

THE T CELL RECEPTOR

FactsBook

Marie-Paule Lefranc
G rard Lefranc



**THE
T CELL
RECEPTOR**
FactsBook

Other books in the FactsBook Series:

Robin Callard and Andy Gearing

The Cytokine FactsBook

Steve Watson and Steve Arkinstall

The G-Protein Linked Receptor FactsBook

Shirley Ayad, Ray Boot-Handford, Martin J. Humphries, Karl E. Kadler
and C. Adrian Shuttleworth

The Extracellular Matrix FactsBook, 2nd edn

Grahame Hardie and Steven Hanks

The Protein Kinase FactsBook

The Protein Kinase FactsBook CD-Rom

Edward C. Conley

The Ion Channel FactsBook

I: Extracellular Ligand-Gated Channels

Edward C. Conley

The Ion Channel FactsBook

II: Intracellular Ligand-Gated Channels

Edward C. Conley and William J. Brammar

The Ion Channel FactsBook

IV: Voltage-Gated Channels

Kris Vaddi, Margaret Keller and Robert Newton

The Chemokine FactsBook

Marion E. Reid and Christine Lomas-Francis

The Blood Group Antigen FactsBook

A. Neil Barclay, Marion H. Brown, S.K. Alex Law, Andrew J. McKnight,
Michael G. Tomlinson and P. Anton van der Merwe

The Leucocyte Antigen FactsBook, 2nd edn

Robin Hesketh

The Oncogene and Tumour Suppressor Gene FactsBook, 2nd edn

Jeffrey K. Griffith and Clare E. Sansom

The Transporter FactsBook

Tak W. Mak, Josef Penninger, John Rader, Janet Rossant
and Mary Saunders

The Gene Knockout FactsBook

Bernard J. Morley and Mark J. Walport

The Complement FactsBook

Steven G.E. Marsh, Peter Parham and Linda Barber

The HLA FactsBook

Hans G. Drexler

The Leukemia-Lymphoma Cell Line FactsBook

Clare M. Isacke and Michael A. Horton

The Adhesion Molecule FactsBook, 2nd edn

Marie-Paule Lefranc and Gérard Lefranc

The Immunoglobulin FactsBook

THE T CELL RECEPTOR

FactsBook

Marie-Paule Lefranc
Gérard Lefranc

IMGT, the international ImMunoGeneTics database
Laboratoire d'ImmunoGénétique Moléculaire
Université Montpellier II,
Institut de Génétique Humaine CNRS,
Montpellier, France



ACADEMIC PRESS

A Harcourt Science and Technology Company

San Diego San Francisco New York Boston
London Sydney Tokyo

This book is printed on acid-free paper.

Copyright © 2001 by ACADEMIC PRESS

All Rights Reserved.

No part of this publication may be reproduced or transmitted in any form or by any means, electronic or mechanical, including photocopying, recording, or any information storage and retrieval system, without permission in writing from the publisher.

Academic Press
A Harcourt Science and Technology Company
Harcourt Place, 32 Jamestown Road, London NW1 7BY, UK
<http://www.academicpress.com>

Academic Press
A Harcourt Science and Technology Company
525 B Street, Suite 1900, San Diego, California 92101-4495, USA
<http://www.academicpress.com>

ISBN 0-12-441352-8

Library of Congress Catalog Number: 2001 091534

A catalogue record for this book is available from the British Library

Typeset by Mackreth Media Services, Hemel Hempstead, UK
Printed in Great Britain by St Edmundsbury Press Limited,
Bury St Edmunds, Suffolk

01 02 03 04 05 SE 9 8 7 6 5 4 3 2 1

Contents

Preface	ix
Abbreviations	x
IMGT standardized labels used in this book	xi
Aide-Mémoire	xiv

Section I THE INTRODUCTORY CHAPTERS

<i>Chapter 1</i>	
Introduction	3
<i>Chapter 2</i>	
T cell receptor structural and biological properties	14
<i>Chapter 3</i>	
Synthesis of the T cell receptor chains	25
<i>Chapter 4</i>	
Chromosomal localization, organization of the loci, and potential repertoire ...	47

Section II THE HUMAN T CELL RECEPTOR TRA GENES

Part 1 TRAC	75	TRAV9-1	116
TRAC	76	TRAV9-2	118
Part 2 TRAJ	79	TRAV10	120
TRAJ group	80	TRAV12-1	122
Part 3 TRAV	87	TRAV12-2	124
TRAV1-1	88	TRAV12-3	126
TRAV1-2	90	TRAV13-1	128
TRAV2	92	TRAV13-2	130
TRAV3	94	TRAV14/DV4	132
TRAV4	96	TRAV16	134
TRAV5	98	TRAV17	136
TRAV6	100	TRAV18	138
TRAV7	102	TRAV19	140
TRAV8-1	104	TRAV20	142
TRAV8-2	106	TRAV21	144
TRAV8-3	108	TRAV22	146
TRAV8-4	110	TRAV23/DV6	148
TRAV8-6	112	TRAV24	151
TRAV8-7	114	TRAV25	153
		TRAV26-1	155
		TRAV26-2	157

TRAV27	159	TRAV38-2/DV8	173
TRAV29/DV5	161	TRAV39	175
TRAV30	163	TRAV40	177
TRAV34	165	TRAV41	179
TRAV35	167	TRAV protein display	181
TRAV36/DV7	169	TRAV recombination signals	183
TRAV38-1.....	171	TRAV references.....	184

Section III THE HUMAN T CELL RECEPTOR TRB GENES

Part 1 TRBC	187	TRBV7-3	247
TRBC1	188	TRBV7-4	250
TRBC2	190	TRBV7-6	252
Part 2 TRBD	193	TRBV7-7	254
TRBD group	194	TRBV7-8	256
Part 3 TRBJ	195	TRBV7-9	258
TRBJ group	196	TRBV9	261
Part 4 TRBV	199	TRBV10-1	263
TRBV2	200	TRBV10-2	265
TRBV3-1	202	TRBV10-3	267
TRBV4-1	204	TRBV11-1	269
TRBV4-2	206	TRBV11-2	271
TRBV4-3	208	TRBV11-3	273
TRBV5-1	210	TRBV12-3	275
TRBV5-3	212	TRBV12-4	277
TRBV5-4	214	TRBV12-5	279
TRBV5-5	216	TRBV13.....	281
TRBV5-6	218	TRBV14.....	283
TRBV5-7	220	TRBV15.....	285
TRBV5-8	222	TRBV16.....	287
TRBV6-1	224	TRBV17.....	289
TRBV6-2	226	TRBV18.....	291
TRBV6-3	229	TRBV19.....	293
TRBV6-4	231	TRBV20-1	295
TRBV6-5	233	TRBV23-1	297
TRBV6-6	235	TRBV24-1	299
TRBV6-7	237	TRBV25-1	301
TRBV6-8	239	TRBV27.....	303
TRBV6-9	241	TRBV28.....	305
TRBV7-1	243	TRBV29-1	307
TRBV7-2	245	TRBV30.....	309
		TRBV protein display.....	311
		TRBV recombination signals	313
		TRBV references	314

Section IV THE HUMAN T CELL RECEPTOR TRG GENES

Part 1 TRGC	319	TRGV3	336
TRGC1	320	TRGV4	338
TRGC2 {2x}	322	TRGV5	340
TRGC2 {3x}	324	TRGV8	342
Part 2 TRGJ	327	TRGV9	344
TRGJ group	328	TRGV10	346
Part 3 TRGV	331	TRGV11	348
TRGV1	332	TRGV protein display	350
TRGV2	334	TRGV recombination signals and references	351

Section V THE HUMAN T CELL RECEPTOR TRD GENES

Part 1 TRDC	355	Part 4 TRDV	363
TRDC	356	TRDV1	364
Part 2 TRDD	359	TRDV2	366
TRDD group	360	TRDV3	368
Part 3 TRDJ	361	TRDV protein display	370
TRDJ group	362	TRDV recombination signals and references	371
 TRAC, TRBC, TRGC, and TRDC protein displays	 372		
Index	373		

This Page Intentionally Left Blank

Preface

The authors wish to acknowledge the IMGT team that contributed to the completion of this book. In particular, we would like to thank Nathalie Bosc, Valérie Contet, Géraldine Folch, Christèle Jean, and Dominique Scaviner, the motivated and enthusiastic IMGT annotators for their invaluable contribution and expertise. Sandrine Béranger, Chantal Ginestoux, Chrystel Godiris, and Manuel Ruiz helped with figures for the introductory chapters. We are very grateful to Gérard Mennessier for the IMGT/Collier de Perles tool development, and to Véronique Giudicelli and Denys Chaume for the bioinformatics and computer management of IMGT, the international ImMunoGeneTics database (<http://imgt.cines.fr>).

The authors wish to acknowledge the funding by the Ministère de l'Education Nationale, the Ministère de la Recherche, the Université Montpellier II, the CNRS, the European Community, and the Région Languedoc-Roussillon.

The authors hope that there are a minimum of omissions and inaccuracies and that these can be rectified in later editions. We would appreciate if such points were forwarded to the Editor, The T Cell Receptor FactsBook, Academic Press Ltd, Harcourt Place, 32 Jamestown Road, London NW1 7BY, UK.



Back row from left: *Sandrine Béranger, Christèle Jean, Valérie Contet, Géraldine Folch, Chantal Ginestoux, Dominique Scaviner, Nathalie Bosc*
Front row from left: *Manuel Ruiz, Chrystel Godiris, **Marie-Paule Lefranc**.*

Abbreviations

a or A	Adenine (purine base of DNA and RNA)
c or C	Cytosine (pyrimidine base of DNA and RNA)
C	Constant
CDR	Complementarity Determining Region
CH	Immunoglobulin heavy constant exon or domain
CNRS	Centre National de la Recherche Scientifique
D	Diversity
DDBJ	DNA DataBank of Japan
E	Enhancer
EMBL	European Molecular Biology Laboratory Nucleotide Sequence Database
ER	Endoplasmic reticulum
FR	Framework
g or G	Guanine (purine base of DNA and RNA)
GDB	Genome Database
GenBank	US Nucleotide Sequence Database
HUGO	HUman Genome Organization
Ig	Immunoglobulin
IG	Immunoglobulin gene
IMGT	The international ImMunoGeneTics database
J	Joining
kb	Kilobase
kDa	Kilodalton
LIGM-DB	Laboratoire d'ImmunoGénétique Moléculaire DataBase (Immunoglobulin and T cell receptor database), part of IMGT
MHC	Major Histocompatibility Complex
nt	Nucleotide
OMIM	Online Mendelian Inheritance in Man (MIM)
ORF	Open Reading Frame
pMHC	peptide-MHC complex
RS	Recombination signal
SRS	Sequence Retrieval System, a database query system developed by EMBL
t or T	Thymine (pyrimidine base of DNA)
TcR	T cell Receptor
TR	T cell Receptor gene
V	Variable

Links to database or molecular biology server web sites quoted in this book are available from IMGT Bloc-notes, <http://imgt.cines.fr>

IMGT Standardized Labels Used in this Book

Label name	Definition
1st-CYS	codon (3 nucleotides) for cysteine in conserved position in FR1-IMGT
2nd-CYS	codon (3 nucleotides) for cysteine in conserved position in FR3-IMGT
3'D-HEPTAMER	7-nucleotide recombination site like CACAGTG, part of a 3'D-RS
3'D-NONAMER	9-nucleotide recombination site like ACAAAAACC, part of a 3'D-RS
3'D-RS	recombination signal including the 3'D-HEPTAMER, 3'D-SPACER, and 3'D-NONAMER in 3' of the D-REGION of a D-GENE
3'UTR	3' untranslated sequence, EMBL feature Key signification
5'D-HEPTAMER	7-nucleotide recombination site like CACTGTG, part of a 5'D-RS
5'D-NONAMER	9-nucleotide recombination site like GGTTTTTGT, part of a 5'D-RS
5'D-RS	recombination signal including the 5'D-NONAMER, 5'D-SPACER and 5'D-HEPTAMER in 5' of the D-REGION of a D-GENE or in 5' of the D-REGION of D-J-GENE
5'UTR	5' untranslated sequence, EMBL feature Key signification
ACCEPTOR-SPLICE	splicing site in 5' of coding region (nagnn), with splicing occurring after g
C-GENE	genomic DNA including C-REGION (and INTRONS if present) with 5'UTR and 3'UTR
C-REGION	coding region of C-GENE or corresponding region in cDNA
CDR1-IMGT	first complementarity determining region according to the IMGT unique numbering
CDR2-IMGT	second complementarity determining region according to the IMGT unique numbering
CDR3-IMGT	third complementarity determining region according to the IMGT unique numbering
CONSERVED-TRP	codon (3 nucleotides) for tryptophan in conserved position in FR2-IMGT
D-J-C-CLUSTER	genomic DNA in germline configuration including at least one D-GENE, one J-GENE and one C-GENE
D-REGION	coding region of D-SEGMENT (plus 1 or 2 nucleotide(s) after the 5'D-HEPTAMER and/or before the 3'D-HEPTAMER, if present), or corresponding region in cDNA
D-GENE	germline genomic DNA including D-REGION with 5'UTR and 3'UTR
DELETION	point out a deletion compared to other sequences
DONOR-SPLICE	splicing site in 3' of coding region (ngt), with splicing occurring before g

Label name	Definition
EX1	first exon of TR C-GENE, or corresponding region in cDNA
EX2	second exon of TR C-GENE, or corresponding region in cDNA
EX2R	duplicated exon 2 of human TRG C-GENE, or corresponding region in cDNA
EX2T	triplicated exon 2 of human TRG C-GENE, or corresponding region in cDNA
EX3	third exon of TR C-GENE, or corresponding region in cDNA
EX4	fourth exon of TR C-GENE, or corresponding region in cDNA
FR1-IMGT	first framework according to the IMGT unique numbering
FR2-IMGT	second framework according to the IMGT unique numbering
FR3-IMGT	third framework according to the IMGT unique numbering
INSERTION	point out an insertion of one or more nucleotide compared with old release of the sequence or with a similar sequence
INT-DONOR-SPLICE	alternative donor splice site located in a coding region
J-C-CLUSTER	genomic DNA in germline configuration including at least one J-GENE and one C-GENE
J-HEPTAMER	7-nucleotide recombination site, like CACAGTG, part of a J-RS
J-NONAMER	9-nucleotide recombination site, like GGTTTTGT, part of a J-RS
J-REGION	coding region of J-GENE (plus 1 or 2 nucleotide(s) after J-HEPTAMER, if present) or corresponding region in cDNA
J-RS	recombination signal including J-HEPTAMER, J-SPACER and J-NONAMER in 5' of J-REGION of a J-GENE or J-SEQUENCE
J-GENE	germline genomic DNA including J-REGION with 5'UTR and 3'UTR
JUNCTION	coding region encompassing the V-J or V-D-J junction from 2nd-CYS to the J-PHE or J-TRP of the J-REGION
L-INTRON-L	sequence including L-PART1, V-INTRON and L-PART2 in genomic DNA or corresponding sequence in unspliced cDNA
L-PART1	exon encoding the first part of the leader peptide of a V-, V-D-, V-D-J-, or V-J-GENE or corresponding region in unspliced cDNA
L-PART2	5' region of V-EXON encoding the second part of leader peptide of a V-, V-D-, V-D-J- or V-J-GENE or corresponding region in unspliced cDNA
N-AND-D-REGION	coding region encompassing the N diversity sequence and coding region of D-GENE(s) when limits between N- and D-REGIONS are unknown or corresponding region in cDNA
N-REGION	coding region encompassing the N diversity sequence
OCTAMER	8-nucleotide regulation site or octanucleotide, in the 5'UTR of a V-, V-D-, V-D-J- or V-J-GENE
STOP-CODON	codon that stops gene translation
TATA_BOX	TATA signal in eukaryotic promoters
V-CLUSTER	genomic DNA in germline configuration including more than one V-GENE
V-D-J-EXON	rearranged genomic DNA including L-PART2, V-, any D- and N-REGION, and J-REGION

Label name	Definition
V-D-J-GENE	rearranged genomic DNA including L-PART1, V-INTRON, and V-D-J-EXON, with the 5'UTR and 3'UTR
V-D-J-REGION	coding region including V-, any D- and N-REGION, and J-REGION, in rearranged genomic DNA, or corresponding region in cDNA
V-EXON	germline genomic DNA including L-PART2 and V-REGION
V-HEPTAMER	7-nucleotide recombination site, like CACAGTG, part of V-RS
V-INTRON	non-coding sequence between L-PART1 and V-EXON in genomic DNA or corresponding sequence in unspliced cDNA
V-J-EXON	rearranged genomic DNA including L-PART2, V- and J- REGION
V-J-GENE	rearranged genomic DNA including L-PART1, V-INTRON and V-J-EXON, with the 5'UTR and 3'UTR
V-J-REGION	coding region including V- and J-REGION, in rearranged genomic DNA or corresponding region in cDNA
V-NONAMER	9-nucleotide recombination site, like ACAAAAACC, part of V-RS
V-REGION	coding region of V-GENE without the leader peptide (plus 1 or 2 nucleotide(s) before the V-HEPTAMER, if present) or corresponding region in cDNA
V-RS	recombination signal including V-HEPTAMER, V-SPACER and V-NONAMER in 3' of V-REGION of a V-GENE or V-SEQUENCE
V-SPACER	12- or 23-nucleotide spacer between the V-HEPTAMER and the V-NONAMER of a V-RS

Aide-Mémoire

Useful restriction sites

<i>Bam</i> HI	G↓GATCC
<i>Eco</i> RI	G↓AATTC
<i>Hind</i> III	A↓AGCTT
<i>Kpn</i> I	GGTAC↓C
<i>Pst</i> I	CTGCA↓G
<i>Pvu</i> II	CAG↓CTG
<i>Sac</i> I (<i>Sst</i> I)	GAGCT↓C
<i>Taq</i> I	T↓CGA
<i>Xba</i> I	T↓CTAGA
<i>Xho</i> I	C↓TCGAG

Amino Acid Abbreviations

Amino acid	Abbreviations	
Alanine	Ala	A
Arginine	Arg	R
Asparagine	Asn	N
Aspartic acid	Asp	D
Asparagine or Aspartic acid	Asx	B
Cysteine	Cys	C
Glutamine	Gln	Q
Glutamic acid	Glu	E
Glutamine or Glutamic acid	Glx	Z
Glycine	Gly	G
Histidine	His	H
Isoleucine	Ile	I
Leucine	Leu	L
Lysine	Lys	K
Methionine	Met	M
Phenylalanine	Phe	F
Proline	Pro	P
Serine	Ser	S
Threonine	Thr	T
Tryptophan	Trp	W
Tyrosine	Tyr	Y
Valine	Val	V

Genetic code

Nucleotide position in codon						
first	second				third	
	U	C	A	G		
U	UUU Phe	UCU Ser	UAU Tyr	UGU Cys	U	
	UUC Phe	UCC Ser	UAC Tyr	UGC Cys	C	
	UUA Leu	UCA Ser	UAA Stop	UGA Stop	A	
	UUG Leu	UCG Ser	UAG Stop	UGG Trp	G	
C	CUU Leu	CCU Pro	CAU His	CGU Arg	U	
	CUC Leu	CCC Pro	CAC His	CGC Arg	C	
	CUA Leu	CCA Pro	CAA Gln	CGA Arg	A	
	CUG Leu	CCG Pro	CAG Gln	CGG Arg	G	
A	AUU Ile	ACU Thr	AAU Asn	AGU Ser	U	
	AUC Ile	ACC Thr	AAC Asn	AGC Ser	C	
	AUA Ile	ACA Thr	AAA Lys	AGA Arg	A	
	AUG Met	ACG Thr	AAG Lys	AGG Arg	G	
G	GUU Val	GCU Ala	GAU Asp	GGU Gly	U	
	GUC Val	GCC Ala	GAC Asp	GGC Gly	C	
	GUA Val	GCA Ala	GAA Glu	GGA Gly	A	
	GUG Val	GCG Ala	GAG Glu	GGG Gly	G	

**THE
INTRODUCTORY
CHAPTERS**

This Page Intentionally Left Blank

1 Introduction

SCOPE OF THE BOOK

The primary aim of this book is to provide a compendium of the human germline T cell Receptor genes which are used to create the human T cell receptor repertoire. The book includes entries for 168 genes and for 271 alleles, with a total of 393 sequences displayed (Section II). Prior to the entries there are four introductory chapters (Section I). The first introductory chapter defines the data content and data selection criteria based on the International ImMunoGeneTics database (IMGT) Scientific chart¹ and IMGT-ONTOLOGY concepts². Chapter 2 is a short overview on the structural and biological properties of the human T cell receptors. Chapter 3 provides a summary of the molecular mechanisms of the synthesis of the human T cell receptor chains. Chapter 4 represents a major IMGT contribution by providing, in a unique document, the first complete description of the T cell receptor germline repertoire in the human.

SELECTION OF THE DATA

The individual entries comprise all the human T cell receptor constant genes, and germline variable, diversity, and joining genes which have at least one functional or ORF (Open Reading Frame) allele, and which are localized in the four major loci. Selected data are from IMGT, the international ImMunoGeneTics database^{1,3-5} (<http://imgt.cines.fr>), created in Montpellier in 1989 by M.-P. Lefranc (Université Montpellier II, CNRS), and more particularly from the IMGT/LIGM-DB database, and from the IMGT Repertoire⁶. The selection criteria of the individual entries are defined in the IMGT Scientific chart¹ (<http://imgt.cines.fr>) and in the IMGT-ONTOLOGY 'IDENTIFICATION' and 'CLASSIFICATION' concepts², some of which are briefly summarized in the following paragraphs.

The 'IDENTIFICATION' concept

The 'IDENTIFICATION' concept allows scientists to identify T cell receptor sequences according to fundamental biological and immunogenetic characteristics². These are as follows.

'molecule type':

Three instances are considered: genomic DNA, cDNA, and protein.

'gene type':

Four types of genes are involved in T cell receptor synthesis, the variable (V), diversity (D) and joining (J) genes which encode the antigen binding sites, and the constant (C) genes which encode the part of the polypeptide chains that has effector properties.

'configuration':

The configuration defines the status of the genes: 'germline' or 'rearranged' for the V, D, and J genes. This concept is particularly important because it is unique to the immunoglobulin and T cell receptor V, D, and J genes. Note that the C genes do not rearrange directly and therefore their configuration is not defined.

‘chain type’:

The chain type identifies the nature of the polypeptide chain potentially encoded by the T cell receptor genes. There are four main instances which are defined by the C gene sequence characteristics: TcR-Alpha, TcR-Beta, TcR-Gamma, and TcR-Delta.

‘functionality’:

The definition of functionality is based on the sequence analysis. As examples, the instances functional (for germline V, D, J, and for C genes), and productive (for rearranged V-J-C and V-D-J-C sequences) mean that the coding regions have an open reading frame without a stop codon, and that there is no described defect in the splicing sites, and/or recombination signals and/or regulatory elements. According to the gravity of the identified defects, the functionality can be defined as ORF, pseudogene, or vestigial (for germline V, D, J, and for C genes)⁷. Complete definitions are available in the IMGT Scientific chart at <http://imgt.cines.fr>.

The ‘CLASSIFICATION’ concept

The ‘CLASSIFICATION’ concept (Fig. 1) organizes the immunogenetic knowledge useful to name and classify the T cell receptor (TR) genes².

‘locus’:

A locus is a group of T cell receptor genes that are ordered and are localized in the same chromosomal location in a given species. The human genome includes four main T cell receptor loci: TRA (14q11.2), TRB (7q34), TRG (7p14), and TRD (14q11.2), this last one being nestled within the TRA locus. T cell receptor genes have also been identified in other chromosomal locations outside the main loci which represent new instances of the concept locus. However, the genes they contain, designated as orphans, are not functional.

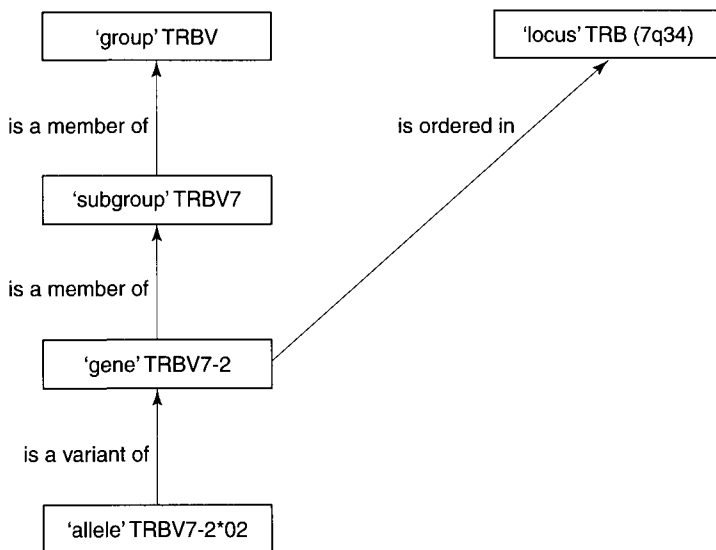


Figure 1. The ‘CLASSIFICATION’ concept in the IMGT-ONTOLOGY.

‘group’:

A group is a set of genes that share the same ‘gene type’ (V, D, J or C) and participate potentially in the synthesis of a polypeptide of the same ‘chain type’. By extension, a group includes the related pseudogenes and orphans.

‘subgroup’:

A subgroup is a set of genes that belong to the same group, in a given species, and that share at least 75% identity at the nucleotide level (in the germline configuration for V, D, and J).

‘gene’:

A gene is defined as a DNA sequence that can be potentially transcribed and/or translated (this definition includes the regulatory elements in 5' and 3', and the introns, if present). Instances of the ‘gene’ concept are gene names. By extension, orphans and pseudogenes are also instances of the ‘gene’ concept. For each gene, IMGT has defined a reference sequence¹. For the V, D, and J genes, the reference sequence corresponds to a germline entity. The rules for the choice of the reference sequences are described in the IMGT Scientific chart.

‘allele’:

An allele is a polymorphic variant of a gene. Alleles are described, exhaustively and in a standardized way, for the four ‘core’ coding regions, that is for the germline V-REGIONS, D-REGIONS, and J-REGIONS, and for the C-REGIONS, from T cell receptor genes. These alleles refer to sequence polymorphisms, with mutations described at the sequence level^{4,7}. Their sequences are compared to the reference sequence designated as *01 (see IMGT Scientific chart at for IMGT description of mutations, and IMGT allele nomenclature for sequence polymorphisms).

Due to the usual absence of somatic hypermutations in V-REGIONS from T cell receptors, rearranged genomic DNA or cDNA can be found included in the alignments of alleles (Section II), when the corresponding germline gene has not yet been isolated. Note that nucleotide mutations and amino acid changes in the CDR3-IMGT of these TR V-REGIONS are not taken into account for the description of allele polymorphisms.

DESCRIPTION OF THE DATA

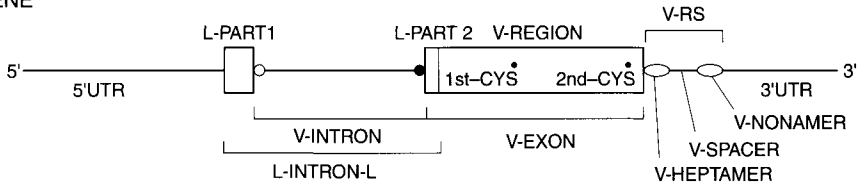
The description of the individual gene entries is based on the ‘DESCRIPTION’ concept of the IMGT-ONTOLOGY², and, for the V-REGIONS, on the setting up of the IMGT unique numbering⁷⁻⁹.

The ‘DESCRIPTION’ concept

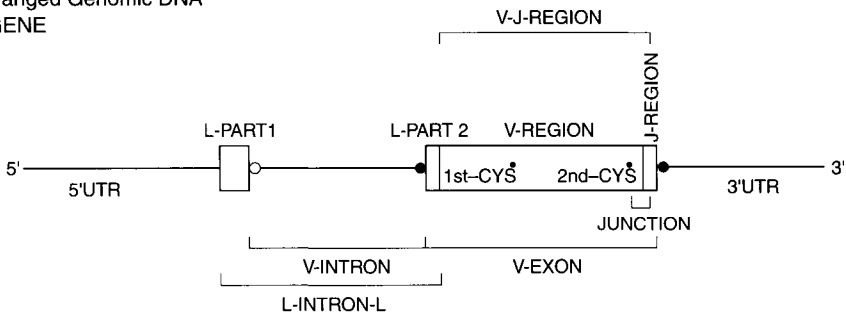
The ‘DESCRIPTION’ concept provides a standardized description of the organization and of the components of the T cell receptor sequences, and a characterization of their specific and conserved motifs. A list of the IMGT labels used in this book is provided. Prototypes have been set up to graphically represent the description and configuration of a T cell receptor gene³ (Fig. 2). For

example, the prototype V-GENE represents a genomic V gene in the germline configuration, whereas V-J-GENE represents genomic V and J genes in the rearranged configuration for an alpha or a gamma chain, and V-D-J-GENE represents genomic V, D, and J genes in the rearranged configuration for a beta or a delta chain (Fig. 2).

Germline Genomic DNA
V-GENE



Rearranged Genomic DNA
V-J-GENE



V-D-J-GENE

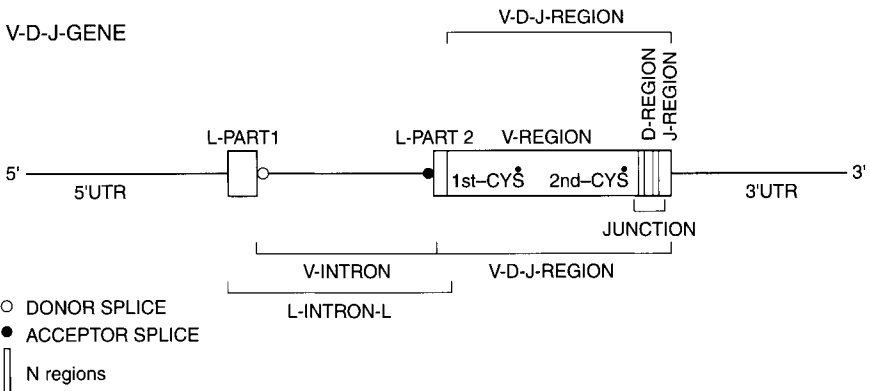


Figure 2. Prototypes of a variable gene in the germline (V-GENE) or rearranged (V-J-GENE for a T cell receptor alpha or gamma chain, V-D-J-GENE for a T cell receptor beta or delta chain) configuration. Labels (in capital letters) are those used for the sequence description in IMGT (<http://imgt.cines.fr>).

THE IMGT UNIQUE NUMBERING FOR THE V-REGIONS

The IMGT unique numbering⁷⁻⁹ relies on the high conservation of the structure of the variable region. This numbering, set up after aligning more than 5000 sequences, takes into account and combines the definition of the framework (FR) and complementarity determining regions (CDR)¹⁰, structural data from X-ray diffraction studies¹¹, and the characterization of the hypervariable loops¹². The delimitations of the FR-IMGT and CDR-IMGT regions have been defined, and correspondence between the IMGT numbering and the other numberings has been established⁹.

The IMGT unique numbering has many advantages:

- It allows an easy comparison between sequences coding the variable regions, whatever the antigen receptor (immunoglobulins or T cell receptors), the chain type (alpha, beta, gamma, or delta chains for T cell receptors), or the species.
- In the IMGT unique numbering, the conserved amino acids always have the same position, for instance Cysteine 23, Tryptophan 41, Leucine 89, Cysteine 104. The hydrophobic amino acids of the framework regions are also found in conserved positions.
- This unique numbering has allowed the redefinition of the limits of the FR and CDR. The FR-IMGT and CDR-IMGT lengths themselves become crucial information characterizing the variable regions belonging to a group, a subgroup and/or a gene.
- Framework amino acids (and codons) located at the same position in different sequences can be compared without requiring sequence alignments. This also holds for amino acids belonging to CDR-IMGT of the same length.
- The IMGT unique numbering has allowed a standardized IMGT description of mutations for the IMGT description of allele polymorphisms of the T cell receptor variable regions^{4,7}.
- The unique numbering is used as the output of the IMGT/V-QUEST alignment tool (<http://imgt.cines.fr>) which analyses your T cell receptor variable (germline or rearranged) sequences according to IMGT criteria¹. In IMGT/V-QUEST, a variable rearranged sequence is compared to the appropriate sets of V-REGION, D-REGION, and J-REGION alleles from the IMGT reference directory. The results show, aligned with the input sequence, the sequences of the most homologous V-REGION alleles and, if appropriate, D-REGION (for beta and delta chains) and J-REGION alleles. The aligned V-REGION sequences are displayed according to the IMGT unique numbering and with the FR-IMGT and CDR-IMGT delimitations.

By facilitating comparisons between the sequences and the descriptions of alleles and mutations, the IMGT unique numbering represents a big step forward in the analysis of the T cell receptor sequences of all species. Moreover, it gives insight to the structural configuration of the variable domain and opens interesting views on the evolution of the sequences of the V-set, since this numbering has been applied with success to all the sequences belonging to the V-set of the immunoglobulin superfamily, including nonrearranging sequences in vertebrates (CD4, *Xenopus* CTX,...) and in invertebrates (*Drosophila* Amalgam, *Drosophila* Fasciclin II, etc.)⁷⁻⁹.

Correspondence between numberings

Table 1 gives the correspondence between the IMGT unique Lefranc numbering⁷⁻⁹ and the different Kabat numberings¹³ for the T cell receptor variable regions.

Table 1. *Correspondence between the V-REGION numberings.*

TRBV					TRAV					TRDV					TRGV					
Human TRBV6-5					Human TRAV8-6					Human TRDV2					Human TRGV3					
FR1-IMGT	1	1	aat	ASN	N	1	0	agc	ALA	A	1	00	gcc	ALA	A	1	01	tct	SER	S
	2	2	gct	ALA	A	2	1	cag	GLN	Q	2	1	att	ILE	I	2	00	tcc	SER	S
	3	3	ggt	GLY	G	3	2	tct	SER	S	3	2	gag	GLU	E	3	1	aac	ASN	N
	4	4	gtc	VAL	V	4	3	gtg	VAL	V	4	3	ttg	LEU	L	4	2	ttg	LEU	L
	5	5	act	THR	T	5	4	acc	THR	T	5	4	gtg	VAL	V	5	3	gaa	GLU	E
	6	6	cag	GLN	Q	6	5	cag	GLN	Q	6	5	cct	PRO	P	6	4	ggg	GLY	G
	7	7	acc	THR	T	7	6	ctt	LEU	L	7	6	gaa	GLU	E	7	5	aga	ARG	R
	8	8	cca	PRO	P	8	7	gac	ASP	D	8	7	cac	HIS	H	8	6	acg	THR	T
	9	9	aaa	LYS	K	9	8	agc	SER	S	9	8	caa	GLN	Q	9	7	aag	LYS	K
	10	10	ttc	PHE	F	10	9	caa	GLN	Q	10	9	aca	THR	T	10	8	tca	SER	S
	11	11	cag	GLN	Q	11	10	gtc	VAL	V	11	10	gtg	VAL	V	11	9	gtc	VAL	V
	12	12	gtc	VAL	V	12	11	cct	PRO	P	12	11	cct	PRO	P	12	10	acc	THR	T
	13	13	ctg	LEU	L	13	12	gtc	VAL	V	13	12	gtg	VAL	V	13	11	agg	ARG	R
	14	14	aag	LYS	K	14	13	ttt	PHE	F	14	13	tca	SER	S	14	12	cag	GLN	Q
	15	15	aca	THR	T	15	14	gaa	GLU	E	15	14	ata	ILE	I	15	13	act	THR	T
	16	16	gga	GLY	G	16	15	gaa	GLU	E	16	15	ggg	GLY	G	16	14	ggg	GLY	G
	17	17	cag	GLN	Q	17	16	gcc	ALA	A	17	16	gtc	VAL	V	17	15	tca	SER	S
	18	18	agc	SER	S	18	17	cct	PRO	P	18	17	cct	PRO	P	18	16	tct	SER	S
	19	19	atg	MET	M	19	18	gtg	VAL	V	19	18	gcc	ALA	A	19	17	gct	ALA	A
	20	20	aca	THR	T	20	19	gag	GLU	E	20	19	acc	THR	T	20	18	gaa	GLU	E
	21	21	ctg	LEU	L	21	20	ctg	LEU	L	21	20	ctc	LEU	L	21	19	atc	ILE	I
	22	22	cag	GLN	Q	22	21	agg	ARG	R	22	21	agg	ARG	R	22	20	act	THR	T
	23	23	tgt	CYS	C	23	22	tgc	CYS	C	23	22	tgc	CYS	C	23	21	tgc	CYS	C
	24	24	gcc	ALA	A	24	23	aac	ASN	N	24	23	tcc	SER	S	24	22	gat	ASP	D
	25	25	cag	GLN	Q	25	24	tac	TYR	Y	25	24	atg	MET	M	25	23	ctt	LEU	L
	26	26	gat	ASP	D	26	25	tca	SER	S	26	25	aaa	LYS	K	26	24	act	THR	T
CDR1-IMGT	27	27	atg	MET	M	27	26	tcg	SER	S	27	26	gga	GLY	G	27	25	gta	VAL	V
	28	28	aac	ASN	N	28	27	tct	SER	S	28	27	gaa	GLU	E	28	26	aca	THR	T
	29	29	cat	HIS	H	29	28	gtt	VAL	V	29	28	gcg	ALA	A	29	27	aat	ASN	N
	30	30	gaa	GLU	E	30	29	tca	SER	S	30	29	atc	ILE	I	30	28	acc	THR	T
	31	*31	tac	TYR	Y	31	30	gtg	VAL	V	31	30	ggt	GLY	G	31	29	ttc	PHE	F
	32	*	---	---	-	32	*31	tat	TYR	Y	32	31	aac	ASN	N	32	30	tac	TYR	Y
	33		---	---	-	33	*	---	---	-	33	32	tac	TYR	Y	33	31	---	---	-
	34		---	---	-	34	*	---	---	-	34	33	tat	TYR	Y	34	32	---	---	-
	35		---	---	-	35		---	---	-	35		---	---	-	35		---	---	-
	36		---	---	-	36		---	---	-	36		---	---	-	36		---	---	-
	37		---	---	-	37		---	---	-	37		---	---	-	37		---	---	-
	38		---	---	-	38		---	---	-	38		---	---	-	38		---	---	-

Table 1. Continued.

