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Protein Displays of the Human T Cell Receptor Alpha, Beta, Gamma and Delta Variable and Joining Regions

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Key Words

Human · IMGT · T cell receptor · Alpha variable and joining regions · Beta variable and joining regions · Gamma variable and joining regions · Delta variable and joining regions

Abstract

'Protein Displays of the Human T Cell Receptor Alpha, Beta, Gamma and Delta Variable and Joining Regions', the 13th report of the 'IMGT Locus in Focus' section, comprises 8 figures: (1) 'Protein display of the human TRA V-REGIONs'; (2) 'Protein display of the human TRB V-REGIONs'; (3) 'Protein display of the human TRG V-REGIONs'; (4) 'Protein display of the human TRD V-REGIONs'; (5) 'Protein display of the human TRA J-REGIONs'; (6) 'Protein display of the human TRB J-REGIONs'; (7) 'Protein display of the human TRG J-REGIONs'; (8) 'Protein display of the human TRD J-REGIONs', and 4 tables entitled: (1) 'FR-IMGT and CDR-IMGT length of the human TRAV genes'; (2) 'FR-IMGT and CDR-IMGT length of the human TRBV genes'; (3) 'FR-IMGT and CDR-IMGT length of the human TRGV genes'; (4) 'FR-IMGT and CDR-IMGT length of the human TRDV genes'. These figures and tables are available at the IMGT Marie-Paule page from **IMGT**, the international ImMunoGeneTics database **(http://imgt.cines.fr:8104)** created by Marie-Paule Lefranc, Université Montpellier II, CNRS, Montpellier, France.

