



**SEQUENCES OF
PROTEINS OF
IMMUNOLOGICAL
INTEREST**

16
S477
1991
v.1

FIFTH EDITION

B.M.L.

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

1991

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**U.S. DEPARTMENT OF HEALTH
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Public Health Service
National Institutes of Health

NIH Publication No. 91-3242

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MOUSE B-CHAIN E-LOCUS OF THE BETA-2 REGION.....1764
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MOUSE.....1948

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MOUSE BETA CHAIN.....1959
MOUSE DELTA CHAIN.....1961

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HUMAN KAPPA.....1963
HUMAN LAMBDA.....1965

MOUSE KAPPA.....1967
MOUSE LAMBDA.....1969

RAT KAPPA.....1971
RAT LAMBDA.....1973

RABBIT KAPPA.....1975

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HUMAN GAMMA CHAIN.....	1997
HUMAN DELTA CHAIN.....	1999
MOUSE ALPHA CHAIN.....	2001
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	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	PRO				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					45	4,5	29 (GLU), 28 (GLU)	6.2,8.
106					46	7	30 (ILE)	11.
106A								
107					45	3	42 (LYS)	3.2
108					33	2	31 (ARG)	2.1
109					22	1	22 (THR)	1.

ANTIBODY SPECIFICITIES: HUMAN KAPPA LIGHT CHAINS SUBGROUP I

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

ALLOTYPE: HUMAN KAPPA LIGHT CHAINS SUBGROUP I

- 14) 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

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- 43) AG: TITANI, K., SHINODA, T. & PUTNAM, F. W. (1969) J. BIOL. CHEM., 244, 3550-3560. (CHECKED BY AUTHOR 06/15/83)
- 44) SCW: EULITZ, M., GOTZE, D. & HILSCHMANN, N. (1972) Z. PHYSIOL. CHEM., 353, 487-491; EULITZ, M. & HILSCHMANN, N. (1974) Z. PHYSIOL. CHEM., 355, 842-866. (CHECKED BY AUTHOR)
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- 101) **H-G2b**: SCOTT, M.G., TARRAND, J.J., CRIMMINS, D.L., MCCOURT, D.W., SIEGEL, N.R., SMITH, C.E. AND NAHM, M.H. (1989) J.IMMUNOL., 143, 293-298.
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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],HAH 14.2'CL[8],HAH 16.1'CL[9],NOV'CL[10],HIC(R)'CL[11],PAY[15],BOR[17],HEW'CL[18], ROB'CL[19],BR'CL[21],HAG'CL[22],HIC'CL[24],WOL[31],EVI-15'CL[32],GOL[33],Taykv322'CL[54],GF4/1.1'CL[54], REE[56],HAH(R)'CL[73],VKAPPA3'CL[85]; AND 1 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(N2B)[46],vkl-B'CL[51],PC2567(N2B)[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],VKAPPA3'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],HAH 14.2'CL[8],HAH 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