	TRBV Human TRBV6-5			TRAV Human TRAV8-6			TRDV Human TRDV2			TRGV Human TRGV3		
FR2 - IMGT	39	32	atg MET M	39	32	ctc LEU L	39	34	atc ILE I	39	33	atc ILE I
	40	33	tcc SER S	40	33	ttc PHE F	40	34A	aac ASN N	40	34	cac HIS H
	41	34	tgg TRP W	41	34	tgg TRP W	41	35	tgg TRP W	41	35	tgg TRP W
	42	35	tat TYR Y	42	35	tat TYR Y	42	36	tac TYR Y	42	36	tac TYR Y
	43	36	cga ARG R	43	36	gtg VAL V	43	37	agg ARG R	43	37	cta LEU L
	44	37	caa GLN Q	44	37	caa GLN Q	44	38	aag LYS K	44	38	cac HIS H
	45	38	gac ASP D	45	38	tac TYR Y	45	39	acc THR T	45	39	cag GLN Q
	46	39	cca PRO P	46	39	ccc PRO P	46	40	caa GLN Q	46	40	gag GLU E
	47	40	ggc GLY G	47	40	aac ASN N	47	41	ggg GLY G	47	41	ggg GLY G
	48	41	atg MET M	48	41	caa GLN Q	48	42	aac ASN N	48	42	aag LYS K
	49	42	ggg GLY G	49	42	gga GLY G	49	43	aca THR T	49	43	gcc ALA A
	50	43	ctg LEU L	50	43	ctc LEU L	50	44	atc ILE I	50	44	cca PRO P
	51	44	agg ARG R	51	44	cag GLN Q	51	45	act THR T	51	45	cag GLN Q
	52	45	ctg LEU L	52	45	ctt LEU L	52	46	ttc PHE F	52	46	cgt ARG R
	53	46	att ILE I	53	46	ctc LEU L	53	47	ata ILE I	53	47	ctt LEU L
	54	47	cat HIS H	54	47	ctg LEU L	54	48	tac TYR Y	54	48	ctg LEU L
	55	48	tac TYR Y	55	48	aag LYS K	55	49	cga ARG R	55	49	tac TYR Y
CDR2 - IMGT	56	49	tca SER S	56	49	tat TYR Y	56	50	gaa GLU E	56	50	tat TYR Y
	57	50	gtt VAL V	57	50	tta LEU L	57	51	aag LYS K	57	51	gac ASP D
	58	51	ggg GLY G	58	51	tca SER S	58	52	gac ASP D	58	52	gtc VAL V
	59	52	gct ALA A	59	52	gga GLY G	59	*	--- --- -	59	53	tcc SER S
	60	53	ggg GLY G	60		--- --- -	60		--- --- -	60	54	acc THR T
	61	54	atc ILE I	61		--- --- -	61		--- --- -	61	55	gca ALA A
	62		--- --- -	62		--- --- -	62		--- --- -	62	56	agg ARG R
	63		--- --- -	63		--- --- -	63		--- --- -	63	57	gat ASP D
	64		--- --- -	64		--- --- -	64		--- --- -	64		--- --- -
	65		--- --- -	65		--- --- -	65		--- --- -	65		--- --- -
FR3 - IMGT	66	55	act THR T	66	53	tcc SER S	66	53	atc ILE I	66	58	gtg VAL V
	67	56	gac ASP D	67	54	acc THR T	67	54	tat TYR Y	67	59	ttg LEU L
	68	57	caa GLN Q	68	55	ctg LEU L	68	55	ggc GLY G	68	60	gaa GLU E
	69	58	gga GLY G	69	56	gtt VAL V	69	56	cct PRO P	69	61	tca SER S
	70	59	gaa GLU E	70	57	gaa GLU E	70	57	ggg GLY G	70	62	gga GLY G
	71	60	gtc VAL V	71	58	agc SER S	71	57A	ttc PHE F	71	63	ctc LEU L
	72	61	ccc PRO P	72	59	atc ILE I	72	57B	aaa LYS K	72	64	agt SER S
	73	62	--- --- -	73	*	--- --- -	73	57C	--- --- -	73	64A	cca PRO P
	74	63	aat ASN N	74	60	aac ASN N	74	58	gac ASP D	74	65	gga GLY G
	75	64	ggc GLY G	75	61	ggg GLY G	75	59	aat ASN N	75	66	aag LYS K
	76	65	tac TYR Y	76	62	ttt PHE F	76	60	ttc PHE F	76	67	tat TYR Y
	77	66	aat ASN N	77	63	gag GLU E	77	61	caa GLN Q	77	68	tat TYR Y
	78	67	gtc VAL V	78	64	gct ALA A	78	62	ggg GLY G	78	69	act THR T
	79	68	tcc SER S	79	65	gaa GLU E	79	63	gac ASP D	79	70	cat HIS H
	80	69	aga ARG R	80	66	ttt PHE F	80	64	att ILE I	80	71	aca THR T
	81	70	tca SER S	81	67	aac ASN N	81	65	gat ASP D	81	72	ccc PRO P
	82		--- --- -	82	68	aag LYS K	82	66	att ILE I	82	*	--- --- -

Table 1. Continued.

	TRBV					TRAV					TRDV					TRGV				
	Human TRBV6-5					Human TRAV8-6					Human TRDV2					Human TRGV3				
FR3-IMGT - continued	83	71	acc	THR	T	83	69	agt	SER	S	83	67	gca	ALA	A	83	73	agg	ARG	R
	84	72	aca	THR	T	84	70	caa	GLN	Q	84	68	aag	LYS	K	84	74	agg	ARG	R
	85	73	gag	GLU	E	85	71	act	THR	T	85	69	aac	ASN	N	85	75	tgg	TRP	W
	86	74	gat	ASP	D	86	72	tcc	SER	S	86	70	ctg	LEU	L	86	76	agc	SER	S
	87	75	ttc	PHE	F	87	73	ttc	PHE	F	87	71	gct	ALA	A	87	77	tgg	TRP	W
	88	76	ccg	PRO	P	88	74	cac	HIS	H	88	72	gta	VAL	V	88	78	ata	ILE	I
	89	77	ctc	LEU	L	89	75	ttg	LEU	L	89	73	ctt	LEU	L	89	79	ttg	LEU	L
	90	78	agg	ARG	R	90	76	agg	ARG	R	90	74	aag	LYS	K	90	80	aga	ARG	R
	91	79	ctg	LEU	L	91	77	aaa	LYS	K	91	75	ata	ILE	I	91	81	ctg	LEU	L
	92	80	ctg	LEU	L	92	78	ccc	PRO	P	92	76	ctt	LEU	L	92	82	caa	GLN	Q
	93	81	tcg	SER	S	93	79	tca	SER	S	93	77	gca	ALA	A	93	83	aat	ASN	N
	94	82	gct	ALA	A	94	80	gtc	VAL	V	94	78	cca	PRO	P	94	84	cta	LEU	L
	95	83	gct	ALA	A	95	81	cat	HIS	H	95	79	tca	SER	S	95	85	att	ILE	I
	96	84	ccc	PRO	P	96	82	ata	ILE	I	96	80	gag	GLU	E	96	86	gaa	GLU	E
	97	85	tcc	SER	S	97	83	agc	SER	S	97	81	aga	ARG	R	97	87	aat	ASN	N
	98	86	cag	GLN	Q	98	84	gac	ASP	D	98	82	gat	ASP	D	98	88	gat	ASP	D
	99	87	aca	THR	T	99	85	acg	THR	T	99	83	gaa	GLU	E	99	89	tct	SER	S
	100	88	tct	SER	S	100	86	gct	ALA	A	100	84	ggg	GLY	G	100	90	ggg	GLY	G
	101	89	gtg	VAL	V	101	87	gag	GLU	E	101	85	tct	SER	S	101	91	gtc	VAL	V
	102	90	tac	TYR	Y	102	88	tac	TYR	Y	102	86	tac	TYR	Y	102	92	tac	TYR	Y
	103	91	ttc	PHE	F	103	89	ttc	PHE	F	103	87	tac	TYR	Y	103	93	tac	TYR	Y
CDR3-IMGT	104	92	tgt	CYS	C	104	90	tgt	CYS	C	104	88	tgt	CYS	C	104	94	tgt	CYS	C
	105	93	gcc	ALA	A	105	91	gct	ALA	A	105	89	gcc	ALA	A	105	95	gcc	ALA	A
	106	94	agc	SER	S	106	92	gtg	VAL	V	106	90	tgt	CYS	C	106	96	acc	THR	T
	107	95	agt	SER	S	107	93	agt	SER	S	107	91	gac	ASP	D	107	97	tgg	TRP	W
	108	96	tat	TYR	Y						108	92	acc	THR	T	108	98	gac	ASP	D
	109	97	---	---	-											109	99	agg	ARG	R

For each V-REGION group, one germline sequence is shown with, on the left hand side of each column, the IMGT unique Lefranc numbering (in bold)⁷⁻⁹ and the corresponding Kabat numbering¹³.

Positions of missing amino acids (shown with dashes) are reported to the 3' end of the CDR-IMGT. Asterisks (*) indicate positions for which it is not possible to make changes from one numbering to the other, automatically.

1st-CYS 23, CONSERVED-TRP 41, and 2nd-CYS 104 are in bold.

ORGANIZATION OF THE DATA

Nomenclature

The IMGT gene name (gene symbol) and the IMGT full name are given. The concepts of classification (Fig. 1) have been used to set up a unique nomenclature of the T cell receptor genes¹⁴⁻²³. A four-letter root designates the 'group': TRAV,

TRAJ, and TRAC for the T cell receptor alpha genes; TRBV, TRBD, TRBJ, and TRBC for the T cell receptor beta genes; TRGV, TRGJ, and TRGC for the T cell receptor gamma genes; and TRDV, TRDD, TRDJ, and TRDC for the T cell receptor delta genes.

Gene names are derived from the four-letter root, by adding, if necessary, number(s) and/or letter(s) to allow unambiguous identification of the gene, a single number or letter being used whenever it is possible. IMGT nomenclature was approved by the HUGO (HUMAN Genome Organization) Nomenclature Committee (<http://www.gene.ucl.ac.uk/nomenclature>) in 1999.

Definition and functionality

The definition includes information on the functionality of a gene, and if necessary, that of its alleles. It also comprises eventual structural or biological particularities.

Gene location

The chromosomal location of the gene is given.

Nucleotide and amino acid sequences

Alignments of all known germline sequences assigned to the different alleles, by comparison to the allele*01, are displayed. The translation of the allele*01, and the nucleotide mutations and corresponding amino acid changes of the other alleles, are shown.

Dashes indicate identical nucleotides. Dots indicate gaps according to the IMGT numbering.

Allele names of the V-REGIONS, D-REGIONS, J-REGIONS, and C-REGIONS comprise the IMGT gene name followed by an asterisk and a two-figure number. The V-REGIONS, D-REGIONS, J-REGIONS and C-REGIONS selected as references for the allele polymorphism description have the number *01; other alleles are designated by increasing numbers (*02, *03, ...) based, if possible, on chronological order of their publication, and/or confirmation of data by different authors.

Note that the number *01 does not mean necessarily that other alleles are already known; it signifies that any new polymorphic sequence will be described by comparison to that allele, *01.

IMGT accession numbers are indicated for each allele. Although the IMGT accession numbers are the same as those from the EMBL/GenBank/DDBJ generalist databases, the content of the IMGT/LIGM-DB flat files differs by the expertised annotations added by IMGT. IMGT data are available from the IMGT/LIGM-DB sequence database, from the IMGT Repertoire, and via SRS sites (available from the IMGT Home page, <http://imgt.cines.fr>). References indicated by a number between brackets are listed at the end of the group entries.

Framework and complementarity determining regions

For the V-GENE entries, the length (in number of amino acids) of the framework (FR) and Complementarity Determining Regions (CDR) are indicated. The limits of the FR and CDR are based on the IMGT unique numbering⁷⁻⁹.

Colliers de Perles

The IMGT Colliers de Perles^{1,4,5,9} are 2D graphical representations of the T cell receptor variable regions, with FR-IMGT and CDR-IMGT delimitations. Colliers de Perles 2D representation provides information on the amino acid positions in the beta-strands and loops of the variable domain and allows quick visualization of amino acids which are important for the structural configuration of the V-REGION.

Amino acids are shown in the one letter abbreviation. Hydrophobic amino acids (hydropathy index with positive value) and Tryptophan (W) found at a given position in more than 50% of analysed T cell receptor sequences are shown in dark grey. All Proline (P) are shown in pale grey. The CDR-IMGT are limited by amino acids shown in squares, which belong to the neighbouring FR-IMGT. Hatched circles or squares correspond to missing positions according to the IMGT unique numbering.

Arrows indicate the direction of the beta-strands and their different designations in 3D structure. This information has to be used carefully if not supported by experimental data.

For a given germline V-GENE, the lengths of the three CDR-IMGT are shown in brackets after the gene name, and separated by full points. For example, TRGV9 [8.7.5] means that in the germline TRGV9 gene, the CDR1-IMGT, CDR2-IMGT, and CDR3-IMGT regions are 8, 7, and 5 amino acids long, respectively.

Genome database accession numbers

All IMGT human T cell receptor genes¹⁴⁻²³ have been entered into GDB, Genome Database, Toronto, Canada (<http://www.gdb.org>), and into LocusLink at NCBI (National Center for Biotechnology Information), Bethesda, USA (<http://www.ncbi.nlm.nih.gov/LocusLink>), and accession numbers are provided. Links to the individual IMGT, GDB and LocusLink gene entries are available from <http://imgt.cines.fr> from IMGT Repertoire>List of human Ig and TcR genes>T cell receptors. Links to OMIM (Online Mendelian Inheritance in Man, MIM) (<http://www.ncbi.nlm.nih.gov/Omim>) are cited when there are existing entries in OMIM.

References

- ¹ Lefranc, M.-P. et al. (1999) *Nucleic Acids Res.* 27, 209–212.
- ² Giudicelli, V., et al. (1999) *Bioinformatics* 15, 1047–1054.
- ³ Giudicelli, V., et al. (1997) *Nucleic Acids Res.* 25, 206–211.
- ⁴ Lefranc, M.-P. et al. (1998) *Nucleic Acids Res.* 26, 297–303.
- ⁵ Ruiz, M. et al. (2000) *Nucleic Acids Res.* 28, 219–221.
- ⁶ Lefranc, M.-P. (2000) *BIOforum International* 4, 98–100.
- ⁷ Lefranc, M.-P. (1998) *Exp. Clin. Immunogenet.* 15, 1–7.
- ⁸ Lefranc, M.-P. (1997) *Immunol. Today* 18, 509.
- ⁹ Lefranc, M.-P. (1999) *The Immunologist.* 7, 132–136.
- ¹⁰ Kabat, E.A. et al. (1987) In 'Sequences of Proteins of Immunological Interest'. Public Health Service, NIH, Washington DC.
- ¹¹ Satow, Y. et al. (1986) *J. Mol. Biol.* 190, 593–604.
- ¹² Chothia, C. and Lesk, A.M. (1987) *J. Mol. Biol.* 196, 901–917.

- ¹³ Kabat, E.A. et al. (1991) In 'Sequences of Proteins of Immunological Interest'. NIH Publication 91-3242 Washington DC.
- ¹⁴ Lefranc, M.-P. et al. (1989) *Eur. J. Immunol.* 19, 989-994.
- ¹⁵ Lefranc, M.-P. and Rabbitts, T.H. (1990) *Res. Immunol.* 141, 615-618.
- ¹⁶ Lefranc, M.-P. (1990) *Res. Immunol.* 141, 692-695.
- ¹⁷ Lefranc, M.-P. (2000) In *Curr. Protocols Immunol.* A.10.1-A.10.23, John Wiley and Sons, New York, USA.
- ¹⁸ Folch, G. and Lefranc, M.-P. (2000) *Exp. Clin. Immunogenet.* 17, 42-54.
- ¹⁹ Folch, G. and Lefranc, M.-P. (2000) *Exp. Clin. Immunogenet.* 17, 107-114.
- ²⁰ Scaviner, D. and Lefranc, M.-P. (2000) *Exp. Clin. Immunogenet.* 17, 83-96.
- ²¹ Scaviner, D. and Lefranc, M.-P. (2000) *Exp. Clin. Immunogenet.* 17, 97-106.
- ²² Folch, G. et al. (2000) *Exp. Clin. Immunogenet.* 17, 205-215.
- ²³ Lefranc, M.-P. *The Immunologist* 8, 72-79.

2 T cell receptor structural and biological properties

INTRODUCTION

The T cell receptors (TcR), like the immunoglobulins (Ig) or antibodies, are clonotypic antigen-specific receptors which are essential to the immune response. T cell receptors which are present on the cell surface of T lymphocytes (T cells) differ in several ways from the immunoglobulins: (1) immunoglobulins are tetramers, made up of four polypeptide chains (two heavy chains and two light chains) and possess two antigen-recognition sites, T cell receptors are dimers and possess only one antigen-recognition site (Fig. 1) (2) immunoglobulins are found either as membrane bound surface receptors on B lymphocytes or in a secreted form, T cell receptors exist only as membrane-bound surface receptors (3) immunoglobulins recognize soluble and native antigens (Ag), T cell receptors recognize protein antigens once they have been processed and converted into small surface peptides and bound to the major histocompatibility complex (MHC) molecules at the surface of antigen-presenting cells (APC) (e.g., macrophages, monocytes, B cells, and dendritic cells). This phenomenon is known as MHC-restricted recognition, or MHC restriction.

The 'education' of T cells to recognize the MHC molecules of their own body (i.e., self-MHC) takes place in the thymus. The conventional T cell receptor, or $\alpha\beta$ TcR, is expressed on most T lymphocytes and consists of two glycosylated polymorphic disulfide-linked chains α and β (Fig. 2), noncovalently associated with the nonpolymorphic membrane-bound CD3 proteins to form the functional TcR-CD3 at the cell surface. The $\alpha\beta$ TcR must discriminate among different peptides embedded in the surfaces of the MHC molecules whose dimensions and shape are relatively constant. The α and β chains participate in the interaction with the pMHC (peptide-MHC) complex, whereas the CD3 proteins participate in signal transduction. Recombinant DNA technology has led to the identification of another locus γ , in the mouse¹ and in humans². Two years thereafter, the γ chain was demonstrated to be part of another type of T cell receptor, or $\gamma\delta$ TcR, which comprises two chains, γ and δ , also associated with the CD3 proteins, at the cell surface of a subset of T cells³⁻⁶ (Fig. 2). The $\gamma\delta$ TcR recognize carbohydrate-, nucleotide-, or phospho-carrying antigens for which the mode of presentation is still poorly characterized. T cells express either the $\alpha\beta$ TcR or the $\gamma\delta$ TcR^{7,8}.

The $\alpha\beta$ and $\gamma\delta$ T cell receptors are associated with the CD3 complex (Fig. 2), which comprises the CD3 γ , CD3 δ , CD3 ϵ , CD3 ζ (dzêta), and CD3 η (êta) proteins organized in CD3 $\gamma\epsilon$, $\delta\epsilon$, and $\zeta\zeta$ or $\zeta\eta$ dimers⁹⁻¹⁰; CD4 and CD8, which act as coreceptors for MHC class II or class I molecules, respectively, with their attendant T cell specific tyrosine kinase p56lck¹¹; and the transmembrane protein tyrosine phosphatase CD45.

After specific recognition of foreign antigen by the T cell receptor, T cells are activated. They acquire activation antigens such as CD69, and express cytokine receptors including CD25 (IL-2 receptor α chain), and start to proliferate. Both $\alpha\beta$ and $\gamma\delta$ T cells display two types of effector functions: cytokine production and cytotoxic activity against microorganisms and tumor cells¹²⁻¹⁴. The effector cytotoxic activity of $\alpha\beta$ and $\gamma\delta$ T cells comprises two pathways: cytotoxicity mediated via the granzyme/perforin pathway and apoptosis via the Fas/Fas-ligand interaction.

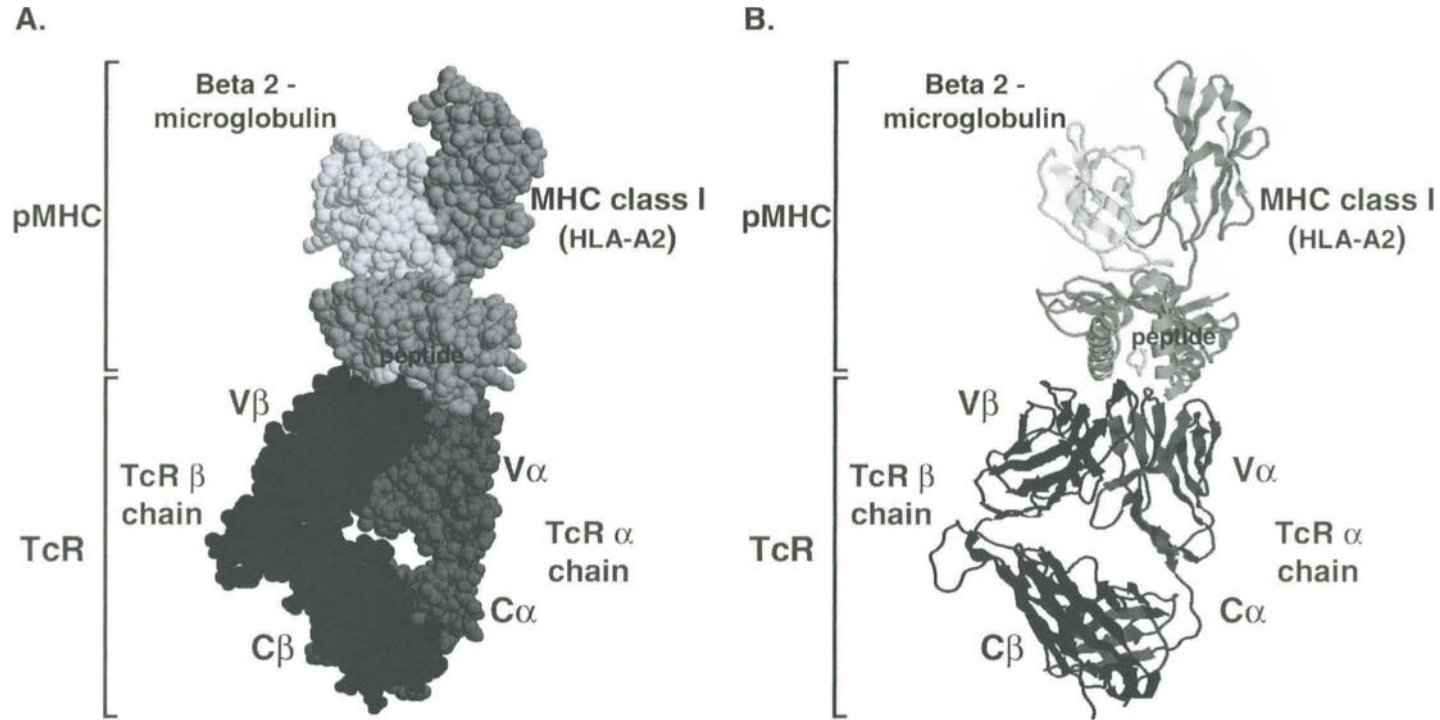


Figure 1. 3D representations of a human $\alpha\beta$ T cell receptor recognizing a viral peptide presented by the human Major Histocompatibility Complex (MHC) class I molecule HLA-A2. **(A)** Spacefill model. **(B)** Cartoon model. The corresponding PDB file is 1BD2. Carbohydrates are not shown. Only the extracellular domains of the TcR and of the MHC are displayed. In vivo, the TcR and the pMHC (peptide-MHC) are membrane-bound on the surface of a T cell, and of an antigen presenting cell (APC), respectively. V = variable domain, C = constant domain.

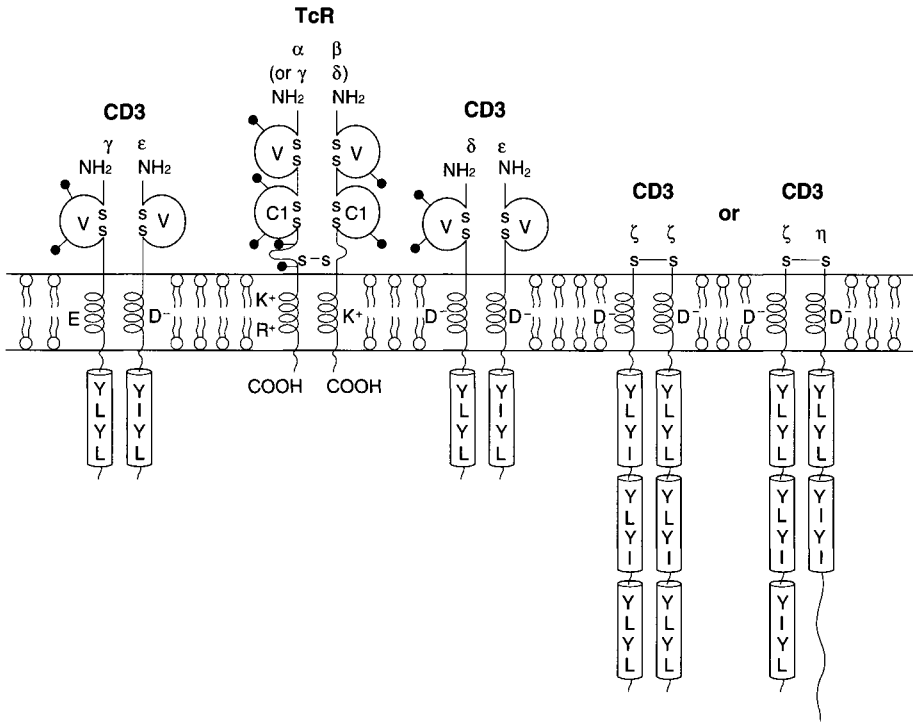


Figure 2. Representation of an $\alpha\beta$ (or $\gamma\delta$) TcR-CD3 complex. Positively and negatively charged amino acids of the transmembrane region as well as intracytoplasmic CD3 ITAMs are indicated. ITAMs, shown as grey cylinders, are not to scale. The TcR N-glycosylation sites are from an $\alpha\beta$ TcR. The $\gamma\delta$ TcR N-glycosylation sites are shown in Fig. 4.

$\alpha\beta$ AND $\gamma\delta$ T CELLS

$\alpha\beta$ T cells

The $\alpha\beta$ T cell receptors are expressed at the surface of T cells that also express the CD antigens CD3 and either CD4 or CD8, these $\text{CD3}^+\text{CD4}^+\text{CD8}^-$ and $\text{CD3}^+\text{CD4}^-\text{CD8}^+$ $\alpha\beta$ T cells represent 90–99 % of the mature peripheral T cells in humans. The $\text{CD3}^+\text{CD4}^+$ $\alpha\beta$ T cells (about 60% of the $\alpha\beta$ T cells) recognize peptides (generally derived from exogenous antigens such as microorganisms) bound to MHC class II molecules and are, for the most part, helper T cells. The $\text{CD3}^+\text{CD8}^+$ $\alpha\beta$ T cells (about 30% of the $\alpha\beta$ T cells) recognize peptides (generated by endogenous processing) bound to MHC class I molecules and are mostly cytotoxic T cells, responsible for finding infected or cancerous cells^{15,16}. CD4 and CD8 are molecules that interact with a nonpolymorphic region of class II and class I molecules, respectively. There is a small subset of $\alpha\beta$ T cells that lack CD4 and

CD8 ('double negative'). These cells, as well as some CD8⁺ αβ T cells, recognize microbial lipid antigens in a CD1-restricted fashion¹⁷.

The ability of αβ T cells to recognize a potentially infinite array of antigen-MHC combinations resides in the variable N-terminal portions of the TcR α and β chains. A single pMHC on an APC cell surface can sequentially engage and trigger as many as 200 αβ TcR¹⁸, consistent with the low affinities and rapid dissociation rates that have been measured for TcR binding to pMHC^{19,20}. A major issue is to explain how a TcR can recognize specific pMHC which are as few as 100 among the 100 000 irrelevant pMHC found on the surface of an APC²¹⁻²³.

TcR α and β chains are subject to allelic exclusion so that a unique αβ receptor type is usually expressed at the surface of a given T cell clone. However, αβ T cells expressing two different alpha chains, and therefore two different αβ receptors, have been identified on the membrane surface of up to one-third of mature T cells²⁴. A small proportion (approximately 1%) of human peripheral T cells has also been shown to express two different V beta^{25,26}.

γδ T cells

The γδ T cells represent 1–10% of peripheral T cells (mean 3%) and 0.2–0.9% of the thymocytes in humans. The γδ T cell receptors are mainly expressed at the surface of T cells that express CD3, but lack CD4 or CD8. Thus the CD4[−]CD8[−] γδ T cells (about 60% of the γδ T cells) recognize antigens independently of the classic MHC class I or class II molecules. A subset of CD4[−]CD8⁺ γδ T cells exist (about 30% of the γδ T cells), along with some very rare CD4⁺CD8[−] γδ T cells. The CD4[−]CD8⁺ γδ T cells usually express CD8αα, not the CD8αβ heterodimer expressed by conventional αβ T cells.

The γδ T cells can recognize a heterogeneous array of ligands, for example in mouse, stress-induced heat-shock proteins from either bacteria or autologous cells^{27,28}, and in human, stress-induced MHC molecules (MICA and MICB), and non-peptidic carbohydrate-, nucleotide- and mycobacterial phospho-carrying antigens¹²⁻¹⁴. The function of these γδ cells could be to eliminate body cells that are under stress, for example as a result of infection or transformation to malignancy. The function of the γδ T cell receptors, the nature of their cognate antigens, and the context in which these antigens are recognized are still poorly characterized and are the object of extensive studies.

Like the α and β chains, the γ and δ chains have clonally unique structures and are subject to allelic exclusion. However, γδ T cells expressing two different gamma chains^{29,30} and, at a lower frequency, two different delta chains³¹, have been identified.

THE T CELL RECEPTOR CHAINS

Structure of the T cell receptor chains

The α and β chains of the αβ TcR, and the γ and δ chains of the γδ TcR possess an N-terminal extracellular region which comprises a variable domain of 104–125 amino acids and a constant domain of 91–129 amino acids, a connecting peptide of 21–62 amino acids, a transmembrane region of 17–26 amino acids, and a small cytoplasmic tail of 0–7 amino acids^{7,8} (Table 1). Each variable and constant domain

Table 1. Human T cell Receptor and CD3 chain characteristics.

Chain Types		T cell Receptor						CD3					
		alpha	beta		gamma		delta	gamma	delta	epsilon	zeta	eta	
Chain characteristics		α	β1	β2	γ1	γ2 (2x)	γ2 (3x)	δ	γ	δ	ε	ζ	η
Molecular weight (kDa) (1)		43–49 (32)		38–44 (34)	40 (30)	40,44 (32)	55 (34)	40–45 (37)	25 (16)	20 (16)	20 (20)	16 (16)	21 (21)
Number of Ig-like domains (2)		2	2	2	2	2	2	2	1	1	1	0	0
Length in number of amino acids	Total length (3)	~241	~277	~279	~273	~289	~305	~254	160	150	185	142	184
	Constant domain (for TcR) (4) or Ig-like domain (for CD3)	91	129	129	110	110	110	93	80	67	91	–	–
	Connecting peptide (4)	30	21	21	30	46	62	36	9	12	13	9	9
	Transmembrane region	17	22	22	26	26	26	25	27	27	26	21	21
	Intracytoplasmic region	3	5	7	7	7	7	0	44	44	55	112	154
N-glycosylation sites (5)		4	1	1	3	4 or 5	5	2	2	2	0	0	0
Charges in transmembrane region (6)		2+ (K, R)	1+ (K)	1+ (K)	3+ (K, R, R)	2 or 3+ (K, R*, R)	2+ (K,R)	3+ (R, K, K)	1– (E)	1– (D)	1– (D)	1– (D)	1– (D)
ITAMs		–	–	–	–	–	–	–	1	1	1	3	2

(1) The relative masses are given in kilodalton (kDa), with those of the backbone proteins in parentheses.

(2) The Ig-like domains of the TcR chain comprises one variable (V) domain and one constant (C) domain of type C1. The Ig-like domain of the CD3 γ , CD3 δ , and CD3 ϵ chains is of type C2³².

(3) The total length for the TcR chains has been calculated by including a V domain with an arbitrary length of 100 amino acids, to facilitate data comparison of the length of the C domain, connecting peptide, and transmembrane and intracytoplasmic regions which, thus, is equal to the total length minus 100.

(4) The TcR chain constant domain is encoded by EX1 whereas the connecting peptide is encoded by EX2 and the 5' part of EX3 (see Chapter 3).

(5) For the TcR chains, N-glycosylation sites of the variable domains (zero or one N-glycosylation site) are not taken into account (see Section II).

(6) Number of negatively (–) or positively (+) charged amino acids are indicated with, between parentheses, involved amino acids. An asterisk indicates an Arginine which can be either present or absent depending on the allelic polymorphism.

has a structure similar to that of the immunoglobulin domain³² and is characterized by a series of multistranded antiparallel β -sheet bilayers and an intradisulfide loop of 51–66 amino acids (Fig. 3). The strands weave back and forth, forming a pleated sheet which folds into a sandwich-like structure. X-ray crystallographic structures of $\alpha\beta$ TcR components have been reported^{34–42}, including murine β chain^{34,35}, V α homodimer³⁶, and intact $\alpha\beta$ TcR³⁷; complex between a human TcR, a viral peptide, and a human class I MHC molecule^{38,39}; complex between a murine TcR, a peptide, and MHC class II⁴⁰; human V δ domain⁴¹; and murine TcR in complex with an anti-

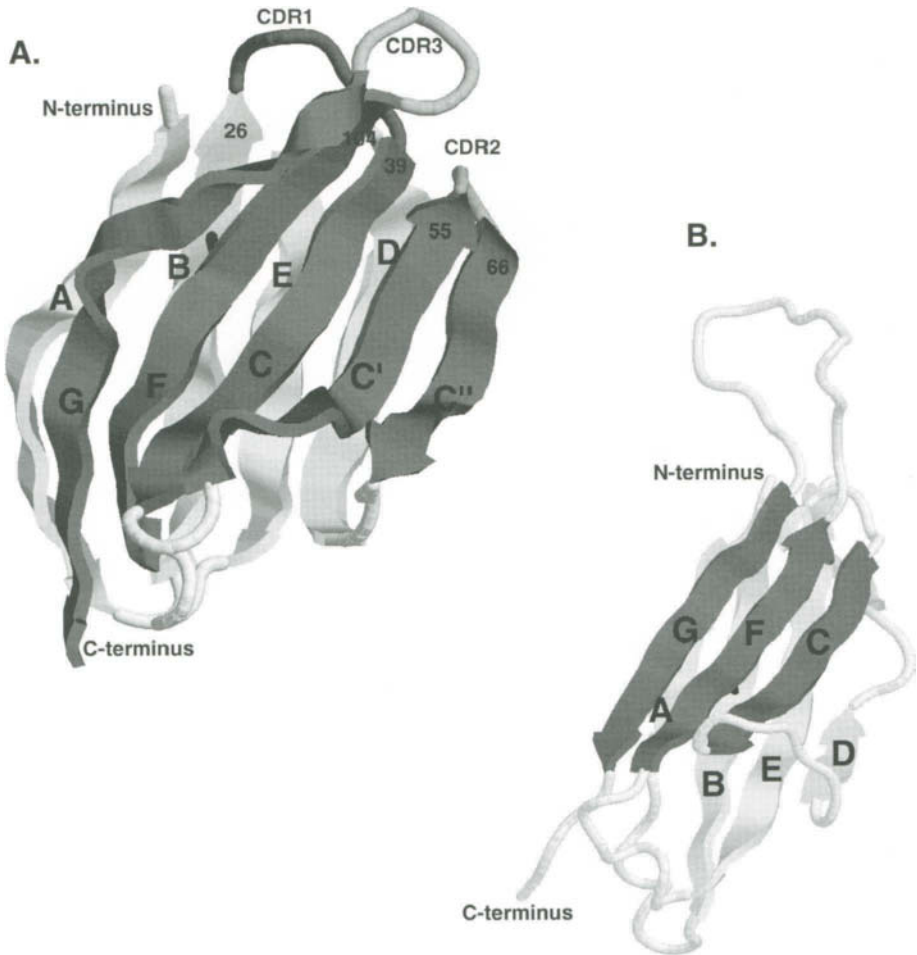


Figure 3. 3D representation (cartoon model) of the variable domain (A) and of the constant domain (B) of a TcR beta chain. These figures show the spreading of the strands labeled A to G, in the two antiparallel sheets (the beta sheet in contact with the domain of the other chain is in dark grey, and the external beta sheet is in light grey). The disulfide bridges of the domains are shown as black cylinders. The FR-IMGT amino acids positions which limit the CDR-IMGT of the variable domain (A) are indicated³³ (see Section II, *Colliers de Perles*).