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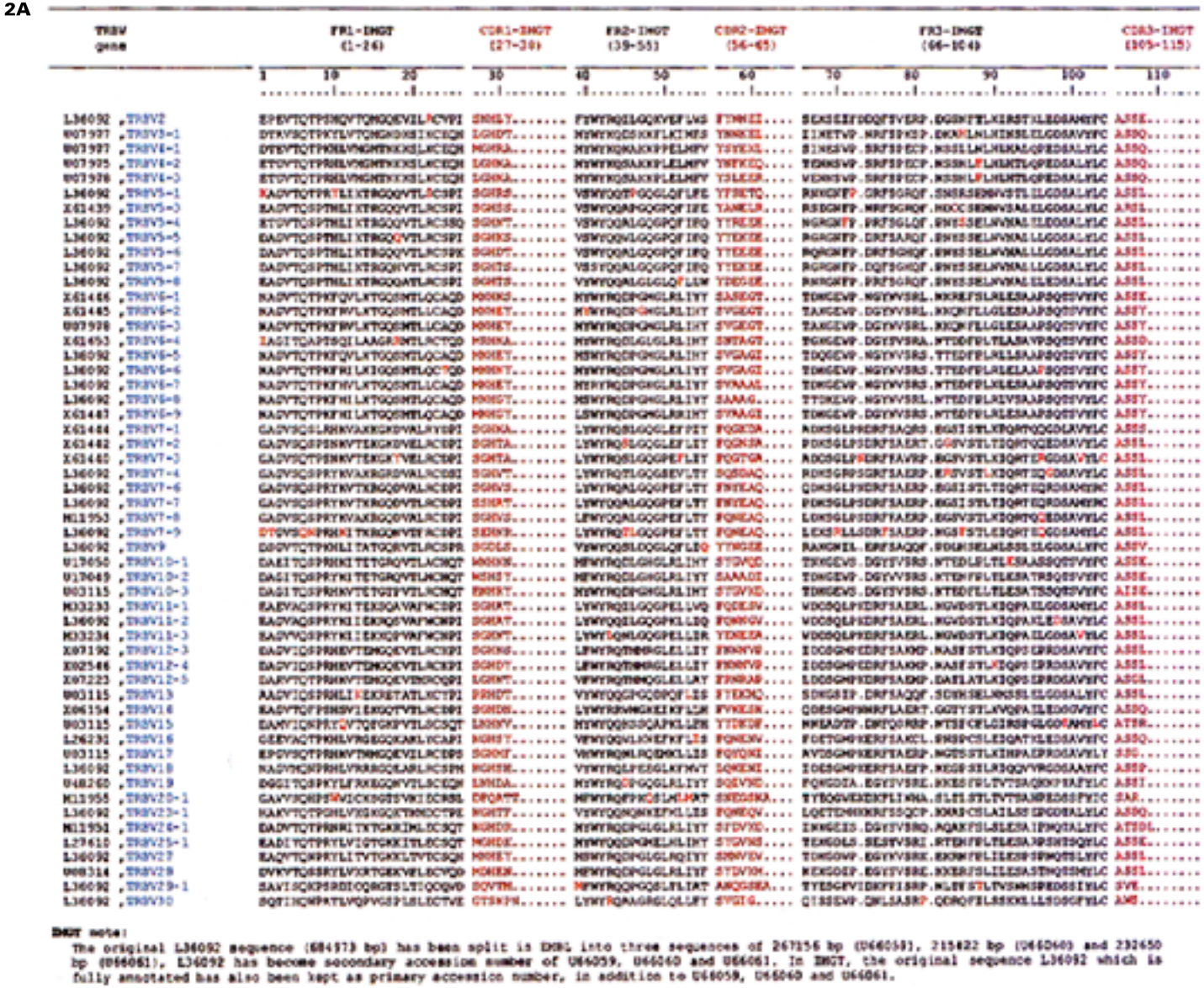
'Protein Displays of the Human T cell Receptor Alpha, Beta, Gamma and Delta Variable and Joining Regions' is the 13th report of the 'IMGT Locus in Focus' section launched in the April 1998 issue of *Experimental and Clinical Immunogenetics* [1]. We have previously reported the complete repertoire of the human germline TRAV [2] and TRAJ [3], TRBV [4], TRBD and TRBJ [5] genes, localized at the TRA (14q11.2) locus and at the TRB locus (7q35), respectively, as well as TRBV orphon genes identified on chromosome 9 (9p21) [4]. This 13th report completes these data by providing the protein displays of the corresponding reference coding regions. It comprises 8 figures: (1) 'Protein display of the human TRA V-REGIONs'; (2) 'Protein display of the human TRB V-REGIONs'; (3) 'Protein display of the human TRG V-REGIONs'; (4) 'Protein display of the human TRD V-REGIONs'; (5) 'Protein display of the human TRA J-REGIONs'; (6) 'Protein display of the human TRB J-REGIONs'; (7) 'Protein display of the human TRG J-REGIONs'; (8) 'Protein display of the human TRD J-REGIONs'; and 4 tables entitled: (1) 'FR-IMGT and CDR-IMGT length of the human TRAV genes'; (2) 'FR-IMGT and CDR-IMGT length of the human TRBV genes'; (3) 'FR-IMGT and CDR-IMGT length of the human TRGV genes'; (4) 'FR-IMGT and CDR-IMGT length of the human TRDV genes'. These figures and tables are available at the IMGT Marie-Paule page from **IMGT**, the international ImMunoGeneTics database **(http://imgt.cines.fr:8104)** created by Marie-Paule Lefranc, Université Montpellier II, CNRS, Montpellier, France [6–9]. Nucleotide and amino acid numbering of the V-REGION is according to the IMGT unique numbering system [1, 10, 11]. Detailed protein displays of the human TRB D-REGIONs [5] and TRD D-REGIONs are available in IMGT Repertoire > Alignments of alleles > Human TRBD and TRDD Overviews, respectively.