	INVARIANT RESIDUES	1* L2	2* L5	3* L6	4* L1	5* L4	6* L8	7 B9/F2	8 21-2	9 3-1	10* 21/28	11* 8E10	12 HG3	13 V35	14 51P1	15 AND	16 NEI	17 HP1	18 E3-10	19 1-92	20 hv1263	21 783c	22 X17115
		'CL	'CL	'CL	'CL	'CL	'CL	#	'CL	'CL	'CL	'CL	'CL	'CL	'CL	'CL	'CL	'CL	'CL	'CL	'CL	'CL	'CL
0																							
1		GLN	VAL	VAL	GLN	GLN	GLN		GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN
2		VAL	VAL	VAL	VAL	VAL	VAL		ile	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
3		GLN	GLN	GLN	GLN	GLN	GLN		GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN
4	LEU (.98)	LEU	LEU	LEU	LEU	LEU	LEU		LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
5		VAL	VAL	VAL	VAL	VAL	VAL		VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
6		ALA	ALA	ALA	ALA	ALA	ALA		ala	ala	ala	ala	ala	ala	ala	ala	ala	ala	ala	ala	ala	ala	ala
7	SER	SER	SER	SER	SER	SER	SER		ser	ser	ser	ser	ser	ser	ser	ser	ser	ser	ser	ser	ser	ser	ser
8	GLY (.98)	GLY	GLY	GLY	GLY	GLY	GLY		gly	gly	gly	gly	gly	gly	gly	gly	gly	gly	gly	gly	gly	gly	gly
9		ALA	ALA	ALA	ALA	ALA	ALA		ala	ala	ala	ala	ala	ala	ala	ala	ala	ala	ala	ala	ala	ala	ala
10		GLU	GLU	GLU	GLU	GLU	GLU		glu	glu	glu	glu	glu	glu	glu	glu	glu	glu	glu	glu	glu	glu	glu
11		VAL	VAL	VAL	VAL	VAL	VAL		val	val	val	val	val	val	val	val	val	val	val	val	val	val	val
12	LYS (.98)	ASN	ASN	ASN	ASN	ASN	ASN		lys	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys
13	PRO (.98)	LYS	LYS	LYS	LYS	LYS	LYS		pro	pro	pro	pro	pro	pro	pro	pro	pro	pro	pro	pro	pro	pro	pro
14	GLY (.96)	GLY	GLY	GLY	GLY	GLY	GLY		gly	gly	gly	gly	gly	gly	gly	gly	gly	gly	gly	gly	gly	gly	gly
15		ALA	ALA	ALA	ALA	ALA	ALA		ala	ala	ala	ala	ala	ala	ala	ala	ala	ala	ala	ala	ala	ala	ala
16	SER (.98)	SER	SER	SER	SER	SER	SER		ser	ser	ser	ser	ser	ser	ser	ser	ser	ser	ser	ser	ser	ser	ser
17		VAL	VAL	VAL	VAL	VAL	VAL		val	val	val	val	val	val	val	val	val	val	val	val	val	val	val
18		LYS	LYS	LYS	LYS	LYS	LYS		lys	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys
19		VAL	VAL	VAL	VAL	VAL	VAL		val	val	val	val	val	val	val	val	val	val	val	val	val	val	val
20	CYS (.98)	SER	SER	SER	SER	SER	SER		ser	ser	ser	ser	ser	ser	ser	ser	ser	ser	ser	ser	ser	ser	ser
21		CYS	CYS	CYS	CYS	CYS	CYS		cys	cys	cys	cys	cys	cys	cys	cys	cys	cys	cys	cys	cys	cys	cys
22		ALA	ALA	ALA	ALA	ALA	ALA		ala	ala	ala	ala	ala	ala	ala	ala	ala	ala	ala	ala	ala	ala	ala
23		SER	SER	SER	SER	SER	SER		ser	ser	ser	ser	ser	ser	ser	ser	ser	ser	ser	ser	ser	ser	ser
24		TYR	TYR	TYR	TYR	TYR	TYR		tyr	tyr	tyr	tyr	tyr	tyr	tyr	tyr	tyr	tyr	tyr	tyr	tyr	tyr	tyr
25	SER (.96)	SER	SER	SER	SER	SER	SER		ser	ser	ser	ser	ser	ser	ser	ser	ser	ser	ser	ser	ser	ser	ser
26	GLY (.96)	GLY	GLY	GLY	GLY	GLY	GLY		gly	gly	gly	gly	gly	gly	gly	gly	gly	gly	gly	gly	gly	gly	gly
27		THR	THR	THR	THR	THR	THR		thr	thr	thr	thr	thr	thr	thr	thr	thr	thr	thr	thr	thr	thr	thr
28	PHE (.96)	PHE	PHE	PHE	PHE	PHE	PHE		phe	phe	phe	phe	phe	phe	phe	phe	phe	phe	phe	phe	phe	phe	phe
29		THR	THR	THR	THR	THR	THR		thr	thr	thr	thr	thr	thr	thr	thr	thr	thr	thr	thr	thr	thr	thr
30		SER	SER	SER	SER	SER	SER		ser	ser	ser	ser	ser	ser	ser	ser	ser	ser	ser	ser	ser	ser	ser
31		TYR	TYR	TYR	TYR	TYR	TYR		tyr	tyr	tyr	tyr	tyr	tyr	tyr	tyr	tyr	tyr	tyr	tyr	tyr	tyr	tyr
32		GLY	GLY	GLY	GLY	GLY	GLY		gly	gly	gly	gly	gly	gly	gly	gly	gly	gly	gly	gly	gly	gly	gly
33		ILE	ILE	ILE	ILE	ILE	ILE		ile	ile	ile	ile	ile	ile	ile	ile	ile	ile	ile	ile	ile	ile	ile
34		MET	MET	MET	MET	MET	MET		met	met	met	met	met	met	met	met	met	met	met	met	met	met	met
35		SER	SER	SER	SER	SER	SER		ser	ser	ser	ser	ser	ser	ser	ser	ser	ser	ser	ser	ser	ser	ser
35A		---	---	---	---	---	---		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
35B		---	---	---	---	---	---		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
36	TRP (.98)	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
38	ARG (.98)	ARG	ARG	ARG	ARG	ARG	ARG		arg	arg	arg	arg	arg	arg	arg	arg	arg	arg	arg	arg	arg	arg	arg
39	GLN (.98)	GLN	GLN	GLN	GLN	GLN	GLN		glu	glu	glu	glu	glu	glu	glu	glu	glu	glu	glu	glu	glu	glu	glu
40		ALA	ALA	ALA	ALA	ALA	ALA		ala	ala	ala	ala	ala	ala	ala	ala	ala	ala	ala	ala	ala	ala	ala
41	PRO (.98)	PRO	PRO	PRO	PRO	PRO	PRO		pro	pro	pro	pro	pro	pro	pro	pro	pro	pro	pro	pro	pro	pro	pro
42	GLY (.98)	GLY	GLY	GLY	GLY	GLY	GLY		gly	gly	gly	gly	gly	gly	gly	gly	gly	gly	gly	gly	gly	gly	gly
43		GLN	GLN	GLN	GLN	GLN	GLN		glu	glu	glu	glu	glu	glu	glu	glu	glu	glu	glu	glu	glu	glu	glu
44		GLY	GLY	GLY	GLY	GLY	GLY		arg	arg	arg	arg	arg	arg	arg	arg	arg	arg	arg	arg	arg	arg	arg
45	LEU (.98)	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
47	TRP (.98)	TRP	TRP	TRP	TRP	TRP	TRP		trp	trp	trp	trp	trp	trp	trp	trp	trp	trp	trp	trp	trp	trp	trp
48	GLY (.98)	MET	MET	MET	MET	MET	MET		met	met	met	met	met	met	met	met	met	met	met	met	met	met	met
49		GLY	GLY	GLY	GLY	GLY	GLY		gly	gly	gly	gly	gly	gly	gly	gly	gly	gly	gly	gly	gly	gly	gly
50		TRP	TRP	TRP	TRP	TRP	TRP		trp	trp	trp	trp	trp	trp	trp	trp	trp	trp	trp	trp	trp	trp	trp
51		ILE	ILE	ILE	ILE	ILE	ILE		ile	ile	ile	ile	ile	ile	ile	ile	ile	ile	ile	ile	ile	ile	ile
52		SER	SER	SER	SER	SER	SER		asn	asn	asn	asn	asn	asn	asn	asn	asn	asn	asn	asn	asn	asn	asn
52A		VAL	VAL	VAL	VAL	VAL	VAL		gly	pro	pro	ala	ala	pro	pro	pro	pro	pro	ala	val	pro	pro	pro
52B		---	---	---	---	---	---		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
52C		---	---	---	---	---	---		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
53		TYR	TYR	TYR	TYR	TYR	TYR		tyr	tyr	tyr	tyr	tyr	tyr	tyr	tyr	tyr	tyr	tyr	tyr	tyr	tyr	tyr
54		ASN	ASN	ASN	ASN	ASN	ASN		asn	asn	asn	asn	asn	asn	asn	asn	asn	asn	asn	asn	asn	asn	asn
55		GLY	GLY	GLY	GLY	GLY	GLY		gly	gly	gly	gly	gly	gly	gly	gly	gly	gly	gly	gly	gly	gly	gly
56		ASP	ASP	ASP	ASP	ASP	ASP		asn	ser	asn	asn	asn	asn	asn	asn	asn	asn	asn	asn	asn	asn	asn
57		THR	THR	THR	THR	THR	THR		thr	thr	thr	thr	thr	thr	thr	thr	thr	thr	thr	thr	thr	thr	thr
58		ASN	ASN	ASN	ASN	ASN	ASN		asn	ser	asn	asn	asn	asn	asn	asn	asn	asn	asn	asn	asn	asn	asn
59		TYR	TYR	TYR	TYR	TYR	TYR		tyr	tyr	tyr	tyr	tyr	tyr	tyr	tyr	tyr	tyr	tyr	tyr	tyr	tyr	tyr
60		ALA	ALA	ALA	ALA	ALA	ALA		ala	ala	ala	ala	ala	ala	ala	ala	ala	ala	ala	ala	ala	ala	ala
61		GLN	GLN	GLN	GLN	GLN	GLN		glu	glu	glu	glu	glu	glu	glu	glu	glu	glu	glu	glu	glu	glu	glu
62		ASN	ASN	ASN	ASN	ASN	ASN		lys	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys
63		LEU	LEU	LEU	LEU	LEU	LEU		leu	leu	leu	leu	leu	leu	leu	leu	leu	leu	leu	leu	leu	leu	leu
64		GLN	GLN	GLN	GLN	GLN	GLN		glu	glu	glu	glu	glu	glu	glu	glu	glu	glu	glu	glu	glu	glu	glu
65		ARG	GLY	GLY	GLY	GLY	GLY		asp	gly	gly	gly	gly	gly	gly	gly	gly	gly	gly	gly	gly	gly	gly
66		VAL	VAL	VAL	VAL	VAL	VAL		arg	arg	arg	arg	arg	arg	arg	arg	arg	arg	arg	arg	arg	arg	arg
67		THR	THR	THR	THR	THR	THR		thr	thr	thr	thr	thr	thr	thr	thr	thr	thr	thr	thr	thr	thr	thr
68		MET	MET	MET	MET	MET	MET		ile	met	ser	ile	ile	ile	ile	met	ile	val	ile	ile	ile	ile	ile
69		---	---	---	---	---	---		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
70		THR	THR	THR	THR	THR	THR		thr	thr	thr	thr	thr	thr	thr	thr	thr	thr	thr	thr	thr	thr	thr
71		THR	THR	THR	THR	THR	THR		arg	arg	arg	arg	arg	arg	arg	arg	arg	arg	arg	arg	arg	arg	arg
72		ASP	ASP	ASP	ASP	ASP	ASP		asn	asn	asn	asn	asn	asn	asn	asn	asn	asn	asn	asn	asn	asn	asn
73		THR	THR	THR	THR	THR	THR		thr	thr													