TcR Fab⁴². Each chain contains a Cysteine proximal to the transmembrane region which is involved in the formation of an α - β and γ - δ interchain disulfide bond, respectively. The human TcR $\gamma 2$ chain, encoded by the constant gene TRGC2, is an exception in that it has no Cysteine in that region and is non-disulfide-linked to the δ chain (Fig. 4)^{7,8}. The $\gamma 2$ chain is 16 or 32 amino acids longer than $\gamma 1$. This results from an allelic polymorphism of the TRGC2 gene which displays a duplication [TRGC2(2x)] or a triplication [TRGC2 (3x)] of exon 2⁴³⁻⁴⁵. All the clonotypic α , β , γ , and δ chains and the associated CD3 proteins possess a hydrophobic and probably helicoidal membrane-spanning region that has the unusual feature of containing charged amino acids: one or two positive charges for the TcR α , β , γ and δ chains, and one negative charge for the CD3 proteins, which probably interact to stabilize the TcR-CD3 complex (Fig. 2).

Glycosylation of the T cell receptor chains

The T cell receptor chains are glycoproteins. The human TcR α chain (43–49 kDa) contains four to five N-linked oligosaccharides of the complex type, attached to a polypeptide backbone of 32 kDa (Table 1). The human TcR β chain (38–44 kDa) contains one or two (one high-mannose and one complex) N-linked glycan side chains attached to a polypeptide backbone of 34 kDa^{7,8}.

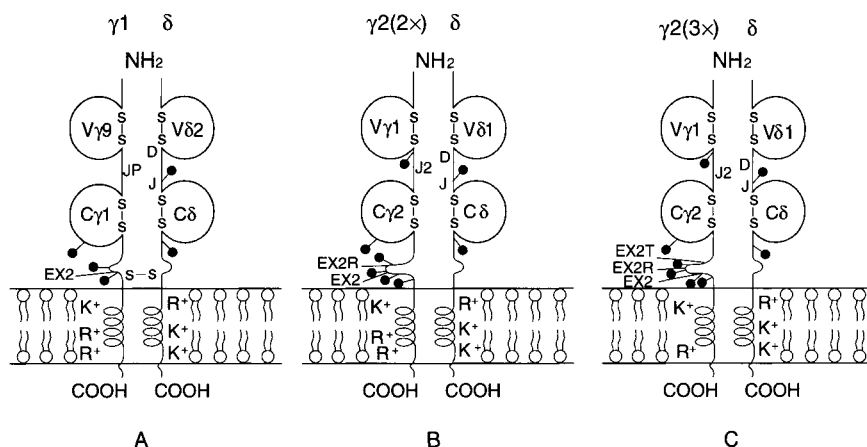


Figure 4. Schematic representation of the three types of human $\gamma\delta$ T cell receptor. There are three types of human $\gamma\delta$ TcR, distinguished by their γ chains^{7,8}: (A) the $\gamma 1\delta$ TcR, in which the 40 kDa $\gamma 1$ chain is disulfide-linked to the δ chain; (B) the $\gamma 2(2x)\delta$ TcR; and (C) the $\gamma 2(3x)\delta$ TcR, in which the 40 or 44 kDa $\gamma 2(2x)$ chain and the 55 kDa $\gamma 2(3x)$ chain are characterized by a duplication or triplication of exon 2, respectively, and are non-disulfide-linked to the δ chain. The $\gamma 2(2x)$ 'exon 2 region' may comprise EX2R (with one N-glycosylation site) or EX2T (no N-glycosylation site). The $\gamma 2(3x)$ 'exon 2 region' comprises EX2, EX2R and EX2T^{7,8}. The V $\gamma 9$, C $\gamma 1$, C $\gamma 2$, V $\delta 1$, V $\delta 2$, and C δ domains are encoded by the TRGV9, TRGC1, TRGC2, TRDV1, TRDV2, and TRDC genes, respectively. The V $\gamma 1$ domain can be encoded by any of the 3–5 functional TRGV1 subgroup genes (see Section II).

There are three types of human γ chains depending on the constant domain^{7,8} (Fig. 4): the $\gamma 1$ chain (40 kDa), whose constant region encoded by the TRGC1 gene is disulfide-linked to the δ chain and has three N-glycosylation sites; the $\gamma 2(2x)$ chains (40 and 44 kDa, which represent two different degrees of glycosylation), encoded by the allelic TRGC2 gene, with duplication of exon 2 (and therefore 16 amino acids longer than $\gamma 1$); and the $\gamma 2(3x)$ chains (55 kDa) encoded by the allelic TRGC2 gene, with triplication of exon 2 (and therefore 32 amino acids longer than $\gamma 1$). The $\gamma 2(2x)$ and $\gamma 2(3x)$ chains are non-disulfide-linked to the δ chain and have four or five N-glycosylation sites (Table 1). These variations in the number of exons and differences in the degree of glycosylation explain the difference in relative molecular mass of the $\gamma 1$ (40 kDa) and $\gamma 2$ (40 or 44 kDa, 55 kDa) chains. Depending on the γ chain, there are, therefore, three types of T cell receptor $\gamma\delta$ dimers: the disulfide-linked $\gamma 1\delta$ receptor, and the nondisulfide-linked $\gamma 2(2x)\delta$ and $\gamma 2(3x)\delta$ receptors (Fig. 4).

THE T CELL RECEPTOR-CD3 COMPLEX

Organization of the T cell receptor-CD3 complex

In addition to the $\alpha\beta$ or $\gamma\delta$ heterodimers which are structurally unique for each clone of T cells, the T cell receptor-CD3 complex comprises the additional nonpolymorphic CD3 γ , CD3 δ , CD3 ϵ , CD3 ζ , and CD3 η proteins, which are identical in all T cells^{9,10}. The CD3 proteins are responsible for coupling TcR occupancy to intracellular signal transduction pathways that result in the events comprising T cell activation. The CD3 γ , CD3 δ , and CD3 ϵ chains contain an N-terminal Ig-like extracellular domain of type C2³², a connecting peptide, a transmembrane region, and a cytoplasmic region (Fig. 2) (Table 1). The CD3 ζ and CD3 η lack the Ig-like domain. The transmembrane regions of the CD3 proteins have a predicted α -helix configuration and contain a negatively charged amino acid (aspartic acid for the CD3 δ , CD3 ϵ , CD3 ζ , and CD3 η chains, glutamic acid for the CD3 γ chain) (Table 1). The cytoplasmic regions of the CD3 chains are considerably longer than those of the TcR α , β , γ , and δ chains and have an important role in the interaction with cytoplasmic components that are directly involved in the transduction of the antigen-binding signal. Indeed, the cytoplasmic region of the CD3 proteins possesses a characteristic motif Yxx(L/I)_{x₆₋₈}Yxx(L/I), designated as ITAM (Immunoreceptor Tyrosine-based Activation Motif). CD3 γ , CD3 δ , and CD3 ϵ have one ITAM, whereas CD3 ζ and CD3 η have three and two ITAMs, respectively (Fig. 2) (Table 1). The phosphorylation of the CD3 ζ ITAMs leads to the recruitment of SH2 (src homology 2) carrying proteins such as ZAP-70 (Zeta Associated Protein of 70 kDa).

The CD3 γ , CD3 δ , and CD3 ϵ chains

The human CD3 γ (25 kDa) and CD3 δ (20 kDa) are glycoproteins bearing two N-linked oligosaccharide side chains and whose protein size is 16 kDa. CD3 ϵ (20 kDa) is not glycosylated. These chains contain one Ig-like domain with an intrachain disulfide bond. The CD3G, CD3D, and CD3E genes encoding the γ , δ , and ϵ chains, respectively, are found within 60 kb on human chromosome 11q23

and probably arose by gene duplication. The highly homologous CD3 γ and CD3 δ genes lie within 1.5 kb of each other. Activation of T cells results in phosphorylation of CD3 γ and CD3 δ .

The CD3 ζ and CD3 η chains

The human CD3 ζ chain is a 16 kDa nonglycosylated protein with no sequence or structural homology to the other CD3 or TcR chains. In contrast to the other chains, ζ has a very short extracellular region of 9 amino acids, with the vast majority of the ζ protein (112 amino acids out of 142) existing as the cytoplasmic region. As for the other CD3 chains, the transmembrane region has a negatively charged amino acid. The ζ chain is encoded by the CD3Z gene found on chromosome 1 at 1q22-q23.

In the majority of receptors, ζ exists as a disulfide-linked 32 kDa ($\zeta\zeta$) homodimer. Five to twenty percent of ζ is disulfide-linked to CD3 η (CD3 *eta*), a 21 kDa splice variant of ζ , in a 37 kDa ($\zeta\eta$) heterodimer. Note that the ζ chain is related to the γ chain of the Fc ϵ RI, Fc γ RI (CD64) and Fc γ RIII (CD16) and can associate with CD16. Cells possess both $\zeta\zeta$ homodimers and $\zeta\eta$ heterodimers, with a ratio of homodimers to heterodimers ranging from 5:1 to 10:1. Activation of T cells results in tyrosine phosphorylation of CD3 ζ and CD3 η .

Biosynthesis and assembly of the T cell receptor-CD3 complex

A T cell cannot recognize antigen unless the TcR-CD3 complex is correctly assembled and efficiently transported and expressed at the cell surface^{9,10,46}. The genes encoding the TcR-CD3 proteins are expressed sequentially during the stages of T cell maturation. CD3 γ , CD3 δ , and CD3 ϵ are synthesized by the earliest recognizable thymocytes, but the proteins remain inside the cell. Assembly of the TcR components takes place within the endoplasmic reticulum (ER) and begins soon after biosynthesis. Within the endoplasmic reticulum there is a transient, noncovalent association with a 26 kDa nonglycosylated protein, the CD3 ω (omega) or TRAP (T cell Receptor Associated Protein). Upon further maturation, T cells begin to express the pre-T cell receptor, a heterodimer of pT α (pre-T cell receptor alpha chain 'substitute') and TcR β chains, on the cell surface of the pre-T cells. After synthesis of the TcR α chain, there is assembly of the full TcR receptor within the ER, and glycosylation processing of the N-linked side chains of the TcR and CD3 chains in the Golgi apparatus. The TcR-CD3 complex is then transported to the plasma membrane. Incomplete TcRs are directed from the Golgi to the lysosomes, where they are rapidly degraded, or are retained for a long period within the ER.

Activation of the T cell receptor-CD3 complex

The TcR-CD3 complex initiates signaling by engaging proximal src-related protein tyrosine kinases (PTKs), such as p56lck and p59fyn. Binding of p56lck to the CD4 and CD8 coreceptors brings the kinases into proximity with the TcR-CD3 complex. A CXCP motif in the cytoplasmic domain of CD4 and CD8 mediates binding to p56lck. This non-covalent interaction requires two cysteines in the N-terminal portion of lck. The activity of p56lck is under the control of CD45, which

initially dephosphorylates the inhibitory site of p56lck. Following the antigen recognition by the $\alpha\beta$ or $\gamma\delta$ T cell receptors^{47,48}, phosphorylation of the ITAM Tyrosines of the CD3 γ , CD3 δ , CD3 ϵ and CD3 ζ chains by p56lck and p59fyn represents one of the earliest events on the signaling cascade. Phosphorylation of both Tyrosines within an ITAM (diphosphorylation) is essential for signaling, as this is required for efficient recruitment of the tandem SH2 domain of ZAP-70. Subsequent phosphorylation of ZAP-70 by p56lck leads to ZAP-70 activation and results in the recruitment and ZAP-70-mediated phosphorylation of effector molecules such as the adaptor proteins LAT (Linker for Activation of T cells) and SLP-76 (SH2 domain-containing Leukocyte Protein of 76 kDa), which couple immune receptors to downstream signaling pathways⁴⁹. Thus these adaptor proteins link the T cell receptors to PLC- γ 1, Grb-2/Sos, and PI3K, resulting in the activation of the calcium and MAP (Mitogen-Activated Protein) kinase pathways^{48–50}.

T cell activation leads to membrane reorganization and to the formation of a SMAC (SupraMolecular Activation Cluster) or mature immunological synapse with the APC. This contact shows a TcR receptor segregation together with their signaling protein complexes and is associated to coalescing lipid rafts⁵¹. These rafts, also referred to as GEMs, membrane glycosphingolipid-enriched microdomains, contain GPI (Glycosylphosphatidylinositol)-linked proteins, src-like tyrosine kinases and other proteins targeted to rafts through saturated acyl chains^{52–55}. The central area of a SMAC contains the TcR-CD3 complex, CD4 or CD8 coreceptors, CD28 costimulatory molecule, CD2 adhesion molecule, p56lck and p59fyn kinases, and the Ca²⁺ independent Protein Kinase C (PKC) θ (thêta), while the peripheral regions are enriched in LFA-1 (Lymphocyte Function-Associated-1) adhesion molecule and the cytoskeletal protein talin⁵⁶. TcR induced cytoskeletal changes involve signaling through SLP76-Vav-Nck to activate effectors of the Rho-family of GTPases⁵⁰. CD45 is excluded from the vicinity of the ligated TcR⁵⁷. The segregation of TcR and signaling molecules appears critical for lymphocyte activation⁵⁶.

References

- ¹ Saito, H. et al. (1984) *Nature* 309, 757–762.
- ² Lefranc, M.-P. and Rabbitts T. H. (1985) *Nature* 316, 464–466.
- ³ Brenner, M.B. et al. (1986) *Nature* 322, 145–149.
- ⁴ Bank, I. et al. (1986) *Nature* 322, 179–181.
- ⁵ Weiss, A. et al. (1986) *Proc. Natl Acad. Sci. USA* 83, 6998–7002.
- ⁶ Moingeon, P. et al. (1986) *Nature* 323, 638–640.
- ⁷ Lefranc, M.-P. (1990) *Eur. Cytokine Network* 1, 121–130.
- ⁸ Lefranc, M.-P. (1994) *In: Immunochemistry*, van Oss C. J. and van Regenmortel M.H.V. eds. Marcel Dekker Inc., New York, pp 129–157.
- ⁹ Clevers, H. et al. (1988) *Annu. Rev. Immunol.* 6, 629–662.
- ¹⁰ Ashwell, J.D. and Klausner, R. D. (1990) *Annu. Rev. Immunol.* 8, 139–167.
- ¹¹ Bierer, B.E. et al. (1989) *Annu. Rev. Immunol.* 7, 579–599.
- ¹² Kabelitz, D. et al. (1999) *Microbes and Infection* 1, 255–261.
- ¹³ Kabelitz, D. et al. (1999) *Springer Semin. Immunopathol.* 21, 55–75.
- ¹⁴ Kabelitz, D. et al. (2000) *Int. Arch. Allergy Immunol.* 122, 1–7.
- ¹⁵ Kronenberg, M. et al. (1986) *Annu. Rev. Immunol.* 4, 529–591.
- ¹⁶ Harty, J.T. et al. (2000) *Annu. Rev. Immunol.* 18, 275–308.

- ¹⁷ Rosat, J.P. et al. (1999) *J. Immunol.* 162, 366–371.
- ¹⁸ Valittuti, S. et al. (1995) *Nature* 375, 148–151.
- ¹⁹ Matsui, K. et al. (1994) *Proc. Natl Acad. Sci. USA* 91, 862–866.
- ²⁰ Corr, M. et al. (1994) *Science* 265, 946–948.
- ²¹ Demotz, S. et al. (1990) *Science* 249, 1028–1031.
- ²² Harding, C.V. and Unanue, E.R. (1990) *Nature* 346, 574–576.
- ²³ Christinck, E.R. et al. (1990) *Nature* 352, 67–70.
- ²⁴ Padovan, E. et al. (1993) *Science* 262, 422–424.
- ²⁵ Padovan, E. et al. (1995) *J. Exp. Med.* 181, 1587–1591.
- ²⁶ Davodeau, F. et al. (1995) *J. Exp. Med.* 181, 1391–1398.
- ²⁷ Haas, W. et al. (1993) *Annu. Rev. Immunol.* 11, 637–685.
- ²⁸ Hayday, A.C. (2000) *Annu. Rev. Immunol.* 18, 975–1026.
- ²⁹ Davodeau, F. et al. (1993) *Science* 260, 1800–1802.
- ³⁰ Hinz, T. et al. (1996) *Br. J. Hematol.* 94, 62–64.
- ³¹ Peyrat, M.A. et al. (1995) *J. Immunol.* 155, 3060–3067.
- ³² Williams, A. F. and Barclay, A. N. (1988) *Annu. Rev. Immunol.* 6, 381–405.
- ³³ Lefranc, M.-P. (1999) *The Immunologist* 7, 132–136.
- ³⁴ Bentley, G.A. et al. (1995) *Science* 267, 1984–1987.
- ³⁵ Fields, B.A. et al. (1996) *Science* 270, 1821–1824.
- ³⁶ Fields, B.A. et al. (1995) *Nature* 384, 188–192.
- ³⁷ Garcia, K.C. et al. (1996) *Science* 274, 209–219.
- ³⁸ Garboczi, D.N. et al. (1996) *Nature* 384, 134–141.
- ³⁹ Ding, Y.H. et al. (1998) *Immunity* 8, 409–411.
- ⁴⁰ Reinherz, E.L. et al. (1999) *Science* 286, 1913–1921.
- ⁴¹ Li, H. et al. (1998) *Nature* 391, 502–506.
- ⁴² Wang, J. et al. (1998) *EMBO J.* 17, 10–26.
- ⁴³ Lefranc, M.-P. et al. (1986) *Proc. Natl Acad. Sci. USA* 83, 9596–9600.
- ⁴⁴ Lefranc, M.-P. and Rabbitts, T. H. (1989) *TIBS* 14, 214–218.
- ⁴⁵ Buresi, C. et al. (1989) *Immunogenetics* 29, 161–172.
- ⁴⁶ Klausner, R. D. et al. (1990) *Annu. Rev. Cell. Biol.* 6, 403–431.
- ⁴⁷ Janeway, C.A., Jr. (1992) *Annu. Rev. Immunol.* 10, 645–674.
- ⁴⁸ Love, P.E. and Shores E. W. (2000) *Immunity* 12, 591–597.
- ⁴⁹ Rudd, C.E. (1999) *Cell* 96, 5–8.
- ⁵⁰ Van Leeuwen, J.E. and Samelson, L. E. (1999) *Curr. Opin. Immunol.* 11, 242–248.
- ⁵¹ Xavier, R. et al. (1998) *Immunity* 8, 723–732.
- ⁵² Montixi, C. et al. (1998) *EMBO J.* 17, 5334–5348.
- ⁵³ Simons, K. and Ikonen, E. (1997) *Nature* 387, 569–572.
- ⁵⁴ Harder, T. et al. (1998) *J. Cell. Biol.* 141, 929–942.
- ⁵⁵ Acuto, O. and Cantrell, D. (2000) *Annu. Rev. Immunol.* 18, 165–184.
- ⁵⁶ Penninger, J.M. and Crabtree, G.R. (1999) *Cell* 96, 9–12.
- ⁵⁷ Sykulev, Y. (2000) *The Immunologist* 8, 51–57.

3 Synthesis of the T cell receptor chains

Synthesis of the T cell receptor chains occurs during T cell differentiation in the thymus. The normal human thymus develops early on in fetal development, and is colonized by stem cells at 7 to 8 weeks of gestational age. Recent data on human postnatal thymus function support the notion that the human thymus is functional well into adult life (into the sixth decade)¹. The thymus is essential for the initial establishment of the peripheral T cell pool expressing the $\alpha\beta$ and $\gamma\delta$ TcR. Children born without a thymus (complete DiGeorge syndrome) lack functional peripheral T cells.

As for immunoglobulins², the constant region (C-REGION) of the TcR chains is encoded by a constant gene, whereas the variable domain (V-J-REGION of an α or γ chain, V-D-J-REGION of a β or δ chain) is encoded by the joining together of noncontiguous DNA genes: a variable (V) gene and a joining (J) gene for the α and γ chains, a V gene, a diversity (D) gene, and a J gene for the β and δ chains (Fig. 1). As with immunoglobulins, three hypervariable regions or CDR (Complementarity Determining Regions) determine the recognition and binding to the antigen, in the three-dimensional structure. Both CDR1 and CDR2 are encoded within the V genes, whereas the CDR3 occur at the V-J junction in the α and γ chains, and at the V-D-J junction in the β and δ chains. The somatic V-J and V-D-J rearrangements occur during lymphocyte development in the thymus (Fig. 2). There is a chronological order of the rearrangements, with the TRD locus rearranging first, then TRG, TRB, and, at the last, TRA³.

SYNTHESIS OF THE T CELL RECEPTOR CHAINS

Somatic V-J rearrangements in the TRA and TRG loci

For the synthesis of a TcR α chain or a TcR γ chain (Fig. 3), there is first a joining of a V gene to one of the J genes, with deletion of the DNA located between these genes (V-J rearrangement). The rearranged V-J gene, the intermediary DNA between the J gene that has been used and the C gene, and the C gene itself, are transcribed. The primary transcript is then spliced (RNA maturation). The messenger RNA is translated into a polypeptide chain by the ribosomes. The signal peptide is cleaved off following the entry of the polypeptide chain into the endoplasmic reticulum (ER) and a mature TcR α or γ chain is produced.

Somatic V-D-J rearrangements in the TRB and TRD loci

For the synthesis of a TcR β chain (Fig. 4) or a TcR δ chain, two successive rearrangements are required: first, one of the D and one of the J genes are joined together, then one of the V genes is joined to the partially rearranged D-J genes. The rearranged V-D-J gene is transcribed with the downstream C gene into a V-D-J-C premessenger RNA. The primary transcript is then spliced into mature RNA. The messenger RNA is translated into a polypeptide chain by the ribosomes. The signal peptide is cleaved off following the entry of the polypeptide chain into the ER and a mature TcR β or δ chain is produced.

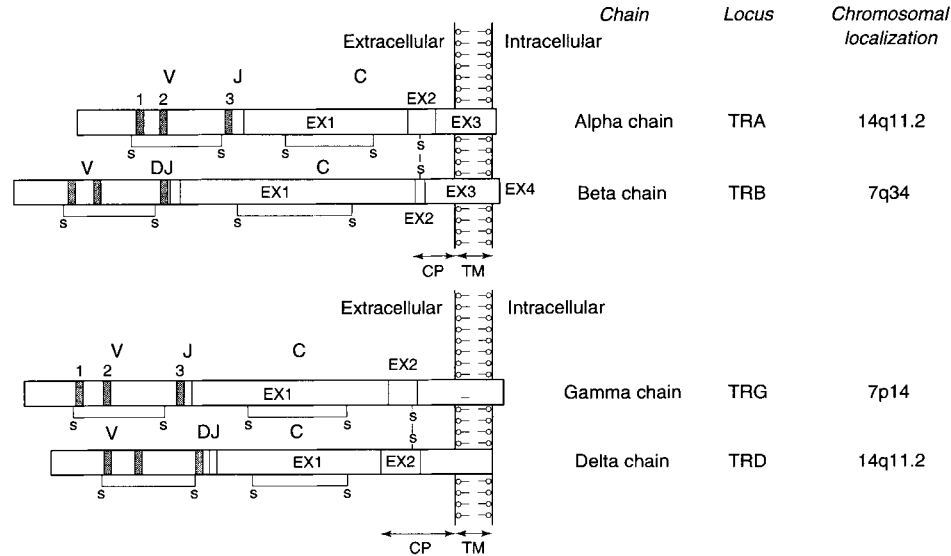


Figure 1. Schematic representation of $\alpha\beta$ and $\gamma\delta$ T cell receptors. The variable domain of an alpha or gamma chain, or V-J-REGION, is encoded by two rearranged genes (one TRAV rearranged to one TRAJ for an alpha chain, one TRGV rearranged to one TRGJ for a gamma chain). The variable domain of a beta or delta chain, or V-D-J-REGION, is encoded by three rearranged genes (TRBV, TRBD, and TRBJ for a beta chain; TRDV, TRDD, and TRDJ for a delta chain). The three hypervariable regions or CDR (Complementarity Determining Regions) 1, 2, and 3 (hatched in the figure) determine the recognition and binding site to the antigen, in the three-dimensional structure. The C-REGION of the alpha, beta, gamma, and delta chains, is encoded by the TRAC, TRBC, TRGC, and TRDC genes, respectively, and comprises a constant (C) domain, a connecting peptide (CP), a transmembrane region (TM), and a very short (absent for the delta chain) intracytoplasmic region. A $\gamma 1$ chain as represented in the figure, has a single exon 2 and is disulfide-linked to the δ chain. In contrast the two types of $\gamma 2$ chain, $\gamma 2(2x)$ and $\gamma 2(3x)$, have a duplicated and triplicated exon 2 coding region, respectively, without cysteine in the connecting peptide and, therefore, there is no $\gamma 2$ - δ interchain disulfide bridge. V = V-REGION, J = J-REGION, D = D-REGION (or more exactly N-AND-D-REGION to take into account the N-diversity), C = C-REGION.

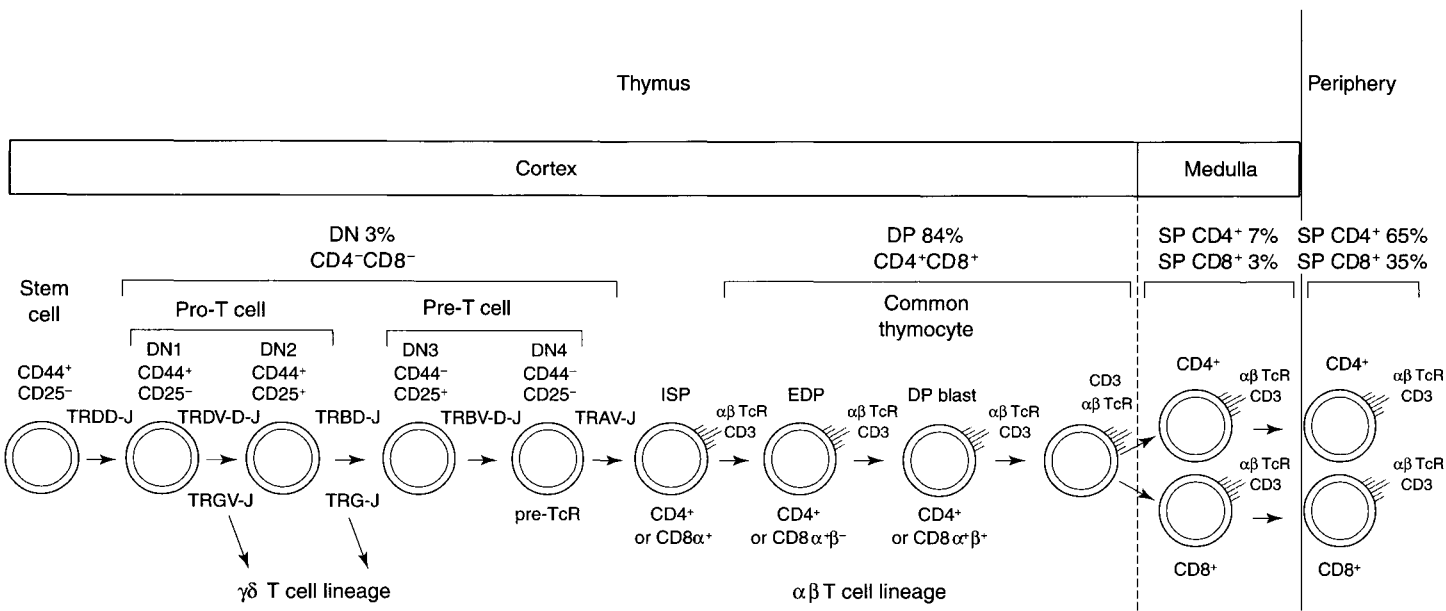


Figure 2. T cell differentiation from the hematopoietic stem cell to the mature $\alpha\beta$ T cells. See also paragraph 'Chronological order of the T cell receptor gene rearrangements' in this chapter. CD44 and CD25 are surface markers, extensively used to characterize the mouse early T cell differentiation populations. The ISP and EDP cells have been characterized in the human thymus³. The pre-TcR plays a crucial role at the checkpoint between DN and DP stages. The $\gamma\delta$ T cell lineage diverges from the $\alpha\beta$ T cell lineage prior to the expression of the pre-TcR. DN = double negative (CD4⁻CD8⁻), DP = double positive (CD4⁺CD8⁺), SP = single positive (CD4⁺ or CD8⁺), ISP = immature single positive (CD4⁺ or CD8⁺), EDP = early double positive (CD4⁺CD8^αβ⁻), lo = low, hi = high.

TRG 7p14

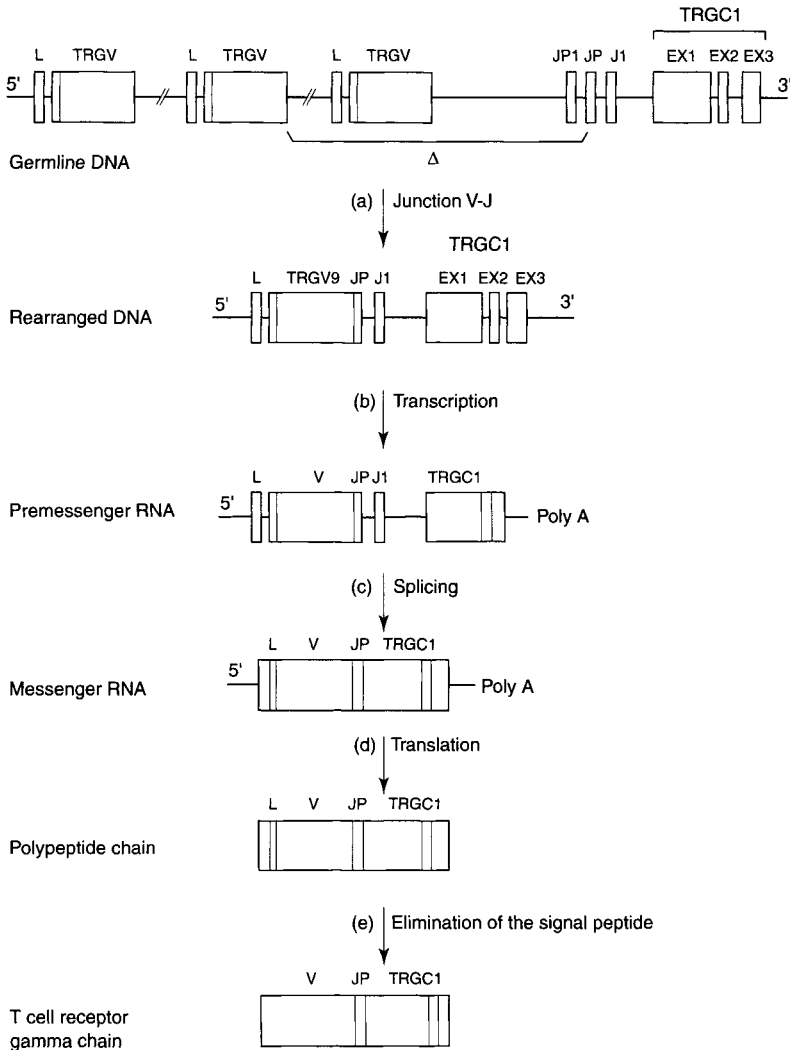


Figure 3. Synthesis of a TcR gamma chain. (a) At the DNA level, one of the TRGV genes is joined to one of the TRGJ genes, with deletion of the intermediary DNA, to create a rearranged TRGV-J gene. (b) The rearranged TRGV-J gene is transcribed with the downstream TRGC gene into a TRGV-J-C premessenger RNA. (c) The RNA sequences corresponding to the introns and to non-used TRGV genes are excised by splicing, and a mature messenger which comprises the spliced coding regions, and the 5' and 3' untranslated sequences, is obtained. (d) The messenger RNA is translated into a polypeptide chain by the ribosomes. (e) The signal peptide is cleaved off by a peptidase following the entry of the polypeptide chain into the endoplasmic reticulum, and a mature TcR gamma chain is produced. L = L-PART1 (L for Leader).

ORIGIN OF THE VARIABLE DOMAIN DIVERSITY OF THE T CELL RECEPTORS

The diversity of the T cell receptor chains depends on two mechanisms: combinatorial diversity, which is a consequence of the number of V, D, and J genes (Chapter 4), and the N-region diversity, which creates an extensive and clonal somatic diversity at the V-J and V-D-J junctions.

Combinatorial diversity

Recombination signals

The junction of T cell receptor genes results, as for the immunoglobulin genes, from the activity of the recombinase enzyme which recognizes the recombination signals, or heptamer-nonamer, present 3' (downstream) from the V genes, 5' (upstream) from the J genes, and on both sides of the D genes (Fig. 5). The heptamer-nonamer sequences are separated by 12 ± 1 or 23 ± 1 nucleotides. Effective recombination takes place between signals separated by a 12 ± 1 base pair (bp) spacer and a 23 ± 1 bp spacer (12/23 rule), as first observed in immunoglobulin rearrangements⁴. Therefore, rearrangements between two V genes or two J genes do not usually occur. In contrast, the TRBD and TRDD genes possess a 12 bp spacer in 5' and a 23 bp spacer in 3', which allow V-D-D-J rearrangements (rare for the TRB locus, but quite common for the TRD locus, where V-D1-D2-D3-J joinings have even been described). These types of rearrangements are not possible in the immunoglobulin heavy chain locus.

Rearrangements by deletion or inversion

In most cases, rearrangements in the T cell receptor loci result from deletional joining. This is in agreement with the V genes being localized upstream from the J (or D and J) and C genes, and in the same orientation of transcription. In such deletional rearrangements, the V and J (or D-J) genes form a contiguous coding sequence, or coding joint, whereas the reciprocal fusion of the recombination signals, or signal joint, leads to the excision of a circular DNA molecule⁵⁻⁷(Fig. 6A). When the V and J (or D-J) genes to be joined are in opposite orientation of transcription on the chromosome, rearrangements occur by inversional joinings.

As a result, the DNA sequences initially located between the V and J (or D-J) genes which rearrange, as well as the signal joints, remain on the chromosome (Fig. 6B). This is exemplified by the rearrangements of the murine TRBV31⁸ and human TRBV30⁹ located downstream from the TRBC2 gene, the murine TRDV5¹⁰ and human TRDV3¹¹⁻¹³ located downstream from the TRDC gene. According to the recombination model proposed by Alt and Baltimore¹⁴ and by Alt and Yancopoulos¹⁵, whether or not joining leads to deletion or inversion is simply based on the relative orientation of the participating genes in the chromosome.