In figures 1–4, the T cell receptor genes are designated according to the IMGT gene tables [2–5] and locus representations (see IMGT Repertoire at IMGT Home page, http://imgt.cines.fr:8104, IMGT Repertoire >1. Locus and Genes). Only FUNCTIONAL and ORF V-GENEs are shown. In tables 1–4, numbers in bold, on the second line at the top of each column, represent the IMGT unique numbering for the FR-IMGT and CDR-IMGT. Numbers in parentheses, on the third line, correspond to the range of FR-IMGT and CDR-IMGT lengths (in number of amino acids) observed for the TRAV, TRBV, TRGV and TRDV genes (tables 1–4, respectively). Numbers in the CDR1-IMGT, CDR2-IMGT and CDR3-IMGT columns show the CDR lengths in number of amino acids. Information in the FR1-IMGT, FR2-IMGT and FR3-IMGT columns shows the gaps compared to the IMGT numbering: the number of missing amino acids is indicated following the sign '–' with, in parentheses, the position(s) of the missing amino acid(s) compared to the IMGT numbering. Columns are left blank if there are no gaps. The proteolytic cleavage site between the leader peptide and the V-REGION is putative and the assignment of amino acid 1 (IMGT numbering) to one or the other region is uncertain.

Fig. 1. Protein display of the human TRA V-REGIONs. Only the *01 allele of each functional or ORF V-REGION is shown. Letters in red correspond to amino acids which are polymorphic in the other alleles. TRAV genes are listed, for each subgroup, according to their position from 5′ to 3′ in the locus. The 8 amino acids in 5′ of TRAV23/DV6 and the 6 amino acids in 5′ of TRAV29/DV5, as predicted by the program SIGSEQ2 and as described by Wülfung and Plückthun [12], are not shown.

2A



IMGT note:

The original L36092 sequence (684979 bp) has been split in EMBL into three sequences of 267256 bp (U66059), 215822 bp (U66060) and 232650 bp (U66061). L36092 has become secondary accession number of U66059, U66060 and U66061. In IMGT, the original sequence L36092 which is fully annotated has also been kept as primary accession number, in addition to U66059, U66060 and U66061.

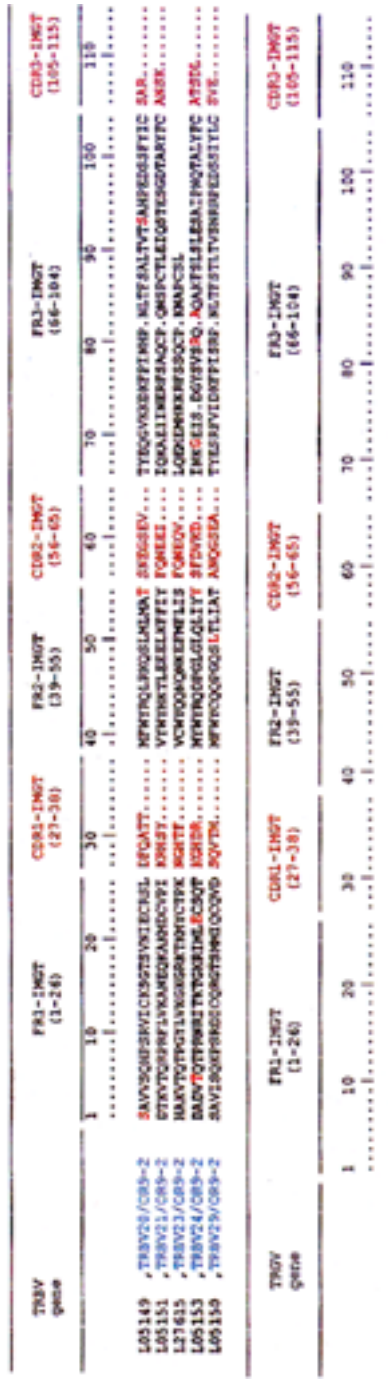


Fig. 2. Protein display of the human TRB V-REGIONs. Only the *01 allele of each functional or ORF V-REGION is shown. Letters in red correspond to amino acids which are polymorphic in the other alleles. **A** TRBV genes at the TRB locus (7q35). TRBV genes are listed, for each subgroup, according to their position from 5′ to 3′ in the locus. **B** Orphons on chromosome 9 (9p21).

Fig. 3. Protein display of the human TRG V-REGIONs. Only the *01 allele of each functional or ORF V-REGION is shown. Letters in red (T29 of TRGV9, W108 and V109 of TRGV10) correspond to amino acids which are polymorphic in the other alleles. Human TRGV genes are listed from 5′ to 3′ in the locus.