HUMAN HEAVY CHAINS SUBGROUP I (cont'd)

	23 TH9 CL #	24 WIL2 CL #	25* EVL-15 CL #	26* KAS CL #	27* BOR #	28* RF-TS1 CL #	29* L57 CL #	30 ND CL #	31 71-5 CL	32 EU	33* RF-TS3 CL #	34 5-1R1 CL	35 VNAU CL	36 5-2R1 CL	37 VH251 CL	38 83P2 CL	39 MOT #	40 WS1 CL	41* Ab2022 CL	42* SIE	43 lambda IGD-1 CL #	44 Ab2 CL	
0																							
1	GLN	GLN	GLN	pca	pca	GLN	GLN	GLN	pca	GLN	GLN	glu	glu	glu	glu		pca	glu	glu	pca	GLN	glu	
2	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL		VAL	VAL	VAL	VAL	VAL	VAL	
3	GLN	GLN	GLN	his	his	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN		GLN	GLN	GLN	GLN	GLN	GLN	
4	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU		LEU	LEU	LEU	LEU	LEU	LEU	
5	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL		VAL	VAL	VAL	VAL	VAL	met	
6	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	
8	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY		GLY	GLY	GLY	GLY	GLY	GLY	
9	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA		ALA	ALA	ALA	ALA	ALA	ser	
10	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU		GLU	GLU	GLU	GLU	GLU	GLU	
11	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL		VAL	VAL	VAL	VAL	VAL	VAL	
12	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys		lys	lys	lys	lys	lys	val	
13	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys		Lys	Lys	Lys	Lys	Lys	Lys	
14	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	
16	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA		ALA	ALA	ALA	ALA	ALA	ALA	
17	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER		SER	SER	SER	SER	SER	SER	
18	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL		VAL	VAL	VAL	VAL	VAL	VAL	
19	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys		Lys	Lys	Lys	Lys	Lys	Lys	
20	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL		VAL	VAL	VAL	VAL	VAL	VAL	
21	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER		SER	SER	SER	SER	SER	SER	
22	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS		CYS	CYS	CYS	CYS	CYS	CYS	
23	Lys	glu	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys		Lys	Lys	Lys	Lys	Lys	arg	
24	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	
26	TYR	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY		TYR	TYR	TYR	TYR	TYR	GLY	
27	TYR	val	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY		TYR	TYR	TYR	TYR	TYR	GLY	
28	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	
30	ala	THR	ser	ser	ser	ser	ser	ser	ser	ser	ser	ser	ser	ser	ser		ala	asn	ser	ser	ser	glu	
31	thr	gln	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER		thr	thr	thr	thr	thr	thr	
32	TYR	his	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER		TYR	TYR	TYR	TYR	TYR	TYR	
33	asp	tyr	ala	ala	ala	ala	ala	ala	ala	ala	ala	ala	ala	ala	ala		asp	tyr	tyr	tyr	tyr	glu	
34	ILE	met	phe	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE		ILE	ILE	ILE	ILE	ILE	thr	
35	asn	his	SER	SER	SER	SER	SER	SER	his	gln	ile	asn	gly	gly	SER		asn	his	ala	gly	SER	glu	
35A																							
35B																							
36	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	
38	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	
40	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA		ALA	ALA	ALA	ALA	ALA	ALA	
41	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY		GLY	GLY	GLY	GLY	GLY	GLY	
42	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN		GLN	GLN	GLN	GLN	GLN	GLN	
43	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU		LEU	LEU	LEU	LEU	LEU	LEU	
44	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU		GLU	GLU	GLU	GLU	GLU	GLU	
45	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP		TRP	TRP	TRP	TRP	TRP	TRP	
46	MET	MET	MET	MET	MET	MET	MET	MET	ile	MET	MET	MET	MET	MET	MET		MET	MET	MET	MET	MET	MET	
47	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY		GLY	GLY	GLY	GLY	GLY	GLY	
48	TRP	TRP	gln	gln	gln	gln	gln	gln	gln	gln	gln	gln	gln	gln	gln		TRP	TRP	TRP	TRP	TRP	TRP	
49	met	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE		met	ile	ile	ile	ile	ile	
50	asn	asn	ile	ile	ile	ile	ile	ile	asn	val	asn	tyr	asn	tyr	asn		asn	asn	asn	asn	asn	asn	
51	met	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE		met	ile	ile	ile	ile	ile	
52	asn	asn	ile	ile	ile	ile	ile	ile	asn	val	asn	tyr	asn	tyr	asn		asn	asn	asn	asn	asn	asn	
52A	pro	pro	pro	pro	pro	pro	pro	pro	VAL	pro	thr	pro	pro	pro	pro		pro	pro	ala	pro	lys	pro	
52B	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		---	---	---	---	---	---	
52C	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		---	---	---	---	---	---	
53	ser	ser	leu	ile	ile	met	phe	asn	gly	met	asn	gln	gln	gln	gln		ser	ser	gln	gln	trp	cys	
54	ser	ser	leu	ile	ile	met	phe	asn	gly	met	asn	gln	gln	gln	gln		ser	ser	gln	gln	trp	cys	
55	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY		GLY	GLY	GLY	GLY	GLY	GLY	
56	asn	asn	arg	arg	arg	arg	arg	arg	asn	asn	asn	asn	asn	asn	asn		asn	asn	asn	asn	asn	asn	
57	THR	THR	thr	ala	pro	ala	THR	THR	THR	pro	pro	THR	THR	THR	THR		THR	THR	THR	THR	THR	THR	
58	GLY	ASN	his	ASN	ASN	ASN	ASN	ASN	ASN	ASN	THR	arg	arg	ASN	ASN		GLY	arg	thr	arg	gln	thr	
59	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR		TYR	TYR	TYR	TYR	TYR	TYR	
60	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA		ALA	ALA	ALA	ALA	ALA	ALA	
61	GLN	glu	GLN	GLN	GLN	GLN	GLN	GLN	pro	GLN	GLN	GLN	pro	pro	pro		GLN	pro	pro	pro	pro	pro	
62	Lys	lys	lys	lys	lys	lys	lys	lys	asn	lys	lys	lys	asn	asn	asn		Lys	asn	asn	asn	asn	asn	
63	phe	phe	phe	phe	phe	phe	phe	phe	phe	phe	phe	phe	phe	phe	phe		phe	phe	phe	phe	phe	phe	
64	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN		GLN	GLN	GLN	GLN	GLN	GLN	
65	GLY	GLY	asp	GLY	GLY	GLY	GLY	GLY	glu	GLY	GLY	GLY	GLY	GLY	GLY		GLY	ala	GLY	GLY	glu	ala	
66	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG		ARG	ARG	ARG	ARG	ARG	ARG	
67	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL		VAL	VAL	VAL	VAL	VAL	VAL	
68	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR		THR	THR	THR	THR	THR	THR	
69	MET	ile	ile	ile	ile	ile	MET	ile	ile	ile	phe	ile	ile	ile	ile		MET	ile	ile	arg	val	ile	
70	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	ser	ser	ser	ser	ser		THR	THR	THR	THR	THR	THR	
71	arg	arg	THR	ala	THR	ala	THR	arg	ala	ala	ala	ala	ala	ala	ala		arg	arg	ala	ala	ala	ala	
72	asn	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP		asn	asn	asn	asn	asn	asn	
73	THR	THR	glu	glu	glu	glu	THR	ala	met	glu	THR	lys	lys	lys	lys		THR	THR	THR	THR	THR	THR	
74	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER		SER	SER	SER	SER	SER	SER	
75	ile	ile	THR	THR	THR	THR	THR	THR	THR	THR	val	ile	ile	ile	ile		ile	THR	THR	ile	phe	arg	
76	SER	asn	arg	asn	SER																		

