'CL[24], KAS[26], BOR'27, L57'CL[29], WOL[45]; 7 HUMAN V-H-II: 15P1'CL[1], MLI'CL[3], MCE'46, DRI2910-2F8'CL[48], Ab17'CL[49], M44'CL[52], N2U[55]; 1 MOUSE V-H-IIB: PING2006E'CL[29]; 1 MOUSE V-H-IIIA: MOPC47A[110]; AND 1 MOUSE V-H-IIID: H37-40'CL[25].)  
 SET 2: TIL[33]. (IDENTICAL TO 2 HUMAN V-H-I: 8E10'CL[11], TH3'CL[55]; AND 1 MOUSE V-H-IIIA: MOPC47A[110].)  
 SET 3: 38P1'CL[36], 3D6'CL[43], 13P1'CL[97]. (3 IDENTICAL HUMAN V-H-III; ALSO 6 HUMAN V-H-I: 51P1'CL[14], 51P1'CL[4], CB2'CL[14], 58P2'CL[16], CE-1'CL[41], 37P1'CL[47].)  
 SET 4: RF-SJ2'CL[31], RF-SJ1'CL[46]. (2 IDENTICAL HUMAN V-H-III; ALSO 1 HUMAN V-H-I: AND'CL[15]; AND 1 HUMAN V-H-II: Paq-1'CL[22].)  
 SET 5: 4G12'CL[10], Ab21'CL[24], M72'CL[27], KIM46H'CL[29], U266'CL[136], 70P1'CL[183]. (6 IDENTICAL HUMAN V-H-III; ALSO 5 HUMAN V-H-I: 783c'CL[21], X17115'CL[22], EV1-15'CL[25], ND'CL[30], Ab2'CL[44]; 6 HUMAN V-H-II: FK-01'CL[14], HIG'CL[24], Ab4'CL[29], 200-8'CL[49], AF2'CL[65]; AND 2 MOUSE V-H-IIA: HDEX12[15], MBI'CL[16]; AND 1 MOUSE V-H-IIC: MuRSV19VH'CL[37].)  
 SET 6: Ab18'CL[11], RF-KL1'CL[13], 1B11'CL[74], 1H1'CL[75], 2C12'CL[80]. (5 IDENTICAL HUMAN V-H-III; ALSO 1 HUMAN V-H-I: 83P2'CL[38]; AND 2 HUMAN V-H-II: Ab26'CL[18], M60'CL[42].)