Fig. 4. Protein display of the human TRD V-REGIONs. Only the *01 allele of each functional or ORF V-REGION is shown. Letters in red correspond to amino acids which are polymorphic in the other alleles. Human TRDV genes are listed from 5′ to 3′ in the locus.

Fig. 5. Protein display of the human TRA J-REGIONs. Only the *01 allele of each functional or ORF J-REGION is shown. Letters in red correspond to amino acids which are polymorphic in the other alleles and to the conserved motif FGXG. Human TRAJ segments are listed from 5′ to 3′ in the locus.

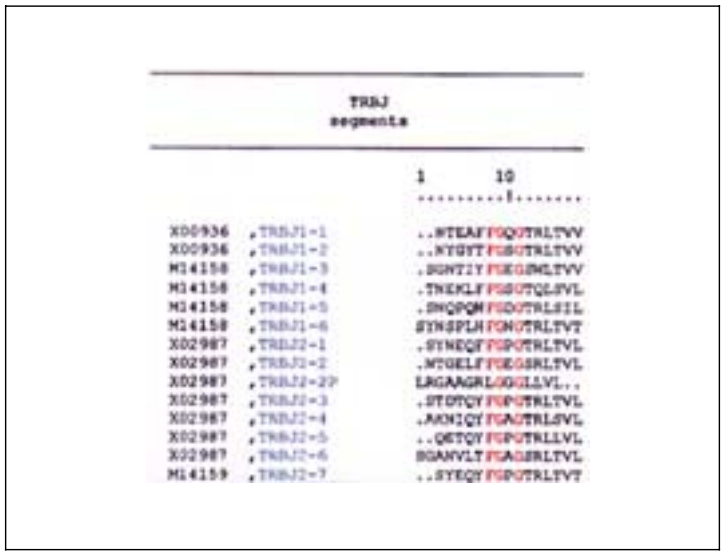


Fig. 6. Protein display of the human TRB J-REGIONs. Only the *01 allele of each functional or ORF J-REGION is shown. The letter F (Phe) of TRBJ2–7 corresponds to an amino acid which is polymorphic in another allele. The conserved motif FGXG is in red. Human TRBJ segments are listed from 5′ to 3′ in the locus.

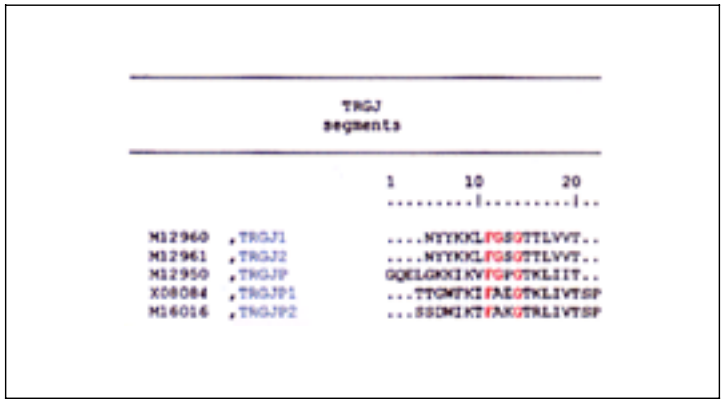


Fig. 7. Protein display of the human TRG J-REGIONs. Only the *01 allele of each functional or ORF J-REGION is shown. The conserved motif FGXG is in red.

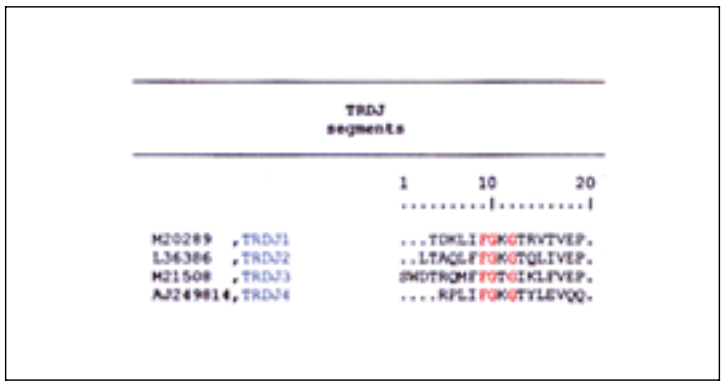


Fig. 8. Protein display of the human TRD J-REGIONs. Only the *01 allele of each functional or ORF J-REGION is shown. The conserved motif FGXG is in red.