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								51	2	49 (LEU)	
83								51	5	33 (ARG)	7.7
84								51	5	34 (SER)	7.5
85								51	4, 5	24 (GLU), 23 (GLU)	8, 5, 11.
86								51	1, 2	51 (ASP), 50 (ASP)	1, 2.
87								51	3	48 (THR)	3.2
88								51	3	48 (ALA)	3.2
89								51	5	34 (VAL)	7.5
90								51	2	50 (TYR)	2.
91								51	2	48 (TYR)	2.1
92								51	1	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	6 (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.
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- 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.
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- 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.
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- 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.

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- 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.
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- 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.
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- 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, 2482-2498. (CHECKED BY AUTHOR 06/15/83)
- 49) **60P1'** CL: SCHROEDER, H.W., JR., HILLSON, J.L. & PERLMUTTER, R.M. (1987) SCIENCE, 238, 791-793.
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- 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.
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- 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)
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- 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)
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- 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)
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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], WIL2'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], WIL2'CL[24], KAS[26], BOR' [27], LS7'CL[29], WOL[45]. (14 IDENTICAL HUMAN V-H-I; ALSO 7 HUMAN V-H-II: 15P1'CL[11], M11'CL[13], MCE' [46], DR12910-2F8'CL[48], Ad17'CL[49], M44'CL[52], NZU[55]; 34 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], HE2-1/7'CL[25], 25'CL[12], Vh383'CL[12], Vh383'CL[15], Vh383'CL[16], Vh383'CL[17], 80P2'CL[18], 6331'CL[19], SF471-1'CL[20], Vh383'CL[21], Vh383'CL[22], 56P1'CL[25], 2P1'CL[26], M74'CL[28], TIL[33], HN. 14'CL[41], WEA[47], 4B4'CL[48], M26'CL[49], NIE[60], DOB[62], VH10.7'CL[63], K6H6'CL[68], K4B8'CL[69], K5B8'CL[70], 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: MOPC47A[110].)
SET 3: 21/28'CL[10]. (IDENTICAL TO 1 HUMAN V-H-III: TIL[33].)
SET 4: 51P1'CL[14],RF-TS1'CL[28],M61'CL[47],60P1'CL[49],AF2'CL[65]. (5 IDENTICAL HUMAN V-H-I; ALSO 6 HUMAN V-H-II:
L16'CL[2],M71'CL[4],C6B2'CL[14],58P2'CL[16],CE-1'CL[41],37P1'CL[47]; AND 3 HUMAN V-H-III: 38P1'CL[36],
3D6'CL[43],13P1'CL[97].)
SET 5: AND'CL[15]. (IDENTICAL TO 1 HUMAN V-H-II: Pag-1'CL[22]; AND 2 HUMAN V-H-III: RF-SJ2'CL[31],RF-SJ1'CL[46].)
SET 6: 783c'CL[21],X17115'CL[22],EV1-15'CL[25],ND'CL[30],Ab2'CL[44]. (5 IDENTICAL HUMAN V-H-I; ALSO 3 HUMAN
V-H-II: RF-001'CL[11],HG3'CL[12],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%
HOMOLOGY 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									49	3	46 (GLY)
	9	PRO	PRO				PRO	PRO									49	3	43 (PRO)
	10	thr	thr				GLY	GLY									49	3	41 (GLY)
	11	LEU	LEU				LEU	LEU									49	1	49 (LEU)
	12	VAL	VAL				VAL	VAL									49	2	45 (VAL)
	13	LYS	LYS				LYS	arg									49	2	41 (LYS)
	14	PRO	PRO				PRO	PRO									49	2	48 (PRO)
	15	thr	thr				SER	pro									49	4	38 (SER)
	16	glu	GLN				asp										48	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			CYS	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				SER	SER			SER	SER					52	3	45 (SER)
	26	GLY	GLY				ser	GLY			SER	GLY					51	1	50 (GLY)
	27	phe	phe				asp				gly						50	6	19 (GLY)
	28	SER	SER				ile				SER						50	4	41 (SER)
	29	leu	ile				leu										50	4	18 (VAL)
	30	SER	SER				SER										50	4	46 (SER)
	31	thr	SER				leu										50	8	28 (SER)
	32	ser	tyr				leu										50	3	13 (TYR)
	33	glu	tyr				tyr										50	3	13 (TYR)
	34	val	trp				pro										50	7	14 (TRP)
	35	gly	ser				asp										50	12	13 (SER)
	35A	val	val				asn										53	6	18 (TRP)
	35B	gly	gly				arg										27	5	12 (ASN)
	36	TRP	TRP			TRP	TRP	TRP			TRP						52	2	51 (TRP)
	37	ILE	ILE			ILE	ILE	ILE			ILE						52	4	40 (ILE)
	38	ARG	ARG			ARG	ARG	ARG			ARG						51	1	51 (ARG)
	39	GLN	GLN			GLN	GLN	GLN			GLN						51	3	49 (GLN)
	40	arg	pro			pro	pro	pro			pro						51	3	36 (PRO)
	41	PRO	PRO			PRO	PRO	PRO			PRO						51	3	50 (PRO)
	42	gly	gly			gly	gly	gly			gly						51	2	39 (GLY)
	43	lys	lys			lys	lys	lys			lys						51	3	30 (LYS)
	44	ala	ala			ala	ala	ala			ala						51	2	44 (GLY)
	45	LEU	LEU			LEU	LEU	LEU			LEU						51	2	49 (LEU)
	46	GLU	GLU			GLU	GLU	GLU			GLU						51	1	51 (GLU)
	47	TRP	TRP			ser	TRP	TRP			TRP						51	2	50 (TRP)
	48	LEU	ile			val	ile	ile			ile						51	3	31 (ILE)
	49	ala	GLY			ala	GLY	GLY			GLY						51	2	43 (GLY)
	50	phe	tyr			leu	glu	glu			glu						51	6	18 (ARG)
	51	ile	ile			ile	THR	ile			ile						51	2	34 (ILE)
	52	asn	TYR			asn	asn	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	his			his						51	10,11	14 (TYR)
	54	asp	ser			asp	arg	ser			ser						51	8	23 (SER)
	55	asp	gly			asp	gly	gly			gly						51	4	28 (GLY)
	56	asp	ser			asp	ser	arg			arg						51	4	19 (SER)
	57	ASN	thr			lys	val	thr			thr						51	2	26 (THR)
	58	arg	asn			lys	thr	thr			thr						51	10	13 (+)
	59	TYR	TYR			TYR	TYR	TYR			TYR						51	6	45 (TYR)
	60	ser	asn			ser	asn	asn			asn						51	6,7	27 (ASN), 26 (ASN)
	61	pro	pro			pro	pro	pro			pro						51	6	30 (PRO)
	62	SER	SER			SER	SER	SER			SER						51	4	46 (SER)
	63	leu	leu			leu	leu	leu			leu						52	3	36 (LEU)
	64	arg	LYS			LYS	glu	thr			LYS						52	5	37 (LYS)
	65	SER	SER			SER	SER	SER			SER						52	3	43 (SER)
	66	ARG	ARG			ARG	ARG	ARG			ARG						52	1	52 (ARG)
	67	leu	val			leu	val	val			leu						52	4	30 (VAL)
	68	THR	THR			THR	THR	THR			THR						52	5	49 (THR)
	69	gly	ILE			ILE	ILE	ILE			ILE						52	5	38 (ILE)
	70	thr	ser			thr	ser	ser			thr						52	4	30 (SER)
	71	lys	val			lys	val	val			lys						52	6	28 (VAL)
	72	ASP	ASP			ASP	ASP	ASP			ASP						52	2	51 (ASP)
	73	THR	THR			THR	ser	THR			THR						52	2	47 (THR)
	74	SER	SER			SER	SER	SER			SER						52	2	51 (SER)
	75	arg	LYS			LYS	LYS	LYS			LYS						52	3	48 (LYS)
	76	ASN	ASN			ASN	ASN	ASN			ASN						52	3	52 (ASN)
	77	GLN	GLN			GLN	GLN	GLN			GLN						52	4	49 (GLN)
	78	val	PHE			val	PHE	PHE			val						52	2	43 (PHE)
	79	val	SER			val	phe	SER			SER						52	4	41 (SER)
	80	LEU	LEU			LEU	LEU	LEU			LEU						52	1	52 (LEU)
	81	thr	lys			thr	lys	lys			thr						52	8	22 (LYS)
	82	ile	LEU			met	met	leu			met						52	4	42 (LEU)
	82A	thr	ser			thr	thr	thr			thr						51	2	22 (SER)
	82B	asn	SER			asn	SER	SER			asn						50	3	42 (SER)
	82C																		