Recombinase

Two genes, RAG1¹⁶ (Recombination Activating Gene 1) and RAG2¹⁷, were characterized in 1989 and 1990, respectively. These two genes are transcribed in

TRB 7q34

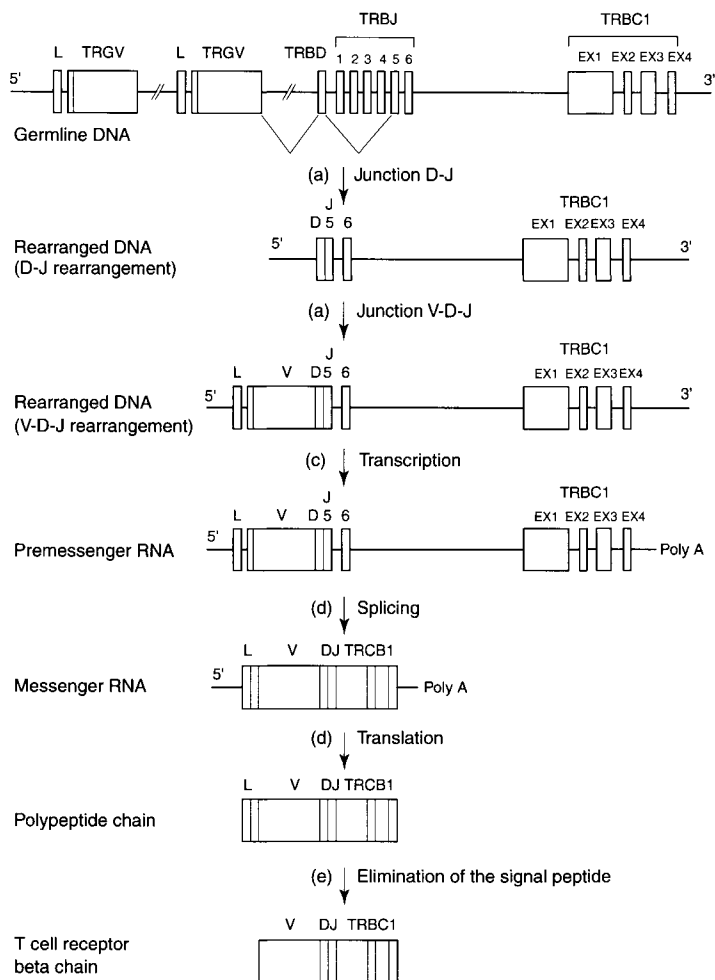
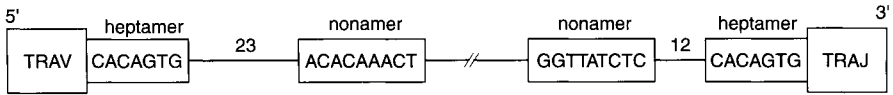
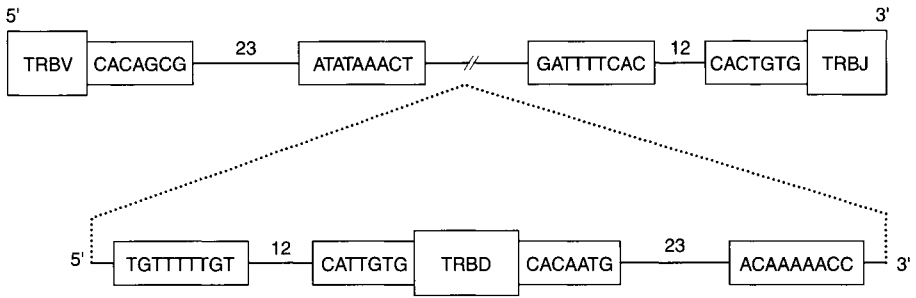


Figure 4. Synthesis of a TcR beta chain. (a) At the DNA level, in a first step, one of the TRBD genes is joined to one of the TRBJ genes, with deletion of the intermediary DNA, to create a partially rearranged D-J gene. In a second step, one of the TRBV genes is joined to D-J, with deletion of the intermediary DNA, to generate a completely rearranged TRBV-D-J gene. (b) The rearranged TRBV-D-J gene is transcribed with the downstream TRBC gene into a TRBV-D-J-C premessenger RNA. (c) The RNA sequences corresponding to the introns and to the non-used TRBJ genes are excised by splicing, and a mature messenger which comprises the spliced coding regions, and the 5' and 3' untranslated sequences, is obtained. (d) The messenger RNA is translated into a polypeptide chain by the ribosomes. (e) The signal peptide is cleaved off by a peptidase following the entry of the polypeptide chain into the endoplasmic reticulum, and a mature TcR beta chain is produced. L = L-PART1 (L for Leader).

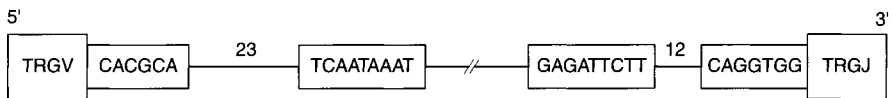
Chromosome 14q11.2



Chromosome 7q34



Chromosome 7p14



Chromosome 14q11.2

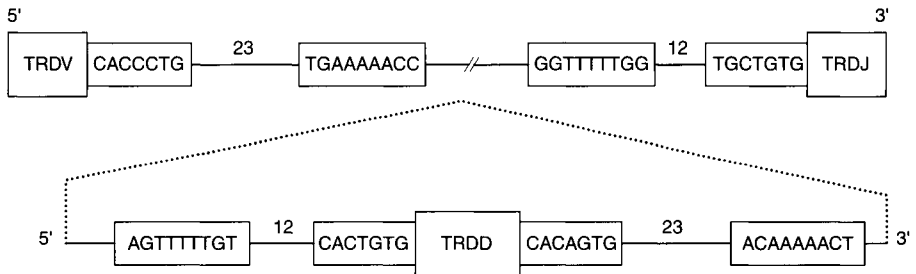


Figure 5. Examples of human T cell receptor V, D, and J gene recombination signals. Although the heptamer and the nonamer sequences are well conserved, there are sequence differences between individual genes as shown in the recombination signal tables in Section II. Spacer lengths are 12 ± 1 or 23 ± 1 bp. This is known as the 12/23 rule.

lymphocytes that have a recombinase activity (that is, the B and T lymphocytes at an early stage of their development). In-vitro nonlymphoid cells are able to recombine transfected V-D-J recombination substrates following introduction of expressed RAG1 and RAG2¹⁷. These two genes are unrelated in amino acid sequence, but are located only 8 kb apart on the same chromosome (11p13). Although the 5' untranslated regions of the cDNAs of both genes contain spliced exons, the RAG1 and RAG2 coding sequences are contained within a single exon. The two genes and their organization have been highly conserved in vertebrate evolution. By homologous recombination, Mombaerts et al.¹⁸ and Shinkai et al.¹⁹

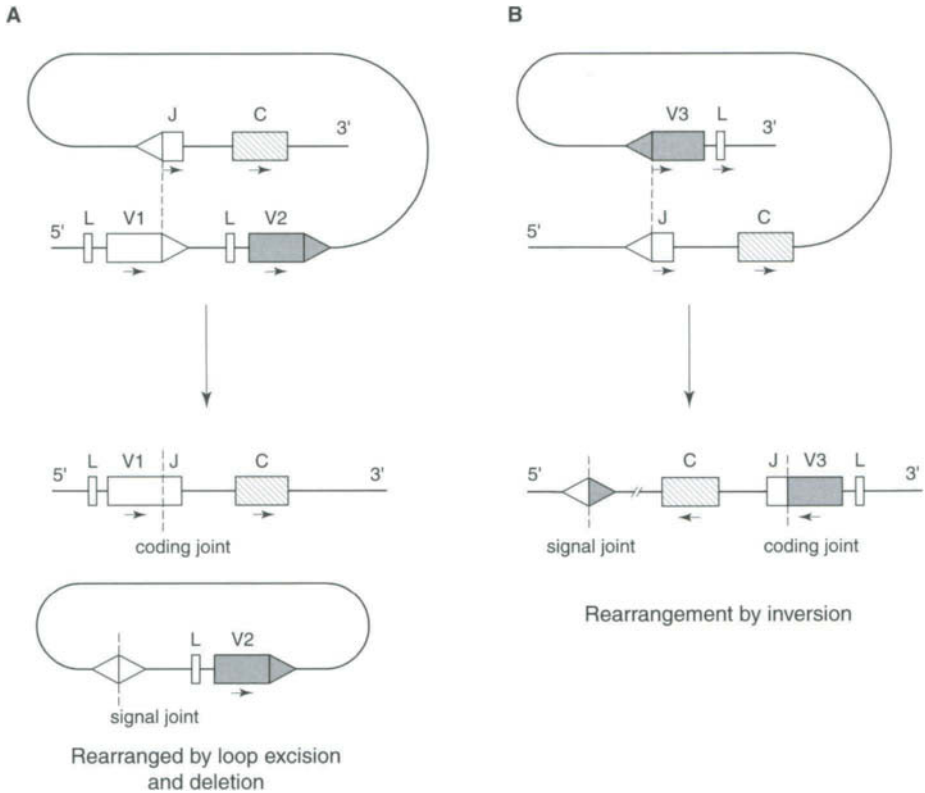


Figure 6. *Rearrangements by loop excision and deletion (A), and by inversion (B). L = L-PART1 (L for Leader).*

have disrupted RAG1 and RAG2, respectively, in the mouse genome. The RAG1 or RAG2 deficient mice have identical phenotypes (i.e., their lymphoid organs are devoid of mature B and T cells). The arrest of B and T cell development occurs at a very early stage, preventing a significant accumulation of immature lymphoid cells. Apart from the complete deficiency of B and T cells, the knock-out RAG1 or RAG2 mice have no other developmental defects and are fertile. The RAG1 and RAG2 proteins are responsible for sequence-specific recognition and DNA cleavage, and they appear to perform multiple post-cleavage roles in the reaction as well²⁰.

Junctional diversity

The N-diversity results from the deletion of nucleotides at the extremities of the coding V, D and J genes by action of an exonuclease and the addition, at random, of nucleotides by the terminal deoxynucleotidyl transferase (TdT)¹⁴. This enzyme preferentially adds G and C nucleotides at the junctions and is specifically transcribed during lymphocytic maturation. In contrast with the immunoglobulin

N-regions, T cell receptor N-regions are less rich in G and C and occasionally display short nucleotide sequences, identical with those found at the extremities of the coding region of the germline V and J genes. These sequences from the V and J ends could be used, in some cases, as templates by the enzyme²¹.

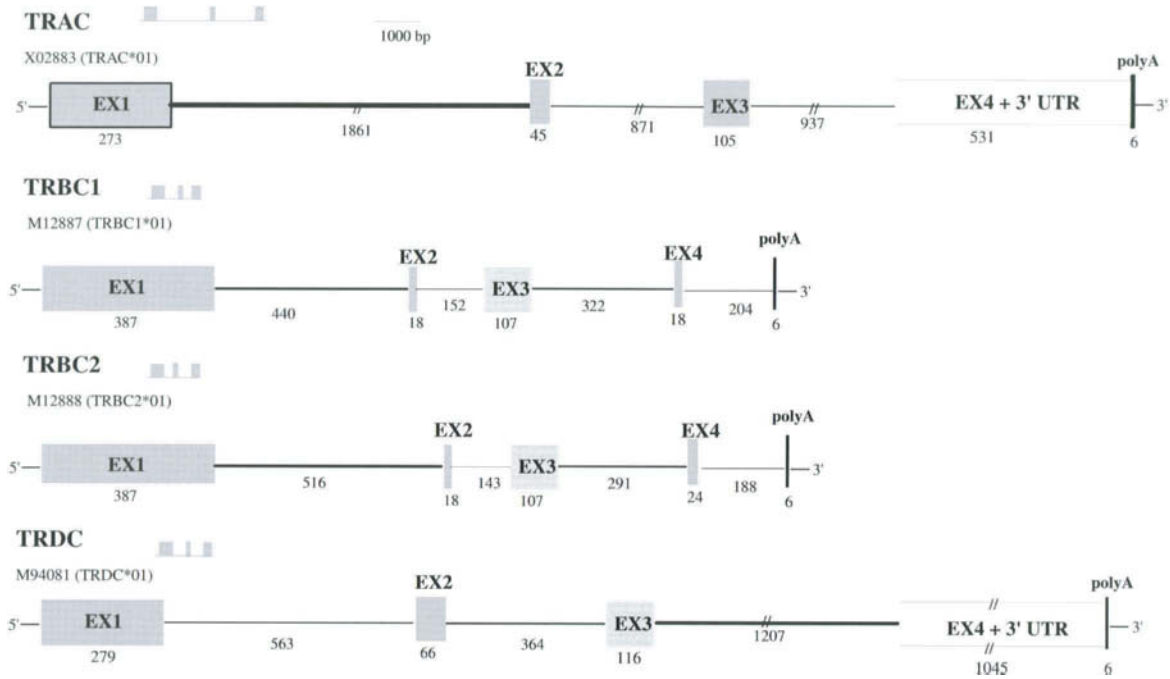
The rearranged TcR genes have a junctional diversity that is more important than that of the immunoglobulins. Indeed, (1) the N-diversity affects all the TcR loci, whereas it affects only the immunoglobulin heavy chain genes; (2) the possibility to join two or even three D genes in the TRD locus still increases the diversity in originating three (or four) N-sequences at the V-D-D-(D-)J junctions; (3) the TRBD and TRDD genes can be read in the three reading frames (which is not generally the case for the IGHD genes).

Nucleotides that are palindromic to the last nucleotides of the germline V genes, to the first nucleotides of the germline J genes, and to the ends of the germline D genes, are designated as 'P' nucleotides and are found at the V-J or V-D-J junctions in cells in which the TcR genes seem not to have been submitted to the exonuclease activity. Indeed, these P nucleotides are only identified when the ends of the respective V, D, and J coding regions are intact²².

In the T cell receptor loci, there are no somatic mutations. This has been demonstrated by the complete identity of several rearranged genes with their germline counterparts and represents an important difference from the immunoglobulin genes²³. As a consequence, oligonucleotides that correspond to V and J sequences can be used as specific primers for in-vitro DNA amplification by the polymerase chain reaction (PCR)²⁴⁻²⁷, and the sequencing of the N-region of the rearranged genes. This method can be applied to the identification of the N-region of malignant clones. Specific oligonucleotides can then be used to detect the residual malignant cells during the treatment of leukemia or in bone marrow samples before an autograft. Anchored-PCR, which uses only one specific primer, has been extensively used for the analysis of TcR V, D, and J gene usage, and for the detection of TcR expression^{27,28}.

THE T CELL RECEPTOR CONSTANT REGIONS AND GENES

The constant regions of the TcR chains are encoded by the constant genes. Figure 7 shows the characteristics of the TRAC, TRBC1 and TRBC2, TRGC1 and TRGC2, and TRDC genes which encode the constant region of the TcR alpha, beta 1 and beta 2, gamma 1 and gamma 2, and delta chains, respectively. TRBC1 and TRBC2, and TRGC1 and TRGC2, represent duplicated genes. TRGC2(2x) and TRGC2(3x) are allelic forms of the TRGC2 gene with duplication (2x) or triplication (3x) of exon 2. These constant genes encode the constant domain, the connecting peptide, the transmembrane region and the intracytoplasmic region as described in Table 1 of Chapter 2. At the genomic level, each constant gene consists of several exons, EX1 to EX4 (Table 1). EX1 encodes the constant domain (91 to 129 amino acids). The EX2, EX2T and/or EX2R, and the 5' part of EX3 encode the connecting peptide, whereas the 3' part of EX3 encodes the transmembrane region. The TRBC1 and TRBC2 EX4 exon encodes the short intracytoplasmic region (the TRAC and TRDC EX4 are not translated).



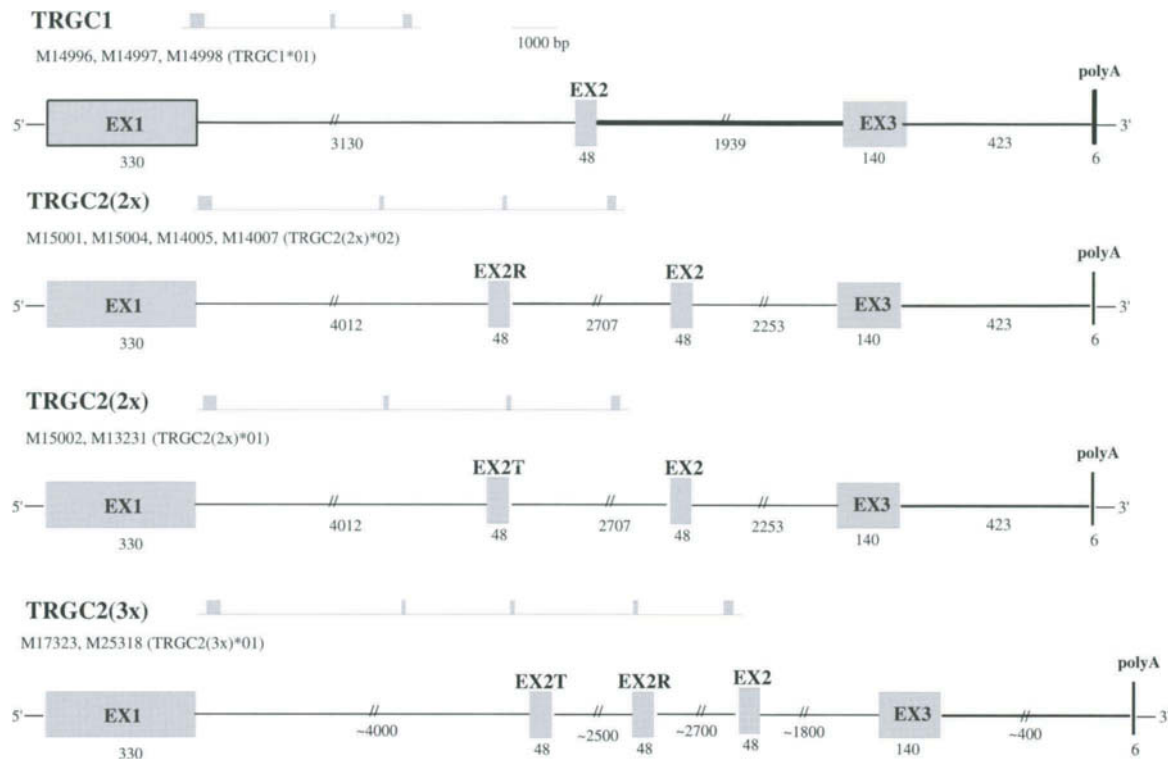


Figure 7. Structure of the human T cell receptor constant genes. Sequences and references for the individual genes and alleles are given in Section II. Size of the exons and introns are in base pairs (bp). Schematic gene representations (scale indicated on the first line) are also shown besides each gene name. The TRAC and TRDC “EX4 + 3’ UTR” are untranslated. The genomic organization of TRGC1 and TRGC2(2x)*02 is from reference 29. Size of the introns is from AF159056. The genomic organization of the TRGC2(2x)*03 and TRGC2(3x) is from reference 30.

Table 1. *Characteristics of the human T cell receptor constant regions*

C genes	TRAC	TRBC1	TRBC2	TRGC1	TRGC2 (2x)	TRGC2 (3x)	TRDC
Characteristics							
EX1	Length in number of amino acids	91	129	129	110	110	93
	1st-CYS (1)	23	31	31	32	32	21
	2nd-CYS (1)	73	96	96	88	88	72
	N-glycosylation sites (1)	33 67 78	70	70	66	66	15 78
EX2T	Length in number of amino acids	–	–	–	–	16*	16
	N-glycosylation sites (1)	–	–	–	–	0	0
EX2R	Length in number of amino acids	–	–	–	–	16*	16
	N-glycosylation sites (1)	–	–	–	–	10	10
EX2	Length in number of amino acids	15	6	6	16	16	16
	N-glycosylation sites (1)	–	–	–	10, 16	10,16	10,16
EX3	Length in number of amino acids	35	36	36	47	47	47
	N-glycosylation sites (1)	8	–	–	–	9	9
	Cysteine (1) (2)	4	2	2	11	–	–
EX4	Length in number of amino acids	n.t.	6	8	0	0	0
C-REGION							
Length in number of amino acids		141	177	179	173	189	205
							154

* polymorphism of the TRGC2(2x) duplicated exon 2 which can be from the EX2T or EX2R type.
n.t. not translated.

(1) Amino acid position. Numbering starts from the first codon of each individual exon.

(2) Cysteine involved in the interdisulfide bridge, and localized in the TcR chain connecting peptide.

REPERTOIRE OF THE $\alpha\beta$ AND $\gamma\delta$ T CELLS

The diversity of the T cell receptors that results from both the combinatorial association of α and β chains, or γ and δ chains, and the junctional N-diversity affect the specificity of the T cell receptors and, therefore, play a major role in the development of the T cell repertoire.

Repertoire of the $\alpha\beta$ T cells

The functional $\alpha\beta$ TcR repertoire in an individual is selected from a population of cells containing randomly rearranged TRAV and TRBV genes, by a combination of positive and negative selective events that occur during intrathymic maturation. Both helper and cytotoxic $\alpha\beta$ T cells draw upon the same pool of germline TRAV and TRBV genes in the production of their antigen receptors (Chapter 4). Both V α and V β domains contribute to the antigen-binding site. There is no simple and general correlation between use of any TRAV or TRBV genes and phenotype, function, specificity, or MHC restriction. However, in some systems, receptors encoded by particular TRAV and TRBV genes may be selected by particular antigen-MHC configurations.

Repertoire of the $\gamma\delta$ T cells

The potential combinatorial diversity of the γ and δ chains is more limited than that of the α and β chains (Chapter 4). Moreover, it is restricted by the preferential usage of some V, D and J genes. In humans, most of the peripheral $\gamma\delta$ T cells express a preferential TRGV and TRDV rearrangement³¹⁻³³. Indeed, TRGV9-JP and TRDV2 are preferentially expressed in human peripheral $\gamma\delta$ T cells (80-95 % of the $\gamma\delta$ T cells) and the corresponding TRGV9-JP-C1 chains are frequently associated with TRDV2-D3-J-C chains³¹⁻³³. These $\gamma\delta$ T cells respond to microbial phosphoantigens.

Antibodies that recognize specifically epitopes of the human C δ (TCR δ -1³⁴, TCR $\gamma\delta$ -1³⁵), V δ 1-J δ 1 (δ TCS-1³⁶), V δ 2 (BB3³⁷), V δ 3 (p11.10b³⁸), V γ 1 subgroup, and V γ 9 regions³⁹⁻⁴¹ are precious tools in the characterization of the human $\gamma\delta$ T cells.

In the human, epithelial tissues contain $\gamma\delta$ T cells in significantly lower numbers than in the mouse. Representation of the $\gamma\delta$ T cells in adult human skin is not significantly different from that in peripheral blood, whereas, in intestinal intraepithelium, most of the $\gamma\delta$ T cells express TRGV1 subgroup genes and the TRDV1 gene. The $\gamma\delta$: $\alpha\beta$ ratio among intestinal intraepithelial lymphocytes (IELs) is about 1:5, compared with about 1:50 in the lymph node.

Polymorphism of the TRGV1 subgroup genes by insertion/deletion^{42,43} and differences in the structural characteristics of the TRGC2 alleles^{30,43} create a polymorphic repertoire in the different populations (Fig. 8).

CHRONOLOGICAL ORDER OF THE T CELL RECEPTOR GENE REARRANGEMENTS

The human T cell receptor genes are rearranged and expressed in a specific order, TRD, TRG, TRB, and TRA³, during thymic development, and the $\gamma\delta$ T cells appear before the $\alpha\beta$ T cells during thymic ontogeny⁴⁴. In humans, a distinct wave has been described in the early fetal thymus, and a chronology of the TRG rearrangements has

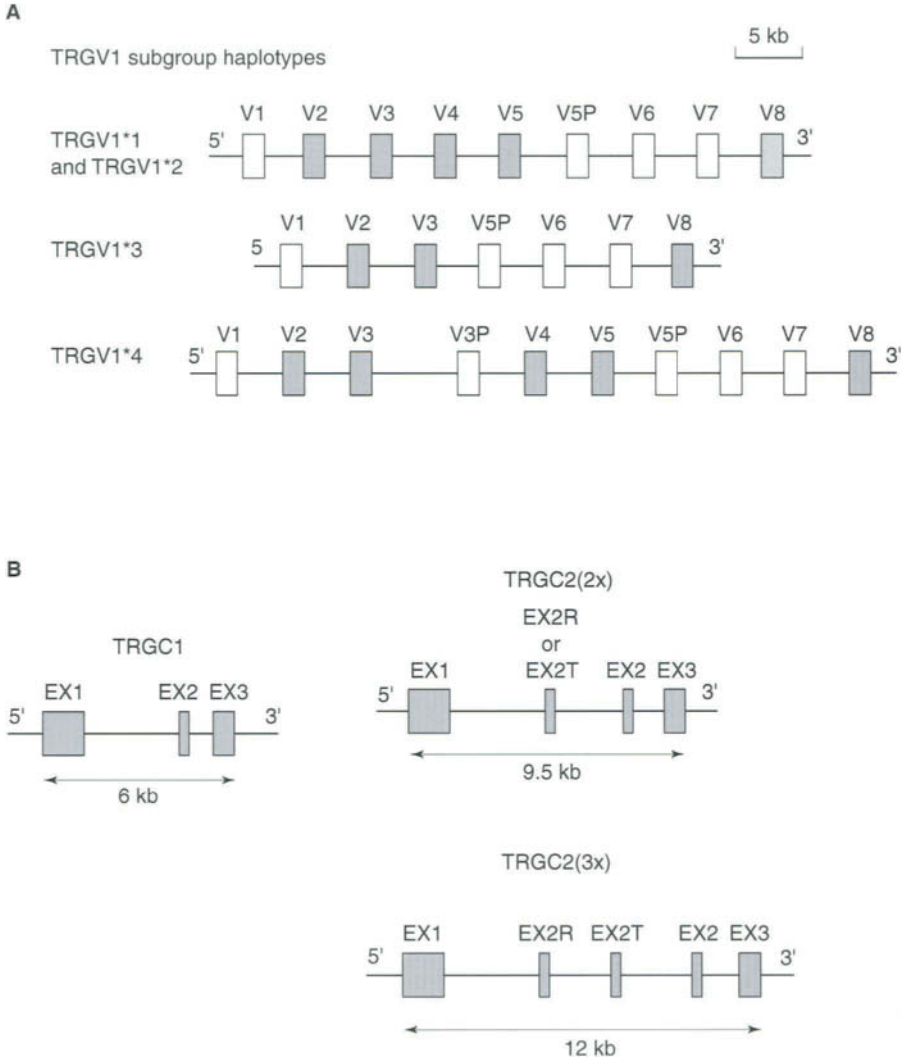


Figure 8. Allelic polymorphism of the human TRG genes. (A) Schematic representation of the TRGV1 subgroup haplotypes^{42,43}. Functional variable genes are shown as grey boxes, and pseudogenes or ORF as white boxes. The TRGV1*1 and TRGV1*2 subgroup haplotypes result from the presence or absence, respectively, of polymorphic restriction sites. The TRGV1*3 subgroup haplotype corresponds to a deletion of the V4 and V5 genes and the TRGV1*4 subgroup haplotype to an insertion of 6 kb corresponding to an additional gene, V3P. (B) Schematic representation of the TRGC genes^{30,43}. Exons are shown as boxes. The allelic TRGC2 genes with duplication or triplication of exon 2 are designated as TRGC2(2x) and TRGC2(3x), respectively.

been proposed^{45,46}. Indeed, most of the $\gamma\delta$ T cells from the peripheral blood express TRGV9-JP³¹, with frequently a nonproductive TRGV10-JP1 subgroup rearrangement on the other chromosome³². The other $\gamma\delta$ T cells express a TRGVI gene joined to J1 or J2. These rearrangements, which use genes that are located upstream of TRGV9 and downstream from JP on the chromosome, most probably occur after the TRGV9-JP rearrangements. This has been suggested by two observations: (1) all $\alpha\beta$ T cells (which appear after the $\gamma\delta$ T cells) display TRGV1 subgroup genes rearranged to J1 or J2, and this on both chromosomes⁴⁷; (2) two successive rearrangements, first TRGV9-JP, and second involving TRGV3 and TRGJ1, have been described on the same chromosome in the SP-F7 cell line⁴⁵. Such a situation was observed because the second rearrangement occurred by inversion and, therefore, maintained the intermediary DNA and the first TRGV9-JP rearrangement on the chromosome (Fig. 9). Thus, the order of the rearrangements and the developmentally regulated V gene expression seem to depend, in part, on the location of V and J genes in the TRG and TRD loci, the first waves using the most proximal V and J genes, and the last waves using the most distal V and J genes⁴⁶ (Fig. 10). However, other factors may also be involved, such as transcriptional regulation of V genes, structural constraint for the pairing of some γ and δ chains, and intrathymic selection by determinants with a programmed expression during thymic development.

The TRD and TRG loci are the first loci to rearrange during thymic ontogeny (Fig. 1). If both loci show a functional (in-frame) rearrangement, and if both the γ and δ chains are synthesized, the T cells express a $\gamma\delta$ TcR at the cell surface. Partial TRBD-J rearrangements may be observed in the $\gamma\delta$ T cells, and some of them express immature TRBC transcripts or even sterile TRAC transcripts. However, the expression of a functional $\gamma\delta$ TcR at the surface stops further rearrangements of the TRB and TRA loci. If the $\gamma\delta$ TcR cannot be expressed at the cell surface, either as a consequence of nonfunctional (out-of-frame) or nonproductive (absence of γ or δ membrane protein) rearrangements, or as a consequence of the activity of a silencer downregulating the TRG locus in *cis*, the TRB locus continue to rearrange. Partial TRBD-J rearrangements are followed by complete TRBV-D-J rearrangements. The pre-TcR, a heterodimer which consists of a rearranged TcR β chain disulfide-linked to the invariant surrogate α chain, pT α , is expressed at the cell surface of immature thymocytes. The expression of the pre-TcR associated with the CD3 proteins signals cessation of TRBV-D-J rearrangements, and thymocyte developmental progression in the $\alpha\beta$ T cell lineage. Indeed, signals delivered through the pre-TcR are crucial for cell survival and for proper transition from the DN (CD4⁻CD8⁻) to DP (CD4⁺CD8⁺) stage of the immature $\alpha\beta$ lineage thymocytes. TRAV-J rearrangements start to occur. Functional rearrangements of one TRA locus and one TRB locus, if productive, allow the expression of a $\alpha\beta$ TcR at the surface of a T cell.

As a consequence of the chronological order of rearrangements, all $\gamma\delta$ and $\alpha\beta$ T cells display rearranged TRG genes, which are, therefore, excellent markers of clonality for the cells of both phenotypes: $\gamma\delta$ and $\alpha\beta$ ^{21,23,48-51}. The localization of the TRD locus, nestled in the TRA locus, results in its deletion on rearrangement of TRAV and TRAJ genes and, therefore, at least one of the two TRD loci is deleted in $\alpha\beta$ T cells. That deletion could occur in two steps: a deletion of the TRD locus, involving specific sequences located upstream from TRDD1 (sequence δ REC) and downstream from the TRDC gene (sequence ϕ) α ^{52,53}, would take place before the TRAV-J rearrangements.

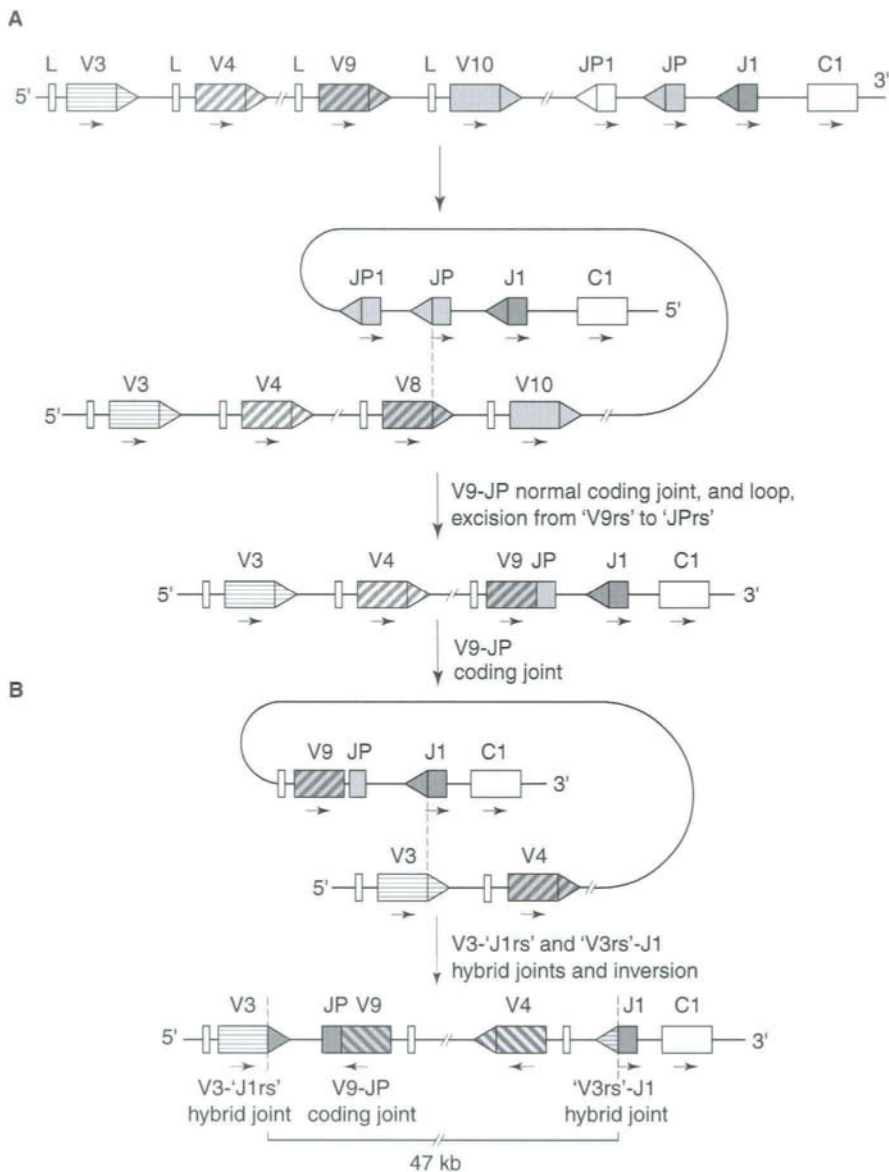


Figure 9. Schematic representation of two successive TRGV-J rearrangements on the same chromosome⁴⁵. (A) A standard rearrangement by loop excision and deletion led to a V9-JP joining. (B) A second rearrangement between V3 and J1 resulted in the formation of reciprocal hybrid joints, and in a 47 kb inversion and, therefore, the maintenance on the chromosome of the previous V9-JP rearrangement. Horizontal arrows indicate orientation of the transcription. Recombination signals are shown by triangles, and coding regions by rectangles. L = L-PART1 (L for leader).

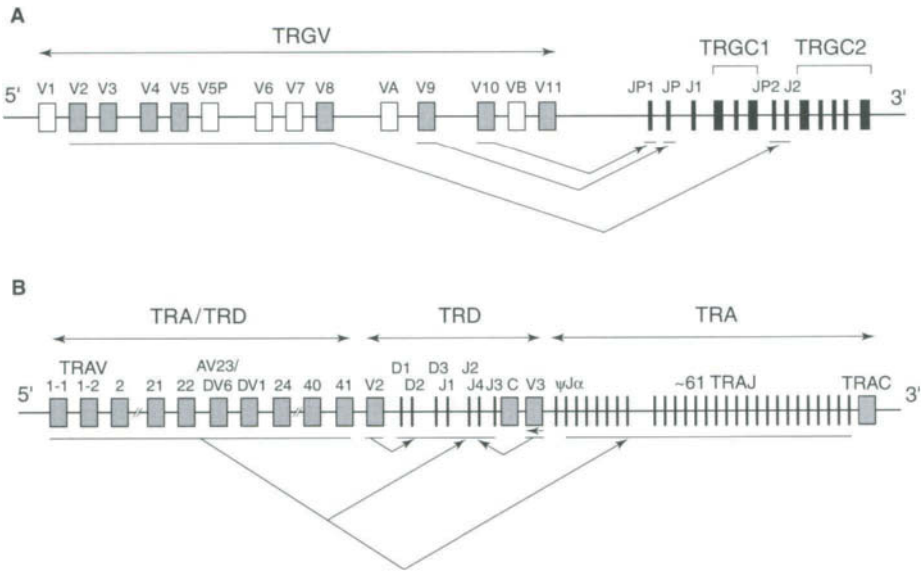


Figure 10. Chronological order of the human TRG (A) and TRD/TRA (B) rearrangements (modified from reference 46). Exons of the TRAC and TRDC genes are not shown. The non-productive TRGV10-JP1 rearrangements (TRGV10 is not functional) precede the frequent TRGV9-JP rearrangements which characterize most of the circulating $\gamma\delta$ T cells. Later productive rearrangements involve functional TRGV1 subgroup genes (V2, V3, V4, V5, V8) and more downstream TRGJ genes (J1, JP2, J2). The TRDV and TRAV/DV (for example, AV23/DV6) rearrangements to TRDD and TRDJ genes precede the TRA rearrangements in the TRA/TRD locus. In the $\alpha\beta$ T cell lineage the TRAV and TRAV/DV genes rearrange to the TRAJ genes, therefore deleting the intermediate TRA genes and the TRD locus.

ANALYSIS OF THE T CELL RECEPTOR GENE REARRANGEMENTS IN HUMANS

The TRG and TRB rearrangements are the most commonly analyzed⁵⁴. Indeed, (1) the TRA rearrangements are difficult to study. Given the extent of the TRAJ region, a high number of J α probes are necessary to cover all the region. Moreover, nonfunctional J-J rearrangements can be observed upstream of the functional TRAV-J rearrangement, making the Southern blot interpretation difficult⁵⁵; (2) TRD rearrangements can be studied in immature T cells or in $\gamma\delta$ T cells. However, in most of the $\alpha\beta$ T cells, the TRD locus is deleted on at least one chromosome as a consequence of the TRAV-J rearrangement.

