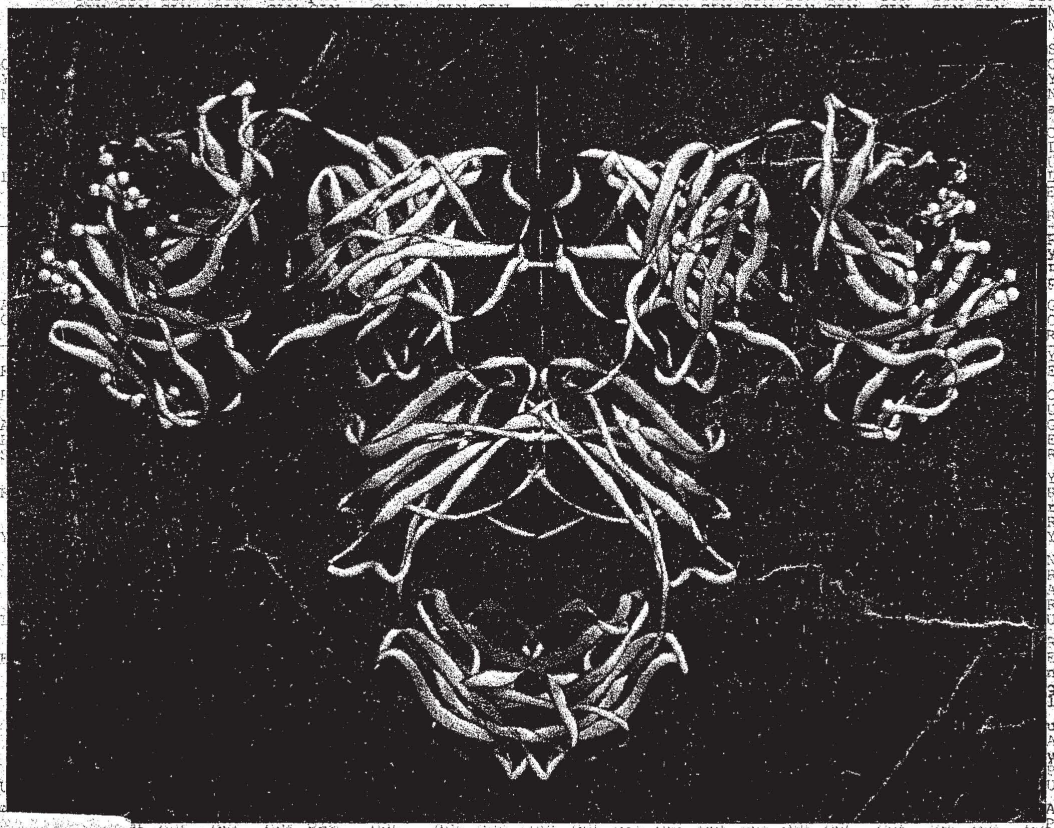
SEQUENCES OF PROTEINS OF IMMUNOLOGICAL INTEREST

VOL. I

FIFTH EDITION



1991

U.S. DEPARTMENT OF HEALTH AND HUMAN SERVICES

Public Health Service

National Institutes of Health

SEQUENCES OF PROTEINS OF IMMUNOLOGICAL INTEREST

FIFTH EDITION

Tabulation and Analysis of Amino Acid and Nucleic Acid Sequences of Precursors, V-Regions, C-Regions, J-Chain, T-Cell Receptors for Antigen, T-Cell Surface Antigens, 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

Elvin A. Kabat, Tai Te Wu†, Harold M. Perry†, Kay S. Gottesman‡, and Carl Foeller†*

*Depts. of Microbiology, Genetics and Development, and Neurology, Cancer Center/Institute of Cancer Research, College of Physicians and Surgeons, Columbia University, New York, NY 10032 and the National Institute of Allergy and Infectious Diseases, Office of the Director National Institutes of Health, Bethesda, MD 20892

†Depts. of Biochemistry, Molecular Biology, and Cell Biology, and Engineering Sciences and Applied Mathematics and Biomedical Engineering, Northwestern University, Evanston, IL 60208 and the Cancer Center, Northwestern University Medical School, Chicago, IL 60611

†BBN Systems and Technologies, 10 Moulton Street, Cambridge, MA 02138

‡Formerly with BBN. Present address Laboratory for Applied Research in Academic Information, William H. Welch Medical Library, The Johns Hopkins University, Baltimore, Md 21205

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U.S. DEPARTMENT OF HEALTH AND HUMAN SERVICES

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Dr. E.A. Kabat
National Institutes of Health
Building 8, Room 126
9000 Rockville Pike
Bethesda, Maryland 20892

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When published, three reprints should be provided.

If any published sequences have been overlooked or if any errors are found, please bring them to our attention.

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	INVARIANT RESIDUES	1 2C12 'CL #	2 1B11 'CL #	3 1H1 'CL #	4 2A12 'CL #	5 BR	6 DEN	7* 3D6 'CL	8 HK102 'CL #	9 EU	10 CAR	11 PA	12 HK 137 'CL #	13 HAU	14 KUE	15* HF2- 1/17	16 Vb 'CL	17 Vb' 'CL	18 GAL (I)	19 OU (IOC)	20* WEA	21 WIL (=) #	22 WES	23 DAUDI 'CL	24 HK 134 'CL #
		---	---	---	---	---	---	---	#	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	#
	1		ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP
	2	ILE(.98)	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE
	3		GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN
	4		MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET
	5	THR(.98)	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
	6		GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLX	GLN	GLN	GLN	GLN	GLN
	7	SER(.99)	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
	8	PRO(.99)	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO
	9	SER(.97)	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
FR1	10		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	**ser**	**ser**	THR	**ser**	**ser**	**ser**	**ser**	**ser**	**ser**	THR	**ser**	**ser**	**ser**
FR1	11		LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	**gln**	LEU	**val**	**val**	LEU	LEU	LEU	LEU	**val**	LEU	LEU
FR1	12	SER(.97)	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	**pro**	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
FR1	13		ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA
FR1	14		SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
	15	VAL(.96)	**VAL**	VAL	**VAL**	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
	16	GLY(.99)	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
	17		ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASX	ASP	ASP	ASP	ASP	ASP
	18		SER	SER	SER	**thr**	**arg**	**arg**	**arg**	**arg**	**arg**	**arg**	**arg**	**arg**	**arg**	**arg**	**arg**	**arg**	**arg**	**arg**	**arg**	**arg**	**arg**	**arg**	**arg**
	19		ILE	ILE	ILE	ILE	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**
	20	THR(.96)	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	**ala**	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
	21	ILE(.95)	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE
	22		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	**ile**	THR	THR	THR	THR	THR	THR
	23	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS
	24		ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG
	25		ALA	ALA	ALA	ALA	ALA	**thr**	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	**pro**	ALA	ALA	ALA
	26		SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	**gly**	SER	SER
	27		GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLX	GLN	GLN	**his**	GLN	GLN
	27A		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	27B		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	27C		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
CDR1	27D		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
CDR1	27E		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
CDR1	27F		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
CDR1	28		SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	**asn**	SER	**gly**	SER	SER	**gly**	**gly**	**gly**	**thr**	**gly**	**ala**	**asp**	**asn**
	29		ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	**phe**	ILE	ILE
	30		GLY	GLY	GLY	GLY	**ser**	**ser**	**ser**	**ser**	**asn**	**ser**	**ser**	**ser**	**asn**	**arg**	**ser**	**ser**	**arg**	**ser**	**arg**	GLY	**ser**	**thr**	**ser**
	31		ASN	ASN	ASN	ASN	**gly**	**arg**	**arg**	**ser**	**thr**	**ser**	**ser**	ASN	**ser**	**ile**	ASN	**ser**	**ser**	ASN	**ser**	ASN	**ser**	**his**	ASN	**ser**
	32		TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	**ser**	**tyr**	**tyr**	TRP	**asp**	TRP	TRP	**asp**	**tyr**	**asp**	TRP	TRP	**phe**
	33	LEU(.95)	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
	34		ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	**ser**	ALA	**gly**	ALA	ALA	**thr**	**asx**	**thr**	ALA	ALA	**ser**	ALA
	35	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP
	36		PHE	PHE	PHE	PHE	PHE	**tyr**	**tyr**	**tyr**	**tyr**	**tyr**	**tyr**	PHE	**tyr**	**tyr**	**tyr**	**tyr**	**tyr**	**tyr**	**tyr**	**tyr**	**tyr**	**tyr**	**tyr**
	37		GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLX	GLN	GLN	GLN	GLN	GLN
	38		GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLX	GLN	GLN	GLN	GLN	GLN
	39		LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS
	40	PRO(.97)	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	**ser**	PRO	PRO
	41		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	**glu**	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	**glu**
FR2	42		LYS	LYS	LYS	LYS	LYS	**glu**	LYS	LYS	LYS	LYS	**glu**	LYS	LYS	LYS	LYS	LYS	LYS	LYS	**thr**	LYS	LYS	LYS	LYS
FR2	43		ALA	ALA	ALA	ALA	ALA	ALA	**val**	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA
	44	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO
	45		ASN	ASN	ASN	ASN	ASN	**lys**	**lys**	**lys**	**lys**	**lys**	**lys**	**gln**	**lys**	**lys**	**lys**	**lys**	**lys**	ASX	**lys**	**glu**	**lys**	**thr**	**lys**
	46		VAL	VAL	VAL	VAL	**leu**	VAL	**leu**	**leu**	**leu**	**leu**	**ser**	VAL	**leu**	**arg**	**leu**	**leu**	**glu**	**leu**	**arg**	**leu**	**leu**	**leu**	**ser**
	47	LEU(.98)	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
	48	ILE(.98)	ILE	ILE	ILE	ILE	ILE	ILE	ILE	**met**	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE
	49		TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR
	50		LYS	LYS	LYS	LYS	LYS	**gly**	LYS	**asp**	LYS	LYS	**glu**	**ala**	**ala**	LYS	**ala**	**ala**	**ala**	**ala**	**ala**	**gly**	**arg**	**ser**	**ala**	**ala**
CDR2	51		ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	**ser**	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	**val**	ALA	**val**	ALA	ALA
CDR2	52		SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	**thr**	SER	SER	SER	SER
CDR2	53		ASN	ASN	ASN	ASN	**thr**	ASN	**ser**	**ser**	**ser**	**ser**	**ser**	**ser**	**thr**	**ser**	**ser**	**ser**	**ser**	ASX	**ser**	**ser**	**ser**	ASN	**ser**
CDR2	54	LEU(.97)	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
CDR2	55		LYS	LYS	LYS	**lys**	**glu**	**glu**	**glu**	**glu**	**glu**	**glu**	**gln**	**pro**	**glu**	**gln**	**gln**	**gln**	**gln**	**his**	**gln**	**gln**	**glu**	**gln**	**gln**
CDR2	56		ASN	ASN	ASN	**lys**	**ser**	**ser**	**ser**	**ser**	**ser**	**ser**	**ser**	**ser**	**thr**	**ser**	**ser**	**ser**	**ser**	**ser**	**ser**	**ser**	ASN	**val**	**ser**
	57	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
	58		ILE	ILE	ILE	ILE	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**
	59	PRO(.95)	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO
	60	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
	61	ARG(.97)	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG
	62	PHE(.96)	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE
	63		SER	SER	SER	SER	SER	SER	SER	SER	**ile**	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
	64	GLY(.96)	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
	65		SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
	66	GLY(.95)	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
	67		SER	SER	SER	SER	**phe**	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	**ala**	SER	SER	SER	SER	SER	SER
	68	GLY(.95)	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
	69		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	**ala**	THR	
	70		GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	**asp**	GLU	**asp**	**asp**	**gln**	GLU	**asp**	**asp**	GLU	**asx**	GLU	GLU	GLU	GLU	**asp**
	71		PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE
FR3	72		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
FR3	73		LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	**phe**	LEU	LEU	LEU	LEU	LEU
	74		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
	75		VAL	VAL	VAL	VAL	**ile**	**ile**	**ile**	**ile**	**ile**	**ile**	**ile**	**ile**	**ile**	**ile**	**ile**	**ile**	**ile**	**ile**	**ile**	**ile**	**ile**	**ile**	**ile**
	76		ILE	ILE	ILE	ILE	**asn**	**ser**	**ser**	**ser**	**ser**	**ser**	**ser**	**ser**	**asn**	**ser**	**ser**	**ser**	**ser**	**ser**	**asn**	**ser**	**ser**	**ser**	**ser**
	77		ASN	ASN	ASN	ASN	**ser**	**ser**	**ser**	**ser**	**ser**	**ser**	**ser**	**ser**	**ser**	**ser**	**ser**	**ser**	**gly**	**ser**	**ser**	**ser**	**ser**	**ser**	**ser**
	78	LEU(.98)	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
	79		GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLX	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLX	GLN	GLN	GLN	GLN	GLN	GLN
	80		SER	SER	SER	SER	**pro**	SER	**pro**	**pro**	**pro**	**pro**	**pro**	**pro**	**pro**	**pro**	**pro**	**pro**	**pro**	**pro**	**pro**	**pro**	**pro**	**pro**	**pro**
	81		ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASX	ASP	**glu**	**glu**	ASP	**glu**	**glu**	**glu**	**glx**	**glu**	ASP	**glu**	**glu**	**glu**
	82		ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASX	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP
	83		PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	**val**	PHE	PHE	PHE	PHE
	84	ALA(.98)	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA
	85		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
	86	TYR(.98)	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR
	87	TYR(.95)	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	**phe**	TYR	TYR	TYR
	88	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS
	89		HIS	HIS	HIS	HIS	**gln**	**gln**	**gln**	**gln**	**gln**	**gln**	**gln**	**gln**	**gln**	**leu**	**gln**	**gln**	**leu**	**glx**	**leu**	**gln**	**gln**	**gln**	**gln**
	90		HIS	HIS	HIS	HIS	HIS	**gln**	**gln**	**gln**	**gln**	**gln**	**gln**	**gln**	**gln**	**gln**	**gln**	**gln**	**gln**	**glx**	**gln**	**gln**	**gln**	**gln**	**gln**
	91		ASN	ASN	ASN	ASN	**tyr**	**tyr**	**tyr**	**tyr**	**tyr**	**tyr**	**tyr**	**tyr**	ASN	**tyr**	**his**	**ala**	**ala**	**gln**	**ser**	**tyr**	**ala**	**ala**	ASN	**tyr**
	92		ASP	ASP	ASP	**glu**	ASP	ASP	**asn**	**asn**	**asn**	**asn**	**asn**	**tyr**	**ser**	**asn**	**asn**	**asn**	**asn**	**tyr**	**ser**	**asn**	**his**	**tyr**	**asn**
	93		SER	SER	**thr**	**thr**	SER	SER	SER	SER	SER	**thr**	**asn**	SER	**ile**	**arg**	SER	SER	SER	SER	SER	**arg**	SER	**asn**	SER
CDR3	94		PHE	PHE	PHE	**ile**	PHE	PHE	**tyr**	**tyr**	**asp**	PHE	**leu**	**tyr**	**thr**	**tyr**	**tyr**	PHE	PHE	**tyr**	**ser**	PHE	**tyr**	**val**	PHE	**tyr**
CDR3	95		SER	SER	SER	SER	**pro**	**pro**	SER	SER	---	---	**pro**	**pro**	**pro**	**pro**	**pro**	**pro**	**pro**	**pro**	**pro**	---	**pro**	SER	**pro**
CDR3	95A		---	---	---	---	---	---	---	#	---	---	---	---	---	---	---	---	---	---	---	---	---	---	#
CDR3	95B		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
CDR3	95C		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
CDR3	95D		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
CDR3	95E		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
CDR3	95F		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
CDR3	96		TRP	TRP	TRP	TRP	TRP	TYR	---	---	LYS	PHE	TRP	---	THR	TYR	LEU	---	---	ARG	THR	TRP	---	LEU	PHE	---
CDR3	97		THR	THR	THR	THR	THR	THR	---	---	MET	THR	THR	---	SER	THR	THR	---	---	SER	THR	THR	---	THR	THR	---
	98	PHE(.96)	PHE	PHE	PHE	PHE	PHE	PHE	PHE	---	PHE	PHE	PHE	---	PHE	PHE	PHE	---	---	PHE	PHE	PHE	PHE	PHE	PHE	---
	99	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	---	GLY	GLY	GLY	---	GLY	GLY	GLY	---	---	GLY	GLY	GLY	GLY	GLY	GLY	---
	100		GLN	GLN	GLN	GLN	GLN	GLN	PRO	---	GLN	PRO	PRO	---	GLN	GLN	GLY	---	---	GLN	GLX	GLN	GLN	GLY	GLY	---
	101	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	---	GLY	GLY	GLY	---	GLY	GLY	GLY	---	---	GLY	GLY	GLY	GLY	GLY	GLY	---
	102	THR(.98)	THR	THR	THR	THR	THR	THR	THR	---	THR	THR	THR	---	THR	THR	THR	---	---	THR	THR	THR	THR	THR	THR	---
FR4	103		LYS	LYS	LYS	LYS	LYS	LYS	LYS	---	LYS	LYS	LYS	---	ARG	LYS	LYS	---	---	LYS	ARG	LYS	LYS	THR	LYS	---
FR4	104		VAL	VAL	VAL	VAL	VAL	LEU	VAL	---	VAL	VAL	VAL	---	VAL	LEU	VAL	---	---	VAL	LEU	VAL	LEU	VAL	VAL	---
FR4	105		LEU	LEU	LEU	LEU	GLU	GLU	ASP	---	GLU	ASP	GLU	---	GLU	ASP	GLU	---	---	GLU	GLX	GLU	GLU	ASP	ASP	---
FR4	106		ILE	ILE	ILE	ILE	ILE	ILE	ILE	---	VAL	ILE	ILE	---	ILE	ILE	ILE	---	---	ILE	ILE	VAL	ILE	ILE	ASN	---
FR4	106A		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	107		LYS	LYS	LYS	LYS	LYS	LYS	LYS	---	LYS	LYS	LYS	---	LYS	LYS	LYS	---	---	LYS	LYS	LYS	LYS	LYS	LYS	---
	108		ARG	ARG	ARG	ARG		ARG		---	GLY	ARG		---	ARG	ARG	ARG	---	---	ARG	ARG	ARG	ARG	ARG	---	---
	109	THR						THR		---	THR	THR		---	THR	THR		---	---	THR	THR	THR	THR		---	---

HUMAN KAPPA LIGHT CHAINS SUBGROUP 1 (cont'd)

		25 Vd 'CL	26 WALKER 'CL	27 HK101 'CL #	28 Va' 'CL	29 VKI-Chr1 'CL	30 AMYLOID BAN #	31 Ve 'CL	32 Vl3 'CL	33 DEE	34 WIL (-) #	35 AND #	36 v108 'CL #	37 VKI-ZI 'CL	38 REI	39 AU	40 ROY	41 BI	42* HuVH CAMP 'CL	43 AG #	44 SCW	45 MEV	46 KA	47* LAY	48 BEL	49 NI
	0	---	---	#	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	1	ASP	ASP	ASP	**ala**	ASP	ASP	**ala**	**val**	ASX	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP
	2	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	**val**	ILE	ILE	ILE
	3	GLN	GLN	GLN	GLN	GLN	GLN	**arg**	**trp**	GLX	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN
	4	**leu**	MET	MET	**leu**	MET	**leu**	MET	MET	MET	MET	MET	**val**	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	**leu**	MET
	5	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
	6	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN
	7	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
	8	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO
	9	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
FR1	10	**phe**	**ser**	**ser**	**ser**	**ser**	**ser**	**ser**	**leu**	**ser**	**THR**	**ser**	**ser**	**ser**	**ser**	**ser**	**ser**	**pro**	**ser**	**ser**	**ser**	**ser**	**THR**	**ser**	**ser**	**ser**
	11	LEU	LEU	LEU	LEU	LEU	**ser**	**phe**	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
	12	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
	13	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	**val**	**val**	ALA	ALA
	14	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	**thr**
	15	VAL	VAL	VAL	VAL	VAL	VAL	**thr**	**thr**	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
	16	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
	17	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	**gly**	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP
	18	**arg**	**arg**	**arg**	**arg**	**arg**	**arg**	**arg**	**arg**	**arg**	**arg**	**arg**	**arg**	**arg**	**arg**	**arg**	**arg**	SER	**arg**	**arg**	**arg**	**arg**	**arg**	**arg**	**arg**	**arg**
	19	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**
	20	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	**ile**	THR	THR	THR	THR	THR
	21	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	**phe**	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	**leu**
	22	THR	THR	THR	THR	THR	THR	**ser**	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	**leu**
	23	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS
	24	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	**gln**	**gln**	**gln**	**gln**	**lys**	**gln**	**gln**	ARG	**glu**	**gln**	**glx**	**glu**
	25	ALA	ALA	ALA	ALA	ALA	ALA	ALA	**met**	ALA	**val**	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA
	26	SER	SER	**arg**	SER	SER	SER	SER	SER	**gly**	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
	27	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	**his**	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLX	GLN
	27A	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	**ser**
	27B	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	**val**
CDR1	27C	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	**leu**
	27D	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	**glu**
	27E	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	27F	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	28	**gly**	SER	**gly**	**gly**	**gly**	SER	**gly**	**gly**	SER	SER	SER	**gly**	**gly**	**asp**	**asp**	**asp**	**asp**	**asn**	**asp**	**asp**	SER	**thr**	**asn**	**asx**	SER
	29	ILE	ILE	ILE	ILE	ILE	**val**	ILE	ILE	**val**	**val**	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	**ser**	**val**	**val**	ILE	**gly**
	30	**ser**	**ser**	**ser**	**ser**	**ser**	**tyr**	**ser**	**ser**	**asn**	**ser**	GLY	**ser**	**ser**	**ile**	**ser**	**ser**	**arg**	**asp**	**asn**	**arg**	**val**	**leu**	**asn**	**ser**	**asn**
	31	**ser**	ASN	**ser**	**ser**	ASN	ASN	**ser**	**ser**	**lys**	**tyr**	**gly**	ASN	ASN	**lys**	**asp**	**ile**	ASN	**lys**	**his**	**lys**	**asp**	**ser**	**ala**	**lys**	**thr**
	32	**tyr**	**tyr**	TRP	**ala**	**asn**	**tyr**	**tyr**	**tyr**	**tyr**	TRP	**ser**	**gly**	**asn**	**tyr**	**tyr**	**phe**	**ser**	**tyr**	**tyr**	**his**	**tyr**	**tyr**	**tyr**	**phe**
	33	LEU	LEU	LEU	LEU	LEU	**val**	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
	34	ALA	**asn**	ALA	ALA	**asn**	ALA	ALA	ALA	**asn**	ALA	**asn**	**ser**	**asn**	**asn**	**asn**	**asn**	**ile**	**asn**	**asn**	**asn**	**asn**	**asn**	**asn**		ALA
	35	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP		TRP
	36	**tyr**	**tyr**	**tyr**	**tyr**	**tyr**	PHE	**tyr**	**tyr**	**tyr**	**tyr**	**tyr**	**tyr**	**tyr**	**tyr**	**tyr**	**tyr**	**tyr**	**tyr**	**tyr**	**tyr**	**tyr**	**tyr**	**tyr**		**tyr**
	37	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	**his**	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	**asp**	GLN	GLN	GLN		GLN
	38	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN		GLN
	39	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	**thr**	LYS	LYS	LYS	LYS	#	LYS	LYS	LYS	LYS		LYS
	40	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO		PRO
FR2	41	GLY	GLY	**glu**	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	#	GLY	GLY	GLY	GLY	GLY	**lys**
	42	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	**gln**	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	**leu**	LYS	LYS	LYS
	43	ALA	ALA	ALA	ALA	**thr**	ALA	ALA	ALA	ALA	ALA	ALA	**thr**	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	**pro**	ALA	
	44	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO
	45	**lys**	**lys**	**lys**	**lys**	**lys**	**lys**	**glu**	**lys**	ASN	**ser**	**thr**	**lys**	**lys**	**lys**	**lys**	**lys**	**lys**	**arg**	**lys**	**lys**	**glu**	**lys**		
	46	**leu**	**leu**	**ser**	**leu**	**leu**	**ser**	**leu**	**leu**	VAL	**leu**	**leu**	**leu**	**leu**	**leu**	**leu**	**leu**	**phe**	**leu**	**ile**	**leu**	**leu**	**leu**	**leu**	**leu**	**leu**
	47	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
	48	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE		ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE
	49	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR		TYR	**phe**	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	**phe**	TYR	TYR	TYR	TYR
	50	**ala**	**ala**	**ala**	**asp**	**ala**	**asp**	**ala**	**ala**	**ala**	**gln**	**gly**	**ala**	**ala**	**glu**	**asp**	**asp**	**asp**	**asn**	**asp**	**gly**	**asp**	**ala**	**gly**	**asp**	**asp**
	51	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	**thr**	ALA	ALA	**thr**	ALA	ALA	ALA	ALA
CDR2	52	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	**glu**	**asn**	SER	SER	SER	SER	SER	SER	SER
	53	**thr**	**ser**	**ser**	**ser**	**ser**	**thr**	**thr**	**thr**	**ser**	**ile**	**ser**	**ser**	**ser**	ASN	ASN	**lys**	ASN	ASN	ASN	**ser**	**thr**	**thr**	ASN	**ser**	**thr**
	54	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	**arg**	LEU	LEU	
	55	**gln**	**gln**	**gln**	**glu**	**gln**	**gln**	**gln**	**gln**	LYS	**asp**	**arg**	**gln**	**gln**	**gln**	**glu**	**glu**	**glu**	**gln**	**glu**	**glu**	**gln**	**glu**	LYS	**glu**	
	56	**ser**	**ser**	**ser**	**ser**	**ser**	**ser**	**ser**	**ser**	**ser**	**ala**	**ser**	**ser**	**ser**	**ala**	**ser**	**ala**	**ile**	**thr**	**thr**	**thr**	**ser**	**thr**	**ala**	**thr**	**thr**
	57	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
	58	**val**	**val**	**val**	**val**	ILE	**val**	**val**	**val**	**val**	**val**	**val**	**val**	ILE	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**
	59	PRO	**thr**	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO		PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO
	60	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
	61	ARG	ARG	ARG	ARG	ARG	**asn**	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG
	62	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE
	63	SER	SER	SER	SER	SER	**thr**	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	**arg**	SER	SER	SER	SER	SER	SER	SER	SER
	64	GLY	GLY	GLY	GLY	**asp**	GLY	GLY	GLY	GLY	GLY	GLY	GLY	**asp**	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
	65	SER	SER	SER	SER	SER	SER	SER	SER	**asn**	SER	SER	SER	SER	SER	**gly**	**thr**	SER	SER	SER	SER	**gly**	**gln**	SER	SER	SER
	66	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	**ile**	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	**arg**	GLY	GLY	GLY	GLY	GLY
	67	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	**phe**	SER	SER	SER	SER	SER	SER	SER
	68	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	**glu**	GLY	
	69	THR	THR	THR	THR	**ala**	THR	THR	THR	THR	THR	THR	THR	**ala**	THR	**ala**	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
	70	GLU	**asp**	**asp**	**asp**	**asp**	**asp**	**asp**	**asp**	**asp**	**asp**	**asp**	**asp**	**asp**	**asp**	**his**	**asp**	**asp**	**asp**	**asp**	**asp**	**asp**	**asx**	**asp**	**his**	**asp**
	71	PHE	PHE	PHE	PHE	**tyr**	PHE	PHE	PHE	PHE	PHE	PHE	PHE	**tyr**	**tyr**	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE
FR3	72	THR	THR	THR	THR	THR	**ile**	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	**ala**	THR	THR	THR	THR	THR	THR	THR	THR
	73	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	**phe**	**phe**	**phe**	LEU	LEU	LEU	LEU	**phe**	**phe**	LEU	**phe**	LEU
	74	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	**ser**	THR	THR	THR	THR	THR	THR	THR	THR
	75	**ile**	**ile**	**ile**	**ile**	**ile**	**ile**	**ile**	**ile**	**ile**	**ile**	**ile**	**ile**	**ile**	**ile**	**ile**	**ile**	**ile**	**ile**	**ile**	**ile**	**ile**	**ile**	**ile**	**ile**	**ile**
	76	**ser**	**ser**	**ser**	**ser**	**arg**	**ser**	**ser**	**ser**	**ser**	**ser**	**thr**	**ser**	**ser**	**ser**	**ser**	**ser**	**ser**	**ser**	**ser**	**ser**	**ser**	**ser**	**ser**		**ser**
	77	**ser**	**ser**	**ser**	**ser**	**ser**	**ser**	**cys**	**cys**	**gly**	**ser**	**ser**	**ser**	**ser**	**ser**	**ser**	**gly**	**ser**	**ser**	**gly**	**thr**	**ser**	**ser**	**ser**	**gly**	
	78	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	**val**	LEU	LEU	LEU
	79	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	**leu**	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLX	GLN	GLN
	80	**pro**	**pro**	**pro**	**pro**	**pro**	**pro**	SER	SER	**pro**	**pro**	**pro**	**pro**	**pro**	**pro**	**pro**	**pro**	**pro**	**pro**	**pro**	**pro**	**pro**	**pro**	**pro**	**pro**	**pro**
	81	**glu**	**glu**	**glu**	**glu**	**glu**	**glu**	**glu**	**glu**	**glu**	ASP	**glu**	**glu**	**glu**	**glu**	**glu**	**glu**	**glu**	**glu**	**glu**	ASP	**glx**	**glu**	**ala**	**glx**	
	82	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	**asn**	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASX	ASP	ASP	ASX	
	83	PHE	**ser**	PHE	PHE	PHE	PHE	PHE	PHE	PHE	**ser**	PHE	**val**	PHE	**ile**	**ile**	**ile**	PHE	**ile**	**ile**	**ile**	PHE	PHE	PHE	PHE	
	84	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	**gly**	ALA	ALA	ALA	ALA	ALA
	85	THR	THR	THR	THR	THR	THR	THR	THR	THR	**arg**	**ala**	THR	**ala**	THR	THR	THR	THR	THR	THR	**asn**	THR	THR	THR	THR	**val**
	86	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR
	87	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	**phe**	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR
	88	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS
	89	**gln**	**gln**	**gln**	**gln**	**gln**	**gln**	**gln**	**gln**	**glx**	**gln**	**gln**	**leu**	**gln**	**gln**	**gln**	**gln**	**leu**	**gln**	**gln**	**gln**	**gln**	**gln**	**gln**	**gln**	**gln**
	90	**gln**	**gln**	**gln**	**gln**	**gln**	**gln**	**gln**	**gln**	**glx**	**gln**	**gln**	**gln**	**gln**	**gln**	**gln**	**gln**	**gln**	**gln**	**gln**	**gln**	**glx**	**gln**	**gln**	**glx**	
	91	**leu**	**ser**	**tyr**	**phe**	**ser**	**tyr**	**tyr**	**tyr**	**ser**	**tyr**	**ser**	**asp**	**ser**	**tyr**	**tyr**	**phe**	**tyr**	**his**	**tyr**	**tyr**	**ser**	**tyr**	**tyr**	**tyr**	
	92	**asn**	**tyr**	**asn**	**asn**	ASP	**asn**	**tyr**	**tyr**	**tyr**	**asn**	**tyr**	**tyr**	ASP	**gln**	ASP	ASP	**tyr**	**ile**	ASP	ASP	**tyr**	**leu**	**asn**	ASX	ASP
	93	SER	SER	SER	SER	SER	SER	SER	SER	**thr**	**arg**	SER	**thr**	SER	SER	**tyr**	**asn**	**asn**	SER	**thr**	**asn**	**thr**	**asp**	**asn**	**his**	**thr**
CDR3	94	**tyr**	**thr**	**tyr**	**tyr**	**thr**	**tyr**	**tyr**	PHE	**thr**	**tyr**	**ser**	**thr**	**thr**	**leu**	**leu**	**leu**	**leu**	**arg**	**leu**	**val**	**asn**	**leu**	**trp**	PHE	**leu**
	95	**pro**	**leu**	**pro**	**pro**	**pro**	**pro**	**pro**	**pro**	**pro**	---	**pro**	**pro**	**pro**	**pro**	**pro**	**pro**	**pro**	**pro**	**pro**	**pro**	**pro**	**pro**	**pro**	**pro**	
	95A	---	---	#	---		---	---	---	---	---	---			---	---	---	---	---	---	---	GLU	---	---	---	---	
	95B	---	---	---	---		---	---	---	---	---	---			---	---	---	---	---	---	---	---	---	---	---	---	
	95C	---	---	---	---		---	---	---	---	---	---			---	---	---	---	---	---	---	---	---	---	---	---	
	95D	---	---	---	---		---	---	---	---	---	---			---	---	---	---	---	---	---	---	---	---	---	---	
	95E	---	---	---	---		---	---	---	---	---	---			---	---	---	---	---	---	---	---	---	---	---	---	
	95F	---	---	---	---		---	---	---	---	---	---			---	---	---	---	---	---	---	---	---	---	---	---	
	96	---	ILE	---	---		TYR	---	---	TYR	---	TRP			TYR	TRP	LEU	TYR	ARG	ARG	ILE	VAL	ARG	PRO	LEU	SER
	97	---	THR	---	---		THR	---	---	THR	---	THR			THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
	98	---	PHE	---	---		PHE	---	---	PHE	PHE	PHE			PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE
	99	---	GLY	---	---		GLY	---	---	GLY	GLY	GLY			GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
	100	---	GLN	---	---		GLN	---	---	PRO	GLN	GLN			GLN	GLN	GLY	GLN	GLN	GLN	GLN	GLY	GLN	GLN	GLY	VAL
	101	---	GLY	---	---		GLY	---	---	GLY	GLY	GLY			GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
	102	---	THR	---	---		THR	---	---	THR	THR	THR			THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	SER
FR4	103	---	ARG	---	---		LYS	---	---	LYS	LYS	LYS			LYS	LYS	LYS	LYS	LYS	LYS	ARG	THR	LYS	LYS	GLU	LYS
	104	---	LEU	---	---		#	---	---	VAL	LEU	VAL			LEU	VAL	VAL	LEU	VAL	LEU	VAL	VAL	VAL	VAL	VAL	VAL
	105	---	GLU	---	---		#	---	---	GLU	GLU	GLU			GLN	GLU	ASP	GLU	GLU	GLU	GLU	ASP	ASP	GLU	GLU	
	106	---	ILE	---	---		ILE	---	---	MET	ILE	ILE			ILE	ILE	PHE	ILE	ILE	ILE	ASN	ILE	LEU	VAL	VAL	SER
	106A	---	---	---	---		---	---	---	---	---	---			---	---	---	---	---	---	---	---	---	---	---	---
	107	---	LYS	---	---		LYS	---	---	THR	LYS	ARG			THR	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS
	108	---	---	---	---		ARG	---	---	ARG	ARG				ARG	ARG	ARG	ARG	ARG	ARG	GLY	ARG	ARG	ARG		ARG
	109	---	---	---	---			---	---	THR	THR				THR	THR	THR	THR		THR	THR		THR	.		THR

HUMAN KAPPA LIGHT CHAINS SUBGROUP I (cont'd)

		50 RZ	51* Hu RSV19 VK #	52 HBJ 4	53 BJ 26 #	54 BJ 19 #	55 RFZ	56 HA	57 PAU	58 PSM	59 JBL #	60 NE	61 FRA	62 BJ 48	63 HF3- 16/6	64 HF2- 1/13B	65 HF2² 18/2	66 GR'	67 G1 'CL #	68 HOM	69 KER	70 ESM IGG	71 ESM IGM	72* DAV	73* FIN	74 PW #	75 SHE	76 ADA
	0	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		---	---	---	---	---	---	---	---
	1	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP		ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP
	2	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE		ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE
	3	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	**his**	GLN	GLN	GLN	GLN	GLN	GLN		GLN	GLN	GLN	GLN	GLN	**his**	GLN	GLN
	4	MET	**leu**	MET	MET	**leu**	MET	MET	MET	MET	MET	**leu**	MET	MET	MET	MET	MET	MET		MET	MET	MET	MET	MET	MET	**leu**	**val**
	5	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR		THR	THR	THR	THR	THR	THR	THR	THR
	6	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLX	GLN	GLN	GLN	GLN	GLN	GLN		GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN
	7	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER		SER	SER	SER	SER	SER	SER	SER	SER
	8	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO		PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO
	9	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER		SER	SER	SER	SER	SER	**thr**	SER	
F	10	**ser**	**ser**	THR	**ser**	**ser**	**ser**	**ser**	THR	**ser**	**ser**	**ser**	THR	**ser**	**ser**	**ser**	**ser**	THR		**ser**	**ser**	**ser**	**ser**	**ser**	**ser**	**ser**	**ser**
R	11	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU		LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
1	12	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER		SER	SER	SER	SER	SER	SER	SER	SER
	13	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA		ALA	ALA	ALA	ALA	**thr**	**thr**	ALA	**val**
	14	SER	SER	SER	SER	SER	SER	SER	SER	SER	**tyr**	SER	SER	SER	SER	SER	SER	SER		SER	SER	SER	SER	**val**	**val**	SER	**phe**
	15	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL		VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
	16	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
	17	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASX	ASP	ASP	ASP	ASP	ASP	ASP		ASP	ASP	ASP	ASP	ASP	ASP	ASX	ASP
	18	**arg**	**arg**	**arg**	**arg**	**arg**	**arg**	**arg**	**arg**	**arg**	**arg**	**arg**	**arg**	**arg**	**arg**	**arg**	**arg**	**arg**		**arg**	**arg**	**arg**	**arg**	**arg**	**arg**	**arg**	**arg**
	19	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**		**val**	ILE	**val**	**val**	**val**	**val**	**val**	**val**
	20	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR		THR	THR	THR	THR	THR	THR	THR	THR
	21	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE		ILE	ILE	ILE	ILE	ILE	**val**	**phe**	ILE
	22	THR	THR	THR	THR	THR	THR	THR	THR	THR	**ala**	THR	THR	THR	THR	THR	THR	THR		THR	THR	THR	THR	THR	**arg**	THR	THR
	23	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS		CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS
	24	**gln**	ARG	ARG	**gln**	**gln**	**gln**	**gln**	ARG	**gln**	ARG	**glx**	ARG		ARG	ARG	ARG	ARG		**gln**	**gln**	ARG	ARG	**asp**	**asp**	ARG	**glx**	**glx**
	25	ALA	**ser**	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA		ALA	ALA	ALA	ALA		ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA
	26	**asn**	SER	SER	SER	SER	**asn**	SER	SER	SER	SER	SER	SER		SER	SER	SER	SER		**arg**	SER	SER	SER	SER	SER	SER	SER	SER
	27	GLN	GLN	GLN	GLN	GLN	GLN	---	GLN	GLN	GLN	GLX			GLN	GLN	GLN	**arg**		**his**	GLN	GLX	GLX	GLN	GLN	GLX	GLX	GLX
	27A	---	**thr**	---	---	---	---	---	---	---	---	---	---		---	---	---	---		---	---	---	---	---	---	---	---	---
	27B	---	**leu**	---	---	---	---	---	---	---	---	---	---		---	---	---	---		---	---	---	---	---	---	---	---	---
C	27C	---	**val**	---	---	---	---	---	---	---	---	---	---		---	---	---	---		---	---	---	---	---	---	---	---	---
C	27D	---	**his**	---	---	---	---	---	---	---	---	---	---		---	---	---	---		---	---	---	---	---	---	---	---	---
D	27E	---	**thr**	---	---	---	---	---	---	---	---	---	---		---	---	---	---		---	---	---	---	---	---	---	---	---
R	27F	---	---	---	---	---	---	---	---	---	---	---	---		---	---	---	---		---	---	---	---	---	---	---	---	---
1	28	**val**	**asp**	SER	SER	**asp**	**val**	---	SER	**asp**	SER	**asx**	**asx**		**gly**	**gly**	**gly**	SER		**asp**	**asp**	SER	SER	**asx**	**asx**	SER	**asx**	**asx**
	29	ILE	**gly**	**val**	ILE	ILE	ILE	---	ILE	ILE	ILE	ILE	ILE		ILE	ILE	ILE	ILE		ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE
	30	**ser**	**asn**	**asn**	**asn**	**asn**	**ser**	**arg**	**ser**	**arg**	**ser**	**ser**	**asx**		**arg**	**arg**	**arg**	**ser**		**ser**	**lys**	**ser**	**ser**	**asx**	**asx**	GLY	**ser**	
	31	**lys**	**thr**	ASN	**lys**	**thr**	**lys**	ASN	**ser**	**ser**	**thr**	ASX	ASX		ASN	ASN	ASN	**ser**		ASN		**ser**	**ser**	**ser**	**ser**		ASX	ASX
	32	**ser**	**tyr**	TRP	**tyr**	**phe**	**ser**	**tyr**	**ser**	**tyr**	**phe**	**tyr**	**tyr**		**asp**	**asp**	**asp**	TRP		**tyr**		**tyr**	**tyr**	TRP	TRP	**tyr**	**tyr**	**tyr**
	33	LEU	LEU	LEU	**ala**	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU		LEU	LEU	LEU	LEU		LEU		LEU	LEU	LEU	LEU	**ser**	LEU	LEU
	34	**asn**	**glu**	ALA	**asn**	**asn**	**asn**	**asn**	ALA	**asn**	#	**asx**	ALA		**gly**	**gly**	**gly**	ALA		**asn**		**asx**	**asx**	**ile**	**ile**	**asx**	**asx**	**asx**
	35	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP		TRP	TRP	TRP	TRP		TRP		TRP	TRP	TRP	TRP	TRP	TRP	TRP
	36	**tyr**	**tyr**	**tyr**	**tyr**	**tyr**	**tyr**	**tyr**	**tyr**	**tyr**	**tyr**	**tyr**	**tyr**		**tyr**	**tyr**	**tyr**	**tyr**		PHE		**tyr**	**tyr**	**tyr**	**tyr**		**tyr**	**tyr**
	37	GLN	GLN	GLN	**glu**	**glu**	GLN	GLN	GLX	GLN	GLN	GLX	GLX		GLN	GLN	GLN	GLN		GLN		GLX	GLX	GLN	GLN	GLN	**his**	GLX
	38	GLN	GLN	**glu**	GLN	GLN	GLN	GLN	GLX	GLN	GLN	GLX	GLX		GLN	GLN	GLN	**gly**		GLN				GLN	GLN	GLN	GLX	**tyr**
	39	**arg**	LYS	LYS	#	#	**arg**	LYS	LYS	LYS	LYS	LYS	LYS		LYS	LYS	LYS	**arg**		LYS				**tyr**	**tyr**	LYS	LYS	LYS
	40	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	**gln**	PRO	PRO	PRO		PRO	PRO	PRO	PRO		PRO				PRO	PRO		PRO	PRO
	41	GLY	GLY	GLY	#	#	GLY	GLY	GLY	GLY	GLY	GLY								GLY								
F	42	**gln**	LYS	**glx**	LYS	LYS	**gln**	**arg**	**glx**	LYS	LYS	**glx**																
R	43	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA		ALA														
2	44	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO		PRO														
	45	**lys**	**lys**	**lys**	**lys**	**lys**	**lys**	**lys**	**lys**	**lys**	**lys**	**lys**		**lys**														
	46	**leu**	**leu**	**leu**	**leu**	**leu**	**leu**	**leu**	**leu**	**leu**	**leu**	VAL																
	47	LEU	LEU	LEU		LEU	LEU	LEU	LEU	LEU	LEU	**met**																
	48	ILE	ILE	ILE		ILE	ILE	ILE	ILE	ILE		ILE																
	49	TYR	TYR	**ser**		TYR	TYR	TYR	TYR	TYR	TYR	TYR		**gly**														
	50	**asp**	**arg**	LYS		**asp**	**asp**	**asp**	**glx**	**asp**				**asp**														
	51	ALA	**val**	**thr**	**asp**	ALA	ALA	ALA		ALA				ALA														
C	52	SER	SER	SER	SER	SER	**ala**	**phe**		SER				SER														
D	53	ASN	ASN	**ser**	**arg**	**ser**	ASX	ASN						**ser**														
R	54	LEU	**arg**	LEU	LEU	LEU	LEU	LEU		LEU				LEU														
2	55	**glu**	**phe**	**glu**	**glu**	**glu**	**glu**	**glu**		**glu**				**asx**														
	56	**ser**	**ser**	**arg**	**thr**	**thr**		**ala**						**ser**														
	57	GLY	GLY	GLY	GLY	GLY	GLY	GLY						GLY														
	58	**val**	**val**	**val**	**asx**	**val**	**val**	**val**						**val**					ILE								
	59	PRO	PRO	PRO	PRO	**glx**	PRO	PRO						**val**					PRO								
	60	SER	SER	SER	SER	SER		SER						SER					SER								
	61	ARG	ARG	ARG	**lys**	ARG	ARG	ARG						ARG					ARG								
	62	PHE	PHE	PHE	**val**	PHE	PHE							**gln**					PHE								
	63	**thr**	SER	**ala**	SER	**leu**	**thr**							SER					SER								
	64	GLY	GLY	GLY	GLY	GLY	GLY							GLY					GLY								
	65	SER	SER	SER	SER	SER								SER					SER								
	66	GLY	GLY	GLY	GLY	**asx**	GLY							GLY					GLY								
	67	SER	SER		SER	**phe**								SER					SER								
	68	GLY	GLY		**glu**	**asx**								GLY					GLY								
	69	THR	THR		THR	THR								THR					THR								
	70	**asp**	**asp**		**asp**	**lys**								**asp**					GLU								
	71	PHE	PHE		**val**									**pro**					PHE								
F	72	**phe**	THR		THR									**ser**					THR								
R	73	LEU	**phe**		**val**									LEU					LEU								
3	74	THR	THR		**asx**									**ala**					THR								
	75	**ile**	**ile**		**glx**									VAL					VAL								
	76	**ser**	**ser**		**ser**									**ser**					ILE								
	77	**ser**	**ser**		**ser**									**arg**					ASN								
	78	LEU	LEU		LEU														LEU								
	79	**arg**	GLN		GLN														GLN								
	80	**pro**	**pro**		**pro**														SER								
	81	**glu**	**glu**		**glu**														ASP								
	82	ASP	ASP		ASP														ASP								
	83	**val**	**ile**		**ile**														PHE								
	84	ALA	ALA		ALA														ALA								
	85	THR	THR		**pro**														THR								
	86	TYR	TYR		**lys**														TYR		TYR						
	87	**phe**	TYR																TYR		TYR						
	88	CYS	CYS																CYS		CYS						
	89	**gln**	**phe**		**gln**														HIS		**gln**						
	90	**gln**	**gln**		**gln**														HIS		**gln**						
	91	**tyr**	**gly**		**arg**	**phe**								**gly**					ASN		**tyr**						
	92	**his**	**ser**		ASP	ASP								**glu**					ASP		ASP						
	93	**asn**	**his**		**asp**	**asp**								SER					**thr**		**asp**						
C	94	**leu**	**leu**		**leu**	**leu**								**asp**					PHE		**leu**						
D	95	**pro**	**pro**		**pro**	**pro**								SER					SER		**pro**						
R	95A	---	---		---	---								---					---		---						
3	95B	---	---		---	---								---					---		---						
	95C	---	---		---	---								---					---		---						
	95D	---	---		---	---								---					---		---						
	95E	---	---		---	---								---					---		---						
	95F	---	---		---	---								---					---		---						
	96	LEU	ARG		TYR	TYR								ARG					TRP		PRO						
	97	THR	THR		THR	THR								THR					THR		THR						
	98	PHE	PHE		LEU	PHE								PHE					PHE		PHE						
	99	GLY	GLY		GLY	GLY								GLY					GLY		GLY						
	100	GLY	GLY		GLY	PRO								GLN					GLN		PRO						
	101	GLY	GLY		GLY	GLY								GLY					GLY		GLY						
	102	THR	THR		THR	THR								THR					THR		THR						
F	103	LYS	LYS		LYS	LYS								LYS					LYS		LYS						
R	104	VAL	VAL		VAL	VAL								VAL					VAL		VAL						
4	105	GLU	GLU		GLU	GLU								GLU					LEU		ASP						
	106	ILE	ILE		MET	LEU								VAL					ILE		LEU						
	106A	---			---	---								---					---		---						
	107	LYS			LYS	LYS								LYS					LYS		LYS						
	108																		ARG								
	109																										

HUMAN KAPPA LIGHT CHAINS SUBGROUP I (cont'd)