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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IDENTICAL SETS OF FRAMEWORK SEGMENTS:

- FR1: SET 1: 15P1'CL[1], L16'CL[2], ML1'CL[3], M71'CL[4], F19L16'CL[5], F19M1'CL[6], 6-1G1'CL[7], VHVI'CL[8], VH6'CL[9], A10'CL[10], FK-001'CL[11], A431'CL[12]. (12 IDENTICAL)
- SET 2: 71-2'CL[13], 71-4'CL[15]. (2 IDENTICAL)
- SET 3: 1-9II'CL[19], 12G-1'CL[20]. (2 IDENTICAL)
- SET 4: HuVNP'CL[25], HuVHLYS'CL[27], HuVHCAMP'CL[32]. (3 IDENTICAL)
- SET 5: HuRSV19VH[36], HuRSV19CHFNS[38]. (2 IDENTICAL)
- FR2: SET 1: 15P1'CL[1], L16'CL[2], ML1'CL[3], M71'CL[4], F19L16'CL[5], F19M1'CL[6], 6-1G1'CL[7], VHVI'CL[8], VH6'CL[9], A10'CL[10], FK-001'CL[11], A431'CL[12]. (12 IDENTICAL)
- SET 2: 71-2'CL[13], C6B2'CL[14], 71-4'CL[15], 58P2'CL[16], SUP-T1 VH-JA'CL[17], 1-9II'CL[19], 12G-1'CL[20], 2-1'CL[21], 58'CL[28], 6S-3C4'CL[33], GER[35], WAB[37], 37P1'CL[47], Ab17'CL[49], LES-B'CL[50], LES-A'CL[51]. (16 IDENTICAL HUMAN V-H-II; ALSO 5 MISCELLANEOUS V-H: LG2-1 (II)'CL[18], LL2-8 (II)'CL[32], XENOPUS LAEVIS II'CL[38], Xenopus laevis c14 (II)'CL[55], Xenopus laevis c40 (II)'CL[57].)
- SET 3: 11'CL[23], 79'CL[26], Fog-B'CL[30]. (3 IDENTICAL)
- SET 4: HuVNP'CL[25], HuVHLYS'CL[27], HuVHCAMP'CL[32], NEWM[34], HuRSV19VH[36], HuRSV19CHFNS[38]. (6 IDENTICAL)
- SET 5: CE-1'CL[41], M60'CL[42]. (2 IDENTICAL)
- FR3: SET 1: 15P1'CL[1], L16'CL[2], ML1'CL[3], M71'CL[4], F19L16'CL[5], F19M1'CL[6], 6-1G1'CL[7], VHVI'CL[8], VH6'CL[9], A10'CL[10]. (10 IDENTICAL)
- SET 2: 71-2'CL[13], C6B2'CL[14], 71-4'CL[15], 58P2'CL[16], SUP-T1 VH-JA'CL[17], Ab44'CL[29], 37P1'CL[47]. (7 IDENTICAL)
- SET 3: 1-9II'CL[19], 12G-1'CL[20]. (2 IDENTICAL)
- SET 4: HuVNP'CL[25], HuVHLYS'CL[27], HuVHCAMP'CL[32], NEWM[34], HuRSV19VH[36]. (5 IDENTICAL)
- FR4: SET 1: 15P1'CL[1], ML1'CL[3], MCE'[46], DR12910-2F8'CL[48], A 17'CL[49], M44'CL[52], NZU[55]. (7 IDENTICAL HUMAN V-H-II; 7H9'CL[23], RL2'CL[24], KAS[26], BOR[27], L57'CL[29], NOL[45]; 34 HUMAN V-H-III: 18'2'CL[11], 18'7'CL[16], 18'9'CL[13], 1'17'CL[14], 30P1'CL[15], M43'CL[6], HF2-1/17[7], Ab25'CL[12], Vh38C1.10'CL[15], Vh38C1.8'CL[16], Vh38C1.9'CL[17], 60P1'CL[18], 63P1'CL[19], GF4/1'CL[20], Vh38C1.4'CL[21], Vh38C1.5'CL[22], 56P1'CL[25], 2P1'CL[26], M6'CL[28], RL[33], HN.14'CL[41], WEA[47], AB'CL[48], M26'CL[49], NIF[60], DOR[62], Vh10.7'CL[63], K6E6'CL[68], K5B8'CL[69], K5B8'CL[70], K5G5'CL[71], K5G5'CL[72], K6F5'CL[73], 20P1'CL[82]; 1 MOUSE V-H-IIB: PING2006E'CL[29]; 1 MOUSE V-H-IIIA: MOPC47A[110]; AND 1 MOUSE V-H-IIID: H37-40'CL[25].)
- SET 2: L16'CL[2], M71'CL[4], C6B2'CL[14], 58P2'CL[16], CE-1'CL[41], 37P1'CL[47]. (6 IDENTICAL HUMAN V-H-II; ALSO 6 HUMAN V-H-I: 51P1'CL[14], RF-TS'CL[28], Ab2022'CL[41], M61'CL[47], 60P1'CL[49], AF2'CL[65]; AND 3 HUMAN V-H-III: 38P1'CL[36], 306'CL[43], 13P1'CL[97].)
- SET 3: Pag-1'CL[22]. (IDENTICAL TO 1 HUMAN V-H-I: AND'CL[15]; AND 2 HUMAN V-H-III: RF-SJ2'CL[31], RF-SJ1'CL[46].)
- SET 4: FK-001'CL[11], HIG1'CL[24], Ab44'CL[29], Fog-B'CL[30], HuRSV19VH[36], HuRSV19CHFNS[38]. (6 IDENTICAL HUMAN V-H-I; ALSO 5 HUMAN V-H-II: 783'CL[21], 71-15'CL[12], 15'CL[15], 567'CL[17], 843'CL[38], 132.16'CL[39], NIG9'CL[50], 4G12'CL[103], Ab21'CL[24], M72'CL[27], KIM46B'CL[29], Q266'CL[136], 70P1'CL[183]; 2 MOUSE V-H-IIA: HDEX12[15], M61'CL[160]; AND 1 MOUSE V-H-IIC: MuRSV19VH[37].)
- SET 5: Ab26'CL[18], M60'CL[42]. (2 IDENTICAL HUMAN V-H-II; ALSO 1 HUMAN V-H-I: 83P2'CL[38]; AND 5 HUMAN V-H-III: A18'CL[11], RF-KL1'CL[13], 1B11'CL[74], 1H1'CL[75], 2C12'CL[180].)
- SET 6: HuVNP'CL[25], HuVHLYS'CL[27], HuVHCAMP'CL[32], NEWM[34]. (4 IDENTICAL)