Practically, the TRG and TRB rearrangements are studied with the TRGJ1 probe pH60^{48,56} and the C β probe, respectively, which detect the rearranged restriction fragments in Southern blot analysis⁵⁴ (Fig. 11). A TRBV-D-J rearrangement leads to a decrease, by half, in the intensity of the 24 kb germline *Bam*HI band and to the appearance of a new rearranged *Bam*HI band. The analysis of the *Eco*RI and *Hind*III restriction fragments allow assignment of the TRGV rearrangements to the TRBJ1 or TRBJ2 genes, respectively⁵⁴. Since the TRGJ1 and TRGJ2 genes are highly homologous⁴⁸, it is possible by using the pH60 probe to first detect the V rearrangements with respect to J1 and J2 and, second, to identify the rearranged TRGV genes by the sizes of the rearranged *Bam*HI, *Eco*RI, and *Hind*III restriction fragments⁴⁹ (Table 2). Moreover, rearrangements to the additional TRGJ genes JP, JP1, and JP2, can be identified by hybridization of the *Kpn*I digests to the TRGJ1 pH60 probe⁵⁰ (Table 2, Fig. 11). Therefore, this unique probe can detect all the TRG rearrangements, whatever the TRGJ gene involved in the rearrangements^{49,50}. Thus, it is a very useful tool to establish the clonality of $\alpha\beta$ T cell clones⁴⁸, leukemic cells^{57,58}, and T lymphocytes expressing $\gamma\delta$ receptor^{31,32,59}. The TRDJ1 and TRDJ2 probes allow the characterization of the TRD rearrangements in the $\gamma\delta$ T cells^{59,60}.

TRANSCRIPTIONAL REGULATION OF T CELL RECEPTOR GENE EXPRESSION: ENHANCERS AND SILENCERS

Rearrangements and expression of the TcR genes are coordinate- and lineage-specific. Extensive studies are currently underway to characterize the regulatory elements (promoters, enhancers, or silencers) and to identify the nuclear proteins that bind to these elements involved in the transcriptional regulation of the TcR genes. Promoters of some TcR genes, such as the TRGV9 and TRDV2 genes, do not display a TATA box⁶¹. A TRA enhancer has been identified at 4.5 kb 3' from the TRAC gene⁶², and several nuclear transcription factors have been characterized⁶³⁻⁶⁶. A TRA enhancer has been described between the most 3' TRAJ and the TRAC gene in humans⁶⁷ but it has not been confirmed in the mouse⁶⁸ and its existence in humans is controversial. A TRB enhancer has been mapped to 5.5 kb 3' from the human TRBC2 gene⁶⁹. A TRD enhancer has been located between TRDJ3 and TRDC in the human TRD locus^{70,71}. Negative regulatory elements or silencers seem to play an important role in restricting the lineage specificity of certain TcR genes.

Three *cis*-acting sequences in 3' of the human TRG locus, and upstream of an enhancer located 6.5 kb downstream of the TRGC2 gene have been characterized⁷². The association of the enhancer with either silencer was shown to restrict transcription to the $\gamma\delta$ T cell lines⁷². Some regulatory elements seem to function as both a silencer and an enhancer, depending on the particular set of nuclear proteins expressed by a given cell type or the precise DNA context in which they are located⁶⁵.

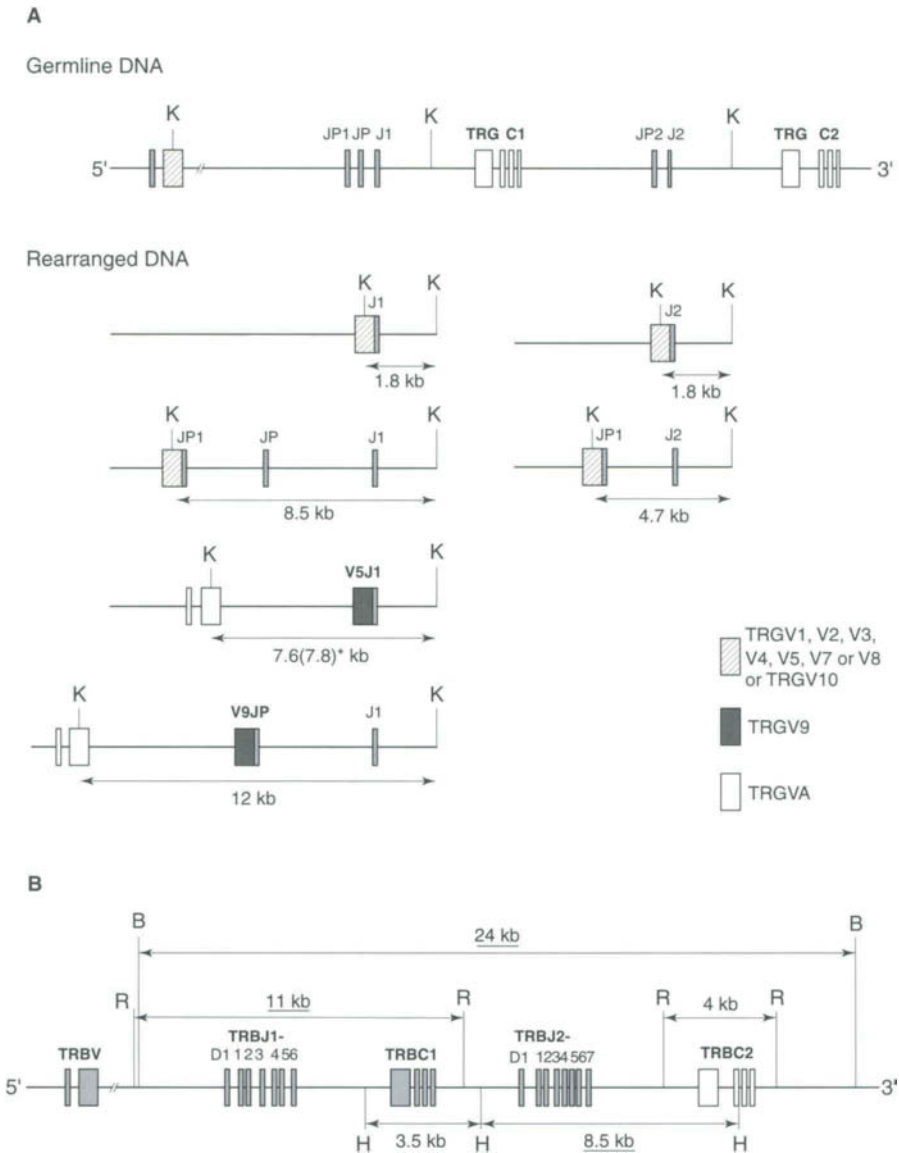


Figure 11. Restriction fragments for the analysis of the human TRGV-J (A) and TRBV-D-J (B) rearrangements. *KpnI* restriction fragments hybridized to the pH60 probe^{48,56} allow the assignment of the TRGV-J rearrangements to given TRGJ-genes⁵⁰ (see Table 2 for a complete description of the TRGV-J rearrangement restriction fragments). The asterisk indicates a rearranged fragment related to a RFLP (Restriction Fragment Length Polymorphism). Lengths of the *Bam*HI, *Eco*RI, and *Hind*III restriction fragments that are informative for the detection of the TRBV-D-J rearrangements⁵⁴ are underlined. B = *Bam*HI, H = *Hind*III, K = *Kpn*I, R = *Eco*RI.

Table 2. Assignments of the human TRGV-J rearranged restriction fragments to given TRGV and TRGJ genes by hybridization to the pH60 probe^{49,50}. Note that V7 is a pseudogene, and V10 and V11 are ORF.

A. Assignments of the TRGV-J rearrangements to given TRGV genes (joined to J1 or J2) by hybridization to *Bam*HI, *Hind*III, and *Eco*RI restriction fragments to the pH60 probe⁴⁹.

Assignment to TRGV genes		Restriction fragments		
TRGV subgroup	TRGV gene	<i>Bam</i> HI	<i>Hind</i> III	<i>Eco</i> RI
TRGV1	V2	11.7	4.3	0.9
	V3	16	3.7	5.4 (+V2)
	V4	21	4.3	0.9
	V5	25	3.6	2.2
	V7	35	2.9	3.1
	V8	40	2.9	4.2
TRGV2	V9	15.5	4.0	2.4
TRGV3	V10	19	5.1	0.65
TRGV4	V11	12	5.6	9.5

B. Assignments of the human TRGV-J rearrangements to given TRGJ genes by hybridization of *Kpn*I restriction fragments to the pH60 probe⁵⁰. TRGV genes that have been found rearranged are shown in parentheses.

TRGV subgroup	TRGV1 (V2,V3,V4, V5,V7,V8)	TRGV2 (V9)	TRGV3 (V10)	TRGV4 (V11)
J1 or 2	1.8	7.5 (7.8)*	1.8	6.0
JP1	8.5	14.5	8.5	12.7
JP	5.9	12	5.9	10
JP2	4.7	10.7	4.7	9.0

Sizes of the *Kpn*I rearranged restriction fragments are indicated in kilobases (kb). The asterisk indicates a rearranged fragment related to an RFLP (Restriction Fragment Length Polymorphism). The rearrangements illustrated in Fig. 11 are shown in bold.

References

- ¹ Haynes, B.H. et al. (2000) Annu. Rev. Immunol. 18, 529–560.
- ² Tonegawa, S. (1983) Nature 302, 575–581.
- ³ Blom, B. et al. (1999) Blood 93, 3033–3043.

- ⁴ Early, P. et al. (1980) *Cell* 19, 981–992.
- ⁵ Fujimoto, S. and Yamagishi, H. (1987) *Nature* 327, 242–243.
- ⁶ Okazaki, K. et al. (1987) *Cell* 49, 477–485.
- ⁷ Toda, M. et al. (1988) *J. Mol. Biol.* 202, 219–231.
- ⁸ Malissen, M. et al. (1986) *Nature* 319, 28–33.
- ⁹ Rowen, L. et al. (1996) *Science* 272, 1755–1762.
- ¹⁰ Iwashima, M. et al. (1988) *Proc. Natl Acad. Sci. USA* 85, 8161–8165.
- ¹¹ Hata, S. et al. (1989) *J. Exp. Med.* 169, 41–57.
- ¹² Loh, E.Y. et al. (1988) *Proc. Natl Acad. Sci. USA* 85, 9714–9718.
- ¹³ Takihara, Y. et al. (1989) *Eur. J. Immunol.* 19, 571–574.
- ¹⁴ Alt, F. and Baltimore, D. (1982) *Proc. Natl Acad. Sci. USA* 79, 4118–4122.
- ¹⁵ Alt, F. and Yancopoulos, G. D. (1987) *Nature* 327, 189–190.
- ¹⁶ Schatz, D.G. et al. (1989) *Cell* 59, 1035–1048.
- ¹⁷ Oettinger, M.A. et al. (1990) *Science* 248, 1517–1522.
- ¹⁸ Mombaerts, P. et al. (1992) *Cell* 68, 869–877.
- ¹⁹ Shinkai, Y. et al. (1992) *Cell* 68, 855–867.
- ²⁰ Fugmann, S.D. et al. (2000) *Annu. Rev. Immunol.* 18, 495–527.
- ²¹ Lefranc, M.-P. et al. (1986) *Cell* 45, 237–246.
- ²² Lafaille, J.L. et al. (1989) *Cell* 59, 857–870.
- ²³ Huck, S. et al. (1988) *EMBO J.* 7, 719–726.
- ²⁴ Saiki, R. et al. (1985) *Science* 230, 1350–1354.
- ²⁵ Saiki, R.K. et al. (1988) *Science* 239, 487–491.
- ²⁶ Erlich, H.A. et al. (1991) *Science* 252, 1643–1651.
- ²⁷ Panzara, M.A. et al. (1992) *Curr. Opin. Immunol.* 4, 205–210.
- ²⁸ Loh, E.Y. et al. (1989) *Science* 243, 217–220.
- ²⁹ Lefranc, M.-P. et al. (1989) *Proc. Natl Acad. Sci. USA* 83, 9596–9600.
- ³⁰ Buresi, C. et al. (1989) *Immunogenetics* 29, 161–172.
- ³¹ Triebel, F. et al. (1988) *J. Exp. Med.* 167, 694–699.
- ³² Triebel, F. et al. (1988) *J. Immunol.* 18, 789–794.
- ³³ Triebel, F. and Hercend, T. (1989) *Immunol. Today* 10, 186–188.
- ³⁴ Band, H. et al. (1987) *Science* 238, 682–684.
- ³⁵ Borst, J. et al. (1988) *J. Exp. Med.* 167, 1625–1644.
- ³⁶ Ciccone, E. et al. (1988) *J. Exp. Med.* 168, 1–11.
- ³⁷ Wu, Y.J. et al. (1988) *J. Immunol.* 141, 1476–1479.
- ³⁸ Peyrat, M.A. et al. (1995) *J. Immunol.* 155, 3060–3067.
- ³⁹ Kabelitz, D. et al. (1994) *J. Immunol.* 152, 3128–3136.
- ⁴⁰ Hinz, T. et al. (1997) *Int. Immunol.* 9, 1065–1072.
- ⁴¹ Kabelitz, D. (1999) *Microbes and Infection* 1, 255–261.
- ⁴² Ghanem, N. et al. (1989) *Immunogenetics* 30, 350–360.
- ⁴³ Ghanem, N. et al. (1991) *Hum. Genet.* 6, 450–456.
- ⁴⁴ Ikuta, K. et al. (1992) *Annu. Rev. Immunol.* 10, 759–783.
- ⁴⁵ Alexandre, D. et al. (1991) *Int. Immunol.* 3, 973–982.
- ⁴⁶ Alexandre, D. and Lefranc, M.-P. (1992) *Mol. Immunol.* 29, 447–451.
- ⁴⁷ Moisan, J.P. et al. (1989) *Hum. Immunol.* 24, 95–110.
- ⁴⁸ Lefranc, M.-P. et al. (1986) *Nature* 319, 420–422.
- ⁴⁹ Forster, A. et al. (1987) *EMBO J.* 6, 1945–1950.
- ⁵⁰ Huck, S. and Lefranc, M.-P. (1987) *FEBS Lett.* 224, 291–296.
- ⁵¹ Lefranc, M.-P. (1990) *Eur. Cytokine Network* 1, 121–130.
- ⁵² De Villartray, J.P. et al. (1988) *Nature* 335, 170–174.

- ⁵³ Begley, C.G. et al. (1989) *J. Exp. Med.* 170, 339–342.
- ⁵⁴ Soua, Z., et al. (1995) *Exp. Clin. Immunogenet.* 12, 16–30.
- ⁵⁵ Baer, R. et al. (1988) *EMBO J.* 7, 1661–1668.
- ⁵⁶ Lefranc, M.-P. and Rabbitts T.H. (1985) *Nature* 316, 464–466.
- ⁵⁷ Chen, Z. et al. (1988) *Blood* 72, 776–783.
- ⁵⁸ Migone, N. et al. (1988) *Eur. J. Immunol.* 18, 173–178.
- ⁵⁹ Sturm, E. et al. (1989) *Eur. J. Immunol.* 19, 1261–1265.
- ⁶⁰ Kanavaros, P. et al. (1991) *J. Clin. Invest.* 87, 666–672.
- ⁶¹ Dariavach, P. and Lefranc, M.-P. (1988) *FEBS Lett.* 256, 185–191.
- ⁶² Ho, I.C. et al. (1989) *Proc. Natl Acad. Sci. USA* 86, 6714–6718.
- ⁶³ Ho, I.C. et al. (1990) *Science* 250, 814–818.
- ⁶⁴ Ho, I.C. and Leiden, J.M. (1990) *Mol. Cell. Biol.* 10, 4720–4727.
- ⁶⁵ Ho, I.C. and Leiden, J.M. (1990) *J. Exp. Med.* 172, 1443–1449.
- ⁶⁶ Leiden, J.M. (1992) *Immunol. Today* 13, 22–30.
- ⁶⁷ Luria, S. et al. (1987) *EMBO J.* 6, 3307–3312.
- ⁶⁸ Winoto, A. and Baltimore, D. (1989) *EMBO J.* 8, 729–733.
- ⁶⁹ Gottschalk, L.R. and Leiden, J.M. (1990) *Mol. Cell. Biol.* 10, 5486–5495.
- ⁷⁰ Bories, J.C. et al. (1990) *J. Exp. Med.* 171, 75–83.
- ⁷¹ Redondo, J.M. et al. (1990) *Science* 247, 1225–1229.
- ⁷² Lefranc, M.-P. and Alexandre, D. (1995) *Eur. J. Immunol.* 25, 617–622.

4 Chromosomal localization, organization of the loci, and potential repertoire

THE HUMAN TRA LOCUS

Chromosomal localization of the human TRA locus

The human TRA locus is located on chromosome 14¹⁻³, on the long arm at band 14q11.2 (Fig. 1). The TRD locus is nestled within the TRA locus. The orientation of the TRA and TRD loci has been determined by the analysis of translocations involving these loci, in leukemia and lymphoma.

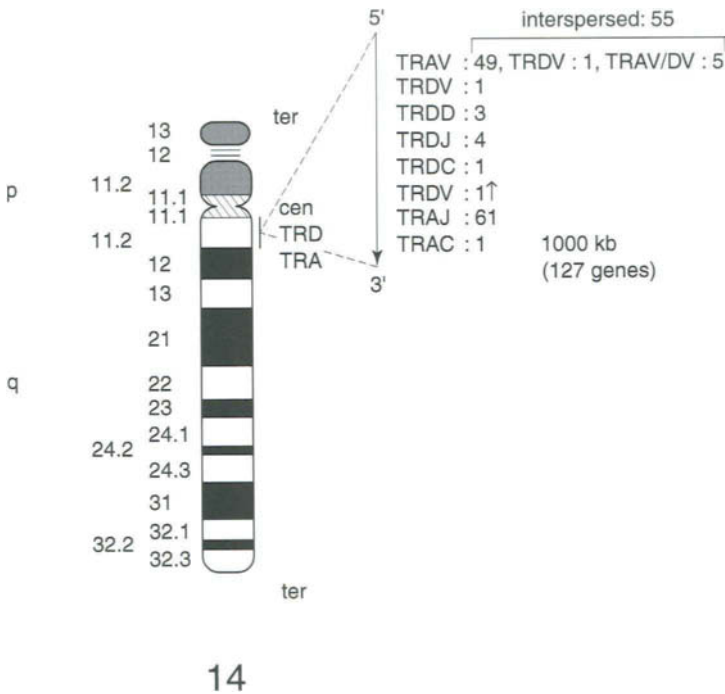


Figure 1. Chromosomal localization of the human TRA locus at 14q11.2. A vertical line indicates the localization of the TRA and TRD loci at 14q11.2. The arrow indicates the orientation 5' -> 3' of the loci, and the gene group order in the loci. The length of the arrow is proportional to the total size of the loci, indicated in kilobases (kb). The total number of genes in the TRA and TRD loci is shown between parentheses. The number of functional genes defines the potential TRA repertoire which comprises 95-97 genes (40-41 TRAV, 4-5 TRAV/DV, 50 TRAJ, and 1 TRAC) per haploid genome. The five genes, designated as TRAV/DV, have been found rearranged to J genes of the TRA locus, and to D and J genes of the TRD locus, and can therefore be used in the synthesis of alpha or delta chains⁴.

Organization of the human TRA locus

The human TRA locus at 14q11.2 spans 1000 kilobases (kb) (Fig. 2). It consists of 54 TRAV genes belonging to 41 subgroups⁴⁻⁸, 61 TRAJ genes localized on 71 kb⁹⁻¹⁰, and a unique TRAC gene¹¹⁻¹². The most 5' TRAV genes occupy the most centromeric position, whereas the TRAC gene, 3' of the locus, is the most telomeric gene in the TRA locus. The organization of the TRAJ genes on a large area is quite unusual and has not been observed in the other immunoglobulin or T cell receptor loci¹². Moreover, the TRD locus is nestled in the TRA locus between the TRAV and TRAJ genes. V-J rearrangements in the TRA locus therefore result in deletion of the TRD genes localized on the same chromosome¹³. That deletion occurs in two steps, that is a deletion of the TRD genes, involving specific sequences located upstream from TRDC (sequence $\phi\alpha$)^{14,15}, would take place before the TRAV-J rearrangement.

The potential genomic TRA repertoire comprises 44–46 functional TRAV genes belonging to 32–34 subgroups, 50 functional TRAJ genes, and the unique TRAC gene^{4,10}. Among the variable genes are included five genes designated as TRAV/DV which belong to five different subgroups and which have been found rearranged either to TRAJ or to TRDD genes and can therefore be used in the synthesis of alpha or delta chains⁴.

The total number of human TRA genes per haploid genome (including the 5 TRAV/DV genes) is 116, of which 95 to 97 genes are functional (see Tables 9 and 10). Enhancer sequences have been characterized 4.5kb 3' from TRAC¹⁶.

List of the TRA genes on chromosome 14 at 14q11.2, and correspondence between nomenclatures

TRAJ gene nomenclature

TRAJ genes are designated by a number for the localization from 3' to 5' in the locus¹⁰.

TRAV gene nomenclature

TRAV genes are designated by a number for the subgroup, followed whenever there are several genes belonging to the same subgroup, by a hyphen and a number for their relative localization in the locus⁴. Numbers increase from 5' to 3' in the locus. Functionality is shown in parentheses when the germline TRAV genes have not yet been isolated. The TRAV14/DV4, TRAV23/DV6, TRAV29/DV5, TRAV36/DV7, and TRAV38-2/DV8 genes have been found rearranged to J genes of the TRA locus, and to D and J genes of the TRD locus.

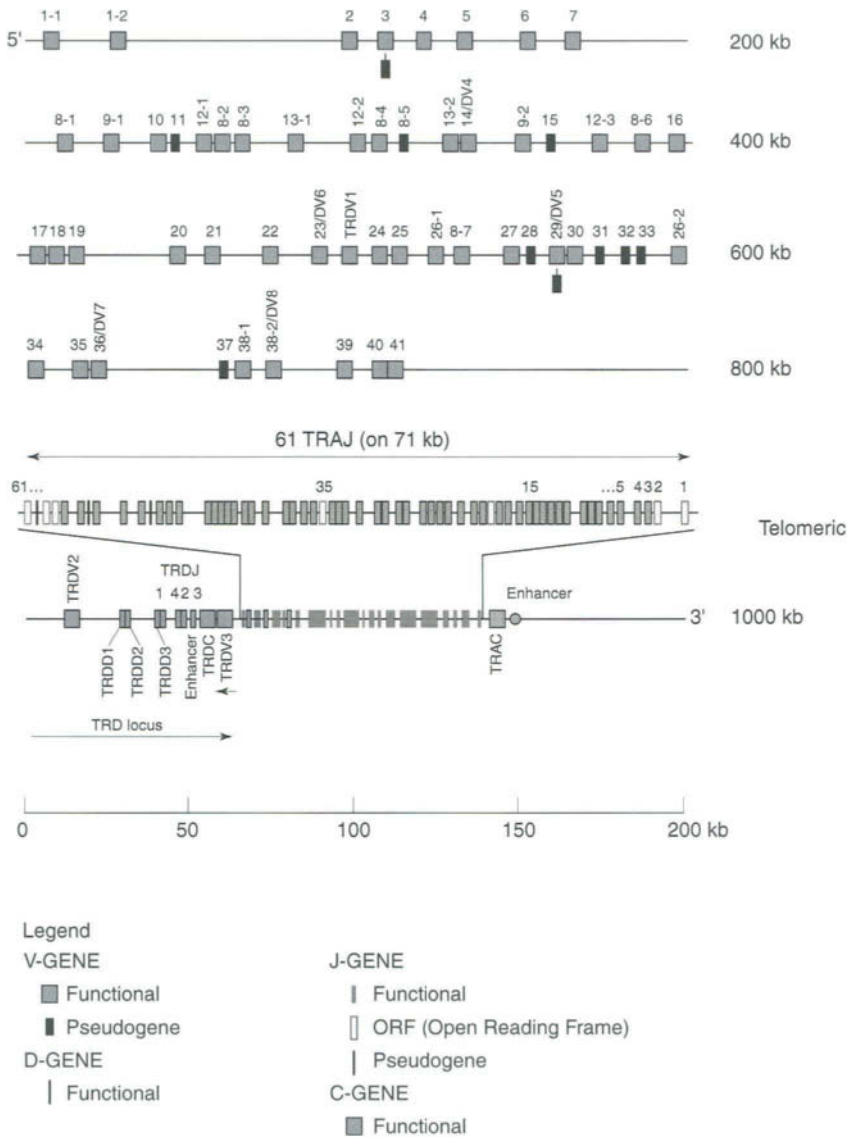


Figure 2. Representation of the human TRA locus at 14q11.2. The boxes representing the genes are not to scale. Exons are not shown. The TRAV genes are designated by a number for the subgroup, followed, whenever there are several genes belonging to the same subgroup, by a hyphen and a number for their relative localization in the locus. Numbers increase from 5' to 3' in the locus. The TRD genes which are nestled in the TRA locus are also represented.

Table 1. List of functional or ORF human TRA genes. Only the genes with at least one functional or ORF allele are shown. For a complete listing of the human TRA genes including the pseudogenes, see references 4 and 10 and IMGT gene data: <http://imgt.cines.fr/cgi-bin/IMGTlect.jv?query=203>.
For information on individual TRA genes:
<http://imgt.cines.fr/cgi-bin/IMGTlect.jv?query=202+genename>.
Example: IMGT Repertoire for TRAV6:
<http://imgt.cines.fr/cgi-bin/IMGTlect.jv?query=202+TRAV6>.

IMGT gene groups	IMGT gene names	IMGT functionality	IMGT number of alleles	Other nomenclatures	
				TRAV (1)	Ref. 7
TRAC	TRAC	F	1		
TRAJ	TRAJ1	ORF	1		
	TRAJ2	ORF	1		
	TRAJ3	F	1		
	TRAJ4	F	1		
	TRAJ5	F	1		
	TRAJ6	F	1		
	TRAJ7	F	1		
	TRAJ8	F	1		
	TRAJ9	F	1		
	TRAJ10	F	1		
	TRAJ11	F	1		
	TRAJ12	F	1		
	TRAJ13	F	1		
	TRAJ14	F	1		
	TRAJ15	F	2		
	TRAJ16	F	1		
	TRAJ17	F	1		
	TRAJ18	F	1		
	TRAJ19	ORF	1		
	TRAJ20	F	1		
	TRAJ21	F	1		
	TRAJ22	F	1		
	TRAJ23	F	1		
	TRAJ24	F	2		
	TRAJ25	ORF	1		
	TRAJ26	F	1		
	TRAJ27	F	1		
	TRAJ28	F	1		
	TRAJ29	F	1		
	TRAJ30	F	1		

Table 1. *Continued.*

IMGT gene groups	IMGT gene names	IMGT functionality	IMGT number of alleles	Other nomenclatures	
				TRAV (1)	Ref. 7
	TRAJ31	F	1		
	TRAJ32	F	1		
	TRAJ33	F	1		
	TRAJ34	F	1		
	TRAJ35	ORF	1		
	TRAJ36	F	1		
	TRAJ37	F	1		
	TRAJ38	F	1		
	TRAJ39	F	1		
	TRAJ40	F	1		
	TRAJ41	F	1		
	TRAJ42	F	1		
	TRAJ43	F	1		
	TRAJ44	F	1		
	TRAJ45	F	1		
	TRAJ46	F	1		
	TRAJ47	F	1		
	TRAJ48	F	1		
	TRAJ49	F	1		
	TRAJ50	F	1		
	TRAJ52	F	1		
	TRAJ53	F	1		
	TRAJ54	F	1		
	TRAJ56	F	1		
	TRAJ57	F	1		
	TRAJ58	ORF	1		
	TRAJ59	ORF	1		
	TRAJ61	ORF	1		
TRAV	TRAV1-1	F	2	1S1	7S1
	TRAV1-2	F	2	1S2	7S2
	TRAV2	F	2	2S1	11S1
	TRAV3	F, (P)	2	3S1	16S1
	TRAV4	F	1	4S1	20S1
	TRAV5	F	1	5S1	15S1
	TRAV6	F	6	6S1	5S1
	TRAV7	F	1	7S1	
	TRAV8-1	F	2	8S1	1S1
	TRAV8-2	F	2	8S2	1S5

Continued

Table 1. *Continued.*

IMGT gene groups	IMGT gene names	IMGT functionality	IMGT number of alleles	Other nomenclatures	
				TRAV (1)	Ref. 7
	TRAV8-3	F	3	8S3	1S4
	TRAV8-4	F	7	8S4	1S2
	TRAV8-6	F	2	8S6	1S3
	TRAV8-7	F	1	8S7	
	TRAV9-1	F	1	9S1	
	TRAV9-2	F	4	9S2	22S1
	TRAV10	F	1	10S1	24S1
	TRAV12-1	F	2	12S1	2S3
	TRAV12-2	F	3	12S2	2S1
	TRAV12-3	F	2	12S3	2S2
	TRAV13-1	F	3	13S1	8S1
	TRAV13-2	F	2	13S2	8S2
	TRAV14/DV4	F	4	hADV14S1	6S1-ADV6S1
	TRAV16	F	1	16S1	9S1
	TRAV17	F	1	17S1	3S1
	TRAV18	F	1	18S1	
	TRAV19	F	1	19S1	12S1
	TRAV20	F	4	20S1	30S1
	TRAV21	F	2	21S1	23S1
	TRAV22	F	1	22S1	13S1
	TRAV23/DV6	F	4	hADV23S1	17S1-ADV17S1
	TRAV24	F	2	24S1	18S1
	TRAV25	F	1	25S1	32S1
	TRAV26-1	F	3	26S1	4S2
	TRAV26-2	F	2	26S2	4S1
	TRAV27	F	3	27S1	10S1
	TRAV29/DV5	F, (P)	3	hADV29S1	21S1-ADV21S1
	TRAV30	F	4	30S1	29S1
	TRAV34	F	1	34S1	26S1
	TRAV35	F	2	35S1	25S1
	TRAV36/DV7	F	4	hADV36S1	28S1-DV28S1
	TRAV38-1	F	4	38S1	14S2
	TRAV38-2/DV8	F	1	hADV38S2	14S1-ADV14S1
	TRAV39	F	1	39S1	27S1
	TRAV40	F	1	40S1	31S1
	TRAV41	F	1	41S1	19S1

(1) Boysen, C. et al. (AE000658-AE000661) unpublished

Number of the human TRAV germline variable genes at 14q11.2 and potential repertoire

Overview

54 TRAV and TRAV/DV genes belonging to 41 subgroups, on 700 kilobases:

44 FUNCTIONAL

8 PSEUDOGENE

2 FUNCTIONAL or PSEUDOGENE (TRAV3, TRAV29/DV5)

Potential repertoire

40–41 FUNCTIONAL TRAV genes belonging to 28 to 29 subgroups, and 4–5 FUNCTIONAL TRAV/DV genes belonging to 4 to 5 subgroups. One subgroup (TRAV38) has one 'TRAV' gene and one 'TRAV/DV' gene. There is therefore a total of 44–46 FUNCTIONAL TRAV and TRAV/DV genes belonging to 32 to 34 subgroups.

Table 2. *Repertoire of the human TRAV germline variable genes at 14q11.2.*

Subgroup	Functional	ORF	Pseudogene	Total
TRAV1	2	–	–	2
TRAV2	1	–	–	1
TRAV3	(1)*	–	(1)*	1
TRAV4	1	–	–	1
TRAV5	1	–	–	1
TRAV6	1	–	–	1
TRAV7	1	–	–	1
TRAV8	6	–	1	7
TRAV9	2	–	–	2
TRAV10	1	–	–	1
TRAV11	–	–	1	1
TRAV12	3	–	–	3
TRAV13	2	–	–	2
TRAV14/DV4	1	–	–	1
TRAV15	–	–	1	1
TRAV16	1	–	–	1
TRAV17	1	–	–	1
TRAV18	1	–	–	1
TRAV19	1	–	–	1
TRAV20	1	–	–	1
TRAV21	1	–	–	1
TRAV22	1	–	–	1
TRAV23/DV6	1	–	–	1
TRAV24	1	–	–	1
TRAV25	1	–	–	1

Continued

Table 2. *Continued.*

Subgroup	Functional	ORF	Pseudogene	Total
TRAV26	2	–	–	2
TRAV27	1	–	–	1
TRAV28	–	–	1	1
TRAV29/DV5	(1)*	–	(1)*	1
TRAV30	1	–	–	1
TRAV31	–	–	1	1
TRAV32	–	–	1	1
TRAV33	–	–	1	1
TRAV34	1	–	–	1
TRAV35	1	–	–	1
TRAV36/DV7	1	–	–	1
TRAV37	–	–	1	1
TRAV38/DV8 ^a	2	–	–	2
TRAV39	1	–	–	1
TRAV40	1	–	–	1
TRAV41	1	–	–	1
Total	44(+2)*	0	8(+2)*	54

* Indicates that the following genes have alleles with different functionality: FUNCTIONAL or PSEUDOGENE (TRAV3, TRAV29/DV5)

^a Only the TRAV38-2 gene has so far been found rearranged to TRDD genes.

THE HUMAN TRB LOCUS

Chromosomal localization of the human TRB locus

The human TRB locus is located on chromosome 7^{17–19}, on the long arm, at band 7q34¹⁹ (Fig. 3). The orientation of the locus has been determined by the analysis of translocations, involving the TRB locus, in leukemia and lymphoma.

Organization of the human TRB locus

The human TRB locus at 7q34 spans 620 kb (Fig. 4). It consists of 64–67 TRBV genes belonging to 32 subgroups^{7,8,20–26}. Except for TRBV30, localized downstream of the TRBC2 gene, in inverted orientation of transcription²⁵, all the other TRBV genes are located upstream of a duplicated D-J-C-cluster, which comprises, for the first part one TRBD, six TRBJ, and the TRBC1 gene, and for the second part, one TRBD, eight TRBJ, and the TRBC2 gene^{13,27–29}. The two constant genes, TRBC1 and TRBC2, encode proteins which differ by six amino acids. TRBV30 rearranges by an inversion mechanism as this has been described for the murine TRBV31 gene, similarly located in the mouse TRB locus, downstream of the TRBC2 gene, and in inverted orientation of transcription³⁰. Twenty-three of the 32 TRBV subgroups are

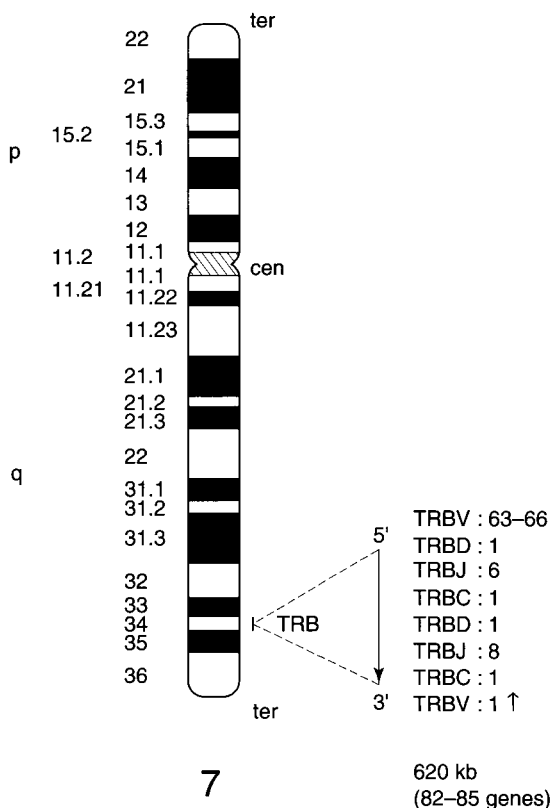


Figure 3. Chromosomal localization of the human TRB locus at 7q34. A vertical line indicates the localization of the TRB locus at 7q34. The arrow indicates the orientation 5' → 3' of the locus, and the gene group order in the locus. The TRBV gene localized at the 3' end of the TRB locus is in inverted orientation of transcription (shown by a small arrow). The length of the arrow is proportional to the size of the locus, indicated in kilobases (kb). The total number of genes in the locus is shown between parentheses. The number of functional genes defines the potential TRB repertoire, which comprises 56–65 genes (40–48 TRBV, 2 TRBD, 12–13 TRBJ, and 2 TRBC) per haploid genome.

found to consist of a single member each. The most 5' TRBV genes occupy the most centromeric position, whereas the TRBV30 gene, 3' of the locus, is the most telomeric gene in the TRB locus. The potential repertoire consists of 40–48 functional TRBV genes belonging to 21–23 subgroups, the two TRBD, twelve to thirteen TRBJ (6 from the first cluster and 6–7 from the second cluster), and the two TRBC genes. Six TRBV orphans have been localized on chromosome 9 at 9p21^{31–32}. Enhancer sequences have been characterized 5.5 kb 3' from TRBC2³³.

