



**SEQUENCES OF
PROTEINS OF
IMMUNOLOGICAL
INTEREST**

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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, β_2 -Microglobulins,
Major Histocompatibility Antigens, Thy-1, Complement,
C-Reactive Protein, Thymopoietin, Integrins, Post-gamma Globulin,
 α_2 -Macroglobulins, and Other Related Proteins

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T-CELL SURFACE ANTIGENS.....1824

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HUMAN GAMMA CHAIN.....	1997
HUMAN DELTA CHAIN.....	1999
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0																								
1	ASP	ASP	ASP	ASP	ASP	ASP	ASP	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	---
3	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	leu	GLX	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	---
4	MET	MET	leu	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	leu	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	---
6	GLN	GLX	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	---
7	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	---
9	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	thr	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	---
F 10	ser	ser	phe	THR	ser	ser	ser	ser	ser	THR	ser	ser	ser	ser	THR	ser	THR	ser	ser	ser	ser	ser	ser	---
R 11	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	---
R 12	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	val	ALA	ALA	val	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	---
15	VAL	VAL	VAL	VAL	VAL	VAL	leu	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	---
16	GLY	GLY	GLY	GLY	GLY	GLY	arg	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	---
17	ASP	glx	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	---
18	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	---
20	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	---
22	THR	THR	THR	THR	ala	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	---
23			CYS																					---
24																								---
25																								---
26																								---
27																								---
27A																								---
27B																								---
27C																								---
27D																								---
27E																								---
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77																								---
78																								---
79																						LEU		---
80																						GLN		---
81																						pro		---
82																						glu		---
83																						ASP		---
84																						PHE		---
85																						ALA		---
86																						THR		---
87																						TYR		---
88																						CYS		---
89																								---
90																							gln	---
91																							gln	---
92																								

HUMAN KAPPA LIGHT CHAINS SUBGROUP I (cont'd)

	125 AMYLOID	126 HEJ	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	124	4	109 (MET)	4.6
4	MET	MET	MET	MET				
5	pro	THR	THR		124	3	122 (THR)	3.
6	GLN	GLN			123	1,2	123 (GLN), 116 (GLN)	1.,2.1
7	SER				121	2	120 (SER)	2.
8	SER				121	4	120 (PRO)	2.
9	SER				121	4	117 (SER)	4.1
10	ser				120	5	89 (SER)	6.7
11	LEU				118	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	3	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	3	1 (+)	
27E					2	2	1 (+)	
27F					84	7	29 (SER)	20.
28					83	5	72 (ILE)	5.8
29					81	11	41 (SER)	22.
30					79	12	27 (ASN), 24 (SER)	35.,39.
31					79	9	34 (TYR)	21.
32					79	9	34 (TYR)	21.
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 (LXS)	4.4
40					68	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
50					59	9	19 (ALA)	28.
51					59	6	50 (ALA)	5.9
52					58	6	53 (SER)	6.6
53					57	6,7	26 (SER)	13.,15.
54					58	2	56 (LEU)	2.1
55					58	8,9	25 (GLU)	19.,21.
56					56	8	34 (SER)	13.
57					57	1	57 (GLY)	1.
58					58	3	50 (VAL)	3.5
59					57	4	54 (PRO)	4.2
60					57	1	57 (SER)	1.
61					57	1	56 (ARG)	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)	5.5
66					57	2	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					5,6	33	33 (ASP), 31 (ASP)	8.3,11.
71					54	4	49 (PHE)	4.4
72					54	5	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					54	3	43 (SER)	3.2
77					54	6	40 (SER)	8.1
78					54	2	53 (LEU)	2.
79					3,4	52	52 (GLN), 48 (GLN)	3.1,4.5
80					54	2	46 (PRO)	2.3
81					3,5	37	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					56	2	52 (TYR)	2.1
88					56	1	56 (CYS)	1.
89					57	4,5	46 (GLN), 43 (GLN)	5.,6.6
90					2,3	51	51 (GLN), 46 (GLN)	2.2,3.7
91					11,12	28	28 (TYR)	27.,28.
92					60	9	20 (ASN), 19 (+)	27.,28.
93					60	9	29 (SER)	19.
94					60	12	15 (LEU)	48.
95					56	4	44 (PRO)	5.1
95A					1	1	1 (GLU)	
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					4,5	29	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) KUE: 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) PW: IGG1-KAPPA
- 79) RI: IGG1-KAPPA
- 89) F-GUI: IGG3-KAPPA
- 90) S-GUI: IGG3-KAPPA

REFERENCE: HUMAN KAPPA LIGHT CHAINS SUBGROUP I

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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],HEJ4[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[100],WEA[20],DAUDI'CL[23],HK134'CL[24],WALKER'CL[26],HK101'CL[27],VKI-Chr1'CL[29],DEE[33],AND[35],REI[38],AU[39],ROY[40],HUVCAMP'CL[42],AG[43],SCW[44],RZ[50],BJ26[53],RF2[55],HA[56],ESM[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],WAG[90],LOW[81],F-GUI[89],DIE[92],CAR A[93],TEL[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],EJ19[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],HUVCAMP'CL[42],KA[48],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-2I'CL[37]. (2 IDENTICAL)
 SET 8: OU[100],WIL(-)[34]. (2 IDENTICAL)
 SET 9: RZ[50],RF2[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*1[24]. (5 IDENTICAL HUMAN V-KAPPA-I; ALSO 6 HUMAN V-KAPPA-II: GM 607'CL[11],RPM16410'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],HAR 14.1'CL[7],HAR 14.2'CL[8],HAR 16.1'CL[9],NOV'CL[10],HIC (R)'CL[11],PAY[15],BOR[17],HEW'CL[18],ROB'CL[19],ROB'CL[21],HAR'CL[22],HIC'CL[24],WOL[31],EVI-15'CL[32],GOL[33],Taykv322'CL[54],GF4/1.1'CL[54],REI[56],HAH (R)'CL[73],VKRPA3'CL[85]; AND 2 HUMAN V-KAPPA-IV: FR-001'CL[1],EB17IV'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],B-G2a[13]; 10 HUMAN V-KAPPA-III: GAR[1],FLO[3],TH3'CL[13],GOT[16],NEU[26],IARC/BL41'CL[46],FR[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[35],Taykv320'CL[36],LS1'CL[39],LS2'CL[40],LS4'CL[41],LS5'CL[42],LS6'CL[43],LS7'CL[44],LS8'CL[45],Taykv308'CL[58]; 2 HUMAN V-KAPPA-IV: VJ1'CL[4],LV661'CL[12]; 4 MOUSE V-KAPPA-V: SE20.2'CL[29],HV65-212'CL[47],DNA9'CL[127],DNA2'CL[128]; AND 2 MOUSE V-KAPPA-MISC: DNA2'CL[11],DNA9'CL[2].)
 SET 9: WES[22],MEV[45]. (2 IDENTICAL)
 SET 10: OU[100],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-2I'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],RF2[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-2I'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],vkl-B'CL[51],PC2567 (NZB) [55],G8 CA 1.7[56],L XIX 27'CL[67],95 BB 2.6[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: mAb 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: RPM16410'CL[11]; 6 HUMAN V-KAPPA-III: PIE[2],HIC (R)'CL[11],ROB'CL[19],HIC'CL[24],GF4/1.1'CL[54],VKRPA3'CL[85]; AND 1 HUMAN V-KAPPA-IV: EB17IV'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]; AND 1 HUMAN V-KAPPA-IV: FR-001'CL[1].)
 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],HAR 14.2'CL[8],HAR 16.1'CL[9],HAR'CL[22],WOL[31],EVI-15'CL[32],HAH (R)'CL[73]; AND 1 HUMAN V-KAPPA-IV: FR-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 51 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 RE1 WITH SOME MODIFICATIONS, AND CDR'S OF HuRSV19VL. WHEN HuRSV19VK IS COMBINED WITH HuRSV19VH, FV DOES NOT BIND VIRUS; BUT WHEN COMBINED WITH HuRSV19VHFS, 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	pca	pca	pca	---	---	pca	68	5	32 (GLN)	11.
2	VAL	VAL	VAL	VAL	---	---	VAL	67	9	59 (VAL)	10.
3	GLN	glu	GLN	GLN	pca	pca	leu	67	6	59 (GLN)	6.8
4	LEU	LEU			LEU	LEU		63	4	62 (LEU)	2.
5								53	4	49 (VAL)	4.3
6								53	1	43 (GLN)	3.7
7								53	1	53 (SER)	1.7
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								54	2	41 (LYS)	9.
13								54	2	53 (PRO)	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	4	37 (VAL)	6.9
19								53	4	44 (LYS)	3.6
20								52	4	36 (VAL)	5.8
21								49	2	48 (SER)	3.2
22								49	2	48 (CYS)	3.2
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								49	6	32 (TYR)	9.6
28								49	3	32 (TYR)	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	2	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	2	32 (GLN)	6.
62								48	2	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	3	19 (ALA)	13.2
72								49	3	46 (ASP)	3.2
73								49	8	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	4	43 (ALA)	4.4
79								50	4	45 (TYR)	4.4
80								50	2	36 (MET)	2.8
81								50	5	35 (GLU)	7.1
82								51	5	37 (LEU)	6.9
82A								51	7	31 (SER)	
82B								51	6	37 (SER)	
82C											
83								51	2	49 (LEU)	7.7
84								51	5	33 (ARG)	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	53 (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	30 (SER)	