IDENTICAL SETS OF COMPLEMENTARITY DETERMINING REGIONS:

- CDR1: SET 1: 15P1'CL[1], L16'CL[2], ML1'CL[3], M71'CL[4], F19L16'CL[5], F19M1'CL[6], 6-1G1'CL[7], VHVI'CL[8], VH6'CL[9]. (9 IDENTICAL)
- SET 2: 71-4'CL[15], 58P2'CL[16], 37P1'CL[47]. (3 IDENTICAL)
- SET 3: 1-9II'CL[19], 12G-1'CL[20]. (2 IDENTICAL)
- SET 4: 11'CL[23], 79'CL[26]. (2 IDENTICAL)
- SET 5: HIG1'CL[24], 58'CL[28], Ab44'CL[29], 6H-3C4'CL[33], LES-C'CL[39]. (5 IDENTICAL)
- SET 6: HuVNP'CL[25]. (IDENTICAL TO 1 HUMAN V-H-III: H11'CL[23]; 9 MOUSE V-H-IIA: 4m4 GL'CL[94], 5D3'CL[112], 8E3'CL[119], AM9'CL[120], AM10'CL[139], AM12'CL[131], 7C6'CL[142], 2.9 GL'CL[169], #139'CL[266]; AND 69 MOUSE V-H-IIB: B1-8'CL[14], B1-8 DELTA1V3[2], B1-48'CL[13], N-HYB'CL[4], 18C10'CL[5], 186-2'CL[6], B1-8. V4'CL[11], S2B8'CL[8], 6F6'CL[9], S2E9'CL[10], F17.170.2[11], 186-1'CL[12], B4'CL[13], S2H5'CL[14], S1F12'CL[15], ANTI-TGAL 17'CL[16], H1-9'CL[19], CR12'CL[22], 4m5 GL'CL[24], 22.11.1'CL[27], 73'CL[28], PING2006E'CL[29], B10.8. V1'CL[30], 3.9. V1'CL[34], 6B3'CL[31], 783'CL[31], 254'CL[32], 153'CL[34], 567'CL[37], 843'CL[38], 132.16'CL[39], NIG9'CL[50], 102'CL[51], 33'CL[52], CH-51'CL[55], DB1-314.3'CL[56], DF4-12.6'CL[57], A1-45'CL[59], S1E2'CL[60], CH14'CL[64], CH10'CL[68], CH-55'CL[74], CH31'CL[76], H1-29'CL[78], DF1-608.1'CL[89], AC38.15.3[93], H1-59'CL[94], 102B'CL[101], 20.119.25'CL[104], SB9C'CL[106], MYA6'CL[138], 119.13'CL[139], 8C7S'CL[188], 3B1S'CL[188], 4A8S'CL[184], CH17'CL[199], F17.59.2'CL[127], vgd5 GL'CL[138], 119.13'CL[139], 8C7S'CL[188], 3B1S'CL[188], 4A8S'CL[184], NO22.87.1'CL[165], AC38.251.5[168], 4m110 GL'CL[174], AC38.260.2[175], 4F5S'CL[178], 10H12S'CL[180], VNP'CL[185].)
- SET 7: HuVHLYS'CL[27]. (IDENTICAL TO 6 MOUSE V-H-IB: P14'CL[33], D1.3[38], MOPC141'CL[56], G2b-4'CL[60], 56P-1'CL[73], G3-3'CL[86].)
- SET 8: HuVHCAMP'CL[32]. (IDENTICAL TO 2 MOUSE V-H-IIA: 26-10VH'CL[74], 26-10[188]; 4 MOUSE V-H-IIIA: CBA/J V3'CL[91], V84.4'CL[99], C57BL/10 V3'CL[100], C57BL V3'CL[101]; AND 1 RAT V-H: YTH 34.5HL'CL[11].)
- SET 9: HuRSV19VH[36], HuRSV19CHFNS[38]. (2 IDENTICAL HUMAN V-H-II; ALSO 1 MOUSE V-H-IIA: L13'CL[173]; 5 MOUSE V-H-IIC: 38P1'CL[36], 306'CL[43], 13P1'CL[97], F4.18.25'CL[25], H4a-3'CL[28], H2b-3'CL[32], MuRSV19VH'CL[37]; AND 1 MISCELLANEOUS V-H: XENOPUS LAEVIS V'CL[42].)
- CDR2: SET 1: 15P1'CL[1], L16'CL[2], ML1'CL[3], M71'CL[4], F19L16'CL[5], F19M1'CL[6], 6-1G1'CL[7], VHVI'CL[8], VH6'CL[9]. (9 IDENTICAL)
- SET 2: 71-2'CL[13], 71-4'CL[15], 58P2'CL[16], 37P1'CL[47]. (4 IDENTICAL)
- SET 3: Ab26'CL[18], 1-9II'CL[19], 12G-1'CL[20]. (3 IDENTICAL)
- SET 4: HuVNP'CL[25]. (IDENTICAL TO 19 MOUSE V-H-IIB: B1-8'CL[11], B1-8 DELTA1V3[2], B1-48'CL[13], N-HYB'CL[4], 18C10'CL[5], 186-2'CL[6], S2B8'CL[8], 6F6'CL[9], S2E9'CL[10], 186-1'CL[12], 186-1'CL[12], ANTI-TGAL 17'CL[16], H1-9'CL[19], CR12'CL[22], 4m5 GL'CL[24], 22.11.1'CL[27], 73'CL[28], PING2006E'CL[29], B10.8. V1'CL[30], 3.9. V1'CL[34], 6B3'CL[31], 783'CL[31], 254'CL[32], 153'CL[34], 567'CL[37], 843'CL[38], 132.16'CL[39], NIG9'CL[50], 102'CL[51], 33'CL[52], CH-51'CL[55], DB1-314.3'CL[56], DF4-12.6'CL[57], A1-45'CL[59], S1E2'CL[60], CH14'CL[64], CH10'CL[68], CH-55'CL[74], CH31'CL[76], H1-29'CL[78], DF1-608.1'CL[89], AC38.15.3[93], H1-59'CL[94], 102B'CL[101], 20.119.25'CL[104], SB9C'CL[106], MYA6'CL[138], 119.13'CL[139], 8C7S'CL[188], 3B1S'CL[188], 4A8S'CL[184], CH17'CL[199], F17.59.2'CL[127], vgd5 GL'CL[138], 119.13'CL[139], 8C7S'CL[188], 3B1S'CL[188], 4A8S'CL[184], NO22.87.1'CL[165], AC38.251.5[168], 4m110 GL'CL[174], AC38.260.2[175], 4F5S'CL[178], 10H12S'CL[180], VNP'CL[185].)
- SET 5: HuVHLYS'CL[27]. (IDENTICAL TO 1 MOUSE V-H-IB: D1.3[38].)
- SET 6: HuVHCAMP'CL[32]. (IDENTICAL TO 1 RAT V-H: YTH 34.5HL'CL[11].)
- SET 7: HuRSV19VH[36], HuRSV19CHFNS[38]. (2 IDENTICAL HUMAN V-H-II; ALSO 1 MOUSE V-H-IIC: MuRSV19VH'CL[37].)