The total number of human TRB genes per haploid genome is 82 to 85 (88 to 91 genes, if the orphans are included) of which 56 to 65 are functional (see Tables 9 and 10).

Centromeric

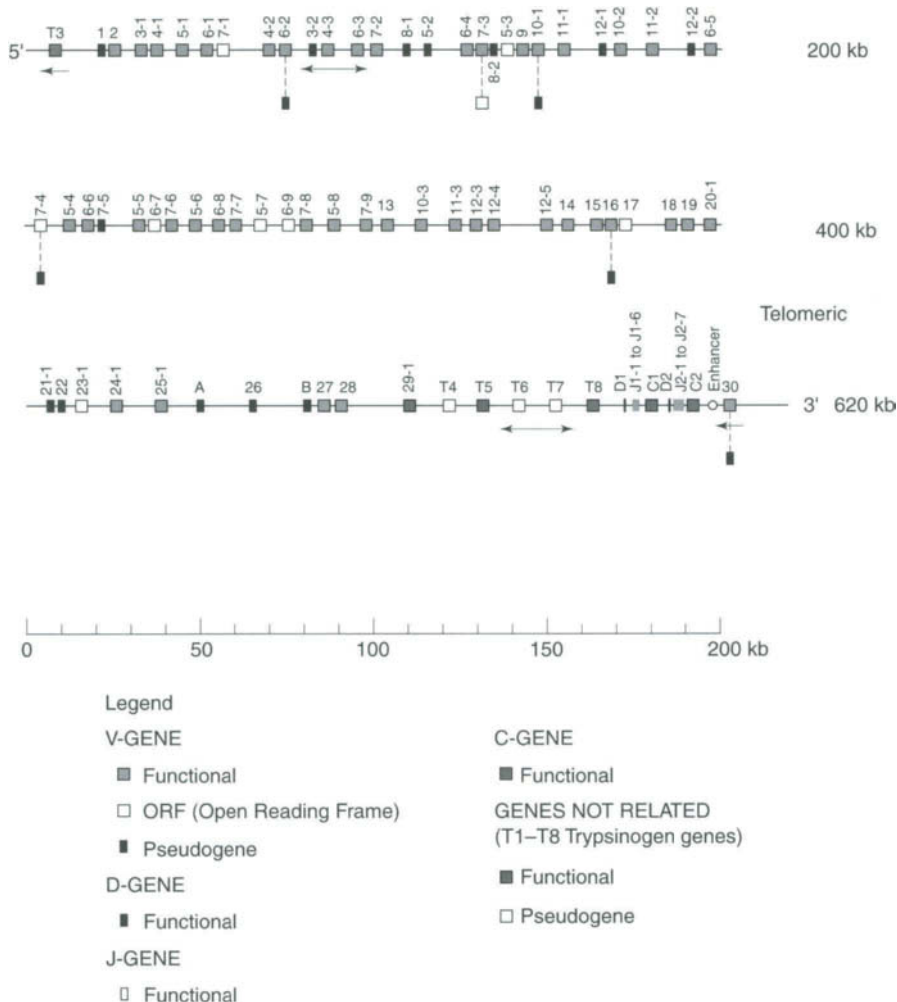


Figure 4. Representation of the human TRB locus at 7q34. The boxes representing the genes are not to scale. Exons are not shown. The TRBV genes are designated by a number for the subgroup followed, whenever there are several genes belonging to the same subgroup, by a hyphen and a number for their relative localization in the locus. Numbers increase from 5' to 3' in the locus. Single arrows show genes whose polarity is opposite to that of the D-J-C-CLUSTER. Double arrows indicate insertion/deletion polymorphisms.

List of the TRB genes on chromosome 7 at 7q34, and correspondence between nomenclatures

TRBV gene nomenclature

TRBV genes are designated by a number for the subgroup followed, whenever there are several genes belonging to the same subgroup, by a hyphen and a number for their relative localization in the locus. Numbers increase from 5' to 3' in the locus²⁶.

Functionality is shown in:

- parentheses when the accession number refers to a rearranged sequence and the corresponding germline gene has not yet been isolated;
- brackets when the accession number refers to a DNA genomic sequence, but not known as being germline or rearranged.

Since orphans have been described for each of the following TRBV subgroups: 20, 21, 23, 24, 25, and 29, the single member gene in the main locus is designated by the subgroup number followed by a hyphen and the number 1. To date, no orphon has been reported that belongs to subgroup 22, therefore the IMGT designation of the single member gene is TRBV22.

Table 3. List of functional or ORF human TRB genes. Only the genes with at least one functional or ORF allele are shown. For a complete listing of the human TRBV genes including the pseudogenes, see references 26 and 29, and IMGT gene data: <http://imgt.cines.fr/cgi-bin/IMGTlect.jv?query=203>.

For information on individual TRA genes:

<http://imgt.cines.fr/cgi-bin/IMGTlect.jv?query=202+genename>.

Example: IMGT Repertoire for TRBV3-1:

<http://imgt.cines.fr/cgi-bin/IMGTlect.jv?query=202+TRBV3-1>.

IMGT gene groups	IMGT gene names	IMGT functionality	IMGT number of alleles	Other nomenclatures		
				Ref. 23	Ref. 7	Ref. 25
TRBC	TRBC1	F	2			
	TRBC2	F	2			
TRBD	TRBD1	F	1			
	TRBD2	F	2			
TRBJ	TRBJ1-1	F	1			
	TRBJ1-2	F	1			
	TRBJ1-3	F	1			
	TRBJ1-4	F	1			
	TRBJ1-5	F	1			
	TRBJ1-6	F	1			

Continued

Table 3. *Continued.*

IMGT gene groups	IMGT gene names	IMGT functionality	IMGT number of alleles	Other nomenclatures		
				Ref. 23	Ref. 7	Ref. 25
	TRBJ2-1	F	1			
	TRBJ2-2	F	1			
	TRBJ2-2P	ORF	1			
	TRBJ2-3	F	1			
	TRBJ2-4	F	1			
	TRBJ2-5	F	1			
	TRBJ2-6	F	1			
	TRBJ2-7	F, ORF	2			
TRBV	TRBV2	F	3	22S1	22S1	2
	TRBV3-1	F	2	9S1	9S1	3-1
	TRBV4-1	F	2	7S1	7S1	4-1
	TRBV4-2	F	2	7S3	7S3	4-2
	TRBV4-3	F	4	7S2	7S2	4-3
	TRBV5-1	F	2	5S1	5S1	5-1
	TRBV5-3	ORF	2	5S5	5S5	5-3
	TRBV5-4	F	4	5S6	5S6	5-4
	TRBV5-5	F	3	5S3	5S3	5-5
	TRBV5-6	F	1	5S2	5S2	5-6
	TRBV5-7	ORF	1	5S7	5S7	5-7
	TRBV5-8	F	2	5S8	5S4	5-8
	TRBV6-1	F	1	13S3	13S3	6-1
	TRBV6-2	F, (P)	3	13S2a	13S2a	6-2
	TRBV6-3	F	1	13S2b	13S2b	6-3
	TRBV6-4	F	2	13S5	13S5	6-4
	TRBV6-5	F	1	13S1	13S1	6-5
	TRBV6-6	F	5	13S6	13S6	6-6
	TRBV6-7	ORF	1	13S8	13S8	6-7
	TRBV6-8	F	1	13S7	13S7	6-8
	TRBV6-9	F	1	13S4	13S4	6-9
	TRBV7-1	ORF	1	6S10	6S7	7-1
	TRBV7-2	F	4	6S7	6S5	7-2
	TRBV7-3	F, ORF	5	6S1	6S1	7-3
	TRBV7-4	F, (P)	3	6S11	6S8	7-4
	TRBV7-6	F	2	6S4	6S3	7-6
	TRBV7-7	F	2	6S14	6S6	7-7
	TRBV7-8	F	3	6S3	6S2	7-8
	TRBV7-9	F	7	6S5	6S4	7-9
	TRBV9	F	3	1S1	1S1	9

Continued

Table 3. *Continued.*

IMGT gene groups	IMGT gene names	IMGT functionality	IMGT number of alleles	Other nomenclatures		
				Ref. 23	Ref. 7	Ref. 25
	TRBV10-1	F, [P]	3	12S4	12S2	10-1
	TRBV10-2	F	2	12S3	12S3	10-2
	TRBV10-3	F	4	12S2	12S1	10-3
	TRBV11-1	F	1	21S1	21S1	11-1
	TRBV11-2	F	3	21S3	21S3	11-2
	TRBV11-3	F	4	21S4	21S2	11-3
	TRBV12-3	F	1	8S1	8S1	12-3
	TRBV12-4	F	2	8S2	8S2	12-4
	TRBV12-5	F	1	8S3	8S3	12-5
	TRBV13	F	2	23S1	23S1	13
	TRBV14	F	2	16S1	16S1	14
	TRBV15	F	3	24S1	24S1	15
	TRBV16	F, P	3	25S1	25S1	16
	TRBV17	ORF	1	26S1[1]	26S1	17
	TRBV18	F	1	18S1	18S1	18
	TRBV19	F	3	17S1	17S1	19
	TRBV20-1	F	7	2S1	2S1	20-1
	TRBV23-1	ORF	1	19S1	19S1	23-1
	TRBV24-1	F	1	15S1	15S1	24-1
	TRBV25-1	F	1	11S1	11S1	25-1
	TRBV27	F	1	14S1	14S1	27
	TRBV28	F	1	3S1	3S1	28
	TRBV29-1	F	3	4S1	4S1	29-1
	TRBV30	F, P	5	20S1	20S1	30

[1] 26S1 was defined in Slightom et al. (1994).

Number of the human TRBV germline variable genes at 7q34 and potential repertoire

Overview

64–67 TRBV genes belonging to 30 subgroups, on 620 kilobases:

40–42 FUNCTIONAL

6 ORF (Open Reading Frame)

12–13 PSEUDOGENE

5 FUNCTIONAL or PSEUDOGENE

1 FUNCTIONAL or ORF

Potential repertoire

40–48 FUNCTIONAL TRBV genes belonging to 21–23 subgroups

Table 4. *Repertoire of the human TRBV germline variable genes at 7q34.*

Subgroup	Functional	ORF	Pseudogene	Total
TRBV1	–	–	1	1
TRBV2	1	–	–	1
TRBV3	1	–	0–1**	1–2**
TRBV4	2–3**	–	–	2–3**
TRBV5	5	2	1	8
TRBV6	6–7** (+1)*	1	(1)*	8–9**
TRBV7	5(+2)*	1(+1)*	1(+1)*	9
TRBV8	–	–	2	2
TRBV9	1	–	–	1
TRBV10	2(+1)*	–	(1)*	3
TRBV11	3	–	–	3
TRBV12	3	–	2	5
TRBV13	1	–	–	1
TRBV14	1	–	–	1
TRBV15	1	–	–	1
TRBV16	(1)*	–	(1)*	1
TRBV17	–	1	–	1
TRBV18	1	–	–	1
TRBV19	1	–	–	1
TRBV20	1	–	–	1
TRBV21	–	–	1	1
TRBV22	–	–	1	1
TRBV23	–	1	–	1
TRBV24	1	–	–	1
TRBV25	1	–	–	1
TRBV26	–	–	1	1
TRBV27	1	–	–	1
TRBV28	1	–	–	1
TRBV29	1	–	–	1
TRBV30	(1)*	–	(1)*	1
TRBVA	–	–	1	1
TRBVB	–	–	1	1
Total	40–42(+6)*	6(+1)*	12–13(+5)*	64–67

* Indicates that the following genes have alleles with different functionality:

FUNCTIONAL or PSEUDOGENE (TRBV6-2, TRBV7-4, TRBV10-1, TRBV16, TRBV30)

FUNCTIONAL or ORF (TRBV7-3)

** Indicate allelic polymorphisms by insertion/deletion which concern TRBV3-2, TRBV4-3, TRBV6-3.

THE HUMAN TRG LOCUS

Chromosomal localization of the human TRG locus

The human TRG locus³⁴⁻⁴⁸ is located on chromosome 7⁴⁹, at band 7p14^{50,51}. The orientation of the locus has been determined by the analysis of chromosome 7 inversions inv(7)(p14-q34), involving the TRG and TRB loci in ataxia telangiectasia patients, and in leukemia.

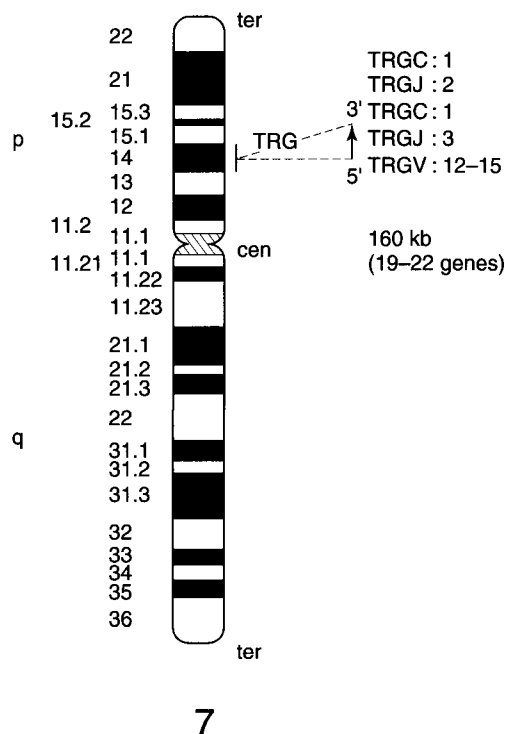


Figure 5. Chromosomal localization of the human TRG locus at 7p14. A vertical line indicates the localization of the TRG locus at 7p14. The arrow indicates the orientation 5' -> 3' of the locus, and the gene group order in the locus. The length of the arrow is proportional to the size of the locus, indicated in kilobases (kb). The total number of genes in the locus is shown in parentheses.

Organization of the human TRG locus

The human TRG locus³⁴⁻⁴⁸ at 7p14 spans 160 kb⁴¹. It consists of 12-15 TRGV genes belonging to 6 subgroups^{34-36,38,40,47-48}, upstream of a duplicated J-C cluster, which comprises, for the first part, three TRGJ and the TRGC1 gene, and for the second part, two TRGJ and the TRGC2 gene^{35,37,39,43}. The most 5' TRGV genes occupy the most centromeric position, whereas the TRGC2 gene, 3' of the locus, is the most telomeric in the TRG locus⁴¹. There is no cross-hybridization between the TRGV genes

belonging to the six different subgroups, which are only 30% homologous at the protein level^{36,40}. TRGV9, expressed in 80–95% of the human peripheral $\gamma\delta$ T cells, is the unique member of subgroup 2. TRGV10 and TRGV11, single members of subgroups 3 and 4, respectively, have been found rearranged⁴⁰ and transcribed, but they are ORF that cannot be expressed in a gamma chain, due to a splicing defect of the premessenger^{47,48}. The potential repertoire consists of 4–6 functional TRGV genes belonging to two subgroups, the five TRGJ and the two TRGC genes^{34–41,47,48}.

Polymorphisms in the number of TRGV genes and in the exon number of the TRGC2 gene have been described in different populations^{43,44,46}. A variation of the number of the TRGV subgroup genes (from seven to ten) has been observed^{44,46}. These allelic polymorphisms, which result from the deletion of V4 and V5, or from the insertion of an additional V gene, V3P, between V3 and V4, can be detected by restriction fragment length polymorphism (RFLP)^{44,46} [see Chapter 3]. The two TRGC genes, which are 16 kb apart, result, with their associated TRGJ genes, from a recent duplication in the locus. However, there are several structural differences⁴². TRGJP1, TRGJ1, and TRGC1 cross-hybridize to TRGJP2, TRGJ2, and TRGC2, respectively^{34,37,39}, whereas the TRGJP has no equivalent in the duplicated TRGJP2-J2-C2 cluster³⁶. The TRGC1 gene has three exons³⁷, whereas the TRGC2 gene has four or five exons, owing to the duplication or triplication of a region that includes exon 2⁴³. The allelic polymorphism of the TRGC2 gene with duplication (C2(2x)) or triplication (C2(3x)) of exon 2 can be identified by RFLP⁴³ (see Chapter 3). The exon 2 of the TRGC1 gene has a cysteine³⁷ involved in the interchain disulfide bridge, whereas this cysteine is not conserved in the exon 2 of the human TRGC2 gene. Enhancer and silencer sequences have been characterized 6.5 kb downstream of the TRGC2 gene⁵².

The total number of TRG genes per haploid genome is 19 to 22 of which 11 to 13 are functional (Tables 9 and 10).

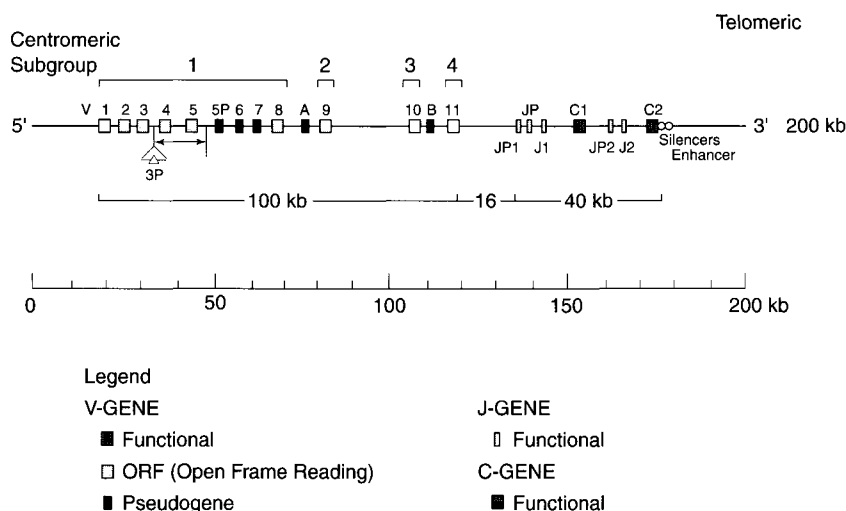


Figure 6. Representation of the human TRG locus at 7p14. The boxes representing the genes are not to scale. Exons are not shown. A double arrow indicates an insertion/deletion polymorphism. The TRGV3P gene, a polymorphic gene by insertion, has been identified by Southern hybridization in a rare haplotype but has not been sequenced⁴⁶.

List of the TRG genes on chromosome 7 at 7p14, and correspondence between nomenclatures

TRGV gene nomenclature

TRGV genes are designated by a number for the localization from 5' to 3' in the locus^{36,41}. Two pseudogenes, single members of their subgroup, are designated by a letter^{40,41}.

Table 5. List of functional or ORF human TRGV genes. Only the genes with at least one functional or ORF allele are shown. For a complete listing of the human TRGV genes including the pseudogenes, see reference 41 and IMGT gene data: <http://imgt.cines.fr/cgi-bin/IMGTlect.jv?query=203>.

For information on individual TRG genes:

<http://imgt.cines.fr/cgi-bin/IMGTlect.jv?query=202+genename>.

Example: IMGT Repertoire for TRGV4:

<http://imgt.cines.fr/cgi-bin/IMGTlect.jv?query=202+TRGV4>.

IMGT gene groups	IMGT gene names	IMGT functionality	IMGT number of alleles
TRGC	TRGC1	F	2
	TRGC2(2x)	F	4
	TRGC2(3x)	F	1
TRGJ	TRGJ1	F	2
	TRGJ2	F	1
	TRGJP	F	1
	TRGJP1	F	1
	TRGJP2	F	1
TRGV	TRGV1	ORF	1
	TRGV2	F	2
	TRGV3	F	2
	TRGV4	F	2
	TRGV5	F	1
	TRGV8	F	1
	TRGV9	F	2
	TRGV10	ORF	2
	TRGV11	ORF	2

Number of the human TRGV germline variable genes at 7p14 and potential repertoire

Overview

12–15 TRGV genes belonging to 6 subgroups, on 120 kilobases:

4–6 FUNCTIONAL

3 ORF (Open Reading Frame)

5 PSEUDOGENE

Potential repertoire

4–6 FUNCTIONAL TRGV genes belonging to 2 subgroups.

Table 6. *Repertoire of the human TRGV germline variable genes at 7p14.*

Subgroup	Gene name	Functional	ORF	Pseudogene	Total
1	TRGV1	–	1	–	1
	TRGV2	1	–	–	1
	TRGV3	1	–	–	1
	TRGV3P				0–1*
	TRGV4	0–1*	–	–	0–1*
	TRGV5	0–1*	–	–	0–1*
	TRGV5P	–	–	1	1
	TRGV6	–	–	1	1
	TRGV7	–	–	1	1
	TRGV8	1	–	–	1
2	TRGV9	1	–	–	1
3	TRGV10	–	1	–	1
4	TRGV11	–	1	–	1
A	TRGVA	–	–	1	1
B	TRGVB	–	–	1	1
	Total	4–6	3	5	12–15

* Indicates allelic polymorphism by insertion/deletion.

The TRGV3P gene, a polymorphic gene by insertion, has been identified by Southern hybridization in a rare haplotype but has not been sequenced⁴⁶.

The most frequent haplotype comprises 14 TRGV genes (6 FUNCTIONAL + 3 ORF + 5 PSEUDOGENES) with V4 and V5 present, and V3P absent^{41,46}.

THE HUMAN TRD LOCUS

Chromosomal localization of the human TRD locus

The human TRD locus is located on chromosome 14, on the long arm at band 14q11.2 (Fig. 7). The TRD locus is embedded in the TRA locus, between the TRAV and TRAJ genes^{53–55}. The orientation of the locus has been determined by the analysis of translocations involving the TRD locus, in leukemia and lymphoma.

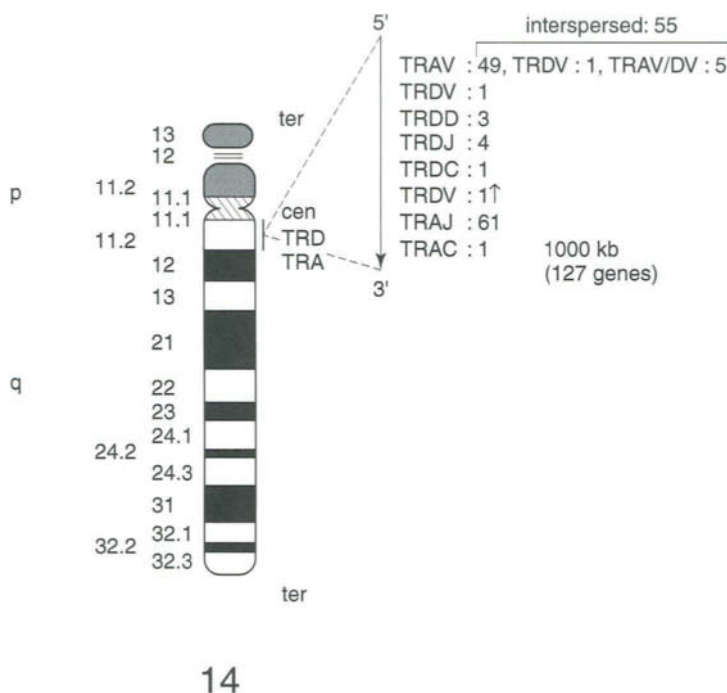


Figure 7. Chromosomal localization of the human TRD locus embedded in the TRA locus at 14q11.2. A vertical line indicates the localization of the TRA and TRD loci at 14q11.2. The arrow indicates the orientation 5' → 3' of the loci, and the gene group order in the loci. The length of the arrow is proportional to the total size of the loci, indicated in kilobases (kb). The total number of genes in the TRA and TRD loci is shown in parentheses. The five genes, designated TRAV/DV, have been found rearranged to J genes of the TRA locus, and to D and J genes of the TRD locus and can therefore be used in the synthesis of alpha or delta chains⁴.

Organization of the human TRD locus

The human TRD locus at 14q11.2 comprises a cluster of one TRDV gene (TRDV2)⁵⁶⁻⁵⁸, three TRDD genes^{59,60}, and four TRDJ genes^{54,60-63}, upstream of the unique TRDC gene⁵⁹; another TRDV gene (TRDV3) is localized downstream of the TRDC gene, in inverted orientation of transcription^{56,60,64}. This cluster spans 60 kb and is localized inside the TRA locus, between the TRAV genes and the TRAJ genes¹³. One TRDV gene (TRDV1)^{65,66} is localized at 360 kb upstream of the TRDC gene, among the TRAV genes⁶⁷. Five variable genes have been found rearranged to both (D)J genes of the TRD locus and TRAJ genes, and can therefore be used for the synthesis of both delta and alpha chains^{4,68,69}. These genes are described as TRAV/DV⁴. The TRDV genes are unique members of different subgroups. All the TRD genes are functional, with the exception of one TRAV/DV, which has been found either functional or as a pseudogene⁴. Enhancer sequences have been described between the TRDJ3 and the TRDC gene^{70,71}.

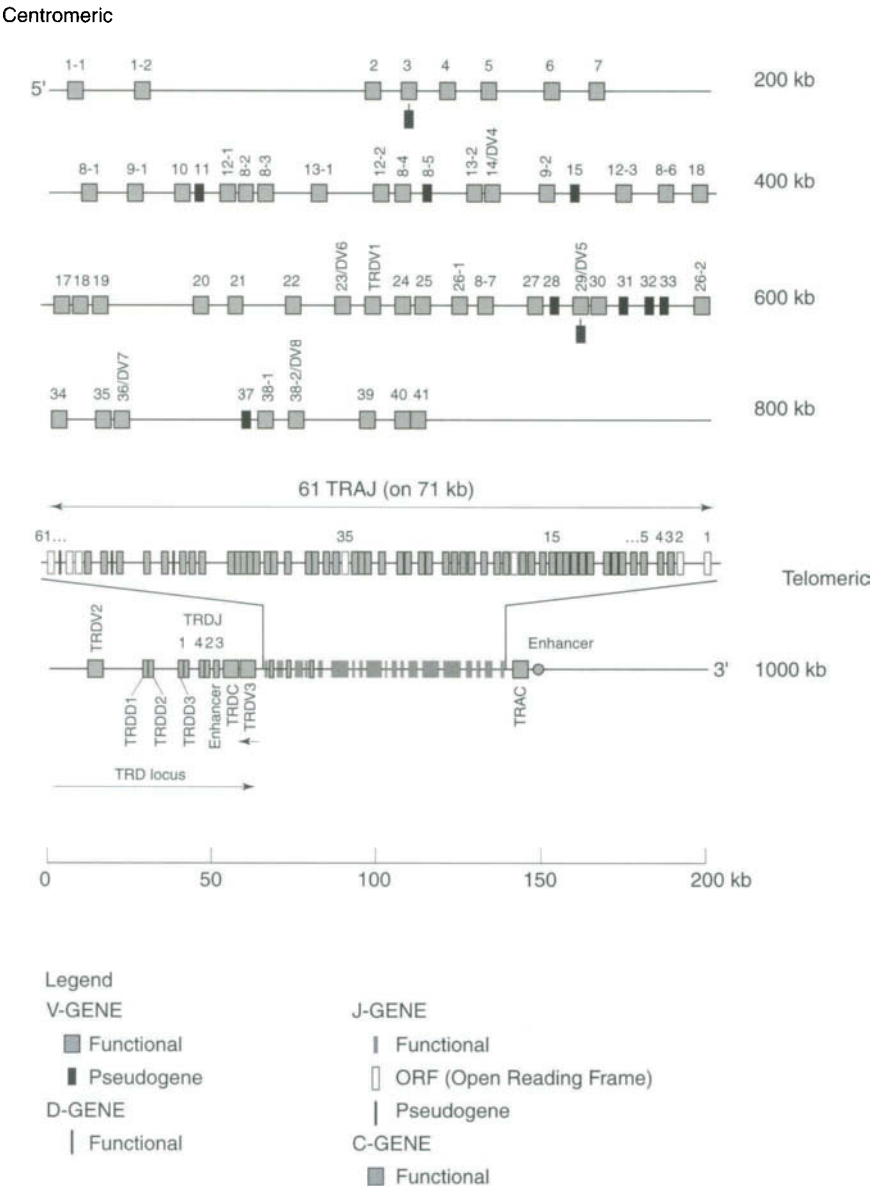


Figure 8. Representation of the human TRD locus nestled in the TRA locus at 14q11.2. The boxes representing the genes are not to scale. Exons are not shown. The three TRDV genes are designated by a number for the subgroup which corresponds to the position from 5' to 3' in the locus. The five TRAV/DV genes can be used for the synthesis of both delta and alpha chains.

List of the TRD genes on chromosome 14 at 14q11.2, and correspondence between nomenclatures

TRDV and TRAV/DV gene nomenclature

TRDV genes (genes only found rearranged to TRDD genes) are designated by a number for the subgroup which corresponds to the position from 5' to 3' in the locus.

TRAV/DV genes (genes found rearranged to TRDD genes and to TRAJ genes) are designated according to the TRAV nomenclature. To indicate that these genes can be involved in TRD rearrangements, a slash is added, followed by the letters DV and a number. These genes have been reported in the TRAV table.

Table 7. List of functional or ORF human TRD genes. Only the genes with at least one functional or ORF allele are shown. The TRAV14/DV4, TRAV23/DV6, TRAV29/DV5, TRAV36/DV7, and TRAV38-2/DV8 genes which have been found rearranged to J genes of the TRA locus, and to D and J genes of the TRD locus are displayed in the human TRAV table. For a complete listing of the human TRD genes including the pseudogenes, see references 4 and 10 and IMGT gene data: <http://imgt.cines.fr/cgi-bin/IMGTElect.jv?query=203>.

For information on individual TRD genes:

<http://imgt.cines.fr/cgi-bin/IMGTElect.jv?query=202+genename>.

Example: IMGT Repertoire for TRDV2

<http://imgt.cines.fr/cgi-bin/IMGTElect.jv?query=202+TRDV2>.

IMGT gene groups	IMGT gene names	IMGT functionality	IMGT number of alleles
TRDC	TRDC	F	1
TRDD	TRDD1	F	1
	TRDD2	F	1
	TRDD3	F	1
TRDJ	TRDJ1	F	1
	TRDJ2	F	1
	TRDJ3	F	1
	TRDJ4	F	1
TRDV	TRDV1	F	1
	TRDV2	F	3
	TRDV3	F	2

Number of the human TRDV germline variable genes at 14q11.2 and potential repertoire

Overview

3 TRDV genes belonging to 3 subgroups

TRDV1 at 360 kb upstream of TRDC, among the TRAV genes

TRDV2 at 44 kb upstream of TRDC

TRDV3 at 3 kb downstream of TRDC and in an inverted orientation of transcription.

5 TRAV/DV genes belonging to 5 subgroups

The TRAV/DV genes have been found rearranged either to TRAJ genes or to D and J genes of the TRD locus, and can therefore be used in the synthesis of alpha or delta chains.

Potential repertoire

3 FUNCTIONAL TRDV genes belonging to 3 subgroups, and 4–5 FUNCTIONAL TRAV/DV genes belonging to 4 to 5 subgroups.

Table 8. *Repertoire of the human TRDV and TRAV/DV germline variable genes at 14q11.2.*

Subgroup	Functional	ORF	Pseudogene	Total
TRDV1	1	–	–	1
TRDV2	1	–	–	1
TRDV3	1	–	–	1
Total	3	0	0	3
TRAV14/DV4	1	–	–	1
TRAV23/DV6	1	–	–	1
TRAV29/DV5	(1)*	–	(1)*	1
TRAV36/DV7	1	–	–	1
TRAV38-2/DV8 ^a	1	–	–	1
Total	4(+1)*	0	(1)*	5

*Indicates that the following gene has alleles with different functionality: FUNCTIONAL or PSEUDOGENE (TRAV29/DV5)

^a The TRAV38/DV8 subgroup comprises two genes; only the TRAV38-2/DV8 gene has so far been found rearranged to TRDD genes.

Table 9. Total number of human T cell receptor genes per haploid genome.

Locus	Major loci						Number of orphans	Total number of genes (including orphans)
	Chromosomal localization	V	D	J	C	Total number of genes in the major locus		
TRA	14q11.2	54 ^a	0	61	1	116 ^a	–	116 ^a
TRB	7q34	64–67	2	14	2	82–85	6	88–91
TRG	7p14	12–15	0	5	2	19–22	–	19–22
TRD	14q11.2	3				11		
		8 ^a	3	4	1	16 ^a	–	11

^a including the 5 TRAV/DV genes.

Major loci refer to the TRA locus at 14q11.2, TRB locus at 7q34, TRG locus at 7p14, and TRD locus at 14q11.2, genes of which are involved in T cell receptor chain synthesis.

Orphans are genes located outside of the main loci, which cannot contribute to the TcR chain synthesis. Six TRBV orphans have been identified on chromosome 9 at 9p21.

Table 10. *Number of functional human T cell receptor genes per haploid genome.*

Locus	Chromosomal localization	Locus size in kb (kilobases)	V	D	J	C	Number of functional genes	Combinatorial diversity (range per locus)
TRA	14q11.2	1000	44–46 ^a	0	50	1	95–97 ^b	44 × 50 = 2200 (m) 46 × 50 = 2300 (M)
TRB	7q34	620	40–48	2	12–13	2	56–65	40 × 2 × 12 = 960 (m) 48 × 2 × 13 = 1248 (M)
TRG	7p14	160	4–6	0	5	2	11–13	4 × 5 = 20 (m) 6 × 5 = 30 (M)
TRD	14q11.2	60 ^b 530 ^c	3 8 ^a	3	4	1	11 16 ^a	3 × 3 × 4 = 36 (m) 8 × 3 × 4 = 96 ^a 8 × 7 × 4 = 224 ^d (M)

^a including the 5 TRAV/DV genes,^b size of the cluster from TRDV2 to TRDV3,^c distance between the most 5' TRAV/DV gene (TRAV14/DV4) and the most 3' gene of the TRD locus (TRDV3).^d taking into account the rearrangement with 2 or 3 TRDD (4 possible combinations: D1,D2; D1,D3; D2,D3; D1,D2,D3)

The range of the theoretical combinatorial diversity is indicated taking into account the minimum (m) and the maximum (M) number of functional V, D, and J genes in each of the major TRA, TRB, TRG, and TRD loci.

References

- ¹ Collins, M.K.L. et al. (1984) *EMBO J.* 3, 2347–2349.
- ² Croce, C. et al. (1984) *Science* 227, 1044–1047.
- ³ Rabbitts, T.H. et al. (1985) *EMBO J.* 4, 1461–1465.
- ⁴ Scaviner, D. and Lefranc, M.-P. (2000) *Exp. Clin. Immunogenet.* 17, 83–96.
- ⁵ Wilson, R.K. et al. (1988) *Immunol. Rev.* 101, 149–172.
- ⁶ Roman-Roman, S. et al. (1991) *Eur. J. Immunol.* 21, 927–933.
- ⁷ Arden, B. et al. (1995) *Immunogenetics* 42, 455–500.
- ⁸ Folch, G. et al. (2000) *Exp. Clin. Immunogenet. in press.*
- ⁹ Koop, B.F. et al. (1994) *Genomics* 19, 478–493.
- ¹⁰ Scaviner, D. and Lefranc, M.-P. (2000) *Exp. Clin. Immunogenet.* 17, 97–106.
- ¹¹ Baer, R. et al. (1986) *Mol. Biol. Med.* 3, 265–277.
- ¹² Yoshikai, Y. et al. (1985) *Nature* 316, 837–740.
- ¹³ Lefranc, M.-P. (1990) *Eur. Cytokine Net.* 1, 121–130.
- ¹⁴ De Villartray, J.P. et al. (1988) *Nature* 335, 170–174.
- ¹⁵ Begley, C.G. et al. (1989) *J. Exp. Med.* 170, 339–342.
- ¹⁶ Ho, I.C. et al. (1989) *Proc. Natl Acad. Sci USA.* 86, 6714–6718.
- ¹⁷ Barker, P.E. et al. (1984) *Science* 226, 348–349.
- ¹⁸ Caccia, N. et al. (1984) *Cell.* 37, 1091–1099.
- ¹⁹ Isobe, M. et al. (1985) *Science* 228, 580–582.
- ²⁰ Wilson, R.K. et al. (1988) *Immunol. Rev.* 101, 149–172.
- ²¹ Lai, E. et al. (1988) *Nature* 333, 543–588.
- ²² Ferradini, L. et al. (1991) *Eur. J. Immunol.* 21, 935–942.
- ²³ Wei, S. et al. (1994) *Immunogenetics* 40, 27–36.
- ²⁴ Posnett, D.N. et al. (1996) *The Immunologist* 4, 5–8.
- ²⁵ Rowen, L. et al. (1996) *Science* 272, 1755–1762.
- ²⁶ Folch, G. and Lefranc, M.-P. (2000) *Exp. Clin. Immunogenet.* 17, 42–54.
- ²⁷ Toyonaga, B. et al. (1985) *Proc. Natl Acad. Sci. USA* 82, 8624–8628.
- ²⁸ Tunnacliffe, A. et al. (1985) *Proc. Natl Acad. Sci. USA* 82, 5068–5072.
- ²⁹ Folch, G. and Lefranc, M.-P. (2000) *Exp. Clin. Immunogenet.* 17, 107–114.
- ³⁰ Malissen, M. et al. (1986) *Nature* 319, 28–33.
- ³¹ Robinson, M.A. et al. (1993) *Proc. Natl Acad. Sci. USA* 90, 2433–2437.
- ³² Charmley, P. et al. (1995) *Genomics* 25, 150–156.
- ³³ Gottschalk, L.R. and Leiden, J.M. (1990) *Mol. Cell. Biol.* 10, 5486–5495.
- ³⁴ Lefranc, M.-P. and Rabbitts, T.H. (1985) *Nature* 316, 464–466.
- ³⁵ Lefranc, M.-P. et al. (1986) *Nature* 319, 420–422.
- ³⁶ Lefranc, M.-P. et al. (1986) *Cell* 45, 237–246.
- ³⁷ Lefranc, M.-P. et al. (1986) *Proc. Natl Acad. Sci. USA* 83, 9596–9600.
- ³⁸ Forster, A. et al. (1987) *EMBO J.* 6, 1945–1950.
- ³⁹ Huck, S. and Lefranc, M.-P. (1987) *FEBS Lett.* 224, 291–296.
- ⁴⁰ Huck, S. et al. (1988) *EMBO J.* 7, 719–726.
- ⁴¹ Lefranc, M.-P. et al. (1989) *Eur. J. Immunol.* 19, 989–994.
- ⁴² Lefranc, M.-P. and Rabbitts, T.H. (1989) *TIBS* 14, 214–218.
- ⁴³ Buresi, C. et al. (1989) *Immunogenetics* 29, 161–172.
- ⁴⁴ Ghanem, N. et al. (1989) *Immunogenetics* 30, 350–360.
- ⁴⁵ Lefranc, M.-P. and Rabbitts, T.H. (1990) *Res. Immunol.* 141, 565–577 ; 615–618.
- ⁴⁶ Ghanem, N. et al. (1991) *Hum. Genet.* 86, 450–456.
- ⁴⁷ Zhang, X.M. et al. (1994) *Eur. J. Immunol.* 24, 571–578.