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
- 10) **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) **1ambda IGD-1'CL:** IGD-
- 45) **WOL:** IGM-KAPPA
- 48) **DI:** IGM-
- 49) **60F1'CL:** IGM-
- 50) **CA:** IGG1-
- 51) **BR0'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) **DUN:** IGG4-
- 74) **SAW:** IGG2-
- 75) **ADA:** IGA-
- 76) **NOR:** IGA-
- 79) **RIC:** IGG3-

REFERENCE: HUMAN HEAVY CHAINS SUBGROUP I

- 1) **LS2'CL:** SILBERSTEIN, L.E., LITWIN, S. & CARMACK, C.E. (1989) J. EXP. MED., 169, 1631-1643.
- 2) **LS5'CL:** SILBERSTEIN, L.E., LITWIN, S. & CARMACK, C.E. (1989) J. EXP. MED., 169, 1631-1643.
- 3) **LS6'CL:** SILBERSTEIN, L.E., LITWIN, S. & CARMACK, C.E. (1989) J. EXP. MED., 169, 1631-1643.
- 4) **LS1'CL:** SILBERSTEIN, L.E., LITWIN, S. & CARMACK, C.E. (1989) J. EXP. MED., 169, 1631-1643.
- 5) **LS4'CL:** SILBERSTEIN, L.E., LITWIN, S. & CARMACK, C.E. (1989) J. EXP. MED., 169, 1631-1643.
- 6) **LS8'CL:** SILBERSTEIN, L.E., LITWIN, S. & CARMACK, C.E. (1989) J. EXP. MED., 169, 1631-1643.
- 7) **1B9/F2'CL:** CARROLL, W.L., YU, M., LINK, M.P. & KORSMEYER, S.J. (1989) J. IMMUNOL., 143, 692-698.
- 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.
- 9) **3-1'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.
- 10) **21/28'CL:** DERSIMONIAN, H., SCHWARTZ, R.S., BARRETT, K.J. & STOLLAR, B.D. (1987) J. IMMUNOL., 139, 2496-2501.
- 11) **8E10'CL:** DERSIMONIAN, H., SCHWARTZ, R.S., BARRETT, K.J. & STOLLAR, B.D. (1987) J. IMMUNOL., 139, 2496-2501.
- 12) **HG3'CL:** RECHAVI, G., RAM, D., GLAZER, L., ZAKUT, R. & GIVOL, D. (1983) PROC. NATL. ACAD. SCI. USA, 80, 855-859. (CHECKED BY AUTHOR 01/04/83)
- 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.
- 16) **NEI'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.
- 17) **HP1'CL:** SHEN, A., HUMPHRIES, C., TUCKER, P. & BLATTNER, F. (1987) PROC. NATL. ACAD. SCI. USA, 84, 8563-8567.
- 18) **E3-10'CL:** KODAIRA, M., KINASHI, T., UMEMURA, I., MATSUDA, F., NOMA, T., ONO, Y. & HONJO, T. (1986) J. MOL. BIOL., 190, 529-541.
- 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.
- 20) **hvi1263'CL:** CHEN, P.P., LIU, M.-F., GLASS, C.A., SINHA, S., KIPPS, T.J. & CARSON, D.A. (1989) ARTHRITIS & RHEUMATISM, 32, 72-76.
- 21) **783'CL:** CHEN, P.P., LIU, M.-F., GLASS, C.A., SINHA, S., KIPPS, T.J. & CARSON, D.A. (1989) ARTHRITIS & RHEUMATISM, 32, 72-76; 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.
- 22) **X17115'CL:** FRIEDLANDER, R.M., NUSSENZWEIG, M.C. & LEDER, P. (1990) NUCL. ACIDS RES., 18, 4278.
- 23) **TH9'CL:** DERSIMONIAN, H., MCADAM, K.P.W.J., MACKWORTH-YOUNG, C. & STOLLAR, B.D. (1989) J. IMMUNOL., 142, 4027-4033.
- 24) **WIL2'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.

REFERENCE: HUMAN HEAVY CHAINS SUBGROUP I (cont'd)