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

- SET 8: LES-C'CL[39],LES-B'CL[50],LES-A'CL[51]. (3 IDENTICAL)
- CDR3: SET 1: HuVHLYS'CL[27]. (IDENTICAL TO 1 MOUSE V-H-IB: D1.3[38].)
- SET 2: HuVHCAMP'CL[32]. (IDENTICAL TO 1 RAT V-H: YTH 34.5HL'CL[1].)
- SET 3: HuRSV19VH[36],HuRSV19CHFNS[38]. (2 IDENTICAL HUMAN V-H-II; ALSO 1 MOUSE V-H-IIC: MuRSV19VH'CL[37].)
- SET 4: LES-C'CL[39],LES-B'CL[50],LES-A'CL[51]. (3 IDENTICAL)

IDENTICAL SETS OF J-MINIGENES:

- SET 1: 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],20P1'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)

	21 Vh38 Cl.4 Cl.5	22 Vh38 Cl.5	23 H11 Cl.1	24* A821 Cl.1	25 5P1 Cl.1	26 2P1 Cl.1	27 W22 Cl.1	28 K74 Cl.1	29* K46H Cl.1	30 111 Cl.1	31* RF1 Cl.1	32 21-2B Cl.1	33 T1L Cl.1	34 F12-2 Cl.1	35 v65-4 Cl.1	36 38P1 Cl.1	37 13-2 Cl.1	38 BRO TGM	39 BU TGM	40 CAM	41* HN.14 Cl.1	42* RF-TS2 Cl.1	
0																							
1				GLU	GLU	gln	gln	gln	gln	gln	gln	gln	GLU	gln	GLU	GLU	GLU	GLU	GLU	GLU	pca	gln	gln
2			VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
3	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	
4																							
5	LEU	LEU	val	LEU	val	val	val	val	val	val	val	val	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	
7	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	
8	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	
9																							
10	asp	asp	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	
11	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	
12	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	
14	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	
15	LEU	LEU	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	
16	GLY	GLY	GLY	GLY	arg	arg	arg	arg	arg	arg	arg	arg	arg	arg	arg	arg	arg	arg	arg	arg	arg	arg	
17	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	
18	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	
20	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	
22	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	
23	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	
24	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	
26	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	
27	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	
28	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	
30	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	
31	asn	asn	SER	SER	SER	SER	SER	SER	SER	SER	SER	asp	thr	SER	asn	SER	SER	tyr	asn	asn	arg	SER	
32	TYR	TYR	TYR	asp	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	his	TYR	TYR	his	TYR	TYR	TYR	TYR	
33	val	val	val	val	val	val	val	val	val	val	val	val	val	val	val	val	val	val	val	val	val	val	
34	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	
35	SER	SER	his	SER	his	his	his	his	his	his	his	his	his	his	SER	his	SER	his	SER	his	his	his	
36	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	
37	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	
38	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	
39	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	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	
42	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	
43	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	
44	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	
45	GLU	GLU	val	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	
46	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	
47	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	
48	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	
49	ala	ala	ala	ala	ala	ala	ala	ala	ala	ala	ala	ala	ala	ala	ala	ala	ala	ala	ala	ala	ala	ala	
50	ser	ser	arg	gly	val	val	val	val	val	val	val	val	val	val	val	val	val	val	val	val	val	val	
51	ile	ile	ile	ile	ile	ile	ile	ile	ile	ile	ile	ile	ile	ile	ile	ile	ile	ile	ile	ile	ile	ile	
52	SER	SER	asn	gly	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	
52A	GLY	GLY	ser	GLY	tyr	tyr	tyr	tyr	tyr	tyr	tyr	tyr	ser	GLY	tyr	GLY	tyr	GLY	tyr	GLY	tyr	GLY	
52B	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
52C	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
53	SER	SER	asp	arg	asp	asp	asp	asp	asp	asp	asp	ser	leu	asp	asp	thr	thr	thr	thr	asp	asp	asp	
54	GLY	GLY	asp	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	ser	GLY	ser	ala	ala	GLY	GLY	GLY	GLY	GLY	
55	asn	asn	SER	GLY	ser	ser	ser	ser	ser	ser	ser	ser	ser	ser	GLY	GLY	GLY	GLY	GLY	asn	asn	asn	
56	thr	thr	thr	thr	asn	asn	asn	asn	asn	asn	asn	thr	asn	thr	asn	thr	asn	thr	asn	thr	thr	thr	
57	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys	
58	TYR	TYR	TYR	asn	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	
59	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	
60	thr	thr	ala	ala	ala	ala	ala	ala	ala	ala	ala	ala	ala	ala	ala	pro	pro	ala	ala	ala	ala	ala	
61	ala	ala	asp	asp	asp	asp	asp	asp	asp	asp	asp	asp	asp	asp	asp	gly	gly	asp	asp	asp	asp	asp	
62	ser	ser	ser	ser	ser	ser	ser	ser	ser	ser	ser	ser	ser	ser	ser	ser	ser	ser	ser	ser	ser	ser	
63	val	val	val	val	val	val	val	val	val	val	val	val	val	val	val	val	val	val	val	val	val	val	
64	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys	
65	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	
66	ARG	ARG	ARG	gln	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	
67	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	
68	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	
69	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
70	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	
71	ARG	ARG	ARG	met	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	
72	ASP	ASP	ASP	asp	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	glu	glu	asn	asp	asp	asp	asp	
73	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	asn	asn	asn	asn	asn	asn	asn	
74	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	ala	ala	SER	SER	SER	SER	SER	
75	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	asn	lys	lys	lys	asn	lys	lys	asn	
76	ASN	ASN	ASN	asn	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	asn	asn	asn	asn	asn	asn	asn	
77																							