		77 AMYLOID VIII-B	78 PAUL	79 RI #	80 WAT	81* LOW	82 AMYLOID ES305 #	83 OCO	84 BOL	85 AMYLOID X	86 SAC	87 BJ	88 GO	89 F-GUI #	90 S-GUI #	91 HF6-21/28	92 DIE	93 CAR A	94 TEI	95 MON	96 ALE	97 JOH	98 POT	99 CON	100 TRA	101* H-G2b
	0	---	---	pca	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	1	ASP	ASP	ASP	ASP	ASP	ASP	ASX	ASP	ASP	ASP	ASX	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASX	ASP	ASP	ASP	ASP	ASP
	2	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE		val	ILE	ILE	val	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE
	3	GLN	GLN	GLN	GLN	GLN	GLN	GLX	GLN	GLN	MET	MET	MET	MET	MET	val	GLN	GLN	GLN	GLN	GLX	GLN	GLN	GLN	GLN	GLN
	4	MET	MET	MET	MET	MET	leu	MET	ile	MET						MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET
	5	THR	THR	THR	THR	THR	THR	THR	met	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
	6	GLN	GLN	GLN	GLN	GLN	GLN	GLX	GLX	GLN	GLN	GLN	GLX	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLX	GLN	GLN	GLN	GLN	GLN
	7	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER		SER	SER	ala	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
	8	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	ala	PRO		PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO
	9	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER		SER	SER	SER	leu	SER	SER	SER	SER	SER	ala	SER	SER	SER	SER
FR1	10	ser	THR	THR	ser	ser	ser	ser	ser	ser	ser		phe	ser	ser	ser	ser	ser	ser	THR		ser	ser	ser	ser	ser
	11	LEU	LEU	LEU	LEU	LEU	LEU	LEU	val	LEU	LEU		val	LEU	LEU	LEU	LEU	LEU	LEU	LEU		LEU	LEU	LEU	LEU	LEU
	12	SER	SER	SER	SER	SER	SER	val	SER	SER	SER		SER	SER	SER	pro	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
	13	ALA	ALA	ALA	ALA	ALA	ALA	ser	ALA	ALA	ALA		ALA	ALA	ALA	val	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA
	14	SER	SER	SER	SER	SER	SER	pro	SER	SER	SER		SER	SER	SER	thr	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
	15	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL		VAL	VAL	VAL	leu	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
	16	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
	17	ASP	ASP	ASP	ASP	ASP	ASP	ASX	ASX	ASP	ASP		ASX	ASX	ASX	gly	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP
	18	arg	arg	gly	arg	arg		leu	arg	arg	---	arg	arg	arg	arg	pro	arg	arg	arg	arg	arg	arg	arg	arg	arg	arg
	19	val	val	val	val	val	val	val	val	val	---	val	val	val	val	ala	val	val	val	val	val	val	val	val	val	val
	20	THR	THR	THR	THR	THR	THR	THR	THR	ile	---	THR	THR	THR	THR	ser	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
	21	ILE	ILE	ILE	ILE	ILE	#	ILE	ILE	ILE	---	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	leu	ILE	ILE	ILE	ILE	ILE
	22	THR	THR	ser	THR	THR	THR	THR	THR		---	THR	THR	THR	THR	ser	THR	THR	THR	THR	THR	ser	THR	THR	THR	THR
	23	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	---	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS		CYS	CYS	CYS			
	24	gln	ARG	ARG	glx	ala	gln	glx	ARG	glx	---	gln	ARG		ARG	ARG					ARG					
	25	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	---	ALA	ALA	ALA	ALA	ser										
	26	SER	SER	SER	SER	SER	SER	SER	SER		---	SER	SER			SER										
	27	GLN	GLN	GLX	GLN	GLN	glu	GLX	GLX	GLX	---	GLN				GLN										
	27A	---	---	---	---	---	---	---	---	---	---	---				ser										
	27B	---	---	---	---	---	---	---	---	---	---	---				leu										
	27C	---	---	---	---	---	---	---	---	---	---	---				val										
CDR1	27D	---	---	---	---	---	---	---	---	---	---	---				trp										
	27E	---	---	---	---	---	---	---	---	---	---	---				ser										
	27F	---	---	---	---	---	---	---	---	---	---	---				---										
	28	asx	SER	SER	asp	asx	ala	asx	gly	asx	---	asp				asp										
	29	ILE	ILE	ILE	ILE	ILE	#	ILE	ILE	ILE	---	ILE				gly										
	30	GLY	ser	ser	ser	ser		ser			---	asn				arg										
	31		ser		asp		ASN	ASX		pro	---	lys				ser										
	32	tyr	ser		tyr		tyr	tyr		tyr	---					tyr										
	33	LEU			val		LEU			LEU	---					LEU										
	34				asn						---					glu										
	35	TRP			TRP		TRP				---					TRP										
	36						tyr			tyr	---					tyr										
	37										---					GLN										
	38										---					GLN										
	39										---					LYS										
	40										---					PRO										
	41										---															
FR2	42										---															
	43										---															
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	47										---															
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	50										LYS															
	51										ser															
CDR2	52										---															
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	71										---															
FR3	72										---															
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	86										---	TYR														
	87										---	TYR														
	88										CYS	CYS														
	89										glx	gln														
	90										glx	gln														
	91										glx	tyr														
	92										ASX	glu														
	93										ala	asn														
	94										ala	leu														
CDR3	95										thr	pro														
	95A										---	---														
	95B										---	---														
	95C										---	---														
	95D										---	---														
	95E										---	---														
	95F										---	---														
	96										ILE	TYR														
	97										PRO															
	98										ILE															
	99										GLY															
	100										GLY															
	101										GLY															
	102										THR															
FR4	103										LYS															
	104										VAL															
	105										ASX															
	106										VAL															
	106A										---															
	107										LYS															
	108										ARG															
	109										THR															

HUMAN KAPPA LIGHT CHAINS SUBGROUP I (cont'd)

		102* K-G2	103 BRA	104 LUX	105* HEI	106 PAP	107* H-G2a	108 CRA	109 AMYLOID LEP	110* WAG	111 HOE	112 HBJ 1	113 AMYLOID 547	114 WEB	115 HBJ 10	116 LOD	117 BEN	118 MAA	119 GR	120 MUK	121 GM131 'CL #	122 AMYLOID 594	123* MAR	124 CL*
	0	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		---	---	---
	1	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP		ASP	ASP	---
	2	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE		ILE	ILE	---
	3	GLN	GLN	GLN	GLN	GLN		GLN	GLN	GLN	GLN	**leu**	GLX	GLN	GLN	GLN	GLN	GLN	GLN	GLN		GLN	GLN	---
	4	MET	MET	**leu**	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET		MET	**leu**	MET	MET		MET	**leu**	---
	5	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR		THR	THR	---
	6	GLN	GLX	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN		GLN	GLN	---
	7	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER		SER	SER	---
	8	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO		PRO	PRO	---
	9	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	**thr**	SER	SER	SER	SER	SER	SER	SER	SER		SER	SER	---
F	10	**ser**	**ser**	**phe**	THR	**ser**	**ser**	**ser**	**ser**	**ser**	THR	**ser**	**ser**	**ser**	**ser**	THR	**ser**	THR	**ser**	**ser**		**ser**	**ser**	---
R	11	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	**val**	LEU		LEU	LEU	LEU	LEU		LEU	LEU	---
1	12	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER				---
	13	ALA	**val**	ALA	ALA	**val**	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	**val**					---
	14	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER									---
	15	VAL	VAL	VAL	VAL	VAL	VÁL	**leu**	VAL	VAL	VAL	VAL	VAL	VAL		VAL								---
	16	GLY	GLY	GLY	GLY	GLY	GLY	**arg**	GLY	GLY		GLY												---
	17	ASP	**glx**	ASP	ASP	ASP	ASP	ASP	ASP	ASP		ASP												---
	18	**arg**	**arg**	**arg**	**arg**	**arg**	**arg**	**arg**	**arg**															---
	19	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**															---
	20	THR	THR	THR	THR	THR		THR	THR															---
	21	ILE	ILE	ILE		ILE	ILE	ILE																---
	22	THR	THR	THR		**ala**	THR	THR																---
	23		CYS																					---
	24																							---
	25																							---
	26																							---
	27																							---
	27A																							---
	27B																							---
C	27C																							---
D	27D																							---
R	27E																							---
1	27F																							---
	28																							---
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	40																							---
F	41																							---
R	42																							---
2	43																							---
	44																							---
	45																							---
	46																							---
	47																							---
	48																							---
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	83																				PHE			---
	84																				ALA			---
	85																				THR			---
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	87																				TYR			---
	88																				CYS			---
	89																				**gln**			---
	90																				**gln**			---
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	92																				ASP			ASP
	93																				**his**			**ile**
C	94																				**leu**			PHE
D	95																				**pro**			**pro**
R	95A																				---			---
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	95F																				---			---
	96																				LEU			GLY
	97																				THR			THR
	98																				PHE			PHE
	99																				GLY			GLY
	100																				GLY			GLN
	101																				GLY			GLY
	102																				THR			THR
F	103																				THR			LYS
R	104																				VAL			VAL
4	105																				GLU			GLU
	106																				MET			ILE
	106A																				---			---
	107																				LYS			LYS
	108																				ARG			ARG
	109																				THR			THR

HUMAN KAPPA LIGHT CHAINS SUBGROUP I (cont'd)

		125 AMYLOID	126 HBJ 6	127 AMYLOID MS #	128 PEN	# OF SEQUENCES	# OF AMINO ACIDS	OCCURRENCES OF MOST COMMON AMINO ACID	VARIABILITY
	0	---	---	---	---	1	1	1(PCA)	
	1	ASP	ASP	ASP	ASP	125	3,4	122(ASP),118(ASP)	3.1,4.2
	2	ILE	ILE	#	ILE	123	2	120(ILE)	2.
	3	glu	GLN	GLN	GLN	123	7	116(GLN),112(GLN)	7.4,7.7
	4	MET	MET	MET	MET	124	4	109(MET)	4.6
	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	2	120(PRO)	2.
	9	SER				121	4	117(SER)	4.1
FR1	10	ser				120	5	89(SER)	6.7
	11	LEU				119	4	111(LEU)	4.3
	12					118	3	115(SER)	3.1
	13					117	4	107(ALA)	4.4
	14					113	6	106(SER)	6.4
	15					113	3	109(VAL)	3.1
	16					109	2	108(GLY)	2.
	17					109	3,4	106(ASP),98(ASP)	3.1,4.4
	18					106	6	97(ARG)	6.6
	19					107	3	101(VAL)	3.2
	20					106	4	102(THR)	4.2
	21					104	4	99(ILE)	4.2
	22					104	6	95(THR)	6.6
	23					96	1	96(CYS)	1.
	24					88	6	57(ARG)	9.3
	25					88	6	82(ALA)	6.4
	26					85	4	79(SER)	4.3
	27					84	4	79(GLN),66(GLN)	4.3,5.1
	27A					3	2	2(SER)	
	27B					3	2	2(LEU)	
	27C					3	2	2(VAL)	
CDR1	27D					3	3	1(+)	
	27E					2	2	1(+)	
	27F								
	28					84	7	29(SER)	20.
	29					83	5	72(ILE)	5.8
	30					81	11	41(SER)	22.
	31					79	12	27(ASN),24(SER)	35.,39.
	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(LYS)	4.4
	40					70	3	68(PRO)	3.1
FR2	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	5	50(ALA)	5.9
CDR2	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					58	3	56(ARG)	3.1
	62					57	3	55(PHE)	3.1
	63					57	6	50(SER)	6.8
	64					57	2	55(GLY)	2.1
	65					56	5	51(SER)	5.5
	66					57	4	54(GLY)	4.2
	67					55	3	51(SER)	3.2
	68					55	3	52(GLY)	3.2
	69					55	2	51(THR)	2.2
	70					55	5,6	33(ASP),31(ASP)	8.3,11.
	71					54	4	49(PHE)	4.4
FR3	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					53	5	43(SER)	6.2
	77					54	6	40(SER)	8.1
	78					54	2	53(LEU)	2.
	79					54	3,4	52(GLN),48(GLN)	3.1,4.5
	80					54	2	46(PRO)	2.3
	81					54	3,5	37(GLU),34(GLU)	4.4,7.9
	82					54	2	53(ASP),50(ASP)	2.,2.2
	83					54	4	40(PHE)	5.4
	84					54	2	53(ALA)	2.
	85					54	6	48(THR)	6.7
	86					56	2	55(TYR)	2.
	87					55	2	52(TYR)	2.1
	88					56	1	56(CYS)	1.
	89					57	4,5	46(GLN),43(GLN)	5.,6.6
	90					57	2,3	51(GLN),46(GLN)	2.2,3.7
	91					59	11,12	28(TYR)	23.,25.
	92					60	9	20(ASN),19(+)	27.,28.
	93					60	9	29(SER)	19.
	94					60	12	15(LEU)	48.
CDR3	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.
FR4	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

REFERENCE: HUMAN KAPPA LIGHT CHAINS SUBGROUP I

1) **2C12'CL:** LEVY,S.,MENDEL,E.,KON,S.,AVNUR,Z. & LEVY,R. (1988) J.EXP.MED.,168,475-489.
2) **1B11'CL:** LEVY,S.,MENDEL,E.,KON,S.,AVNUR,Z. & LEVY,R. (1988) J.EXP.MED.,168,475-489.
3) **1H1'CL:** LEVY,S.,MENDEL,E.,KON,S.,AVNUR,Z. & LEVY,R. (1988) J.EXP.MED.,168,475-489.
4) **2A12'CL:** LEVY,S.,MENDEL,E.,KON,S.,AVNUR,Z. & LEVY,R. (1988) J.EXP.MED.,168,475-489.
5) **BR:** KIM,H.S. & DEUTSCH,H.F. (1988) IMMUNOL.,64,573-579.
6) **DEN:** YANG,C.Y.,PAULY,E.,KRATZIN,H. & HILSCHMANN,N. (1981) Z.PHYSIOL.CHEM.,362,1131-1146.
7) **3D6'CL:** FELGENHAUER,M.,KOHL,J. & RUKER,F. (1990) NUCL.ACIDS RES., 18,4927.
8) **HK102'CL:** BENTLEY,D.L. & RABBITTS,T.H. (1980) NATURE,288,730-733. (CHECKED BY AUTHOR 11/30/82)
9) **EU:** GOTTLIEB,P.D.,CUNNINGHAM,B.A.,RUTISHAUSER,U. & EDELMAN,G.M. (1970) BIOCHEMISTRY,9,3155-3161. (CHECKED BY AUTHOR)
10) **CAR:** MILSTEIN,C.P. & DEVERSON,E.V. (1974) EUR.J.BIOCHEM.,49,377-391. (CHECKED BY AUTHOR)
11) **PA:** KIM,H.S. & DEUTSCH,H.F. (1988) IMMUNOL.,64,573-579.
12) **HK137'CL:** BENTLEY,D.L. & RABBITTS,T.H. (1983) CELL,32,181-189.
13) **HAU:** WATANABE,S. & HILSCHMANN,N. (1970) Z.PHYSIOL.CHEM.,351,1291-1295. (CHECKED BY AUTHOR)
14) **KUE:** EULITZ,M.,KLEY,H.P. & ZEITLER,H.J. (1979) Z.PHYSIOL.CHEM.,360,725-734. (CHECKED BY AUTHOR 07/17/79)
15) **HF2-1/17:** ATKINSON,P.M.,LAMPMAN,G.W.,FURIE,B.C.,NAPARSTEK,Y.,SCHWARTZ,R.S.,STOLLAR,B.D. & FURIE,B. (1985) J.CLIN.INVEST.,75,1138-1143. (CHECKED BY AUTHOR 08/21/85); LAMPMAN,G.W.,FURIE,B.,SCHWARTZ,R.S.,STOLLAR,B.D. & FURIE,B.C. (1989) BLOOD,74,262-269.
16) **Vb'CL:** PECH,M.,JAENICHEN,H.-R.,POHLENZ,H.-D.,NEUMAIER,P.S.,KLOBECK,H.-G. & ZACHAU,H.G. (1984) J.MOL.BIOL.,176,189-204. (CHECKED BY AUTHOR 12/14/84)
17) **Vb''CL:** PECH,M.,JAENICHEN,H.-R.,POHLENZ,H.-D.,NEUMAIER,P.S.,KLOBECK,H.-G. & ZACHAU,H.G. (1984) J.MOL.BIOL.,176, 189-204. (CHECKED BY AUTHOR 12/14/84)
18) **GAL(I):** LAURE,C.J.,WATANABE,S. & HILSCHMANN,N. (1973) Z.PHYSIOL.CHEM.,354,1503-1504. (CHECKED BY AUTHOR)
19) **OU(IOC):** KOHLER,H.,SHIMIZU,A.,PAUL,C. & PUTNAM,F.W. (1970) SCIENCE,169,56-59. (KAPLAN,A.P. & METZGER,H. (1969) BIOCHEMISTRY,8,3944-3951.) (CHECKED BY AUTHOR 06/15/83)
20) **WEA:** GONI,F. & FRANGIONE,B. (1983) PROC.NAT.ACAD.SCI.USA,80,4837-4841. (CHECKED BY AUTHOR 03/23/84)
21) **WIL(=):** GONI,F.,CHUBA,J.,BUXBAUM,J. & FRAGIONE,B. (1988) J.IMMUNOL.,140,551-557.
22) **WES:** KRATZIN,H.,YANG,C.Y.,KRUSCHE,J.U. & HILSCHMANN,N. (1980) Z.PHYSIOL.CHEM.,361,1591-1598.
23) **DAUDI'CL:** KLOBECK,H.G.,COMBRIATO,G. & ZACHAU,H.G. (1984) NUC.ACIDS RES.,12,18,6995-7006.
24) **HK134'CL:** BENTLEY,D.L. & RABBITTS,T.H. (1983) CELL,32,181-189.
25) **Vd'CL:** PECH,M.,JAENICHEN,H.-R.,POHLENZ,H.-D.,NEUMAIER,P.S.,KLOBECK,H.-G. & ZACHAU,H.G. (1984) J.MOL.BIOL.,176,189-204. (CHECKED BY AUTHOR 12/14/84)
26) **WALKER'CL:** KLOBECK,H.G.,COMBRIATO,G. & ZACHAU,H.G. (1984) NUC.ACIDS RES.,12,18,6995-7006. (CHECKED BY AUTHOR 08/22/85 WHO CORRECTED RESIDUE 34)
27) **HK101'CL:** BENTLEY,D.L. & RABBITTS,T.H. (1980) NATURE,288,730-733. (CHECKED BY AUTHOR 11/30/82)
28) **Va''CL:** PECH,M.,JAENICHEN,H.-R.,POHLENZ,H.-D.,NEUMAIER,P.S.,KLOBECK,H.-G. & ZACHAU,H.G. (1984) J.MOL.BIOL.,176, 189-204. (CHECKED BY AUTHOR 12/14/84)
29) **VKI-Chr1'CL:** LOTSCHER,E.,ZIMMER,F.-J.,KLOPSTOCK,T.,GRZESCHIK,K.-H.,JAENICHEN,R.,STRAUBINGER,B. & ZACHAU,H.G. (1988) GENE,69,215-223.
30) **AMYLOID BAN:** DWULET,F.E.,O'CONNOR,T.P. & BENSON,M.D. (1986) MOL.IMMUNOL.,23,73-78. (CHECKED BY AUTHOR 02/06/87)
31) **Ve'CL:** PECH,M.,JAENICHEN,H.-R.,POHLENZ,H.-D.,NEUMAIER,P.S.,KLOBECK,H.-G. & ZACHAU,H.G. (1984) J.MOL.BIOL.,176,189-204. (CHECKED BY AUTHOR 12/14/84)
32) **V13'CL:** JAENICHEN,H.-R.,PECH,M.,LINDENMAIER,W.,WILDGRUBER,N. & ZACHAU,H.G. (1984) NUC.ACIDS RES.,12,5249-5263. (CHECKED BY AUTHOR 12/14/84)
33) **DEE:** MILSTEIN,C. & DEVERSON,E.V. (1971) BIOCHEM.J.,123,945-958. (CHECKED BY AUTHOR)
34) **WIL(-):** GONI,F.,CHUBA,J.,BUXBAUM,J. & FRAGIONE,B. (1988) J.IMMUNOL.,140,551-557.
35) **AND:** LIEPNIEKS,J.J.,DWULET,F.E. & BENSON,M.D. (1990) MOL.IMMUNOL.,27,481-485.
36) **V108'CL:** HUBER,C.,THIEBE,R.,HAMEISTER,H.,SMOLA,H.,LOTSCHER,E. & ZACHAU,G. (1990) NUCL.ACIDS RES.,18,3475-3478.
37) **VKI-ZI'CL:** STRAUBINGER,B.,THIEBE,R.,PECH,M. & ZACHAU,H.G. (1988) GENE,69,209-214.
38) **REI:** PALM,W. & HILSCHMANN,N. (1973) Z.PHYSIOL.CHEM.,354,1651-1654; (1975) Z.PHYSIOL.CHEM.,356,167-191. (CHECKED BY AUTHOR)
39) **AU:** SCHIECHL,H. & HILSCHMANN,N. (1971) Z.PHYSIOL.CHEM.,352,111-115; (1972) Z.PHYSIOL.CHEM.,353,345-370. (CHECKED BY AUTHOR)
40) **ROY:** HILSCHMANN,N. & CRAIG,L.C. (1965) PROC.NAT.ACAD.SCI.USA,53,1403-1409; HILSCHMANN,N. (1967) Z.PHYSIOL.CHEM.,348, 1077-1080; HILSCHMANN,N.,BARNIKOL,H.U.,HESS,M.,LANGER,B.,PONSTINGL,H.,STEINMETZ-KAYNE,M.,SUTER,L. & WATANABE,S. (1969) PROC. 5TH FEBS SYMP.,15,57-74. (CHECKED BY AUTHOR WHO PROVIDED ADDITIONAL RESIDUES TO THOSE PUBLISHED AND CORRECTED RESIDUES 65 AND 67 AS GIVEN IN THE TABLE)
41) **BI:** BRAUN,H.,LEIBOLD,W.,BARNIKOL,H.U. & HILSCHMANN,N. (1971) Z.PHYSIOL.CHEM.,352,647-651; (1972) Z.PHYSIOL.CHEM.,353, 1284-1306. (CHECKED BY AUTHOR WHO PROVIDED AN ADDITIONAL RESIDUE TO THOSE PUBLISHED AND CORRECTED RESIDUE 72 AS GIVEN IN TABLE)
42) **HuVHCAMP'CL:** RIECHMANN,L.,CLARK,M.,WALDMANN,H. & WINTER,G. (1988) NATURE,332,323-327.
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)
45) **MEV:** EULITZ,M. & LINKE,R.P. (1982) Z.PHYSIOL.CHEM.,363,1347-1358. (CHECKED BY AUTHOR 10/10/83)
46) **KA:** SHINODA,T. (1975) J.BIOCHEM.,77,1277-1296. (CHECKED BY AUTHOR)
47) **LAY:** KAPLAN,A.P. & METZGER,H. (1969) BIOCHEMISTRY,8,3944-3951. (CHECKED BY AUTHOR); KLAPPER,D.G. & CAPRA,J.D. (1976) ANN.IMMUNOL.(INST.PASTEUR),127C,261-271. (CHECKED BY AUTHOR 08/01/79)
48) **BEL:** MILSTEIN,C. (1969) PROC. 5TH FEBS SYMP.,15,43-56. (CHECKED BY AUTHOR WHO PROVIDED ADDITIONAL RESIDUES TO THOSE PUBLISHED AND CORRECTED RESIDUES 1,3,6,27,79 AND 82 AS GIVEN IN TABLE)
49) **NI:** SHINODA,T. (1973) J.BIOCHEM.,73,433-446. (CHECKED BY AUTHOR)

REFERENCE: HUMAN KAPPA LIGHT CHAINS SUBGROUP I (cont'd)

50) **RZ:** KIM,H.S. & DEUTSCH,H.F. (1988) IMMUNOL.,64,573-579.
51) **BuRSV19VK:** TEMPEST,P.R.,BREMNER,P.,LAMBERT,M.,TAYLOR,G.,FURZE,J.M.,CARR,F.J. & HARRIS,W.J. (1991) BIO/TECH.,9,266-271.
52) **BBJ4:** SMITH,G.P.,HOOD,L. & FITCH,W.M. (1971) ANN.REV.BIOCHEM.,40,969-1012.
53) **BJ26:** ALESCIO-ZONTA,L. & BAGLIONI,C. (1970) EUR.J.BIOCHEM.,15,450-463. (CHECKED BY AUTHOR)
54) **BJ19:** ALESCIO-ZONTA,L. & BAGLIONI,C. (1970) EUR.J.BIOCHEM.,15,450-463. (CHECKED BY AUTHOR)
55) **RFZ:** SMITHIES,O.,GIBSON,D.,FANNING,E.M.,GOODFLIESH,R.M.,GILMAN,J.G. & BALLANTYNE,D.L. (1971) BIOCHEMISTRY,10,4912-4921. (CHECKED BY AUTHOR)
56) **BA:** KIM,H.S. & DEUTSCH,H.F. (1988) IMMUNOL.,64,573-579.
57) **PAU:** DAYHOFF,M.O. (1972) ATLAS OF PROTEIN SEQUENCE & STRUCTURE,5,D-245. SUBMITTED BY SMITHIES,O.,GIBSON,D.M. AND FANNING,E.M. (CHECKED BY AUTHOR)
58) **PSM:** SEON,B.K. (1982) MOL.IMMUNOL.,19,83-86. (CHECKED BY AUTHOR 05/23/83)
59) **JBL:** SEON,B.K. (1982) MOL.IMMUNOL.,19,83-86. (CHECKED BY AUTHOR 05/23/83)
60) **NE:** MATTHEWS,J.B. & JEFFERIS,R. (1977) IMMUNOCHEM.,14,793-797. (CHECKED BY AUTHOR 08/10/79)
61) **FRA:** MEINKE,G.C.,SIGRIST,P.H. & SPIEGELBERG,H.L. (1974) IMMUNOCHEM.,11,457-460. (CHECKED BY AUTHOR WHO PROVIDED ADDITIONAL RESIDUES TO THOSE PUBLISHED); MEINKE,G.C. & SPIEGELBERG,H.L. (1976) IMMUNOCHEM.,13,915-919. (CHECKED BY AUTHOR 10/17/77)
62) **BJ48:** ALESCIO-ZONTA,L. & BAGLIONI,C. (1970) EUR.J.BIOCHEM.,15,450-463. (CHECKED BY AUTHOR)
63) **HF3-16/6:** 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)
64) **HF2-1/13B:** ATKINSON,P.M.,LAMPMAN,G.W.,FURIE,B.C.,NAPARSTEK,Y.,SCHWARTZ,R.S.,STOLLAR,B.D. & FURIE,B. (1985) J.CLIN.INVEST.,75,1138-1143. (CHECKED BY AUTHOR 08/21/85)
65) **HF2-18/2:** ATKINSON,P.M.,LAMPMAN,G.W.,FURIE,B.C.,NAPARSTEK,Y.,SCHWARTZ,R.S.,STOLLAR,B.D. & FURIE,B. (1985) J.CLIN.INVEST.,75,1138-1143. (CHECKED BY AUTHOR 08/21/85)
66) **GR':** FAIR,D.S.,SLEDGE,C.,KRUEGER,R.G.,MANN,K.G. & HOOD,L.E. (1975) BIOCHEMISTRY,14,5561-5568.
67) **G1'CL:** LEVY,S.,MENDEL,E.,KON,S.,AVNUR,Z. & LEVY,R. (1988) J.EXP.MED.,168,475-489.
68) **HOM:** SAVVIDOU,G.,KLEIN,M.,HORNE,C.,HOFMANN,T. & DORRINGTON,K.J. (1981) MOL.IMMUNOL.,18,793-805.
69) **KER:** MILSTEIN,C. (1966) BIOCHEM.J.,101,352-368. (CHECKED BY AUTHOR WHO PROVIDED ADDITIONAL RESIDUES TO THOSE PUBLISHED)
70) **ESM IGG:** KUAN,T.K.,TUNG,E.,WANG,I.Y. & WANG,A.C. (1981) IMMUNOL.,44,265-271. (CHECKED BY AUTHOR 05/26/83)
71) **ESM IGM:** KUAN,T.K.,TUNG,E.,WANG,I.Y. & WANG,A.C. (1981) IMMUNOL.,44,265-271. (CHECKED BY AUTHOR 05/26/83)
72) **DAV:** CAPRA,J.D. & KUNKEL,H.G. (1970) PROC.NAT.ACAD.SCI.USA,67,87-92. (CHECKED BY AUTHOR)
73) **FIN:** CAPRA,J.D. & KUNKEL,H.G. (1970) PROC.NAT.ACAD.SCI.USA,67,87-92. (CHECKED BY AUTHOR)
74) **PW:** PICK,A.I.,WANG,A.C.,FROHLICHMAN,R. & FUDENBERG,H.H. (1982) ACTA HAEMAT.,68,207-214. (CHECKED BY AUTHOR 05/26/83)
75) **SHE:** MEINKE,G.C. & SPIEGELBERG,H.L. (1976) IMMUNOCHEM.,13,915-919. (CHECKED BY AUTHOR 10/17/77)
76) **ADA:** MEINKE,G.C. & SPIEGELBERG,H.L. (1976) IMMUNOCHEM.,13,915-919. (CHECKED BY AUTHOR 10/17/77)
77) **AMYLOID VIII-B:** GLENNER,G.G.,TERRY,W.,HERADA,M.,ISERSKY,C. & PAGE,D. (1971) SCIENCE,172,1150-1151. (CHECKED BY AUTHOR 09/22/78)
78) **PAUL:** SMITH,G.P.,HOOD,L. & FITCH,W.M. (1971) ANN.REV.BIOCHEM.,40,969-1012.
79) **RI:** PICK,A.I.,WANG,A.C.,FROHLICHMAN,R. & FUDENBERG,H.H. (1982) ACTA HAEMAT.,68,207-214. (CHECKED BY AUTHOR 05/26/83)
80) **WAT:** STEVENS,F.J.,WESTHOLM,F.A.,PANAGIOTOPOULOS,N.,SCHIFFER,M.,POPP,R.A. & SOLOMON,A. (1981) J.MOL.BIOL.,147,185-193. (CHECKED BY AUTHOR 05/26/1983)
81) **LOW:** CAPRA,J.D.,KEHOE,J.M.,WILLIAMS,R.C.,JR.,FEIZI,T. & KUNKEL,H.G. (1972) PROC.NAT.ACAD.SCI.USA,69,40-43. (CHECKED BY AUTHOR WHO CORRECTED RESIDUE 16 AS GIVEN IN TABLE)
82) **AMYLOID ES305:** WESTERMARK,P.,SLETTEN,K. & NATVIG,J.B. (1981) ACTA PATH.MICROBIOL.SCAND.,C89,199-203. (CHECKED BY AUTHOR 11/09/81)
83) **OCO:** WANG,A.C.,WELLS,J.V.,FUDENBERG,H.H. & GERGELY,J. (1974) IMMUNOCHEM.,11,341-345. (CHECKED BY AUTHOR)
84) **BOL:** WANG,A.C.,WELLS,J.V.,FUDENBERG,H.H. & GERGELY,J. (1974) IMMUNOCHEM.,11,341-345. (CHECKED BY AUTHOR)
85) **AMYLOID X:** GLENNER,G.G.,TERRY,W.,HERADA,M.,ISERSKY,C. & PAGE,D. (1971) SCIENCE,172,1150-1151. (CHECKED BY AUTHOR 09/22/78)
86) **SAC:** SMITHIES,O.,GIBSON,O.M.,FANNING,E.M.,PERCY,M.E.,PARR,D.M. & CONNELL,G.E. (1971) SCIENCE,172,574-577. (CHECKED BY AUTHOR)
87) **BJ:** MILSTEIN,C. (1966) BIOCHEM.J.,101,352-368. (CHECKED BY AUTHOR)
88) **GO:** WANG,A.C.,FUDENBERG,H.H. & CREYSSEL,R. (1974) EUR.J.IMMUNOL.,4,446-448. (CHECKED BY AUTHOR)
89) **F-GUI:** WANG,A.C.,FUDENBERG,H.H. & CREYSSEL,R. (1982) ACTA HAEMAT.,68,187-195. (CHECKED BY AUTHOR 05/26/83)
90) **S-GUI:** WANG,A.C.,FUDENBERG,H.H. & CREYSSEL,R. (1982) ACTA HAEMAT.,68,187-195. (CHECKED BY AUTHOR 05/26/83)
91) **HF6-21/28:** ATKINSON,P.M.,LAMPMAN,G.W.,FURIE,B.C.,NAPARSTEK,Y.,SCHWARTZ,R.S.,STOLLAR,B.D. & FURIE,B. (1985) J.CLIN.INVEST.,75,1138-1143. (CHECKED BY AUTHOR 08/21/85)
92) **DIE:** CAPRA,J.D. & KUNKEL,H.G. (1970) PROC.NAT.ACAD.SCI.USA,67,87-92. (CHECKED BY AUTHOR)
93) **CAR A:** CAPRA,J.D. & KUNKEL,H.G. (1970) PROC.NAT.ACAD.SCI.USA,67,87-92. (CHECKED BY AUTHOR)
94) **TEI:** CAPRA,J.D. & KUNKEL,H.G. (1970) PROC.NAT.ACAD.SCI.USA,67,87-92. (CHECKED BY AUTHOR)
95) **MON:** NIALL,H.D. & EDMAN,P. (1967) NATURE,216,262-263. (CHECKED BY AUTHOR 07/25/79)
96) **ALE:** MILSTEIN,C.,MILSTEIN,C.P.& FEINSTEIN,A. (1969) NATURE,221,151-154. (CHECKED BY AUTHOR)
97) **JOH:** CAPRA,J.D. & KUNKEL,H.G. (1970) PROC.NAT.ACAD.SCI.USA,67,87-92. (CHECKED BY AUTHOR)
98) **POT:** CAPRA,J.D. & KUNKEL,H.G. (1970) PROC.NAT.ACAD.SCI.USA,67,87-92. (CHECKED BY AUTHOR WHO CORRECTED RESIDUE 9 AS GIVEN IN TABLE)
99) **CON:** NIALL,H.D. & EDMAN,P. (1967) NATURE,216,262-263. (CHECKED BY AUTHOR 07/25/79)
100) **TRA:** NIALL,H.D. & EDMAN,P. (1967) NATURE,216,262-263. (CHECKED BY AUTHOR 07/25/79)
101) **H-G2b:** SCOTT,M.G.,TARRAND,J.J.,CRIMMINS,D.L.,MCCOURT,D.W.,SIEGEL,N.R.,SMITH,C.E. AND NAHM,M.H. (1989) J.IMMUNOL.,143, 293-298.
102) **K-G2:** SCOTT,M.G.,TARRAND,J.J.,CRIMMINS,D.L.,MCCOURT,D.W.,SIEGEL,N.R.,SMITH,C.E. AND NAHM,M.H. (1989) J.IMMUNOL.,143, 293-298.
103) **BRA:** WANG,A.C.,WELLS,J.V.,FUDENBERG,H.H. & GERGELY,J. (1974) IMMUNOCHEM.,11,341-345. (CHECKED BY AUTHOR)
104) **LUX:** NIALL,H.D. & EDMAN,P. (1967) NATURE,216,262-263. (CHECKED BY AUTHOR 07/25/79)
105) **HEI:** RIESEN,W.F.,MAJANIEMI,I.,HUSER,H.,BRAUN,D.G. & ROELCKE,D. (1978) SCAND.J.IMMUNOL.,8,145-148. (CHECKED BY AUTHOR 10/10/79)
106) **PAP:** NIALL,H.D. & EDMAN,P. (1967) NATURE,216,262-263. (CHECKED BY AUTHOR 07/25/79)
107) **A-G2a:** SCOTT,M.G.,TARRAND,J.J.,CRIMMINS,D.L.,MCCOURT,D.W.,SIEGEL,N.R.,SMITH,C.E. AND NAHM,M.H. (1989) J.IMMUNOL.,143, 293-298.
108) **CRA:** NIALL,H.D. & EDMAN,P. (1967) NATURE,216,262-263. (CHECKED BY AUTHOR 07/25/79)
109) **AMYLOID LEP:** LIAN,J.B.,SKINNER,M.,BENSON,M.D. & COHEN,A.S. (1977) BIOCHIM.BIOPHYS.ACTA,491,167-176.
110) **WAG:** KAPLAN,A.P. & METZGER,H. (1969) BIOCHEMISTRY,8,3944-3951. (CHECKED BY AUTHOR)
111) **HOE:** JOHNSTON,S.L.,ABRAHAM,G.N. & WELCH,E.H. (1975) BIOCHEM.BIOPHYS.RES.COMMUN.,66,842-847. (CHECKED BY AUTHOR 10/17/77)
112) **HBJ1:** HOOD,L.,GRAY,W.R.,SANDERS,B.G. & DREYER,W.J. (1967) COLD SPRING HARBOR SYMP. QUANTITATIVE BIOL.,32,133-145.
113) **AMYLOID 547:** WESTERMARK,P.,SLETTEN,K. & NATVIG,J.B. (1981) ACTA PATH.MICROBIOL.SCAND.,C89,199-203. (CHECKED BY AUTHOR 11/09/81)
114) **WEB:** JOHNSTON,S.L.,ABRAHAM,G.N. & WELCH,E.H. (1975) BIOCHEM.BIOPHYS.RES.COMMUN.,66,842-847. (CHECKED BY AUTHOR 10/17/77)
115) **HBJ10:** HOOD,L.,GRAY,W.R.,SANDERS,B.G. & DREYER,W.J. (1967) COLD SPRING HARBOR SYMP. QUANTITATIVE BIOL.,32,133-145.
116) **LOD:** JOHNSTON,S.L.,ABRAHAM,G.N. & WELCH,E.H. (1975) BIOCHEM.BIOPHYS.RES.COMMUN.,66,842-847. (CHECKED BY AUTHOR 10/17/77)
117) **BEN:** CAPRA,J.D.,KEHOE,J.M.,WILLIAMS,R.C.,JR.,FEIZI,T. & KUNKEL,H.G. (1972) PROC.NAT.ACAD.SCI.USA,69,40-43. (CHECKED BY AUTHOR)
118) **MAA:** CAPRA,J.D.,KEHOE,J.M.,WILLIAMS,R.C.,JR.,FEIZI,T. & KUNKEL,H.G. (1972) PROC.NAT.ACAD.SCI.USA,69,40-43. (CHECKED BY AUTHOR)
119) **GR:** CAPRA,J.D.,KEHOE,J.M.,WILLIAMS,R.C.,JR.,FEIZI,T. & KUNKEL,H.G. (1972) PROC.NAT.ACAD.SCI.USA,69,40-43. (CHECKED BY AUTHOR)
120) **MUK:** LITMAN,G.W.,GERBER-JENSON,B.,LITMAN,R.,MIDDAUGH,C.R. & SCHEFFEL,C. (1980) MOL.IMMUNOL.,17,337-344.
121) **GM131'CL:** MORIN,J.W.,BLACK,A.,WU,M. & BEYCHOK,S. (1985) PROC.NAT.ACAD.SCI.USA,82,7025-7029.
122) **AMYLOID 594:** WESTERMARK,P.,SLETTEN,K. & NATVIG,J.B. (1981) ACTA PATH.MICROBIOL.SCAND.,C89,199-203. (CHECKED BY AUTHOR 11/09/81)
123) **MAR:** KAPLAN,A.P. & METZGER,H. (1969) BIOCHEMISTRY,8,3944-3951. (CHECKED BY AUTHOR)
124) **CL*:** SOLOMON,A.,MCLAUGHLIN,C.L. & CAPRA,J.D. (1975) J.CLINICAL INVESTIGATION,55,579-586. (CHECKED BY AUTHOR)
125) **AMYLOID:** COHEN,A.S.,SHIRAHAMA,T.,SKINNER,M.,BENSON,M.D. & CATHCART,E.S. (1973) PROTIDES BIOL.FLUIDS,20,73-80.
126) **HBJ6:** HOOD,L.,GRAY,W.R.,SANDERS,B.G. & DREYER,W.J. (1967) COLD SPRING HARBOR SYMP. QUANTITATIVE BIOL.,32,133-145.
127) **AMYLOID MS:** PICK,A.I.,SCHREIBMAN,S.,LAVIE,G. & FROHLICHMAN,R. (1973) PROTIDES BIOL.FLUIDS,20,63-72.
128) **PEN:** MOULIN,A. & FOUGEREAU,M. (1973) NATURE NEW BIOLOGY,246,176-178.

GENERAL NOTES: HUMAN KAPPA LIGHT CHAINS SUBGROUP I

IDENTICAL SETS OF FRAMEWORK SEGMENTS:

FR1: SET 1: 2C12'CL[1],1B11'CL[2],1H1'CL[3],2A12'CL[4]. (4 IDENTICAL)
SET 2: DEN[6],3D6'CL[7],HK102'CL[8],EU[9],PA[11],WIL(=)[21],HBJ4[52],PAU[57],FRA[61],GR'[66],PAUL[78],MON[95]. (12 IDENTICAL)
SET 3: HK137'CL[12],HAU[13],HF2-1/17[15],OU(IOC)[19],WEA[20],DAUDI'CL[23],HK134'CL[24],WALKER'CL[26],HK101'CL[27], VKI-Chr1'CL[29],DEE[33],AND[35],REI[38],AU[39],ROY[40],HuVHCAMP'CL[42],AG[43],SCW[44],RZ[50],BJ26[53], RFZ[55],HA[56],PSM[58],BJ48[62],HF3-16/6[63],HF2-1/13B[64],HF2-18/2[65],HOM[68],ESM IGG[70],ESM IGM[71], AMYLOID VIII-B[77],WAT[80],LOW[81],F-GUI[89],DIE[92],CAR A[93],TEI[94],CON[99],TRA[100],H-G2b[101], K-G2[102]. (41 IDENTICAL)
SET 4: Vb'CL[16],Vb''CL[17],WES[22]. (3 IDENTICAL)
SET 5: Vd'CL[25],LUX[104]. (2 IDENTICAL)
SET 6: AMYLOID BAN[30],BEL[48],HuRSV19VK[51],BJ19[54]. (4 IDENTICAL)
SET 7: DAV[72],FIN[73]. (2 IDENTICAL)

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

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

FR4: SET 1: 2C12'CL[1],1B11'CL[2],1H1'CL[3],2A12'CL[4],G1'CL[67]. (5 IDENTICAL)
SET 2: BR[5],GAL(I)[18],AU[39],HuVHCAMP'CL[42],CL*[124]. (5 IDENTICAL HUMAN V-KAPPA-I; ALSO 6 HUMAN V-KAPPA-II: GM 607 'CL[1],RPMI6410'CL[11],A-G1[14],C-G1[15],B-G1[16],E-G1[19]; 23 HUMAN V-KAPPA-III: PIE[2],GLO[4],CUR[5], HAH 14.1'CL[7],HAH 14.2'CL[8],HAH 16.1'CL[9],NOV'CL[10],HIC (R)'CL[11],PAY[15],BOR'[17],HEW'CL[18], ROB'CL[19],BRA'CL[21],HAH'CL[22],HIC'CL[24],WOL[31],EV1-15'CL[32],GOL'[33],Taykv322'CL[34],GF4/1.1'CL[54], REE[56],HAH (R)'CL[73],VKAPPA3'CL[85]; AND 2 HUMAN V-KAPPA-IV: FK-001'CL[1],PB17IV'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],FR4[47], Taykv312'CL[58],Taykv308'CL[66],TH9'CL[90]; AND 1 HUMAN V-KAPPA-IV: LEN[3].)
SET 4: 3D6'CL[7],CAR[10]. (2 IDENTICAL)
SET 5: EU[9],WEA[20],LAY[47],BJ48[62]. (4 IDENTICAL)
SET 6: PA[11]. (IDENTICAL TO 1 HUMAN V-KAPPA-III: BRO'CL[20].)
SET 7: HAU[13]. (IDENTICAL TO 2 HUMAN V-KAPPA-III: POM[48],CLL'CL[50].)
SET 8: HF2-1/17[15],RZ[50]. (2 IDENTICAL HUMAN V-KAPPA-I; ALSO 13 HUMAN V-KAPPA-III: SON[14],KAS[28],SIC'CL[30], Taykv310'CL[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], Taykv306'CL[59]; 2 HUMAN V-KAPPA-IV: VJI'CL[4],Ly66rlc1'CL[12]; 4 MOUSE V-KAPPA-V: SE20.2'CL[29], hVH65-212'CL[47],DNA9'CL[127],DNA2'CL[128]; AND 2 MOUSE V-KAPPA-MISC: DNA2'CL[1],DNA9'CL[2].)
SET 9: WES[22],MEV[45]. (2 IDENTICAL)
SET 10: OU(IOC)[19],WALKER'CL[26]. (2 IDENTICAL HUMAN V-KAPPA-I; ALSO 1 HUMAN V-KAPPA-II: TEW[5]; AND 2 HUMAN V-KAPPA-III: 8E10'CL[12],GER[53].)

IDENTICAL SETS OF COMPLEMENTARITY DETERMINING REGIONS:

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

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

CDR3: SET 1: 2C12'CL[1],1B11'CL[2]. (2 IDENTICAL)
SET 2: 1H1'CL[3],G1'CL[67]. (2 IDENTICAL)
SET 3: Vb'CL[16],Vb''CL[17]. (2 IDENTICAL)
SET 4: HK134'CL[24],HK101'CL[27]. (2 IDENTICAL)
SET 5: AMYLOID BAN[30]. (IDENTICAL TO 2 MOUSE V-KAPPA-V: 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: RPMI6410'CL[11]; 6 HUMAN V-KAPPA-III: PIE[2],HIC (R)'CL[11],ROB'CL[19],HIC'CL[24],GF4/1.1'CL[54],VKAPPA3'CL[85]; AND 1 HUMAN V-KAPPA-IV: PB17IV'CL[5].)
SET 3: DEN[6],BI[41]. (2 IDENTICAL HUMAN V-KAPPA-I; ALSO 1 HUMAN V-KAPPA-II: FR[9]; AND 5 HUMAN V-KAPPA-III: GAR'[1],FLO[3],IARC/BL41'CL[46],Taykv312'CL[58],Taykv308'CL[66].)
SET 4: HF2-1/17[15],RZ[50]. (2 IDENTICAL HUMAN V-KAPPA-I; ALSO 7 HUMAN V-KAPPA-III: LS1'CL[39],LS2'CL[40], LS4'CL[41],LS5'CL[42],LS6'CL[43],LS7'CL[44],LS8'CL[45].)
SET 5: GAL(I)[18]. (IDENTICAL TO 1 HUMAN V-KAPPA-III: GOL'[33].)
SET 6: WIL(=)[21],WIL(-)[34]. (2 IDENTICAL)
SET 7: WALKER'CL[26]. (IDENTICAL TO 1 HUMAN V-KAPPA-II: TEW[5]; AND 2 HUMAN V-KAPPA-III: 8E10'CL[12],GER[53].)
SET 8: HuVHCAMP'CL[42]. (IDENTICAL TO 8 HUMAN V-KAPPA-III: CUR[5],HAH 14.1'CL[7],HAH 14.2'CL[8],HAH 16.1'CL[9], HAH'CL[22],WOL[31],EV1-15'CL[32],HAH (R)'CL[73]; AND 1 HUMAN V-KAPPA-IV: FK-001'CL[1].)
SET 9: AG[43]. (IDENTICAL TO 1 HUMAN V-KAPPA-III: GOT[16].)

SEE SIGNAL PEPTIDE TABLE IF # OCCURS AT POSITION 0.

SPECIFIC NOTES: HUMAN KAPPA LIGHT CHAINS SUBGROUP I

1) **2C12'CL:** HETEROHYBRIDOMA FORMED BY FUSING CELLS FROM LYMPH NODES OR SPLEEN FROM A PATIENT SUFFERING FROM FOLLICULAR SMALL CLEAVED CELL LYMPHOMA AND CELL LINE K6H6-B5.

2) **1B11'CL:** HETEROHYBRIDOMA FORMED BY FUSING CELLS FROM LYMPH NODES OR SPLEEN FROM A PATIENT SUFFERING FROM FOLLICULAR SMALL CLEAVED CELL LYMPHOMA AND CELL LINE K6H6-B5.

3) **1H1'CL:** HETEROHYBRIDOMA WAS FORMED BY FUSING CELLS FROM LYMPH NODES OR SPLEEN FROM A PATIENT SUFFERING FROM FOLLICULAR SMALL CLEAVED CELL LYMPHOMA AND CELL LINE K6H6-B5.

4) **2A12'CL:** HETEROHYBRIDOMA WAS FORMED BY FUSING CELLS FROM LYMPH NODES OR SPLEEN FROM A PATIENT SUFFERING FROM FOLLICULAR SMALL CLEAVED CELL LYMPHOMA AND CELL LINE K6H6-B5.

8) **HK102'CL:** THE SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF HUMAN FETAL LIVER DNA.

12) **HK137'CL:** THE AMINO ACID SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF HUMAN FETAL DNA.