## IDENTICAL SETS OF COMPLEMENTARITY DETERMINING REGIONS:

- CDR1:** SET 1: 56P1'CL[25], 2P1'CL[26], M72'CL[27], M74'CL[28], RF-SJ2'CL[31], V65-2'CL[84]. (6 IDENTICAL HUMAN V-H-III; ALSO 3 HUMAN V-H-I: 21/28'CL[10], 8E10'CL[11], E3-10'CL[18]; AND 1 SHARK V-H: Rel10'CL[3].)  
 SET 2: H11'CL[23]. (IDENTICAL TO 1 HUMAN V-H-II: HUVPN'CL[25]; 9 MOUSE V-H-IIA: 4m4 GL'CL[94], 5D3'CL[112], 8E3'CL[119], AM9'CL[120], AM10'CL[130], AM12'CL[131], 7C6'CL[142], 2.9 GL'CL[169], 1L38'CL[206]; AND 69 MOUSE V-H-IIB: B1-8'CL[1], B1-8.DELTA1V3[2], B1-48'CL[3], N-HYB'CL[4], 18C10'CL[15], 186-2'CL[6], B1-8.V4'CL[17], S2D8'CL[18], 6E6'CL[19], S2E9'CL[20], E17.190.2[11], 186-1'CL[12], 84'CL[13], S25'CL[14], SIF12'CL[15], ANI1-TGAL'CL[16], H1-9'CL[18], CH12'CL[21], 455 GL'CL[24], 22.111.1'CL[27], 23'CL[28], PING2006E'CL[29], B1-8.V1[V2[30], B1-8.V1'CL[31], NIC12'CL[33], 124'CL[34], 564'CL[35], 550'CL[36], 567'CL[37], 563'CL[38], 132.16'CL[39], N169'CL[50], 102'CL[51], 33'CL[52], CH-51'CL[55], DB1-314.3'CL[56], DF4-12.6'CL[57], H1-5'CL[59], 31E-2'CL[60], C1H4'CL[64], CH10'CL[69], CH-55'CL[74], CH3'CL[76], H49'CL[79], DBF1-608.1'CL[89], AC38.15.3[93], H1-59'CL[84], 104B'CL[101], 20.119.25'CL[104], 3B9P'CL[106], MVAR1'CL[109], 167.1'CL[113], 219.7'CL[114], 5D65'CL[122], 167.2'CL[127], CH12'CL[129], F17.59.2'CL[137], vpd15 GL'CL[138], 119.13'CL[149], 6C7S'CL[158], 3B1S'CL[161], 4A9S'CL[164], NQ22.87.1'CL[165], AC38.251.5[168], 4m10 GL'CL[174], AC38.260.2[175], 4F5'CL[178], 10H2S'CL[180], VNB'CL[185].)  
 SET 3: 18/2'CL[1], 18/17'CL[2], 18/9'CL[3], 1/17'CL[4], 30P1'CL[5], M43'CL[6], HF2-1/17[7], vh26c'CL[8], LAMBDA-VH26'CL[9], Ab25'CL[12], RF-KL1'CL[13], H11'CL[23], 38P1'CL[36], 13-2'CL[37], BRO'IGM[38], TEI[54], 12-2'CL[55], GR'V[90]. (13 IDENTICAL HUMAN V-H-III; ALSO 15 MOUSE V-H-IIID: 1F2-76'CL[6], 8-1-12A'CL[7], 8-1-12-5A'CL[8], 914'CL[22], H28-A2'CL[24], H37-40'CL[25], 129-48'CL[42], AF2'CL[52], 5.4KL.2V'CL[53], H37-82'CL[54], 40-20[68], AF1'CL[69], 40-90[76], 40-100[77], SP1/HL'CL[81]; AND 4 RABBIT V-H: VHL-a1'CL[8], 3374[16], p26.9a3'CL[24], RVH139'CL[37].)  
 SET 4: 4G12'CL[10]. (IDENTICAL TO 2 MOUSE V-H-IIID: 5-27'CL[35], 40-60[75].)  
 SET 5: Ab18'CL[11], POM[45]. (2 IDENTICAL)  
 SET 6: 8-1B'CL[14], 60P2'CL[18], 63P1'CL[19]. (3 IDENTICAL HUMAN V-H-III; ALSO 1 MISCELLANEOUS V-H: GOLDFISH 5A'CL[64].)  
 SET 7: Vh38C1.10'CL[15], Vh38C1.8'CL[16], Vh38C1.9'CL[17], Vh38C1.4'CL[21], Vh38C1.5'CL[22]. (5 IDENTICAL)  
 SET 8: GF4/1.1'CL[20]. (IDENTICAL TO 1 MOUSE V-H-IIID: 5-76'CL[21].)  
 SET 9: KIM46H'CL[29], 1-9III'CL[30], FL2-2'CL[34], RF-TS2'CL[42], RF-SJ1'CL[46]. (5 IDENTICAL)  
 SET 10: 22-2B'CL[32]. (IDENTICAL TO 36 MOUSE V-H-IIIA: V11'CL[60], CLA-2/Cn V11'CL[61], WSA V11'CL[62], 38C'CL[63], 38C4'CL[64], 38C9'CL[65], 666'CL[66], CB8/J V11'CL[67], NZB V11'CL[68], NZW V11'CL[69], 36-7'CL[71], N4-1'CL[76], CH2'CL[77], CH5'CL[78], 6E8'CL[79], 9A6'CL[81], C57BL/10 V11'CL[82], VB6.5'CL[83], C57BL V11'CL[84], CBA/J 666[86], N010.2.22'CL[88], H210-56'CL[89], G2a-1'CL[90], VB4.8'CL[93], C57BL V13'CL[94], C57BL/10 V13'CL[95], 36-17'CL[98], DF1'CL[103], N011.8.4'CL[106], V13'CL[108], N4-18'CL[109], MOPC47A[110], 17G5'CL[113], CBA/J V13'CL[114], H220-17'CL[123], HFG015[172].)  
 SET 11: 38P1'CL[36], 13-2'CL[37]. (2 IDENTICAL)  
 SET 12: 3D6'CL[43], BUR[52]. (2 IDENTICAL HUMAN V-H-III; ALSO 2 MOUSE V-H-IIA: BCL1'CL[102], mAb 123'CL[106]; AND 1 MOUSE V-H-MISC: Zhi'CL[45].)  
 SET 13: 4B4'CL[48], M26'CL[49], 9-1'CL[50], 20P1'CL[82]. (4 IDENTICAL)  
 SET 14: VH10.7'CL[63]. (IDENTICAL TO 1 MOUSE V-H-MISC: H51.54.33[71].)