HUMAN HEAVY CHAINS SUBGROUP III (cont'd)

	69 K4B8 CL #	70 K5B8 CL #	71 K5C7 CL #	72 K5G5 CL #	73 K6F5 CL #	74* 1B11 CL	75* 1H1 CL	76* 333 CL	77* 112 CL	78* 126 CL	79* 115 CL	80* C12 CL	81* 2A12 CL	82 20P1 CL	83* FR #	84 V65-2 CL	85 MU	86 DAU	87 HF2- 1/13B	88 HF2- 18/2	89 KEA	90 GR	91 VIN	92 HF3- 16/6	93 GO
0																									
1	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU				GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	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
3	arg	arg	arg	arg	arg	arg	arg	arg	arg	arg	arg				arg	arg	arg	arg	arg	arg	arg	arg	arg	arg	arg
4	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU				LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
5	val	val	val	val	val	val	val	val	val	val	val				val	val	val	val	val	val	val	val	val	val	val
6	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU			GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU
7	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER			SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	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
9	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY			GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
10	asp	asp	asp	asp	asp	ala	ala	ala	ala	ala	ala	ala	ala		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
11	LEU	LEU	LEU	LEU	LEU	phe	phe	phe	phe	phe	phe	phe	phe		LEU	LEU	LEU	LEU	LEU	LEU	LEU	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
13	glu	glu	glu	glu	glu	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
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
16	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
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
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
19	ARG	ARG	ARG	ARG	ARG	lys	lys	lys	lys	lys	lys	lys	lys		ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG
20	val	val	val	val	val	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
22	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS		CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS
23	PRO	PRO	PRO	PRO	PRO	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA		ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA
24	val	val	val	val	val	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
26	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY		SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
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
28	ile	ile	ile	ile	ile	asn	asn	asn	asn	asn	asn	asn	asn		THR	THR	THR	THR	THR	lys	THR	ile	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
30	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER		SER	SER	SER	SER	SER	thr	SER	pro	SER	SER	SER
31	lys	lys	lys	lys	lys	asp	asp	asp	asp	asp	asp	asp	asp		asp	asn	asn	asn	asn	asn	asn	asn	asn	asn	asn
32	ala	ala	ala	ala	ala	ser	ser	ser	ser	ser	ser	ser	ser		ser	ala	phe	tyr	tyr	tyr	tyr	tyr	tyr	tyr	tyr
33	trp	trp	trp	trp	trp	thr	thr	thr	thr	thr	thr	thr	thr		thr	tyr	tyr	tyr	tyr	tyr	tyr	tyr	tyr	tyr	tyr
34	MET	MET	MET	MET	MET	ile	ile	ile	ile	ile	ile	ile	ile		MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET
35	asn	asn	asn	asn	asn	his	his	his	his	his	his	his	his		SER	asp	his	glu	met	SER	SER			SER	SER
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
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
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
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
40	ALA	ALA	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	ser	ser	ser	ser	ser	ser	ser	ser		PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO
42	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	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	GLY	GLY	GLY	GLY	GLY	ser	ser	ser	ser	ser	ser	ser	ser		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
46	glu	glu	glu	glu	glu	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU		GLU	GLU	GLU	GLU	GLX	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
48	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL		VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
49	glu	glu	glu	glu	glu	glu	glu	glu	glu	glu	glu	glu	glu		glu	glu	glu	glu	glu	glu	glu	glu	glu	glu	glu
50	ile	ile	ile	ile	ile	his	his	his	his	his	his	his	his		ile	arg	ALA	ALA	val	val					
51	lys	lys	lys	lys	lys	glu	glu	glu	glu	glu	glu	glu	glu		lys	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys
52A	asn	asn	asn	asn	asn	lys	asn	asn	glu	asn	lys	lys	asp		ser	thr	val								
52B	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys		lys	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys
52C	val	val	val	val	val	ser	thr	thr	ser	thr	ser	ser	thr		thr	thr	thr	thr	thr	thr	thr	thr	thr	thr	thr
53	asp	asp	asp	asp	asp	lys	lys	lys	asn	lys	lys	lys	lys		asp	asp	thr	asn	asp	thr	asn	thr	asn	thr	asn
54	GLY	GLY	GLY	GLY	GLY	lys	asn	asn	lys	asn	lys	asn	asn		GLY	thr	GLY		GLY						
55	GLY	GLY	GLY	GLY	GLY	tyr	tyr	tyr	tyr	tyr	tyr	tyr	tyr		tyr	tyr	tyr	tyr	tyr	tyr	tyr	tyr	tyr	tyr	tyr
56	thr	thr	thr	thr	thr	ala	ala	ala	ala	ala	ala	ala	ala		thr	thr	thr	thr	thr	thr	thr	thr	thr	thr	thr
57	ile	ile	ile	ile	ile	thr	thr	thr	thr	thr	thr	thr	thr		ile	thr	thr	thr	thr	thr	thr	thr	thr	thr	thr
58	asp	asp	asp	asp	asp	ile	met	ile	ile	val	ile	ile	ile		asp	asp	asp	asp	asp	asp	asp	asp	asp	asp	asp
59	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	phe	TYR	TYR	TYR	TYR		TYR	TYR	TYR	TYR	TYR	ser	TYR	TYR	TYR	TYR	TYR
60	ALA	ALA	ALA	ALA	ALA	arg	arg	arg	arg	arg	arg	arg	arg		ALA	ALA	ALA	ALA	ALA	val	thr	ile			
61	ala	ala	ala	ala	ala	ala	ala	ala	ala	ala	ala	ala	ala		ala	ala	ala	ala	ala	lys	glu	ASX			
62	pro	pro	pro	pro	pro	ser	ser	ser	ser	ser	ser	ser	ser		pro	pro	pro	pro	pro	glu	ser	ser			
63	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL		VAL	VAL	VAL	VAL	VAL	arg	leu	VAL			
64	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS		LYS	LYS	LYS	LYS	LYS	phe	asn				
65	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY		GLY	GLY	GLY	GLY	GLY	thr	GLY				
66	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG		ARG	ARG	ARG	ARG	ARG	ile					
67	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE		PHE	PHE	PHE	PHE	PHE	ser	PHE				

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., SIOUD, 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.
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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.
- 36) **38P1'CL**: SCHROEDER, H.W., JR., HILLSON, J.L. & PERLMUTTER, R.M. (1987) SCIENCE, 238, 791-793.
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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.)
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- 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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- 53) **KOL**: SCHMIDT, W.E., JUNG, H.-D., PALM, W. & HILSCHMANN, N. (1983) Z. PHYSIOL. CHEM., 364, 713-747.
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- 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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- 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],1-9III'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-IIB: 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],NEI'CL[16],WIL2'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)