21) **WIL(=):** WIL(-) AND WIL(=) ARE PRODUCED BY THE SAME PATIENT WITH MULTIPLE MYELOMA.

24) **HK134'CL:** THE AMINO ACID SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF HUMAN FETAL DNA.

27) **HK101'CL:** THE SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF HUMAN FETAL LIVER DNA.

30) **AMYLOID BAN:** AMINO ACID RESIDUE ASN AT POSITION 61 IS LINKED TO CARBOHYDRATE. AMINO ACID RESIDUES FOUND AT POSITIONS 104 AND 105 ARE VAL,LEU AND GLN,GLU RESPECTIVELY.

34) **WIL(-):** WIL(-) AND WIL(=) ARE PRODUCED BY THE SAME PATIENT WITH MULTIPLE MYELOMA.

35) **AND:** IT IS ISOLATED FROM THE AMYLOID FIBRILS FROM THE SPLEEN OF THE PATIENT,

36) **V108'CL:** HUMAN IMMUNOGLOBULIN KAPPA ORPHON GENE LOCATED ON CHROMOSOME 2 IN THE REGION 2q12-14.

43) **AG:** THE AMINO ACID RESIDUES AT POSITIONS 39 AND 41 WERE REPORTED BY THE AUTHORS AS GLY AND LYS RESPECTIVELY; HOWEVER, THE PROOF WAS NOT ABSOLUTE. THUS, THEY ARE OMITTED.

51) **HuRSV19VK:** THIS SEQUENCE CONTAINS THE FR'S OF REI WITH SOME MODIFICATIONS, AND CDR'S OF MuRSV19VL. WHEN HuRSV19VK IS COMBINED WITH HuRSV19VH, FV DOES NOT BIND VIRUS; BUT WHEN COMBINED WITH HuRSV19VHFNS, 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* LS2 'CL	2* LS5 'CL	3* LS6 'CL	4* LS1 'CL	5* LS4 'CL	6* LS8 'CL	7 1B9/F2 'CL #	8 21-2 'CL	9 3-1 'CL	10* 21/28 'CL #	11* 8E10 'CL #	12 HG3 'CL #	13 V35 'CL	14 51P1 'CL #	15 AND 'CL	16 NEI 'CL #	17 HP1 'CL	18 E3-10 'CL	19 1-92 'CL	20 hv1263 'CL	21 783c 'CL #	22 X17115 'CL #
	0		---	---	---	---	---	---	---	---	---	---	---	#	---	---	---	---	---	---	---	---	---	---
	1		GLN	GLN	GLN	GLN	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	**glu**	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	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	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		ALA	ALA	ALA	ALA	ALA	ALA	**gln**	**gln**	**gln**	**gln**	**gln**	**gln**	**gln**	**gln**	**gln**	**gln**	**gln**	**gln**	**gln**	**gln**	**gln**	**gln**
	7	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
	8	GLY(.98)	GLY	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	**gly**	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	GLU
	11		VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
	12		ASN	ASN	ASN	ASN	ASN	ASN	**lys**	**lys**	**lys**	**lys**	**lys**	**lys**	**lys**	**lys**	**lys**	**lys**	**lys**	**lys**	**lys**	**lys**	**lys**	**lys**
	13	LYS(.98)	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS
FR1	14	PRO(.98)	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO
	15	GLY(.96)	GLY	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	**ser**	**ser**	**ser**	ALA	ALA	ALA	**ser**	**ser**	**ser**
	17	SER(.98)	SER	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	VAL
	19		LYS	LYS	LYS	LYS	LYS	LYS	**arg**	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	VAL
	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(.98)	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS
	23		LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS
	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(.96)	SER	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	GLY
	27		TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	**gly**	**gly**	**gly**	TYR	**phe**	TYR	**gly**	**gly**	**gly**
	28		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	**ser**	THR	THR	THR	THR	THR
	29	PHE(.96)	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE
	30		THR	THR	THR	THR	THR	**ser**	**his**	THR	THR	THR	THR	**asn**	THR	**ser**	**ser**	**ser**	**ile**	THR	THR	**ser**	**ser**	**ser**
	31		SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	**gly**	SER	SER	SER	**val**	SER	SER	SER	SER	SER
CDR1	32		TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR
	33		GLY	GLY	GLY	GLY	GLY	GLY	GLY	**tyr**	**tyr**	**ala**	**ala**	**tyr**	**tyr**	**ala**	**ala**	**ala**	**tyr**	**ala**	**ala**	**ala**	**ala**	**ala**
	34		ILE	ILE	ILE	ILE	ILE	ILE	ILE	**met**	**met**	**met**	**met**	**met**	**met**	ILE	ILE	ILE	ILE	**met**	ILE	ILE	ILE	ILE
	35		SER	SER	SER	SER	SER	SER	**thr**	**his**	**his**	**his**	**his**	**his**	**his**	SER	SER	SER	**his**	**his**	**his**	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	TRP
	37		VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	**leu**	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	ARG
	39	GLN(.98)	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
FR2	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(.98)	GLY	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	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN
	44		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	**arg**	**arg**	GLY	GLY	GLY	GLY	GLY	**arg**	**arg**	GLY	GLY	GLY	GLY
	45	LEU(.98)	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
	46	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU
	47	TRP(.98)	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	**TRP**	TRP	TRP	TRP	TRP	TRP
	48		MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET
	49	GLY(.98)	GLY	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	**ile**	**ile**	TRP	TRP	**ile**	**arg**	**gly**	**gly**	**gly**	TRP	TRP	TRP	**arg**	**gly**	**gly**
	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	SER	SER	SER	SER	SER	**asn**	**asn**	**asn**	**asn**	**asn**	**asn**	**ile**	**ile**	**ile**	**asn**	**asn**	**asn**	**ile**	**ile**	**ile**
	52A		VAL	VAL	VAL	VAL	VAL	VAL	**gly**	**pro**	**pro**	**ala**	**ala**	**pro**	**pro**	**pro**	**pro**	**pro**	**pro**	**ala**	VAL	**pro**	**pro**	**pro**
	52B		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	52C		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	53		TYR	TYR	TYR	TYR	TYR	TYR	TYR	**ser**	**ser**	**gly**	**gly**	**ser**	**asn**	**ile**	**ile**	**ile**	**arg**	**gly**	**gly**	**ile**	**ile**	**ile**
CDR2	54		ASN	ASN	ASN	ASN	ASN	ASN	ASN	**gly**	**gly**	ASN	ASN	**gly**	**ser**	**phe**	**phe**	**phe**	**thr**	ASN	ASN	**leu**	**phe**	**phe**
	55		GLY	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**	**ser**	**asn**	**asn**	**ser**	**gly**	**thr**	**thr**	**thr**	ASP	**asn**	**asn**	**ile**	**thr**	**thr**
	57		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	**ala**	**ala**	**ala**	THR	THR	THR	**ala**	**ala**	**ala**
	58		ASN	ASN	ASN	ASN	ASN	ASN	ASN	**ser**	**ser**	**lys**	**lys**	**ser**	ASN	ASN	ASN	ASN	ASN	**lys**	**lys**	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	TYR
	60		ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	**ser**	**ser**	ALA	ALA	ALA	ALA	ALA	ALA	**ser**	**ser**	ALA	ALA	ALA
	61		GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN
	62		ASN	ASN	ASN	ASN	ASN	ASN	**lys**	**lys**	**lys**	**lys**	**lys**	**lys**	**lys**	**lys**	**lys**	**lys**	**thr**	**lys**	**lys**	**lys**	**lys**	**lys**
	63		LEU	LEU	LEU	LEU	LEU	LEU	LEU	**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	GLN
	65		GLY	GLY	GLY	GLY	GLY	GLY	**asp**	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
	66		ARG	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	VAL
	68		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
	69		MET	MET	MET	MET	MET	MET	MET	MET	MET	**ile**	ile	MET	**ser**	**ile**	**ile**	**ile**	MET	**ile**	**val**	**ile**	**ile**	**ile**
	70		THR	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	THR	**arg**	**arg**	**arg**	**arg**	**arg**	**arg**	**ala**	**ala**	**ala**	**arg**	**arg**	**arg**	**ala**	**ala**	**ala**
	72		ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP
	73		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	**glu**	**glu**	**glu**	THR	THR	THR	**lys**	**glu**	**glu**
	74	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
	75		THR	THR	THR	THR	THR	THR	THR	THR	THR	**ala**	**ala**	THR	**ile**	THR	THR	THR	**ile**	**ala**	**ala**	THR	THR	THR
	76		SER	SER	SER	SER	SER	SER	**asn**	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
	77		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
	78		ALA	ALA	ALA	ALA	ALA	ALA	**val**	**val**	**val**	ALA	ALA	**val**	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA
	79		TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR
	80		MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	**leu**	MET	MET	MET
FR3	81		GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	**asp**	GLU	GLU	GLU	GLU	GLU
	82		LEU	LEU	LEU	LEU	LEU	LEU	**val**	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
	82A		ARG	ARG	ARG	ARG	ARG	ARG	ARG	**ser**	**ser**	**ser**	**ser**	**ser**	**ser**	**ser**	**ser**	**gly**	**ser**	**asn**	**ser**	**ser**	**ser**	**ser**
	82B		ASN	ASN	ASN	ASN	ASN	ASN	**ser**	**ser**	**ser**	**ser**	**ser**	**ser**	**arg**	**ser**	**ser**	**arg**	**ser**	**ser**	**ser**	**ser**	**ser**	**ser**
	82C	LEU(.96)	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
	83		ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	**thr**	ARG	ARG	ARG	ARG
	84		SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	**phe**	SER	SER	SER	SER	SER
	85		ASP	ASP	ASP	ASP	ASP	ASP	ASP	**glu**	**glu**	**glu**	**glu**	**glu**	ASP	**glu**	**glu**	**glu**	ASP	**glu**	**glu**	**glu**	**glu**	**glu**
	86	ASP	ASP	ASP	ASP	ASP	ASP	**ASP**	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP
	87		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
	88		ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	**val**	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA
	89		VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	**ile**	VAL	VAL	VAL
	90	TYR(.98)	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR
	91		TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR
	92	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS
	93	ALA(.96)	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA
	94		ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	**lys**	**lys**
	95		ALA	ALA	ALA	ALA	ALA	ALA	ASP	---	---	GLY	ALA	#		ASP	VAL	GLY	ASP	---			THR	THR
	96		PRO	PRO	PRO	PRO	PRO	PRO	ASP	---	---	GLY	MET	---		VAL	SER	PRO	VAL	---			GLY	GLY
	97		GLY	GLY	GLY	GLY	GLY	GLY	CYS	---	---	TYR	ILE	---		PRO	ILE	ARG	GLU	---			ILE	ILE
	98		TYR	TYR	TYR	TYR	TYR	TYR	SER	---	---	TYR	LEU	---		GLY	PHE	LEU	LEU	---			LEU	LEU
	99		CYS	CYS	CYS	CYS	CYS	CYS	GLY	---	---	GLY	ARG	---		GLU	GLY	LEU	ARG	---			GLY	GLY
	100		SER	SER	SER	SER	SER	SER	ASP	---	---	SER	ILE	---		LEU	VAL	ALA	TYR	---			PRO	PRO
	100A		GLY	GLY	GLY	GLY	GLY	GLY	ASN	---	---	GLY	GLY	---		GLY	VAL	ASP	GLY	---			TYR	TYR
	100B		GLY	GLY	GLY	GLY		GLY	CYS	---	---	SER	HIS	---		THR	GLN	VAL	THR	---			SER	SER
CDR3	100C		GLY	GLY	GLY	GLY		GLY	TYR	---	---	---	GLY	---		ASP	HIS	LEU	GLY	---			SER	SER
	100D		CYS	CYS	CYS	CYS		CYS	MET	---	---	---	GLN	---		---	---	LEU	---	---			GLY	GLY
	100E		TYR	TYR	TYR	TYR		TYR	SER	---	---	---	PRO	---		---	TYR	TRP	---	---			TRP	#
	100F		ARG	ARG	ARG	ARG		ARG	---	---	---	---	GLN	---		---	TYR	PHE	---	---			TYR	TYR
	100G		GLY	GLY	GLY	GLY		GLY	---	---	---	---	---	---		---	TYR	GLY	---	---			#	TYR
	100H		ASP	ASP	ASP	ASP		ASP	---	---	---	---	---	---		---	TYR	GLU	---	---			TYR	TYR
	100I		---	---	---	---		---	---	---	---	---	---	---		---	TYR	LEU	---	---			TYR	TYR
	100J		---	---	---	---		---	---	---	---	---	---	---		ALA	TYR	#	TRP	---			GLY	GLY
	100K		---	---	---	---		---	---	---	---	---	---	---		PHE	MET	PHE	PHE	---			MET	MET
	101		ASP	ASP	ASP	ASP		ASP	ALA	---	---	ASN	GLY	---		ASP	ASP	ASP	ASP	---			ASP	ASP
	102		TYR	TYR	TYR	TYR		TYR	TYR	---	---	TYR	TYR	---		ILE	VAL	TYR	PRO	---			VAL	VAL
	103	TRP(.95)	**TRP**	**TRP**	**TRP**	TRP		**TRP**	TRP	---	---	TRP	TRP	---		TRP	**TRP**	**TRP**	**TRP**	---			**TRP**	TRP
	104		GLY	GLY	GLY	GLY		GLY	GLY	---	---	GLY	GLY	---		GLY	GLY	GLY	GLY	---			GLY	GLY
	105		GLN	GLN	GLN	GLN		GLN	GLN	---	---	GLN	GLU	---		GLN	LYS	GLN	GLN	---			GLN	GLN
	106	GLY	GLY	GLY	GLY	GLY		GLY	GLY	---	---	GLY	GLY	---		GLY	GLY	GLY	GLY	---			GLY	GLY
FR4	107		THR	THR	THR	THR		THR	THR	---	---	THR	THR	---		THR	THR	THR	THR	---			THR	THR
	108		LEU	LEU	LEU	LEU		LEU	LEU	---	---	LEU	LEU	---		MET	THR	LEU	LEU	---			THR	THR
	109	VAL(.95)	VAL	VAL	VAL	VAL		VAL	VAL	---	---	VAL	VAL	---		VAL	VAL	VAL	VAL	---			VAL	VAL
	110		THR	THR	THR	THR		THR	THR	---	---	THR	THR	---		THR	THR	THR	THR	---			THR	THR

HUMAN HEAVY CHAINS SUBGROUP I (cont'd)

		23 TH9 'CL #	24 WIL2 'CL	25* EV1-15 'CL, #	26* KAS #	27* BOR' #	28* RF-TS1 'CL	29* LS7 '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	glu	glu	glu	glu		pca	glu	glu	pca	GLN	glu
	2	VAL	VAL	VAL	VAL	VAL	VAL		thr	met	VAL	VAL	VAL	VAL	VAL	VAL		VAL	VAL	VAL	VAL	gly	VAL
	3	GLN	GLN	GLN	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
	5	VAL	VAL	VAL	VAL	VAL	VAL		VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	met	VAL
	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	pro	ALA	ser	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ser	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	leu	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
	12	lys	lys	lys	lys	lys	lys		arg	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys	lys	val	lys
	13	LYS	LYS	LYS	LYS	LYS	LYS		LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS
FR1	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	ser	ser	ser	ser		ALA	thr	ser	ALA	glu	glu	glu	glu	glu	ser	glu	glu	ser	ALA	glu
	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	leu	leu	leu	leu	leu	ala	leu	leu	VAL	VAL	leu
	19	LYS	LYS	LYS	LYS	LYS	LYS		LYS	LYS	LYS	LYS	LYS	LYS	arg	LYS	LYS	arg	LYS	LYS	arg	arg	LYS
	20	VAL	VAL	VAL	VAL	VAL	VAL		VAL	VAL	VAL	VAL	ile	ile	ile	ile	ile	leu	ile	ile	VAL	VAL	ile
	21	SER	SER	SER	SER	thr	SER		SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	thr	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	arg	LYS	LYS
	24	ALA	ALA	ALA	ALA	ALA	ALA		ALA	ALA	ALA	ALA	gly	gly	gly	gly	gly	val	gly	gly	thr	ALA	gly
	25	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	GLY	GLY	GLY	GLY	GLY	GLY	glu	GLY
	27	TYR	val	gly	gly	asp	gly	TYR	TYR	phe	gly	TYR	TYR	TYR	TYR	TYR	TYR	asp	TYR	TYR	gly	asp	TYR
	28	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	ser	ser	ser	ser	ser	asp	ser	ser	THR	ile	ser
	29	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	thr	PHE
	30	ala	THR	ser	ser	ser	ser	THR	ile	THR	ser	THR	THR	THR	THR	THR	THR	asn	ser	ser	ser	gly	ser
	31	thr	gly	SER	SER	SER	thr	SER	asp	SER	arg	SER	SER	SER	SER	SER	SER	thr	thr	SER	gly	thr	thr
CDR1	32	TYR	his	TYR	TYR	ser	TYR	TYR	ser	ser	ser	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	glu	ser
	33	asp	tyr	ala	ala	ala	ala	GLY	tyr	ala	ala	trp	trp	trp	trp	trp	trp	asp	trp	trp	thr	GLY	trp
	34	ILE	met	phe	ILE	ILE	ILE	ILE	ILE	val	ILE	met	ILE	ILE	ILE	thr	ILE	ILE	ILE	ILE	ILE	phe	ILE
	35	asn	his	SER	SER	SER	SER	SER	his	gln	ile	asn	gly	gly	SER	gly	gly	his	ala	gly	SER	SER	gly
	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
	37	VAL	VAL	VAL	VAL	VAL	VAL	VAL	ile	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	leu	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
	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	met	met	met	met	met	ALA	met	ALA	ALA	ALA	met
	41	thr	PRO	PRO	PRO	PRO	PRO	PRO	PRO	arg	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO
FR2	42	GLY	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	GLN	his	GLN	GLN	GLN	lys	lys	lys	lys	lys	arg	lys	lys	arg	GLN	lys
	44	GLY	GLY	GLY	GLY	GLY	GLY	GLY	arg	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
	45	LEU	LEU	LEU	LEU	pro	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	TRP	TRP	TRP	TRP	ser	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP
	48	MET	MET	MET	MET	MET	MET	MET	val	ile	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	val	MET	leu
	49	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	ala	GLY	GLY	GLY	GLY	GLY
	50	TRP	TRP	gly	gly	gly	gly	TRP	TRP	TRP	gly	TRP	ile	ile	arg	ile	ile	val	ile	ile	ser	ala	thr
	51	met	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	val	ILE	ILE	pro	ILE	ILE
	52	asn	asn	ile	ile	ile	thr	SER	asn	val	val	asn	tyr	tyr	asp	tyr	tyr	his	tyr	tyr	ala	ala	his
	52A	pro	pro	pro	pro	pro	pro	VAL	pro	VAL	pro	thr	pro	pro	pro	pro	pro	pro	ala	pro	lys	pro	pro
	52B	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	tyr	---
	52C	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	#	---
	53	asn	asn	phe	ile	ile	met	TYR	asn	gly	met	asn	gly	gly	ser	gly	gly	ser	gly	gly	trp	cys	gly
CDR2	54	ser	ser	leu	phe	phe	phe	ASN	ser	ser	phe	thr	asp	asp	asp	asp	asp	asp	asp	asp	thr	arg	asp
	55	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	ser	ser	ser	ser	ser	asp	ser	ser	asp	arg	ser
	56	asn	gly	thr	gln	thr	arg	ASP	gly	asn	pro	asn	ASP	ASP	tyr	ASP	ASP	arg	glu	ASP	pro	arg	ASP
	57	THR	THR	THR	ala	pro	ala	THR	THR	THR	pro	pro	THR	THR	THR	THR	THR	THR	THR	THR	phe	THR	THR
	58	gly	ASN	his	ASN	ASN	ASN	ASN	ASN	ASN	ASN	thr	arg	arg	ASN	arg	arg	thr	arg	arg	gln	thr	arg
	59	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	gly	phe	asn
	60	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ser	ser	ser	ser	ser	gly	thr	ser	val	ALA	ser
	61	GLN	glu	GLN	GLN	GLN	GLN	GLN	pro	GLN	GLN	GLN	pro	pro	pro	pro	pro	pro	pro	pro	tyr	pro	pro
	62	lys	lys	lys	lys	lys	lys	ASN	arg	lys	lys	gly	ser	ser	ser	ser	ser	arg	ser	ser	ile	met	ser
	63	phe	phe	phe	phe	phe	phe	LEU	phe	phe	phe	phe	phe	phe	phe	phe	phe	ser	phe	LEU	lys	phe	phe
	64	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	thr	GLN	GLN	GLN	GLN	GLN	GLN	arg	GLN	trp	GLN	GLN
	65	GLY	GLY	asp	GLY	GLY	GLY	GLY	glu	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	ala	GLY	GLY	glu	ala	GLY
	66	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	gln	gln	his	gln	gln	ARG	gln	gln	ARG	ARG	gln
	67	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	pha	VAL	VAL	VAL	VAL	VAL	phe	VAL	VAL	VAL	leu	VAL
	68	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	val	THR	THR	THR	THR	THR	THR	THR	THR	THR	lys	THR
	69	MET	ile	ile	ile	ile	ile	MET	MET	ile	ile	phe	ile	ile	ile	ile	ile	val	ile	arg	val	leu	ile
	70	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	ser	ser	ser	ser	ser	ser	THR	ser	ser	ser	THR	ser
	71	arg	arg	THR	ala	THR	ala	THR	arg	arg	ala	leu	ala	ala	ala	ala	ala	arg	ala	ala	leu	ala	val
	72	asn	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	lys	ASP	ASP
	73	THR	THR	glu	glu	glu	glu	THR	ala	met	glu	THR	lys	lys	lys	lys	lys	ser	lys	lys	pro	arg	lys
	74	SER	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	phe	THR	THR	val	ile	ile	ile	ile	ile	THR	THR	ile	phe	arg	ile
	76	SER	asn	arg	asn	SER	SER	SER	SER	SER	asn	SER	SER	SER	SER	SER	SER	thr	SER	SER	asn	asn	SER
	77	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	gln	met	THR
	78	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	val	ALA	ALA	ALA	ALA	ALA
	79	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	ser
	80	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	leu	leu	leu	leu	leu	leu	MET	leu	leu	MET	MET	leu
FR3	81	GLU	GLU	GLU	GLU	GLU	GLU	GLU	asp	GLU	GLU	gln	gln	gln	gln	gln	gln	GLU	gln	gln	GLU	GLU	gln
	82	LEU	LEU	LEU	LEU	val	LEU	LEU	LEU	LEU	LEU	ile	trp	trp	trp	trp	trp	LEU	trp	trp	LEU	LEU	trp
	82A	ser	ser	his	ARG	ser	ser	ARG	ARG	ser	ser	ser	ser	ser	ser	ser	ser	thr	ser	ser	val	ARG	gly
	82B	ser	arg	ile	ser	ser	ser	ASN	ser	ser	ser	ser	ser	ser	ser	ser	ser	ala	ser	ser	ASN	gly	ser
	82C	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
	83	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	lys	lys	lys	lys	lys	lys	ile	lys	lys	phe	thr	lys
	84	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	ala	ala	ala	ala	ala	ala	SER	ala	ala	asn	phe	ala
	85	glu	ASP	glu	ASP	glu	glu	ASP	ASP	glu	glu	ASP	ser	ser	ser	ser	ser	ala	ser	ser	glu	glu	ser
	86	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP
	87	THR	THR	THR	THR	THR	ser	THR	ser	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	gly	THR	THR
	88	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	gly	gly
	89	VAL	VAL	ile	met	leu	VAL	VAL	VAL	VAL	phe	VAL	met	met	met	met	met	ile	met	met	VAL	ile	ile
	90	TYR	TYR	TYR	TYR	TYR	TYR	TYR	phe	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR		TYR	TYR	TYR
	91	TYR	TYR	TYR	TYR	TYR	phe	TYR	TYR	TYR	phe	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR		TYR	phe	TYR
	92	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS		CYS	CYS	CYS
	93	pro	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA		ALA	ALA	ALA
	94	ARG	ARG	ARG	lys	ARG	ARG	ARG	lys	ala	gly	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG		ARG	ARG	ARG
	95	ARG	ALA	ASP	GLU	GLU	GLU	ALA	SER	---	GLY	GLU				---	HIS	GLY	LEU	PRO	GLU	GLY	LEU
	96	THR	SER	GLN	GLY	GLY	ASP	PRO	ASP	---	TYR	ASP				---	ASN	ALA	GLU	PRO	TRP	PRO	ILE
	97	ARG	TYR	SER	TYR	ARG	LEU	GLY	PRO	---	GLY	SER				---	SER	HIS	GLY	GLU	LYS	LEU	THR
	98	TRM	CYS	LEU	GLY	ARG	TYR	TYR	PHE	---	ILE	ASN				---	GLN	TYR	ARG	GLY	GLY	LYS	GLY
	99	GLY	GLY	GLU	ASP	MET	GLY	CYS	TRP	---	TYR	GLY				---	THR	SER	GLY	TYR	GLN	ASN	PRO
	100	GLY	TYR	ASN	TYR	ALA	ASP	SER	SER	---	SER	TYR				---	GLY	ASP	TYR	CYS	VAL	MET	ARG
	100A	ARG	ASP	ILE	GLY	ILE	TYR	GLY	ASP	---	---	LYS				---	ALA	THR	THR	THR	ASN	ASN	HIS
	100B	GLY	CYS	GLU	ARG	ASN	VAL	GLY	TYR	---	---	ILE				---	SER	ASP	GLY	ASN	VAL	ILE	TYR
CDR3	100C	GLY	TYR	VAL	PRO	PRO	ALA	GLY	TYR	---	---	---				---	LEU	ASP	TYR	ASP	ASN	VAL	TYR
	100D	ASN	TYR	VAL	---	---	ASN	CYS	ASN	---	---	---				---	TRP	SER	ALA	ILE	PRO	GLY	TYR
	100E	---	---	PRO	---	---	---	TYR	PHE	---	---	---				---	TYR	GLY	LEU	CYS	---	GLY	TYR
	100F	---	---	LEU	---	---	---	ARG	ASP	---	---	---				---	PHE	THR	PRO	SER	---	VAL	ALA
	100G	---	---	ASP	---	---	---	GLY	TYR	---	---	---				---	---	SER	TYR	LEU	---	MET	---
	100H	---	---	PRO	---	---	---	ASP	SER	---	---	---				---	---	LEU	---	ASP	---	ASP	---
	100I	---	---	ASN	---	---	---	---	TYR	---	---	---				---	---	---	---	---	---	LEU	---
	100J	TRP	PHE	TYR	---	---	PRO	---	THR	---	---	---				---	---	---	TYR	---	---	#	---
	100K	PHE	PHE	#	PHE	PHE	PHE	---	LEU	---	---	PHE				---	---	---	PHE		PHE	MET	MET
	101	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	---	PRO	ASP				---	ASP	GLY	ASP	TYR	ASP	ASP	ASP
	102	SER	TYR	VAL	PHE	TYR	ILE	TYR	VAL	---	GLU	TYR				---	LEU	PRO	TYR	ILE	TYR	VAL	VAL
	103	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	---	GLU	TRP				---	TRP	TRP	TRP	TRP	TRP	TRP	TRP
	104	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	---	TYR	ASP				---	GLY	GLY	GLY	GLY	GLY	GLY	GLY
	105	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	---	ASN	GLN				---	ARG	GLN	GLN	GLN	GLN	GLN	GLN
	106	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	---	GLY	GLY				---	GLY	GLY	GLY	GLY	GLY	GLY	GLY
FR4	107	THR	THR	THR	THR	THR	THR	THR	THR	---	GLY	THR				---	THR	THR	PRO	THR	VAL	THR	THR
	108	LEU	LEU	THR	LEU	LEU	MET	LEU	THR	---	LEU	LEU				---	LEU	LEU	LEU	MET	LEU	THR	THR
	109	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	---	VAL	VAL				---	VAL	LEU	VAL	VAL	VAL	VAL	VAL
	110	THR	THR	THR	THR	THR	THR	THR	THR	---	THR	ILE				---	THR	ILE	THR	THR	THR	SER	THR

HUMAN HEAVY CHAINS SUBGROUP I (cont'd)

		45* WOL	46 Vh 383ex 'CL	47 M61 'CL	48 DI	49 60P1 'CL #	50 CA	51 BRO 'IGG	52 THO	53* STE	54 ZUC #	55* TH3 'CL #	56 HUS	57 OMM 'CL #	58 BOT #	59 BEN (I)	60 ZUC' #	61 WIS #	62 VAU #	63 LEB #	64 SAC #	65 AF2 'CL #	66 DEE	67* KOH	68* MAR	69 FI	70 VU	71 WAR	72 VIL
	0	---	---		---		---	---	---	---	---			---	---	---	---	---	---	---	---	---		---	---	---	---	---	---
	1	**pca**	**glu**		**pca**		**pca**	**glu**	**glu**	**pca**	**pca**			GLN	**asp**	**glu**	---	**pca**	**pca**	**pca**	**gly**	---		GLN	**pca**	**pca**	**pca**	**pca**	**pca**
	2	VAL	VAL		VAL		VAL	VAL	VAL	VAL	VAL			VAL	**ser**	**leu**	---	**met**	VAL	VAL	**ala**	---		VAL	VAL	VAL	VAL	VAL	VAL
	3	GLN	GLN		GLN		GLN	GLN	GLN	**his**	GLN			**his**	**pro**	GLN	---	GLN	---	---	---	---		GLN	GLN	GLN	GLN	GLN	GLN
	4	LEU	LEU		LEU		LEU	LEU	LEU	LEU	**val**			LEU	LEU	LEU	---	---	---	---	---	---		LEU	LEU	LEU	LEU	LEU	LEU
	5	**met**	VAL				VAL	VAL	VAL	VAL	VAL			**gln**	**glu**	VAL	---	---	---	---	---	---							
	6	**gln**	**gln**				**glu**	**gln**	**gln**	**glu**	**glu**			**glu**	**gln**	**gln**	---	---	---	---	---	---							
	7	SER	SER				SER	SER	SER	SER	SER			SER	SER	SER	---	---	---	---	---	---							
	8	GLY	GLY		GLY		GLY	GLY	GLY	**ser**	GLY			GLY	GLY	GLY	---	---	---	---	---	---							
	9	ALA	ALA		**gly**		ALA	ALA	ALA	ALA	ALA			**pro**	**his**	ALA	---	---	---	---	---	---							
	10	GLU	GLU				GLU	GLU	GLU	GLU	**asp**			**gly**	GLU	GLU	**asp**	---	---	---	---	---							
	11	VAL	VAL				VAL	VAL	VAL	VAL	**leu**			**leu**	VAL	VAL	**leu**	---	---	---	---	---							
	12	**lys**	**lys**		**lys**		**arg**	**lys**	**lys**	**lys**	**val**			**gly**	**gly**	**ser**	**val**	---	---	---	---	---							
	13	LYS	LYS		LYS		LYS	LYS	LYS	LYS	LYS			LYS	**ile**		LYS	---	---	---	---	---							
FR1	14	PRO	PRO				PRO	PRO	PRO	PRO	PRO			PRO	**leu**	PRO	PRO	---	---	---	---	---							
	15	GLY	GLY				GLY	GLY	GLY	GLY	GLY			**pro**	**lys**	GLY	GLY	---	---	---	---	---							
	16	**ser**	**glu**				ALA	**glu**	**glu**	ALA	**gly**			---	**glu**		**gly**	---	---	---	---	---							
	17	SER	SER				SER	SER	SER	SER	---			---	**thr**		---	---	---	---	---	---							
	18	VAL	**leu**				VAL	**leu**	**leu**	**met**	---			---	**glu**		---	---	---	---	---	---	VAL						
	19	**arg**	LYS	LYS	LYS		LYS	LYS	**arg**	LYS	---			---	**ala**		---	---	---	---	---	---	**arg**						
	20	VAL	**ile**	**ile**			**ile**	**ile**	**ile**	VAL	---			---	**glu**		---	---	---	---	---	---	**ile**						
	21	SER	SER	SER			SER	SER	SER	SER	---			---	**asp**		---	---	---	---	---	---							
	22	CYS	CYS	CYS			CYS			CYS	---			---	**arg**		---	---	---	---	---	---							
	23	LYS	LYS	LYS			LYS	LYS	LYS	**arg**	---			---	**ile**		---	---	---	---	---	---							
	24	**thr**	**gly**	**gly**			**thr**	**gly**	**gly**	ALA	---			---	**ile**		---	---	---	---	---	---							
	25	SER	SER	SER			SER	SER	**phe**		---			---	**lys**		---	---	---	---	---	---							
	26	GLY	GLY	GLY			GLY	GLY	GLY		---			---	**glu**		---	---	---	---	---	---							
	27	**gly**	TYR	TYR			TYR	TYR	TYR		---			---	**glu**		---	---	---	---	---	---							
	28	THR	**ser**	**ser**			THR				---			---	**glu**		---	---	---	---	---	---							
	29	PHE	PHE	PHE			PHE				---			---	**ala**		---	---	---	---	---	---							
	30	**val**	**ser**	THR			**ser**				---			---	**arg**		---	---	---	---	---	---							
	31	**asp**	**thr**	SER			**his**				---			---	**leu**		---	---	---	---	---	---							
	32	TYR	**phe**	TYR			TYR				---			---	**ser**		---	---	---	---	---	---							
CDR1	33	**lys**	**trp**	**trp**			**ala**				---			---	GLY		---	---	---	---	---	---							
	34	**gly**	ILE	ILE			**met**				---			---	**arg**		---	---	---	---	---	---							
	35	**leu**	**gly**	**gly**	SER						---			---	**asp**		---	---	---	---	---	---							
	35A	---	---	---	---						---			---	---		---	---	---	---	---	---							
	35B	---	---	---	---						---			---	---		---	---	---	---	---	---							
	36	TRP	TRP	TRP	TRP						---			---	**met**		---	---	---	---	---	---							
	37	VAL	VAL	VAL	**ile**						---			---	**gln**		---	---	---	---	---	---							
	38	ARG	ARG	ARG	ARG						---			---	**val**		---	---	---	---	---	---							
	39	GLN	GLN	GLN	GLN						---			---	**thr**		---	---	---	---	---	---							
	40	ALA	**met**	**met**	**pro**						---			---	**ser**		---	---	---	---	---	---							
	41	PRO	PRO	PRO	PRO						---			---	**gln**		---	---	---	---	---	---							
FR2	42	GLY	GLY	GLY	GLY						---			---	**pro**		---	---	---	---	---	---							
	43	**lys**	**lys**	**lys**	**lys**						---			---	---		---	---	---	---	---	---							
	44	GLY	GLY	GLY	GLY						---			---	---		---	---	---	---	---	---							
	45	LEU	LEU	LEU	LEU						---			---	---		---	---	---	---	---	---							
	46	GLU	GLU	GLU	GLU						---			---	---		---	---	---	---	---	---							
	47	TRP	TRP	TRP	TRP						---			---	---		---	---	---	---	---	---							
	48	**val**	**leu**	MET	**val**						---			---	---		---	---	---	---	---	---							
	49	GLY	GLY	GLY	GLY						---			---	---		---	---	---	---	---	---							
	50	**gln**	**thr**	**ile**	**glu**						---			---	---		---	---	---	---	---	---							
	51	ILE	ILE	ILE	ILE						---			---	---		---	---	---	---	---	---							
	52	**pro**	**his**	**tyr**	**asp**						---			---	---		---	---	---	---	---	---							
	52A	**leu**	**pro**	**pro**	---						---			---	---		---	---	---	---	---	---							
	52B	---	---	---	---						---			---	---		---	---	---	---	---	---							
	52C	---	---	---	---						---			---	---		---	---	---	---	---	---							
	53	**arg**	**gly**	**gly**	TYR						---			---	---		---	---	---	---	---	---							
CDR2	54	**phe**	**asp**	**asp**	**ser**						---			---	---		---	---	---	---	---	---							
	55	**asn**	**ser**	**ser**	GLY						---			---	---		---	---	---	---	---	---							
	56	**gly**	ASP	ASP	**thr**						---			---	---		---	---	---	---	---	---							
	57	**glu**	THR	THR	THR						---			---	---		---	---	---	---	---	---							
	58	**val**	**arg**	**arg**	**asp**						---			---	---		---	---	---	---	---	---							
	59	**lys**	**asn**	TYR	TYR						---			---	---		---	---	---	---	---	---							
	60	**asn**	**ser**	**ser**							---			---	---		---	---	---	---	---	---							
	61	**pro**	**pro**	**pro**		GLN					---			---	---		---	---	---	---	---	---							
	62	**gly**	**ser**	**ser**		**lys**					---			---	---		---	---	---	---	---	---							
	63	**ser**	**phe**	**phe**		**phe**					---			---	---		---	---	---	---	---	---							
	64	**val**	GLN	GLN	**lys**	GLN					---			---	---		---	---	---	---	---	---							
	65	**val**	GLY	GLY	**ser**	GLY					---			---	---		---	---	---	---	---	---							
	66	ARG	**gln**	**gln**	ARG	ARG					---			---	---		---	---	---	---	---	---							
	67	VAL	VAL	VAL		VAL					---			---	---		---	---	---	---	---	---							
	68	**ser**	THR	THR		THR					---			---	---		---	---	---	---	---	---							
	69	**val**	**ile**	**ile**	MET	**ile**					---			---	---		---	---	---	---	---	---							
	70	**ser**	**ser**	**ser**	**ser**	THR					---			---	---		---	---	---	---	---	---							
	71	**leu**	**val**	**ala**	**leu**	**ala**					---			---	---		---	---	---	---	---	---							
	72	**lys**	ASP	ASP	ASP	ASP					---			---	---		---	---	---	---	---	---							
	73	**pro**	**lys**	**lys**	THR	**glu**					---			---	---		---	---	---	---	---	---							
	74	SER	SER	SER	SER	SER					---	SER		---	---		---	---	---	---	---	---							
	75	**phe**	**ile**	**ile**	**val**	THR					---	**lys**		---	---		---	---	---	---	---	---							
	76	**asn**	SER	SER	**asn**	SER					---	**lys**		---	---		---	---	---	---	---	---							
	77	**gln**	THR	THR	**leu**	THR					---	**pro**		---	---		---	---	---	---	---	---							
	78	ALA	ALA	ALA	**phe**	ALA					---	**val**		---	---		---	---	---	---	---	---							
	79	**his**	**phe**	TYR	**ser**	TYR					---	**ser**		---	---		---	---	---	---	---	---							
FR3	80	MET	**leu**	**leu**	**leu**	MET					---	**leu**		---	---		---	---	---	---	---	---							
	81	GLU	**gln**	**gln**	**ser**	GLU					---	**lys**		---	---		---	---	---	---	---	---							
	82	LEU	**trp**	**trp**	LEU	LEU					---	LEU	**met**	---	---		---	---	---	---	---	---							
	82A	**ser**	**gly**	**ser**	**thr**	**ser**					---	**ser**	**asn**	---	---		---	---	---	---	---	---							
	82B	**ser**	**ser**	**ser**	**ser**	**ser**					---	**ser**	**ser**	---	---		---	---	---	---	---	---							
	82C	LEU	LEU	LEU	**val**	LEU					---	**val**	LEU	---	---		---	---	---	---	---	---							
	83	**phe**	**lys**	**lys**	**thr**	ARG					---	**thr**	ARG	---	---		---	---	---	---	---	---							
	84	SER	**ala**	**ala**	**ala**	SER					---	**ala**	**val**	---	---		---	---	---	---	---	---							
	85	**glu**	**ser**	**ser**	**ala**	**glu**					---	**ala**	**glx**	---	---		---	---	---	---	---	---							
	86	ASP	ASP	ASP	ASP	ASP					---	ASP	ASX	---	---		---	---	---	---	---	---							
	87	THR	THR	THR	THR	THR					---	THR	THR	---	---		---	---	---	---	---	---							
	88	ALA	**gly**	ALA	ALA	ALA					---	ALA	ALA	---	---		---	---	---	---	---	---							
	89	VAL	**ile**	**met**	VAL	VAL					---	VAL	VAL	---	---		---	---	---	---	---	---							
	90	TYR	TYR	TYR	TYR	TYR					---	TYR	TYR	---	---		---	---	---	---	---	---	TYR						
	91	TYR	TYR	TYR	TYR	TYR					---	TYR	TYR	---	---		---	---	---	---	---	---	TYR						
	92	CYS	CYS	CYS	CYS	CYS					---	CYS	CYS	---	---		---	---	---	---	---	---	CYS						
	93	**ALA**	**ALA**	**ALA**	ALA	ALA					---	ALA	ALA	---	---		---	---	---	---	---	---	**thr**						
	94	ARG	ARG	ARG	ARG	**thr**					---	ARG	ARG	---	---		---	---	---	---	---	---	**gly**						
	95	GLU		ARG		ALA					---	ARG	ASX	---	---		---	---	---	---	---	---	ARG						
	96	TYR		ARG		THR					---	ARG	ARG	---	---		---	---	---	---	---	THR	GLY						
	97	GLY		TYR		GLY					---	GLY	ASX	---	---		---	---	---	---	---	THR	MET						
	98	PHE		MET		ASP					---	GLY	ASX	---	---		---	---	---	---	---	VAL							
	99	ASP		GLY		---					---	TYR	TYR	---	---		---	---	---	---	---	VAL							
	100	THR		TYR		---					---	TYR	GLY	---	---		---	---	---	---	---	ILE							
	100A	SER		GLY		---					---	TYR	ASX	---	---		---	---	---	---	---	PRO							
	100B	ASP		ASP		---					---	GLY	PHE	---	---		---	---	---	---	---	PRO							
CDR3	100C	TYR		GLN		---					---	SER	---	---	---		---	---	---	---	---	VAL							
	100D	TYR		ALA		---					---	GLY	---	---	---		---	---	---	---	---	---							
	100E	---		PHE		---					---	SER	---	---	---		---	---	---	---	---	---							
	100F	---		---		---					---	TYR	---	---	---		---	---	---	---	---	---							
	100G	---		---		---					---	PHE	---	---	---		---	---	---	---	---	---							
	100H	---		---		---					---	GLY	---	---	---		---	---	---	---	---	---							
	100I	---		---		---					---	VAL	---	---	---		---	---	---	---	---	ASP							
	100J	---		---		ALA					---	LEU	---	---	---		---	---	---	---	---	ALA							
	100K	TYR		---		PHE					---	---	---	---	---		---	---	---	---	---	PHE							
	101	TYR		ASP		ASP					---	ASP	ASX	---	---		---	---	---	---	PRO	ASP							
	102	TYR		ILE	ARG	ILE					---	TYR	TYR	---	---		---	---	---	---	GLX	ILE							
	103	TRP		TRP	TRP	TRP					---	TRP	TRP	---	---		---	---	---	---	GLX	TRP							
	104	GLY		GLY	GLY	GLY					---	GLY	GLY	---	---		---	---	---	---	THR	GLY							
	105	GLN		GLN	SER	GLN					---	GLU	GLX	---	---		---	---	---	---	ASX	GLN							
	106	GLY		GLY	GLY	GLY					---	GLY	GLY	---	---		---	GLY	---	---	---	GLY							
F	107	THR		THR	GLY	THR					---	THR	THR	---	---		---	VAL	---	---	LEU	THR							
FR4	108	LEU		MET	LEU	MET					---	LEU	LEU	---	---		---	#	---	---	VAL	MET							
	109	VAL		VAL	VAL	VAL					---	VAL	VAL	---	---		---	#	---	---	ILE	VAL							
	110	THR		THR	THR	THR					---	THR	THR	---	---		---	THR	---	---	THR	THR							

HUMAN HEAVY CHAINS SUBGROUP I (cont'd)

		73 DUN	74 SAW	75 ADA	76 NOR	77 LEA	78 HAR	79 RIC	# OF SEQUENCES	# OF AMINO ACIDS	OCCURRENCES OF MOST COMMON AMINO ACID	VARIABILITY
	0	---	---	---	---	---	---	---				
	1	**pca**	**pca**	**pca**	**pca**	---	---	**pca**	68	5	32(GLN)	11.
	2	VAL	VAL	VAL	VAL	---	---	VAL	68	9	59(VAL)	10.
	3	GLN	**glu**	GLN	GLN	**pca**	**pca**	**leu**	67	6	59(GLN)	6.8
	4	LEU	LEU			LEU	LEU		63	2	62(LEU)	2.
	5								53	4	49(VAL)	4.3
	6								53	3	43(GLN)	3.7
	7								53	1	53(SER)	1.
	8								54	2	53(GLY)	2.
	9								54	5	47(ALA)	5.7
	10								54	3	51(GLU)	3.2
	11								54	2	50(VAL)	2.2
	12								55	6	41(LYS)	8.
	13								54	2	53(LYS)	2.
FR1	14								54	2	53(PRO)	2.
FR1	15								54	3	52(GLY)	3.1
FR1	16								52	5	23(ALA)	11.
FR1	17								50	2	49(SER)	2.
FR1	18								51	5	37(VAL)	6.9
FR1	19								53	3	44(LYS)	3.6
FR1	20								52	4	36(VAL)	5.8
FR1	21								51	3	48(SER)	3.2
FR1	22								49	2	48(CYS)	2.
FR1	23								51	4	47(LYS)	4.3
FR1	24								51	5	34(ALA)	7.5
FR1	25								50	3	48(SER)	3.1
FR1	26								50	2	48(GLY)	2.1
FR1	27								51	6	32(TYR)	9.6
FR1	28								49	5	35(THR)	7.
FR1	29								49	3	47(PHE)	3.1
FR1	30								49	9	22(THR)	20.
CDR1	31								49	8	33(SER)	12.
CDR1	32								49	5	40(TYR)	6.1
CDR1	33								49	7	18(ALA)	19.
CDR1	34								49	7	33(ILE)	10.
CDR1	35								49	10	21(SER)	23.
CDR1	35A											
CDR1	35B											
FR2	36								49	2	48(TRP)	2.
FR2	37								49	4	44(VAL)	4.5
FR2	38								49	2	48(ARG)	2.
FR2	39								49	2	48(GLN)	2.
FR2	40								49	4	37(ALA)	5.3
FR2	41								49	4	46(PRO)	4.3
FR2	42								49	2	48(GLY)	2.
FR2	43								48	4	33(GLN)	5.8
FR2	44								48	2	43(GLY)	2.2
FR2	45								48	2	47(LEU)	2.
FR2	46								48	1	48(GLU)	1.
FR2	47								48	2	47(TRP)	2.
FR2	48								48	4	41(MET)	4.7
FR2	49								48	2	47(GLY)	2.
CDR2	50								48	10	18(TRP)	27.
CDR2	51								48	4	45(ILE)	4.3
CDR2	52								48	10	13(ASN)	37.
CDR2	52A								47	7	30(PRO)	
CDR2	52B								1	1	1(TYR)	
CDR2	52C											
CDR2	53								48	10	14(GLY)	34.
CDR2	54								48	8	12(ASN)	32.
CDR2	55								48	5	34(GLY)	7.1
CDR2	56								48	11	16(ASP)	33.
CDR2	57								48	5	35(THR)	6.9
CDR2	58								48	10	24(ASN)	20.
CDR2	59								48	5	43(TYR)	5.6
CDR2	60								47	6	30(ALA)	9.4
CDR2	61								48	4	32(GLN)	6.
CDR2	62								48	8	24(LYS)	16.
CDR2	63								48	4	36(PHE)	5.3
CDR2	64								49	6	44(GLN)	6.7
CDR2	65								49	6	41(GLY)	7.2
FR3	66								49	3	39(ARG)	3.8
FR3	67								48	3	45(VAL)	3.2
FR3	68								48	4	45(THR)	4.3
FR3	69								49	7	26(ILE)	13.
FR3	70								49	2	35(THR)	2.8
FR3	71								49	5	19(ALA)	13.
FR3	72								49	3	46(ASP)	3.2
FR3	73								49	8	21(THR)	19.
FR3	74								50	1	50(SER)	1.
FR3	75								50	7	26(THR)	13.
FR3	76								50	5	39(SER)	6.4
FR3	77								50	5	45(THR)	5.6
FR3	78								50	3	43(ALA)	3.5
FR3	79								50	4	45(TYR)	4.4
FR3	80								50	2	36(MET)	2.8
FR3	81								50	5	35(GLU)	7.1
FR3	82								51	5	37(LEU)	6.9
FR3	82A								51	7	31(SER)	
FR3	82B								51	6	37(SER)	
FR3	82C								51	2	49(LEU)	
FR3	83								51	5	33(ARG)	7.7
FR3	84								51	5	34(SER)	7.5
FR3	85								51	4,5	24(GLU),23(GLU)	8.5,11.
FR3	86								51	1,2	51(ASP),50(ASP)	1.,2.
FR3	87								51	3	48(THR)	3.2
FR3	88								51	3	48(ALA)	3.2
FR3	89								51	5	34(VAL)	7.5
FR3	90								51	2	50(TYR)	2.
FR3	91								51	2	48(TYR)	2.1
FR3	92								51	1	51(CYS)	1.
FR3	93								51	3	49(ALA)	3.1
FR3	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)	
CDR3	100B								35	15	9(GLY)	
CDR3	100C								32	11	9(GLY)	
CDR3	100D								26	13	6(CYS)	
CDR3	100E								21	8	9(TYR)	
CDR3	100F								20	11	6(ARG)	
CDR3	100G								16	7	7(GLY)	
CDR3	100H								16	7	8(ASP)	
CDR3	100I								9	5	4(TYR)	
CDR3	100J								14	8	3(+)	
CDR3	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
FR4	106								39	1	39(GLY)	1.
FR4	107								40	5	34(THR)	5.9
FR4	108								39	4	25(LEU)	6.2
FR4	109								39	3	37(VAL)	3.2
FR4	110								40	3	37(THR)	3.2
FR4	111								40	1	40(VAL)	.