- 25) **EV1-15'** CL: NEWKIRK, M.M., MAGEED, R.A., JEFFERIS, R., CHEN, P.P. & CAPRA, J.D. (1988) J. CLIN. INVEST., 81, 1511-1518.
- 26) **KAS:** NEWKIRK, M.M., MAGEED, R.A., JEFFERIS, R., CHEN, P.P. & CAPRA, J.D. (1987) J. EXP. MED., 166, 550-564.
- 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: PASQUAL, V., RANDEN, I., THOMPSON, K., SLOUD, M., FORRE, O., NATVIG, J. & CAPRA, J.D. (1990) J. CLIN. INVEST., 86, 1320-1328.
- 29) **LS7'** CL: SILBERSTEIN, L.E., LITWIN, S. & CARMACK, C.E. (1989) J. EXP. MED., 169, 1631-1643.
- 30) **ND'** CL: BENNICH, H. & VON BARR-LINDSTROM, H. (1974) PROGRESS IN IMMUNOLOGY, 1, 49-58; BENNICH, H.H., JOHANSSON, S.G.O. & VON BARR-LINDSTROM, H. (1978) IN IMMEDIATE HYPERSENSITIVITY: MODERN CONCEPTS AND DEVELOPMENTS. BACH, M.K. (ED.), PP. 1-36. MARCEL DEKKER, NEW YORK; KENTEN, J., H. MOULARD, H.V., HOUGHTON, M., DERBYSHIRE, R.B., VINEY, J., BELL, L.O. & GOULD, H.J. (1982) PROC. NAT. ACAD. SCI. USA, 79, 6661-6665.
- 31) **71-5'** CL: KODAIRA, M., KINASHI, T., UMEMURA, T., MATSUDA, F., NOMA, T., ONO, Y. & HONJO, T. (1986) J. MOL. BIOL., 190, 529-541.
- 32) **EU:** CUNNINGHAM, B.A., RUTISHAUSER, U., GALL, W.E., GOTTLIEB, P.D., WAXDAL, M.J. & EDELMAN, G.M. (1970) BIOCHEMISTRY, 9, 3161-3170. (CHECKED BY AUTHOR)
- 33) **RF-TS3'** CL: PASQUAL, V., RANDEN, I., THOMPSON, K., SLOUD, M., FORRE, O., NATVIG, J. & CAPRA, J.D. (1990) J. CLIN. INVEST., 86, 1320-1328.
- 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.
- 35) **VhAU'** CL: VAN DER HEIJDEN, R.W.J., BUNSCHOTEN, H., PASQUAL, V., UYTDEHAAG, F.G.C.M., OSTERHAUS, A.D.M.E. & CAPRA, J.D. (1990) J. IMMUNOL., 144, 2835-2839.
- 36) **5-2R1'** 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.
- 37) **VH251'** CL: HUMPHRIES, C.G., SHEN, A., KUZIEL, W.A., CAPRA, J.D., BLATTNER, F.R. & TUCKER, P.W. (1988) NATURE, 331, 446-449.
- 38) **83P2'** CL: SCHROEDER, H.W., JR. & WANG, J.Y. (1990) PROC. NATL. ACAD. SCI. USA, 87, 6146-6150.
- 39) **MOT:** KOJIMA, M., ODANI, S. & ONO, T. (1982) MOL. IMMUNOL., 19, 1095-1103; KOJIMA, M., KOIDE, T., ODANI, S. & ONO, T. (1986) MOL. IMMUNOL., 23, 169-174. (CHECKED BY AUTHOR 08/08/86)
- 40) **WS1'** CL: SHEN, A., HUMPHRIES, C., TUCKER, P. & BLATTNER, F. (1987) PROC. NATL. ACAD. SCI. USA, 84, 8563-8567.
- 41) **Ab2022'** CL: SANZ, I., CASALI, P., THOMAS, J.W., NOTKINS, A.L. & CAPRA, J.D. (1989) J. IMMUNOL., 142, 4054-4061.
- 42) **STE:** ANDREWS, D.W. & CAPRA, J.D. (1981) PROC. NAT. 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.
- 43) **lambda IGD-1'** CL: YASUI, H., AKAHORI, Y., HIRANO, M., YAMADA, K. & KUROSAWA, Y. (1989) EUR. J. IMMUNOL., 19, 1399-1403.
- 44) **Ab2'** CL: VAN DER HEIJDEN, R.W.J., BUNSCHOTEN, H., PASQUAL, V., UYTDEHAAG, F.G.C.M., OSTERHAUS, A.D.M.E. & CAPRA, J.D. (1990) J. IMMUNOL., 144, 2835-2839.
- 45) **WOL:** ANDREWS, D.W. & CAPRA, J.D. (1981) PROC. NAT. 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.
- 46) **Vh383ex'** CL: VAN DER HEIJDEN, R.W.J., BUNSCHOTEN, H., PASQUAL, V., UYTDEHAAG, F.G.C.M., OSTERHAUS, A.D.M.E. & CAPRA, J.D. (1990) J. IMMUNOL., 144, 2835-2839.
- 47) **M61'** CL: SCHROEDER, H.W., JR. & WANG, J.Y. (1990) PROC. NATL. ACAD. SCI. USA, 87, 6146-6150.
- 48) **DI:** KOHLER, H., SHIMIZU, A., PAUL, C., MOORE, V. & PUTNAM, F.W. (1970) NATURE, 227, 1318-1320; FLORENT, G., LEHMAN, D. & PUTNAM, F.W. (1974) BIOCHEMISTRY, 13, 2482-2488. (CHECKED BY AUTHOR 06/15/83)
- 49) **60P1'** CL: SCHROEDER, H.W., JR., HILLSON, J.L. & PERLMUTTER, R.M. (1987) SCIENCE, 238, 791-793.
- 50) **CA:** PITCHER, S.E. & KONIGSBERG, W. (1970) J. BIOL. CHEM., 245, 1267-1274. (CHECKED BY AUTHOR)
- 51) **BRO' IGG:** HOPPER, J.E., NOYES, C., HEINRIKSON, R. & KESSEL, J.W. (1976) J. IMMUNOL., 116, 743-746; HOPPER, J.E. & BRAHN, E. (1977) J. IMMUNOL., 119, 847-849. (CHECKED BY AUTHOR 08/25/78 WHO POINTED OUT THAT BRO' IS SAME AS BRIGG AND SUGGESTED THAT IT SHOULD BE RENAMED AS BROIGG)
- 52) **THO:** HOPPER, J.E. & BRAHN, E. (1977) J. IMMUNOL., 119, 847-849. (CHECKED BY AUTHOR 08/25/78)
- 53) **STE:** FISHER, C.E., PALM, W.H. & PRESS, E.M. (1969) FEBS LETTERS, 5, 20-22. (CHECKED BY AUTHOR)
- 54) **ZUC:** FRANGIONE, B. & MILSTEIN, C. (1969) NATURE, 224, 597-599. (CHECKED BY AUTHOR)
- 55) **TH3'** CL: DERSIMONIAN, H., MCADAM, K.P.W.J., MACKWORTH-YOUNG, C. & STOLLAR, B.D. (1989) J. IMMUNOL., 142, 4027-4033.
- 56) **HUS:** WANG, A.C. & FUDENBERG, H.H. (1975) ARCH. BIOCHEM. BIOPHYS., 168, 657-664. (CHECKED BY AUTHOR 09/23/77)
- 57) **OHM'** CL: ALEXANDER, A., STEINMETZ, M., BARRIPAL, D., FRANGIONE, B., FRANKLIN, E.C., HOOD, L. & BUXBAUM, J.N. (1982) PROC. NAT. ACAD. SCI. USA, 79, 3260-3264. (CHECKED BY AUTHOR 06/17/83)
- 58) **BOT:** BARNIKOL-WATANABE, S., MIHAESCO, E., MIHAESCO, C., BARNIKOL, H.U. & HILSCHMANN, N. (1984) Z. PHYSIOL. CHEM., 365, 105-118.
- 59) **BEN (I):** KAPLAN, A.P., HOOD, L., TERRY, W.D. & METZGER, H. (1971) IMMUNOCHEMISTRY, 8, 801-811. (CHECKED BY AUTHOR)
- 60) **ZUC'** CL: TAKAHASHI, N., TAKAHASHI, Y., ISHIOKA, N., HEINY, M.E. & PUTNAM, F.W. (1986) PROTIDES BIOL. FLUIDS, 33, 541-544.
- 61) **WIS:** FRANKLIN, E.C., PRELLI, F. & FRANGIONE, B. (1979) PROC. NAT. ACAD. SCI. USA, 76, 452-456. (CHECKED BY AUTHOR 07/18/79)
- 62) **VAU:** FRANKLIN, E.C., KYLE, R., SELIGMANN, M. & FRANGIONE, B. (1979) MOL. IMMUNOL., 16, 919-921. (CHECKED BY AUTHOR 12/10/82)
- 63) **LEB:** FRANKLIN, E.C., KYLE, R., SELIGMANN, M. & FRANGIONE, B. (1979) MOL. IMMUNOL., 16, 919-921. (CHECKED BY AUTHOR 12/10/82)
- 64) **SAC:** PARR, D.M. (1981) MOL. IMMUNOL., 18, 257-259. (CHECKED BY AUTHOR 03/02/82)
- 65) **AF2'** CL: SONNTAG, D., WEINGARTNER, B. & GRUTZMANN, R. (1989) NUCL. ACIDS RES., 17, 1267.
- 66) **DEE:** FRANGIONE, B. & MILSTEIN, C. (1967) NATURE, 216, 939-941. (CHECKED BY AUTHOR)
- 67) **KOH:** KAPLAN, A.P., HOOD, L., TERRY, W.D. & METZGER, H. (1971) IMMUNOCHEMISTRY, 8, 801-811. (CHECKED BY AUTHOR)
- 68) **NAR:** KAPLAN, A.P., HOOD, L., TERRY, W.D. & METZGER, H. (1971) IMMUNOCHEMISTRY, 8, 801-811. (CHECKED BY AUTHOR)
- 69) **FT:** MONTGOMERY, P.C., BELLO, A.C. & ROCKEY, J.H. (1970) BIOCHIM. BIOPHYS. ACTA, 200, 258-266. (CHECKED BY AUTHOR)
- 70) **VU:** MONTGOMERY, P.C., BELLO, A.C. & ROCKEY, J.H. (1970) BIOCHIM. BIOPHYS. ACTA, 200, 258-266. (CHECKED BY AUTHOR)
- 71) **WAR:** KAPLAN, A.P., HOOD, L., TERRY, W.D. & METZGER, H. (1971) IMMUNOCHEMISTRY, 8, 801-811. (CHECKED BY AUTHOR)
- 72) **VIL:** KAPLAN, A.P., HOOD, L., TERRY, W.D. & METZGER, H. (1971) IMMUNOCHEMISTRY, 8, 801-811. (CHECKED BY AUTHOR)
- 73) **DUN:** KAPLAN, A.P., HOOD, L., TERRY, W.D. & METZGER, H. (1971) IMMUNOCHEMISTRY, 8, 801-811. (CHECKED BY AUTHOR)
- 74) **SAW:** KAPLAN, A.P., HOOD, L., TERRY, W.D. & METZGER, H. (1971) IMMUNOCHEMISTRY, 8, 801-811. (CHECKED BY AUTHOR)
- 75) **ADA:** KAPLAN, A.P., HOOD, L., TERRY, W.D. & METZGER, H. (1971) IMMUNOCHEMISTRY, 8, 801-811. (CHECKED BY AUTHOR)
- 76) **NOR:** KAPLAN, A.P., HOOD, L., TERRY, W.D. & METZGER, H. (1971) IMMUNOCHEMISTRY, 8, 801-811. (CHECKED BY AUTHOR)
- 77) **LEA:** FRANGIONE, B. & FRANKLIN, E.C. (1977) PROG. IMMUNOL., 3, 278-288. (CHECKED BY AUTHOR 07/18/79)
- 78) **HAR:** FRANGIONE, B. & FRANKLIN, E.C. (1977) PROG. IMMUNOL., 3, 278-288. (CHECKED BY AUTHOR 07/18/79)
- 79) **RIC:** KAPLAN, A.P., HOOD, L., TERRY, W.D. & METZGER, H. (1971) IMMUNOCHEMISTRY, 8, 801-811. (CHECKED BY AUTHOR)