## GENERAL NOTES: HUMAN HEAVY CHAINS SUBGROUP III (cont'd)

SET 15: K6H6'CL[68],K4B8'CL[69],K5B8'CL[70],K5C7'CL[71],K5G5'CL[72],K6F5'CL[73]. (6 IDENTICAL)  
 SET 16: 1B11'CL[74],1H1'CL[75],333'CL[76],112'CL[77],126'CL[78],115'CL[79],2C12'CL[80],2A12'CL[81]. (8 IDENTICAL)

CDR2: SET 1: 18/2'CL[1],18/17'CL[2],18/9'CL[3],1/17'CL[4],30P1'CL[5],M43'CL[6],HF2-1/17[7],vh26c'CL[8],4G12'CL[10]. (9 IDENTICAL)  
 SET 2: 8-1B'CL[14],60P2'CL[18],63P1'CL[19]. (3 IDENTICAL HUMAN V-H-III; ALSO 1 MISCELLANEOUS V-H: GOLDFISH 5A'CL[64].)  
 SET 3: Vh38C1.10'CL[15],Vh38C1.8'CL[16],Vh38C1.9'CL[17],Vh38C1.4'CL[21],Vh38C1.5'CL[22]. (5 IDENTICAL)  
 SET 4: 56P1'CL[25],2P1'CL[26],M72'CL[27],M74'CL[28],KIM46H'CL[29],1-9111'CL[30],RF-SJ2'CL[31],FL2-2'CL[34]. (8 IDENTICAL)  
 SET 5: 38P1'CL[36],13-2'CL[37]. (2 IDENTICAL)  
 SET 6: POM[45],LAY[51]. (2 IDENTICAL)  
 SET 7: 4B4'CL[48],M26'CL[49],9-1'CL[50],20P1'CL[82]. (4 IDENTICAL)  
 SET 8: K6H6'CL[68],K4B8'CL[69],K5B8'CL[70],K5C7'CL[71],K5G5'CL[72],K6F5'CL[73]. (6 IDENTICAL)  
 SET 9: 1B11'CL[74],115'CL[79]. (2 IDENTICAL)

CDR3: SET 1: LAMBDA-VH26'CL[9]. (IDENTICAL TO 1 HUMAN V-H-I: HG3'CL[12]; 1 MOUSE V-H-IB: PJ14'CL[33]; AND 5 MOUSE V-H-IB: 186-2'CL[6],186-1'CL[12],23'CL[28],102'CL[51],3'CL[72].)  
 SET 2: U266'CL[136]. (IDENTICAL TO 1 HUMAN V-H-I: ND'CL[30].)  
 SET 3: 18/2'CL[1],18/17'CL[2],18/9'CL[3],1/17'CL[4]. (4 IDENTICAL)  
 SET 4: Vh38C1.10'CL[15],Vh38C1.8'CL[16],Vh38C1.9'CL[17],Vh38C1.4'CL[21],Vh38C1.5'CL[22]. (5 IDENTICAL)  
 SET 5: POM[45],LAY[51]. (2 IDENTICAL)  
 SET 6: K6H6'CL[68],K4B8'CL[69],K5B8'CL[70],K5C7'CL[71],K6F5'CL[73]. (5 IDENTICAL)  
 SET 7: 1B11'CL[74],1H1'CL[75],333'CL[76],112'CL[77],126'CL[78],115'CL[79],2C12'CL[80],2A12'CL[81]. (8 IDENTICAL)