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) **lambda IGD-1'CL**: IGD-
45) **WOL**: IGM-KAPPA
48) **DI**: IGM-
49) **60F1'CL**: IGM-
50) **CA**: IGG1-
51) **BRO'IGG**: IGG-KAPPA
53) **STE**: IGG1-
54) **ZUC**: IGG3-
55) **TH3'CL**: IGM-KAPPA
56) **HUS**: IGG3-
57) **OMM'CL**: IGG3-
58) **BOT**: IGM-
59) **BEN(I)**: IGG3-
60) **ZUC'**: IGG3-
61) **WIS**: IGG3-
62) **VAU**: IGG1-
63) **LEB**: IGG1-
64) **SAC**: IGG1-KAPPA
67) **KOH**: IGM-LAMBDA
68) **MAR**: IGM-
71) **WAR**: IGG1-
72) **VIL**: IGG3-LAMBDA
73) **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.NAT.ACAD.SCI.USA,80,855-859. (CHECKED BY AUTHOR 01/04/83)
13) **V35'CL**: MATSUDA,F.,LEE,K.H.,NAKAI,S.,SATO,T.,KODAIRA,M.,ZONG,S.Q.,OHNO,H.,FUKUHARA,S. & HONJO,T. (1988) EMBO J.,7, 1047-1051.
14) **51P1'CL**: SCHROEDER,H.W.,JR.,HILLSON,J.L. & PERLMUTTER,R.M. (1987) SCIENCE,238,791-793; CHEN,P.P.,LIU,M.-F.,GLASS,C.A., SINHA,S.,KIPPS,T.J. & CARSON,D.A. (1989) ARTHRITIS & RHEUMATISM,32,72-76.
15) **AND'CL**: KIPPS,T.J.,TOMHAVE,E.,PRATT,L.F.,DUFFY,S.,CHEN,P.P. & CARSON,D.A. (1989) PROC.NATL.ACAD.SCI.USA,86,5913-5917.
16) **NEI'CL**: KIPPS,T.J.,TOMHAVE,E.,PRATT,L.F.,DUFFY,S.,CHEN,P.P. & CARSON,D.A. (1989) PROC.NATL.ACAD.SCI.USA,86,5913-5917.
17) **HP1'CL**: SHEN,A.,HUMPHRIES,C.,TUCKER,P. & BLATTNER,F. (1987) PROC.NATL.ACAD.SCI.USA,84,8563-8567.
18) **E3-10'CL**: KODAIRA,M.,KINASHI,T.,UMEMURA,I.,MATSUDA,F.,NOMA,T.,ONO,Y. & HONJO,T. (1986) J.MOL.BIOL.,190,529-541.
19) **1-92'CL**: BERMAN,J.E.,MELLIS,S.J.,POLLOCK,R.,SMITH,C.L.,SUH,H.,HEINKE,B.,KOWAL,C.,SURTI,U.,CHESS,L.,CANTOR,C.R & ALT,F.W. (1988) EMBO J.,7,727-738.
20) **hv1263'CL**: CHEN,P.P.,LIU,M.-F.,GLASS,C.A.,SINHA,S.,KIPPS,T.J. & CARSON,D.A. (1989) ARTHRITIS & RHEUMATISM,32,72-76.
21) **783c'CL**: CHEN,P.P.,LIU,M.-F.,GLASS,C.A.,SINHA,S.,KIPPS,T.J. & CARSON,D.A. (1989) ARTHRITIS & RHEUMATISM,32,72-76; KIPPS, T.J.,TOMHAVE,E.,PRATT,L.F.,DUFFY,S.,CHEN,P.P. & CARSON,D.A. (1989) PROC.NATL.ACAD.SCI.USA,86,5913-5917.
22) **X17115'CL**: FRIEDLANDER,R.M.,NUSSENZWEIG,M.C. & LEDER,P. (1990) NUCL.ACIDS RES.,18,4278.
23) **TH9'CL**: DERSIMONIAN,H.,MCADAM,K.P.W.J.,MACKWORTH-YOUNG,C. & STOLLAR,B.D. (1989) J.IMMUNOL.,142,4027-4033.
24) **WIL2'CL**: KIPPS,T.J.,TOMHAVE,E.,PRATT,L.F.,DUFFY,S.,CHEN,P.P. & CARSON,D.A. (1989) PROC.NATL.ACAD.SCI.USA,86,5913-5917.

25) **EV1-15'CL:** NEWKIRK,M.M.,GRAM,H.,HEINRICH,G.F.,OSTBERG,L.,CAPRA,J.D. & WASSERMAN,R.L. (1988) J.CLIN.INVEST.,81,1511-1518.

26) **KAS:** NEWKIRK,M.M.,MAGEED,R.A.,JEFFERIS,R.,CHEN,P.P. & CAPRA,J.D. (1987) J.EXP.MED.,166,550-564.

27) **BOR':** NEWKIRK,M.M.,MAGEED,R.A.,JEFFERIS,R.,CHEN,P.P. & CAPRA,J.D. (1987) J.EXP.MED.,166,550-564.

28) **RF-TS1'CL:** PASCUAL,V.,RANDEN,I.,THOMPSON,K.,SIOUD,M.FORRE,O.,NATVIG,J. & CAPRA,J.D. (1990) J.CLIN.INVEST.,86,1320-1328.

29) **LS7'CL:** SILBERSTEIN,L.E.,LITWIN,S. & CARMACK,C.E. (1989) J.EXP.MED.,169,1631-1643.

30) **ND'CL:** BENNICH,H. & VON BAHR-LINDSTROM,H. (1974) PROGRESS IN IMMUNOLOGY,1,49-58; BENNICH,H.H.,JOHANSSON,S.G.O. & VON BAHR-LINDSTROM,H. (1978) IN IMMEDIATE HYPERSENSITIVITY: MODERN CONCEPTS AND DEVELOPMENTS, BACH,M.K., ED.,PP.1-36, MARCEL DEKKER,NEW YORK; KENTEN,J.H.,MOLGAARD,H.V.,HOUGHTON,M.,DERBYSHIRE,R.B.,VINEY,J.,BELL,L.O. & GOULD,H.J. (1982) PROC.NAT.ACAD.SCI.USA,79,6661-6665.

31) **71-5'CL:** KODAIRA,M.,KINASHI,T.,UMEMURA,I.,MATSUDA,F.,NOMA,T.,ONO,Y. & HONJO,T. (1986) J.MOL.BIOL.,190,529-541.

32) **EU:** CUNNINGHAM,B.A.,RUTISHAUSER,U.,GALL,W.E.,GOTTLIEB,P.D.,WAXDAL,M.J. & EDELMAN,G.M. (1970) BIOCHEMISTRY,9,3161-3170. (CHECKED BY AUTHOR)

33) **RF-TS3'CL:** PASCUAL,V.,RANDEN,I.,THOMPSON,K.,SIOUD,M.FORRE,O.,NATVIG,J. & CAPRA,J.D. (1990) J.CLIN.INVEST.,86,1320-1328.

34) **5-1R1'CL:** BERMAN,J.E.,MELLIS,S.J.,POLLOCK,R.,SMITH,C.L.,SUH,H.,HEINKE,B.,KOWAL,C.,SURTI,U.,CHESS,L.,CANTOR,C.R & ALT, F.W. (1988) EMBO J.,7,727-738.

35) **VhAU'CL:** VAN DER HEIJDEN,R.W.J.,BUNSCHOTEN,H.,PASCUAL,V.,UYTDEHAAG,F.G.C.M.,OSTERHAUS,A.D.M.E. & CAPRA,J.D. (1990) J.IMMUNOL.,144,2835-2839.

36) **5-2R1'CL:** BERMAN,J.E.,MELLIS,S.J.,POLLOCK,R.,SMITH,C.L.,SUH,H.,HEINKE,B.,KOWAL,C.,SURTI,U.,CHESS,L.,CANTOR,C.R & ALT, F.W. (1988) EMBO J.,7,727-738.

37) **VH251'CL:** HUMPHRIES,C.G.,SHEN,A.,KUZIEL,W.A.,CAPRA,J.D.,BLATTNER,F.R. & TUCKER,P.W. (1988) NATURE,331,446-449.

38) **83P2'CL:** SCHROEDER,H.W.,JR. & WANG,J.Y. (1990) PROC.NATL.ACAD.SCI.USA,87,6146-6150.

39) **MOT:** KOJIMA,M.,ODANI,S. & ONO,T. (1982) MOL.IMMUNOL.,19,1095-1103; KOJIMA,M.,KOIDE,T.,ODANI,S. & ONO,T. (1986) MOL.IMMUNOL.,23,169-174. (CHECKED BY AUTHOR 08/08/86)

40) **WS1'CL:** SHEN,A.,HUMPHRIES,C.,TUCKER,P. & BLATTNER,F. (1987) PROC.NATL.ACAD.SCI.USA,84,8563-8567.

41) **Ab2022'CL:** SANZ,I.,CASALI,P.,THOMAS,J.W.,NOTKINS,A.L. & CAPRA,J.D. (1989) J.IMMUNOL.,142,4054-4061.

42) **SIE:** ANDREWS,D.W. & CAPRA,J.D. (1981) PROC.NAT.ACAD.SCI.USA,78,3799-3803; ANDREWS,D.W. & CAPRA,J.D. (1981) BIOCHEMISTRY, 20,5816-5822. (CHECKED BY AUTHOR 11/15/82); ANDREWS,D.W. & CAPRA,J.D. (1981) BIOCHEMISTRY,20,5822-5830.

43) **lambda IGD-1'CL:** YASUI,H.,AKAHORI,Y.,HIRANO,M.,YAMADA,K. & KUROSAWA,Y. (1989) EUR.J.IMMUNOL.,19,1399-1403.

44) **Ab2'CL:** VAN DER HEIJDEN,R.W.J.,BUNSCHOTEN,H.,PASCUAL,V.,UYTDEHAAG,F.G.C.M.,OSTERHAUS,A.D.M.E. & CAPRA,J.D. (1990) J.IMMUNOL.,144,2835-2839.

45) **WOL:** ANDREWS,D.W. & CAPRA,J.D. (1981) PROC.NAT.ACAD.SCI.USA,78,3799-3803; ANDREWS,D.W. & CAPRA,J.D. (1981) BIOCHEMISTRY, 20,5816-5822. (CHECKED BY AUTHOR 11/15/82); ANDREWS,D.W. & CAPRA,J.D. (1981) BIOCHEMISTRY,20,5822-5830.

46) **Vh383ex'CL:** VAN DER HEIJDEN,R.W.J.,BUNSCHOTEN,H.,PASCUAL,V.,UYTDEHAAG,F.G.C.M.,OSTERHAUS,A.D.M.E. & CAPRA,J.D. (1990) J.IMMUNOL.,144,2835-2839.

47) **M61'CL:** SCHROEDER,H.W.,JR. & WANG,J.Y. (1990) PROC.NATL.ACAD.SCI.USA,87,6146-6150.

48) **DI:** KOHLER,H.,SHIMIZU,A.,PAUL,C.,MOORE,V. & PUTNAM,F.W. (1970) NATURE,227,1318-1320; FLORENT,G.,LEHMAN,D. & PUTNAM,F.W. (1974) BIOCHEMISTRY,13,2482-2498. (CHECKED BY AUTHOR 06/15/83)

49) **60P1'CL:** SCHROEDER,H.W.,JR.,HILLSON,J.L. & PERLMUTTER,R.M. (1987) SCIENCE,238,791-793.

50) **CA:** PITCHER,S.E. & KONIGSBERG,W. (1970) J.BIOL.CHEM.,245,1267-1274. (CHECKED BY AUTHOR)

51) **BRO'IGG:** HOPPER,J.E.,NOYES,C.,HEINRIKSON,R. & KESSEL,J.W. (1976) J.IMMUNOL.,116,743-746; HOPPER,J.E. & BRAHN,E. (1977) J.IMMUNOL.,119,847-849. (CHECKED BY AUTHOR 08/25/78 WHO POINTED OUT THAT BRO' IS SAME AS BRIGG AND SUGGESTED THAT IT SHOULD BE RENAMED AS BROIGG)

52) **THO:** HOPPER,J.E. & BRAHN,E. (1977) J.IMMUNOL.,119,847-849. (CHECKED BY AUTHOR 08/25/78)

53) **STE:** FISHER,C.E.,PALM,W.H. & PRESS,E.M. (1969) FEBS LETTERS,5,20-22. (CHECKED BY AUTHOR)

54) **ZUC:** FRANGIONE,B. & MILSTEIN,C. (1969) NATURE,224,597-599. (CHECKED BY AUTHOR)

55) **TH3'CL:** DERSIMONIAN,H.,MCADAM,K.P.W.J.,MACKWORTH-YOUNG,C. & STOLLAR,B.D. (1989) J.IMMUNOL.,142,4027-4033.

56) **HUS:** WANG,A.C. & FUDENBERG,H.H. (1975) ARCH.BIOCHEM.BIOPHYS.,168,657-664. (CHECKED BY AUTHOR 09/23/77)

57) **OMM'CL:** ALEXANDER,A.,STEINMETZ,M.,BARRITAULT,D.,FRANGIONE,B.,FRANKLIN,E.C.,HOOD,L. & BUXBAUM,J.N. (1982) PROC.NAT.ACAD.SCI.USA,79,3260-3264. (CHECKED BY AUTHOR 06/17/83)

58) **BOT:** BARNIKOL-WATANABE,S.,MIHAESCO,E.,MIHAESCO,C.,BARNIKOL,H.U. & HILSCHMANN,N. (1984) Z.PHYSIOL.CHEM.,365,105-118.

59) **BEN(I):** KAPLAN,A.P.,HOOD,L.,TERRY,W.D. & METZGER,H. (1971) IMMUNOCHEMISTRY,8,801-811. (CHECKED BY AUTHOR)

60) **ZUC':** TAKAHASHI,N.,TAKAHASHI,Y.,ISHIOKA,N.,HEINY,M.E. & PUTNAM,F.W. (1986) PROTIDES BIOL.FLUIDS,33,541-544.

61) **WIS:** FRANKLIN,E.C.,PRELLI,F. & FRANGIONE,B. (1979) PROC.NAT.ACAD.SCI.USA,76,452-456. (CHECKED BY AUTHOR 07/18/79)

62) **VAU:** FRANKLIN,E.C.,KYLE,R.,SELIGMANN,M. & FRANGIONE,B. (1979) MOL.IMMUNOL.,16,919-921. (CHECKED BY AUTHOR 12/10/82)

63) **LEB:** FRANKLIN,E.C.,KYLE,R.,SELIGMANN,M. & FRANGIONE,B. (1979) MOL.IMMUNOL.,16,919-921. (CHECKED BY AUTHOR 12/10/82)

64) **SAC:** PARR,D.M. (1981) MOL.IMMUNOL.,18,257-259. (CHECKED BY AUTHOR 03/02/82)

65) **AF2'CL:** SONNTAG,D.,WEINGARTNER,B. & GRUTZMANN,R. (1989) NUCL.ACIDS RES.,17,1267.

66) **DEE:** FRANGIONE,B. & MILSTEIN,C. (1967) NATURE,216,939-941. (CHECKED BY AUTHOR)

67) **KOH:** KAPLAN,A.P.,HOOD,L.,TERRY,W.D. & METZGER,H. (1971) IMMUNOCHEMISTRY,8,801-811. (CHECKED BY AUTHOR)

68) **MAR:** KAPLAN,A.P.,HOOD,L.,TERRY,W.D. & METZGER,H. (1971) IMMUNOCHEMISTRY,8,801-811. (CHECKED BY AUTHOR)

69) **FI:** MONTGOMERY,P.C.,BELLO,A.C. & ROCKEY,J.H. (1970) BIOCHIM.BIOPHYS.ACTA,200,258-266. (CHECKED BY AUTHOR)

70) **VU:** MONTGOMERY,P.C.,BELLO,A.C. & ROCKEY,J.H. (1970) BIOCHIM.BIOPHYS.ACTA,200,258-266. (CHECKED BY AUTHOR)

71) **WAR:** KAPLAN,A.P.,HOOD,L.,TERRY,W.D. & METZGER,H. (1971) IMMUNOCHEMISTRY,8,801-811. (CHECKED BY AUTHOR)

72) **VIL:** KAPLAN,A.P.,HOOD,L.,TERRY,W.D. & METZGER,H. (1971) IMMUNOCHEMISTRY,8,801-811. (CHECKED BY AUTHOR)

73) **DUN:** KAPLAN,A.P.,HOOD,L.,TERRY,W.D. & METZGER,H. (1971) IMMUNOCHEMISTRY,8,801-811. (CHECKED BY AUTHOR)

74) **SAW:** KAPLAN,A.P.,HOOD,L.,TERRY,W.D. & METZGER,H. (1971) IMMUNOCHEMISTRY,8,801-811. (CHECKED BY AUTHOR)

75) **ADA:** KAPLAN,A.P.,HOOD,L.,TERRY,W.D. & METZGER,H. (1971) IMMUNOCHEMISTRY,8,801-811. (CHECKED BY AUTHOR)

76) **NOR:** KAPLAN,A.P.,HOOD,L.,TERRY,W.D. & METZGER,H. (1971) IMMUNOCHEMISTRY,8,801-811. (CHECKED BY AUTHOR)

77) **LEA:** FRANGIONE,B. & FRANKLIN,E.C. (1977) PROG.IMMUNOL.,3,278-288. (CHECKED BY AUTHOR 07/18/79)

78) **HAR:** FRANGIONE,B. & FRANKLIN,E.C. (1977) PROG.IMMUNOL.,3,278-288. (CHECKED BY AUTHOR 07/18/79)

79) **RIC:** KAPLAN,A.P.,HOOD,L.,TERRY,W.D. & METZGER,H. (1971) IMMUNOCHEMISTRY,8,801-811. (CHECKED BY AUTHOR)

IDENTICAL SETS OF FRAMEWORK SEGMENTS:

FR1:
- SET 1: LS2'CL[1],LS5'CL[2],LS6'CL[3],LS1'CL[4],LS4'CL[5]. (5 IDENTICAL)
- SET 2: 21-2'CL[8],3-1'CL[9],21/28'CL[10],8E10'CL[11],V35'CL[13],1-92'CL[19]. (6 IDENTICAL)
- SET 3: 51P1'CL[14],AND'CL[15],NEI'CL[16],hv1263'CL[20],783c'CL[21],X17115'CL[22],EV1-15'CL[25],RF-TS1'CL[28]. (8 IDENTICAL)
- SET 4: 5-1R1'CL[34],VhAU'CL[35],VH251'CL[37]. (3 IDENTICAL)
- SET 5: WS1'CL[40],Ab2022'CL[41],Ab2'CL[44],Vh383ex'CL[46]. (4 IDENTICAL)
- SET 6: VAU[62],LEB[63]. (2 IDENTICAL)

FR2:
- SET 1: LS2'CL[1],LS5'CL[2],LS6'CL[3],LS1'CL[4],LS4'CL[5],LS8'CL[6],1B9/F2'CL[7],21-2'CL[8],3-1'CL[9],HG3'CL[12], V35'CL[13],51P1'CL[14],AND'CL[15],NEI'CL[16],hv1263'CL[20],783c'CL[21],X17115'CL[22],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],LS5'CL[2],LS6'CL[3],LS1'CL[4],LS4'CL[5],LS8'CL[6],LS7'CL[29]. (7 IDENTICAL)
- SET 2: 21-2'CL[8],3-1'CL[9],HG3'CL[12]. (3 IDENTICAL)
- SET 3: 21/28'CL[10],8E10'CL[11],E3-10'CL[18]. (3 IDENTICAL)
- SET 4: 51P1'CL[14],AND'CL[15],NEI'CL[16]. (3 IDENTICAL)
- SET 5: 783c'CL[21],X17115'CL[22]. (2 IDENTICAL)
- SET 6: ND'CL[30]. (IDENTICAL TO 1 HUMAN V-H-III: U266'CL[136].)
- SET 7: 5-1R1'CL[34],VhAU'CL[35],VH251'CL[37],83P2'CL[38],M61'CL[47]. (5 IDENTICAL)

FR4:
- SET 1: LS2'CL[1],LS5'CL[2],LS6'CL[3],LS1'CL[4],LS8'CL[6],1B9/F2'CL[7],21/28'CL[10],NEI'CL[16],TH9'CL[23], WIL2'CL[24],KAS[26],BOR'[27],LS7'CL[29],WOL[45]. (14 IDENTICAL HUMAN V-H-I; ALSO 7 HUMAN V-H-II: 15P1'CL[1], ML1'CL[3],MCE'[46],DR12910-2F8'CL[48],Ab17'CL[49],M44'CL[52],NZU[55]; 34 HUMAN V-H-III: 18/2'CL[1], 18/17'CL[2],18/9'CL[3],1/17'CL[4],30P1'CL[5],M43'CL[6],HF2-1/17[7],Ab25'CL[12],Vh38C1.9'CL[15], Vh38C1.8'CL[16],Vh38C1.5'CL[17],60P2'CL[18],63P1'CL[19],GF4/1.1'CL[20],Vh38C1.4'CL[21],Vh38C1.5'CL[22], 56P1'CL[25],2P1'CL[26],M74'CL[28],TIL[33],AN.14'CL[41],WEA[47],4B4'CL[48],M26'CL[49],NIE[60],DOB[62], VH10.7'CL[63],K6H6'CL[68],K4B8'CL[69],K5B8'CL[70],K5C7'CL[71],K5G5'CL[72],K6F5'CL[73],20P1'CL[82]; 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: 8E10'CL[11],TH3'CL[55]. (2 IDENTICAL HUMAN V-H-I; ALSO 1 HUMAN V-H-III: TIL[33]; AND 1 MOUSE V-H-IIIA: MOPC47A[110].)
- SET 3: 51P1'CL[14],RF-TS1'CL[28],Ab2022'CL[41],M61'CL[47],60P1'CL[49],AF2'CL[65]. (6 IDENTICAL HUMAN V-H-I; ALSO 6 HUMAN V-H-II: L16'CL[2],M71'CL[4],C6B2'CL[14],58P2'CL[16],CE-1'CL[41],37P1'CL[47]; AND 3 HUMAN V-H-III: 38P1'CL[36],3D6'CL[43],13P1'CL[97].)
- SET 4: AND'CL[15]. (IDENTICAL TO 1 HUMAN V-H-II: 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],HIG1'CL[24],Ab44'CL[29],Eog-B'CL[30],HuRSV19VH[36],HuRSV19CHFNS[38]; 6 HUMAN V-H-III: 4GI2'CL[10],Ab21'CL[24],M72'CL[27],KIM46H'CL[29],U266'CL[136],70P1'CL[183]; 2 MOUSE V-H-IIA: HDEX12[15], MBr1'CL[160]; AND 1 MOUSE V-H-IIC: MuRSV19VH'CL[37].)

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

SET 6: 83P2'CL[38]. (IDENTICAL TO 2 HUMAN V-H-II: Ab26'CL[18],M60'CL[42]; AND 5 HUMAN V-H-III: Ab18'CL[11], RF-KL1'CL[13],1B11'CL[74],1H1'CL[75],2C12'CL[80].)

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

IDENTICAL SETS OF COMPLEMENTARITY DETERMINING REGIONS:

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

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

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

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

SET 5: 51P1'CL[14],AND'CL[15],NEI'CL[16],hv1263'CL[20],783c'CL[21],X17115'CL[22],KAS[26]. (7 IDENTICAL HUMAN V-H-I; ALSO 3 RABBIT V-H: 5C3'CL[1],5.5'CL[2],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: ML1'CL[3],DRI2910-2F8'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],M26'CL[49], VH10.7'CL[63],K6H6'CL[68],K4B8'CL[69],K5B8'CL[70],K5C7'CL[71],K5G5'CL[72],K6F5'CL[73],20P1'CL[82]; AND 1 MOUSE V-H-IIID: H37-40'CL[25].)

SET 2: 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: LI16'CL[2],M71'CL[4],C6B2'CL[14],58P2'CL[16],CE-1'CL[41],37P1'CL[47]; AND 3 HUMAN V-H-III: 38P1'CL[36], 3D6'CL[43],13P1'CL[97].)

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

SET 6: 783c'CL[21],X17115'CL[22],EV1-15'CL[25],ND'CL[30],Ab2'CL[44]. (5 IDENTICAL HUMAN V-H-I; ALSO 3 HUMAN V-H-II: FK-001'CL[1],HIG1'CL[24],Ab44'CL[29]; AND 6 HUMAN V-H-III: 4G12'CL[10],Ab21'CL[24],M72'CL[27], KIM46H'CL[29],U266'CL[136],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:** PAPAIN CLEAVES BETWEEN ARG 56 AND THR 57, AND BETWEEN ARG 62 AND SER 63.

43) **lambda IGD-1'CL:** CLASS SWITCH FROM IGM TO IGD IS PROBABLY DUE TO HOMOLOGOUS RECOMBINATION BETWEEN sigma/mu and SIGMA/mu. RESIDUE 52C IS PHE, WITH ANOTHER RESIDUE GLN BETWEEN 52C AND 53. RESIDUE 100J IS LYS, WITH TWO MORE RESIDUES LEU AND ALA BETWEEN 100J AND 100K.

49) **60P1'CL:** FROM HUMAN FETUS AT 130 DAYS OF GESTATION.

54) **ZUC:** IT WAS FROM A CASE OF HEAVY CHAIN DISEASE.

55) **TH3'CL:** THIS HYBRIDOMA WAS GENERATED BY FUSION OF PERIPHERAL BLOOD CELLS OF A PATIENT WITH LEPROSY AND THE HUMAN MYELOBLASTOID CELL LINE GM4672.

57) **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 DHFL16.

\+ THE FOLLOWING WERE EQUALLY AND MOST FREQUENTLY OCCURRING:

AT POSITION	RESIDUES
100J	(TYR,ALA)

		INVARIANT RESIDUES	1 15P1 'CL #	2* L16 'CL	3* ML1 'CL	4 M71 'CL	5* F19L16 'CL	6* F19ML1 'CL	7 6-1G1 'CL	8 VHVI 'CL	9 VH6 'CL	10* A10 'CL	11* FK-001 'CL #	12* A431 'CL	13 71-2 'CL	14* C6B2 'CL #	15 71-4 'CL	16 58P2 'CL #	17 SUP-T1 VH-JA 'CL #	18* Ab26 'CL	19 1-9II 'CL	20 12G-1 'CL
	0		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	1		GLN	GLN	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	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
	4	LEU(.98)	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
	5		GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN
	6		GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	**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
	8	GLY(.98)	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
	9		PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO
	10		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
	12		VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
	13		LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS
FR1	14	PRO(.98)	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO
	15		SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
	16		GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	**glu**	GLN	**glu**	**glu**	**glu**	GLN	**asp**	**asp**
	17	THR(.96)	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
	18	LEU(.98)	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
	19		SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
	20	LEU(.98)	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
	21	THR(.96)	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
	22	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	**thr**	**thr**	**thr**	**thr**	ALA	ALA	ALA	ALA
	24		ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**
	25		SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
	26	GLY(.98)	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
	27		ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	**gly**	**gly**	**gly**	**gly**	**tyr**	**gly**	**tyr**	**tyr**
	28		SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
	29		VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	**ile**	VAL	**ile**	**ile**	**ile**	**ile**	**ile**
	30		SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	**arg**	SER	SER	SER	SER	SER	SER
	31		SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	**gln**	SER	SER	SER	SER	SER	SER
CDR1	32		ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	**lys**	ASN	ASN	**gly**	**trp**	**tyr**	**tyr**	**gly**	**gly**	**ser**	**ser**
	33		SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	**tyr**	**tyr**	**tyr**	**asp**	**asn**	**asn**	**asn**
	34		ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	**val**	ALA	**tyr**	**tyr**	**trp**	**trp**	**tyr**	**tyr**	**trp**	**trp**
	35		ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	**ser**	**phe**	**tyr**	**tyr**	**ser**	**ser**	**trp**	**trp**	**trp**	**trp**
	35A		TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	---	---	**gly**	**ser**	**gly**	**gly**
	35B		ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	**ser**	**ser**	---	---	---	---	---	---	---
	36	TRP(.98)	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP
	37		ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE
	38	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG
	39	GLN(.96)	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN
	40		SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	**pro**	**pro**	**pro**	**pro**	**pro**	**his**	**pro**	**pro**
FR2	41	PRO(.98)	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO
	42		SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	**gly**	**gly**	**gly**	**gly**	**gly**	**gly**	**gly**	**gly**
	43		ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	**lys**	**lys**	**lys**	**lys**	**lys**	**lys**	**lys**	**lys**
	44		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
	45	LEU(.96)	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
	47	TRP(.98)	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP
	48		LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	**ile**	**ile**	**ile**	**ile**	**ile**	**ile**	**ile**	**ile**
	49		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
	50		ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	**ARG**	**tyr**	ARG	**tyr**	**tyr**	**ser**	**tyr**	**tyr**	**tyr**
	51		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	**ile**	**ile**	**ile**	**ile**	**ile**	**ile**	**ile**	**ile**
	52		TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR
	52A		TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	---	---	---	---	---	---	---	---
	52B		ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	**lys**	ARG	ARG	---	---	---	---	---	---	---	---
	52C		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	53		SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	**tyr**	**thr**	**tyr**	**tyr**	**his**	**tyr**	**tyr**	**tyr**
CDR2	54		LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	**ser**	**ser**	**ser**	**ser**	**ser**	**ser**	**ser**	**ser**	**ser**
	55		TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	**gly**	**gly**	**gly**	**gly**	**gly**	**gly**	**gly**	**gly**
	56		TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	**asn**	**ser**	**ser**	**ser**	**ser**	**ser**	**ser**	**ser**	**ser**
	57		ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	**thr**	**thr**	**thr**	**thr**	**thr**	**thr**	**thr**	**thr**	**thr**
	58		ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	**asn**	**asn**	**asn**	**asn**	**asn**	**tyr**	**tyr**	**tyr**	**tyr**
	59		TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	**ser**	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR
	60		ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	**asn**	**asn**	**asn**	**asn**	**asn**	**asn**	**asn**	**asn**
	61		VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	**glu**	VAL	VAL	**pro**	**pro**	**pro**	**pro**	**pro**	**pro**	**pro**	**pro**
	62		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	**leu**	**leu**	**leu**	**leu**	**leu**	**leu**	**leu**	**leu**
	64		LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS
	65		SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
	66	ARG	ARG	**ARG**	ARG	ARG	**ARG**	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG
	67		ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	**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	**ala**	THR	THR
	69		ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	**thr**	ILE	ILE	ILE	ILE	ILE	**met**	**met**	**met**
	70		ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	**ser**	**ser**	**ser**	**ser**	**ser**	**ser**	**ser**	**ser**
	71		PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**
	72	ASP(.98)	**ASP**	**ASP**	**ASP**	**ASP**	ASP	ASP	ASP	ASP	ASP	ASP	ASP	**ASP**	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP
	73		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
	74	SER(.98)	SER	**SER**	**SER**	**SER**	SER	**SER**	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
	75		LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	**asn**	LYS	LYS
	76	ASN	ASN	ASN	A**S**N	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN
	77		GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN
	78		PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE
	79		SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
FR3	80	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
	81		GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	**lys**	**lys**	**lys**	**lys**	**lys**	**asn**	**lys**	**lys**
	82		LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
	82A		ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	**ser**	**ser**	**ser**	**ser**	**ser**	ASN	**ser**	**ser**
	82B		SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
	82C		VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
	83		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
	84		PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	**ala**	**ala**	**ala**	**ala**	**ala**	**arg**	**ala**	**ala**
	85		GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	**ala**	**ala**	**ala**	**ala**	**ala**	**ala**	**val**	**val**
	86	ASP(.98)	ASP	ASP	ASP	ASP	**ASP**	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP
	87		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
	88		ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA
	89		VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
	90	TYR(.98)	**TYR**	**TYR**	**TYR**	**TYR**	**TYR**	**TYR**	**TYR**	**TYR**	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR
	91		TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR
	92	CYS(.98)	CYS	CYS	C**Y**S	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS
	93		ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	**val**	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA
	94		ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	**thr**	ARG	ARG
	95		ASN	GLU	GLU	ALA	GLU	GLU	---	---		GLU	ALA	GLY	---	GLU	---	VAL	VAL	SER	---	---
	96		GLN	LEU	GLU	LEU	LEU	GLU	---	---		LEU	ARG	ASP	---	GLU	---	PHE	ARG	VAL	---	---
	97		ARG	GLY	THR	THR	GLY	THR	---	---		GLY	PRO	GLN	---	GLN	---	LEU	ARG	SER	---	---
	98		GLY	ASP	GLY	GLY	ASP	GLY	---	---		ASP	GLY	GLY	---	LEU	---	THR	ARG	SER	---	---
	99		THR	ALA	LEU	ASP	---	LEU	---	---		GLY	THR	---	---	LEU	---	GLY	---	MET	---	---
	100		ARG	PHE	PHE	ALA	---	---	---	---		---	THR	---	---	TRP	---	ASP	---	ILE	---	---
	100A		ALA	---	---	PHE	---	---	---	---		---	GLY	---	---	PHE	---	---	---	VAL	---	---
	100B		GLY	---	---	---	---	---	---	---		---	GLY	---	---	GLY	---	---	---	VAL	---	---
CDR3	100C		THR	---	---	---	---	---	---	---		---	---	---	---	ASP	---	---	---	ALA	---	---
	100D		LYS	---	---	---	---	---	---	---		---	---	---	---	LEU	---	---	---	LEU	---	---
	100E		---	---	---	---	---	---	---	---		---	---	---	---	PHE	---	---	---	ASN	---	---
	100F		---	---	---	---	---	---	---	---		---	---	---	---	SER	---	---	TYR	---	---	---
	100G		---	---	---	---	---	---	---	---		---	---	---	---	GLY	---	---	SER	---	---	---
	100H		---	---	---	---	---	---	---	---		---	---	---	---	---	---	---	SER	HIS	---	---
	100I		ASN	---	---	---	---	---	---	---		---	---	---	---	---	---	---	ALA	TRP	---	---
	100J		TRP	---	---	---	---	---	---	---		---	GLY	---	---	ALA	---	ALA	SER	TYR	---	---
	100K		PHE	---	---	---	ALA	---	---	---		---	MET	---	---	PHE	---	PHE	LYS	PHE	---	---
	101		ASP	ASP	ASP	ASP	PHE	PHE	---	---		PHE	ASP	PHE	---	ASP	---	ASP	ILE	ASP	---	---
	102		PRO	ILE	TYR	ILE			---	---			VAL		---	ILE	---	ILE	ILE	LEU	---	---
	103	TRP(.95)	TRP	TRP	TRP	TRP			---	---			TRP		---	TRP	---	TRP	PHE	TRP	---	---
	104	GLY	GLY	GLY	GLY	GLY			---	---			GLY		---	GLY	---	GLY	GLY	GLY	---	---
	105		GLN	GLN	GLN	GLN			---	---			GLN		---	GLN	---	GLN	SER	ARG	---	---
	106	GLY	GLY	GLY	GLY	GLY			---	---			GLY		---	GLY	---	GLY	GLY	GLY	---	---
FR4	107		THR	THR	THR	THR			---	---			THR		---	THR	---	THR	THR	THR	---	---
	108		LEU	MET	LEU	MET			---	---			THR		---	MET	---	MET	ARG	LEU	---	---
	109	VAL(.97)	VAL	VAL	VAL	VAL			---	---			VAL		---	VAL	---	VAL	LEU	VAL	---	---
	110		THR	THR	THR	THR			---	---			THR		---	THR	---	THR	SER	THR	---	---

HUMAN HEAVY CHAINS SUBGROUP II (cont'd)

		21 2-1 'CL	22* Pag-1 'CL #	23 11 'CL	24 HIG1 'CL	25* HuVNP 'CL #	26 79 'CL	27* HuVH LYS 'CL #	28 58 'CL	29* Ab44 'CL	30* Fog-B 'CL #	31 TS2 'CL	32* HuVH CAMP 'CL	33* 6H- 3C4 'CL #	34* NEWM	35* GER	36 Hu RSV19 VH #	37 WAH	38* Hu RSV19 VH FNS #	39* LES-C 'CL #	40 COR	41 CE-1 'CL #	42 M60 'CL	43 DAW	44 HE	45 OU
	0	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----
	1	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	**pca**	GLX	**pca**	**arg**	**pca**	GLN	GLN	**glu**	**pca**	**pca**	**pca**
	2	**leu**	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	**leu**	VAL	VAL	VAL	VAL	**leu**	VAL	**leu**	VAL	VAL	VAL	VAL	VAL	VAL	VAL
	3	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	**arg**	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	**his**	**thr**	**asn**	**thr**	**thr**	**thr**
	4	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
	5	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLX	**glu**	GLN	GLN	GLN	GLN	**arg**	**arg**	**arg**	**arg**	**thr**
	6	**glu**	**glu**	**glu**	GLN	**glu**	**glu**	**glu**	GLN	GLN	**glu**	**glu**	**glu**	GLN	GLX	**glu**	**glu**	**glu**	**glu**	GLN	**glu**	**glu**	**glu**	**glu**	**glu**
	7	SER	SER	SER	**trp**	SER	SER	SER	**trp**	**trp**	SER	SER	SER	**trp**	SER	SER	SER	SER	**trp**	SER	SER	SER	SER	**asn**	SER
	8	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
	9	PRO	PRO	PRO	**ala**	PRO	PRO	PRO	**ala**	**ala**	PRO	PRO	PRO	**ala**	PRO	**ser**	PRO	PRO	PRO	**ala**	PRO	PRO	PRO	PRO	PRO
	10	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	**ala**	**ala**	**ala**	**thr**	**ala**
	11	LEU	LEU	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	**leu**	**leu**	VAL	VAL	VAL	**leu**	VAL	VAL	VAL	VAL	VAL	**leu**	VAL	VAL	VAL	VAL	VAL
	13	LYS	LYS	LYS	LYS	**arg**	LYS	**arg**	LYS	LYS	LYS	LYS	**arg**	LYS	**arg**	LYS	**arg**	LYS	**arg**	LYS	LYS	LYS	LYS	**arg**	LYS
FR1	14	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	**ala**	PRO	PRO	PRO	PRO
	15	SER	SER	SER	SER	SER	**pro**	SER	SER	SER	SER	SER	SER	SER	SER	**thr**	SER	SER	SER	SER	**thr**	**thr**	**thr**	**thr**	**lys**
	16	**glu**	**glu**	**glu**	**glu**	GLN	**gly**	GLN	**glu**	**glu**	**glu**	GLN	GLN	**glu**	GLN	**glu**	GLN	**glu**	GLN	**glu**	GIN	**his**	GLN	GLN	GLN
	17	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	**ala**	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	**pro**
	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	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	**ala**	SER	SER	SER	SER	SER	SER	SER	SER	**thr**	**thr**	**thr**	**thr**	**thr**
	20	**LEU**	**val**	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
	21	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
	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	**thr**	**thr**	**val**	ALA	**thr**	ALA	**thr**	ALA	ALA	**ser**	**thr**	**thr**	**asp**	**thr**	ALA	**thr**	**ile**	**thr**	ALA	**thr**	**thr**	**thr**	**thr**	**thr**
	24	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**phe**	**phe**	**leu**	**phe**	**phe**
	25	SER	SER	SER	**phe**	SER	SER	SER	**tyr**	**tyr**	SER	SER	SER	**tyr**	SER	SER	SER	SER	SER	**tyr**	SER	SER	**tyr**	SER	SER
	26	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
	27	**gly**	**gly**	**gly**	**gly**	**ser**	**gly**	**ser**	**gly**	**gly**	**gly**	**gly**	**ser**	**gly**	**ser**	ASP	**phe**	**gly**	**phe**	**gly**	**phe**	**leu**	**phe**	**phe**	**leu**
	28	SER	SER	SER	SER	**thr**	SER	**thr**	SER	SER	SER	SER	**thr**	SER	**thr**	**pro**	**thr**	**pro**	**thr**	**pro**	SER	SER	SER	SER	SER
	29	**ile**	VAL	**ile**	**phe**	**phe**	**ile**	**phe**	VAL	**phe**	VAL	**phe**	**phe**	**phe**	**phe**	**ile**	**phe**	**ile**	**phe**	**phe**	**leu**	VAL	**leu**	**leu**	**leu**
	30	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	**arg**	SER	SER	SER	SER	**asn**	SER	SER	**thr**
	31	SER	SER	SER	**gly**	SER	SER	**gly**	**gly**	**gly**	SER	**thr**	**asp**	**gly**	**asn**	SER	**asp**	**arg**	**asp**	**gly**	SER	**thr**	**thr**	**gly**	**thr**
CDR1	32	**ser**	**ser**	**ser**	**tyr**	**tyr**	**ser**	**tyr**	**tyr**	**tyr**	**gly**	**asp**	**phe**	**tyr**	**asp**	**ala**	**tyr**	**thr**	**tyr**	**tyr**	**thr**	**arg**	**ser**	**glu**	**asp**
	33	SER	**tyr**	**asn**	**tyr**	**trp**	**asn**	**gly**	**tyr**	**tyr**	**gly**	**asn**	**tyr**	**tyr**	**tyr**	**asn**	**tyr**	**gly**	**tyr**	**tyr**	**gly**	**gly**	**gly**	**thr**	**gly**
	34	**tyr**	**trp**	**trp**	**trp**	**met**	**trp**	**val**	**trp**	**trp**	**leu**	**tyr**	**met**	**trp**	**tyr**	**tyr**	**met**	**tyr**	**met**	**trp**	**met**	**met**	**met**	**met**	**val**
	35	**tyr**	**ser**	**trp**	**ser**	**his**	**trp**	**asn**	**ser**	**ser**	**tyr**	**tyr**	**asn**	**ser**	**thr**	**ser**	**his**	**tyr**	**his**	**ser**	**cys**	**ser**	**cys**	**cys**	ALA
	35A	TRP	---	**ser**	---	---	**ser**	---	---	---	TRP	TRP	---	---	---	---	---	TRP	---	---	**val**	**val**	**val**	**val**	**val**
	35B	**gly**	---	---	---	---	---	---	---	---	**gly**	**ser**	---	---	---	---	---	**gly**	---	---	**gly**	**ser**	**ser**	**ala**	**gly**
	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	ILE	ILE	**val**	ILE	**val**	**val**	**val**	ILE	ILE	**val**	**leu**	**val**	ILE	**val**	ILE	**val**	ILE	**val**	**val**	ILE	ILE	ILE	ILE	ILE
	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	**thr**	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	**arg**
	40	**pro**	**pro**	**pro**	**pro**	**pro**	**pro**	**pro**	**pro**	**pro**	**pro**	**pro**	**pro**	**pro**	**pro**	**pro**	**pro**	**pro**	**pro**	**pro**	**pro**	**pro**	**pro**	**gly**	**pro**
FR2	41	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	**ala**	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**	**gly**	**gly**
	43	**lys**	**lys**	**lys**	ARG	ARG	**lys**	ARG	**lys**	**lys**	**lys**	**lys**	ARG	**lys**	ARG	**lys**	ARG	**lys**	ARG	**lys**	**lys**	**lys**	**lys**	ARG	**lys**
	44	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	**ala**	**ala**	**ala**	**ala**	**ala**
	45	LEU	**pro**	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	**pro**	LEU	LEU	LEU	LEU	LEU
	46	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU
	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	**ile**	**ile**	**ile**	**ile**	**ile**	**ile**	**ile**	**ile**	**ile**	**ile**	**ile**	**ile**	**ile**	**ile**	**ile**	**ile**	**ile**	**ile**	**ile**	LEU	LEU	LEU	LEU	LEU
	49	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	**ala**	**ala**	**ala**	**ala**	**ala**
	50	**ser**	**tyr**	**glu**	**glu**	ARG	**glu**	**met**	**tyr**	**glu**	**ser**	ARG	**phe**	**glu**	**tyr**	**tyr**	**trp**	**gly**	**trp**	**glu**	ARG	ARG	**leu**	**trp**	**trp**
	51	**ile**	**ile**	**ile**	**ile**	**ile**	**ile**	**ile**	**ile**	**ile**	**ile**	**ile**	**ile**	**ile**	**val**	**ile**	**val**	**val**	**ile**	**ile**	**ile**	**ile**	**ile**	**asp**	**leu**
	52	TYR	TYR	TYR	**asn**	**asp**	TYR	**trp**	TYR	**asn**	**phe**	**phe**	**arg**	**asn**	**phe**	TYR	**asp**	TYR	**asp**	**asn**	**asp**	**asp**	**asp**	**ile**	**leu**
	52A	---	---	---	---	**pro**	---	---	---	---	---	---	**asp**	---	---	---	**pro**	---	**pro**	---	---	---	---	TYR	---
	52B	---	---	---	---	---	---	---	---	---	---	---	**lys**	---	---	---	---	---	---	---	---	---	---	---	---
	52C	---	---	---	---	---	---	---	---	---	---	---	**ala**	---	---	---	---	---	---	---	---	---	---	---	---
	53	**tyr**	**tyr**	**his**	**his**	**asn**	**his**	**gly**	**tyr**	**his**	**tyr**	**gly**	**lys**	**his**	**tyr**	**his**	**glu**	**tyr**	**glu**	**his**	**trp**	**trp**	**trp**	**leu**	**trp**
	54	**ser**	**ser**	**ser**	**ser**	**ser**	**ser**	**asp**	**ser**	**ser**	**ser**	**ser**	**gly**	**ser**	**his**	**thr**	**asn**	**thr**	**asn**	**ser**	**asp**	**asp**	**asp**	**asn**	**asp**
	55	**gly**	**gly**	**gly**	**gly**	**gly**	**gly**	**gly**	**gly**	**gly**	**gly**	**gly**	**tyr**	**gly**	**gly**	**gly**	**asp**	**gly**	**asp**	**gly**	**asp**	**asp**	**asp**	**asp**	**asp**
	56	**ser**	**ser**	**asn**	**ser**	**gly**	**ser**	**asn**	**ser**	**gly**	**ser**	**arg**	**thr**	**ser**	**thr**	**ser**	**asp**	**ser**	**asp**	**arg**	**asp**	**asp**	**asp**	**asp**	**lys**
CDR2	57	**thr**	**thr**	**pro**	**thr**	**thr**	**thr**	**thr**	**thr**	**thr**	**thr**	**thr**	**thr**	**thr**	**ser**	**thr**	**val**	**ile**	**val**	**thr**	**lys**	**lys**	**lys**	**lys**	**phe**
	58	**tyr**	**asn**	**asn**	**asn**	**lys**	**asn**	ASP	**asn**	**asn**	**tyr**	**his**	**glu**	**asn**	ASP	**tyr**	**gln**	**tyr**	**gln**	**thr**	**tyr**	**tyr**	**tyr**	**arg**	**tyr**
	59	TYR	TYR	TYR	TYR	TYR	TYR	TYR	**asn**	TYR	TYR	**phe**	TYR	TYR	**asp**	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	**phe**
	60	**asn**	**asn**	**asn**	**lys**	**asn**	**asn**	**asn**	**asn**	**asn**	**asn**	**asn**	**asn**	**asn**	**thr**	**ser**	ALA	**asn**	ALA	**asn**	**asx**	**gly**	**ser**	**gly**	**ser**
	61	**pro**	**pro**	**pro**	**thr**	**glu**	**pro**	**ser**	**pro**	**pro**	**pro**	**pro**	**pro**	**pro**	**thr**	**pro**	**pro**	**pro**	**pro**	**pro**	**thr**	**thr**	**thr**	**ala**	**pro**
	62	SER	SER	SER	SER	**lys**	SER	**ala**	SER	SER	SER	SER	SER	SER	**pro**	SER	**lys**	SER	**lys**	SER	SER	SER	SER	SER	SER
	63	**leu**	**leu**	**leu**	**leu**	**phe**	**leu**	**leu**	**leu**	**leu**	**leu**	**leu**	VAL	**leu**	**leu**	**leu**	**phe**	**leu**	**phe**	**leu**	**leu**	**leu**	**leu**	**leu**	**leu**
	64	LYS	**arg**	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	**arg**	**arg**	LYS	**gln**	**arg**	**gln**	**thr**	**glu**	**glu**	LYS	LYS	**arg**
	65	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	**gly**	SER	SER	SER	**gly**	**gly**	**gly**	SER	**thr**	**thr**	**thr**	SER	**thr**
	66	ARG	ARG	ARG	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**	**ala**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**leu**	**leu**	**leu**	**leu**	**leu**	**leu**
	68	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	**ala**	THR	**ser**	
	69	ILE	ILE	ILE	ILE	**met**	ILE	**met**	ILE	ILE	ILE	ILE	**met**	ILE	**met**	**met**	**met**	ILE	**met**	**met**	ILE	ILE	ILE	**val**	**val**
	70	**ser**	**ser**	**ser**	**ser**	**leu**	**ser**	**leu**	**ser**	**ser**	**ser**	**ser**	**leu**	**ser**	**leu**	**ser**	**leu**	**ser**	**leu**	**ser**	**ser**	**ser**	**ser**	**thr**	**ser**
	71	**val**	**val**	**ile**	**leu**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**leu**	**lys**	**lys**	**lys**	**arg**	**lys**
	72	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	**asn**
	73	THR	THR	**lys**	THR	THR	**lys**	THR	THR	THR	THR	THR	THR	THR	THR	**arg**	THR	THR	THR	THR	THR	THR	THR	THR	**asp**
	74	SER	SER	SER	SER	SER	SER	SER	SER	SER	**leu**	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
	75	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	**arg**	LYS	LYS	**arg**	LYS	LYS	LYS	LYS
	76	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN
	77	**his**	GLN	GLN	**leu**	GLN	GLN	GLN	GLN	GLN	**asn**	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN
	78	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	**val**	**val**	**val**	**val**	**val**
	79	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	**tyr**	SER	SER	SER	SER	**val**	**val**	**val**	**val**	**val**
	80	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
FR3	81	**lys**	**lys**	**lys**	**lys**	**arg**	**lys**	**arg**	**asn**	**lys**	**lys**	**met**	**arg**	**lys**	**arg**	**lys**	**arg**	**asn**	**arg**	**lys**	**thr**	**lys**	**thr**	**ser**	**thr**
	82	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	**met**	**val**	**met**	**met**	**met**
	82A	**ser**	**gly**	**ser**	**ser**	**ser**	**ser**	**ser**	**ser**	**ser**	**ser**	**thr**	**ser**	**arg**	**ser**	**phe**	**ser**	**arg**	**ser**	**thr**	---	**thr**	**thr**	ASN	**thr**
	82B	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER		SER	SER	SER	SER	---	**asn**	**asn**	**thr**	**asn**
	82C	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	**met**	VAL	VAL	---	**met**	**met**	VAL	**met**
	83	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	**ser**	THR	THR	**asp**	**asp**	**asp**	**gly**	**asp**	**asn**
	84	**ala**	**ala**	**ala**	**ala**	**ala**	**ala**	**ala**	**ala**	**ala**	**ala**	**ala**	**ala**	**ala**	**ala**	**ala**	**ala**	**ala**	**ala**	**ala**	PRO	PRO	PRO	PRO	PRO
	85	**ala**	**ala**	**ala**	**ala**	**ala**	**ala**	**ala**	**ala**	**ala**	**ala**	**ala**	**ala**	**ala**	**ala**	**ala**	**ala**	**ala**	**ala**	**ala**	**ala**	**val**	**ala**	**val**	**val**
	86	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP
	87	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	**ser**	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
	88	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA
	89	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	**met**	VAL	VAL	**thr**	**thr**	**thr**	**thr**	**thr**
	90	**TYR**	**TYR**	**TYR**	**TYR**	**TYR**	**TYR**	**TYR**	**TYR**	**TYR**	**TYR**	**TYR**	**TYR**	**TYR**	**TYR**	**TYR**	**TYR**	**TYR**	**TYR**	**TYR**	**TYR**	**TYR**	**TYR**	**TYR**	**TYR**
	91	TYR	TYR	TYR	TYR	TYR	**cys**	TYR	**cys**	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	**phe**	TYR	TYR	TYR	TYR	TYR	TYR	TYR
	92	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS
	93	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	**thr**	ALA	ALA	ALA	ALA	ALA	ALA	**asn**	ALA	ALA	ALA	ALA	ALA	**val**	ALA
	94	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	**ser**	ARG	ARG	ARG	ARG	ARG	**his**	ARG
	95	---	VAL	---	GLY	TYR	---	GLU	---	ALA	PRO	GLY	GLU	GLY	ASN		TRP	GLY	TRP	GLY	ILE	MET	ILE	SER	ARG	VAL
	96	---	LEU	---	LEU	ASP	---	ARG	---	ARG	GLY	TYR	GLY	PHE	LEU		GLY	ASN	GLY	PRO	THR	GLN	ASN	CYS	HIS	VAL
	97	---	VAL	---	LEU	TYR	---	ASP	---	GLY	TYR	ASP	HIS	MET	ILE		SER	PRO	SER	CYS	VAL	VAL	ASN	GLY	PRO	ASN
	98	---	SER	---	ARG	TYR	---	LEU	---	ASP	GLY	THR	THR	VAL	ALA		ASP	PRO	ASP	GLU	ILE	THR	TRP	SER	ARG	SER
	99	---	ARG	---	GLY	GLY	---	ARG	---	LEU	ASP	GLY	ALA	ARG	GLY		PHE	PRO	PHE	ALA	PRO	MET	GLY	GLN	THR	VAL
	100	---	THR	---	GLY	SER	---	LEU	---	GLY	THR	GLY	ALA	GLY	CYS		ASP	TYR	ASP	TYR	ALA	VAL	GLU	TYR	LEU	MET
	100A	---	ILE	---	TRP	SER	---	---	---	VAL	SER	TYR	PRO	ILE	ILE		HIS	TYR	HIS	CYS	PRO	ARG	GLY	PHE	ALA	ALA
	100B	---	SER	---	ASN	TYR	---	---	---	ALA	VAL	MET	PHE	MET	---		---	ASP	---	THR	ALA	GLU	TYR	---	---	GLY
CDR3	100C	---	GLN	---	ASP	PHE	---	---	---	MET	ARG	ALA	---	TRP	---		---	ILE	---	ASP	GLY	VAL	PHE	---	---	TYR
	100D	---	TYR	---	VAL	ASP	---	---	---	VAL	LYS	ARG	---	ASN	---		---	GLY	---	ASP	TYR	MET	---	---	---	TYR
	100E	---	SER	---	ASP	TYR	---	---	---	TYR	ARG	---	---	TYR	---		---	THR	---	ALA	---	ILE	---	---	---	TYR
	100F	---	TYR	---	TYR	---	---	---	---	ALA	VAL	---	---	TYR	---		---	GLY	---	PRO	---	THR	---	---	---	TYR
	100G	---	TYR	---	TYR	---	---	---	---	GLN	TRP	---	---	TYR	---		---	SER	---	GLN	---	SER	---	---	---	TYR
	100H	---	---	---	TYR	---	---	---	---	ASP	ASN	---	---	---	---		---	ASP	---	ALA	---	ASN	---	---	---	---
	100I	---	---	---	---	---	---	---	---	PRO	---	---	---	---	---		---	ASP	---	#	---	ALA	---	---	---	---
	100J	---	---	---	GLY	---	---	---	---	GLY	---	GLY	---	---	---		---	GLY	---	TYR	---	PHE	---	---	---	---
	100K	---	MET	---	MET	---	---	---	---	MET	MET	PHE	---	MET	---		---	ILE	---	PHE	MET	---	---	---	PHE	MET
	101	---	ASP	---	ASP	---	---	ASP	---	ASP	ASP	ASP	ASP	ASP	ASP		---	ASP	---	GLN	ASP	ASP	ASP	ASP	ASP	ASP
	102	---	VAL	---	VAL	---	---	TYR	---	VAL	LEU	TYR	TYR	VAL	VAL		---	VAL	---	HIS	VAL	ILE	LEU	TYR	VAL	VAL
	103	---	TRP	---	TRP	TRP	---	TRP	---	TRP	TRP	TRP	TRP	TRP	TRP		TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP
	104	---	GLY	---	GLY	GLY	---	GLY	---	GLY	GLY	GLY	GLY	GLY	GLY		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
	105	---	LYS	---	GLN	GLN	---	GLN	---	GLN	GLN	PRO	GLN	LYS	GLN		GLN	GLN	GLN	GLN	ARG	GLN	ARG	GLN	LYS	
	106	---	GLY	---	GLY	GLY	---	GLY	---	GLY	GLY	GLY	GLY	GLY	GLY		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
FR	107	---	THR	---	THR	SER	---	SER	---	THR	THR	THR	SER	THR	SER		THR	THR	THR		THR	THR	THR	ILE	THR	THR
	108	---	THR	---	THR	LEU	---	LEU	---	THR	THR	ARG	LEU	THR	LEU		THR	THR	THR		PRO	MET	LEU	LEU	LYS	THR