- ⁴⁸ Zhang, X.M. et al. (1996) *Immunogenetics* 43, 196–203.
- ⁴⁹ Rabbitts, T.H. et al. (1985) *EMBO J.* 4, 1461–1465.
- ⁵⁰ Murre, C. et al. (1985) *Nature* 316, 549–552.
- ⁵¹ Bensmana, M. et al. (1991) *Cytogenet. Cell Genet.* 56, 31–32.
- ⁵² Lefranc, M.-P. and Alexandre, D. (1995) *Eur. J. Immunol.* 25, 617–622.
- ⁵³ Baer, R. et al. (1988) *EMBO J.* 7, 1661–1668.
- ⁵⁴ Satyanarayana, K. et al. (1988) *Proc. Natl Acad. Sci. USA* 85, 8166–8170.
- ⁵⁵ Griesser, H. et al. (1988) *Eur. J. Immunol.* 18, 641–644.
- ⁵⁶ Hata, S. et al. (1989) *J. Exp. Med.* 169, 41–57.
- ⁵⁷ Triebel, Y. et al. (1988) *Eur. J. Immunol.* 18, 2021–2027.
- ⁵⁸ Dariavach, P. and Lefranc, M.-P. (1989) *Nucleic Acids Res.* 17, 4880.
- ⁵⁹ Takihara, Y. et al. (1988) *Proc. Natl Acad. Sci. USA* 85, 6097–6101.
- ⁶⁰ Loh, E.Y. et al. (1988) *Proc. Natl Acad. Sci. USA* 85, 9714–9718.
- ⁶¹ Isobe, M. et al. (1988) *Proc. Natl Acad. Sci. USA* 85, 3933–3937.
- ⁶² Boehm, T. et al. (1988) *EMBO J.* 7, 385–394.
- ⁶³ Davodeau, F. et al. (1994) *J. Immunol.* 153, 137–142.
- ⁶⁴ Takihara, Y. et al. (1989) *Eur. J. Immunol.* 19, 571–574.
- ⁶⁵ Hata, S. et al. (1987) *Science* 238, 678–682.
- ⁶⁶ Loh, E.Y. et al. (1987) *Nature* 330, 569–572.
- ⁶⁷ Boysen, C. et al. unpublished (AE000660, AE000661).
- ⁶⁸ Guglielmi, P. et al. (1988) *Proc. Natl Acad. Sci. USA* 85, 5634–5638.
- ⁶⁹ Casorati, G. and Migone, N. (1989) *Res. Immunol.* 141, 624–626.
- ⁷⁰ Redondo, J.M. et al. (1990) *Science* 247, 1225–1229.
- ⁷¹ Bories, J.C. et al. (1990) *J. Exp. Med.* 171, 75–83.

**THE HUMAN
T CELL RECEPTOR
TRA GENES**

This Page Intentionally Left Blank

Part 1

TRAC

Nomenclature

TRAC: T cell receptor alpha constant.

Definition and functionality

TRAC is the functional and unique constant gene in the TRA locus.

Gene location

TRAC is in the TRA locus on chromosome 14 at 14q11.2. TRAC is the most 3' gene in the TRA/TRD locus.

Nucleotide and amino acid sequences for human TRAC

The nucleotide between parentheses at the beginning of exons comes from a DONOR-SPLICE (n from ngf).

The Cysteines involved in the intrachain disulfide bridges are shown with their number and letter C in bold.

N-Glycosylation sites (NXS/T, where X is different from P) are underlined.

A DONOR-SPLICE, located just after the termination codon, uses a downstream ACCEPTOR-SPLICE, placing part of the 3' non-coding sequence on a separate untranslated exon, designated as EX4. Since EX4 is untranslated, nucleotide differences observed in EX4 are not taken into account for the description of alleles.

		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	
		N	I	Q	N	P	D	P	A	V	Y	Q	L	R	D	S	K	S	S	D	K	
X02883	,TRAC*01 (EX1)	[1]	(A)AT	ATC	CAG	AAC	CCT	GAC	CCT	GCC	GTG	TAC	CAG	CTG	AGA	GAC	TCT	AAA	TCC	AGT	GAC	AAG
X02592	,TRAC*01 (cDNA)	[2]	(-)	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
M14858	,TRAC*01	[3]	(-)	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
AE000662	,TRAC*01	[5]	(-)	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
M94081	,TRAC*01	[4]	(-)	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
		21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	
		S	V	C	L	F	T	D	F	D	S	Q	T	<u>N</u>	<u>V</u>	<u>S</u>	Q	S	K	D	S	
X02883	,TRAC*01	TCT	GTC	TGC	CTA	TTC	ACC	GAT	TTT	GAT	TCT	CAA	ACA	AAT	GTG	TCA	CAA	AGT	AAG	GAT	TCT	
X02592	,TRAC*01	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
M14858	,TRAC*01	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
AE000662	,TRAC*01	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
M94081	,TRAC*01	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
		41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	
		D	V	Y	I	T	D	K	T	V	L	D	M	R	S	M	D	F	K	S	N	
X02883	,TRAC*01	GAT	GTG	TAT	ATC	ACA	GAC	AAA	ACT	GTG	CTA	GAC	ATG	AGG	TCT	ATG	GAC	TTC	AAG	AGC	AAC	
X02592	,TRAC*01	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
M14858	,TRAC*01	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
AE000662	,TRAC*01	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
M94081	,TRAC*01	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
		61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	
		S	A	V	A	W	S	<u>N</u>	<u>K</u>	<u>S</u>	D	F	A	C	A	N	A	F	<u>N</u>	<u>N</u>	<u>S</u>	
X02883	,TRAC*01	AGT	GCT	GTG	GCC	TGG	AGC	AAC	AAA	TCT	GAC	TTT	GCA	TGT	GCA	AAC	GCC	TTC	AAC	AAC	AGC	
X02592	,TRAC*01	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
M14858	,TRAC*01	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
AE000662	,TRAC*01	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
M94081	,TRAC*01	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		

77



X02883 ,TRAC*01GCCCTGCTATGCTGTGTGTCGTGGCGCTGTGTATGTCTGCTGCCGATGCCTTC

X02592 ,TRAC*01-----

X05002/M14861,TRAC*01-----

AE000662,TRAC*01-----

M94081 ,TRAC*01-----

: Nucleotide deletion or insertion



Genome database accession numbers

GDB:9953797

LocusLink: 28755



References

¹ Yoshikai, Y. et al. (1985) Nature 316, 837–840.

² Rabbitts, T.H. et al. (1985) EMBO J. 4, 1461–1465.

³ Baer, R.J. et al. (1986) Mol. Biol. Med. 3, 265–277.

⁴ Koop, B.F. et al. (1994) Genomics 19, 478–493.

⁵ Boysen, C. et al., unpublished.



Protein display

Protein display of the TRAC gene is shown on page 372.

Part 2

TRAJ

Nomenclature

T cell receptor alpha joining group.

Definition and functionality

The human TRAJ group comprises 61 mapped genes of which 52 are functional, eight are ORF (TRAJ1, TRAJ2, TRAJ19, TRAJ25, TRAJ35, TRAJ58, TRAJ59, and TRAJ61) and three are pseudogenes (TRAJ51, TRAJ55, and TRAJ60).

Gene location

The human TRAJ genes are located in the TRA/TRD locus on chromosome 14 at 14q11.2, between the TRDV3 and TRAC genes, at a distance of 71 kb.

Nucleotide and amino acid sequences for the human functional or ORF TRAJ genes with nomenclature

The conserved FGXG motif, characteristic of the TRA J-REGION, is underlined.

TRAJ1

T cell receptor alpha joining 1

X02884 ,TRAJ1*01 [6](1) Y E S I T S Q L Q F G K G T R V S T S P
G TAT GAA AGT ATT ACC TCC CAG TTG CAA TTT GGC AAA GGA ACC AGA GTT TCC ACT TCT CCC C

TRAJ2

T cell receptor alpha joining 2

X02884 ,TRAJ2*01 [6](2) N T G G T I D K L T F G K G T H V F I I S
TG AAT ACT GGA GGA ACA ATT GAT AAA CTC ACA TTT GGC AAA GGG ACC CAT GTA TTC ATT ATA TCT G

TRAJ3

T cell receptor alpha joining 3

X02884 ,TRAJ3*01 [6] G Y S S A S K I I F G S G T R L S I R P
G GGG TAC AGC AGT GCT TCC AAG ATA ATC TTT GGA TCA GGG ACC AGA CTC AGC ATC CGG CCA A

TRAJ4

T cell receptor alpha joining 4

M94081 ,TRAJ4*01 [4] F S G G Y N K L I F G A G T R L A V H P
TG TTT TCT GGT GGC TAC AAT AAG CTG ATT TTT GGA GCA GGG ACC AGG CTG GCT GTA CAC CCA T

TRAJ5

T cell receptor alpha joining 5

M94081 ,TRAJ5*01 [4] D T G R R A L T F G S G T R L Q V Q P
TG GAC ACG GGC AGG AGA GCA CTT ACT TTT GGG AGT GGA ACA AGA CTC CAA GTC CAA CCA A

TRAJ6

T cell receptor alpha joining 6

M16747 ,TRAJ6*01 [1] A S G G S Y I P T F G R G T S L I V H P
T GCA TCA GGA GGA AGC TAC ATA CCT ACA TTT GGA AGA GGA ACC AGC CTT ATT GTT CAT CCG T

TRAJ7

T cell receptor alpha joining 7

M94081 ,TRAJ7*01 [4] D Y G N N R L A F G K G N Q V V V I P
T GAC TAT GGG AAC AAC AGA CTC GCT TTT GGG AAG GGG AAC CAA GTG GTG GTC ATA CCA A

TRAJ8

T cell receptor alpha joining 8

M94081 ,TRAJ8*01 [4] N T G F Q K L V F G T G T R L L V S P
TG AAC ACA GGC TTT CAG AAA CTT GTA TTT GGA ACT GGC ACC CGA CTT CTG GTC AGT CCA A

TRAJ9

T cell receptor alpha joining 9

M94081 ,TRAJ9*01 [4] G N T G G F K T I F G A G T R L F V K A
GGA AAT ACT GGA GGC TTC AAA ACT ATC TTT GGA GCA GGA ACA AGA CTA TTT GTT AAA GCA A

TRAJ10

T cell receptor alpha joining 10

M94081 ,TRAJ10*01 [4] I L T G G G N K L T F G T G T Q L K V E L
ATA CTC ACG GGA GGA GGA AAC AAA CTC ACC TTT GGG ACA GGC ACT CAG CTA AAA GTG GAA CTC A

**TRAJ11****T cell receptor alpha joining 11**

M94081 ,TRAJ11*01 [4]

N S G Y S T L T F G K G T M L L V S P
TG AAT TCA GGA TAG AGC ACC CTC ACC TTT GGG AAG GGG ACT ATG CTT CTA GTC TCT CCA G

TRAJ12**T cell receptor alpha joining 12**

X02885 ,TRAJ12*01 [6]

M D S S Y K L I F G S G T R L L V R P
GG ATG GAT AGC AGC TAT AAA TTG ATC TTC GGG AGT GGG ACC AGA CTG CTG GTC AGG CCT G

TRAJ13**T cell receptor alpha joining 13**

M94081 ,TRAJ13*01 [4]

N S G G Y Q K V T F G I G T K L Q V I P
TG AAT TCT GGG GST TAC CAG AAA GTT ACC TTT GGA ATT GGA ACA AAG CTC CAA GTC ATC CCA A

TRAJ14**T cell receptor alpha joining 14**

M94081 ,TRAJ14*01 [4]

I Y S T F I F G S G T R L S V K P
ATT TAT AGC ACA TTC ATC TTT GGG AGT GGG ACA AGA TTA TCA GTA AAA CCT G

TRAJ15**T cell receptor alpha joining 15**

X05775 ,TRAJ15*01 [5]

N Q A G T A L I F G K G T T L S V S S
CC AAC CAG GCA AGA ACT GCT CTG ATC TTT GGG AAG GGA ACC ACC TTA CTA GTG AGT TCC A
H
----- CA- C-----

M94081 ,TRAJ15*02 [4]

TRAJ16**T cell receptor alpha joining 16**

M94081 ,TRAJ16*01 [4]

F S D G Q K L L F A R G T M L K V D L
GG TTT TCA GAT GGC CAG AAG CTC CTC TTT GCA AGG GGA ACC ATG TTA AAG GTG GAT CTT A

TRAJ17**T cell receptor alpha joining 17**

X05773 ,TRAJ17*01 [5]

I K A A G N K L T F G G G T R V L V K P
TG ATC AAA GCT GCA GGC AAC AAG CTA ACT TTT GGA GGA GGA ACC AGG GTG CTA GTT AAA CCA A

TRAJ18**T cell receptor alpha joining 18**

M94081 ,TRAJ18*01 [4]

D R G S T L G R L Y F G R G T Q L T V W P
CC GAC AGA GGC TCA ACC CTG GGG AGG CTA TAC TTT GGA AGA GGA ACT CAG TTG ACT GTC TGG CCT G

TRAJ19**T cell receptor alpha joining 19**

M94081 ,TRAJ19*01 [4] (3)

Y Q R F Y N F T F G K G S K H N V T P
GC TAT CAA AGA TTT TAC AAT TTC ACC TTT GGA AAG GGA TCC AAA CAT AAT GTC ACT CCA A

TRAJ20**T cell receptor alpha joining 20**

M94081 ,TRAJ20*01 [4]

S N D Y K L S F G A G T T V T V R A
GT TCT AAC GAC TAC AAG CTC AGC TTT GGA GCC GGA ACC ACA GTA ACT GTA AGA GCA A

TRAJ21**T cell receptor alpha joining 21**

M94081 ,TRAJ21*01 [4]

Y N F N K F Y F G S G T K L N V K P
TAC AAC TTC AAC AAA TTT TAC TTT GGA TCT GGG ACC AAA CTC AAT GTA AAA CCA A

TRAJ22**T cell receptor alpha joining 22**

X02886 ,TRAJ22*01 [6]

S S G S A R Q L T F G S G T Q L T V L P
TT TCT TCT GGT TCT GCA AGG CAA CTG ACC TTT GGA TCT GGG ACA CAA TTG ACT GTT TTA CCT G

TRAJ23**T cell receptor alpha joining 23**

M94081 ,TRAJ23*01 [4]

I Y N Q G G K L I F G Q G T E L S V K P
TG ATT TAT AAC CAG GGA GGA AAG CTT ATC TTC GGA CAG GGA ACG GAG TTA TCT GTG AAA CCC A

TRAJ24**T cell receptor alpha joining 24**

X02887 ,TRAJ24*01 [6]

T T D S W G K F E F G A G T Q V V V T P
TG ACA ACT GAC AGC TGG GGG AAA TTC GAG TTT GGA GCA GGG ACC CAG GTT GTG GTC ACC CCA G
L Q
----- -AG C-----

M94081 ,TRAJ24*02 [4]

TRAJ25**T cell receptor alpha joining 25**

X02888 ,TRAJ25*01 [6] (4)

E G Q G F S F I F G K G T R L L V K P
CA GAA GGA CAA GGC TTC TCC TTT ATC TTT GGG AAG GGG ACA AGG CTG CTT GTC AAG CCA A

TRAJ26**T cell receptor alpha joining 26**

M94081 ,TRAJ26*01 [4]

D N Y G Q N F V F G P G T R L S V L P
GG GAT AAC TAT GGT CAG AAT TTT GTC TTT GGT CCC GGA ACC AGA TTG TCC CTG CTG CCC T

TRAJ27**T cell receptor alpha joining 27**

M94081 ,TRAJ27*01 [4]

N T N A G K S T F G D G T T L T V K P
T AAC ACC AAT GCA GGC AAA TCA ACC TTT GGG GAT GGG ACT ACG CTC ACT GTG AAG CCA A

**TRAJ28****T cell receptor alpha joining 28**

Y S G A G S Y Q L T F G K G T K L S V I P
M94081 ,TRAJ28*01 [4] CA TAC TCT GGG GCT GGG AGT TAC CAA CTC ACT TTC GGG AAG GGG ACC AAA CTC TCG GTC ATA CCA A

TRAJ29**T cell receptor alpha joining 29**

N S G N T P L V F G K G T R L S V I A
X02889 ,TRAJ29*01 [6] GG AAT TCA GGA AAC ACA CCT CTT GTC TTT GGA AAG GGC ACA AGA CTT TCT GTG ATT GCA A

TRAJ30**T cell receptor alpha joining 30**

N R D D K I I F G K G T R L H I L P
M94081 ,TRAJ30*01 [4] TG AAC AGA GAT GAC AAG ATC ATC TTT GGA AAA GGG ACA CGA CTT CAT ATT CTC CCC A

TRAJ31**T cell receptor alpha joining 31**

N N N A R L M F G D G T Q L V V K P
M14905 ,TRAJ31*01 [3] G AAT AAC AAT GCC AGA CTC ATG TTT GGA GAT GGA ACT CAG CTG GTG GTG AAG CCC A

TRAJ32**T cell receptor alpha joining 32**

N Y G G A T N K L I F G T G T L L A V Q P
M94081 ,TRAJ32*01 [4] TG AAT TAT GGC GGT GCT ACA AAC AAG CTC ATC TTT GGA ACT GGC ACT CTG CTT OCT GTC CAG CCA A

TRAJ33**T cell receptor alpha joining 33**

D S N Y Q L I H G A G T K L I I K P
M94081 ,TRAJ33*01 [4] TG GAT AGC AAC TAT CAG TTA ATC TGG GGC GCT GGG ACC AGA CTA ATT ATA AAG CCA G

TRAJ34**T cell receptor alpha joining 34**

S Y N T D K L I F G T G T R L Q V F P
M35622 ,TRAJ34*01 [2] TCT TAT AAC ACC GAC AAG CTC ATC TTT GGG ACT GGG ACC AGA TTA CAA GTC TTT CCA A

TRAJ35**T cell receptor alpha joining 35**

I G F G N V L H C G S G T Q V I V L P
M94081 ,TRAJ35*01 [4](5) G ATA GGC TTT GGG AAT GTG CTG CAT TCC GGG TCC GGC ACT CAA GTG ATT GTT TTA CCA C

TRAJ36**T cell receptor alpha joining 36**

Q T G A N N L F F G T G T R L T V I P
M94081 ,TRAJ36*01 [4] T CAA ACT GGG GCA AAC AAC CTC TTC TTT GGG ACT GGA ACG AGA CTC ACC GTT ATT CCC T

TRAJ37**T cell receptor alpha joining 37**

G S G N T G K L I F G Q G T T L Q V K P
M94081 ,TRAJ37*01 [4] T GGC TCT GGC AAC ACA GGC AAA CTA ATC TTT GGG CAA GGG ACA ACT TTA CAA GTA AAA CCA G

TRAJ38**T cell receptor alpha joining 38**

N A G N N R K L I H G L G T S L A V N P
M94081 ,TRAJ38*01 [4] T AAT GCT GGC AAC AAC CGT AAG CTG ATT TGG GGA TTG GGA ACA AGC CTG GCA GTA AAT CCG A

TRAJ39**T cell receptor alpha joining 39**

N N N A G N M L T F G G G T R L M V K P
M94081 ,TRAJ39*01 [4] TG AAT AAT AAT GCA GGC AAC ATG CTC ACC TTT GGA GGG GGA ACA AGS TTA ATG GTC AAA CCC C

TRAJ40**T cell receptor alpha joining 40**

T T S G T Y K Y I F G T G T R L K V L A
M35620 ,TRAJ40*01 [2] ACT ACC TCA GGA ACC TAC AAA TAC ATC TTT GGA ACA GGC ACC AGG CTG AAG GTT TTA GCA A

TRAJ41**T cell receptor alpha joining 41**

N S N S G Y A L N F G K G T S L L V T P
M94081 ,TRAJ41*01 [4] G AAC TCA AAT TCC GGG TAT GCA CTC AAC TTC GGC AAA GGC ACC TCG CTG TTG GTC ACA CCC C

TRAJ42**T cell receptor alpha joining 42**

N Y G G S Q G N L I F G K G T K L S V K P
M94081 ,TRAJ42*01 [4] TG AAT TAT GGA GGA AGC CAA GGA AAT CTC ATC TTT GGA AAA GGC ACT AAA CTC TCT GTT AAA CCA A

TRAJ43**T cell receptor alpha joining 43**

N N N D M R F G A G T R L T V K P
M94081 ,TRAJ43*01 [4] AC AAT AAC AAT GAC ATG CGC TTT GGA GCA GGG ACC AGA CTG ACA GTA AAA CCA A

TRAJ44**T cell receptor alpha joining 44**

N T G T A S K L T F G T G T R L Q V T L
M35619 ,TRAJ44*01 [2] TA AAT ACC GGC ACT GCC AGT AAA CTC ACC TTT GGG ACT GGA ACA CTT CAG GTC ACG CTC G

TRAJ45**T cell receptor alpha joining 45**

Y S G G G A D G L T F G K G T H L I I Q P
M94081 ,TRAJ45*01 [4] TG TAT TCA GGA GGA GGT GCT GAC GGA CTC ACC TTT GGC AAA GGG ACT CAT CTA ATC CTC CAG CCC T

TRAJ46**T cell receptor alpha joining 46**

K K S S G D K L T F G T G T R L A V R P
M94081 ,TRAJ46*01 [4] AG AAG AAA AGC AGC GGA GAC AAG CTG ACT TTT GGG ACC GGG ACT CGT TTA GCA GTT AGG CCC A

**TRAJ47****T cell receptor alpha joining 47**

M94081 ,TRAJ47*01 [4]

E Y G N K L V F G A G T I L R V K S
 TG GAA TAT GGA AAC AAA CTG GTC TTT GGC GCA GGA ACC ATT CTG AGA GTC AAG TCC T

TRAJ48**T cell receptor alpha joining 48**

M94081 ,TRAJ48*01 [4]

S N F G N E K L T F G T G T R L T I I P
 TA TCT AAC TTT GGA AAT GAG AAA TTA ACC TTT GGC ACT GGA ACA AGA CTC ACC ATC ATA CCC A

TRAJ49**T cell receptor alpha joining 49**

M94081 ,TRAJ49*01 [4]

N T G N Q F Y F G T G T S L T V I P
 G AAC ACC GGT AAC CAG TTC TAT TTT GGC ACA GGC ACA AGT TTG ACG GTC ATT CCA A

TRAJ50**T cell receptor alpha joining 50**

M94081 ,TRAJ50*01 [4]

K T S Y D K V I F G P G T S L S V I P
 TG AAA ACC TCC TAC GAC AAG GTG ATA TTT GGC CCA GGC ACA AGC TTA TCA GTC ATT CCA A

TRAJ52**T cell receptor alpha joining 52**

M94081 ,TRAJ52*01 [4]

N A G G T S Y G K L T F G O G T I L T V H P
 CT AAT GCT GGT GGT ACT AGC TAT GGA AAG CTG ACA TTT GGA CAA GGC AGC ATC TTG ACT GTC CAT CCA A

TRAJ53**T cell receptor alpha joining 53**

M94081 ,TRAJ53*01 [4]

N S G G S N Y K L T F G K G T L L T V N P
 AG AAT AGT GGA GGT AGC AAC TAT AAA CTG ACA TTT GGA AAA GGA ACT CTC TTA ACC GTG AAT CCA A

TRAJ54**T cell receptor alpha joining 54**

M94081 ,TRAJ54*01 [4]

I Q G A Q K L V F G O G T R L T I N P
 TA ATT CAG GGA GCC CAG AAG CTG GTA TTT GGC CAA GGA ACC AGG CTG ACT ATC AAC CCA A

TRAJ56**T cell receptor alpha joining 56**

M94081 ,TRAJ56*01 [4]

Y T G A N S K L T F G K G I T L S V R P
 T TAT ACT GGA GCC AAT AGT AAG CTG ACA TTT GGA AAA GGA ATA ACT CTG AGT GTT AGA CCA G

TRAJ57**T cell receptor alpha joining 57**

M94081 ,TRAJ57*01 [4]

T Q G G S E K L V F G K G T K L T V N P
 TA ACT CAG GGC GGA TCT GAA AAG CTG GTC TTT GGA AAG GGA ACG AAA CTG ACA GTA AAC CCA T

TRAJ58**T cell receptor alpha joining 58**

M94081 ,TRAJ58*01 [4] (6)

* E T S G S R L T F G F G T Q L T V N P
 TT TAA GAA ACC AGT GGC TCA TGG TTG ACC TTT GGC GAA GGA ACA CAG CTC ACA GTG AAT CCT G

TRAJ59**T cell receptor alpha joining 59**

M94081 ,TRAJ59*01 [4] (7)

K E G N R K F T F G N G T Q V R V
 GG AAG GAA GGA AAC AGG AAA TTT ACA TTT GGA ATG GGG ACG CAA GTG AGA GTG

TRAJ61**T cell receptor alpha joining 61**

M94081 ,TRAJ61*01 [4] (7)

Y R V N R K L T F G A N T R G I M K L
 GG TAC CGG GTT AAT AGG AAA CTG ACA TTT GGA GCC AAC ACT AGA GGA ATC ATG AAA CTC A

Notes:

- (1) Non-canonical J-HEPTAMER: gggcatg instead of cactgtg.
- (2) Non-canonical J-HEPTAMER: tacggtg instead of cactgtg.
- (3) 7 nucleotides instead of 12 in J-SPACER.
- (4) Non-canonical J-HEPTAMER: cactagt instead of cactgtg.
- (5) Non-canonical J-REGION: Cys-Gly-X-Gly instead of Phe-Gly-X-Gly.
- (6) The first codon of the germline J-REGION is a STOP-CODON which may disappear during rearrangements.
- (7) Defective DONOR-SPLICE.

References:

- ¹ Baer, R.J. et al. (1987) Cell 50, 97-105.
- ² Baer, R.J. et al. (1988) EMBO J. 7, 1661-1668.
- ³ Finger, L.R. et al. (1986) Science 234, 982-985.
- ⁵ Mengle-Gaw, L. et al. (1987) EMBO J. 6, 2273-2280.
- ⁴ Koop, B.F. et al. (1994) Genomics 19, 478-493.
- ⁶ Yoshikai, Y. et al. (1985) Nature 316, 837-839.

Recombination signals

Only the recombination signals of the allele *01 of each functional or ORF J-REGION are shown. Non-conserved nucleotides taken into account for the ORF functionality definition are shown in bold and italics.

J Recombination Signal (J-RS)			TRAJ gene and allele name
J-NONAMER	(bp)	J-HEPTAMER	
GGATTCTGT	12	GGGCATG	TRAJ1*01 (ORF)
AGTTTGTGC	12	TACGGTA	TRAJ2*01 (ORF)
GGTTATCTC	12	CACAGTG	TRAJ3*01
AGTTCTTGT	12	GATTGTG	TRAJ4*01
GGATTTTGT	12	CAGGGTG	TRAJ5*01
GGTTTTATC	12	CACTGTG	TRAJ6*01
GGTTTTTGT	10	CACAGTG	TRAJ7*01
CCATTTTGT	12	CAGAGTG	TRAJ8*01
CCATTTTGT	12	CACTGTG	TRAJ9*01
AGTTTATGT	12	CACTGTG	TRAJ10*01
CATTTTGT	12	TATAGTG	TRAJ11*01
TGTTTTTGA	12	CACTGTG	TRAJ12*01
TCATTTTGT	12	TACAGTG	TRAJ13*01
CATTTTGT	12	TGCTGTG	TRAJ14*01
GGTATTTGC	12	CACTGTG	TRAJ15*01
GGTATTTGC	12	CACTGTG	TRAJ15*02
GGTTTTTGT	12	CACTGTG	TRAJ16*01
GGTATTTGC	12	CATTTGT	TRAJ17*01
GGTTCATGT	12	CATTGTG	TRAJ18*01
TGATTTTGC	7	AGATGTG	TRAJ19*01 (ORF)
GGTTTGTGT	11	CACTGTG	TRAJ20*01
ATTTTTTGT	12	CATGGTG	TRAJ21*01
GGTTTTTGT	12	CATAGTG	TRAJ22*01
TGTTTTTGA	12	CACAGTG	TRAJ23*01
CCATTTTGT	12	CACAGTG	TRAJ24*01
CCATTTTGT	12	CACAGTG	TRAJ24*02
GGTTTTTGA	12	CACTATG	TRAJ25*01 (ORF)
GGTTTTTGC	12	CACTGTG	TRAJ26*01
GGTATTGC	12	GA CTGTG	TRAJ27*01
GGTTTTTGC	12	CTCTGTG	TRAJ28*01
GGTTTTTGT	12	CACTGTG	TRAJ29*01 (1)
AGTTTTTGT	12	CACAGTG	TRAJ30*01
GGTTTCAGT	12	TGCTGTG	TRAJ31*01
GGTTAGTGT	12	GA CTGTG	TRAJ32*01
GGTTTTTGT	12	GTCTGTG	TRAJ33*01
GGTTTTTGT	12	CACTGTG	TRAJ34*01
GGTTTTTGT	12	CATTGTG	TRAJ35*01 (ORF)
TGTTTTTGT	12	CACTGTG	TRAJ36*01
AGTTTTTGT	12	TAGAGTG	TRAJ37*01

Recombination signals – *continued*

J Recombination Signal (J-RS)			TRAJ gene and allele name
J-NONAMER	(bp)	J-HEPTAMER	
GGTTTTGGT	12	GA CTGTG	TRAJ38*01
GGTTTTTGC	12	CA CTGTG	TRAJ39*01
GGTTTATGT	12	CA CTGTG	TRAJ40*01
GTTTTTTGT	12	CA CTGTG	TRAJ41*01
GATTATTGT	12	GA CTGTG	TRAJ42*01
GGTTTTTGT	12	TA CTGTG	TRAJ43*01
GGTTTCTGT	12	CA CAGTG	TRAJ44*01
AGTTTATGT	12	CA GAGTG	TRAJ45*01
TGTTTCTGT	12	AG CCGTG	TRAJ46*01
TGTTTTTGT	12	CG CTGTG	TRAJ47*01
GGTTTTTGC	12	CA CTGTG	TRAJ48*01
GGTTTTTGT	12	CA CAGTG	TRAJ49*01
AGTTATTGT	12	GG CTGTG	TRAJ50*01
GGTTCTTGT	12	TG CAGTG	TRAJ52*01
TGTTTCTGT	12	GG CTGTG	TRAJ53*01
AGTTTCTGT	12	TG TG GTG	TRAJ54*01
AGTTTTTGT	12	CA TTGTG	TRAJ56*01
AGTATTTGT	12	GG GG GTG	TRAJ57*01
GGTTTTTGC	12	CA CAGTG	TRAJ58*01 (ORF)
AGTTTATGT	12	TC CTGTG	TRAJ59*01 (ORF)
GGTTTTTGT	12	TC CTGTG	TRAJ61*01 (ORF)

(1) From M94081.

This Page Intentionally Left Blank

Part 3

TRAV

Nomenclature

TRAV1-1: T cell receptor alpha variable 1-1.

Definition and functionality

TRAV1-1 is one of the two functional genes of the TRAV1 subgroup which comprises two mapped genes.

Gene location

TRAV1-1 is in the TRA/TRD locus on chromosome 14 at 14q11.2.

Nucleotide and amino acid sequences for human TRAV1-1

		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20						
AE000658,TRAV1-1*01	[6]	GGA	CAA	AGC	CTT	GAG	CAG	...	CCC	TCT	GAA	GTG	ACA	GCT	GTG	GAA	GGA	GCC	ATT	GTC	CAG						
M12070 ,TRAV1-1*01	[1]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---						
X04939 ,TRAV1-1*02	[38]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---						
L11161 ,TRAV1-1*02	[7]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---						
		21	22	23	24	25	26	CDR1-IMGT										33	34	35	36	37	38	39	40		
AE000658,TRAV1-1*01		T	N	C	T	Y	Q	T	S	G	F	Y	G											L	S		
M12070 ,TRAV1-1*01		ATA	AAC	TGC	ACG	TAC	CAG	ACA	TCT	GGG	TTT	TAT	GGG	...	...	...	...	...	...	...	...	...	...	CTG	TCC		
X04939 ,TRAV1-1*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
L11161 ,TRAV1-1*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
		41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	CDR2-						56	57	58	59	60
AE000658,TRAV1S1*01		T	W	Y	Q	Q	H	D	G	G	A	P	T	F	L	S	Y	N	A								
M12070 ,TRAV1-1*01		WGG	TAC	CAG	CAA	CAT	GAT	GGC	GGA	GCA	CCC	ACA	TTT	CTT	TCT	TAC	AAT	GCT	...	...	...	...	...	...	...		
X04939 ,TRAV1-1*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
L11161 ,TRAV1-1*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
		IMGT				61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80		
AE000658,TRAV1-1*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
M12070 ,TRAV1-1*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
X04939 ,TRAV1-1*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
L11161 ,TRAV1-1*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
		81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100						
AE000658,TRAV1-1*01		S	R	S	D	S	Y	G	Y	L	L	L	Q	E	L	Q	M	R	D	S	A						
M12070 ,TRAV1-1*01		AGT	CGC	TCT	GAT	AGT	TAT	GGT	TAC	CTC	CTT	CTA	CAG	GAG	CTC	CAG	ATG	AAA	GAC	TCT	GCC						
X04939 ,TRAV1-1*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---						
L11161 ,TRAV1-1*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---						
						CDR3-IMGT				101	102	103	104	105	106	107											
AE000658,TRAV1-1*01										S	Y	F	C	A	V	R											
M12070 ,TRAV1-1*01										TCT	TAC	TTC	TGC	GCT	GTG	AGA	GA										
X04939 ,TRAV1-1*02										---	---	---	---	---	---	---											
L11161 ,TRAV1-1*02										---	---	---	---	---	---	---											

#c: Rearranged cDNA
 #g: Rearranged genomic DNA
 °: Genomic DNA, but not known as being germline or rearranged



Framework and complementarity determining regions

FR1-IMGT: 25 [-1 aa: 7]

CDR1-IMGT: 6

FR2-IMGT: 17

CDR2-IMGT: 2

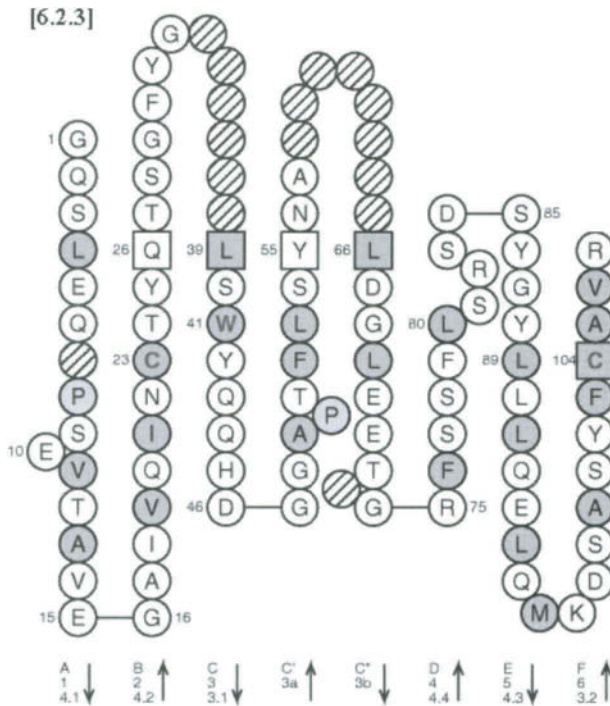
FR3-IMGT: 38 [-1 aa: 73]

CDR3-IMGT: 3

Collier de Perles for human TRAV1-1*01

Accession number: IMGT AE000658

EMBL/GenBank/DDBJ: AE000658



Genome database accession numbers

GDB:9953921

LocusLink: 28693

Nomenclature

TRAV1-2: T cell receptor alpha variable 1-2.