## IDENTICAL SETS OF J-MINIGENES:

SET 1: 30P1'CL[5],Ab25'CL[12],60P2'CL[18],63P1'CL[19],56P1'CL[25],M74'CL[28],TIL[33],HN.14'CL[41],M26'CL[49],VH10.7'CL[63],K6H6'CL[68],K4B8'CL[69],K5B8'CL[70],K5C7'CL[71],K5G5'CL[72],K6F5'CL[73],20P1'CL[82]. (17 IDENTICAL HUMAN V-H-III; ALSO 9 HUMAN V-H-I: L2'CL[1],L5'CL[2],L56'CL[3],L51'CL[4],L58'CL[6],NEI'CL[16],WIL2'CL[24],BOR'CL[27],127'CL[29]; 4 HUMAN V-H-II: MLI'CL[3],DR12910-2F8'CL[48],AD17'CL[49],M44'CL[52]; AND 1 MOUSE V-H-IB: H37-40'CL[25].)  
 SET 2: TIL[33]. (IDENTICAL TO 1 HUMAN V-H-I: 21/28'CL[10].)  
 SET 3: 38P1'CL[36],3D6'CL[43],13P1'CL[97]. (3 IDENTICAL HUMAN V-H-III; ALSO 5 HUMAN V-H-I: 51P1'CL[14],RF-TS1'CL[28],M61'CL[47],60P1'CL[49],AF2'CL[65]; AND 6 HUMAN V-H-II: L16'CL[2],M71'CL[4],C6B2'CL[14],58P2'CL[16],CE-1'CL[41],37P1'CL[47].)  
 SET 4: RF-SJ2'CL[31],RF-SJ1'CL[46]. (2 IDENTICAL HUMAN V-H-III; ALSO 1 HUMAN V-H-I: AND'CL[15]; AND 1 HUMAN V-H-II: Pag-1'CL[22].)  
 SET 5: 4G12'CL[10],Ab21'CL[24],M72'CL[27],KIM46H'CL[29],U266'CL[136],70P1'CL[183]. (6 IDENTICAL HUMAN V-H-III; ALSO 5 HUMAN V-H-I: 785'CL[21],X17,115'CL[22],EVI-15'CL[25],ND'CL[30],Ab2'CL[44]; AND 3 HUMAN V-H-II: FK-001'CL[11],HIG1'CL[24],Ab44'CL[29].)  
 SET 6: DOB[62]. (IDENTICAL TO 1 HUMAN V-H-I: TH9'CL[23].)  
 SET 7: Ab18'CL[11]. (IDENTICAL TO 1 HUMAN V-H-I: 83P2'CL[38]; AND 2 HUMAN V-H-II: Ab26'CL[18],M60'CL[42].)  
 SET 8: TIL[33]. (IDENTICAL TO 1 HUMAN V-H-I: TH3'CL[55].)  
 SET 9: 18/2'CL[1],18/17'CL[2],18/9'CL[3],1/17'CL[4],M43'CL[6],HF2-1/17[7],2P1'CL[26]. (7 IDENTICAL HUMAN V-H-III; ALSO 1 HUMAN V-H-II: 15P1'CL[1].)  
 SET 10: Vh38C1.10'CL[15],Vh38C1.8'CL[16],Vh38C1.9'CL[17],Vh38C1.4'CL[21],Vh38C1.5'CL[22]. (5 IDENTICAL)  
 SET 11: GF4/1.1'CL[20],4B4'CL[48]. (2 IDENTICAL)  
 SET 12: 1B11'CL[74],1H1'CL[75],2C12'CL[80]. (3 IDENTICAL)