HUMAN HEAVY CHAINS SUBGROUP II (cont'd)

		46 MCE' #	47 37P1 'CL #	48* DR 12910 -2F8 'CL	49* Ab17 'CL #	50* LES-B 'CL #	51* LES-A 'CL #	52 M44 'CL	53 Ly66 'CL #	54 JBL2 'CL #	55 NZU #	56 SA	57 CAR	58 SPA #	59 IO	60 64P1 'CL #	61* ERI	# OF SEQUENCES	# OF AMINO ACIDS	OCCURRENCES OF MOST COMMON AMINO ACID
	0	---		---					---	---				---	---					
	1	**pca**		GLN					GLN	GLN				**pca**	**pca**			51	4	39 (GLN), 38 (GLN)
	2	**ile**		**ile**					VAL	**leu**				**glu**	VAL			51	4	43 (VAL)
	3	**thr**		**thr**					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	2	33 (GLU), 32 (GLU)
	7	SER		SER					SER	SER				SER				50	3	44 (SER)
	8	GLY		GLY					**ser**	GLY				---				49	2	48 (GLY)
	9	PRO		PRO					PRO	PRO				---				49	3	43 (PRO)
	10	**thr**		**thr**					GLY	GLY				---				49	3	41 (GLY)
	11	LEU		LEU					LEU	LEU				---				49	1	49 (LEU)
	12	VAL		VAL					VAL	VAL				---				49	2	45 (VAL)
	13	LYS		LYS					LYS	**arg**				---				49	2	41 (LYS)
FR1	14	PRO		PRO					PRO	PRO				---				49	2	48 (PRO)
	15	**thr**		**thr**					SER	**pro**				---				49	4	38 (SER)
	16	**glu**		GLN					**asp**	---				---				48	5	26 (GLN)
	17	THR		THR					THR	---				---				48	3	46 (THR)
	18	LEU		LEU					**phe**	---				---				48	2	47 (LEU)
	19	**thr**		**thr**					SER	**ala**				---				49	3	39 (SER)
	20	LEU		LEU					LEU	LEU			LEU	---				50	2	49 (LEU)
	21	THR		THR					**ile**	**ile**		THR	THR	---				51	2	49 (THR)
	22	CYS		CYS					CYS	CYS		CYS	CYS	---				51	1	51 (CYS)
	23	**thr**		**thr**	ALA				**asn**	**thr**		**thr**	**thr**	---				52	7	25 (THR)
	24	**phe**		**phe**	**val**				**val**	**gly**		**val**	**val**	---				52	5	31 (VAL)
	25	SER		SER	**tyr**				SER	SER		SER	SER	---				52	3	45 (SER)
	26	GLY		GLY	GLY				**ser**	---		GLY	GLY	---				51	2	50 (GLY)
	27	**phe**		**phe**	**gly**				ASP	---		**gly**		---				50	6	19 (GLY)
	28	SER		SER	SER				**ile**	---		SER		---				50	4	41 (SER)
	29	**leu**	**ile**	**leu**	**leu**				**leu**	---				---				50	4	18 (VAL)
	30	SER	SER	SER	SER				SER	---				---				50	4	46 (SER)
	31	**thr**	SER	**thr**	**asn**				**leu**	---				---				50	8	28 (SER)
	32	**ser**	**tyr**	**gly**	**tyr**				**leu**	---				---				50	13	13 (TYR)
CDR1	33	**gly**	**tyr**	**gly**	**tyr**				**cys**	---				---				50	9	15 (+)
	34	**val**	**trp**	**val**	**trp**				**pro**	---				---				50	7	14 (TRP)
	35	**gly**	**ser**	**gly**	**ser**				**asp**	---				---				50	12	13 (SER)
	35A	**val**	---	**val**	---				**asn**	---				---				33	5	18 (TRP)
	35B	**gly**	---	**gly**	---				**arg**	---				---				27	5	12 (ASN)
	36	TRP	TRP	TRP	TRP	TRP	TRP		**thr**	---				---				52	2	51 (TRP)
	37	ILE	ILE	ILE	ILE	ILE	ILE		**gly**	---				---				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	5	36 (PRO)
FR2	41	PRO	PRO	PRO	PRO	PRO	PRO		---	---				---				51	2	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**	GLY	**ala**	GLY	GLY	GLY		---	---				---				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	9	18 (ARG)
	51	**ile**	**ile**	**ile**	THR	**ile**	**ile**		---	---				---				51	5	34 (ILE)
	52	**asn**	TYR	TYR	**asn**	**asn**	**asn**		---	---				---				51	8	29 (TYR)
	52A	---	---	---	---	---	---		---	---				---				17	3	13 (TYR)
	52B	---	---	---	---	---	---		---	---				---				13	2	11 (ARG)
	52C	---	---	---	---	---	---		---	---				---				1	1	1 (ALA)
	53	**trp**	**tyr**	**trp**	**tyr**	**his**	**his**		---	---				---				51	10,11	14 (TYR)
CDR2	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	8	19 (SER)
	57	ASN	**thr**	**lys**	**val**	**thr**	**thr**		---	---				---				51	8	26 (THR)
	58	**arg**	**asn**	**leu**	**lys**	**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**	**leu**	---	---				---				52	3	36 (LEU)
	64	**arg**	LYS	LYS	**glu**	**thr**	**thr**	LYS	---	---				---				52	5	37 (LYS)
	65	SER	SER	SER	SER	SER	SER	SER	---	---				---				52	3	43 (SER)
	66	ARG	ARG	ARG	ARG	ARG	ARG	ARG	---	---				---				52	1	52 (ARG)
	67	**leu**	**val**	**leu**	**val**	**val**	**val**	**leu**	---	---				---				52	4	30 (VAL)
	68	THR	THR	THR	THR	THR	THR	THR	---	---				---				52	3	49 (THR)
	69	**gly**	ILE	ILE	ILE	ILE	ILE	ILE	---	---				---				52	5	38 (ILE)
	70	**thr**	**ser**	**thr**	**ser**	**ser**	**ser**	**thr**	---	---				---				52	4	30 (SER)
	71	**lys**	**val**	**lys**	**val**	**val**	**val**	**lys**	---	---				---				52	6	28 (VAL)
	72	ASP	ASP	ASP	ASP	ASP	ASP	ASP	---	---				---				52	2	51 (ASP)
	73	THR	THR	THR	**ser**	THR	THR	THR	---	---				---				52	5	47 (THR)
	74	SER	SER	SER	SER	SER	SER	SER	---	---				---				52	2	51 (SER)
	75	**arg**	LYS	LYS	LYS	LYS	LYS	LYS	---	---				---				52	3	48 (LYS)
	76	ASN	ASN	ASN	ASN	ASN	ASN	ASN	---	---				---				52	1	52 (ASN)
	77	GLN	GLN	GLN	GLN	GLN	GLN	GLN	---	---				---				52	4	49 (GLN)
	78	**val**	PHE	**val**	PHE	PHE	PHE	**val**	---	---				---				52	2	43 (PHE)
	79	**val**	SER	**val**	**phe**	SER	SER	**val**	---	---				---				52	4	41 (SER)
	80	LEU	LEU	LEU	LEU	LEU	LEU	LEU	---	---				---				52	1	52 (LEU)
FR3	81	**thr**	**lys**	**thr**	**lys**	**lys**	**lys**	**thr**	---	---				---				52	8	22 (LYS)
	82	**ile**	LEU	**met**	**met**	LEU	LEU	**met**	---	---				---				52	4	42 (LEU)
	82A	**thr**	**ser**	**thr**	**ser**	**thr**	**thr**	**thr**	---	---				---				51	7	22 (SER)
	82B	**asn**	SER	**asn**	SER	SER	SER	**asn**	---	---				---				50	3	42 (SER)
	82C	**met**	VAL	**met**	VAL	**ala**	VAL	**met**	---	---	**met**			---				52	3	43 (VAL)
	83	**asp**	THR	**asp**	THR	THR	THR	**asp**	---	---	**asp**			---				53	5	42 (THR)
	84	PRO	**ala**	PRO	**ala**	**ala**	**ala**	PRO	---	---	PRO			---				53	3	30 (ALA)
	85	**val**	**ala**	**val**	**ala**	**ala**	**ala**	**val**	---	---	**val**			---				53	4	30 (ALA)
	86	ASP	ASP	**thr**	ASP	ASP	ASP	ASP	---	---	ASP			---				53	2	52 (ASP)
	87	**ser**	THR	**gln**	THR	THR	THR	THR	---	---	**ser**			---				53	3	49 (THR)
	88	**gly**	ALA	**pro**	ALA	ALA	ALA	ALA	---	---	**gly**			---				53	3	50 (ALA)
	89	**thr**	VAL	**his**	**ile**	VAL	VAL	**thr**	---	---	**thr**			---				53	5	41 (VAL)
	90	TYR	TYR	**ile**	TYR	TYR	TYR	TYR	---	---	TYR			---				53	2	52 (TYR)
	91	**phe**	TYR	**thr**	TYR	TYR	**phe**	TYR	---	---	**phe**			---				53	4	46 (TYR)
	92	CYS	CYS	**met**	**CYS**	CYS	CYS	CYS	---	---	CYS			---				53	2	52 (CYS)
	93	ALA	ALA	**his**	ALA	ALA	ALA	ALA	---	---	ALA			---				53	5	48 (ALA)
	94	**his**	ARG	**thr**	ARG	ARG		**his**	---	---	**his**			---				52	4	45 (ARG)
	95	ARG	GLU	ASP	CYS	GLY	GLY	THR	---	---	ARG			---		ILE		42	15	9 (GLU)
	96	PRO	GLY	VAL	ALA	PRO	PRO	THR	---	---	PRO			---		---		41	15	7 (LEU)
	97	PRO	ALA	PRO	VAL	CYS	CYS	ARG	---	---	PRO			---		---		41	16	6 (PRO)
	98	TRP	TRP	LEU	ILE	GLU	GLU	ILE	---	---	TRP			---		---		41	13	7 (GLY)
	99	ARG	GLY	TYR	THR	ALA	ALA	PHE	---	---	ARG			---		---		38	12	8 (GLY)
	100	PHE	TYR	PHE	LEU	TYR	TYR	---	---	---	PHE			---		---		35	15	6 (TYR)
	100A	THR	SER	GLY	LEU	CYS	CYS	---	---	---	THR			---		---		31	14	3 (+)
	100B	GLY	GLY	SER	GLY	THR	THR	---	---	---	SER			---		---		25	11	7 (GLY)
CDR3	100C	ASN	TYR	THR	TYR	ASP	ASP	---	---	---	ASP			---		---		23	13	6 (ASP)
	100D	LEU	ASP	SER	CYS	ASP	ASP	---	---	---	LEU			---		---		22	11	5 (ASP)
	100E	GLY	TYR	CYS	ALA	ALA	ALA	---	---	---	GLY			---		---		19	11	5 (TYR)
	100F	GLY	---	TYR	ASN	PRO	PRO	---	---	---	SER			---		---		17	8	6 (TYR)
	100G	---	---	TYR	GLY	GLN	GLN	---	---	---	---			---		---		15	5	5 (TYR)
	100H	---	---	ILE	ASP	ALA	ALA	---	---	---	---			---		---		12	7	3 (+)
	100I	---	---	ASN	CYS	#	#	---	---	---	---			---		---		8	6	2 (+)
	100J	---	ALA	PHE	#	TYR	TYR	---	---	---	---			---		---		16	6	5 (GLY)
	100K	PHE	PHE	---	PHE	PHE	PHE	---	---	---	PHE			---		---		24	5	13 (PHE)
	101	ASP	ASP	ASP	ASP	GLN	GLN	ASP	---	---	SER			---		---	ASP	39	5	30 (ASP)
	102		ILE	TYR	TYR	HIS	HIS	TYR	---	---	PRO			---		---	VAL	34	6	11 (VAL)
	103	TRP	TRP	TRP	TRP	TRP	TRP	TRP	---	---	TRP			---		ARG	TRP	39	3	37 (TRP)
	104	GLY	GLY	GLY	GLY	GLY	GLY	GLY	---	---	GLY			---		GLY	GLY	39	1	39 (GLY)
	105	GLN	GLN	GLN	GLN	GLN	GLN	GLN	---	---	GLN			---		GLN	ARG	39	5	30 (GLN)
	106	GLY	**GLY**	**GLY**	**GLY**	**GLY**	**GLY**	GLY	---	---	GLY			---		GLY	GLY	39	1	39 (GLY)
FR4	107	THR	THR	THR	THR			THR	---	---	THR			---		THR	THR	36	3	31 (THR)
	108	LEU	MET	LEU	LEU			LEU	---	---	LEU			---		MET	THR	36	6	14 (LEU)
	109	**VAL**	**VAL**	**VAL**	**VAL**			**VAL**	---	---	VAL			---		VAL	VAL	36	2	35 (VAL)
	110	THR	THR	THR	THR			THR	---	---	THR			---		THR	THR	36	4	33 (THR)

	0	
	1	5.2,5.4
	2	4.7
	3	7.8
	4	2.
	5	7.9,8.1
	6	3.,3.1
	7	3.4
	8	2.
	9	3.4
	10	3.6
	11	1.
	12	2.2
	13	2.4
	14	2.
FR1	15	5.2
FR1	16	9.2
FR1	17	3.1
FR1	18	2.
FR1	19	3.8
FR1	20	2.
FR1	21	2.1
FR1	22	1.
FR1	23	15.
FR1	24	8.4
FR1	25	3.5
FR1	26	2.
FR1	27	16.
FR1	28	4.9
FR1	29	11.
FR1	30	4.3
CDR1	31	14.
CDR1	32	50.
CDR1	33	30.
CDR1	34	25.
CDR1	35	46.
CDR1	35A	
CDR1	35B	
FR2	36	2.
FR2	37	5.2
FR2	38	1.
FR2	39	3.1
FR2	40	7.1
FR2	41	2.
FR2	42	2.6
FR2	43	5.1
FR2	44	2.3
FR2	45	2.1
FR2	46	1.
FR2	47	2.
FR2	48	4.9
FR2	49	2.4
CDR2	50	25.
CDR2	51	7.5
CDR2	52	14.
CDR2	52A	
CDR2	52B	
CDR2	52C	
CDR2	53	36.,40.
CDR2	54	18.
CDR2	55	7.3
CDR2	56	21.
CDR2	57	16.
CDR2	58	39.
CDR2	59	6.8
CDR2	60	11.,14.
CDR2	61	10.
CDR2	62	4.4
CDR2	63	4.3
CDR2	64	7.
CDR2	65	3.6
FR3	66	1.
FR3	67	6.9
FR3	68	3.2
FR3	69	6.8
FR3	70	6.9
FR3	71	11.
FR3	72	2.
FR3	73	5.5
FR3	74	2.
FR3	75	3.2
FR3	76	1.
FR3	77	4.2
FR3	78	2.4
FR3	79	5.1
FR3	80	1.
FR3	81	19.
FR3	82	5.
FR3	82A	
FR3	82B	
FR3	82C	
FR3	83	6.3
FR3	84	5.3
FR3	85	7.1
FR3	86	2.
FR3	87	3.2
FR3	88	3.2
FR3	89	6.5
FR3	90	2.
FR3	91	4.6
FR3	92	2.
FR3	93	5.5
FR3	94	4.6
CDR3	95	70.
CDR3	96	88.
CDR3	97	110.
CDR3	98	76.
CDR3	99	57.
CDR3	100	87.
CDR3	100A	
CDR3	100B	
CDR3	100C	
CDR3	100D	
CDR3	100E	
CDR3	100F	
CDR3	100G	
CDR3	100H	
CDR3	100I	
CDR3	100J	
CDR3	100K	
CDR3	101	6.5
CDR3	102	19.
FR4	103	3.2
FR4	104	1.
FR4	105	6.5
FR4	106	1.
FR4	107	3.5
FR4	108	15.
FR4	109	2.1
FR4	110	4.4
FR4	111	2.1
FR4	112	2.1
FR4	113	2.3

ANTIBODY SPECIFICITIES: HUMAN HEAVY CHAINS SUBGROUP II

2) **L16'CL:** ANTI-POLYdT, CARDIOLIPIN, AND ssDNA
3) **ML1'CL:** ANTI-POLYdT, AND ssDNA
5) **F19L16'CL:** ANTI-ssDNA, CARDIOLIPIN, POLY-dT
6) **F19ML1'CL:** ANTI-ssDNA, POLY-dT
10) **A10'CL:** ANTI-ssDNA, dsDNA, CARDIOLIPIN, POLY-dT, HEN EGG LYSOZYME
11) **FK-001'CL:** ANTI-Pseudomonas aeruginosa EXOTOXIN A HYBRIDOMA
12) **A431'CL:** ANTI-ssDNA, dsDNA, CARDIOLIPIN, POLY-dT, PIGEON CYTOCHROME C
14) **C6B2'CL:** ANTI-DNA HYBRIDOMA
18) **Ab26'CL:** POLYREACTIVE AUTOANTIBODY
22) **Pag-1'CL:** ANTI-D ANTIGEN OF THE Rh-BLOOD-GROUP SYSTEM
25) **HuVNP'CL:** ANTI-4-HYDROXY-3-NITROPHENACETYL CAPROIC ACID (BINDING CONSTANT = 1.9X10EXP6)
27) **HuVHLYS'CL:** ANTI-LYSOZYME HYBRIDOMA
29) **Ab44'CL:** POLYREACTIVE AUTOANTIBODY
30) **Fog-B'CL:** ANTI-D ANTIGEN OF THE Rh-BLOOD-GROUP SYSTEM
32) **HuVHCAMP'CL:** ANTI-HUMAN LYMPHOCYTE HYBRIDOMA
33) **6H-3C4'CL:** HUMAN SPERM-IMMOBILIZING ANTIBODY
34) **NEWM:** ANTI-3-(3'-HYDROXY-3',7',11',15',TETRAMETHYL HEXADECYL) 2-METHYL 1,4 NAPHTHOQUINONE(VIT.K1OH)
35) **GER:** MONOCLONAL CRYOIMMUNOGLOBULIN
38) **HuRSV19CHFNS:** 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) **HuVHCAMP'CL:** IGG1-KAPPA
34) **NEWM:** 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

1) **15P1'CL:** SCHROEDER,H.W.,JR.,HILLSON,J.L. & PERLMUTTER,R.M. (1987) SCIENCE,238,791-793.
2) **L16'CL:** LOGTENBERG,T.,YOUNG,F.M.,VAN ES,J.H.,GMELIG-MEYLING,F.H.J. & ALT,F.W. (1989) J.EXP.MED.,170,1347-1355.
3) **ML1'CL:** LOGTENBERG,T.,YOUNG,F.M.,VAN ES,J.H.,GMELIG-MEYLING,F.H.J. & ALT,F.W. (1989) J.EXP.MED.,170,1347-1355.
4) **M71'CL:** SCHROEDER,H.W.,JR. & WANG,J.Y. (1990) PROC.NATL.ACAD.SCI.USA,87,6146-6150.
5) **F19L16'CL:** LOGTENBERG,T.,YOUNG,F.M.,VAN ES,J.,GMELIG-MEYLING,F.H.J.,BERMAN,J.E. & ALT,F.W. (1989) J.AUTOIMMUNITY,2, 203-213.
6) **F19ML1'CL:** LOGTENBERG,T.,YOUNG,F.M.,VAN ES,J.,GMELIG-MEYLING,F.H.J.,BERMAN,J.E. & ALT,F.W. (1989) J.AUTOIMMUNITY,2, 203-213.
7) **6-1G1'CL:** BERMAN,J.E.,MELLIS,S.J.,POLLOCK,R.,SMITH,C.L.,SUH,H.,HEINKE,B.,KOWAL,C.,SURTI,U.,CHESS,L.,CANTOR,C.R & ALT, F.W. (1988) EMBO J.,7,727-738.
8) **VHVI'CL:** BULUWELA,L. & RABBITTS,T.H. (1988) EUR.J.IMMUNOL.,18,1843-1845.
9) **VH6'CL:** SCHROEDER,H.W.,JR.,WALTER,M.A.,HOFKER,M.H.,EBENS,A.,VAN DIJK,K.W.,LIAO,L.C.,COX,D.W.,MILNER,E.C.B. & PERLMUTTER, R.M. (1988) PROC.NATL.ACAD.SCI.USA,85,8196-8200.
10) **A10'CL:** LOGTENBERG,T.,YOUNG,F.M.,VAN ES,J.,GMELIG-MEYLING,F.H.J.,BERMAN,J.E. & ALT,F.W. (1989) J.AUTOIMMUNITY,2,203-213.
11) **FK-001'CL:** LEHMAN,D.W. & PUTNAM,F.W. (1980) PROC.NAT.ACAD.SCI.USA,77,3239-3243. (CHECKED BY AUTHOR 05/01/80)
12) **A431'CL:** LOGTENBERG,T.,YOUNG,F.M.,VAN ES,J.,GMELIG-MEYLING,F.H.J.,BERMAN,J.E. & ALT,F.W. (1989) J.AUTOIMMUNITY,2,203-213.
13) **71-2'CL:** KODAIRA,M.,KINASHI,T.,UMEMURA,I.,MATSUDA,F.,NOMA,T.,ONO,Y. & HONJO,T. (1986) J.MOL.BIOL.,190,529-541.
14) **C6B2'CL:** HOCH,S. & SCHWABER,J. (1987) J.IMMUNOL.,139,1689-1693.
15) **71-4'CL:** KODAIRA,M.,KINASHI,T.,UMEMURA,I.,MATSUDA,F.,NOMA,T.,ONO,Y. & HONJO,T. (1986) J.MOL.BIOL.,190,529-541.
16) **58P2'CL:** SCHROEDER,H.W.,JR.,HILLSON,J.L. & PERLMUTTER,R.M. (1987) SCIENCE,238,791-793.
17) **SUP-T1 VH-JA'CL:** BAER,R.,CHEN,K.-C.,SMITH,S.D. & RABBITTS,T.H. (1985) CELL,43,705-713; DENNY,C.T.,YOSHIKAI,Y.,MAK,T.W., SMITH,S.D.,HOLLIS,G.F. & KIRSCH,I.R. (1986) NATURE,320,549-551.
18) **Ab26'CL:** SANZ,I.,CASALI,P.,THOMAS,J.W.,NOTKINS,A.L. & CAPRA,J.D. (1989) J.IMMUNOL.,142,4054-4061.
19) **1-9II'CL:** BERMAN,J.E.,MELLIS,S.J.,POLLOCK,R.,SMITH,C.L.,SUH,H.,HEINKE,B.,KOWAL,C.,SURTI,U.,CHESS,L.,CANTOR,C.R & ALT, F.W. (1988) EMBO J.,7,727-738.
20) **12G-1'CL:** LEE,K.H.,MATSUDA,F.,KINASHI,T.,KODAIRA,M. & HONJO,T. (1987) J.MOL.BIOL.,195,761-768.
21) **2-1'CL:** LEE,K.H.,MATSUDA,F.,KINASHI,T.,KODAIRA,M. & HONJO,T. (1987) J.MOL.BIOL.,195,761-768.
22) **Pag-1'CL:** HUGHES-JONES,N.C.,BYE,J.M.,BEALE,D. & COADWELL,J. (1990) BIOCHEM.J.,268,135-140.
23) **11'CL:** LEE,K.H.,MATSUDA,F.,KINASHI,T.,KODAIRA,M. & HONJO,T. (1987) J.MOL.BIOL.,195,761-768.
24) **HIG1'CL:** KUDO,A.,ISHIHARA,T.,NISHIMURA,Y. & WATANABE,T. (1985) GENE,33,181-189. (CHECKED BY AUTHOR 10/01/85)
25) **HuVNP'CL:** JONES,P.T.,DEAR,P.H.,FOOTE,J.,NEUBERGER,M.S. & WINTER,G. (1986) NATURE,321,522-525.
26) **79'CL:** LEE,K.H.,MATSUDA,F.,KINASHI,T.,KODAIRA,M. & HONJO,T. (1987) J.MOL.BIOL.,195,761-768.
27) **HuVHLYS'CL:** VERHOEYEN,M., MILSTEIN,C. & WINTER,G. (1988) SCIENCE,239,1534-1536.
28) **58'CL:** LEE,K.H.,MATSUDA,F.,KINASHI,T.,KODAIRA,M. & HONJO,T. (1987) J.MOL.BIOL.,195,761-768.
29) **Ab44'CL:** SANZ,I.,CASALI,P.,THOMAS,J.W.,NOTKINS,A.L. & CAPRA,J.D. (1989) J.IMMUNOL.,142,4054-4061.
30) **Fog-B'CL:** HUGHES-JONES,N.C.,BYE,J.M.,BEALE,D. & COADWELL,J. (1990) BIOCHEM.J.,268,135-140.
31) **TS2'CL:** SHEN,A.,HUMPHRIES,C.,TUCKER,P. & BLATTNER,F. (1987) PROC.NATL.ACAD.SCI.USA,84,8563-8567.
32) **HuVHCAMP'CL:** RIECHMANN,L.,CLARK,M.,WALDMANN,H. & WINTER,G. (1988) NATURE,332,323-327.

33) **6S-3C4'CL:** KOMORI,S.,YAMASAKI,N.,SHIGETA,M.,ISOJIMA,S. & WATANABE,T. (1988) CLIN.EXP.IMMUNOL.,71,508-516.

34) **NEWM:** POLJAK,R.J.,AMZEL,L.M.,CHEN,B.L.,PHIZACKERLEY, R.P. & SAUL,F. (1974) PROC.NAT.ACAD.SCI.USA,71,3440-3444. (CHECKED BY AUTHOR WHO CORRECTED RESIDUES 6,9,15,16,24,26,27,29 THROUGH 35B,59,60 AS GIVEN IN TABLE OF THE FIRST EDITION OF THIS BOOK, AND HAS MORE RECENTLY REVISED RESIDUES 5,24,28,29,30,31,33,34,35,35A,35B,59,60 AND 101); POLJAK, R.J.,AMZEL,L.M.,CHEN,B.L.,CHU,Y.Y.,PHIZACKERLEY,R.P.,SAUL,F. & YSERN,X. (1976) COLD SPRING HARBOR SYMP. QUANTITATIVE BIOL.,41,639-645; POLJAK,R.J.,NAKASHIMA,Y.,CHEN,B.L. & KONIGSBERG,W. (1977) BIOCHEMISTRY,16, 3412-3420. THE SEQUENCE LISTED IN THE LAST REFERENCE IS GIVEN IN THE TABLE. (CHECKED BY AUTHOR, W.K., 09/30/78)

35) **GER:** MIDDAUGH,C.R. & LITMAN,G.W. (1987) J.BIOL.CHEM.,262,3671-3673.

36) **HuRSV19VH:** TEMPEST,P.R.,BREMNER,P.,LAMBERT,M.,TAYLOR,G.,FURZE,J.M.,CARR,F.J. & HARRIS,W.J. (1991) BIO/TECH.,9,266-271.

37) **WAH:** PUTNAM,F.W.,TAKAHASHI,N.,TETAERT,D.,DEBUIRE,B. & LIN,L.C. (1981) PROC.NAT.ACAD.SCI.USA,78,6168-6172. (CHECKED BY AUTHOR 11/30/81); TAKAHASHI,N.,TETAERT,D.,DEBUIRE,B.,LIN,L. & PUTNAM,F.W. (1982) PROC.NAT.ACAD.SCI.USA,79, 2850-2854.

38) **HuRSV19CHFNS:** TEMPEST,P.R.,BREMNER,P.,LAMBERT,M.,TAYLOR,G.,FURZE,J.M.,CARR,F.J. & HARRIS,W.J. (1991) BIO/TECH.,9,266-271.

39) **LES-C'CL:** ROUDIER,J.,SILVERMAN,G.J.,CHEN,P.P.,CARSON,D.A. & KIPPS,T.J. (1990) J.IMMUNOL.,144,1526-1530.

40) **COR:** PRESS,E.M. & HOGG,N.M. (1970) BIOCHEM.J.,117,641-660. (CHECKED BY AUTHOR)

41) **CS-1 'CL:** TAKAHASHI,N.,NOMA,T. & HONJO,T. (1984) PROC.NAT.ACAD.SCI.USA,81,5194-5198.

42) **M60'CL:** SCHROEDER,H.W.,JR. & WANG,J.Y. (1990) PROC.NATL.ACAD.SCI.USA,87,6146-6150.

43) **DAW:** PRESS,E.M. & HOGG,N.M. (1970) BIOCHEM.J.,117,641-660. (CHECKED BY AUTHOR)

44) **HE:** CUNNINGHAM,B.A.,GOTTLIEB.P.D.,PFLUMM,M.N. & EDELMAN,G.M. (1971) PROGRESS IN IMMUNOLOGY (B.AMOS,ED.),ACADEMIC PRESS, N.Y.,PP.3-24. (CHECKED BY AUTHOR)

45) **OU:** PUTNAM,F.W.,SHIMIZU,A.,PAUL.,C.,SHINODA,T. & KOHLER,H. (1971) ANN.N.Y.ACAD.SCI.,190,83-103. (CHECKED BY AUTHOR 06/15/83)

46) **MCE':** GERBER-JENSON,B.,KAZIN,A.,KEHOE,J.M.,SCHEFFEL,C.,ERICKSON,B.W. & LITMAN,G.W. (1981) J.IMMUNOL.,126,1212-1216. (CHECKED BY AUTHOR 12/15/80)

47) **37P1'CL:** SCHROEDER,H.W.,JR.,HILLSON,J.L. & PERLMUTTER,R.M. (1987) SCIENCE,238,791-793.

48) **DR12910-2F8'CL:** LARRICK,J.W.,DANIELSSON,L.,BRENNER,C.A.,WALLACE,E.F.,ABRAHAMSON,M.,FRY,K.E. & BORREBAECK,C.A.K. (1989) BIO/TECH.,7,934-938.

49) **Ab17'CL:** SANZ,I.,CASALI,P.,THOMAS,J.W.,NOTKINS,A.L. & CAPRA,J.D. (1989) J.IMMUNOL.,142,4054-4061.

50) **LES-B'CL:** ROUDIER,J.,SILVERMAN,G.J.,CHEN,P.P.,CARSON,D.A. & KIPPS,T.J. (1990) J.IMMUNOL.,144,1526-1530.

51) **LES-A'CL:** ROUDIER,J.,SILVERMAN,G.J.,CHEN,P.P.,CARSON,D.A. & KIPPS,T.J. (1990) J.IMMUNOL.,144,1526-1530.

52) **M44'CL:** SCHROEDER,H.W.,JR. & WANG,J.Y. (1990) PROC.NATL.ACAD.SCI.USA,87,6146-6150.

53) **Ly66'CL:** COGNE,M.,MOUNIR,S.,MAHDI,T.,PREUD'HOMME,J.L.,NAU,F. & GUGLIELMI,P. (1990) MOL.IMMUNOL.,27,929-934.

54) **JBL2'CL:** COGNE,M.,MOUNIR,S.,PREUD'HOMME,J.-L.,NAU,F. & GUGLIELMI,P. (1988) EUR.J.IMMUNOL.,18,1485-1489.

55) **NZU:** ERICKSON,B.W.,GERBER-JENSON,B.,WANG,A.C. & LITMAN,G.W. (1981) MOL.IMMUNOL.,19,357-365. (CHECKED BY AUTHOR 11/30/81)

56) **SA:** MILSTEIN,C. & FRANGIONE,B. (1971) BIOCHEM.J.,121,217-225. (CHECKED BY AUTHOR)

57) **CAR:** FRANGIONE,B. (1968) PH.D. THESIS, UNIVERSITY OF CAMBRIDGE. (CHECKED BY AUTHOR)

58) **SPA:** FRANGIONE,B. & FRANKLIN,E.C. (1979) J.IMMUNOL.,122,1177-1179. (CHECKED BY AUTHOR 07/18/79)

59) **IO:** MONTGOMERY,P.C.,BELLO,A.C. & ROCKEY,J.H. (1970) BIOCHIM.BIOPHYS.ACTA,200,258-266. (CHECKED BY AUTHOR)

60) **64P1'CL:** SCHROEDER,H.W.,JR.,HILLSON,J.L. & PERLMUTTER,R.M. (1987) SCIENCE,238,791-793.

61) **ERI:** MILSTEIN,C.P. & DEVERSON,E.V. (1980) IMMUNOLOGY,40,657-664. (CHECKED BY AUTHOR 11/30/82)

IDENTICAL SETS OF FRAMEWORK SEGMENTS:

FR1: SET 1: 15P1'CL[1],L16'CL[2],ML1'CL[3],M71'CL[4],F19L16'CL[5],F19ML1'CL[6],6-1G1'CL[7],VHVI'CL[8],VH6'CL[9], A10'CL[10],FK-001'CL[11],A431'CL[12]. (12 IDENTICAL)

SET 2: 71-2'CL[13],71-4'CL[15]. (2 IDENTICAL)

SET 3: 1-9II'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],F19ML1'CL[6],6-1G1'CL[7],VHVI'CL[8],VH6'CL[9], A10'CL[10],FK-001'CL[11],A431'CL[12]. (12 IDENTICAL)

SET 2: 71-2'CL[13],C6B2'CL[14],71-4'CL[15],58P2'CL[16],SUP-T1 VH-JA'CL[17],1-9II'CL[19],12G-1'CL[20],2-1'CL[21], 58'CL[28],6H-3C4'CL[33],GER[35],WAH[37],37P1'CL[47],Ab17'CL[49],LES-B'CL[50],LES-A'CL[51]. (16 IDENTICAL HUMAN V-H-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],F19ML1'CL[6],6-1G1'CL[7],VHVI'CL[8],VH6'CL[9], A10'CL[10]. (10 IDENTICAL)

SET 2: 71-2'CL[13],C6B2'CL[14],71-4'CL[15],58P2'CL[16],SUP-T1 VH-JA'CL[17],Ab44'CL[29],37P1'CL[47]. (7 IDENTICAL)

SET 3: 1-9II'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; ALSO 14 HUMAN V-H-I: LS2'CL[1],LS5'CL[2],LS6'CL[3],LS1'CL[4],LS8'CL[6],1B9/F2'CL[7],21/28'CL[10],NEI'CL[16], TH9'CL[23],WIL2'CL[24],KAS[26],BOR'[27],LS7'CL[29],WOL[45]; 34 HUMAN V-H-III: 18/2'CL[1],18/17'CL[2], 18/9'CL[3],1/17'CL[4],30P1'CL[5],M43'CL[6],HF2-1/17[7],Ab25'CL[12],Vh38C1.10'CL[15],Vh38C1.8'CL[16], Vh38C1.9'CL[17],60P2'CL[18],63P1'CL[19],GF4/1.1'CL[20],Vh38C1.4'CL[21],Vh38C1.5'CL[22],56P1'CL[25], 2P1'CL[26],M74'CL[28],CTL[31],HN.14'CL[41],NEA[47],4B4'CL[48],M26'CL[49],NIE[60],DOR[62],VH10.7'CL[63], K6H6'CL[68],K4B8'CL[69],K5B8'CL[70],K5C7'CL[71],K5G5'CL[72],K6F5'CL[73],20P1'CL[82]; 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-TS1'CL[28],Ab2022'CL[41],M61'CL[47],60P1'CL[49],AF2'CL[65]; AND 3 HUMAN V-H-III: 38P1'CL[36],3D6'CL[43],13P1'CL[97].)

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

SET 4: FK-001'CL[11],HIG1'CL[24],Ab44'CL[29],Fog-B'CL[30],HuRSV19VH[36],HuRSV19CHFNS[38]. (6 IDENTICAL HUMAN V-H-II; ALSO 5 HUMAN V-H-I: 78C'CL[21],X17115'CL[22],EV1-15'CL[25],ND'CL[30],Ab2'CL[44]; 6 HUMAN V-H-III: 4G12'CL[10],Ab21'CL[24],M72'CL[27],KIM46H'CL[29],U266'CL[136],70P1'CL[183]; 2 MOUSE V-H-IIA: HDEX12[15], MBr1'CL[160]; AND 1 MOUSE V-H-IIC: MuRSV19VH'CL[37].)

SET 5: Ab26'CL[18],M60'CL[42]. (2 IDENTICAL HUMAN V-H-II; ALSO 1 HUMAN V-H-I: 83P2'CL[38]; AND 5 HUMAN V-H-III: Ab18'CL[11],RF-KL1'CL[13],1B11'CL[74],1H1'CL[75],2C12'CL[80].)

SET 6: HuVNP'CL[25],HuVHLYS'CL[27],HuVHCAMP'CL[32],NEWM[34]. (4 IDENTICAL)

IDENTICAL SETS OF COMPLEMENTARITY DETERMINING REGIONS:

CDR1: SET 1: 15P1'CL[1],L16'CL[2],ML1'CL[3],M71'CL[4],F19L16'CL[5],F19ML1'CL[6],6-1G1'CL[7],VHVI'CL[8],VH6'CL[9]. (9 IDENTICAL)

SET 2: 71-4'CL[15],58P2'CL[16],37P1'CL[47]. (3 IDENTICAL)

SET 3: 1-9II'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[130],AM12'CL[131],7C6'CL[142],2.9 GL'CL[169],#L38'CL[206]; AND 69 MOUSE V-H-IIB: B1-8'CL[1],B1-8.DELTA1V3[2],B1-48'CL[3],N-HYB'CL[4],18C10'CL[5],186-2'CL[6],B1-8.V4'CL[7], S2D8'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[18],CH12''CL[22],4m5 GL'CL[24],22.111.1'CL[27],73'CL[28],pING2006E'CL[29],B1-8.V1/V2[30], B1-8.V1'CL[31],N1C12'CL[33],124'CL[34],564'CL[35],550'CL[36],567'CL[37],563'CL[38],132.16'CL[39],N1G9'CL[50], 102'CL[51],33'CL[52],C4-51'CL[55],DB1-314.3'CL[56],DF4-12.6'CL[57],H1-45'CL[59],S1F2'CL[60],C1H4 GL'CL[64], CH10'CL[68],CH-55'CL[74],CH31'CL[76],H1-29'CL[79],DBF1-608.1'CL[89],AC38 15.3[93],H1-59'CL[94],104B'CL[101], 20.119.25'CL[104],3B9PC'CL[106],MVAR1'CL[109],167.1'CL[113],219.7'CL[114],5D6S'CL[122],167.2'CL[127], CH12'CL[129],F17.59.2'CL[137],vpd15 GL'CL[138],119.13'CL[149],6G7S'CL[158],3B11S'CL[161],4A9S'CL[164], NQ22.87.1'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: PJ14'CL[33],D1.3[38],MOPC141'CL[56],G2b-4'CL[61],56-1'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],VB4.4'CL[99],C57BL/10 V3'CL[100],C57BL V3'CL[101]; AND 1 RAT V-H: YTH 34.5HL'CL[1].)

SET 9: HuRSV19VH[36],HuRSV19CHFNS[38]. (2 IDENTICAL HUMAN V-H-II; ALSO 1 MOUSE V-H-IIA: L13'CL[173]; 5 MOUSE V-H-IIC: vpw38 GL'CL[20],P4.16.25'CL[25],H4a-3'CL[28],H2b-3'CL[32],MuRSV19VH'CL[37]; AND 1 MISCELLANEOUS V-H: XENOPUS LAEVIS V'CL[42].)

CDR2: SET 1: 15P1'CL[1],L16'CL[2],ML1'CL[3],M71'CL[4],F19L16'CL[5],F19ML1'CL[6],6-1G1'CL[7],VHVI'CL[8],VH6'CL[9]. (9 IDENTICAL)

SET 2: 71-2'CL[13],71-4'CL[15],58P2'CL[16],37P1'CL[47]. (4 IDENTICAL)

SET 3: Ab26'CL[18],1-9II'CL[19],12G-1'CL[20]. (3 IDENTICAL)

SET 4: HuVNP'CL[25]. (IDENTICAL TO 19 MOUSE V-H-IIB: B1-8'CL[1],B1-8.DELTA1V3[2],B1-48'CL[3],N-HYB'CL[4], 18C10'CL[5],186-2'CL[6],S2D8'CL[8],6F6'CL[9],S2E9'CL[10],186-1'CL[12],ANTI-TGAL 17'CL[16],H1-9'CL[18], H1-5'CL[21],H1-39'CL[43],N1G9'CL[50],3C52'CL[102],20.119.25'CL[104],219.7'CL[114],167.2'CL[127].)