IDENTICAL SETS OF FRAMEWORK SEGMENTS:

- FR1:** SET 1: LS2'CL[1], LSS'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], LSS'CL[2], LS6'CL[3], LS1'CL[4], LS4'CL[5], LS8'CL[6], 1B9/F2'CL[7], 21-2'CL[8], 13-1'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], WL2'CL[24], 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], 20P1'CL[82].)
- FR3:** SET 1: LS2'CL[1], LSS'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], LSS'CL[2], LS6'CL[3], LS1'CL[4], LS4'CL[5], LS8'CL[6], 1B9/F2'CL[7], 21/28'CL[10], NEI'CL[16], TH9'CL[23], WL2'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[11], M11'CL[13], MCE' [46], DR12910-2F8'CL[48], Ad17'CL[49], M44'CL[52], NZU[55]; 24 HUMAN V-H-III: 18/2'CL[11], 18/17'CL[12], 18/9'CL[13], 8/17'CL[4], 30P1'CL[5], 13/19'CL[19], HE2-1/2'CL[25], 25'CL[12], Vh383'CL[12], Vh383'CL[16], Vh383'CL[17], 80P2'CL[18], 6331'CL[19], SF471-1'CL[20], Vh383'CL[4], C[21], Vh383'CL[15], 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], R5C7'CL[71], K6S'CL[72], K6F5'CL[73], 20P1'CL[82]; 1 MOUSE V-H-IIB: PING2006'CL[29]; 1 MOUSE V-H-III: MOP47A[110]; AND 1 MOUSE V-H-IIID: H31-40'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-III: MOP47A[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: 16'CL[2], W17'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: Pag-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-001'CL[11], HIGL'CL[24], Ab44'CL[29], POG-B'CL[30], HuRSV19V[36], HuRSV19CH[38]; 2 HUMAN V-H-III: 4GL2'CL[10], Ab21'CL[24], M72'CL[27], KIM46H'CL[29], U266'CL[136], 70P1'CL[183]; 2 MOUSE V-H-IA: HDEK12[15], M61'CL[160]; AND 1 MOUSE V-H-IC: MURSV19V[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-IA: 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],4K7'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],3'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: M1'CL[3],GR2910-288'CL[48],Ab17'CL[49],M44'CL[52]; 17 HUMAN V-H-III:
30P1'CL[5],Ab25'CL[12],60P2'CL[18],63P1'CL[19],56P1'CL[25],M74'CL[28],TIL[33],HN-14'CL[41],M2'CL[49],
VH10.7'CL[63],K6H6'CL[68],K4B8'CL[69],K5B8'CL[70],K5C7'CL[71],K5G5'CL[72],K6P5'CL[73],20P1'CL[82]; AND 1
MOUSE V-H-IIID: 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: MOPCA47A[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: RF-001'CL[11],H131'CL[24],Ab44'CL[29]; AND 6 HUMAN V-H-III: 4G12'CL[10],Ab21'CL[24],M72'CL[27],
KIM45H'CL[29],U266'CL[136],70P1'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 116J.
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:** PAPAINE 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) **OMM'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% HOMOMOLOGY TO MOUSE DFL16 MINIGENE AND WAS THUS DESIGNATED AS DFL16.

+ THE FOLLOWING WERE EQUALLY AND MOST FREQUENTLY OCCURRING:

AT POSITION	RESIDUES
100J	(TYR,ALA)

HUMAN HEAVY CHAINS SUBGROUP II (cont'd)