# SEE SIGNAL PEPTIDE TABLE IF # OCCURS AT POSITION 0.

## SPECIFIC NOTES: HUMAN HEAVY CHAINS SUBGROUP III

- 1) 18/2'CL: FROM PERIPHERAL BLOOD LYMPHOCYTES OF A SYSTEMIC LUPUS ERYTHEMATOSUS PATIENT.
- 2) 18/17'CL: FROM PERIPHERAL BLOOD LYMPHOCYTES OF A SYSTEMIC LUPUS ERYTHEMATOSUS PATIENT.
- 3) 18/9'CL: FROM PERIPHERAL BLOOD LYMPHOCYTES OF A SYSTEMIC LUPUS ERYTHEMATOSUS PATIENT.
- 4) 1/17'CL: FROM PERIPHERAL BLOOD LYMPHOCYTES OF A SYSTEMIC LUPUS ERYTHEMATOSUS PATIENT.
- 5) 30P1'CL: FROM HUMAN FETUS AT 130 DAYS OF GESTATION.
- 6) LAMBDA-VH26'CL: THE SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF HUMAN FETAL LIVER DNA. TWO OTHER CLONES HAVE SLIGHT DIFFERENT SEQUENCES: LAMBDA-VH52'CL HAS MET AT POSITION 87 AND ARG AT POSITION 94, AND LAMBDA-VH32'CL HAS VAL AT POSITION 93.
- 10) 4G12'CL: IT RECOGNIZES A TUMOR-ASSOCIATED AND DIFFERENTIATION ANTIGEN OF MW 195,000.
- 11) Ab18'CL: THE D-SEGMENT IS EXTRA LONG. EIGHT AMINO ACID RESIDUES ILE TRP ARG LEU ASN PRO ILE ARG ARE PLACED AT POSITION 100G.
- 12) Ab25'CL: AUTHORS PROVIDED THIS ORIGINAL SEQUENCE WHICH IS DIFFERENT FROM THAT IN THE REFERENCE.
- 18) 60P2'CL: FROM HUMAN FETUS AT 130 DAYS OF GESTATION.
- 19) 63P1'CL: FROM HUMAN FETUS AT 130 DAYS OF GESTATION.
- 24) Ab21'CL: AUTHORS PROVIDED THIS ORIGINAL SEQUENCE WHICH IS DIFFERENT FROM THAT IN THE REFERENCE.
- 25) 56P1'CL: FROM HUMAN FETUS AT 130 DAYS OF GESTATION.
- 26) 2P1'CL: FROM HUMAN FETUS AT 130 DAYS OF GESTATION.
- 29) KIM46H'CL: KIM4.6 CELL LINE WAS PRODUCED BY FUSION OF TONSILLAR LYMPHOID CELLS FROM A NORMAL CHILD WITH GM4672, AN IGG-KAPPA PRODUCER. THE CDR3 OF THIS HEAVY CHAIN IS LONGER, REQUIRING 8 RESIDUES, THR THR THR LYS ARG GLY LEU THR, TO BE PLACED AT POSITION 100D.
- 31) RF-SJ2'CL: FOR ALIGNMENT, IT IS REQUIRED TO PLACE TWO RESIDUES, TYR SER, AT POSITION 100D.
- 34) FL2-2'CL: DERIVED FROM HUMAN GENOMIC DNA OF EPSTEIN-BARR VIRUS-TRANSFORMED FETAL B CELL LINE.
- 36) 38P1'CL: FROM HUMAN FETUS AT 130 DAYS OF GESTATION.
- 41) HN.14'CL: THIS HYBRIDOMA WAS MADE BY FUSING PERIPHERAL BLOOD LYMPHOCYTES FROM A PATIENT WITH CHRONIC LYMPHOCYTIC LEUKEMIA AND UC729-6 HUMAN LYMPHOBLASTOID CELLS.
- 46) RF-SJ1'CL: FOR ALIGNMENT, IT IS REQUIRED TO PLACE TWO RESIDUES, TYR SER, AT POSITION 100D.
- 48) 4B4'CL: THE HYBRIDOMA WAS MADE BY FUSING PBMC CELLS FROM AN SLE PATIENT TO THE LYMPHOBLASTOID CELL LINE GM4672. Sm IS THE ABBREVIATION FOR SMALL NUCLEAR RIBONUCLEOPROTEIN.
- 63) VH10.7'CL: FROM PATIENT WITH IGD-SECRETING MYELOMA. THE V- AND C-REGIONS ARE BROUGHT TOGETHER BY A HOMOLOGOUS RECOMBINATION BETWEEN 442/443-BASE-PAIR REPEATS DELETING THE C-MU.
- 67) GRA': PERSONAL COMMUNICATION FROM THE AUTHOR INDICATES THAT IT IS A CRYOGLOBULIN.
- 68) K6H6'CL: FROM A PATIENT WITH B-CELL LYMPHOMA.
- 69) K4B8'CL: FROM A PATIENT WITH B-CELL LYMPHOMA.
- 70) K5B8'CL: FROM A PATIENT WITH B-CELL LYMPHOMA.
- 71) K5C7'CL: FROM A PATIENT WITH B-CELL LYMPHOMA.
- 72) K5G5'CL: FROM A PATIENT WITH B-CELL LYMPHOMA.
- 73) K6F5'CL: FROM A PATIENT WITH B-CELL LYMPHOMA.
- 82) 20P1'CL: FROM HUMAN FETUS AT 130 DAYS OF GESTATION.
- 83) FR: AN IDIOTYPIC ANTIBODY TO FR NOT INHIBITABLE BY PHOSPHORYLCHOLINE REACTED BETTER WITH THE FR HEAVY CHAIN THAN WITH THE LIGHT CHAIN. THE CROSS-REACTION WITH MOPC167 WAS 10,000 TIMES WEAKER. (RIESEN, W.F. (1979) EUR. J. IMMUNOL., 9, 421-425.)
- 96) PS (SHA): PS AND SHA ARE THE SAME PROTEIN AS POINTED OUT BY HASSNER, A. & SAXON, A. (1984) J. IMMUNOL., 132, 2844-2846.
- 97) 13P1'CL: FROM HUMAN FETUS AT 130 DAYS OF GESTATION.
- 111) A-G1: AMINO ACID RESIDUES FOUND AT POSITION 5 ARE VAL AND LEU.
- 113) B-G1: AMINO ACID RESIDUES FOUND AT POSITION 7 ARE SER AND THR.
- 114) B-G2b: AMINO ACID RESIDUES FOUND AT POSITION 7 ARE SER AND THR.
- 122) C-G1: AMINO ACID RESIDUES FOUND AT POSITION 7 ARE SER AND THR.
- 123) K-G1 (+&-): AMINO ACID RESIDUES FOUND AT POSITION 20 ARE LEU AND VAL.
- 125) LR1'CL: THE REGION NOT SEQUENCED CONSISTED OF A LARGE DELETION. THIS HEAVY CHAIN IS EXPRESSED ON THE CELL SURFACE WITHOUT LIGHT CHAIN. LR1 IS A B-CELL LINE THAT SPONTANEOUSLY AROSE FROM CULTURED PERIPHERAL BLOOD LYMPHOCYTES FROM A PATIENT WITH ACUTE LYMPHOCYTIC LEUKEMIA.
- 131) F-G1: AMINO ACID RESIDUES FOUND AT POSITION 7 ARE SER AND THR.
- 133) S98-IGA: THIS MYELOMA PROTEIN IS FROM A PATIENT WITH SMOLDERING MULTIPLE MYELOMA WHO PRODUCES TWO MONOCLONAL IMMUNOGLOBULINS, IGG AND IGA.
- 135) Ly47'CL: FROM BURKITT'S LYMPHOMA CELL LINES WHICH PRODUCE TRUNCATED HEAVY CHAINS LACKING PART OF VARIABLE REGION
- 139) LBW2'CL: THE REGION NOT SEQUENCED CONSISTED OF A LARGE DELETION. THIS HEAVY CHAIN IS EXPRESSED ON THE CELL SURFACE WITHOUT LIGHT CHAIN. LBW2 IS AN EBV-TRANSFORMED B-CELL LINE DERIVED FROM PERIPHERAL BLOOD LYMPHOCYTES FROM A PATIENT WITH COMMON VARIABLE IMMUNODEFICIENCY.