SET 5: HuVHLYS'CL[27]. (IDENTICAL TO 1 MOUSE V-H-IB: D1.3[38].)

SET 6: HuVHCAM 'CL[32]. (IDENTICAL TO 1 RAT V-H: YTH 34.5HL'CL[1].)

SET 7: HuRSV19VH[36],HuRSV19CHFNS[38]. (2 IDENTICAL HUMAN V-H-II; ALSO 1 MOUSE V-H-IIC: MuRSV19VH'CL[37].)

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

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

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

IDENTICAL SETS OF J-MINIGENES:

SET 1: ML1'CL[3],DR12910-2F8'CL[48],Ab17'CL[49],M44'CL[62]. (4 IDENTICAL HUMAN V-H-II; ALSO 9 HUMAN V-H-I: LS2'CL[1],LS5'CL[2],LS6'CL[3],LS3'CL[4],LS8'CL[6],NEI'CL[16],WIL2'CL[24],BOR'[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],K6A6'CL[68],K4B8'CL[69],K5B8'CL[70],K5C7'CL[71],K5G5'CL[72],K6F5'CL[73], 20P1'CL[82]; AND 1 MOUSE V-H-IIID: H37-40'CL[25].)

SET 2: L16'CL[2],M71'CL[4],C6B2'CL[14],58P2'CL[16],CE-1 'CL[41],37P1'CL[47]. (6 IDENTICAL HUMAN V-H-II; ALSO 5 HUMAN V-H-I: 51P1'CL[14],RF-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],HIG1'CL[24],Ab44'CL[29]. (3 IDENTICAL HUMAN V-H-II; ALSO 5 HUMAN V-H-I: 783c'CL[21], X17115'CL[22],EV1-15'CL[25],ND'CL[30],Ab2'CL[44]; AND 6 HUMAN V-H-III: 4G12'CL[10],Ab21'CL[24],M72'CL[27], KIM46H'CL[29],U266'CL[136],70P1'CL[183].)

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

SET 6: 15P1'CL[1]. (IDENTICAL TO 7 HUMAN V-H-III: 18/2'CL[1],18/17'CL[2],18/9'CL[3],1/17'CL[4],M43'CL[6], HF2-1/17[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 NEWM 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 NEWM 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 NEWM WITH MORE MODIFICATIONS THAN HuRSV19VH, AND CDR'S OF MuRSV19VH. WHEN COMBINED WITH HuRSV19VK, THE FV BINDS THE VIRUS.
39) **LES-C'CL:** FROM A PATIENT WITH CHRONIC LYMPHOCYTIC LEUKEMIA. FOR ALIGNMENT, IT IS REQUIRED TO PLACE THREE AMINO ACID RESIDUES, GLY ALA ARG, AT POSITION 100I.
41) **CE-1 'CL:** CELL LINE CESS
46) **MCE':** IT IS A CRYOIMMUNOGLOBULIN AND IS DESIGNATED BY THE AUTHORS AS MCE. IN ORDER TO DIFFERENTIATE IT FROM ANOTHER MCE SEQUENCED BY CAPRA ET AL., IT IS DENOTED AS MCE'.
47) **37P1'CL:** FROM HUMAN FETUS AT 130 DAYS OF GESTATION.
49) **Ab17'CL:** AUTHORS PROVIDED THIS SEQUENCE WHICH IS DIFFERENT FROM THAT IN THE REFERENCE. THE RESIDUE AT POSITION 100J IS GLU, WITH THREE ADDITIONAL RESIDUES PRO GLY ASN BETWEEN POSITIONS 100J AND 100K.
50) **LES-B'CL:** FROM A PATIENT WITH CHRONIC LYMPHOCYTIC LEUKEMIA. FOR ALIGNMENT, IT IS REQUIRED TO PLACE THREE AMINO ACID RESIDUES, GLY ALA ARG, AT POSITION 100I.
51) **LES-A'CL:** FROM A PATIENT WITH CHRONIC LYMPHOCYTIC LEUKEMIA. FOR ALIGNMENT, IT IS REQUIRED TO PLACE THREE AMINO ACID RESIDUES, GLY ALA ARG, AT POSITION 100I.
53) **Ly66'CL:** AT POSITION 40 THE SEQUENCE CONNECTS TO THE CONSTANT REGION.
54) **JBL2'CL:** FROM BURKITT'S LYMPHOMA CELL LINES WHICH PRODUCE TRUNCATED HEAVY CHAINS LACKING PART OF VARIABLE REGION
55) **NZU:** IT IS A CRYOIMMUNOGLOBULIN.
58) **SPA:** IT WAS FROM A CASE OF HEAVY CHAIN DISEASE.
60) **64P1'CL:** FROM HUMAN FETUS AT 130 DAYS OF GESTATION.

\+ THE FOLLOWING WERE EQUALLY AND MOST FREQUENTLY OCCURRING:

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

HUMAN HEAVY CHAINS SUBGROUP III

		INVARIANT RESIDUES	1* 18/2 'CL #	2* 18/17 'CL #	3* 18/9 'CL #	4* 1/17 'CL #	5 30P1 'CL #	6 M43 'CL	7* HF2- 1/17	8 vh 26c 'CL	9 LAMBDA -VH26 'CL #	10* 4G12 'CL #	11* Ab18 'CL #	12* Ab25 'CL #	13* RF-KL1 'CL	14 8-1B 'CL	15 Vh38 Cl.10 'CL	16 Vh38 Cl.8 'CL	17 Vh38 Cl.9 'CL	18 60P2 'CL #	19 63P1 'CL #	20* GF4 /1.1 'CL
	0		---	---	---	---	---	---	---	---	#	---	---	---	---	---	---	---	---	---	---	---
	1		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
	3		GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN
	4	LEU(.97)	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	**val**
	5		LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	**val**	LEU	LEU	**val**	LEU	LEU	LEU	**val**	**val**	LEU
	6		GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU
	7	SER(.98)	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
	8	GLY(.99)	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	**GLY**	GLY	GLY	GLY	GLY	GLY	GLY
	9	GLY(.99)	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
	10		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	**asp**	**asp**	**asp**	GLY	GLY	GLY
	11		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	**ile**	**ile**	VAL
	13		GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN
FR1	14	PRO(.96)	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO
FR1	15	GLY(.99)	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
FR1	16		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
FR1	17	SER(.96)	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
FR1	18	LEU(.97)	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	**LEU**	LEU	LEU	LEU	LEU	LEU
FR1	19		ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG
FR1	20		LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
FR1	21	SER(.96)	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
FR1	22	CYS(.99)	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS
FR1	23		ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA
FR1	24		ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA
FR1	25	SER(.98)	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
FR1	26		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
FR1	27	PHE(.97)	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE
FR1	28		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
FR1	29		PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	**val**	PHE	PHE	PHE	**val**	**val**	PHE
FR1	30		SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
CDR1	31		SER	SER	SER	SER	SER	SER	SER	SER	SER	**thr**	SER	SER	SER	SER	**asn**	**asn**	**asn**	SER	SER	**lys**
CDR1	32		TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	**ser**	TYR	TYR	**asn**	TYR	TYR	**asn**	**asn**	**asn**	TYR
CDR1	33		ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	**tyr**	**val**	**val**	**val**	**tyr**	**tyr**	ALA
CDR1	34		MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET
CDR1	35		SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
CDR1	35A		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
CDR1	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(.97)	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
	38	ARG(.99)	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG
	39	GLN(.99)	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	**ser**	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA
FR2	41		PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO
FR2	42	GLY(.99)	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	**GLY**	**GLY**
FR2	43	LYS(.98)	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	**LYS**	LYS	LYS	LYS	LYS	LYS	LYS
FR2	44		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
FR2	45	LEU(.99)	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
FR2	46		GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	**gln**	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU
FR2	47	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP
FR2	48	VAL(.98)	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
FR2	49		SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
	50		ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	**val**	**ser**	**ser**	**ser**	**val**	**val**	**gly**
	51		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	SER	SER	SER	SER	SER	SER	SER	**tyr**	SER	SER	SER	**tyr**	**tyr**	SER
	52A		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	**asp**	---	GLY	GLY	GLY	---	---	**ala**
	52B	LYS(.95)	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	52C		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	53		SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	**asn**	SER	SER	SER	SER	SER	SER	SER
	54		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	**asp**	**asp**	**asp**	GLY	GLY	GLY
CDR2	55		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	**asp**	**ile**	GLY	GLY	GLY	GLY	GLY	GLY	GLY	**glu**
CDR2	56		SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	**ile**	SER	**gly**	**gly**	**gly**	SER	SER	**asn**
CDR2	57		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
CDR2	58		TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR
CDR2	59		TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR
CDR2	60		ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	**gly**	ALA	ALA	ALA	**thr**	ALA	**thr**	**thr**	**thr**	ALA	ALA	ALA
CDR2	61		ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	**ala**	**ala**	**ala**	ASP	ASP	ASP
CDR2	62		SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	**tyr**	SER	SER	SER	SER	SER	SER	**pro**
CDR2	63	VAL(.95)	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	**VAL**	**VAL**	VAL
CDR2	64		LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	**arg**	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS
	65	GLY(.98)	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
	66	ARG(.98)	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	**ARG**	**ARG**
	67	PHE(.98)	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE
	68		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
	69	ILE(.98)	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE
	70	SER(.98)	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	**SER**	SER	SER	SER
	71	ARG(.98)	ARG	ARG	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	ASP	ASP	ASP	ASP	ASP
	73		ASN	ASN	ASN	ASN	ASN	ASN	ASN	**ile**	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	SER	SER	SER	SER	SER
	75		LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS
	76		ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN
	77		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	**pro**	THR	THR	THR	THR	THR	THR	THR
	78		LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	**val**	LEU
	79		TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR
FR3	80	LEU(.95)	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
FR3	81		GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN
FR3	82	MET(.97)	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET
FR3	82A		ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	**ser**	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN
FR3	82B		SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
FR3	82C	LEU(.96)	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
FR3	83		ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG
FR3	84		ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA
FR3	85		GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	**asp**
FR3	86		ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP
FR3	87		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
FR3	88	ALA(.95)	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	**ALA**
FR3	89		VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	**met**
FR3	90	TYR(.98)	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR
FR3	91	TYR(.97)	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR
	92	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS
	93		ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA
	94		LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	**arg**	**gln**	**gln**	**ser**	**ser**	LYS	
	95		GLY	GLY	GLY	GLY	ASP	LYS	GLY		#	ALA	GLY	ALA	LYS	---	ASN	ASN	ASN	LYS	THR	GLY
	96		GLN	GLN	GLN	GLN	ALA	ASP	GLN		---	VAL	GLY	ALA	LEU	---	MET	MET	MET	GLY	ARG	GLY
	97		VAL	VAL	VAL	VAL	GLY	TRP	VAL		---	VAL	VAL	GLU	ARG	---	GLY	GLY	GLY	SER	GLU	ARG
	98		LEU	LEU	LEU	LEU	TRP	ASN	LEU		---	ARG	GLU	GLY	SER	---	ASP	ASP	ASP	LEU	THR	GLN
	99		TYR	TYR	TYR	TYR	GLY	ASP	TYR		---	GLY	LEU	PHE	GLY	---	ILE	ILE	ILE	TYR	GLY	TRP
	100		TYR	TYR	TYR	TYR	SER	ASN	TYR		---	VAL	ALA	GLY	LEU	---	ARG	ARG	ARG	---	ASP	VAL
	100A		GLY	GLY	GLY	GLY	GLY	TRP	GLY		---	ILE	SER	HIS	VAL	---	LEU	LEU	LEU	---	LEU	VAL
CDR3	100B		SER	SER	SER	SER	---	PHE	SER		---	SER	THR	CYS	PRO	---	THR	THR	THR	---	GLY	LEU
CDR3	100C		GLY	GLY	GLY	GLY	---	---	GLY		---	TYR	LYS	SER	TYR	---	PRO	PRO	PRO	---	TRP	GLY
CDR3	100D		SER	SER	SER	SER	---	---	SER		---	TYR	PRO	THR	---	---	LEU	LEU	LEU	---	---	TYR
CDR3	100E		TYR	TYR	TYR	TYR	---	---	TYR		---	TYR	SER	SER	---	---	ALA	ALA	ALA	---	---	PHE
CDR3	100F		---	---	---	---	---	---	HIS		---	TYR	SER	CYS	---	---	---	---	---	---	---	PHE
	100G		---	---	---	---	---	---	---		---	GLY	#	TYR	---	---	---	---	---	---	---	ASP
	100H		---	---	---	---	---	---	---		---	MET	TYR	THR	---	---	---	---	---	---	---	SER
	100I		HIS	HIS	HIS	HIS	---	---	---		---	---	TRP	GLY	---	---	---	---	---	---	---	---
	100J		TRP	TRP	TRP	TRP	---	---	TRP		---	---	TYR	TYR	TYR	---	---	---	---	TYR	---	---
	100K		PHE	PHE	PHE	PHE	PHE	---	PHE		---	---	PHE	PHE	PHE	---	---	---	---	PHE	PHE	---
	101		ASP	ASP	ASP	ASP	ASP	ASP	ASP		---	ASP	ASP	ASP	ASP	---	---	---	---	ASP	ASP	---
	102		PRO	PRO	PRO	PRO	TYR	PRO	PRO		---	VAL	LEU	TYR	PHE	---	TYR	TYR	TYR	TYR	TYR	---
	103	TRP(.96)	TRP	TRP	TRP	TRP	TRP	TRP	TRP		---	TRP	TRP	TRP	TRP	---	TRP	TRP	TRP	TRP	TRP	TRP
	104	GLY(.99)	GLY	GLY	GLY	GLY	GLY	GLY	GLY		---	GLY	GLY	GLY	GLY	---	GLY	GLY	GLY	GLY	GLY	GLY
	105		GLN	GLN	GLN	GLN	GLN	GLN	GLN		---	GLN	ARG	GLN	ARG	---	GLN	GLN	GLN	GLN	GLN	GLN
	106	GLY(.99)	GLY	GLY	GLY	GLY	GLY	GLY	GLY		---	GLY	GLY	GLY	GLY	---	GLY	GLY	GLY	GLY	GLY	GLY
FR4	107	THR(.96)	THR	THR	THR	THR	THR	THR	THR		---	THR	THR	THR	THR	---	THR	THR	THR	THR	THR	THR
FR4	108		LEU	LEU	LEU	LEU	LEU	LEU	LEU		---	THR	LEU	LEU	LEU	---	LEU	LEU	LEU	LEU	LEU	LEU
FR4	109	VAL(.99)	VAL	VAL	VAL	VAL	VAL	VAL	VAL		---	VAL	VAL	VAL	VAL	---	VAL	VAL	VAL	VAL	VAL	VAL
FR4	110	THR(.96)	THR	THR	THR	THR	THR	THR	THR		---	THR	THR	THR	THR	---	THR	THR	THR	THR	THR	THR

HUMAN HEAVY CHAINS SUBGROUP III (cont'd)

	21 Vh38 Cl.4 'CL	22 Vh38 Cl.5 'CL	23 H11 'CL	24* Ab21 'CL #	25 56P1 'CL #	26 2P1 'CL #	27 M72 'CL	28 M74 'CL	29* KIM46H 'CL #	30 1-9III 'CL	31* RF-SJ2 'CL #	32 22-2B 'CL	33 TIL	34 FL2-2 'CL #	35 v65-4 'CL	36 38P1 'CL #	37 13-2 'CL	38 BRO 'IGM	39 BUT	40 CAM'	41* HN.14 'CL #	42* RF-TS2 'CL
0			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
1			GLU	GLU	gln	gln	gln	gln	gln	gln	gln	gln	GLU	gln	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
3	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	glu	GLN	GLN
4	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
5	LEU	LEU	val	LEU	val	val	val	val	val	val	val	val	LEU	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	thr	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	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	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	val	val	val	val	val	val	val	LEU	LEU	val	LEU	LEU	LEU	LEU	LEU	val	val	val
12	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	ile	VAL	VAL	VAL
13	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	lys	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLX	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
FR1 15	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	arg	arg	arg	arg	arg	arg	arg	GLY	GLY	arg	GLY	GLY	GLY	GLY	GLY	GLY	thr	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	met	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	pro	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	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
27	PHE	PHE	PHE	leu	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE
28	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
29	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	val	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
CDR1 31	asn	asn	SER	SER	SER	SER	SER	SER	SER	SER	SER	asp	thr	SER	asn	SER	SER	tyr	asx	asn	arg	SER
32	TYR	TYR	TYR	asp	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	his	TYR	TYR	TYR	his	TYR	TYR	TYR
33	val	val	trp	ALA	ALA	ALA	ALA	ALA	gly	gly	ALA	tyr	val	gly	tyr	asp	asp	asn	ser	ALA	gly	gly
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	SER	SER	his	SER	his	his	asn	SER	his	his	his
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
37	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	ile	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
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	val	ALA	pro	ALA	ALA
FR2 41	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	leu	PRO	thr	thr	thr	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	gln	LYS	LYS
44	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	ala	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
46	GLU	GLU	val	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLX	GLU	GLU	GLU	GLU	GLX	GLU	GLU	GLU	GLU
47	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP
48	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
49	SER	SER	SER	SER	ala	ala	ala	ala	ala	ala	ala	SER	gly	ala	SER	SER	SER	SER	SER	ala	SER	ala
50	ser	ser	arg	gly	val	val	val	val	val	val	val	tyr	ALA	val	tyr	ALA	ALA	ALA	ALA	val	val	val
51	ILE	ILE	ILE	thr	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	glx	SER	SER	gly	gly	gly	tyr	SER	SER	SER
52A	GLY	GLY	ser	GLY	tyr	tyr	tyr	tyr	tyr	tyr	tyr	tyr	ser	GLY	tyr	GLY	---	---	---	tyr	phe	tyr
52B	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
52C	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
53	SER	SER	asp	arg	asp	asp	asp	asp	asp	asp	asp	SER	leu	asp	asp	thr	thr	arg	asx	asp	asp	asp
CDR2 54	asp	asp	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	ser	GLY	ser	ala	ala	ala	GLY	GLY	GLY	GLY
55	GLY	GLY	ser	GLY	ser	ser	ser	ser	ser	ser	ser	val	ser	GLY	GLY	GLY	GLY	GLY	asx	GLY	ser	ser
56	gly	gly	SER	SER	asn	asn	asn	asn	asn	asn	asn	thr	SER	asn	tyr	asp	asp	asp	thr	asx	thr	asn
57	THR	THR	THR	THR	lys	lys	lys	lys	lys	lys	ile	glx	lys	THR	THR	THR	gln	THR	lys	lys	lys	glu
58	TYR	TYR	thr	asn	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	ser	TYR	asn	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	phe
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	ASX	ASP	ASP	gly	gly	ASP	ASP	ASX	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	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE
68	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
69	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE
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	asp	ASN	ASN	ASN	ASN	asp	asp	ASX	ASN	ASN
74	SER	SER	ala	SER	SER	SER	SER	SER	SER	SER	SER	ala	SER	SER	ala	ala	ala	SER	SER	SER	SER	SER
75	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	asn	LYS	LYS	LYS	arg	LYS	LYS	LYS	asn
76	ASN	ASN	ASN	ser	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASX	ASX	ASN	ASN	ASN
77	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	ser	THR	THR	ser	ser	ser	THR	THR	THR	THR	THR
78	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	---	LEU	pro	LEU	LEU	LEU	val	LEU	ile	LEU
79	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	ser	TYR	---	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR
FR3 80	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	---	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	met
81	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	---	GLN	GLN	GLN	GLN	asn	GLN	GLN	GLN	GLN
82	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET
82A	ASN	ASN	ASN	thr	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASX	ASN	ASN	ASN	ASN
82B	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
82C	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
83	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG
84	ALA	ALA	ALA	val	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	pro	ALA	ALA
85	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	gly	gly	GLU	GLU	GLU	GLU	GLU
86	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASX	ASP	ASP
87	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
88	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA
89	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
90	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR
91	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR
92	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS
93	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	val	ALA	ALA	ALA	ALA	ALA	ALA	ALA
94	gln	gln	arg	LYS	arg	gly	arg	arg	LYS	arg	arg	LYS	LYS	LYS	LYS	arg	arg	arg	arg	arg	LYS	arg
95	ASN	ASN	---	VAL	ARG	TRP	ASP	ASP	VAL	---	GLY	---	GLY	ASP		SER	---	SER	ASP	ASP	LYS	ASP
96	MET	MET	---	ALA	SER	GLY	ARG	ARG	ARG	---	ARG	---	LYS	ARG		PHE	---	PRO	LEU	ARG	ALA	ARG
97	GLY	GLY	---	SER	ALA	LYS	HIS	LYS	GLU	---	PHE	---	VAL	ASN		SER	---	VAL	ALA	PRO	ALA	VAL
98	ASP	ASP	---	TYR	ARG	---	SER	ASP	TYR	---	CYS	---	SER	TRP		GLU	---	SER	ALA	LEU	PRO	ALA
99	ILE	ILE	---	SER	THR	---	SER	TRP	TYR	---	SER	---	ALA	GLY		THR	---	LEU	ALA	TYR	ALA	VAL
100	ARG	ARG	---	PHE	TYR	---	SER	GLY	TYR	---	GLY	---	TYR	PHE		GLY	---	VAL	ARG	GLY	SER	TYR
100A	LEU	LEU	---	ARG	---	---	TRP	TRP	GLY	---	GLY	---	TYR	---		ASP	---	ASP	LEU	ASX	THR	ALA
CDR3 100B	THR	THR	---	PHE	---	---	TYR	ALA	SER	---	SER	---	PHE	---		---	---	GLY	---	TYR	GLY	SER
100C	PRO	PRO	---	ARG	---	---	TYR	LEU	GLY	---	CYS	---	---	---		---	---	TRP	---	ARG	SER	VAL
100D	LEU	LEU	---	---	---	---	GLY	PHE	#	---	#	---	---	---		---	---	LEU	---	ALA	GLY	PHE
100E	ALA	ALA	---	---	---	---	MET	---	TYR	---	TYR	---	---	---		---	---	TYR	---	PHE	VAL	PHE
100F	---	---	---	HIS	---	---	---	---	TYR	---	TYR	---	---	---		---	---	TYR	---	---	---	ILE
100G	---	---	---	TYR	---	---	---	---	TYR	---	TYR	---	---	---		---	---	TYR	---	---	---	ASP
100H	---	---	---	TYR	---	---	---	---	TYR	---	TYR	---	---	---		---	---	TYR	---	---	---	SER
100I	---	---	---	TYR	---	ASN	---	---	TYR	---	TYR	---	---	---		---	---	GLY	---	---	---	---
100J	---	---	---	GLY	TYR	TRP	---	---	GLY	---	TYR	---	---	---		ALA	---	---	---	---	ASP	---
100K	---	---	---	MET	PHE	PHE	---	---	MET	---	MET	---	---	---		PHE	---	---	---	---	PHE	PHE
101	---	---	---	ASP	ASP	ASP	ASP	ASP	ASP	---	ASP	---	ASX	ASP		ASP	---	SER	PHE	ASN	ASP	ASP
102	TYR	TYR	---	VAL	TYR	PRO	VAL	TYR	VAL	---	VAL	---	TYR	TYR		ILE	---			TYR	TYR	ILE
103	TRP	TRP	---	TRP	TRP	TRP	TRP	TRP	TRP	---	TRP	---	TRP	TRP		TRP	---	TRP		TRP	TRP	TRP
104	GLY	GLY	---	GLY	GLY	GLY	GLY	GLY	GLY	---	GLY	---	GLY	GLY		GLY	---	GLY	GLY	GLY	GLY	GLY
105	GLN	GLN	---	GLN	GLN	GLN	GLN	GLN	GLN	---	LYS	---	GLX	GLN		GLN	---	GLN	LYS	GLN	GLN	GLN
106	GLY	GLY	---	GLY	GLY	GLY	GLY	GLY	GLY	---	GLY	---	GLY	GLY		GLY	---	GLY	GLY	GLY	GLY	GLY
FR4 107	THR	THR	---	THR	THR	THR	THR	THR	THR	---	THR	---	THR	THR		THR	---	THR	THR	THR	THR	THR
108	LEU	LEU	---	THR	LEU	LEU	THR	LEU	THR	---	THR	---	LEU	LEU		MET	---	LEU	THR	LEU	LEU	GLY
109	VAL	VAL	---	VAL	VAL	VAL	VAL	VAL	VAL	---	VAL	---	VAL	VAL		VAL	---		VAL	VAL	VAL	VAL
110	THR	THR	---	THR	THR	THR	THR	THR	THR	---	THR	---	THR	THR		THR	---		THR	THR	THR	THR

HUMAN HEAVY CHAINS SUBGROUP III (cont'd)

		43* 3D6 'CL	44 1-91 'CL	45* POM	46* RF-SJ1 'CL #	47* WEA	48* 4B4 'CL #	49 M26 'CL	50 9-1 'CL	51* LAY	52 BUR	53 KOL	54 TEI	55 12-2 'CL	56 HIL	57 TRO	58 WAS	59* TUR	60 NIE	61 GAL	62 DOB	63 VH10.7 'CL #	64 ZAP	65 JON	66 GA	67 GRA' #	68 K6H6 'CL #
	0	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	1	GLU	GLU	GLU	**gln**	**pca**	GLU	GLU	GLU	**ala**	**pca**	**pca**	GLU	GLU	**pca**	**pca**	GLU	GLU	**pca**	GLU	GLU	**gln**	GLU	**asp**	**pca**	GLU	GLU
	2	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
	3	GLN	**his**	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	**lys**	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLX	GLN	**arg**
	4	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
	5	**val**	LEU	LEU	**val**	**val**	**val**	**val**	**val**	LEU	**val**	**val**	**val**	**val**	**val**	**val**	LEU	LEU	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**
	6	GLU	GLU	GLU	GLU	**asp**	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	**gln**	**gln**	GLU	GLU	**gln**	GLU	GLU	GLU	GLU	GLU	GLX	GLU	GLU
	7	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	**ala**	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
	8	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
	9	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
	10	GLY	**asp**	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	**asp**	**asp**	GLY	**ala**	GLY		GLY	**asp**
	11	LEU	LEU	LEU	**val**	LEU	LEU	LEU	LEU	LEU	**val**	**val**	LEU	LEU	**val**	LEU	LEU	LEU	LEU	LEU	LEU	**val**	LEU	LEU		LEU	LEU
	12	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL		VAL	VAL
	13	GLN	GLN	GLN	GLN	**glu**	**lys**	**lys**	GLN	GLN	GLN	GLN	GLN	GLN	GLN	**lys**	GLN	GLN	GLN	GLN	GLN	GLN	GLN	**lys**		GLN	**glu**
FR1	14	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	**ala**	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	**ala**	PRO	PRO		PRO	PRO
	15	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY		GLY	GLY
	16	**arg**	GLY	GLY	**arg**	GLY	GLY	GLY	GLY	GLY	**thr**	**arg**	GLY	GLY	**arg**	GLY	GLY	GLY	**arg**	**arg**	**arg**	**arg**	GLY	GLY	**arg**	GLY	GLY
	17	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	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	**gly**	LEU	LEU	LEU	LEU
	19	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG
	20	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	**val**
	21	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
	22	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS
	23	ALA	ALA	ALA	ALA	**ser**	ALA	ALA	ALA	ALA	**thr**	**ser**	ALA	ALA	**ile**	**val**	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	**glu**
	24	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	**ser**	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	**thr**	ALA	ALA	ALA	ALA	**val**
	25	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
	26	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	**ala**	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
	27	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE
	28	THR	THR	THR	**ser**	THR	THR	THR	THR	THR	**asn**	**ile**	THR	THR	THR	**ser**	**ser**	THR	THR		**asn**	**met**	THR	THR	**ser**	THR	**ile**
	29	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	**leu**	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE		PHE	PHE	PHE	PHE	PHE	**ile**	PHE
	30	**asn**	**asn**	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	**arg**	SER	SER	SER		**his**	SER	SER	SER		SER	SER
CDR1	31	**asp**	**asn**	SER	SER	**ala**	**asn**	**asn**	**asn**	**ala**	**asp**	SER	**thr**	**asp**	**asn**	**asp**	**thr**	**arg**	**arg**		**glu**	**thr**	**thr**	**thr**		**lys**	**lys**
	32	TYR	**his**	**ser**	TYR	**asn**	**ala**	**ala**	**ala**	**ser**	TYR	TYR	**ser**	**his**	TYR	**phe**	**asp**	**val**	TYR		TYR	TYR	TYR	**thr**	**ala**	TYR	**ala**
	33	ALA	ALA	ALA	**gly**	**asp**	**trp**	**trp**	**trp**	ALA	ALA	ALA	ALA	**trp**	**gly**	**tyr**	ALA	**leu**	**thr**		**asn**	ALA	**ser**	**trp**		**val**	**trp**
	34	MET	**leu**	MET	MET	MET	MET	MET	MET	MET	MET	MET	**val**	MET	MET	MET	MET	**ser**	**ile**	MET	MET	MET	**arg**	MET	MET	**tyr**	MET
	35	**his**	**thr**	SER	**his**	**asn**	SER	SER	SER	SER	**his**	**tyr**	**tyr**	**asp**	**his**	SER	**tyr**	SER	**his**	**thr**	**his**	**his**	**phe**	**lys**	**his**	**glu**	**asn**
	35A	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	35B	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	36	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP
	37	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	**ile**	VAL	VAL	VAL	VAL	**leu**	VAL	VAL	VAL	VAL	VAL	VAL
	38	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG
	39	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN
	40	ALA	ALA	ALA	**cys**	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	**thr**	ALA	ALA	ALA	ALA	**gly**	ALA	ALA	ALA	ALA	ALA	ALA
FR2	41	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PPO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO
	42	GLY	**arg**	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
	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	LYS	LYS
	44	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
	45	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	**pro**	LEU	LEU	LEU	LEU	LEU	LEU
	46	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLX	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLX	GLU	**gln**
	47	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP
	48	VAL	VAL	VAL	VAL	**leu**	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	**leu**	VAL	VAL
	49	SER	SER	**ala**	**ala**	SER	**gly**	**gly**	**gly**	**ala**	**ala**	**ala**	**gly**	**gly**	**ala**	SER	**ala**	SER	**ala**	**ala**	SER	**ala**	**glu**	**val**	SER	**thr**	**gly**
	50	**gly**	**thr**	**trp**	**val**	**phe**	**arg**	**arg**	**arg**	**trp**	**leu**	**ile**	**trp**	**arg**	**val**	**tyr**	**trp**	**gly**	**val**	**asn**	**thr**	**val**	**phe**	**trp**	**val**	**tyr**	**gln**
	51	ILE	ILE	**lys**	ILE	ILE	ILE	ILE	ILE	**lys**	ILE	ILE	**arg**	**thr**	ILE	ILE	**lys**	**arg**	**met**	ILE	ILE	ILE	**arg**	**arg**	ILE	**val**	ILE
	52	SER	**asp**	**tyr**	SER	**gly**	**lys**	**lys**	**tyr**	SER	**trp**	**tyr**	**arg**	**arg**	**trp**	**gly**	**tyr**	**leu**	SER	**lys**	**thr**	**trp**	**val**	**val**	SER	**gly**	**lys**
	52A	**trp**	**asn**	**glu**	**asp**	GLY	**ser**	**ser**	**ser**	**glu**	**tyr**	**asp**	**glu**	**asn**	**tyr**	GLY	**gln**	**asn**	**tyr**	**glx**	**trp**	**tyr**	**gln**	**glu**	**tyr**	**gln**	**asn**
	52B	---	---	---	---	---	**lys**	**lys**	**lys**	---	---	---	---	**lys**	---	---	---	---	---	---	---	---	---	---	---	---	**lys**
	52C	---	---	---	---	---	**thr**	**thr**	**thr**	---	---	---	---	**ala**	---	---	---	---	---	---	---	---	---	---	---	---	**val**
CDR2	53	**asp**	SER	**asn**	**asp**	SER	**asp**	**asp**	**asp**	**asn**	**gly**	**asp**	**gly**	**asn**	**asn**	SER	**glu**	**ala**	**asx**	**asx**	**asn**	**asp**	**gly**	**gln**	**asx**	**val**	**asp**
	54	**ser**	**glu**	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	**ser**	**ser**	GLY	GLY	GLY	**ala**	**ser**	GLY	GLY	GLY	GLY	**ser**	**val**	GLY	**ser**	GLY
	55	**ser**	**ile**	**asn**	**ser**	**ser**	GLY	GLY	GLY	**asn**	**ser**	**ser**	**ser**	**tyr**	**ser**	**ser**	**ser**	**ser**	**asx**	**ser**	GLY	**ser**	**ala**	**val**	**asx**	**lys**	GLY
	56	SER	**asn**	**asp**	**asn**	**thr**	**thr**	**thr**	**thr**	**asp**	**asx**	**asp**	**leu**	**thr**	**arg**	**thr**	**asn**	**asn**	**asx**	**glx**	SER	**gln**	**ile**	**glu**	**asx**	**phe**	**thr**
	57	**ile**	THR	**lys**	**lys**	**ile**	THR	THR	THR	**lys**	THR	**gln**	THR	THR	THR	**leu**	**ser**	**leu**	**lys**	**glx**	**val**	**ala**	**ser**	**lys**	**glx**	**ser**	**ile**
	58	**gly**	TYR	**his**	TYR	TYR	**asp**	**asp**	**asp**	**his**	TYR	**his**	**his**	**glu**	TYR	TYR	**his**	**his**	**his**	**asx**	**leu**	**ser**	**his**	**ala**	TYR		**asp**
	59	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	**phe**	**phe**	TYR	TYR	TYR	TYR	TYR	**phe**	TYR	TYR	TYR
	60	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	**gly**	ALA	ALA	ALA	ALA	**val**	ALA	**thr**	ALA	ALA	ALA	ALA	ALA
	61	ASP	**ser**	ASP	ASP	ASP	**ala**	**ala**	**ala**	ASP	ASP	ASP	**val**	**ala**	ASP	ASP	ASP	**val**	ASP	ASP	ASP	ASP	ASP	**asn**	**ala**	**val**	**ala**
	62	SER	SER	SER	SER	SER	**pro**	**pro**	**pro**	SER	SER	SER	SER	SER	SER	SER	**thr**	SER	SER	SER	SER	SER	SER	SER	SER	SER	**pro**
	63	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	**ala**	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
	64	LYS	LYS	**asn**	LYS	LYS	LYS	LYS	LYS	**asn**	**arg**	LYS	**gln**	LYS	LYS	LYS	**asn**	**gln**	**asn**	LYS	LYS	**arg**	**gln**	**asn**	LYS	**gln**	LYS
	65	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	**ala**	GLY	GLY	GLY	GLY
	66	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARC	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG
	67	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE
	68	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	**ala**	THR	THR	THR	THR	THR	**ile**
	69	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE
	70	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
	71	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG
	72	ASP	ASP	**asn**	ASP	**asn**	ASP	ASP	ASP	**asn**	ASX	ASP	**asn**	ASP	ASP	ASP	**asn**	**asn**	**asn**	ASP	ASP	ASP	**asn**	**asn**	ASX	**asn**	ASP
	73	ASN	ASN	**asp**	ASN	ASX	**asp**	**asp**	**asp**	**ile**	ASN	**asp**		**asp**	ASN	ASN	**asp**	**asp**	**asp**	ASN	ASN	ASN	**asp**	**asp**		**asp**	**asp**
	74	**ala**	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	**ala**	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	**gln**	LYS	LYS	LYS	LYS	**gln**	LYS	LYS	LYS	LYS	LYS	LYS
	76	ASN	ASN	ASN	**lys**	ASN	ASN	ASN	ASN	ASN	ASX	ASN	ASN	ASN	**arg**	**lys**	ASN	ASN	ASN	ASN	**lys**	**lys**	ASN	ASN	ASX	ASN	**ser**
	77	**ser**	THR	THR	THR	**ser**	THR	THR	THR	THR	THR	THR	THP	ser	THR	**ser**	THR	THR	THR	**ser**	THR	**ile**	THR	THR	THR	THR	THR
	78	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	**met**	LEU	LEU
	79	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	**phe**	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR
FR3	80	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	**met**	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
	81	GLN	GLN	**leu**	GLN	GLN	GLN	GLN	GLN	GLN	GLX	GLN	GLN	GLN	GLX	GLN	GLN	GLN	**asn**	GLN	GLN	**glu**	GLN	GLN	**glu**	GLU	GLN
	82	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	**leu**	MET	MET	MET	MET	MET	MET
	82A	ASN	ASN	ASN	**asp**	**ser**	ASN	ASN	ASN	**lys**	**asp**	leu		ASN	ASN	ASN	ASN	leu	ASN	ASN	ASN	**ser**	ASN	ile	ASN	**lys**	ASN
	82B	SER	SER	SER	SER	SER	SER	SER	SER	**gly**	**thr**	SER	SER	SER	SER	SER	SER	**arg**	SER	SER	SER	**ile**	**gly**	**thr**	SER	**thr**	**arg**
	82C	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	**gly**	**val**	LEU	**gly**	LEU
	83	ARG	**lys**	**gln**	ARG	ARG	**lys**	**lys**	**lys**	**gln**	ARG	ARG	**glu**	**lys**	ARG	ARG	**glu**	**gln**	ARG	ARG	ARG	ARG	**glu**	**thr**	ARG	**glu**	**lys**
	84	ALA	**val**	ALA	**thr**	ALA	**thr**	**thr**	**thr**	ALA	**thr**	**pro**	**pro**	**thr**	**thr**	**thr**	ALA	ALA	**pro**	**val**	**pro**	ALA	ALA	**pro**	ALA	**pro**	**ile**
	85	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU
	86	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	**val**	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	**asn**	ASP	ASP
	87	**met**	THR	THR	THR	THR	THR	THR	**ser**	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
	88	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	**gly**	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA
	89	**leu**	VAL	**leu**	VAL	VAL	VAL	VAL	VAL	**ile**	VAL	VAL	VAL	VAL	VAL	VAL	VAL	**leu**	VAL	**leu**	**phe**	**thr**	VAL	VAL	VAL	VAL	VAL
	90	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR
	91	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	**phe**	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR
	92	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS
	93	**val**	ALA	ALA	ALA	ALA	**thr**	**thr**	**thr**	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	**val**
	94	LYS	LYS	**arg**	LYS	**arg**	**thr**	**thr**	**thr**	**arg**	LYS	**arg**	**arg**	**arg**	**arg**	**ala**	**arg**	**arg**	**arg**	**arg**	LYS	**thr**	**arg**	**arg**	**arg**	**arg**	**gly**
	95	GLY		ASP	GLY	GLY	ASP	SER	---	ASP	LEU	ASP	VAL	---	ASP	THR	PHE	LEU	ILE	GLY	GLY	GLN	THR	VAL	SER	HIS	ASN
	96	ARG		ALA	VAL	TRP	SER	ILE	---	ALA	ILE	GLY	THR	---	PRO	ASN	ARG	SER	ARG	TRP	TYR	HIS	ARG	VAL	GLY	ILE	TYR
	97	ASP		GLY	TYR	LEU	LEU	PRO	---	GLY	ALA	GLY	PRO	---	ASP	ASN	GLN	VAL	ASP	GLY	ILE	ASP	PRO	VAL	ILE	TYR	THR
	98	TYR		PRO	CYS	---	PRO	GLY	---	PRO	VAL	HIS	ALA	---	ILE	PHE	PRO	THR	THR	GLY	TRP	TYR	GLY	SER	ALA	VAL	GLY
	99	TYR		TYR	SER	---	---	PRO	ILE	---	TYR	ALA	GLY	ALA	---	LEU	ASN	PHE	ALA	ALA	GLY	ASN	SER	GLY	THR	LEU	THR	THR
	100	ASP		VAL	SER	---	---	HIS	ALA	---	VAL	GLY	PHE	ALA	---	THR	TRP	VAL	VAL	MET	---	GLY	HIS	TYR	SER	GLY	LEU	VAL
	100A	SER		SER	SER	---	---	ARG	VAL	---	SER	THR	CYS	SER	---	ALA	SER	GLN	ALA	PHE	---	ASN	GLN	PHE	---	SER	TYR	---
CDR3	100B	GLY		PRO	SER	---	---	VAL	ALA	---	PRO	ARG	SER	LEU	---	PHE	THR	---	PHE	---	---	TRP	ARG	SER	---	VAL	TYR	---
	100C	GLY		THR	CYS	---	---	GLY	---	---	THR	---	SER	THR	---	SER	PHE	---	---	---	---	PHE	---	---	---	ALA	TYR	---
	100D	TYR		PHE	#	---	---	THR	---	---	PHE	---	ALA	---	---	PHE	SER	---	---	---	---	---	---	---	---	GLY	---	---
	100E	PHE		---	TYR	---	---	---	---	---	---	---	SER	---	---	---	LEU	---	---	---	---	---	---	---	---	THR	---	---
	100F	THR		---	TYR	---	---	---	---	---	---	---	CYS	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	100G	VAL		---	TYR	---	---	---	---	---	---	---	PHE	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	100H	---		---	TYR	---	---	---	---	---	---	---	GLY	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	100I	---		---	HIS	---	---	---	---	---	---	---	PRO	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	100J	ALA		---	TYR	---	---	---	---	---	---	---	PHE	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	100K	PHE		PHE	MET	---	---	---	---	---	PHE	---	---	SER	---	---	---	---	PHE	---	---	---	---	---	---	---	MET	---
	101	ASP		ALA	ASP	LEU	---	ASP	---	ALA	ASX	ASP	ALA	---	ASP	ASN	ASP	ASP	ALA	ASP	ASP	ASP	ASP	ASP	ASP	ALA	ASP
	102	ILE		HIS	VAL	ASN	---	TYR	---	HIS	PHE	TYR	VAL	---	TYR	TYR	VAL	VAL	HIS	TYR	SER	TYR	VAL	VAL	TYR	VAL	TYR
	103	TRP		TYR	TRP	TRP	TRP	TRP	---	TRP	TRP	TRP	TRP	---	TRP	TRP	PHE	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP
	104	GLY		GLY	GLY	GLY	GLY	GLY	---	GLY	GLY	GLY	GLY	---	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
	105	GLN		GLN	LYS	GLN	GLN	GLN	---	GLN	GLN	GLN	GLN	---	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLX	GLN	GLN
	106	GLY		GLY	GLY	GLY	GLY	GLY	---	GLY	GLY	GLY	GLY	---	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
	107	THR		THR	THR	THR	THR	THR	---	THR	THR	THR	THR	---	VAL	ASN	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
	108	MET		LEU	THR	LEU	LEU	LEU	---	LEU	LEU	PRO	LEU	---	LEU	LEU	LEU	LEU	LYS	LEU	LEU	LEU	LEU	PRO	LEU	LEU	LEU
FR4	109	VAL		VAL	VAL	VAL	VAL	VAL	---	VAL	VAL	VAL	VAL	---	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL		VAL
	110	THR		THR	THR	THR	THR	THR	---	THR	THR	THR	THR	---	THR	THR	THR	SER	THR	THR	THR	THR	SER	THR	THR		THR