Table 1 - FR-IMGT and CDR-IMGT length of the human TRAV genes

An asterisk (*) indicates a longer N-terminal end as predicted by the program SIGSEQ2 [Wülfing and Plückthun. *Immunology Today* 1995; 16:405-406].

TRAV genes	FR1-IMGT 1 to 26	CDR1-IMGT 27 to 38	FR2-IMGT 39 to 55	CDR2-IMGT 56 to 65	FR3-IMGT 66 to 104	CDR3-IMGT (germline V-GENE) 105 to 115
	(25,26,32,34)	(5 to 7)	(16,17)	(0 to 4)	(36 to 38)	(2 to 5)
TRAV1-1, TRAV1-2	-1 (aa 7)	6		2	-1 (aa73)	3
TRAV2	-1 (aa 7)	6		0	-3 (aa 73,81,82)	3
TRAV3		6		4	-1 (aa 73)	4
TRAV4	-1 (aa 7)	7		1	-1 (aa73)	4
TRAV5	-1 (aa 8)	6		3	-1 (aa 73)	3
TRAV6		6		3	-1 (aa 73)	3
TRAV7		6		3	-3 (aa 73,81,82)	3
TRAV8-1 to 8-4,		6		4	-1 (aa 73)	3
TRAV8-6,		6		4	-1 (aa 73)	3
TRAV8-7		6		4	-1 (aa 73)	5
TRAV9-1, TRAV9-2		6		3	-1 (aa 73)	3
TRAV10		6		3	-1 (aa 73)	3
TRAV11		6		3	-1 (aa 73)	2
TRAV12-1,		6		2	-2 (aa 70,73)	3
TRAV12-2,		6		2	-1 (aa 73)	3
TRAV12-3		6		2	-1 (aa 73)	3
TRAV13-1, TRAV13-2		6		3	-1 (aa 73)	3
TRAV14/DV4		7		4	-1 (aa 73)	4
TRAV16		6		0	-1 (aa 73)	3
TRAV17		5		3	-1 (aa 73)	3
TRAV18		6		2	-1 (aa 73)	3
TRAV19		7		4	-1 (aa 73)	4
TRAV20		6		3	-3 (aa 73,81,82)	3
TRAV21		6		3	-1 (aa 73)	3
TRAV22		5		1	-1 (aa 73)	3
TRAV23/DV6	+8 aa in 5'*	6		3	-1 (aa 73)	3
TRAV24		6		3	-1 (aa 73)	2
TRAV25		5		3	-1 (aa 73)	2
TRAV26-1, TRAV26-2	-1 (aa 7)	7		1	-1 (aa 73)	4
TRAV27		5		3	-1 (aa 73)	2
TRAV29/DV5	+6 aa in 5'*	6		3	-1 (aa 73)	3
TRAV30	-1 (aa 5)	5		3	-1 (aa 73)	3
TRAV34		5		3	-1 (aa 73)	3
TRAV35		5		3	-1 (aa 73)	3
TRAV36/DV7		6	-1 (aa 50)	3	-1 (aa 73)	3
TRAV38-1, TRAV38-2/DV8		7		4	-1 (aa 73)	4
TRAV39		5		3	-1 (aa 73)	3
TRAV40	-1 (aa 8)	6		0	-3 (aa 66,73,82)	3
TRAV41		5		1	-1 (aa 73)	3

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Table 2 - FR-IMGT and CDR-IMGT length of the human TRBV genes