	46 MCE' #	47 7F1 /CL #	48* DR L2F10 /CL #	49* A17 /CL #	50* LES-B /CL #	51* LES-A /CL #	52 M44 /CL #	53 L66 /CL #	54 JBL2 /CL #	55 NZU #	56 SA	57 CAR	58 SPA #	59 IO	60 64P1 /CL #	61* ERI /CL #	# OF SEQUENCES	# OF AMINO ACIDS	OCCURRENCES OF MOST COMMON AMINO ACID
	0																		
	1	pc	GLN				GLN	GLN					pc	pc			51	4	39 (GLN), 38 (GLN)
	2	ie	LEU				VAL	LEU					le	le			51	4	43 (VAL)
	3	thr	LEU				GLN	GLN					glu	thr			51	6	39 (GLN)
	4	LEU	LEU				LEU	LEU					val	LEU			51	2	50 (LEU)
	5	lys	lys				arg	pro					arg				50	6	38 (GLN), 37 (GLN)
	6	glu	glu				glu	glu					glu				50	6	33 (GLU), 32 (GLU)
	7	SER	SER				SER	SER					SER				50	6	44 (SER)
	8	GLY	GLY				SER	GLY					GLY				50	6	46 (GLY)
	9	PRO	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	6	26 (GLN)
	17	THR	THR				THR	---									48	6	46 (THR)
	18	LEU	LEU				phe	---									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			THR	CYS	---				51	1	51 (CYS)
	23	thr	thr				asn	thr			thr	thr	---				52	2	25 (THR)
	24	phe	ALA				val	gly			val	val	---				52	5	31 (VAL)
	25	SER	SER				tyr	SER			SER	SER	---				52	3	45 (SER)
	26	GLY	GLY				tyr	SER			SER	GLY	---				51	1	50 (GLY)
	27	phe	phe				asp	---			GLY	GLY	---				50	6	19 (GLY)
	28	SER	SER				ile	---			SER	---	---				50	4	41 (SER)
	29	leu	ile				leu	---			SER	---	---				50	4	18 (VAL)
	30	SER	SER				SER	---			---	---	---				50	4	46 (SER)
	31	thr	SER				thr	asn			---	---	---				50	8	28 (SER)
	32	ser	tyr				gly	tyr			---	---	---				50	3	13 (TYR)
	33	glu	tyr				tyr	tyr			---	---	---				50	3	50 (GLY)
	34	val	trp				val	trp			---	---	---				50	7	14 (TRP)
	35	gly	ser				gly	ser			---	---	---				50	12	13 (SER)
	35A	val	val				val	asn			---	---	---				53	6	18 (TRP)
	35B	gly	gly				gly	arg			---	---	---				27	5	12 (ASN)
	36	TRP	TRP				TRP	TRP			---	---	---				52	2	51 (TRP)
	37	ILE	ILE				ILE	ILE			---	---	---				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	3	36 (PRO)
	41	PRO	PRO				PRO	PRO			---	---	---				51	3	50 (PRO)
	42	gly	gly				gly	gly			---	---	---				51	2	39 (GLY)
	43	lys	lys				lys	lys			---	---	---				51	3	30 (LYS)
	44	ala	ala				LEU	LEU			---	---	---				51	2	44 (GLY)
	45	LEU	LEU				LEU	LEU			---	---	---				51	2	49 (LEU)
	46	GLU	GLU				GLU	GLU			---	---	---				51	1	51 (GLU)
	47	TRP	TRP				ser	TRP			---	---	---				51	2	50 (TRP)
	48	LEU	ile				val	ile			---	---	---				51	3	31 (ILE)
	49	ala	GLY				ala	GLY			---	---	---				51	2	43 (GLY)
	50	phe	tyr				leu	glu			---	---	---				51	6	18 (ARG)
	51	ile	ile				ile	THR			---	---	---				51	2	34 (ILE)
	52	asn	TYR				asn	asn			---	---	---				51	2	29 (TYR)
	52A	---	---				---	---			---	---	---				17	3	13 (TYR)
	52B	---	---				---	---			---	---	---				13	3	11 (ARG)
	52C	---	---				---	---			---	---	---				1	1	1 (ALA)
	53	trp	tyr				trp	tyr			---	---	---				51	10,11	14 (TYR)
	54	asp	ser				asp	arg			---	---	---				51	8	23 (SER)
	55	asp	gly				asp	gly			---	---	---				51	4	28 (GLY)
	56	asp	ser				asp	arg			---	---	---				51	4	19 (SER)
	57	ASN	thr				lys	val			---	---	---				51	2	26 (THR)
	58	arg	asn				lys	thr			---	---	---				51	10	13 (+)
	59	TYR	TYR				TYR	TYR			---	---	---				51	6	45 (TYR)
	60	ser	asn				ser	asn			---	---	---				51	6,7	27 (ASN), 26 (ASN)
	61	pro	pro				pro	pro			---	---	---				51	6	30 (PRO)
	62	SER	SER				SER	SER			---	---	---				51	4	46 (SER)
	63	leu	leu				leu	leu			---	---	---				52	3	36 (LEU)
	64	arg	LYS				lys	thr			---	---	---				52	5	37 (LYS)
	65	SER	SER				SER	SER			---	---	---				52	3	43 (SER)
	66	ARG	ARG				ARG	ARG			---	---	---				52	1	52 (ARG)
	67	leu	val				val	val			---	---	---				52	4	30 (VAL)
	68	THR	THR				THR	THR			---	---	---				52	4	49 (THR)
	69	gly	ILE				ILE	ILE			---	---	---				52	5	38 (ILE)
	70	thr	ser				ser	thr			---	---	---				52	4	30 (SER)
	71	lys	val				lys	val			---	---	---				52	6	28 (VAL)
	72	ASP	ASP				ASP	ASP			---	---	---				52	2	51 (ASP)
	73	THR	THR				THR	THR			---	---	---				52	2	47 (THR)
	74	SER	SER				SER	SER			---	---	---				52	2	51 (SER)
	75	arg	LYS				lys	lys			---	---	---				52	3	48 (LYS)
	76	ASN	ASN				ASN	ASN			---	---	---				52	3	52 (ASN)
	77	GLN	GLN				GLN	GLN			---	---	---				52	4	49 (GLN)
	78	val	PHE				val	PHE			---	---	---				52	2	43 (PHE)
	79	val	SER				val	SER			---	---	---				52	4	41 (SER)
	80	LEU	LEU				LEU	LEU			---	---	---				52	1	52 (LEU)
	81	thr	lys				thr	lys			---	---	---				52	8	22 (LYS)
	82	ile	LEU				met	lys			---	---	---				52	4	42 (LEU)
	82A	thr	ser				thr	thr			---	---	---				51	2	22 (SER)
	82B	asn	SER				asn	SER			---	---	---				50	3	42 (SER)
	82C	met	VAL				met	VAL			---	---	---				52	3	43 (VAL)
	83	asp	THR				asp	THR			---	---	---				53	5	42 (THR)
	84	PRO	ala				ala	ala			---	---	---				53	3	30 (ALA)
	85	val	ala				ala	ala			---	---	---				53	4	30 (ALA)
	86	ASP	ASP				thr	ASP			---	---	---				53	2	52 (ASP)
	87	ser	THR				glu	THR			---	---	---				53	3	49 (THR)
	88	gly	ALA				pro	ALA			---	---	---				53	3	50 (ALA)
	89	chr	VAL				his	ile			---	---	---				53	3	41 (VAL)
	90	TYR	TYR				ile	TYR			---	---	---				53	2	52 (TYR)
	91	phe	TYR				thr	TYR			---	---	---				53	4	46 (TYR)
	92	CYS	CYS				met	CYS			---	---	---				53	2	52 (CYS)
	93	ALA	ALA				his	ALA			---	---	---				53	5	48 (ALA)
	94	his	ARG				thr	ARG			---	---	---				52	4	45 (ARG)
	95	ARG	GLU				ASP	CYS			---	---	---				42	15	9 (GLU)
	96	PRO	GLY				VAL	ALA			---	---	---				41	15	7 (LEU)
	97	PRO	ALA				PRO	CYS			---	---	---				41	16	6 (PRO)
	98	TRP	TRP				LEU	ILE			---	---	---				41	13	7 (GLY)
	99	ARG	GLY				TYR	ALA			---	---	---				38	13	8 (GLY)
	100	PHE																	

0	
1	5.2, 5.4
2	4.7
3	7.8
4	2.
5	7.9, 8.1
6	3.3, 3.1
7	3.4
8	2.
9	3.4
10	3.6
11	1.
12	2.2
13	2.4
14	2.
15	5.2
16	3.2
17	1.1
18	2.1
19	3.8
20	2.
21	2.1
22	1.
23	15.
24	8.4
25	3.5
26	2.
27	16.
28	4.9
29	11.
30	4.3
31	14.
32	50.
33	30.
34	25.
35	46.
35A	
35B	
36	2.
37	5.2
38	1.
39	3.1
40	7.1
41	2.
42	2.6
43	5.1
44	2.3
45	2.1
46	1.
47	2.
48	4.9
49	2.4
50	25.
51	7.5
52	14.
52A	
52B	
52C	
53	36., 40.
54	18.
55	7.3
56	21.
57	16.
58	39.
59	6.8
60	11., 14.
61	10.
62	4.4
63	4.3
64	7.
65	3.6
66	1.
67	6.9
68	3.2
69	6.8
70	6.9
71	11.
72	2.
73	5.5
74	2.
75	3.2
76	1.
77	4.2
78	2.4
79	5.1
80	1.
81	19.
82	5.
82A	
82B	
82C	
83	6.3
84	5.3
85	7.1
86	2.
87	3.2
88	3.2
89	6.5
90	2.
91	4.6
92	2.
93	5.5
94	4.6
95	70.
96	88.
97	110.
98	76.
99	57.
100	87.
100A	
100B	
100C	
100D	
100E	
100F	
100G	
100H	
100I	
100J	
100K	
101	6.5
102	19.
103	3.2
104	1.
105	6.5
106	1.
107	3.5
108	15.
109	2.1
110	4.4
111	2.1
112	2.1
113	2.