**SPECIFIC NOTES: HUMAN HEAVY CHAINS SUBGROUP III (cont'd)**

- 140) **Ly91'CL:** FROM BURKITT'S LYMPHOMA CELL LINES WHICH PRODUCE TRUNCATED HEAVY CHAINS LACKING PART OF VARIABLE REGION
- 146) **DB'CL:** THE REGION NOT SEQUENCED CONSISTED OF A LARGE DELETION. THIS HEAVY CHAIN IS EXPRESSED ON THE CELL SURFACE WITHOUT LIGHT CHAIN. DB IS AN EBV-TRANSFORMED B-CELL LINE DERIVED FROM PERIPHERAL BLOOD LYMPHOCYTES FROM A HEALTHY INDIVIDUAL.
- 147) **LBW14'CL:** THE REGION NOT SEQUENCED CONSISTED OF A LARGE DELETION. THIS HEAVY CHAIN IS EXPRESSED ON THE CELL SURFACE WITHOUT LIGHT CHAIN. LBW14 IS AN EBV-TRANSFORMED B-CELL LINE DERIVED FROM PERIPHERAL BLOOD LYMPHOCYTES FROM A PATIENT WITH COMMON VARIABLE IMMUNODEFICIENCY.
- 165) **SMM-IGG:** THIS MYELOMA PROTEIN IS FROM A PATIENT WITH SMOLDERING MULTIPLE MYELOMA WHO PRODUCES TWO MONOCLONAL IMMUNOGLOBULINS, IGG AND IGA.
- 178) **CRA:** IT WAS FROM A CASE OF HEAVY CHAIN DISEASE. AT POSITION 3, LEU AND ILE WERE FOUND. AFTER POSITION 9, THE CHAIN CONTINUES IN THE C-REGION AS RESIDUE 216 (EU NUMBERING) GLU.
- 180) **JLN'CL:** IT IS ASSOCIATED WITH A t(14;18) TRANSLOCATION WITH THE BREAK POINT IN THE J4 REGION ON THE NONFUNCTIONAL ALLELE.

+ THE FOLLOWING WERE EQUALLY AND MOST FREQUENTLY OCCURRING:

AT POSITION	RESIDUES
95	(GLY, ASP)
97	(VAL, GLU)
99	(TYR, THR)
100D	(LEU, SER)