TRBV genes	FR1-IMGT 1 to 26	CDR1-IMGT 27 to 38	FR2-IMGT 39 to 55	CDR2-IMGT 56 to 65	FR3-IMGT 66 to 104	CDR3-IMGT (germline V-GENE) 105 to 115
	(26)	(5,6)	(17)	(5 to 7)	(37,38)	(3 to 5)
TRBV2		5		6	-1 (aa 82)	4
TRBV3-1		5		6	-2 (aa 73,82)	4
TRBV4-1 to TRBV4-3		5		6	-2 (aa 73,82)	4
TRBV5-1, TRBV5-3 to TRBV5-8		5		6	-2 (aa 73,82)	4
TRBV6-1 to TRBV6-7		5		6	-2 (aa 73,82)	4
TRBV6-8		5		5	-2 (aa 73,82)	4
TRBV6-9		5		6	-2 (aa 73,82)	4
TRBV7-1 to TRBV7-4, TRBV7-6 to TRBV7-9		5		6	-1 (aa 82)	4
TRBV9		5		6	-2 (aa 73,82)	4
TRBV10-1 to TRBV10-3		5		6	-2 (aa 73,82)	4
TRBV11-1 to TRBV11-3		5		6	-1 (aa 82)	4
TRBV12-3 to TRBV12-5		5		6	-1 (aa 82)	4
TRBV13		5		6	-2 (aa 73,82)	4
TRBV14		5		6	-1 (aa 82)	4
TRBV15		5		6	-2 (aa 73,82)	4
TRBV16		5		6	-1 (aa 82)	4
TRBV17		5		6	-1 (aa 82)	3
TRBV18		5		6	-1 (aa 82)	4
TRBV19		5		6	-2 (aa 73,82)	4
TRBV20-1		6		7	-1 (aa 82)	3
TRBV23-1		5		6	-1 (aa 82)	4
TRBV24-1		5		6	-2 (aa 73,82)	5
TRBV25-1		5		6	-2 (aa 73,82)	4
TRBV27		5		6	-2 (aa 73,82)	4
TRBV28		5		6	-2 (aa 73,82)	4
TRBV29-1		5		7	-1 (aa 82)	3
TRBV30		6		5	-2 (aa 73,82)	3

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Table 3 - FR-IMGT and CDR-IMGT length of the human TRGV genes

TRGV genes	FR1-IMGT 1 to 26	CDR1-IMGT 27 to 38	FR2-IMGT 39 to 55	CDR2-IMGT 56 to 65	FR3-IMGT 66 to 104	CDR3-IMGT (germline V-GENE) 105 to 115
	(26)	(6,8)	(17)	(7,8)	(38,39)	(4 to 6)
TRGV1,		6		8	-2(aa79,82)	5
TRGV2,		6		8	-1 (aa 82)	5
TRGV3,		6		8	-1 (aa 82)	5
TRGV4,		6		8	-1 (aa 82)	5
TRGV5,		6		8	-1 (aa 82)	5
TRGV8		6		8	-1 (aa 82)	5
TRGV9		8		7		5
TRGV10		8		8		4,5*
TRGV11		8		7		6

* polymorphic CDR3-IMGT length (4 or 5 amino acids)

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Table 4 - FR-IMGT and CDR-IMGT length of the human TRDV genes

TRDV genes	FR1-IMGT 1 to 26	CDR1-IMGT 27 to 38	FR2-IMGT 39 to 55	CDR2-IMGT 56 to 65	FR3-IMGT 66 to 104	CDR3-IMGT (germline V-GENE) 105 to 115
	(26)	(7,8)	(17)	(3,5)	(38,39)	(4)
TRDV1		7		3	-1 (aa 73)	4
TRDV2		8		3	-1 (aa 73)	4
TRDV3		7		5		2

Five genes designated as TRAV/DV have been found rearranged either to D and J segments of the TRD locus or to TRAJ segments, and can therefore be used in the synthesis of delta or alpha chains. These genes (TRAV14/DV4, TRAV23/DV6, TRAV29/DV5, TRAV36/DV7 and TRAV38-2/DV8) are reported in Table 1.

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