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) Ab44'CL: POLYREACTIVE AUTOANTIBODY
- 30) Fog-B'CL: ANTI-D ANTIGEN OF THE Rh-BLOOD-GROUP SYSTEM
- 32) HuVBCAMP'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) Ab44'CL: IGA-LAMBDA
- 30) Fog-B'CL: IGG1-LAMBDA
- 32) HuVBCAMP'CL: IGG1-KAPPA
- 34) NEMM: IGG1-LAMBDA
- 35) GER: IGG-KAPPA
- 37) WAH: IGD-LAMBDA
- 39) LES-C'CL: IGM-
- 40) COR: IGG1-
- 43) DAW: IGG1-LAMBDA
- 44) HE: IGG1-
- 45) OU: IGM-KAPPA
- 46) MCE': 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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- 14) C6B2'CL: HOCH, S. & SCHWABER, J. (1987) J.IMMUNOL., 139, 1689-1693.
- 15) 71-4'CL: KODAIRA, M., KINASHI, T., UMEMURA, I., MATSUDA, F., NOMA, T., ONO, Y. & HONJO, T. (1986) J.MOL.BIOL., 190, 529-541.
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- 26) 79'CL: LEE, K.H., MATSUDA, F., KINASHI, T., KODAIRA, M. & HONJO, T. (1987) J.MOL.BIOL., 195, 761-768.
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- 29) Ab44'CL: SANZ, I., CASALI, P., THOMAS, J.W., NOTKINS, A.L. & CAPRA, J.D. (1989) J.IMMUNOL., 142, 4054-4061.
- 30) Fog-B'CL: HUGHES-JONES, N.C., BYE, J.M., BEALE, D. & COADWELL, J. (1990) BIOCHEM.J., 268, 135-140.
- 31) TS2'CL: SHEN, A., HUMPHRIES, C., TUCKER, P. & BLATTNER, F. (1987) PROC.NATL.ACAD.SCI.USA, 84, 8563-8567.
- 32) HuVBCAMP'CL: RECHMANN, L., CLARK, M., WALLMANN, H. & WINTER, G. (1988) NATURE, 332, 323-327.

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: MLI'CL[3],DR12910-2P8'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],NEI'CL[16],WIL2'CL[24],BOR'CL[27],LS7'CL[29]; 17 HUMAN V-H-III: 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],K6B6'CL[68],K4B8'CL[69],K5B8'CL[70],K5C7'CL[71],K5G5'CL[72],K6F5'CL[73],Z0P1'CL[82]; AND 1 MOUSE V-H-III: E57-40'CL[23].)
- 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-TS1'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[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],HIGL'CL[24],Ab44'CL[29]. (3 IDENTICAL HUMAN V-H-II; ALSO 5 HUMAN V-H-I: 783c'CL[21],X1715'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: Ab19'CL[11].)
- SET 6: 15P1'CL[11]. (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],BF2-1/17[7],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 NEW 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 ETAINS 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) Ly56'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)
58	(TYR, ASP, ASN)
100A	(ILE, PHE, CYS, ALA, SER, GLY)
100H	(ALA, ASP)
100I	(ALA, ASN)

HUMAN HEAVY CHAINS SUBGROUP III (cont'd)

	43*	44	45*	46*	47*	48*	49	51*	52	53	54	55	56	57	58	59*	60	62	62	63	64	65	66	67	68		
	3D6	1-91	POM	RF-SJ1	WEA	4B4	M26	9-1	LAY	BUR	KOL	TEI	12-2	HIL	TRO	WAS	TUR	NIE	GAL	DOB	VH10.7	ZAP	JON	GA	GRA	K6H6	
	'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	'CL	
0																											
1	GLU	GLU	GLU	gln	pca	GLU	GLU	GLU	ala	pca	pca	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	gln	GLU	asp	pca	GLU	GLU	
2	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	VAL	VAL
3	LEU	his	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLX	GLN	arg	
4	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	LEU	
5	val	LEU	LEU	val	val	val	val	val	LEU	val	val	val	val	val	LEU	LEU	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	GLX	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	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	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	GLY	GLY	
10	LEU	asp	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	asp	asp	GLY	ala	GLY	GLY	
11	LEU	LEU	LEU	val	val	val	val	val	val	val	val	val	val	val	LEU	LEU	val	val	val	val	val	val	LEU	LEU	LEU	LEU	
12	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	VAL	
13	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	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	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	GLY	GLY	GLY	
16	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	SER	
17	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	LEU	
18	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	LEU	
19	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	
20	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	LEU	
21	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	SER	
22	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	SER	
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	CYS	
24	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	ALA	
25	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	SER	
26	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	
27	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	
28	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	THR	
29	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	
30	asn	asn	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	
31	asp	asn	SER	SER	ala	asn	asn	asn	ala	asp	asp	thr	thr	thr	thr	thr	thr	thr	thr	thr	thr	thr	thr	thr	thr	lys	
32	THR	his	SER	SER	asn	ala	ala	ala	ala	thr	thr	thr	thr	thr	thr	thr	thr	thr	thr	thr	thr	thr	thr	thr	thr	lys	
33	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	ala	
34	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	THR	
35	his	thr	SER	his	asn	SER	SER	SER	his	tyr	tyr	asp	his	SER	tyr	SER	his	thr	his	his	his	phe	lys	his	gln	asn	
35A	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
35B	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
36	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	TRP	
37	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	VAL	
38	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	
39	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	GLN	
40	ALA	ALA	ALA	cys	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	
41	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	PRO	
42	arg	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	
43	LEU	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys	
44	LEU	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	
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	LEU	
46	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	
47	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	TRP	
48	VAL	VAL	VAL	ala	leu	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	
49	SER	SER	SER	ala	SER	gln	gln	gln	ala	ala	ala	gln	ala	SER	ala	SER	ala	ala	SER	ala	SER	ala	SER	ala	SER	thr	
50	gln	thr	trp	val	phe	arg	arg	arg	trp	leu	ile	trp	arg	val	trp	gln	asn	thr	thr	thr	thr	thr	thr	thr	thr	gln	
51	ILE	THR	TRP	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	
52	SER	asp	tyr	ser	gln	lys	lys	lys	tyr	SER	trp	tyr	arg	trp	gln	lys	thr	thr	thr	thr	thr	thr	thr	thr	thr	lys	
52A	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
52B	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
53	asp	SER	asn	SER	SER	asp	asn	gln																			