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* 2C12 'CL	61* 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	**pca**	GLU	GLU	GLU	GLU	GLU	GLU	GLU
2	VAL	VAL	VAL	VAL	VAL	**met**	**met**	**met**	**met**	**met**	**met**				VAL	VAL	VAL	**ser**	VAL	VAL	VAL	VAL	VAL	VAL	VAL
3	**arg**	**arg**	**arg**	**arg**	**arg**	GLN	GLN	GLN	GLN	GLN	GLN				GLN	GLN	GLN	**val**	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**	LEU
5	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**				**val**	**val**	**val**	**asx**	LEU	LEU	**val**	**val**	**val**	LEU	**val**
6	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	**gln**	GLU			**asp**	**gln**	GLU	**gly**	GLY	**gln**	GLY	GLU	GLU	**gln**	GLX
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
11	LEU	LEU	LEU	LEU	LEU	**phe**	**phe**	**phe**	**phe**	**phe**	**phe**	**phe**	**phe**		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	ile	VAL	VAL
13	**glu**	**glu**	**glu**	**glu**	**glu**	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN		GLN	**his**	**lys**		GLN	GLN	**lys**	GLN	GLN	GLN	GLX
14	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	**glu**	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
17	SER	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	LEU
19	ARG	ARG	ARG	ARG	ARG	**lys**	**lys**	**lys**	ARG	**lys**	**lys**	**lys**	**lys**		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
21	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER		SER	SER	SER		SER	SER	SER	SER	SER	**gln**	**gly**
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	**glu**	**glu**	**glu**	**glu**	**glu**	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	**gly**	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
26	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY			GLY	GLY	GLY	GLY	GLY	GLY	GLY
27	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			**lys**	THR	**ile**	THR	THR	**ser**	
29	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE			PHE	PHE	PHE	PHE	**val**	PHE	
30	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	**thr**			SER	SER	**pro**	SER	SER	SER	
31	**lys**	**lys**	**lys**	**lys**	**lys**	**asp**	**asp**	**asp**	**asp**	**asp**	**asp**	**asp**	**asp**	**asn**	**asx**	SER	**arg**		SER	SER		**ala**	**thr**	**pro**	
32	**ala**	**ala**	**ala**	**ala**	**ala**	**ser**	**ser**	**ser**	**ser**	**ser**	**ser**	**ser**	**ser**	**ala**	**phe**	TYR	**gly**		TYR	TYR	TYR	**asx**	**asn**	**ser**	
33	**trp**	**trp**	**trp**	**trp**	**trp**	**thr**	**thr**	**thr**	**thr**	**thr**	**thr**	**thr**	**thr**	**trp**	**tyr**	ALA	**gly**		ALA	ALA		**tyr**	**tyr**	ALA	
34	MET	MET	MET	MET	MET	**ile**	**ile**	**ile**	**ile**	**ile**	**ile**	**ile**	**ile**	MET	MET	MET	**leu**		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	
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	
37	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		**pro**		ARG	
39	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN		**gly**		GLN	
40	ALA	ALA	ALA	**val**	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			
42	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				**arg**			
44	GLY	GLY	GLY	GLY	GLY	**ser**	**ser**	**ser**	**ser**	**ser**	**ser**	**ser**	**ser**	GLY	GLY	GLY	**ala**	GLY				GLY			
45	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU				LEU			
46	**gln**	**gln**	**gln**	**gln**	**gln**	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								
48	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL								
49	**gly**	**gly**	**gly**	**gly**	**gly**	**gly**	**gly**	**gly**	**gly**	**gly**	**gly**	**gly**	**gly**	**gly**	**ala**	SER	**leu**	SER							
50	**gln**	**gln**	**gln**	**gln**	**gln**	**his**	**his**	**his**	**his**	**his**	**his**	**his**	**his**	**arg**	ALA	ALA	**val**	**val**							
51	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	**arg**	ILE	**phe**	ILE							
52	**lys**	**lys**	**lys**	**lys**	**lys**	**glu**	**glu**	**glu**	**glu**	**glu**	**glu**	**glu**	**glu**	**lys**		**gly**	SER	**thr**							
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**		**gly**	---	---							
52C	**val**	**val**	**val**	**val**	**val**	**ser**	**thr**	**thr**	**ser**	**thr**	**ser**	**ser**	**thr**	**thr**		**gly**	---	---							
53	**asp**	**asp**	**asp**	**asp**	**asp**	**lys**	**lys**	**lys**	**lys**	**asn**	**lys**	**lys**	**asp**	**asx**		**gly**	**thr**	**asx**							
54	GLY	GLY	GLY	GLY	GLY	**lys**	**asn**	**asn**	**lys**	**asn**	**lys**	**asn**	**asn**	GLY		**thr**		GLY							
55	GLY	GLY	GLY	GLY	GLY	**tyr**	**tyr**	**tyr**	**tyr**	**tyr**	**tyr**	**tyr**	**tyr**	GLY		**tyr**									
56	**thr**	**thr**	**thr**	**thr**	**thr**	**ala**	**ala**	**ala**	**ala**	**ala**	**ala**	**ala**	**ala**	**thr**		**tyr**									
57	**ile**	**ile**	**ile**	**ile**	**ile**	THR	THR	THR	THR	THR	THR	THR	THR	THR		**ala**	**lys**	THR							
58	**asp**	**asp**	**asp**	**asp**	**asp**	**ile**	**met**	**ile**	**ile**	**val**	**ile**	**ile**	**ile**	**asp**		**asp**	**phe**	TYR							
59	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	**phe**	TYR	TYR	TYR	TYR	TYR		**ser**	TYR	TYR							
60	ALA	ALA	ALA	ALA	ALA	**arg**	**arg**	**arg**	**arg**	**arg**	**arg**	**arg**	**arg**	ALA		**val**	**thr**	**ile**							
61	**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**		**gly**	SER	SER							
63	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		**phe**	**asn**								
65	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		**ile**									
67	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE		**ser**		PHE							
68	**ile**	**ile**	**ile**	**ile**	**ile**	THR	THR	THR	**ile**	**asn**	THR	THR	THR	THR		**arg**		THR							
69	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE		**asp**		ILE							
70	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER		**asn**		SER							
71	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG		**ala**		ARG							
72	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP		**lys**									
73	**asp**	**asp**	**asp**	**asp**	**asp**	**asp**	**asp**	**asp**	**asp**	**asp**	**asp**	**asp**	**asp**	ASP		**met**									
74	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER		SER									
75	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	**asn**	LYS	LYS	LYS		**leu**									
76	**ser**	**ser**	**ser**	**ser**	**ser**	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN		**tyr**									
77	THR	THR	THR	THR	THR	THR	**met**	**met**	THR	**met**	THR	THR	THR	THR		**leu**									
78	LEU	LEU	**val**	LEU	LEU	**ala**	**ala**	**ala**	**ala**	**thr**	**ala**	**ala**	**ala**	LEU		**gln**									
79	TYR	TYR	TYR	TYR	TYR	**phe**	**phe**	**phe**	**phe**	**phe**	**phe**	**phe**	**phe**	TYR		**met**									
80	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU		**asn**									
81	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN		**ser**									
82	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	**leu**		MET		MET				MET	
82A	ASN	ASN	ASN	ASN	ASN	**asp**	**asp**	**asp**	**asp**	**asp**	**asp**	**asp**	**asp**	ASN	ASN	**arg**		**ser**		ASN				ASN	
82B	**arg**	**arg**	**arg**	**arg**	**arg**	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	**ala**		SER		**asn**				**gly**	
82C	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	**glu**		LEU		LEU				LEU	
83	**lys**	**lys**	**lys**	**lys**	**lys**	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	**lys**	ARG	**asp**		ARG		ARG				ARG	
84	**ile**	**ile**	**ile**	**ile**	**ile**	**pro**	**pro**	**pro**	**pro**	**pro**	**pro**	**pro**	**pro**	**thr**	ALA	**met**		**thr**		**val**		ALA		ALA	
85	GLU	GLU	GLU	GLU	GLU	**asp**	**asp**	**asp**	**asp**	**asp**	**asp**	**asp**	**asp**	GLU	GLX	**ala**		GLU		GLX		GLU		GLX	
86	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASX	**val**		ASP		ASX		ASP		ASX	
87	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	**tyr**		THR		THR		THR		**gly**	
88	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	**tyr**		ALA		ALA		ALA		**gly**	
89	VAL	VAL	VAL	VAL	VAL	**leu**	**leu**	**leu**	**leu**	**leu**	**leu**	**leu**	**leu**	VAL	VAL	**cys**		VAL		VAL		VAL		VAL	
90	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	**ala**		TYR		TYR		TYR		TYR	
91	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	**arg**		TYR		TYR		TYR		TYR	
92	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS			CYS		CYS		CYS		CYS	
93	**val**	**val**	**val**	**val**	**val**	**thr**	**thr**	**thr**	**thr**	**thr**	**thr**	**thr**	**thr**	**thr**	**lys**	ALA		ALA		ALA		ALA		**val**	
94	**gly**	**gly**	**gly**	**gly**	**gly**	**pro**	**pro**	**pro**	**pro**	**pro**	**pro**	**pro**	**pro**	**pro**	**ala**	**arg**		**leu**		**arg**		**arg**		**ser**	
95	ASN	ASN	ASN	ASN	ASN	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	GLY					ASX				ASX	
96	TYR	TYR	TYR	TYR	TYR	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO			LEU		ARG				VAL	
97	THR	THR	THR	THR	THR	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	---			GLU		LEU					
98	GLY	GLY	GLY	ILE	GLY	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	---				ALA		GLY					
99	THR	THR	THR	THR	THR	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	---						PRO					
100	VAL	VAL	VAL	ILE	VAL	SER	SER	SER	SER	SER	SER	SER	SER	---				TYR		THR					
100A	---	---	---	---	---	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	---				SER		ALA					
100B	---	---	---	---	---	---	---	---	---	---	---	---	---	---				LEU		CYS					
100C	---	---	---	---	---	---	---	---	---	---	---	---	---	---				---		SER					
100D	---	---	---	---	---	---	---	---	---	---	---	---	---	---				---		VAL					
100E	---	---	---	---	---	---	---	---	---	---	---	---	---	---				---							
100F	---	---	---	---	---	---	---	---	---	---	---	---	---	---				---							
100G	---	---	---	---	---	---	---	---	---	---	---	---	---	---				---							
100H	---	---	---	---	---	---	---	---	---	---	---	---	---	---				---							
100I	---	---	---	---	---	---	---	---	---	---	---	---	---	---				---							
100J	---	---	---	---	---	---	---	---	---	---	---	---	---	---				---							
100K	---	---	---	---	---	---	---	---	---	---	---	---	---	---				---							
101	ASP	ASP	ASP	ASP	ASP	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ASP				ASP							
102	TYR	TYR	TYR	TYR	TYR	SER	SER	SER	SER	SER	SER	SER	SER	TYR				VAL							
103	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP				TRP							
104	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY											
105	GLN	GLN	GLN	GLN	GLN	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	GLN											
106	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY				GLY							
107	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR											
108	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU											
109	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL				VAL							
110	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR				THR							

HUMAN HEAVY CHAINS SUBGROUP III (cont'd)

		94 FOR	95 BEN (III)	96 PS (SHA) #	97 13P1 'CL #	98 H11' 'CL	99 WAT	100 LOW	101 JOR	102 BRO	103 V.N.	104 CAM	105 GAA	106 EIK	107 SKI	108 WEI	109 WE	110 AVI	111* A-G1 #	112 EVA	113* B-G1 #	114* B-G2b #	115 ESM	116* B-G2a	117* C-G2a	118* A-G2a
	0	---	---	---		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	1	GLU	GLU	GLU		GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	**asp**	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU
	2	**ile**	VAL	VAL		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		GLN	GLN	GLN	GLN	GLN	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	LEU	LEU	LEU
	5	**val**	**val**	**met**		**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**met**	**val**	**glu**	#	**val**	LEU	LEU	**val**	LEU	**val**	**val**
	6	GLU	GLU	GLU		GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU
	7	SER	SER	SER		SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	#	#	SER	SER	SER	SER	SER
	8	GLY	GLY	GLY		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
	9	GLY	GLY	GLY		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
	10	GLY	GLY	GLY		GLY	GLY	GLY	GLY	**ala**	GLY	GLY	**ala**	GLY	**asx**	**ala**	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
	11	LEU	LEU	**val**		LEU	LEU	LEU	LEU	LEU	**ser**	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
	12	VAL	**ala**	VAL		VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
	13	**lys**	GLN	**lys**		GLN	GLN	**lys**	GLX	**arg**	GLX	GLN			GLN	**lys**	GLN	**lys**	GLN		GLN	GLN	**lys**	GLN	GLN	**lys**
FR1	14	**gly**	PRO	PRO		PRO	PRO	PRO	PRO	PRO	PRO	**lys**	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	**glu**	GLY	GLY	GLY	**glu**	GLY	GLY	GLY	GLY	GLY	GLY
	17	SER	SER	SER		SER	SER	SER	SER	SER	**ala**	SER	SER	SER	**thr**	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	LEU	LEU
	19	ARG	ARG	ARG		**lys**	ARG	ARG	ARG	ARG	ARG	**lys**	ARG	ARG	**lys**	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG
	20	LEU	LEU	LEU		LEU	LEU	LEU	**val**	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	**val**	LEU	LEU	LEU	LEU	LEU	LEU
	21	SER	**ala**	SER		SER	SER	SER	SER	SER		SER	SER	SER	**gly**	SER	SER	SER		SER			SER			
	22	CYS	CYS	CYS		CYS	CYS	CYS	CYS	CYS			CYS	CYS	CYS	CYS		CYS		CYS			CYS			
	23	ALA	ALA			ALA	ALA	ALA	**val**	**glx**	ALA	ALA	ALA	ALA	ALA	**val**	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA
	24	ALA	ALA			ALA	ALA	ALA	ALA	ALA	ALA	ALA	**val**	**thr**	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA
	25	SER	SER			SER	SER	SER		SER	SER	SER	SER	**thr**	SER	SER	SER	SER	SER	SER	SER		SER	SER	SER	SER
	26	GLY	GLY			GLY	GLY	**val**	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY				GLY	GLY
	27	PHE	PHE			PHE	PHE	PHE	PHE	PHE	**ile**	PHE	PHE	PHE	PHE	PHE			PHE	PHE						
	28	**pro**	THR			THR	THR	THR	THR	THR		THR	THR	**ala**	THR	**leu**				THR						
	29	PHE	PHE			PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	**leu**	PHE				PHE						
	30	**gly**	SER			SER	**asx**	**phe**	SER	**ala**		SER	**asx**	SER	**gly**	SER										
	31	**thr**	**thr**			SER	**thr**	**thr**	**asx**	**ala**			**asx**	**gly**	**asx**	**thr**										
	32	**ala**	**thr**			TYR	TYR	TYR	TYR	TYR	**ala**		TYR	**ser**	TYR	TYR										
CDR1	33	**gly**	**phe**				**thr**	**val**	**ser**	**thr**				ALA	**glx**	**gly**										
	34	MET	MET				MET	MET	MET	MET	MET			**val**	MET	MET										
	35	SER	**arg**				**val**	**asx**	**asx**	**lys**						**asx**	**asx**									
	35A		---								---															
	35B		---								---															
	36		TRP																							
	37		VAL								VAL															
	38		**ARG**																							
	39																									
	40										ALA															
FR2	41																									
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	54																									
CDR2	55																									
	56																									
	57																									
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	59																									
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	62																									
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	66				ARG																					
	67				PHE																					
	68				THR																					
	69				ILE																					
	70				SER																					
	71				ARG																					
	72				ASP																					
	73				ASN																					
	74				SER																					
	75				LYS																					
	76				ASN																					
	77				THR																					
	78				LEU																					
	79				TYR																					
	80				LEU																					
	81				GLN																					
FR3	82	MET		MET	MET																					
	82A	ASX		ASX	ASN																					
	82B	**gly**		SER	SER																					
	82C	LEU		LEU	LEU																					
	83	**lys**		ARG	ARG																					
	84	**ile**		**leu**	ALA																					
	85	GLX		GLX	GLU																					
	86	ASX		ASX	ASP																					
	87	THR		THR	THR																					
	88	**gly**		**gly**	ALA																					
	89	VAL		VAL	VAL																					
	90	TYR		TYR	TYR																					
	91	TYR		**phe**	TYR																					
	92	CYS		CYS	CYS																					
	93	**thr**		ALA	ALA																					
	94	**thr**		**thr**	**phe**																					
	95	ASX		LEU	SER																					
	96	GLX		ASX	GLY																					
	97	SER			ALA																					
	98	ALA			ALA																					
	99	THR			---																					
	100	ALA			---																					
	100A	PHE			---																					
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CDR3	100C				---																					
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	100H				---																					
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	100J				ALA																					
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	101				ASP																					
	102				ILE																					
	103				TRP																					
	104				GLY																					
	105				GLN																					
	106				GLY																					
FR4	107				THR																					
	108				MET																					
	109				VAL																					
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		119* H-G2a	120* A-G2b	121* K-G2	122* C-G1 #	123* K-G1 (+&-) #	124 ERI	125 LR1 'CL #	126 WO	127* HEI	128* KN	129* H-G2b	130* C-G2b	131* F-G1 #	132* L. TH.	133 SNM -IGA #	134 HI	135 Ly47 'CL #	136 U266 'CL	137* WAG	138 LR	139 LB W2 'CL #	140 Ly91 'CL #	141 LAMBDA -VH52 'CL
	0	---		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		---	---	---	---	
	1	GLU		GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	**pca**	**gly**	GLU		GLU	GLU	GLU	GLU	
	2	VAL	VAL	VAL	VAL	VAL	**ala**	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL		VAL	VAL	VAL	VAL	
	3		GLN	GLN	GLN	GLN	GLN	**his**	GLN	GLN	GLN	GLN	GLN	GLN		GLN	**leu**	GLN		GLN	**lys**	**his**	GLN	
	4	**LEU**	**LEU**	**LEU**	LEU	LEU	LEU	**LEU**	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	**met**		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	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	**asp**		GLU	GLU	GLU	GLU	
	7	**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	**GLY**	**GLY**	**GLY**	**GLY**	**GLY**	**GLY**	**GLY**	**GLY**	**GLY**	**GLY**	**GLY**	**GLY**	**GLY**	**GLY**	**GLY**	**GLY**	**GLY**		**GLY**	**GLY**	**GLY**	**GLY**	
	10	GLY	GLY	GLY		GLY	GLY	**asp**	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	**val**	**asp**		GLY	GLY	**asp**	GLY	
	11	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	**val**	**ser**	**ser**		LEU	LEU	LEU	**ser**	
	12	VAL	VAL	VAL	VAL	VAL	**ile**	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	**ile**	VAL		VAL	VAL		**ile**	
	13	GLN	GLN	GLN	GLN	GLN	GLN	**lys**	GLN	GLN	GLN	GLN	GLN	GLN	GLX	**lys**		**arg**		GLN	**glu**	**lys**	GLN	
FR1	14	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	**ser**		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	**pro**	
	16	GLY	GLY		GLY		**arg**	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	**ser**		GLY	**glu**	GLY	GLY	
	17	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER		SER	SER	SER	SER	**phe**		SER	SER	**phe**	**arg**	
	18	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU		LEU	LEU	LEU	**ser**	
	19	ARG	ARG		ARG		ARG	**lys**	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG		ARG			ARG	**lys**	**gln**	
	20	LEU	LEU	LEU	LEU	#	**ile**	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU			LEU	LEU	**arg**	
	21						SER	SER								SER		SER				SER	**pro**	
	22						CYS	CYS								CYS	CYS	CYS			CYS	CYS	**ser**	
	23	ALA	ALA			ALA	**thr**	**glu**										**glu**				**glu**	**tyr**	
	24	ALA	ALA	ALA	ALA	ALA	ALA	**val**									ALA	**thr**					**thr**	
	25	SER		SER	SER	SER		SER									SER	SER				SER	**cys**	
	26	GLY		GLY	GLY	GLY	GLY	**glu**									GLY	---				**asp**	**ser**	
	27						PHE	PHE									PHE	---				PHE	**gly**	
	28																	---					**ser**	
	29							PHE									**ile**	---					**thr**	
	30																**gly**	---					SER	
	31																	---					**gly**	
	32																**phe**	---					**asp**	
CDR1	33																	---					**his**	
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FR2	42																	---					---	
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CDR2	55																	---					---	
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	64																	---	**gln**				---	
	65																	---	GLY				---	
	66																	---	ARG				---	
	67																	---	**val**				---	
	68																	---	THR				---	
	69																	---	**met**				---	
	70																	---	**thr**				---	
	71																	---	ARG				---	
	72																	---	ASP				---	
	73																	---	**ala**				---	
	74																	---	SER				---	
	75																	---	**phe**				---	
	76																	---	**ser**				---	
	77																	---	THR				---	
	78																	---	**ala**				---	
	79																	---	TYR				---	TYR
FR3	80																	---	**met**				---	LEU
	81																	---	**asp**				---	GLN
	82																	---	**leu**				---	MET
	82A																	---	**arg**				---	ASN
	82B																	---	SER				---	SER
	82C																	---	LEU				---	LEU
	83																	---	ARG				---	ARG
	84																	---	**ser**				---	ALA
	85																	---	**asp**				---	GLU
	86																	---	ASP				---	ASP
	87																	---	**ser**				---	**met**
	88																	---	ALA				---	ALA
	89																	---	VAL				---	VAL
	90																	---	**phe**				---	TYR
	91																	---	TYR				---	TYR
	92																	---	CYS				---	CYS
	93																	---	ALA				---	ALA
	94																	---	LYS				---	**thr**
	95																	---	SER				---	---
	96																	---	ASP				---	---
	97																	---	PRO				---	---
	98																	---	PHE				---	---
	99																	---	TRP				---	---
	100																	---	SER				---	---
	100A																	---	ASP				---	---
	100B																	---	TYR				---	---
CDR3	100C																	---	TYR				---	---
	100D																	---	ASN				---	---
	100E																	---	PHE				---	---
	100F																	---	ASP				---	---
	100G																	---	TYR				---	---
	100H																	---	SER				---	---
	100I																	---	TYR				---	---
	100J																	---	THR				---	---
	100K																	---	LEU				---	---
	101																	---	ASP				---	---
	102																	---	VAL				---	---
	103																	---	TRP				---	---
	104																	---	GLY				---	---
	105																	---	GLN				---	---
	106																	---	GLY				---	---
FR4	107																	---	THR				---	---
	108																	---	THR				---	---
	109																	---	VAL				---	---
	110																	---	THR				---	---
	111																	---	VAL				---	---

HUMAN HEAVY CHAINS SUBGROUP III (cont'd)

		142* R.K.	143* GOE II	144 PAL	145 POD	146 DB 'CL #	147 LBW 14 'CL #	148 LAMBDA -VH32 'CL	149 HA	150 GIT	151 SEI	152 KOO	153 BER	154 HIN	155 KNI	156 SHE	157 LIV	158 PUT	159 HER	160 MOY	161 PIT	162 TOL	163 CRI	164 GLU	165 SMM -IGG #	166 PAC	167 THA	168 KAR	169 PAR
	0	---	---	---	---	---	---		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	1	GLU	GLU	GLU	GLU	GLU	GLU		GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	**pca**	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	VAL	**leu**	VAL	VAL	VAL
	3	GLN	GLN	GLN	GLN	**his**	**his**		GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	**lys**	GLN
	4	LEU	LEU			LEU	LEU		LEU		LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU		LEU	LEU	
	5	**val**	**val**	LEU	**val**	**val**	**val**		**val**	**val**	LEU	**val**	**val**	**vai**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**val**	**glx**	**val**	**val**	**val**
	6	GLU	GLU			GLU	GLU		GLU		GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU		**gln**	GLU		
	7	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	GLY	GLY	GLY	GLY	GLY	GLY		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
	10	GLY	GLY	GLY	GLY	**asp**	**val**		GLY	**ala**	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
	11	**val**	LEU	LEU	LEU	LEU	**ser**		LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	**val**	LEU	LEU	LEU	**val**
	12	VAL	VAL	VAL	VAL		VAL		VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	**ala**
	13	**arg**	**leu**	GLN	GLN	**lys**	**lys**		**gly**	**lys**															**lys**	**lys**			**arg**
FR1	14	PRO	PRO	PRO	PRO		PRO		PRO	PRO															PRO	**lys**			PRO
FR1	15	GLY	GLY			GLY	GLY		GLY																GLY				
FR1	16	GLY	GLY	GLY	GLY					GLY																GLY			GLY
FR1	17	SER	SER			SER	SER																						
FR1	18	LEU		LEU	LEU	LEU	LEU			LEU																LEU			LEU
FR1	19	ARG		ARG	ARG	**lys**	**lys**			ARG																**thr**			ARG
FR1	20	**val**		LEU	LEU	LEU	LEU			LEU																LEU			LEU
FR1	21					SER	SER																						
FR1	22					CYS	CYS																						
FR1	23				ALA					ALA																ALA			**val**
FR1	24			ALA	ALA		**val**			ALA																ALA			**gly**
FR1	25					SER	SER																						
FR1	26					**ala**	**asp**																						
FR1	27																												
FR1	28																												
FR1	29						**ser**																						
FR1	30																												
CDR1	31																												
CDR1	32																												
CDR1	33																												
CDR1	34																												
CDR1	35																												
CDR1	35A																												
CDR1	35B																												
FR2	36																												
FR2	37																												
FR2	38																												
FR2	39																												
FR2	40																												
FR2	41																												
FR2	42																												
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FR2	45																												
FR2	46																												
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FR2	49																												
CDR2	50																												
CDR2	51																												
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FR3	81																												
FR3	82																												
FR3	82A							ASN																					
FR3	82B							SER																					
FR3	82C							LEU																					
FR3	83							ARG																					
FR3	84							ALA																					
FR3	85							GLU																					
FR3	86							ASP																					
FR3	87							THR																					
FR3	88							ALA																					
FR3	89							VAL																					
FR3	90							TYR																					
FR3	91							TYR																					
FR3	92							CYS																					
FR3	93							**val**																					
FR3	94							LYS																					
CDR3	95							---																					
CDR3	96							---																					
CDR3	97							---																					
CDR3	98							---																					
CDR3	99							---																					
CDR3	100							---																					
CDR3	100A							---																					
CDR3	100B							---																					
CDR3	100C							---																					
CDR3	100D							---																					
CDR3	100E							---																					
CDR3	100F							---																					
CDR3	100G							---																					
CDR3	100H							---																					
CDR3	100I							---																					
CDR3	100J							---																					
CDR3	100K							---																					
CDR3	101							---																					
CDR3	102							---																					
FR4	103							---																					
FR4	104							---																					
FR4	105							---																					
FR4	106							---																					
FR4	107							---																					
FR4	108							---																					
FR4	109							---																					
FR4	110							---																					

HUMAN HEAVY CHAINS SUBGROUP III (cont'd)

		170 PAV	171 NA	172 SLA	173 LES	174 ANT	175 GRA	176 ARP	177 HOW	178 CRA #	179 GUI	180 JLN 'CL #	181 BUS	182 RE	183 70P1 'CL	184 DOS	185 BAL	# OF SEQUENCES	# OF AMINO ACIDS	OCCURRENCES OF MOST COMMON AMINO ACID	VARIABILITY
	0	---	---	---	---	---	---	---	---	---	---		---	---		---	---				
	1	GLU	GLU	GLU	**asp**	GLU		**leu**	GLU	**gly**	**gly**		**pca**	**pca**		**pca**	**pca**	172	7	136 (GLU)	8.9
	2	VAL	VAL	VAL	**ile**	VAL	VAL	VAL	VAL	**phe**	VAL		**ser**	**ser**		**ser**	**ser**	174	7	158 (VAL)	7.7
	3	GLN	GLN	**glu**	GLN	**his**		**arg**	GLN	#	GLN		**val**	**ala**		**val**	**val**	172	8	148 (GLN), 147 (GLN)	9.3, 9.4
	4	LEU	LEU	LEU	LEU				LEU	**asp**	LEU		LEU	LEU		**ala**	**ala**	168	5	163 (LEU)	5.2
	5	**ala**	**val**	**val**	**val**	**val**	**val**	**val**		**asn**			**asx**			**asx**	**glx**	172	6,8	129 (VAL)	8., 11.
	6	GLU	GLU	**gln**	GLU					**arg**			**gly**					164	5	149 (GLU), 146 (GLU)	5.5, 5.6
	7	SER	SER	SER	SER					**thr**								158	3	155 (SER)	3.1
	8	GLY	GLY	GLY	GLY					**thr**								163	2	162 (GLY)	2.
	9	GLY	GLY	GLY	GLY	GLY	GLY	**ala**		**glu**								171	3	169 (GLY)	3.
	10	GLY	**ala**	GLY	GLY	**asp**	GLY	**glx**		---								168	5,6	131 (GLY)	6.4, 7.7
	11		LEU	LEU	LEU	LEU		**val**		---								167	4	131 (LEU)	5.1
	12			VAL	VAL	VAL				---								163	3	154 (VAL)	3.2
	13					GLN		GLN		---								144	7	106 (GLN), 101 (GLN)	9.5, 10.
FR1	14					PRO	PRO	PRO		---								148	5	142 (PRO)	5.2
	15									---								141	3	139 (GLY)	3.
	16						GLY	**ser**		---								143	5	116 (GLY)	6.2
	17									---								136	5	131 (SER)	5.2
	18							**val**		---								145	5	141 (LEU)	5.1
	19									---								140	4	124 (ARG)	4.5
	20							**val**		---								143	4	131 (LEU)	4.4
	21									---								116	5	111 (SER)	5.2
	22									---								117	2	116 (CYS)	2.
	23							ALA		---								128	8,9	107 (ALA)	9.6, 11.
	24							ALA		---								132	5	116 (ALA)	5.7
	25									---								124	3	122 (SER)	3.
	26									---								124	6	117 (GLY)	6.4
	27									---								112	4	109 (PHE)	4.1
	28									---								104	9	75 (THR)	12.
	29									---								108	6	97 (PHE)	6.7
	30									---								103	9,10	90 (SER)	10., 11.
	31									---								100	11	35 (SER)	31.
CDR1	32									---								103	10	55 (TYR)	19.
	33									---								98	13	35 (ALA)	36.
	34									---								101	7	85 (MET)	8.3
	35									---								97	12	39 (SER)	30.
	35A									---											
	35B									---											
	36									---								91	1	91 (TRP)	1.
	37									---								92	3	89 (VAL)	3.1
	38									---								90	2	89 (ARG)	2.
	39									---								90	2	89 (GLN)	2.
	40									---								91	7	84 (ALA)	7.6
FR2	41									---								87	4	75 (PRO)	4.6
	42									---								87	2	86 (GLY)	2.
	43									---								87	3	85 (LYS)	3.1
	44									---								87	3	77 (GLY)	3.4
	45									---								87	2	86 (LEU)	2.
	46									---								86	3	78 (GLU), 73 (GLU)	3.3, 3.5
	47									---								85	1	85 (TRP)	1.
	48									---								86	2	84 (VAL)	2.
	49									---								86	7	40 (SER)	15.
	50									---								86	14	21 (VAL)	57.
	51									---								86	7	73 (ILE)	8.2
	52									---								85	12,13	38 (SER)	27., 29.
	52A									---								77	13	22 (GLY)	
	52B									---								20	2	19 (LYS)	
	52C									---								20	5	8 (THR)	
	53									---								85	12	31 (ASP), 26 (ASP)	33., 39.
	54									---								84	9	56 (GLY)	13.
CDR2	55									---								83	10	37 (GLY)	22.
	56									---								83	13	20 (SER)	54.
	57									---								85	9	46 (THR)	17.
	58									---								84	14	46 (TYR)	26.
	59									---								85	3	79 (TYR)	3.2
	60									---								85	7	62 (ALA)	9.6
	61									---								85	8	51 (ASP), 48 (ASP)	13., 14.
	62									---								86	6	71 (SER)	7.3
	63									---								86	5	82 (VAL)	5.2
	64									---								85	5	70 (LYS)	6.1
	65									---								85	3	83 (GLY)	3.1
	66									---								85	3	83 (ARG)	3.1
	67									---								86	3	84 (PHE)	3.1
	68									---								86	5	76 (THR)	5.7
	69									---								86	3	84 (ILE)	3.1
	70									---								86	3	84 (SER)	3.1
	71									---								86	3	84 (ARG)	3.1
	72									---								85	4	71 (ASP), 69 (ASP)	4.8, 4.9
	73									---								84	4	50 (ASN), 48 (ASN)	6.7, 7.
	74									---								84	2	75 (SER)	2.2
	75									---								85	6	77 (LYS)	6.6
	76									---								85	5,6	71 (ASN), 67 (ASN)	6., 7.6
	77									---								85	6	70 (THR)	7.3
	78									---								84	8	68 (LEU)	9.9
	79									---								85	4	74 (TYR)	4.6
	80									---								85	3	81 (LEU)	3.1
FR3	81									---								85	6	77 (GLN), 75 (GLN)	6.6, 6.8
	82									---								92	2	89 (MET)	2.1
	82A									---								93	8	71 (ASN), 68 (ASN)	
	82B									---								93	7	76 (SER)	
	82C									---								93	4	89 (LEU)	
	83									---								93	6	71 (ARG)	7.9
	84									---								94	8	55 (ALA)	14.
	85									---								94	4,5	81 (GLU), 76 (GLU)	4.6, 6.2
	86									---								94	3	91 (ASP), 85 (ASP)	3.1, 3.3
	87									---								94	5	88 (THR)	5.3
	88									---								94	3	89 (ALA)	3.2
	89									---								94	7	77 (VAL)	8.5
	90									---		TYR						95	3	93 (TYR)	3.1
	91									---		TYR						95	3	92 (TYR)	3.1
	92									---		CYS						94	1	94 (CYS)	1.
	93									---		thr						94	4	70 (ALA)	5.4
	94									---		pro			cys			95	11	31 (ARG)	34.
	95									---		PRO			GLU			79	17	15 (+), 15 (GLY)	90.
	96									---		PRO			ARG			80	18,19	14 (ARG)	100., 110.
	97									---		PRO			PRO			77	18	12 (+)	120.
	98	SER								---		PRO			GLY			76	18	11 (GLY)	120.
	99	ASP								---		GLU			ASP			74	14	11 (+)	94.
	100	TYR								---		VAL			GLY			73	16	14 (SER)	83.
	100A	HIS								---		GLU			SER			64	17	15 (LEU)	
	100B	TYR								---		SER			TYR			51	12	13 (SER)	
CDR3	100C	TYR								---		LEU			TYR			42	13	9 (GLY)	
	100D	ALA								---		---			TYR			32	10	6 (+)	
	100E	---								---		---			TYR			28	8	11 (TYR)	
	100F	---								---		---			GLY			15	9	5 (TYR)	
	100G	---								---		---			MET			13	6	7 (TYR)	
	100H	---								---		---			---			12	5	6 (TYR)	
	100I	---								---		---			---			15	7	5 (HIS)	
	100J	---								---		---			---			24	8	7 (TYR)	
	100K	MET										---			---			29	4	21 (PHE)	
	101	VAL								---		ARG			ASP			70	8	50 (ASP), 48 (ASP)	11., 12.
	102	THR								---		SER			VAL			73	10	29 (TYR)	25.
	103	VAL								---		TRP			TRP			76	4	73 (TRP)	4.2
	104	SER								---		GLY			GLY			76	2	75 (GLY)	2.
	105	SER								---		ARG			GLN			76	4,5	61 (GLN), 59 (GLN)	5., 6.4
	106	ALA								---		GLY			GLY			77	2	76 (GLY)	2.
FR4	107	SER								---		THR			THR			76	4	73 (THR)	4.2
	108	THR								---		LEU			THR			76	6	59 (LEU)	7.7
	109	LYS								---		VAL			VAL			75	2	74 (VAL)	2.
	110	GLY								---		THR			THR			75	3	72 (THR)	3.1
	111									---					VAL			60	2	59 (VAL)	2.

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) **NEI:** COLD AGGLUTININ WITH ANTI-GD (MEMBRANE-GLYCOLIPID-DEPENDENT) ACTIVITY
128) **KN:** COLD AGGLUTININ WITH ANTI-GD (MEMBRANE-GLYCOLIPID-DEPENDENT) ACTIVITY
129) **H-G2b:** ANTI-Haemophilus influenzae TYPE b CAPSULAR POLYSACCHARIDE
130) **C-G2b:** ANTI-Haemophilus influenzae TYPE b CAPSULAR POLYSACCHARIDE
131) **F-G1:** ANTI-Haemophilus influenzae TYPE b CAPSULAR POLYSACCHARIDE
132) **L.TH.:** COLD AGGLUTININ WITH ANTI-PR2 ACTIVITY (RBC MEMBRANE ANTIGEN ON HUMAN, RAT AND GUINEA PIG ERYTHROCYTES INACTIVATED BY PROTEOLYTIC ENZYMES AND NEURAMINIDASE)
137) **WAG:** ANTI-DINITROPHENYL
142) **R.K.:** COLD AGGLUTININ WITH ANTI-PR1H ACTIVITY (RBC MEMBRANE ANTIGEN ON HUMAN ERYTHROCYTES INACTIVATED BY PROTEOLYTIC ENZYMES AND NEURAMINIDASE)
143) **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) **CAM':** IGM-KAPPA
41) **HN.14'CL:** IGM-
42) **RF-TS2'CL:** IGM-KAPPA
43) **3D6'CL:** IGG1-KAPPA
45) **POM:** IGM-KAPPA
46) **RF-SJ1'CL:** IGM-LAMBDA
47) **WEA:** IGM-KAPPA
48) **4B4'CL:** IGM-
51) **LAY:** IGM-KAPPA
52) **BUR:** IGA1-LAMBDA
53) **KOL:** IGG1-LAMBDA
54) **TEI:** IGG1-KAPPA
56) **HIL:** IGG1-LAMBDA
57) **TRO:** IGA1-LAMBDA
58) **WAS:** IGG1-
59) **TUR:** IGA1-KAPPA
60) **NIE:** IGG1-
61) **GAL:** IGM-KAPPA
62) **DOB:** IGG1 GM(1,-17)-KAPPA KM(3)
63) **VH10.7'CL:** IGD-

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

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

REFERENCE: HUMAN HEAVY CHAINS SUBGROUP III

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) **HF2-1/17:** ATKINSON,P.M.,LAMPMAN,G.W.,FURIE,B.C.,NAPARSTEK,Y.,SCHWARTZ,R.S.,STOLLAR,B.D. & FURIE,B. (1985) J.CLIN.INVEST.,75,1138-1143. (CHECKED BY AUTHOR 08/21/85); LAMPMAN,G.W.,FURIE,B.,SCHWARTZ,R.S.,STOLLAR,B.D. & FURIE,B.C. (1989) BLOOD,74,262-269.
8) **vh26c'CL:** CHEN,P.P.,LIU,M.-F.,SINHA,S. & CARSON,D.A. (1988) ARTH.RHEUM.,31,1429-1431.
9) **LAMBDA-VH26'CL:** RABBITTS,T.H.,BENTLEY,D.L.,DUNNICK,W.,FORSTER,A.,MATTHYSSENS,G. & MILSTEIN,C. (1980) COLD SPRING HARB.SYMP.QUANTI.BIOL.,45,867-878; MATTHYSSENS,G. & RABBITTS,T.H. (1980) PROC.NAT.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) **Vh38C1.10'CL:** MEEKER,T.C.,GRIMALDI,J.,O'ROURKE,R.,LOEB,J.JULIUSSON,G. & EINHORN,S. (1988) J.IMMOL.,141,3994-3998.

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

16) **Vh38C1.8'CL:** MEEKER,T.C.,GRIMALDI,J.,O'ROURKE,R.,LOEB,J.JULIUSSON,G. & EINHORN,S. (1988) J.IMMOL.,141,3994-3998.
17) **Vh38C1.9'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) **GF4/1.1'CL:** GILLIES,S.D.,DORAI,H.,WESOLOWSKI,J.,MAJEAU,G.,YOUNG,D.,BOYD,J.,GARDNER,J. & JAMES,K. (1989) BIO/TECH.,7, 799-804.
21) **Vh38C1.4'CL:** MEEKER,T.C.,GRIMALDI,J.,O'ROURKE,R.,LOEB,J.JULIUSSON,G. & EINHORN,S. (1988) J.IMMOL.,141,3994-3998.
22) **Vh38C1.5'CL:** MEEKER,T.C.,GRIMALDI,J.,O'ROURKE,R.,LOEB,J.JULIUSSON,G. & EINHORN,S. (1988) J.IMMOL.,141,3994-3998.
23) **Ei11'CL:** RECHAVI,G.,BIENZ,B.,RAM,D.,BEN-NERIAH,Y.,COHEN,J.B.,ZAKUT,R. & GIVOL,D. (1982) PROC.NAT.ACAD.SCI.USA,79, 4405-4409.
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) **XIM46H'CL:** CAIRNS,E.,KWONG,P.C.,MISENER,V.,IP,P.,BELL,D.A. & SIMINOVITCH,K.A. (1989) J.IMMUNOL.,143,685-691.
30) **1-9III'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.
32) **22-2B'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.
33) **TIL:** WANG,A.C.,GERGELY,J. & FUDENBERG,H.H. (1973) BIOCHEMISTRY,12,528-534. (CHECKED BY AUTHOR); WANG,A.C. & FUDENBERG, H.H. (1975) ARCH.BIOCHEM.BIOPHYS.,168,657-664; WANG,A.C.,WANG,I.T. & FUDENBERG,H.H. (1977) J.BIOL.CHEM.,252, 7192-7199. (CHECKED BY AUTHOR 09/23/77)
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.
37) **13-2'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.
38) **BRO'IGM:** CAPRA,J.D. & HOPPER,J.E. (1976) IMMUNOCHEMISTRY,13,995-999; HOPPER,J.E.,NOYES,C.,HEINRIKSON,R. & KESSEL,J.W. (1976) J.IMMUNOL.,116,743-746. (CHECKED BY AUTHOR 08/01/79)
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.W. & PUTNAM,F.W. (1980) PROC.NAT.ACAD.SCI.USA,77,3239-3243. (CHECKED BY AUTHOR 05/01/80)
41) **HN.14'CL:** DESAI,R.,SPATZ,L.,MATSUDA,T.,ILYAS,A.A.,BERMAN,J.E.,ALT,F.W.,KABAT,E.A. & LATOV,N. (1990) J.NEUROIMMUNOL.,26, 35-41. (CHECKED BY AUTHORS WHO CORRECTED RESIDUES 44 TO 47 AS SHOWN, SEE DESAI,R.,SPATZ,L.,MATSUDA,T.,ILYAS, A.A.,BERMAN,J.E.,ALT,F.W.,KABAT,E.A. & LATOV,N. (1990) J.NEUROIMMUNOL.,30,245.)
42) **RF-TS2'CL:** PASCUAL,V.,RANDEN,I.,THOMPSON,K.,SIOUD,M.FORRE,O.,NATVIG,J. & CAPRA,J.D. (1990) J.CLIN.INVEST.,86,1320-1328.
43) **3D6'CL:** FELGENHAUER,M.,KOHL,J. & RUKER,F. (1990) NUCL.ACIDS RES., 18,4927.
44) **1-91'CL:** BERMAN,J.E.,MELLIS,S.J.,POLLOCK,R.,SMITH,C.L.,SUH,H.,HEINKE,B.,KOWAL,C.,SURTI,U.,CHESS,L.,CANTOR,C.R & ALT, F.W. (1988) EMBO J.,7,727-738.
45) **POM:** CAPRA,J.D. & KEHOE,J.M. (1974) PROC.NAT.ACAD.SCI.USA,71,4032-4036. (CHECKED BY AUTHOR WHO CORRECTED RESIDUES 85,86 AS GIVEN IN TABLE)
46) **RF-SJ1'CL:** PASCUAL,V.,RANDEN,I.,THOMPSON,K.,SIOUD,M.FORRE,O.,NATVIG,J. & CAPRA,J.D. (1990) J.CLIN.INVEST.,86,1320-1328.
47) **WEA:** GONI,F. & FRANGIONE,B. (1983) PROC.NAT.ACAD.SCI.USA,80,4837-4841. (CHECKED BY AUTHOR 03/23/84)
48) **4B4'CL:** SANZ,I.,DANG,H.,TAKEI,M.,TALAL,N. & CAPRA,J.D. (1989) J.IMMUNOL.,142,883-887.
49) **M25'CL:** SCHROEDER,H.W.,JR. & WANG,J.Y. (1990) PROC.NATL.ACAD.SCI.USA,87,6146-6150.
50) **9-1'CL:** BERMAN,J.E.,MELLIS,S.J.,POLLOCK,R.,SMITH,C.L.,SUH,H.,HEINKE,B.,KOWAL,C.,SURTI,U.,CHESS,L.,CANTOR,C.R & ALT,F.W. (1988) EMBO J.,7,727-738.
51) **LAY:** CAPRA,J.D. & KEHOE,J.M. (1974) PROC.NAT.ACAD.SCI.USA,71,4032-4036. (CHECKED BY AUTHOR WHO CORRECTED RESIDUE 85 AS GIVEN IN TABLE)
52) **BUR:** LIU,V.Y.S.,LOW,T.L.K.,INFANTE,A. & PUTNAM,F.W. (1976) SCIENCE,193,1017-1020. (CHECKED BY AUTHOR 06/15/83)
53) **KOL:** SCHMIDT,W.E.,JUNG,H-.D.,PALM,W. & HILSCHMANN,N. (1983) Z.PHYSIOL.CHEM.,364,713-747.
54) **TEI:** CAPRA,J.D. & KEHOE,J.M. (1974) PROC.NAT.ACAD.SCI.USA,71,845-848. (CHECKED BY AUTHOR WHO CORRECTED RESIDUES 85,86 AS GIVEN IN TABLE)
55) **12-2'CL:** BERMAN,J.E.,MELLIS,S.J.,POLLOCK,R.,SMITH,C.L.,SUH,H.,HEINKE,B.,KOWAL,C.,SURTI,U.,CHESS,L.,CANTOR,C.R & ALT, F.W. (1988) EMBO J.,7,727-738.
56) **HIL:** CHIU,Y.Y.H.,LOPEZ DE CASTRO,J.A. & POLJAK,R.J. (1979) BIOCHEMISTRY,18,553-560. (CHECKED BY AUTHOR 07/16/79)
57) **TRO:** KRATZIN,H.,ALTEVOGT,P.,RUBAN,E.,KORTT,A.,STAROSCIK,K. & HILSCHMANN,N. (1975) Z.PHYSIOL.CHEM.,356,1337-1342; KRATZIN,H.,ALTEVOGT,P.,KORTT,A.,RUBAN,E. & HILSCHMANN,N. (1978) Z.PHYSIOL.CHEM.,359,1717-1745.
58) **WAS:** CAPRA,J.D. & KEHOE,J.M. (1974) PROC.NAT.ACAD.SCI.USA,71,845-848. (CHECKED BY AUTHOR WHO CORRECTED RESIDUES 85,86 AS GIVEN IN TABLE)
59) **TUR:** CAPRA,J.D. & KEHOE,J.M. (1974) PROC.NAT.ACAD.SCI.USA,71,845-848. (CHECKED BY AUTHOR WHO CORRECTED RESIDUES 85,86 AS GIVEN IN TABLE)
60) **NIE:** PONSTINGL,H.,SCHWARZ,J.,REICHEL,W. & HILSCHMANN,N. (1970) Z.PHYSIOL.CHEM.,351,1591-1594. (CHECKED BY AUTHOR WHO CORRECTED RESIDUES 85,86 AS GIVEN IN TABLE); PONSTINGL,H. & HILSCHMANN,N. (1976) Z.PHYSIOL.CHEM.,357,1571-1604.
61) **GAL:** WATANABE,S.,BARNIKOL,H.U.,HORN,J.,BERTRAM,J. & HILSCHMANN,N. (1973) Z.PHYSIOL.CHEM.,354,1505-1509. (CHECKED BY AUTHOR)
62) **DOB:** STEINER,L.A.,GARCIA-PARDO,A. & MARGOLIES,M.N. (1979) BIOCHEMISTRY,18,4068-4080. (CHECKED BY AUTHOR 07/20/79)
63) **VH10.7'CL:** WHITE,M.B.,WORD,C.J.,HUMPHRIES,C.G.,BLATTNER,F.R. & TUCKER,P.W. (1990) MOL.CELL.BIOL.,10,3690-3699.
64) **ZAP:** CAPRA,J.D. & KEHOE,J.M. (1974) PROC.NAT.ACAD.SCI.USA,71,845-848. (CHECKED BY AUTHOR WHO CORRECTED RESIDUES 85,86 AS GIVEN IN TABLE)
65) **JON:** CAPRA,J.D. & KEHOE,J.M. (1974) PROC.NAT.ACAD.SCI.USA,71,845-848. (CHECKED BY AUTHOR WHO CORRECTED RESIDUES 85,86 AS GIVEN IN TABLE)
66) **GA:** FLORENT,G.,LEHMAN,D. & PUTNAM,F.W. (1974) BIOCHEMISTRY,13,2482-2498. (CHECKED BY AUTHOR 06/15/83)
67) **GRA':** CAPRA,J.D. (1977) IN ANTIBODIES IN HUMAN DIAGNOSIS AND THERAPY,RAVEN PRESS,NEW YORK,87-102. (CHECKED BY AUTHOR 03/18/81)
68) **K6H6'CL:** KON,S.,LEVY,S. & LEVY,R. (1987) PROC.NATL.ACAD.SCI.USA,84,5053-5057.
69) **K4B8'CL:** KON,S.,LEVY,S. & LEVY,R. (1987) PROC.NATL.ACAD.SCI.USA,84,5053-5057.
70) **K5B8'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.
72) **K5G5'CL:** KON,S.,LEVY,S. & LEVY,R. (1987) PROC.NATL.ACAD.SCI.USA,84,5053-5057.
73) **K6F5'CL:** KON,S.,LEVY,S. & LEVY,R. (1987) PROC.NATL.ACAD.SCI.USA,84,5053-5057.
74) **1B11'CL:** CLEARY,M.L.,MEEKER,T.C.,LEVY,S.,LEE,E.,TRELA,M.,SKLAR,J. & LEVY,R. (1986) CELL,44,97-106. (CHECKED BY AUTHOR 10/31/86)
75) **1H1'CL:** CLEARY,M.L.,MEEKER,T.C.,LEVY,S.,LEE,E.,TRELA,M.,SKLAR,J. & LEVY,R. (1986) CELL,44,97-106. (CHECKED BY AUTHOR 10/31/86)
76) **333'CL:** CLEARY,M.L.,MEEKER,T.C.,LEVY,S.,LEE,E.,TRELA,M.,SKLAR,J. & LEVY,R. (1986) CELL,44,97-106. (CHECKED BY AUTHOR 10/31/86)
77) **112'CL:** CLEARY,M.L.,MEEKER,T.C.,LEVY,S.,LEE,E.,TRELA,M.,SKLAR,J. & LEVY,R. (1986) CELL,44,97-106. (CHECKED BY AUTHOR 10/31/86)
78) **126'CL:** CLEARY,M.L.,MEEKER,T.C.,LEVY,S.,LEE,E.,TRELA,M.,SKLAR,J. & LEVY,R. (1986) CELL,44,97-106. (CHECKED BY AUTHOR 10/31/86)
79) **115'CL:** CLEARY,M.L.,MEEKER,T.C.,LEVY,S.,LEE,E.,TRELA,M.,SKLAR,J. & LEVY,R. (1986) CELL,44,97-106. (CHECKED BY AUTHOR 10/31/86)
80) **2C12'CL:** CLEARY,M.L.,MEEKER,T.C.,LEVY,S.,LEE,E.,TRELA,M.,SKLAR,J. & LEVY,R. (1986) CELL,44,97-106. (CHECKED BY AUTHOR 10/31/86)
81) **2A12'CL:** CLEARY,M.L.,MEEKER,T.C.,LEVY,S.,LEE,E.,TRELA,M.,SKLAR,J. & LEVY,R. (1986) CELL,44,97-106. (CHECKED BY AUTHOR 10/31/86)
82) **20P1'CL:** SCHROEDER,H.W.,JR.,HILLSON,J.L. & PERLMUTTER,R.M. (1987) SCIENCE,238,791-793.
83) **FR:** RIESEN,W.,RUDIKOFF,S.,ORIOL,R. & POTTER,M. (1975) BIOCHEMISTRY,14,1052-1057; RIESEN,W.F.,BRAUN,D.G. & JATON,J.C. (1976) PROC.NAT.ACAD.SCI.USA,73,2096-2100. (CHECKED BY AUTHOR WHO PROVIDED ADDITIONAL RESIDUES FOR POSITIONS 39 TO 51 AND 82 TO 94. 12/05/77)
84) **v65-2'CL:** MATSUDA,F.,SHIN,E.K.,HIRABAYASHI,Y.,NAGAOKA,H.,YOSHIDA,M.C.,ZONG,S.Q. & HONJO,T. (1990) EMBO J.,9,2501-2506.
85) **MU:** SHINODA,T. (1973) BIOCHEM.BIOPHYS.RES.COMMUN.,52,1246-1251. (CHECKED BY AUTHOR WHO CORRECTED RESIDUE 46 AS GIVEN IN TABLE)
86) **DAU:** BENNETT,J.C. (1968) BIOCHEMISTRY,7,3340-3344. (CHECKED BY AUTHOR 11/01/77); FLORENT,G.,LEHMAN,D. & PUTNAM,F.W. (1974) BIOCHEMISTRY,13,2482-2498. (CHECKED BY AUTHOR 02/15/82)
87) **HF2-1/13B:** ATKINSON,P.M.,LAMPMAN,G.W.,FURIE,B.C.,NAPARSTEK,Y.,SCHWARTZ,R.S.,STOLLAR,B.D. & FURIE,B. (1985) J.CLIN.INVEST.,75,1138-1143. (CHECKED BY AUTHOR 08/21/85)
88) **HF2-18/2:** ATKINSON,P.M.,LAMPMAN,G.W.,FURIE,B.C.,NAPARSTEK,Y.,SCHWARTZ,R.S.,STOLLAR,B.D. & FURIE,B. (1985) J.CLIN.INVEST.,75,1138-1143. (CHECKED BY AUTHOR 08/21/85)
89) **KEA:** WANG,A.C. & FUDENBERG,H.H. (1975) IMMUNOL.COMMUN.,4,483-497. (CHECKED BY AUTHOR 09/23/77)
90) **GR':** FAIR,D.S.,SLEDGE,C.,KRUEGER,R.G.,MANN,K.G. & HOOD,L.E. (1975) BIOCHEMISTRY,14,5561-5568.
91) **VIN:** PINK,J.R.L. & MILSTEIN,C. (1969) PROC. 5TH FEBS SYMP.,15,177-182. (CHECKED BY AUTHOR)
92) **HF3-16/6:** 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)

