

Proposed name <sup>a</sup>	Origin		CDR Region <sup>c</sup>		Investigator <sup>d</sup>		GenBank <sup>e</sup> Accn #	Comments <sup>f</sup>
	cDNA	DNA	CDR1	CDR2				
V <sub>H</sub> A-1 <sup>*</sup>	+	+	A	A	B		AF064686	A in FR3
V <sub>H</sub> A-2 <sup>*b</sup>	+	+	A	A	B			G in FR3
V <sub>H</sub> B <sup>*</sup>	+	+	B	B	B		AF064687	
V <sub>H</sub> C <sup>*</sup>	+	+	C	C	B		AF064688	
V <sub>H</sub> D	+	+	C	D	B			
V <sub>H</sub> E <sup>*</sup>	+	+	E	E	B		AF064689	
V <sub>H</sub> F <sup>*</sup>	+	+	F	F	B		AF064690	
V <sub>H</sub> N <sup>*</sup>	+	+	N	N	B	K	AY911499 AF321841	
V <sub>H</sub> L	+	+	E	L	B	K	AY911500 AF321839	
V <sub>H</sub> Psg1		+	E	I	B		AF064691	Pseudogene
V <sub>H</sub> J		+	J	F	B		AY911501	
V <sub>H</sub> K		+	K	K	B		AF064692	
V <sub>H</sub> H		+	O	H	B		DQ886392	
V <sub>H</sub> M	+		F	X		K	AF321840	Truncated
V <sub>H</sub> O	+		O	O	B	K	AF321842	Truncated
V <sub>H</sub> P	+		P	O	B	K	AF321843	Truncated
V <sub>H</sub> Q	+		C	Q		K	AF321844	Truncated
V <sub>H</sub> R	+		O	I		K	AF321845	Truncated
V <sub>H</sub> S	+		S	S		K	AF321846	Truncated
V <sub>H</sub> T	+	+	E	F	B	K	AF321847	Truncated
V <sub>H</sub> U	+		C	U	B	K	AF321848	Truncated
V <sub>H</sub> V	+		A	B	B	K	AF321849	Truncated
V <sub>H</sub> W	+	+	A	F	B	K	AF321850	
V <sub>H</sub> X	+	+	X	X	B	K	AY911502	
V <sub>H</sub> Psg2		+	Y	A	B		AY911503	Pseudogene
V <sub>H</sub> ZZ	+	+	N	I	B		AY911504	
V <sub>H</sub> Y <sup>*</sup>	+	+	C	A	B		DQ886393	
V <sub>H</sub> Z	+	+	E	C	B		DQ886394	
V <sub>H</sub> G	+	+	G	E	B		DQ886395	

- Proposed name after comparison to sequences in GenBank. \* = Denotes major V<sub>H</sub> genes used in the pre-immune repertoire.
- V<sub>H</sub>A-2 differs from V<sub>H</sub>A-1 in FR3 and is located upstream of V<sub>H</sub>A-1 in the locus.
- The single Arabic designator indicates the CDR region. The sequence for each is given below the table. Various V<sub>H</sub> genes share CDR sequences with other genes. Some V<sub>H</sub> genes share one CDR but possess a second unique CDR, e.g. V<sub>H</sub>L shares CDR1 with V<sub>H</sub>E but has a unique CDR2 called "L".
- B = Butler Lab based on repeated recovery; K = Sequences reported by Y.B. Kim.
- Sequences entered in GenBank as protein sequences by other investigators are not included since they cannot be identified without their nucleotide sequences.
- Certain V<sub>H</sub> genes may be alleles of others. Conclusions await further studies.

CDR1			CDR2		
A	AGTACCTACA	TTAAC	A	~~~~~GCTA	TTAGTACTAG TGGTGGT
B	GACAACGCTT	TCAGC	B	GCCATTGCTA	GTAGTGACTA TGACGGT
C	AGTTATGAAA	TCAGC	C	~~~~~GGTA	TTTATAGTAG TGGTGGT
E	AGTTATGCAG	TGAGC	D	~~~~~G	ATATTTGTAG TGGTGGT
F	AGTTATGGCG	TAGGC	E	GGTATTGATA	GTGGTAGTTA TAGTGGT
G	AGTTATGGCA	TGAGC	F	TCTATTGGTA	GTGGTAGTTA TATTGGT
J	AGTTATGCAG	TGGAG	H	TCTATTGGTC	GTGGTCGTTA TCGTGGT
K	AGTTCTCCCA	TAGGC	I	~~~~~TGTA	TTTATAGTAG TGGTAGT
N	AGTTATAGCA	TGAGC	K	TCTATTGGTA	GTGGTAGTTA TAGTGGT
O	AGTTATCCCA	TAGGC	L	~~~~~G	CTATTTATAG TGGTGGT
P	GACTACGCTT	TCAGC	N	~~~~~GGTA	TTTATAGTAG TGGTAGT
S	AGCTACAACA	TGATC	O	~~~~~GCTA	TTAGTACTAG TGGTAGT
X	AGTTATGGCA	TAGGC	Q	~~~~~GCTA	TCAGTACTAG TGGTGCT
Y	AGTTATGAAA	TCAGA	S	~~~~~TATA	TTACTAGTAG TGGTGGT
			U	GCTATTGGTT	GTGGTAGTTA TAGTGGT
			X	~~~~~G	GTATTTATAG TGGTGGT