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																				
1	GLU	GLU	GLU	asp	GLU	leu	GLU	gly	gly	pca	pca	pca	pca	172	7			136 (GLU)	8.9	
2	VAL	VAL	VAL	ile	VAL	VAL	VAL	phe	VAL	ser	ser	ser	ser	174	7			158 (VAL)	7.7	
3	GLN	GLN	glu	GLN	his	arg	GLN	GLN	GLN	val	ala	val	val	177	8	148	(GLN), 147 (GLN)	149 (GLU), 146 (GLU)	9.3, 9.4	
4	LEU	LEU	LEU	LEU			LEU	asp	LEU	LEU	LEU	LEU	LEU	172	5			163 (LEU)	5.2	
5	ala	val	val	val	val	val	asn			asx	gly			172	6, 8			129 (VAL)	8.1, 11	
6	GLU	GLU	glu	GLU			arg							164	3			155 (SER)	5.3, 5.6	
7	SER	SER	SER	SER			thr							158	3			162 (GLY)	3.1	
8	GLY	GLY	GLY	GLY			thr							163	2			169 (GLY)	2	
9	GLY	GLY	GLY	GLY	GLY	ala	glu							171	3			131 (GLY)	6.4, 7.7	
10		ala	GLY	GLY	asp	GLY	glx							168	5, 6			131 (LEU)	5.1	
11		LEU	LEU	LEU	LEU	val	val							167	4			154 (VAL)	3.2	
12			VAL	VAL	GLN	GLN								144	7	106	(GLN), 101 (GLN)	142 (PRO)	9.5, 10	
13					GLN	PRO	PRO							148	5			139 (GLY)	5.2	
14														141	3			116 (GLY)	3	
15														143	4			131 (SER)	6.2	
16					GLY	ser								136	5			141 (LEU)	5.2	
17						val								146	5			124 (ARG)	5.2	
18														140	4			131 (LEU)	4.5	
19														143	4			111 (SER)	4.4	
20						val								116	5			116 (CYS)	5.2	
21														117	2			107 (ALA)	2	
22						ALA								128	8, 9			116 (ALA)	9.6, 11.1	
23						ALA								132	5			122 (SER)	5.7	
24														124	3			117 (GLY)	3	
25														124	6			109 (PHE)	6.4	
26														112	2			75 (THR)	4.1	
27														104	9			97 (PHE)	12.1	
28														108	6			90 (SER)	6.7	
29														103	9, 10				10., 11.	
30														100	11			35 (SER)	31	
31														103	10			55 (TYR)	19	
32														98	13			35 (ALA)	36	
33														101	7			85 (MET)	8.3	
34														97	12			39 (SER)	30	
35																				
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	7			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), 73 (GLU)	85 (TRP)	3.3, 3.5	
47														85	1				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	2			8 (THR)		
53														85	12	31	(ASP), 26 (ASP)	56 (GLY)	33., 39.	
54														84	9				13	
55														83	10			37 (GLY)	22	
56														83	13			20 (SER)	54	
57														85	5			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)	71 (SER)	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														85	8			68 (LEU)	9.9	
79														85	4			74 (TYR)	4.6	
80														85	3			81 (LEU)	3.1	
81														85	6			77 (GLN), 75 (GLN)	6.6, 6.8	
82														92	2			89 (MET)	2.1	
82A														93	3			71 (ASN), 68 (ASN)		
82B														93	7			76 (SER)		
82C														93	4			89 (LEU)		
83														93	6			71 (ARG)	7.9	
84														94	8			55 (ALA)	14.	
85														94	4, 5			81 (GLU), 76 (GLU)	4.6, 6.2	
86														94	3			91 (ASP), 85 (ASP)	3.1, 3.3	
87														94	5			88 (THR)	5.3	
88														94	3			89 (ALA)	3.2	
89														94	7			77 (VAL)	6.5	
90														95	3			93 (TYR)	3.1	
91														95	3			92 (TYR)	3.1	
92														94	1			94 (CYS)	1.	
93														94	4			70 (ALA)	5.4	
94														95	11			31 (ARG)	34.	
95														79	17	15	(+), 15 (GLY)		90.	
96														80	18, 19			14 (ARG)	100., 110.	
97														77	18			12 (+)	120.	
98	SER													76	18			11 (GLY)	120.	
99	ASP													74	14			11 (+)	94.	
100	TYR													73	16			14 (SER)	83.	
100A	HIS													64	17			15 (LEU)		
100B	TYR													51	12			13 (SER)		
100C	TYR													42	13			9 (GLY)		

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-PHOSPHOCHOLINE (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(+/-): 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.TR.: 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) GOEII: 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) CRM': 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) VELO.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) LRI'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) HIN: IGA1-KAPPA
 155) KMI: IGA1-KAPPA
 156) SEE: 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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- 1) 18/2'CL: DERSIMONIAN, H., SCHWARTZ, R.S., BARRETT, K.J. & STOLLAR, B.D. (1987) J. IMMUNOL., 139, 2496-2501; CHEN, P.P., LIU, M.-F., SINHA, S. & CARSON, D.A. (1988) ARTH. RHEUM., 31, 1429-1431.
- 2) 18/17'CL: DERSIMONIAN, H., SCHWARTZ, R.S., BARRETT, K.J. & STOLLAR, B.D. (1987) J. IMMUNOL., 139, 2496-2501.
- 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.
- 6) M43'CL: SCHROEDER, H.W., JR. & WANG, J.Y. (1990) PROC. NATL. ACAD. SCI. USA, 87, 6146-6150.
- 7) H22-1/17: 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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- 9) LAMBDA-VH26'CL: RABBITTS, T.H., BENTLEY, D.L., DUNNICK, W., FORSTER, A., MATTHYSSENS, G. & MILSTEIN, C. (1980) COLD SPRING HARB. SYMP. QUANT. BIOL., 45, 887-898; MATTHYSSENS, G. & RABBITTS, T.H. (1980) PROC. NATL. ACAD. SCI. USA, 77, 6561-6565. (CHECKED BY AUTHOR 12/09/80)
- 10) 4G12'CL: KISHIMOTO, T., OKAJIMA, H., OKUMOTO, T. & TANIGUCHI, M. (1989) NUCL. ACIDS RES., 17, 4385.
- 11) Ab18'CL: SANZ, I., CASALI, P., THOMAS, J.W., NOTKINS, A.L. & CAPRA, J.D. (1989) J. IMMUNOL., 142, 4054-4061.
- 12) Ab25'CL: SANZ, I., CASALI, P., THOMAS, J.W., NOTKINS, A.L. & CAPRA, J.D. (1989) J. IMMUNOL., 142, 4054-4061.
- 13) RF-KL1'CL: PASCUAL, V., RANDEN, I., THOMPSON, K., SLOUD, M., FORRE, O., NATVIG, J. & CAPRA, J.D. (1990) J. CLIN. INVEST., 86, 1320-1328.
- 14) 8-1B'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.
- 15) vh38cl.10'CL: MEEKER, T.C., GRIMALDI, J., O'ROURKE, R., LOEB, J., JULIUSSON, G. & EINHORN, S. (1988) J. IMMOL., 141, 3994-3998.