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

93) **GO:** WANG,A.C.,FUDENBERG,H.H. & CREYSSEL,R. (1974) EUR.J.IMMUNOL.,4,446-448. (CHECKED BY AUTHOR)
94) **FOR:** WANG,A.C.,FUDENBERG,H.H. & PINK,J.R.L. (1971) PROC.NAT.ACAD.SCI.USA,68,1143-1147. (CHECKED BY AUTHOR); WANG,A.C. & FUDENBERG,H.H. (1975) ARCH.BIOCHEM.BIOPHYS.,168,657-664. (CHECKED BY AUTHOR 09/23/77)
95) **BEN(III):** CAPRA,J.D. (1971) NATURE NEW BIOLOGY,230,61-63. (CHECKED BY AUTHOR)
96) **PS (SHA):** TERRY,W.D.,OGAWA,M. & KOCHWA,S. (1970) J.IMMUNOL.,105,783-785; KOCHWA,S.,TERRY,W.D.,CAPRA,J.D. & YANG,N.Y. (1971) ANN.N.Y.ACAD.SCI.,190,49-70. (CHECKED BY AUTHOR WHO PROVIDED ADDITIONAL RESIDUES TO THOSE PUBLISHED)
97) **13P1'CL:** SCHROEDER,H.W.,JR.,HILLSON,J.L. & PERLMUTTER,R.M. (1987) SCIENCE,238,791-793.
98) **H11'CL:** POLLOK,B.A.,ANKER,R.,ELDRIDGE,P.,HENDERSHOT,L. & LEVITT,D. (1987) PROC.NATL.ACAD.SCI.USA,84,9199-9203.
99) **NAT:** WANG,A.C.,FUDENBERG,H.H. & PINK,J.R.L. (1971) PROC.NAT.ACAD.SCI.USA,68,1143-1147. (CHECKED BY AUTHOR)
100) **LOW:** WANG,A.C.,FUDENBERG,H.H. & PINK,J.R.L. (1971) PROC.NAT.ACAD.SCI.USA,68,1143-1147. (CHECKED BY AUTHOR)
101) **JOR:** WANG,A.C.,FUDENBERG,H.H. & PINK,J.R.L. (1971) PROC.NAT.ACAD.SCI.USA,68,1143-1147. (CHECKED BY AUTHOR)
102) **BRO:** WANG,A.C.,FUDENBERG,H.H. & PINK,J.R.L. (1971) PROC.NAT.ACAD.SCI.USA,68,1143-1147. (CHECKED BY AUTHOR)
103) **V.N.:** WANG,A.C.,FUDENBERG,H.H.,GOLDROSEN,M.H. & FREEDMAN,M.H. (1972) IMMUNOCHEMISTRY,9,473-479. (CHECKED BY AUTHOR 09/23/77)
104) **CAM:** HOPPER,J.E.,NOYES,C.,HSU,R.,HEINRIKSON,R. & GALLAGHER,W. (1979) J.IMMUNOL.,122,2007-2010. (CHECKED BY AUTHOR 01/26/83)
105) **GAA:** WANG,A.C.,FUDENBERG,H.H. & PINK,J.R.L. (1971) PROC.NAT.ACAD.SCI.USA,68,1143-1147. (CHECKED BY AUTHOR)
106) **EIK:** SMITH,G.P.,HOOD,L. & FITCH,W.M. (1971) ANN.REV.BIOCHEM.,40,969-1012.
107) **SKI:** WANG,A.C.,FUDENBERG,H.H. & PINK,J.R.L. (1971) PROC.NAT.ACAD.SCI.USA,68,1143-1147. (CHECKED BY AUTHOR)
108) **WEI:** WANG,A.C.,FUDENBERG,H.H. & PINK,J.R.L. (1971) PROC.NAT.ACAD.SCI.USA,68,1143-1147. (CHECKED BY AUTHOR)
109) **WE:** DWORSKY,E.,SLETTEN,K.,HARBOE,M. & WETTELAND,P. (1980) SCAND.J.IMMUNOL.,12,281-287. (CHECKED BY AUTHOR 02/28/1984)
110) **AVI:** PINK,J.R.L.,MCNALLY,M.P.,WANG,A.C. & FUDENBERG,H.H. (1972) IMMUNOCHEMISTRY,9,84-88; WOLFENSTEIN-TODEL,C.,FRANGIONE,B. & FRANKLIN,E.C. (1975) BIOCHIM.BIOPHYS.ACTA,379,627-637. (CHECKED BY AUTHOR WHO PROVIDED ADDITIONAL RESIDUES TO THOSE PUBLISHED)
111) **A-G1:** 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.
112) **EVA:** WANG,A.C.,FUDENBERG,H.H. & PINK,J.R.L. (1971) PROC.NAT.ACAD.SCI.USA,68,1143-1147. (CHECKED BY AUTHOR)
113) **B-G1:** 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.
114) **B-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.
115) **ESM:** WANG,A.C.,MATHER,S.,TUNG,E.,SARVAS,H.,RIVAT,C. & RIVAT,L. (1980) MOL.IMMUNOL.,17,313-318. (CHECKED BY AUTHOR 11/15/82.)
116) **B-G2a:** SCOTT,M.G.,TARRAND,J.J.,CRIMMINS,D.L.,MCCOURT,D.W.,SIEGEL,N.R.,SMITH,C.E. AND NAHM,M.H. (1989) J.IMMUNOL.,143, 293-298.
117) **C-G2a:** SCOTT,M.G.,TARRAND,J.J.,CRIMMINS,D.L.,MCCOURT,D.W.,SIEGEL,N.R.,SMITH,C.E. AND NAHM,M.H. (1989) J.IMMUNOL.,143, 293-298.
118) **A-G2a:** SCOTT,M.G.,TARRAND,J.J.,CRIMMINS,D.L.,MCCOURT,D.W.,SIEGEL,N.R.,SMITH,C.E. AND NAHM,M.H. (1989) J.IMMUNOL.,143, 293-298.
119) **H-G2a:** SCOTT,M.G.,TARRAND,J.J.,CRIMMINS,D.L.,MCCOURT,D.W.,SIEGEL,N.R.,SMITH,C.E. AND NAHM,M.H. (1989) J.IMMUNOL.,143, 293-298.
120) **A-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.
121) **K-G2:** SCOTT,M.G.,TARRAND,J.J.,CRIMMINS,D.L.,MCCOURT,D.W.,SIEGEL,N.R.,SMITH,C.E. AND NAHM,M.H. (1989) J.IMMUNOL.,143, 293-298.
122) **C-G1:** 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.
123) **K-G1(+&-):** 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.
124) **ERI:** MILSTEIN,C.P. & NORTHROP,F. (1976) EUR.J.IMMUNOL.,6,222-224. (CHECKED BY AUTHOR 09/08/78)
125) **LR1'CL:** POLLOK,B.A.,ANKER,R.,ELDRIDGE,P.,HENDERSHOT,L. & LEVITT,D. (1987) PROC.NATL.ACAD.SCI.USA,84,9199-9203.
126) **WO:** KOHLER,H.,SHIMIZU,A.,PAUL,C.,MOORE,V. & PUTNAM,F.W. (1970) NATURE,227,1318-1320. (CHECKED BY AUTHOR 06/15/83)
127) **HEI:** RIESEN,W.F.,MAJANIEMI,I.,HUSER,H.,BRAUN,D.G. & ROELCKE,D. (1978) SCAND.J.IMMUNOL.,8,145-148. (CHECKED BY AUTHOR 10/10/79)
128) **KW:** RIESEN,W.F.,MAJANIEMI,I.,HUSER,H.,BRAUN,D.G. & ROELCKE,D. (1978) SCAND.J.IMMUNOL.,8,145-148. (CHECKED BY AUTHOR 10/10/79)
129) **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.
130) **C-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.
131) **F-G1:** 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.
132) **L.TH.:** WANG,A.C.,FUDENBERG,H.H.,WELLS,J.V. & ROELCKE,D. (1973) NATURE NEW BIOLOGY,243,126-128. (CHECKED BY AUTHOR)
133) **SMM-IGA:** TAKAHASHI,M.,TSUKADA,T.,KOJIMA,M.,KOIDA,T.,KOIKE,T.,TAKAHASHI,H.,SAKAI,C.,KASHIMURA,M. & SHIBATA,A. (1986) BLOOD,67,1710-1713.
134) **HI:** TERRY,W.D. & OHMS,J. (1970) PROC.NAT.ACAD.SCI.USA,66,558-563.
135) **Ly47'CL:** COGNE,M.,MOUNIR,S.,PREUD'HOMME,J.-L.,NAU,F. & GUGLIELMI,P. (1988) EUR.J.IMMUNOL.,18,1485-1489.
136) **U266'CL:** SENO,M.,KUROKAWA,T.,ONO,Y.,ONDA,H.,SASADA,R.,IGARASHI,K.,KIKUCHI,M.,SUGINO,Y.,NISHIDA,Y. & HONJO,T. (1983) NUC.ACIDS RES.,11,719-726.
137) **WAG:** KAPLAN,A.P.,HOOD,L.,TERRY,W.D. & METZGER,H. (1971) IMMUNOCHEMISTRY,8,801-811.
138) **LR:** CAULIN-GLASER,T.,PRELLI,F. & FRANKLIN,E.C. (1982) J.LAB.CLIN.MED.,99,845-851. (CHECKED BY AUTHOR 12/10/82)
139) **LBW2'CL:** POLLOK,B.A.,ANKER,R.,ELDRIDGE,P.,HENDERSHOT,L. & LEVITT,D. (1987) PROC.NATL.ACAD.SCI.USA,84,9199-9203.
140) **Ly91'CL:** COGNE,M.,MOUNIR,S.,PREUD'HOMME,J.-L.,NAU,F. & GUGLIELMI,P. (1988) EUR.J.IMMUNOL.,18,1485-1489.
141) **LAMBDA-VH52'CL:** RABBITTS,T.H.,BENTLEY,D.L.,DUNNICK,W.,FORSTER,A.,MATTHYSSENS,G. & MILSTEIN,C. (1980) COLD SPRING HARB.SYMP.QUANTI.BIOL.,45,867-878.
142) **R.K.:** WANG,A.C.,FUDENBERG,H.H.,WELLS,J.V. & ROELCKE,D. (1973) NATURE NEW BIOLOGY,243,126-128. (CHECKED BY AUTHOR)
143) **GOEII:** STROSBERG,A.D.,KARCHER,D. & LOWENTHAL,A. (1975) J.IMMUNOL.,115,157-160. (CHECKED BY AUTHOR)
144) **PAL:** WANG,A.C.,MATHER,S.,TUNG,E.,SARVAS,H.,RIVAT,C. & RIVAT,L. (1980) MOL.IMMUNOL.,17,313-318. (CHECKED BY AUTHOR 11/15/82.)
145) **POD:** WANG,A.C.,MATHER,S.,TUNG,E.,SARVAS,H.,RIVAT,C. & RIVAT,L. (1980) MOL.IMMUNOL.,17,313-318. (CHECKED BY AUTHOR 11/15/82.)
146) **DB'CL:** POLLOK,B.A.,ANKER,R.,ELDRIDGE,P.,HENDERSHOT,L. & LEVITT,D. (1987) PROC.NATL.ACAD.SCI.USA,84,9199-9203.
147) **LBW14'CL:** POLLOK,B.A.,ANKER,R.,ELDRIDGE,P.,HENDERSHOT,L. & LEVITT,D. (1987) PROC.NATL.ACAD.SCI.USA,84,9199-9203.
148) **LAMBDA-VH32'CL:** RABBITTS,T.H.,BENTLEY,D.L.,DUNNICK,W.,FORSTER,A.,MATTHYSSENS,G. & MILSTEIN,C. (1980) COLD SPRING HARB.SYMP.QUANTI.BIOL.,45,867-878.
149) **HA:** KOHLER,H.,SHIMIZU,A.,PAUL,C.,MOORE,V. & PUTNAM,F.W. (1970) NATURE,227,1318-1320. (CHECKED BY AUTHOR 06/15/83)
150) **GIT:** WANG,A.C.,MATHER,S.,TUNG,E.,SARVAS,H.,RIVAT,C. & RIVAT,L. (1980) MOL.IMMUNOL.,17,313-318. (CHECKED BY AUTHOR 11/15/82.)
151) **SEI:** CAPRA,J.D. & KEHOE,J.M. (1975) J.IMMUNOLOGY,114,678-681. (CHECKED BY AUTHOR)
152) **KOO:** CAPRA,J.D. & KEHOE,J.M. (1975) J.IMMUNOLOGY,114,678-681. (CHECKED BY AUTHOR)
153) **BER:** CAPRA,J.D. & KEHOE,J.M. (1975) J.IMMUNOLOGY,114,678-681. (CHECKED BY AUTHOR)
154) **HIN:** CAPRA,J.D. & KEHOE,J.M. (1975) J.IMMUNOLOGY,114,678-681. (CHECKED BY AUTHOR)
155) **KNI:** CAPRA,J.D. & KEHOE,J.M. (1975) J.IMMUNOLOGY,114,678-681. (CHECKED BY AUTHOR)
156) **SHE:** CAPRA,J.D. & KEHOE,J.M. (1975) J.IMMUNOLOGY,114,678-681. (CHECKED BY AUTHOR)
157) **LIV:** CAPRA,J.D. & KEHOE,J.M. (1975) J.IMMUNOLOGY,114,678-681. (CHECKED BY AUTHOR)
158) **PUT:** CAPRA,J.D. & KEHOE,J.M. (1975) J.IMMUNOLOGY,114,678-681. (CHECKED BY AUTHOR)
159) **HER:** CAPRA,J.D. & KEHOE,J.M. (1975) J.IMMUNOLOGY,114,678-681. (CHECKED BY AUTHOR)
160) **MOY:** CAPRA,J.D. & KEHOE,J.M. (1975) J.IMMUNOLOGY,114,678-681. (CHECKED BY AUTHOR)
161) **PIT:** CAPRA,J.D. & KEHOE,J.M. (1975) J.IMMUNOLOGY,114,678-681. (CHECKED BY AUTHOR)
162) **TOL:** CAPRA,J.D. & KEHOE,J.M. (1975) J.IMMUNOLOGY,114,678-681. (CHECKED BY AUTHOR)
163) **CRI:** CAPRA,J.D. & KEHOE,J.M. (1975) J.IMMUNOLOGY,114,678-681. (CHECKED BY AUTHOR)
164) **GLU:** CAPRA,J.D. & KEHOE,J.M. (1975) J.IMMUNOLOGY,114,678-681. (CHECKED BY AUTHOR)
165) **SMM-IGG:** TAKAHASHI,M.,TSUKADA,T.,KOJIMA,M.,KOIDA,T.,KOIKE,T.,TAKAHASHI,H.,SAKAI,C.,KASHIMURA,M. & SHIBATA,A. (1986) BLOOD,67,1710-1713.
166) **PAC:** WANG,A.C.,MATHER,S.,TUNG,E.,SARVAS,H.,RIVAT,C. & RIVAT,L. (1980) MOL.IMMUNOL.,17,313-318. (CHECKED BY AUTHOR 11/15/82.)
167) **THA:** CAPRA,J.D. & KEHOE,J.M. (1975) J.IMMUNOLOGY,114,678-681. (CHECKED BY AUTHOR)
168) **KAR:** CAPRA,J.D. & KEHOE,J.M. (1975) J.IMMUNOLOGY,114,678-681. (CHECKED BY AUTHOR)
169) **PAR:** WANG,A.C.,MATHER,S.,TUNG,E.,SARVAS,H.,RIVAT,C. & RIVAT,L. (1980) MOL.IMMUNOL.,17,313-318. (CHECKED BY AUTHOR 11/15/82.)
170) **PAV:** PARR,D.M. (1977) BIOCHEM.J.,165,303-308; PARR,D.M. & HOFMANN,T. (1980) MOL.IMMUNOL.,17,1-7. (CHECKED BY AUTHOR 05/29/80 WHO PROVIDED ADDITIONAL RESIDUES FOR POSITIONS 98 TO 100H)
171) **NA:** KOHLER,H.,SHIMIZU,A.,PAUL,C.,MOORE,V. & PUTNAM,F.W. (1970) NATURE,227,1318-1320. (CHECKED BY AUTHOR 06/15/83)
172) **SLA:** CAPRA,J.D. & KEHOE,J.M. (1975) J.IMMUNOLOGY,114,678-681. (CHECKED BY AUTHOR)

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

173) **LES:** CAPRA,J.D. & KEHOE,J.M. (1975) J.IMMUNOLOGY,114,678-681. (CHECKED BY AUTHOR)

174) **ANT:** WANG,A.C.,MATHER,S.,TUNG,E.,SARVAS,H.,RIVAT,C. & RIVAT,L. (1980) MOL.IMMUNOL.,17,313-318. (CHECKED BY AUTHOR 11/15/82.)

175) **GRA:** WANG,A.C.,MATHER,S.,TUNG,E.,SARVAS,H.,RIVAT,C. & RIVAT,L. (1980) MOL.IMMUNOL.,17,313-318. (CHECKED BY AUTHOR 11/15/82.)

176) **ARP:** WANG,A.C.,MATHER,S.,TUNG,E.,SARVAS,H.,RIVAT,C. & RIVAT,L. (1980) MOL.IMMUNOL.,17,313-318. (CHECKED BY AUTHOR 11/15/82.)

177) **HOW:** KAPLAN,A.P.,HOOD,L.,TERRY,W.D. & METZGER,H. (1971) IMMUNOCHEMISTRY,8,801-811.

178) **CRA:** FRANGIONE,B. & FRANKLIN,E.C. (1977) PROG.IMMUNOL.,3,278-288. (CHECKED BY AUTHOR 07/18/79)

179) **GUI:** PINK,J.R.L.,MCNALLY,M.P.,WANG,A.C. & FUDENBERG,H.H. (1972) IMMUNOCHEMISTRY,9,84-88. (CHECKED BY AUTHOR)

180) **JLN'CL:** CLEARY,M.L. & SKLAR,J. (1985) PROC.NAT.ACAD.SCI.USA,82,7439-7443.

181) **BUS:** BENNETT,J.C. (1968) BIOCHEMISTRY,7,3340-3344. (CHECKED BY AUTHOR 11/01/77)

182) **RE:** KOHLER,H.,SHIMIZU,A.,PAUL,C.,MOORE,V. & PUTNAM,F.W. (1970) NATURE,227,1318-1320. (CHECKED BY AUTHOR 06/15/83)

183) **70P1'CL:** SCHROEDER,H.W.,JR. & WANG,J.Y. (1990) PROC.NATL.ACAD.SCI.USA,87,6146-6150.

184) **DOS:** BENNETT,J.C. (1968) BIOCHEMISTRY,7,3340-3344. (CHECKED BY AUTHOR 11/01/77)

185) **BAL:** BENNETT,J.C. (1968) BIOCHEMISTRY,7,3340-3344. (CHECKED BY AUTHOR 11/01/77)

GENERAL NOTES: HUMAN HEAVY CHAINS SUBGROUP III

IDENTICAL SETS OF FRAMEWORK SEGMENTS:

FR1:

SET 1: 18/2'CL[1],18/17'CL[2],18/9'CL[3],1/17'CL[4],30P1'CL[5],M43'CL[6],HF2-1/17[7],vh26c'CL[8],LAMBDA-VH26'CL[9], 4G12'CL[10],Ab25'CL[12],RF-KL1'CL[13],TIL[33],POM[45],TUR[59]. (15 IDENTICAL)

SET 2: Ab18'CL[11],H11'CL[23],38P1'CL[36],13-2'CL[37],BRO'IGM[38],TEI[54],12-2'CL[55],GR'[90]. (8 IDENTICAL)

SET 3: Vh38C1.10'CL[15],Vh38C1.8'CL[16],Vh38C1.9'CL[17]. (3 IDENTICAL)

SET 4: 60P2'CL[18],63P1'CL[19],VIN[91]. (3 IDENTICAL HUMAN V-H-III; ALSO 1 MISCELLANEOUS V-H: GOLDFISH 5A'CL[64].)

SET 5: 56P1'CL[25],2P1'CL[26],M72'CL[27],M74'CL[28],KIM46H'CL[29],1-9III'CL[30],R -SJ2'CL[31],FL2-2'CL[34], RF-TS2'CL[42]. (9 IDENTICAL)

SET 6: 4B4'CL[48],M26'CL[49],9-1'CL[50]. (3 IDENTICAL HUMAN V-H-III; ALSO 2 MOUSE V-H-IIID: H28-A2'CL[24], H37-82'CL[54].)

SET 7: K6H6'CL[68],K4B8'CL[69],K5B8'CL[70],K5C7'CL[71],K5G5'CL[72]. (5 IDENTICAL)

SET 8: 1B11'CL[74],1H1'CL[75],333'CL[76],126'CL[78]. (4 IDENTICAL)

SET 9: H11''CL[98]. (IDENTICAL TO 2 MOUSE V-H-IIID: 36-18'CL[48],36-15'CL[49].)

FR2:

SET 1: TIL[33],4B4'CL[48],M26'CL[49],9-1'CL[50],TEI[54],12-2'CL[55],20P1'CL[82]. (7 IDENTICAL HUMAN V-H-III; ALSO 1 HUMAN V-H-I: WOL[45].)

SET 2: 18/2'CL[1],18/17'CL[2],18/9'CL[3],1/17'CL[4],30P1'CL[5],M43'CL[6],HF2-1/17[7],vh26c'CL[8],LAMBDA-VH26'CL[9], 4G12'CL[10],Ab18'CL[11],RF-KL1'CL[13],8-1B'CL[14],Vh38C1.10'CL[15],Vh38C1.8'CL[16],Vh38C1.9'CL[17], 60P2'CL[18],63P1'CL[19],GF4/1.1'CL[20],Vh38C1.4'CL[21],Vh38C1.5'CL[22],Ab21'CL[24],v65-4'CL[35],3D6'CL[43], TUR[59],v65-2'CL[84]. (25 IDENTICAL HUMAN V-H-III; ALSO 1 MISCELLANEOUS V-H: GOLDFISH 3'CL[63].)

SET 3: 56P1'CL[25],2P1'CL[26],M72'CL[27],M74'CL[28],KIM46H'CL[29],1-9III'CL[30],RF-SJ2'CL[31],RF-TS2'CL[42], POM[45],LAY[51],BUR[52],KOL[53],HIL[56],WAS[58],NIE[60],GAL[61],VH10.7'CL[63],ER[83]. (18 IDENTICAL HUMAN V-H-III; ALSO 4 MOUSE V-H-IIID: BV04-01'CL[62],MRL-4'CL[64],MRL-DNA4'CL[65],H220-3'CL[70]; AND 1 CHICKEN V-H: Col-3'CL[9].)

SET 4: 22-2B'CL[32]. (IDENTICAL TO 1 MISCELLANEOUS V-H: RTVH431'CL[67].)

SET 5: 38P1'CL[36],13-2'CL[37]. (2 IDENTICAL)

SET 5: WEA[47],GA[66]. (2 IDENTICAL)

SET 7: TIL[33],K6H6'CL[68],K4B8'CL[69],K5B8'CL[70],K5C7'CL[71],K6F5'CL[73]. (6 IDENTICAL)

SET 8: 1B11'CL[74],1H1'CL[75],333'CL[76],112'CL[77],126'CL[78],115'CL[79],2C12'CL[80],2A12'CL[81]. (8 IDENTICAL)

FR3:

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

SET 2: 18/2'CL[1],18/17'CL[2],18/9'CL[3],1/17'CL[4],30P1'CL[5],M43'CL[6],HF2-1/17[7],LAMBDA-VH26'CL[9],4G12'CL[10], Ab18'CL[11],KIM46H'CL[29],1-9III'CL[30],FL2-2'CL[34]. (13 IDENTICAL)

SET 3: 8-1B'CL[14],56P1'CL[25],M72'CL[27],M74'CL[28],CAM'[40]. (5 IDENTICAL HUMAN V-H-III; ALSO 1 MISCELLANEOUS V-H: GOLDFISH 5A'CL[64].)

SET 4: Vh38C1.10'CL[15],Vh38C1.8'CL[16],Vh38C1.9'CL[17],Vh38C1.4'CL[21],Vh38C1.5'CL[22]. (5 IDENTICAL)

SET 5: 60P2'CL[18],63P1'CL[19]. (2 IDENTICAL)

SET 6: 38P1'CL[36],13-2'CL[37]. (2 IDENTICAL)

SET 7: 4B4'CL[48],M26'CL[49],9-1'CL[50]. (3 IDENTICAL)

SET 8: K6H6'CL[68],K4B8'CL[69],K5B8'CL[70],K5G5'CL[72],K6F5'CL[73]. (5 IDENTICAL)

SET 9: 1B11'CL[74],2C12'CL[80],2A12'CL[81]. (3 IDENTICAL)

SET 10: 1H1'CL[75],333'CL[76]. (2 IDENTICAL)

FR4:

SET 1: 18/2'CL[1],18/17'CL[2],18/9'CL[3],1/17'CL[4],30P1'CL[5],M43'CL[6],HF2-1/17[7],Ab25'CL[12],Vh38C1.10'CL[15], Vh38C1.8'CL[16],Vh38C1.9'CL[17],60P2'CL[18],63P1'CL[19],GF4/1.1'CL[20],Vh38C1.4'CL[21],Vh38C1.5'CL[22], 56P1'CL[25],2P1'CL[26],M74'CL[28],TIL[33],HN.14'CL[41],WEA[47],4B4'CL[48],M26'CL[49],NIE[60],DOB[62], VH10.7'CL[63],K6H6'CL[68],K4B8'CL[69],K5B8'CL[70],K5C7'CL[71],K5G5'CL[72],K6F5'CL[73],20P1'CL[82]. (34 IDENTICAL HUMAN V-H-III; ALSO 14 HUMAN V-H-I: LS2'CL[1],LS5'CL[2],LS6'CL[3],LS1'CL[4],LS8'CL[6],1B9/F2'CL[7], 21/28'CL[10],NEI'CL[16],TH9'CL[23],WIL2'CL[24],KAS[26],BOR'[27],LS7'CL[29],WOL[45]; 7 HUMAN V-H-II: 15P1'CL[1],ML1'CL[3],MCE'[46],DR12910-2F8'CL[48],Ab17'CL[49],M44'CL[52],NZO[55]; 1 MOUSE V-H-IIB: pING2006E'CL[29]; 1 MOUSE V-H-IIIA: MOPC47A[110]; AND 1 MOUSE V-H-IIID: H37-40'CL[25].)

SET 2: TIL[33]. (IDENTICAL TO 2 HUMAN V-H-I: 8E10'CL[11],TH3'CL[55]; AND 1 MOUSE V-H-IIIA: MOPC47A[110].)

SET 3: 38P1'CL[36],3D6'CL[43],13P1'CL[97]. (3 IDENTICAL HUMAN V-H-III; ALSO 6 HUMAN V-H-I: 51P1'CL[14], RF-TS1'CL[28],Ab2022'CL[41],M61'CL[47],60P1'CL[49],AF2'CL[65]; AND 6 HUMAN V-H-II: L16'CL[2],M71'CL[4], C6B2'CL[14],58P2'CL[16],CE-1 'CL[41],37P1'CL[47].)

SET 4: RF-SJ2'CL[31],RF-SJ1'CL[46]. (2 IDENTICAL HUMAN V-H-III; ALSO 1 HUMAN V-H-I: AND'CL[15]; AND 1 HUMAN V-H-II: Pag-1'CL[22].)

SET 5: 4G12'CL[10],Ab21'CL[24],M72'CL[27],KIM46H'CL[29],U266'CL[136],70P1'CL[183]. (6 IDENTICAL HUMAN V-H-III; ALSO 5 HUMAN V-H-I: 783G'CL[21],X17115'CL[22],EV1-15'CL[25],ND'CL[30],Ab2'CL[44]; 6 HUMAN V-H-II: FK-001'CL[11],HIG1'CL[24],Ab44'CL[29],Fog-B'CL[30],HuRSV19VH[36],HuRSV19CHFNS[38]; 2 MOUSE V-H-IIA: HDEX12[15],MBr1'CL[160]; AND 1 MOUSE V-H-IIC: MuRSV19VH'CL[37].)

SET 6: Ab18'CL[11],RF-KL1'CL[13],1B11'CL[74],1H1'CL[75],2C12'CL[80]. (5 IDENTICAL HUMAN V-H-III; ALSO 1 HUMAN V-H-I: 83P2'CL[38]; AND 2 HUMAN V-H-II: Ab26'CL[18],M60'CL[42].)

IDENTICAL SETS OF COMPLEMENTARITY DETERMINING REGIONS:

CDR1:

SET 1: 56P1'CL[25],2P1'CL[26],M72'CL[27],M74'CL[28],RF-SJ2'CL[31],v65-2'CL[84]. (6 IDENTICAL HUMAN V-H-III; ALSO 3 HUMAN V-H-I: 21/28'CL[10],8E10'CL[11],E3-10'CL[18]; AND 1 SHARK V-H: Rel07'CL[3].)

SET 2: H11'CL[23]. (IDENTICAL TO 1 HUMAN V-H-II: HuVNP'CL[25]; 9 MOUSE V-H-IIA: 4m4 GL'CL[94],5D3'CL[112], 8E3'CL[119],AM9'CL[120],AM10'CL[130],AM12'CL[131],7C6'CL[142],2.9 GL'CL[169],#L38'CL[206], AND 69 MOUSE V-H-IIB: B1-8'CL[1],B1-8.DELTA1V3[2],B1-48'CL[3],N-HYB'CL[4],18C10'CL[5],186-2'CL[6],B1-8.V4'CL[7], S2D8'CL[8],6F6'CL[9],S2E9'CL[10],F1'.170.2[11],186-1'CL[12],B4'CL[13],S2H5'CL[14],S1F12'CL[15],ANTI-TGAL 17'CL[16],H1-9'CL[18],CH12''CL[22],4m5 GL'CL[24],22.111.1'CL[27],23'CL[28],pING2006E'CL[29],B1-8.V1/V2[30], B1-8.V1'CL[31],N1C12'CL[33],124'CL[34],564'CL[35],550'CL[36],567'CL[37],563'CL[38],132.16'CL[39],N1G9'CL[50], 102'CL[51],33'CL[52],CH-51'CL[55],DB1-314.3'CL[56],DF4-12.6'CL[57],B1-45'CL[59],S1F2'CL[60],C1H4 GL'CL[64], CH10'CL[68],CH-55'CL[74],CH31'CL[76],H1-29'CL[79],DBF1-608.1'CL[89],AC38 15.3[93],H1-59'CL[94],104B'CL[101], 20.119.25'CL[104],3B9PC'CL[106],MVAR1'CL[109],167.1'CL[113],219.7'CL[114],5D6S'CL[122],167.2'CL[127], CH12'CL[129],F17.59.2'CL[137],vpd15 GL'CL[138],119.13'CL[149],6C7S'CL[158],3B11S'CL[161],4A9S'CL[164], NQ22.87.1'CL[165],AC38 251.5[168],4m110 GL'CL[174],AC38 260.2[175],4F5S'CL[178],10H12S'CL[180],VNP'CL[185].)

SET 3: 18/2'CL[1],18/17'CL[2],18/9'CL[3],1/17'CL[4],30P1'CL[5],M43'CL[6],HF2-1/17[7],vh26c'CL[8],LAMBDA-VH26'CL[9], Ab25'CL[12],RF-KL1'CL[13],HF2-1/13B[87],HF2-18/2[88]. (13 IDENTICAL HUMAN V-H-III; ALSO 15 MOUSE V-H-IIID: TF2-76'CL[6],8-1-12A'CL[7],8-1-12-5A'CL[8],914'CL[22],H28-A2'CL[24],H37-40'CL[25],129-48'CL[42],AF2'CL[52], 5.4KL.2Y.B'CL[53],H37-82'CL[54],40-20[64],AF1'CL[69],40-90[76],40-100[77],SP1/HL'CL[81]; AND 4 RABBIT V-H: VH1-a1'CL[8],3374[16],p26.9a3'CL[24],RVH139'CL[37].)

SET 4: 4G12'CL[10]. (IDENTICAL TO 2 MOUSE V-H-IIID: 5-27'CL[35],40-60[75].)

SET 5: Ab18'CL[11],POM[45]. (2 IDENTICAL)

SET 6: 8-1B'CL[14],60P2'CL[18],63P1'CL[19]. (3 IDENTICAL HUMAN V-H-III; ALSO 1 MISCELLANEOUS V-H: GOLDFISH 5A'CL[64].)

SET 7: Vh38C1.10'CL[15],Vh38C1.8'CL[16],Vh38C1.9'CL[17],Vh38C1.4'CL[21],Vh38C1.5'CL[22]. (5 IDENTICAL)

SET 8: GF4/1.1'CL[20]. (IDENTICAL TO 1 MOUSE V-H-IIID: 5-76'CL[21].)

SET 9: KIM46H'CL[29],1-9III'CL[30],FL2-2'CL[34],RF-TS2'CL[42],RF-SJ1'CL[46]. (5 IDENTICAL)

SET 10: 22-2B'CL[32]. (IDENTICAL TO 36 MOUSE V-H-IIIA: V11'CL[60],CLA-2/Cn V11'CL[61],WSA V11'CL[62],38C'CL[63], 38CV4'CL[64],38CV1'CL[65],6G6'CL[66],CBA/J V11'CL[67],NZB V11'CL[68],NZW V11'CL[69],36-7'CL[72],N4-1'CL[76], CH2'CL[77],CH5'CL[78],6F9'CL[79],9A6'CL[81],C57BL/10 V11'CL[82],VB6.5'CL[83],C57BL V11'CL[84],CBA/J 6G6[86], NQ10.2.22'CL[88],H210-56'CL[89],G2a-1'CL[90],VP4.8'CL[93],C57BL V13'CL[94],C57BL/10 V13'CL[95],36-17'CL[98], DPI'CL[103],NQ11.8.4'CL[106],V13'CL[108],N4-18'CL[109],MOPC47A[110],17G5'CL[113],CBA/J V13'CL[114], H220-17'CL[123],HPCG15[172].)

SET 11: 38P1'CL[36],13-2'CL[37]. (2 IDENTICAL)

SET 12: 3D6'CL[43],BUR[52]. (2 IDENTICAL HUMAN V-H-III; ALSO 2 MOUSE V-H-IIA: BCL1'CL[102],mAb 123'CL[106]; AND 1 MOUSE V-H-MISC: 2H1'CL[45].)

SET 13: 4B4'CL[48],M26'CL[49],9-1'CL[50],20P1'CL[82]. (4 IDENTICAL)

SET 14: VH10.7'CL[63]. (IDENTICAL TO 1 MOUSE V-H-MISC: H51.54.33[71].)

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

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

CDR2: SET 1: 18/2'CL[1],18/17'CL[2],18/9'CL[3],1/17'CL[4],30P1'CL[5],M43'CL[6],HF2-1/17[7],vh26c'CL[8],4G12'CL[10]. (9 IDENTICAL)
SET 2: 8-1B'CL[14],60P2'CL[18],63P1'CL[19]. (3 IDENTICAL HUMAN V-H-III; ALSO 1 MISCELLANEOUS V-H: GOLDFISH 5A'CL[64].)
SET 3: Vh38C1.10'CL[15],Vh38C1.8'CL[16],Vh38C1.9'CL[17],Vh38C1.4'CL[21],Vh38C1.5'CL[22]. (5 IDENTICAL)
SET 4: 56P1'CL[25],2P1'CL[26],M72'CL[27],M74'CL[28],KIM46H'CL[29],1-9III'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: Vh38C1.10'CL[15],Vh38C1.8'CL[16],Vh38C1.9'CL[17],Vh38C1.4'CL[21],Vh38C1.5'CL[22]. (5 IDENTICAL)
SET 5: POM[45],LAY[51]. (2 IDENTICAL)
SET 6: K6H6'CL[68],K4B8'CL[69],K5B8'CL[70],K5C7'CL[71],K6F5'CL[73]. (5 IDENTICAL)
SET 7: 1B11'CL[74],1H1'CL[75],333'CL[76],112'CL[77],126'CL[78],115'CL[79],2C12'CL[80],2A12'CL[81]. (8 IDENTICAL)

IDENTICAL SETS OF J-MINIGENES:

SET 1: 30P1'CL[5],Ab25'CL[12],60P2'CL[18],63P1'CL[19],56P1'CL[25],M74'CL[28],TIL[33],HN.14'CL[41],M26'CL[49], VH10.7'CL[63],K6H6'CL[68],K4B8'CL[69],K5B8'CL[70],K5C7'CL[71],K5G5'CL[72],K6F5'CL[73],20P1'CL[82]. (17 IDENTICAL HUMAN V-H-III; ALSO 9 HUMAN V-H-I: 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]; 4 HUMAN V-H-II: ML1'CL[3],DR12910-2F8'CL[48],Ab17'CL[49],M44'CL[52]; AND 1 MOUSE V-H-IIID: H37-40'CL[25].)
SET 2: TIL[33]. (IDENTICAL TO 1 HUMAN V-H-I: 21/28'CL[10].)
SET 3: 38P1'CL[36],3D6'CL[43],13P1'CL[97]. (3 IDENTICAL HUMAN V-H-III; ALSO 5 HUMAN V-H-I; 51P1'CL[14], RF-TS1'CL[28],M61'CL[47],60P1'CL[49],AF2'CL[65]; AND 6 HUMAN V-H-II: L16'CL[2],M71'CL[4],C6B2'CL[14], 58P2'CL[16],CE-1 'CL[41],37P1'CL[47].)
SET 4: RF-SJ2'CL[31],RF-SJ1'CL[46]. (2 IDENTICAL HUMAN V-H-III; ALSO 1 HUMAN V-H-I: AND'CL[15]; AND 1 HUMAN V-H-II: Pag-1'CL[22].)
SET 5: 4G12'CL[10],Ab21'CL[24],M72'CL[27],KIM46H'CL[29],U266'CL[136],70P1'CL[183]. (6 IDENTICAL HUMAN V-H-III; ALSO 5 HUMAN V-H-I: 783C'CL[21],X17115'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: Vh38C1.10'CL[15],Vh38C1.8'CL[16],Vh38C1.9'CL[17],Vh38C1.4'CL[21],Vh38C1.5'CL[22]. (5 IDENTICAL)
SET 11: GF4/1.1'CL[20],4B4'CL[48]. (2 IDENTICAL)
SET 12: 1B11'CL[74],1H1'CL[75],2C12'CL[80]. (3 IDENTICAL)

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

SPECIFIC NOTES: HUMAN HEAVY CHAINS SUBGROUP III

1) **18/2'CL:** FROM PERIPHERAL BLOOD LYMPHOCYTES OF A SYSTEMIC LUPUS ERYTHEMATOSUS PATIENT.
2) **18/17'CL:** FROM PERIPHERAL BLOOD LYMPHOCYTES OF A SYSTEMIC LUPUS ERYTHEMATOSUS PATIENT.
3) **18/9'CL:** FROM PERIPHERAL BLOOD LYMPHOCYTES OF A SYSTEMIC LUPUS ERYTHEMATOSUS PATIENT.
4) **1/17'CL:** FROM PERIPHERAL BLOOD LYMPHOCYTES OF A SYSTEMIC LUPUS ERYTHEMATOSUS PATIENT.
5) **30P1'CL:** FROM HUMAN FETUS AT 130 DAYS OF GESTATION.
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 SLIGHT DIFFERENT SEQUENCES: LAMBDA-VH52'CL HAS MET AT POSITION 87 AND ARG AT POSITION 94, AND LAMBDA-VH32'CL HAS VAL AT POSITION 93.
10) **4G12'CL:** IT RECOGNIZES A TUMOR-ASSOCIATED AND DIFFERENTIATION ANTIGEN OF MW 195,000.
11) **Ab18'CL:** THE D-SEGMENT IS EXTRA LONG. EIGHT AMINO ACID RESIDUES ILE TRP ARG LEU ASN PRO ILE ARG ARE PLACED AT POSITION 100G.
12) **Ab25'CL:** AUTHORS PROVIDED THIS ORIGINAL SEQUENCE WHICH IS DIFFERENT FROM THAT IN THE REFERENCE.
18) **60P2'CL:** FROM HUMAN FETUS AT 130 DAYS OF GESTATION.
19) **63P1'CL:** FROM HUMAN FETUS AT 130 DAYS OF GESTATION.
24) **Ab21'CL:** AUTHORS PROVIDED THIS ORIGINAL SEQUENCE WHICH IS DIFFERENT FROM THAT IN THE REFERENCE.
25) **56P1'CL:** FROM HUMAN FETUS AT 130 DAYS OF GESTATION.
26) **2P1'CL:** FROM HUMAN FETUS AT 130 DAYS OF GESTATION.
29) **KIM46H'CL:** Kim4.6 CELL LINE WAS PRODUCED BY FUSION OF TONSILLAR LYMPHOID CELLS FROM A NORMAL CHILD WITH GM4672, AN IGG-KAPPA PRODUCER. THE CDR3 OF THIS HEAVY CHAIN IS LONGER, REQUIRING 8 RESIDUES, THR THR THR LYS ARG GLY LEU THR, TO BE PLACED AT POSITION 100D.
31) **RF-SJ2'CL:** FOR ALIGNMENT, IT IS REQUIRED TO PLACE TWO RESIDUES, TYR SER, AT POSITION 100D.
34) **FL2-2'CL:** DERIVED FROM HUMAN GENOMIC DNA OF EPSTEIN-BARR VIRUS-TRANSFORMED FETAL B CELL LINE.
36) **38P1'CL:** FROM HUMAN FETUS AT 130 DAYS OF GESTATION.
41) **HN.14'CL:** THIS HYBRIDOMA WAS MADE BY FUSING PERIPHERAL BLOOD LYMPHOCYTES FROM A PATIENT WITH CHRONIC LYMPHOCYTIC LEUKEMIA AND UC729-6 HUMAN LYMPHOBLASTOID CELLS.
46) **RF-SJ1'CL:** FOR ALIGNMENT, IT IS REQUIRED TO PLACE TWO RESIDUES, TYR SER, AT POSITION 100D.
48) **4B4'CL:** THE HYBRIDOMA WAS MADE BY FUSING PBMC CELLS FROM AN SLE PATIENT TO THE LYMPHOBLASTOID CELL LINE GM4672. Sm IS THE ABBREVIATION FOR SMALL NUCLEAR RIBONUCLEOPROTEIN.
63) **VH10.7'CL:** FROM PATIENT WITH IGD-SECRETING MYELOMA. THE V- AND C-REGIONS ARE BROUGHT TOGETHER BY A HOMOLOGOUS RECOMBINATION BETWEEN 442/443-BASE-PAIR REPEATS DELETING THE C-MU.
67) **GRA':** PERSONAL COMMUNICATION FROM THE AUTHOR INDICATES THAT IT IS A CRYOGLOBULIN.
68) **K6H6'CL:** FROM A PATIENT WITH B-CELL LYMPHOMA.
69) **K4B8'CL:** FROM A PATIENT WITH B-CELL LYMPHOMA.
70) **K5B8'CL:** FROM A PATIENT WITH B-CELL LYMPHOMA.
71) **K5C7'CL:** FROM A PATIENT WITH B-CELL LYMPHOMA.
72) **K5G5'CL:** FROM A PATIENT WITH B-CELL LYMPHOMA.
73) **K6F5'CL:** FROM A PATIENT WITH B-CELL LYMPHOMA.
82) **20P1'CL:** FROM HUMAN FETUS AT 130 DAYS OF GESTATION.
83) **FR:** AN IDIOTYPIC ANTIBODY TO FR NOT INHIBITABLE BY PHOSPHORYLCHOLINE REACTED BETTER WITH THE FR HEAVY CHAIN THAN WITH THE LIGHT CHAIN. THE CROSS-REACTION WITH MOPC167 WAS 10,000 TIMES WEAKER. (RIESEN,W.F. (1979) EUR.J.IMMUNOL.,9, 421-425.)
96) **PS (SHA):** PS AND SHA ARE THE SAME PROTEIN AS POINTED OUT BY HASSNER,A. & SAXON,A. (1984) J.IMMUNOL.,132,2844-2846.
97) **13P1'CL:** FROM HUMAN FETUS AT 130 DAYS OF GESTATION.
111) **A-G1:** AMINO ACID RESIDUES FOUND AT POSITION 5 ARE VAL AND LEU.
113) **B-G1:** AMINO ACID RESIDUES FOUND AT POSITION 7 ARE SER AND THR.
114) **B-G2b:** AMINO ACID RESIDUES FOUND AT POSITION 7 ARE SER AND THR.
122) **C-G1:** AMINO ACID RESIDUES FOUND AT POSITION 7 ARE SER AND THR.
123) **K-G1(+a-):** AMINO ACID RESIDUES FOUND AT POSITION 20 ARE LEU AND VAL.
125) **LR1'CL:** THE REGION NOT SEQUENCED CONSISTED OF A LARGE DELETION. THIS HEAVY CHAIN IS EXPRESSED ON THE CELL SURFACE WITHOUT LIGHT CHAIN. LR1 IS A B-CELL LINE THAT SPONTANEOUSLY AROSE FROM CULTURED PERIPHERAL BLOOD LYMPHOCYTES FROM A PATIENT WITH ACUTE LYMPHOCYTIC LEUKEMIA.
131) **F-G1:** AMINO ACID RESIDUES FOUND AT POSITION 7 ARE SER AND THR.
133) **SMM-IGA:** THIS MYELOMA PROTEIN IS FROM A PATIENT WITH SMOLDERING MULTIPLE MYELOMA WHO PRODUCES TWO MONOCLONAL IMMUNOGLOBULINS, IGG AND IGA.
135) **Ly47'CL:** FROM BURKITT'S LYMPHOMA CELL LINES WHICH PRODUCE TRUNCATED HEAVY CHAINS LACKING PART OF VARIABLE REGION
139) **LBW2'CL:** THE REGION NOT SEQUENCED CONSISTED OF A LARGE DELETION. THIS HEAVY CHAIN IS EXPRESSED ON THE CELL SURFACE WITHOUT LIGHT CHAIN. LBW2 IS AN EBV-TRANSFORMED B-CELL LINE DERIVED FROM PERIPHERAL BLOOD LYMPHOCYTES FROM A PATIENT WITH COMMON VARIABLE IMMUNODEFICIENCY.

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

140) **Ly91'CL:** FROM BURKITT'S LYMPHOMA CELL LINES WHICH PRODUCE TRUNCATED HEAVY CHAINS LACKING PART OF VARIABLE REGION

146) **DB'CL:** THE REGION NOT SEQUENCED CONSISTED OF A LARGE DELETION. THIS HEAVY CHAIN IS EXPRESSED ON THE CELL SURFACE WITHOUT LIGHT CHAIN. DB IS AN EBV-TRANSFORMED B-CELL LINE DERIVED FROM PERIPHERAL BLOOD LYMPHOCYTES FROM A HEALTHY INDIVIDUAL.

147) **LBW14'CL:** THE REGION NOT SEQUENCED CONSISTED OF A LARGE DELETION. THIS HEAVY CHAIN IS EXPRESSED ON THE CELL SURFACE WITHOUT LIGHT CHAIN. LBW14 IS AN EBV-TRANSFORMED B-CELL LINE DERIVED FROM PERIPHERAL BLOOD LYMPHOCYTES FROM A PATIENT WITH COMMON VARIABLE IMMUNODEFICIENCY.

165) **SMM-IGG:** THIS MYELOMA PROTEIN IS FROM A PATIENT WITH SMOLDERING MULTIPLE MYELOMA WHO PRODUCES TWO MONOCLONAL IMMUNOGLOBULINS, IGG AND IGA.

178) **CRA:** IT WAS FROM A CASE OF HEAVY CHAIN DISEASE. AT POSITION 3, LEU AND ILE WERE FOUND. AFTER POSITION 9, THE CHAIN CONTINUES IN THE C-REGION AS RESIDUE 216 (EU NUMBERING) GLU.

180) **JLN'CL:** IT IS ASSOCIATED WITH A t(14:18) TRANSLOCATION WITH THE BREAK POINT IN THE J4 REGION ON THE NONFUNCTIONAL ALLELE.

\+ THE FOLLOWING WERE EQUALLY AND MOST FREQUENTLY OCCURRING:

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