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- 17) **Vh38Cl.9'CL**: MEEKER, T.C., GRIMALDI, J., O'ROURKE, R., LOEB, J. JULIUSSON, G. & EINHORN, S. (1988) J. IMMOL., 141, 3994-3998.
- 18) **60P2'CL**: SCHROEDER, H.W., JR., HILLSON, J.L. & PERLMUTTER, R.M. (1987) SCIENCE, 238, 791-793.
- 19) **63P1'CL**: SCHROEDER, H.W., JR., HILLSON, J.L. & PERLMUTTER, R.M. (1987) SCIENCE, 238, 791-793.
- 20) **GE4/1.1'CL**: GILLIES, S.D., DORAI, H., WESOLOWSKI, J., MAJEAU, G., YOUNG, D., BOYD, J., GARDNER, J. & JAMES, K. (1989) BIO/TECH., 7, 799-804.
- 21) **Vh38Cl.4'CL**: MEEKER, T.C., GRIMALDI, J., O'ROURKE, R., LOEB, J. JULIUSSON, G. & EINHORN, S. (1988) J. IMMOL., 141, 3994-3998.
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- 24) **Ab21'CL**: SANZ, I., CASALI, P., THOMAS, J.W., NOTKINS, A.L. & CAPRA, J.D. (1989) J. IMMUNOL., 142, 4054-4061.
- 25) **56P1'CL**: SCHROEDER, H.W., JR., HILLSON, J.L. & PERLMUTTER, R.M. (1987) SCIENCE, 238, 791-793.
- 26) **2P1'CL**: SCHROEDER, H.W., JR., HILLSON, J.L. & PERLMUTTER, R.M. (1987) SCIENCE, 238, 791-793.
- 27) **M72'CL**: SCHROEDER, H.W., JR. & WANG, J.Y. (1990) PROC. NATL. ACAD. SCI. USA, 87, 6146-6150.
- 28) **M74'CL**: SCHROEDER, H.W., JR. & WANG, J.Y. (1990) PROC. NATL. ACAD. SCI. USA, 87, 6146-6150.
- 29) **KIM46H'CL**: CAIRNS, E., KWONG, P.C., MISENER, V., IP, P., BELL, D.A. & SIMINOVITCH, K.A. (1989) J. IMMUNOL., 143, 685-691.
- 30) **1-9111'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.
- 31) **RF-SJ2'CL**: PASCUAL, V., RANDEN, I., THOMPSON, K., SIOUD, M., FORRE, O., NATVIG, J. & CAPRA, J.D. (1990) J. CLIN. INVEST., 86, 1320-1328.
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- 34) **FL2-2'CL**: NICKERSON, K.G., BERMAN, J., GLICKMAN, E., CHESS, L. & ALT, F.W. (1989) J. EXP. MED., 169, 1391-1403.
- 35) **v65-4'CL**: MATSUDA, F., SHIN, E.K., HIRABAYASHI, Y., NAGAOKA, H., YOSHIDA, M.C., ZONG, S.Q. & HONJO, T. (1990) EMBO J., 9, 2501-2506.
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- 39) **BUT**: TORANO, A. & PUTNAM, F.W. (1978) PROC. NAT. ACAD. SCI. USA, 75, 966-969. (CHECKED BY AUTHOR 06/15/83)
- 40) **CAM'**: LEHMAN, D. & PUTNAM, F.W. (1980) PROC. NAT. ACAD. SCI. USA, 77, 3239-3243. (CHECKED BY AUTHOR 05/01/80)
- 41) **HN.14'CL**: DESAI, R., SPATZ, L., MATSUDA, T., ILYAS, A.A., BERMAN, J.E., ALT, F.W., KABAT, E.A. & LATOV, N. (1990) J. NEUROIMMUNOL., 26, 35-41. (CHECKED BY AUTHORS WHO CORRECTED RESIDUES 44 TO 47 AS SHOWN; SEE DESAI, R., SPATZ, L., MATSUDA, T., ILYAS, A.A., BERMAN, J.E., ALT, F.W., KABAT, E.A. & LATOV, N. (1990) J. NEUROIMMUNOL., 30, 245.)
- 42) **RF-TS2'CL**: PASCUAL, V., RANDEN, I., THOMPSON, K., SIOUD, M., FORRE, O., NATVIG, J. & CAPRA, J.D. (1990) J. CLIN. INVEST., 86, 1320-1328.
- 43) **3D6'CL**: FELGENHAUER, M., KOHL, J. & RUKER, F. (1990) NUCL. ACIDS RES., 18, 4927.
- 44) **1-91'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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- 48) **4B4'CL**: SANZ, I., DANG, H., TAKEI, M., TALAL, N. & CAPRA, J.D. (1989) J. IMMUNOL., 142, 883-887.
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- 50) **9-1'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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- 53) **KOL**: SCHMIDT, W.E., JUNG, H.-D., PALM, W. & HILSCHMANN, N. (1983) Z. PHYSIOL. CHEM., 364, 713-747.
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- 55) **12-2'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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- 57) **PRO**: KRATZ, H., ALTMANN, R., RUBAN, E., KORTT, A., STAROSCIK, K., HILSCHMANN, N. (1975) Z. PHYSIOL. CHEM., 359, 1337-1342; KRATZ, H., ALTMANN, R., RUBAN, E., KORTT, A., STAROSCIK, K., HILSCHMANN, N. (1978) Z. PHYSIOL. CHEM., 359, 1337-1342.
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- 60) **NIE**: PONSTINGL, H., SCHWARZ, J., REICHEL, W. & HILSCHMANN, N. (1970) Z. PHYSIOL. CHEM., 351, 1591-1594. (CHECKED BY AUTHOR WHO CORRECTED RESIDUES 85, 86 AS GIVEN IN TABLE); PONSTINGL, H. & HILSCHMANN, N. (1976) Z. PHYSIOL. CHEM., 357, 1571-1604.
- 61) **GAL**: WATANABE, S., BARNIKOL, H.U., HORN, J., BERTRAM, J. & HILSCHMANN, N. (1973) Z. PHYSIOL. CHEM., 354, 1505-1509. (CHECKED BY AUTHOR)
- 62) **DOB**: STEINER, L.A., GARCIA-PARDO, A. & MARGOLIES, M.N. (1979) BIOCHEMISTRY, 18, 4068-4080. (CHECKED BY AUTHOR 07/20/79)
- 63) **VB10.7'CL**: WHITE, M.B., WORD, C.J., HUMPHRIES, C.G., BLATTNER, F.R. & TUCKER, P.W. (1990) MOL. CELL. BIOL., 10, 3690-3699.
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- 66) **GA**: FLORENT, G., LEHMAN, D. & PUTNAM, F.W. (1974) BIOCHEMISTRY, 13, 2482-2498. (CHECKED BY AUTHOR 06/15/83)
- 67) **GRA'**: CAPRA, J.D. (1977) IN ANTIBODIES IN HUMAN DIAGNOSIS AND THERAPY, RAVEN PRESS, NEW YORK, 87-102. (CHECKED BY AUTHOR 03/18/81)
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- 70) **K5B9'CL**: KON, S., LEVY, S. & LEVY, R. (1987) PROC. NATL. ACAD. SCI. USA, 84, 5053-5057.
- 71) **K5C7'CL**: KON, S., LEVY, S. & LEVY, R. (1987) PROC. NATL. ACAD. SCI. USA, 84, 5053-5057.
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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: Vh38CL.10'CL[15],Vh38CL.8'CL[16],Vh38CL.9'CL[17],Vh38CL.4'CL[21],Vh38CL.5'CL[22]. (5 IDENTICAL)
 SET 4: 56P1'CL[25],2P1'CL[26],M72'CL[27],M74'CL[28],KIM46H'CL[29],1-9I11'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: Vh38CL.10'CL[15],Vh38CL.8'CL[16],Vh38CL.9'CL[17],Vh38CL.4'CL[21],Vh38CL.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: LS2'CL[1],LS5'CL[2],LS6'CL[3],LS1'CL[4],LS8'CL[6],NE1'CL[16],W112'CL[24],BOR'CL[27],67'CL[29], 4 HUMAN V-H-II: ML1'CL[3],DR12910-2F8'CL[48],Ab17'CL[49],M44'CL[52]; AND 1 MOUSE V-H-III: H37-40'CL[55].)
 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: L.6'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: 786'CL[21],M715'CL[22],EV1-15'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: Vh38CL.10'CL[15],Vh38CL.8'CL[16],Vh38CL.9'CL[17],Vh38CL.4'CL[21],Vh38CL.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.
- 9) LAMBDA-VH26'CL: THE SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF HUMAN FETAL LIVER DNA. TWO OTHER CLONES HAVE SLIGHTLY 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 MOPCI67 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) LRI'CL: THE REGION NOT SEQUENCED CONSISTED OF A LARGE DELETION. THIS HEAVY CHAIN IS EXPRESSED ON THE CELL SURFACE WITHOUT LIGHT CHAIN. LRI 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) SMM-TGA: 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) Lw2'CL: THE REGION NOT SEQUENCED CONSISTED OF A LARGE DELETION. THIS HEAVY CHAIN IS EXPRESSED ON THE CELL SURFACE WITHOUT LIGHT CHAIN. Lw2 IS AN EPV-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:

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