Definition and functionality

TRAV1-2 is one of the two functional genes of the TRAV1 subgroup which comprises two mapped genes.

Gene location

TRAV1-2 is in the TRA/TRD locus on chromosome 14 at 14q11.2.



Nucleotide and amino acid sequences for human TRAV1-2

		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
AE000658, TRAV1-2*01	[6]	GGA	CAA	AAC	ATT	GAC	CAG	...	CCC	ACT	GAG	ATG	ACA	GCT	ACG	GAA	GGT	GCC	ATT	GTG	CAG
X58744, TRAV1-2*01	[28]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U32544, TRAV1-2*02	[5]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
AE000658, TRAV1-2*01		ATC	AAC	TGC	ACG	TAC	CAG	ACA	TCT	GGG	TTC	AAC	GGG	...	...	...	...	...	...	CTG	TTC
X58744, TRAV1-2*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U32544, TRAV1-2*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
AE000658, TRAV1-2*01		TGG	TAC	CAG	CAA	CAT	GCT	GGC	GAA	GCA	CCC	ACA	TTT	CTG	TCT	TAC	AAT	GTT	...	...	...
X58744, TRAV1-2*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U32544, TRAV1-2*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
AE000658, TRAV1-2*01		...	...	...	...	...	CTG	GAT	GGT	TTG	GAG	GAG	AAA	...	GGT	CGT	TTT	TCT	TCA	TTC	CTT
X58744, TRAV1-2*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U32544, TRAV1-2*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
AE000658, TRAV1-2*01		AGT	CGG	TCT	AAA	GGG	TAC	AGT	TAC	CTC	CTT	TTG	AAG	GAG	CTC	CAG	ATG	AAA	GAC	TCT	GCC
X58744, TRAV1-2*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U32544, TRAV1-2*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		101	102	103	104	105	106	107													
AE000658, TRAV1-2*01		TCT	TAC	CTC	TGT	GCT	GTG	AGA	GA												
X58744, TRAV1-2*01		---	---	---	---	---	---	---	---												
U32544, TRAV1-2*02		---	---	---	---	---	---	---	---												

#c: Rearranged cDNA
 °: Genomic DNA, but not known as being germline or rearranged

Framework and complementarity determining regions

FR1-IMGT: 25 (-1 aa: 7)
 FR2-IMGT: 17
 FR3-IMGT: 38 (-1 aa: 73)

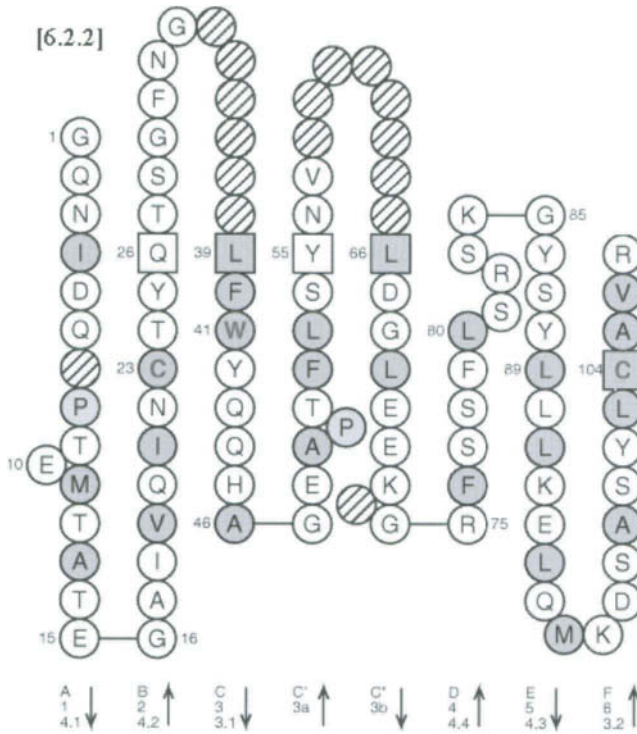
CDR1-IMGT: 6
 CDR2-IMGT: 2
 CDR3-IMGT: 3



Collier de Perles for human TRAV1-2*01

Accession number: IMGT AE000658

EMBL/GenBank/DDBJ: AE000658



Genome database accession numbers

GDB:9953923

LocusLink: 28692

Nomenclature

TRAV2: T cell receptor alpha variable 2.

Definition and functionality

TRAV2 is the unique functional gene of the TRAV2 subgroup which only comprises this mapped gene.

Gene location

TRAV2 is in the TRA/TRD locus on chromosome 14 at 14q11.2.

Nucleotide and amino acid sequences for human TRAV2

		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
		K	D	Q	V	F	Q		P	S	T	V	A	S	S	E	G	A	V	V	E
AE000658, TRAV2*01	[6]	AAG	GAC	CAA	GTG	TTT	CAG	...	CCT	TCC	ACA	GTG	GCA	TCT	TCA	GAG	GGA	GCT	GTG	GTG	GAA
X04936, TRAV2*01	[38]	---	---	---	---	---	---	...	---	---	---	---	---	---	---	---	---	---	---	---	---
U32522, TRAV2*01	[5]	---	---	---	---	---	---	...	---	---	---	---	---	---	---	---	---	---	---	---	---
M17659, TRAV2*02	[17]	---	---	---	---	---	---	...	---	---	---	---	---	---	---	---	---	---	---	---	---
		CDR1-IMGT																			
		21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
		I	F	C	N	H	S	V	S	N	A	Y	N							F	F
AE000658, TRAV2*01		ATC	TTC	TGT	AAT	CAC	TCT	GTG	TCC	AAT	GCT	TAC	AAC	...	...	...	...	...	...	TTC	TTC
X04936, TRAV2*01		---	---	---	---	---	---	---	---	---	---	---	---	...	...	...	...	...	---	---	---
U32522, TRAV2*01		---	---	---	---	---	---	---	---	---	---	---	---	...	...	...	...	---	---	---	---
M17659, TRAV2*02		---	---	---	---	---	---	---	---	---	---	---	---	...	...	...	...	---	---	---	---
		CDR2-																			
		41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
		W	Y	L	H	F	P	G	C	A	P	R	L	L	V	K					
AE000658, TRAV2*01		TGG	TAC	CTT	CAC	TTC	CCG	GGA	TGT	GCA	CCA	AGA	CTC	CTT	GTT	AAA	...	...	...	...	...
X04936, TRAV2*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	...	...	---	---	---
U32522, TRAV2*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	...	...	---	---	---
M17659, TRAV2*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	...	...	---	---	---
		IMGT																			
		61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
		G	S	K	P	S	Q	Q						G	G	A	T	A	C	C	T
AE000658, TRAV2*01		...	...	...	...	...	GGC	TCA	AAG	CCT	TCT	CAG	CAG	...	GGA	GGA	TAC	AAC	ATG	ACC	TAT
X04936, TRAV2*01		---	---	---	---	---	---	---	---	---	---	---	---	...	---	---	---	---	---	---	---
U32522, TRAV2*01		---	---	---	---	---	---	---	---	---	---	---	---	...	---	---	---	---	---	---	---
M17659, TRAV2*02		---	---	---	---	---	---	---	---	---	---	---	---	...	---	---	---	---	---	---	---
		81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
		E	R	F	S	S	S	L	L	I	L	L	Q	V	R	E	A	D	A	A	A
AE000658, TRAV2*01		...	...	GAA	CGG	TTT	TCT	TCA	TCG	CTG	CTC	ATC	CTC	CAG	GTG	CGG	GAG	GCA	GAT	GCT	GCT
X04936, TRAV2*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U32522, TRAV2*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M17659, TRAV2*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		CDR3-IMGT																			
		101	102	103	104	105	106	107													
		V	Y	Y	C	A	V	E													
AE000658, TRAV2*01		GTT	TAC	TAC	TGT	GCT	GTG	GAG	GA												
X04936, TRAV2*01		---	---	---	---	---	---	---	---	#c											
U32522, TRAV2*01		---	---	---	---	---	---	---	---	o											
M17659, TRAV2*02		---	---	---	---	---	---	---	---	#c											

#c: Rearranged cDNA

o: Genomic DNA, but not known as being germline or rearranged

Framework and complementarity determining regions

FR1-IMGT: 25 (-1 aa: 7)

FR2-IMGT: 17

FR3-IMGT: 36 (-3 aa: 73,81,82)

CDR1-IMGT: 6

CDR2-IMGT: 0

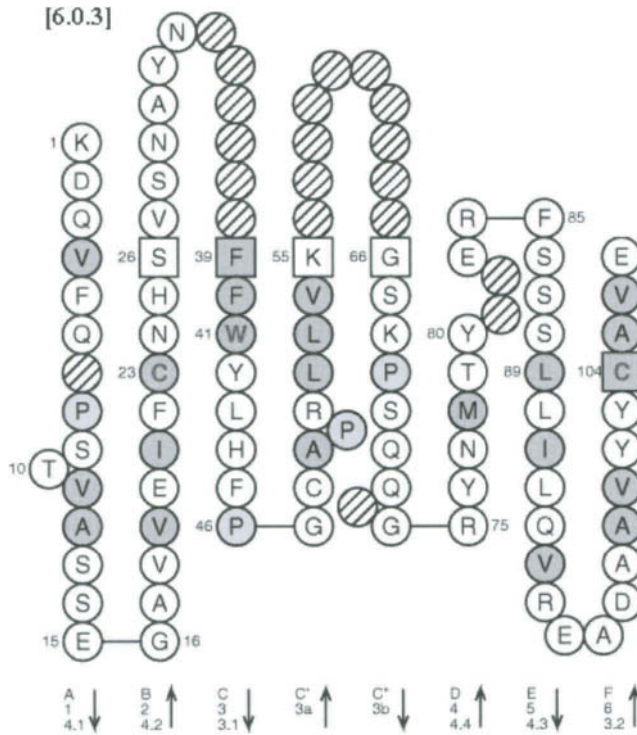
CDR3-IMGT: 3



Collier de Perles for human TRAV2*01

Accession number: IMGT AE000658

EMBL/GenBank/DDBJ: AE000658



Genome database accession numbers

GDB:9953925

LocusLink: 28691

TRAV3 is in the TRA/TRD locus on chromosome 14 at 14q11.2.

94



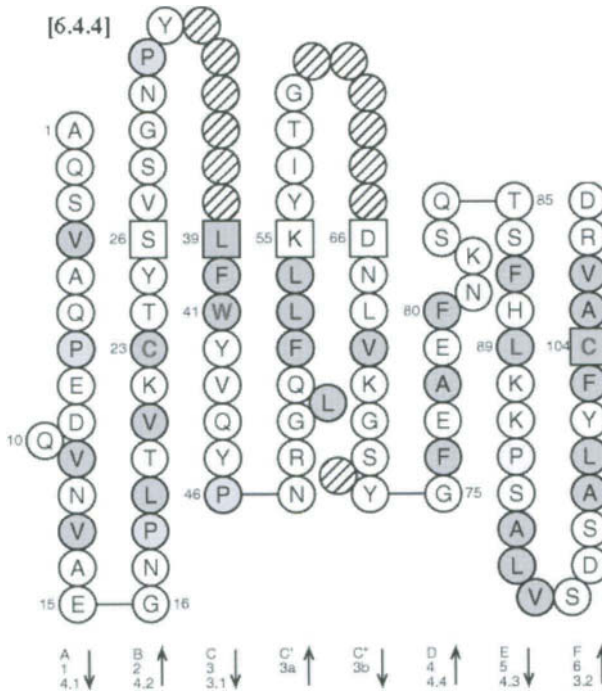
Framework and complementarity determining regions

FR1-IMGT: 26
FR2-IMGT: 17
FR3-IMGT: 38 (-1 aa: 73)

CDR1-IMGT: 6
CDR2-IMGT: 4
CDR3-IMGT: 4

Collier de Perles for human TRAV3*01

Accession number: IMGT AE000658 EMBL/GenBank/DDBJ: AE000658



Genome database accession numbers

GDB:9953927 LocusLink: 28690

Nomenclature

TRAV4: T cell receptor alpha variable 4.

Definition and functionality

TRAV4 is the unique functional gene of the TRAV4 subgroup which only comprises this mapped gene.

Gene location

TRAV4 is in the TRA/TRD locus on chromosome 14 at 14q11.2.

Nucleotide and amino acid sequences for human TRAV4

		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
AE000658, TRAV4*01	[6]	CTT	GCT	AAG	ACC	ACC	CAG	...	CCC	ATC	TCC	ATG	GAC	TCA	TAT	GAA	GGA	CAA	GAA	GTG	AAC
M17663, TRAV4*01	[17]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U32529, TRAV4*01	[5]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
AE000658, TRAV4*01		ATA	ACC	TGT	AGC	CAC	AAC	AAC	ATT	GCT	ACA	AAT	GAT	TAT	...	...	...	...	...	ATC	ACG
M17663, TRAV4*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U32529, TRAV4*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
AE000658, TRAV4*01		TGG	TAC	CAA	CAG	TTT	CCC	AGC	CAA	GGA	CCA	CGA	TTT	ATT	ATT	CAA	GGA	...	...	...	...
M17663, TRAV4*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U32529, TRAV4*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
AE000658, TRAV4*01		...	...	...	...	...	TAC	AAG	ACA	AAA	GTT	ACA	AAC	...	GAA	GTG	GCC	TCC	CTG	TTT	ATC
M17663, TRAV4*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U32529, TRAV4*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
AE000658, TRAV4*01		CCT	GCC	GAC	AGA	AAG	TCC	AGC	ACT	CTG	AGC	CTG	CCC	CGG	GTT	TCC	CTG	AGC	GAC	ACT	GCT
M17663, TRAV4*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U32529, TRAV4*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		101	102	103	104	105	106	107	108												
AE000658, TRAV4*01		V	Y	Y	C	L	V	G	D												
M17663, TRAV4*01		---	---	---	---	---	---	---	---												
U32529, TRAV4*01		---	---	---	---	---	---	---	---												

#c: Rearranged cDNA

°: Genomic DNA, but not known as being germline or rearranged

Framework and complementarity determining regions

FR1-IMGT: 25 (-1 aa: 7)

FR2-IMGT: 17

FR3-IMGT: 38 (-1 aa: 73)

CDR1-IMGT: 7

CDR2-IMGT: 1

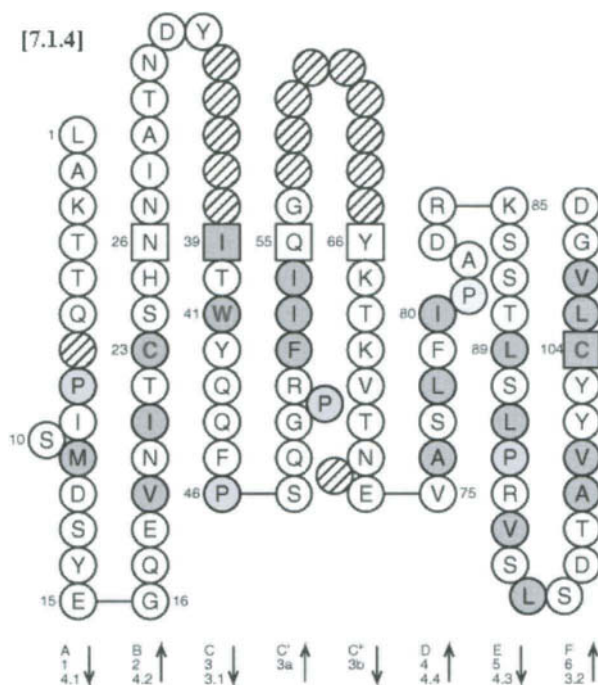
CDR3-IMGT: 4



Collier de Perles for human TRAV4*01

Accession number: IMGT AE000658

EMBL/GenBank/DDBJ: AE000658



Genome database accession numbers

GDB:9953929

LocusLink: 28689



Nomenclature

TRAV5: T cell receptor alpha variable 5.

Definition and functionality

TRAV5 is the unique functional gene of the TRAV5 subgroup which only comprises this mapped gene.

Gene location

TRAV5 is in the TRA/TRD locus on chromosome 14 at 14q11.2.

Nucleotide and amino acid sequences for human TRAV5

		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
AE000659,TRAV5*01	[6]	G	E	D	V	E	Q	S		L	F	L	S	V	R	E	G	D	S	S	V
M27376 ,TRAV5*01	[16]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		CDR1-IMGT																			
AE000659,TRAV5*01		21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
M27376 ,TRAV5*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		CDR2-																			
AE000659,TRAV5*01		41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
M27376 ,TRAV5*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		IMGT																			
AE000659,TRAV5*01		61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
M27376 ,TRAV5*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		CDR3-IMGT																			
AE000659,TRAV5*01		101	102	103	104	105	106	107													
M27376 ,TRAV5*01		---	---	---	---	---	---	---													
		#c																			

#c: Rearranged cDNA

Framework and complementarity determining regions

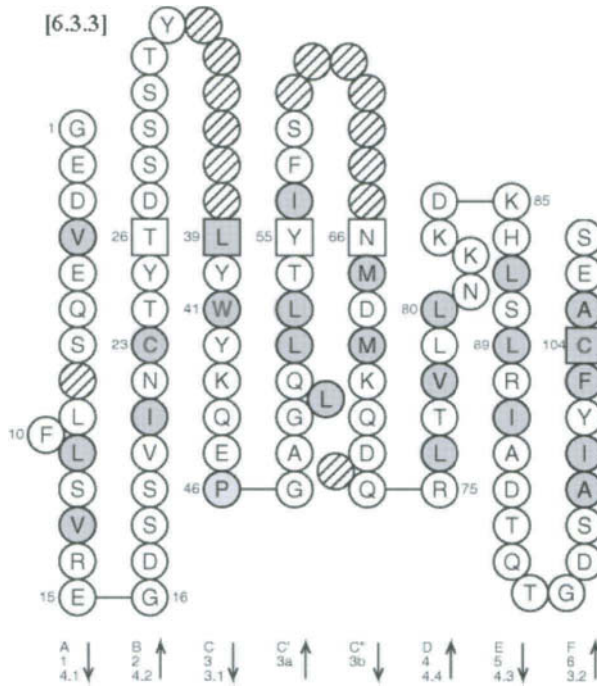
FR1-IMGT: 25 (-1 aa: 8)	CDR1-IMGT: 6
FR2-IMGT: 17	CDR2-IMGT: 3
FR3-IMGT: 38 (-1 aa: 73)	CDR3-IMGT: 3



Collier de Perles for human TRAV5*01

Accession number: IMGT AE000659

EMBL/GenBank/DDBJ: AE000659



Genome database accession numbers

GDB:9953931

LocusLink: 28688

Nomenclature

TRAV6: T cell receptor alpha variable 6.

Definition and functionality

TRAV6 is the unique functional gene of the TRAV6 subgroup which only comprises this mapped gene.

Gene location

TRAV6 is in the TRA/TRD locus on chromosome 14 at 14q11.2.

Nucleotide and amino acid sequences for human TRAV6

		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
AE000659,TRAV6*01	[6]	AGC	CAA	AAG	ATA	GAA	CAG	AAT	TCC	GAG	GCC	CTG	AAC	ATT	CAG	GAG	GGT	AAA	ACG	GCC	ACC
X58747 ,TRAV6*02	[28]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
Z49060 ,TRAV6*03	[13]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
Y10409 ,TRAV6*04	[14]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
Y10410 ,TRAV6*05	[14]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U32542 ,TRAV6*06	[5]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---



Framework and complementarity determining regions

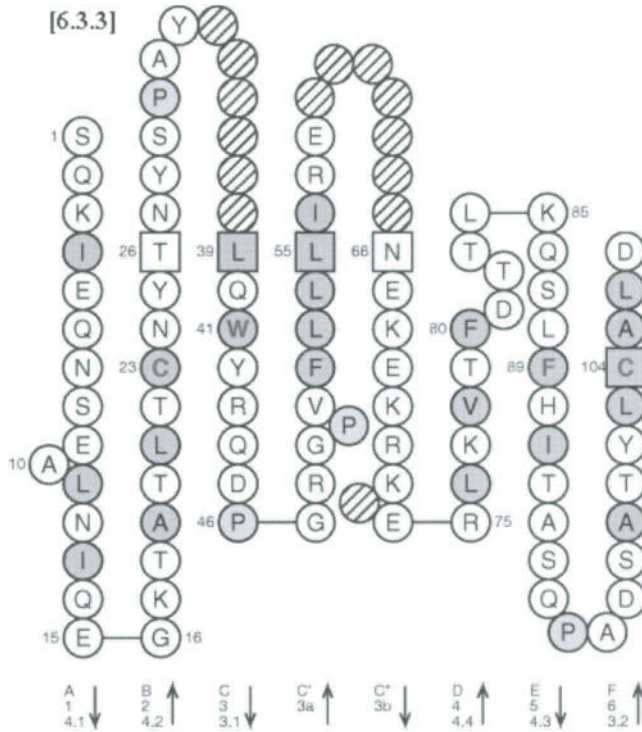
FR1-IMGT: 26
FR2-IMGT: 17
FR3-IMGT: 38 (-1 aa: 73)

CDR1-IMGT: 6
CDR2-IMGT: 3
CDR3-IMGT: 3

Collier de Perles for human TRAV6*01

Accession number: IMGT AE000659

EMBL/GenBank/DDBJ: AE000659



Genome database accession numbers

GDB:9953933

LocusLink: 28687

Nomenclature

TRAV7: T cell receptor alpha variable 7.

Definition and functionality

TRAV7 is the unique functional gene of the TRAV7 subgroup which only comprises this mapped gene.

Gene location

TRAV7 is in the TRA/TRD locus on chromosome 14 at 14q11.2.

Nucleotide and amino acid sequences for human TRAV7

		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	
AE000659,TRAV7*01	(6)	E	N	Q	V	E	H	S	P	H	F	L	G	P	Q	Q	G	D	V	A	S	
		GAA	AAC	CAG	GTG	GAG	CAC	AGC	CCT	CAT	TTT	CTG	GGA	CCC	CAG	CAG	GGA	GAC	GTT	GCC	TCC	
		CDR1-IMGT																				
		21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	
		M	S	C	T	V	S	V	S	R	F	N	N	N	...	...	...	...	...	...	...	
AE000659,TRAV7*01		ATG	AGC	TGC	ACG	TAC	TCT	GTC	AGT	CGT	TTT	AAC	AAT	...	...	...	...	...	...	...	TTG	CAG
		CDR2-																				
		41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	
		W	Y	R	Q	N	T	G	M	G	P	K	H	L	S	M	V	S	...	...	...	
AE000659,TRAV7*01		TGG	TAC	AGG	CAA	AAT	ACA	GGG	ATG	GGT	CCC	AAA	CAC	CTA	TTA	TCC	ATG	TAT	TCA	...	...	
		IMGT																				
		61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	
		L	H	M	A	V	A	G	Y	E	K	Q	K	G	R	L	N	A	T	...	...	
AE000659,TRAV7*01		...	...	...	...	...	GCT	GGA	TAT	GAG	AAG	CAG	AAA	...	GGA	AGA	CTA	AAT	GCT	ACA	TTA	
		81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	
AE000659,TRAV7*01		...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	
		CDR3-IMGT																				
		101	102	103	104	105	106	107														
		T	Y	F	C	A	V	D														
AE000659,TRAV7*01		ACC	TAT	TTG	TGT	GCT	GTA	GAT	G													

Framework and complementarity determining regions

FR1-IMGT: 26

FR2-IMGT: 17

FR3-IMGT: 36 (-3 aa: 73,81,82)

CDR1-IMGT: 6

CDR2-IMGT: 3

CDR3-IMGT: 3

Nomenclature

TRAV8-1: T cell receptor alpha variable 8-1.

Definition and functionality

TRAV8-1 is one of the six functional genes of the TRAV8 subgroup which comprises seven mapped genes.

Gene location

TRAV8-1 is in the TRA/TRD locus on chromosome 14 at 14q11.2.



Nucleotide and amino acid sequences for human TRAV8-1

			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
			A	Q	S	V	S	Q	H	N	H	H	V	I	L	S	E	A	A	S	L	E
AE000659, TRAV8-1*01	[6]		GCC	CAG	TCT	GTG	AGC	CAG	CAT	AAC	CAC	CAC	GTA	ATT	CTC	TCT	GAA	GCA	GCC	TCA	CTG	GAG
X04949, TRAV8-1*01	[38]		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U32520, TRAV8-1*02	[5]		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
			CDR1-IMGT																			
			21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
			L	G	C	N	Y	S	Y	G	G	T	V	N							L	F
AE000659, TRAV8-1*01			TTG	GGA	TGC	AAC	TAT	TCC	TAT	GGT	GGA	ACT	GTT	AAT	...	...	...	...	...	...	CTC	TTC
X04949, TRAV8-1*01			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U32520, TRAV8-1*02			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
			CDR2-																			
			41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
			W	Y	V	Q	Y	P	G	Q	H	L	Q	L	L	K	Y	F	S	G		
AE000659, TRAV8-1*01			TGG	TAT	GTC	CAG	TAC	CCT	GGT	CAA	CAC	CTT	CAG	CTT	CTC	CTC	AAG	TAC	TTT	TCA	GGG	...
X04949, TRAV8-1*01			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U32520, TRAV8-1*02			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
			IMGT																			
			61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
								D	P	L	V	K	G	I		K	G	F	E	A	E	F
AE000659, TRAV8-1*01			---	---	---	---	---	GAT	CCA	CTG	GTT	AAA	GGC	ATC	...	AAG	GGC	TTT	GAG	GCT	GAA	TTT
X04949, TRAV8-1*01			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U32520, TRAV8-1*02			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	V	---	---	---	---
			81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
			I	K	S	K	F	S	F	N	L	R	K	P	S	V	Q	W	S	D	T	A
AE000659, TRAV8-1*01			ATA	AAG	AGT	AAA	TTC	TCC	TTT	AAT	CTG	AGG	AAA	CCC	TCT	GTG	CAG	TGG	AGT	GAC	ACA	GCT
X04949, TRAV8-1*01			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U32520, TRAV8-1*02			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
			CDR3-IMGT																			
			101	102	103	104	105	106	107													
			E	Y	F	C	A	V	N													
AE000659, TRAV8-1*01			GAG	TAC	TTC	TGT	GCC	GTG	AAT	GC												
X04949, TRAV8-1*01			---	---	---	---	---	---	---	---												
U32520, TRAV8-1*02			---	---	---	---	---	---	---	---												

#c: Rearranged cDNA

o: Genomic DNA, but not known as being germline or rearranged

Framework and complementarity determining regions

FR1-IMGT: 26

FR2-IMGT: 17

FR3-IMGT: 38 (-1 aa: 73)

CDR1-IMGT: 6

CDR2-IMGT: 4

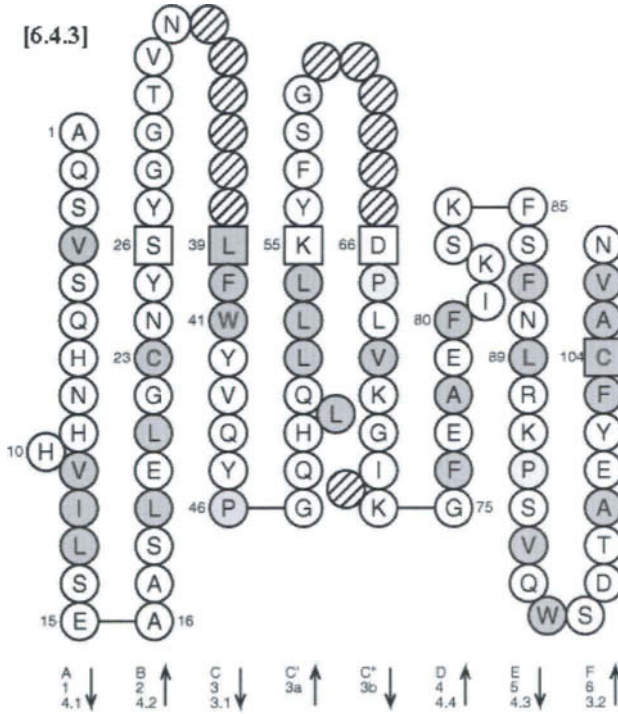
CDR3-IMGT: 3



Collier de Perles for human TRAV8-1*01

Accession number: IMGT AE000659

EMBL/GenBank/DDBJ: AE000659



Genome database accession numbers

GDB:9953937

LocusLink: 28685

Nomenclature

TRAV8-2: T cell receptor alpha variable 8-2.

Definition and functionality

TRAV8-2 is one of the six functional genes of the TRAV8 subgroup which comprises seven mapped genes.

Gene location

TRAV8-2 is in the TRA/TRD locus on chromosome 14 at 14q11.2.

Nucleotide and amino acid sequences for human TRAV8-2

		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
AE000659, TRAV8-2*01	[6]	GCC	CAG	TCG	GTG	ACC	CAG	CTT	GAC	AGC	CAC	GTC	TCT	GTC	TCT	GAA	GGA	ACC	CCG	GTG	CTG
M17650, TRAV8-2*02	[17]	---	---	---	---	---	---	AG-	---	---	---	---	---	---	---	---	---	---	---	---	---
		21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
AE000659, TRAV8-2*01		CTG	AGG	TGC	AAC	TAC	TCA	TCT	TCT	TAT	TCA	CCA	TCT	...	...	...	...	...	...	...	CTC
M17650, TRAV8-2*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
AE000659, TRAV8-2*01		TGG	TAT	GTG	CAA	CAC	CCC	AAC	AAA	GSA	CTC	CAG	CTT	CTC	CTG	AAG	TAC	ACA	TCA	GCG	...
M17650, TRAV8-2*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
AE000659, TRAV8-2*01		...	...	...	...	...	GCC	ACC	CTG	GTT	AAA	GGC	ATC	...	AAC	GGT	TTT	GAG	GCT	GAA	TTT
M17650, TRAV8-2*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
AE000659, TRAV8-2*01		AAG	AAG	AGT	GAA	ACC	TCC	TTC	CAC	CTG	ACG	AAA	CCC	TCA	GCC	CAT	ATG	AGC	GAC	GCG	GCT
M17650, TRAV8-2*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		101	102	103	104	105	106	107													
AE000659, TRAV8-2*01		E	V	F	C	V	V	S													
M17650, TRAV8-2*02		---	---	---	---	---	---	---													

#c: Rearranged cDNA

Framework and complementarity determining regions

FR1-IMGT: 26

FR2-IMGT: 17

FR3-IMGT: 38 (-1 aa: 73)

CDR1-IMGT: 6

CDR2-IMGT: 4

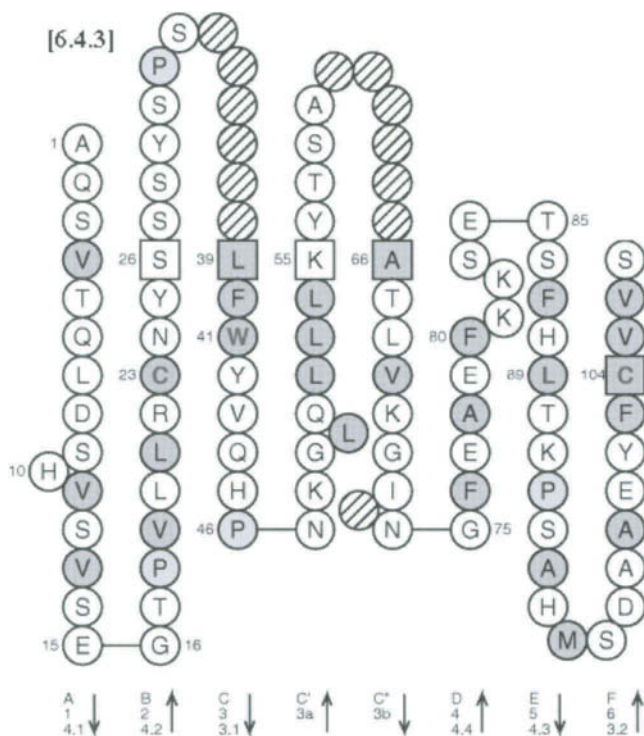
CDR3-IMGT: 3



Collier de Perles for human TRAV8-2*01

Accession number: IMGT AE000659

EMBL/GenBank/DDBJ: AE000659



Genome database accession numbers

GDB:9953939

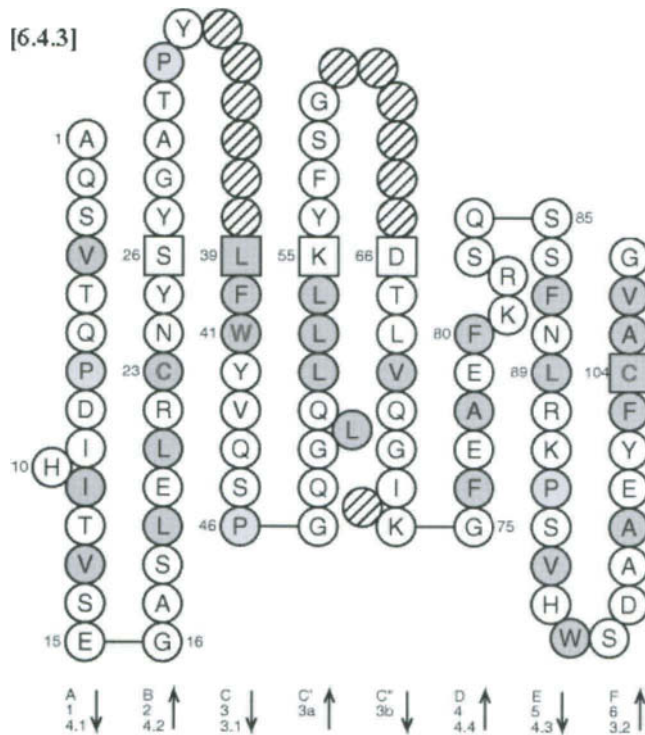
LocusLink: 28684



Collier de Perles for human TRAV8-3*01

Accession number: IMGT AE000659

EMBL/GenBank/DDBJ: AE000659



Genome database accession numbers

GDB:9953941

LocusLink: 28683

Nomenclature

TRAV8-4: T cell receptor alpha variable 8-4.

Definition and functionality

TRAV8-4 is one of the six functional genes of the TRAV8 subgroup which comprises seven mapped genes.

Gene location

TRAV8-4 is in the TRA/TRD locus on chromosome 14 at 14q11.2.

Nucleotide and amino acid sequences for human TRAV8-4

		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
		A	G	S	V	T	Q	L	G	S	H	V	S	V	S	E	G	A	E	V	L
AE000659, TRAV8-4*01	[6]	GCC	CAG	TCG	GTG	ACC	CAG	CTT	GGC	AGC	CAC	GTC	TCT	GTC	TCT	GAA	GGA	GCC	CTG	GTT	CTG
X02592, TRAV8-4*01	[26]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M12423, TRAV8-4*02	[35]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
D13077, TRAV8-4*03	[23]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M12959, TRAV8-4*04	[26]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X63455, TRAV8-4*05	[11]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
K02777, TRAV8-4*06	[9]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M17665, TRAV8-4*07	[17]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

		21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
		L	R	C	N	Y	S	S	S	V	P	P	Y	L	L	K	Y	T	S	A	F
AE000659, TRAV8-4*01		CTG	AGG	TGC	AAC	TAC	TCA	TCG	TCT	GTT	CCA	CCA	TAT	---	---	---	---	---	---	CTC	TTC
X02592, TRAV8-4*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M12423, TRAV8-4*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
D13077, TRAV8-4*03		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M12959, TRAV8-4*04		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X63455, TRAV8-4*05		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
K02777, TRAV8-4*06		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M17665, TRAV8-4*07		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

		41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
		TGG <td>TAT</td> <td>GTG</td> <td>CAA</td> <td>TAC</td> <td>CCC</td> <td>AAC</td> <td>CAA</td> <td>GGA</td> <td>CTC</td> <td>CAG</td> <td>CTT</td> <td>CTC</td> <td>CTG</td> <td>AAG</td> <td>TAC</td> <td>ACA</td> <td>TCA</td> <td>GCG</td> <td>---</td>	TAT	GTG	CAA	TAC	CCC	AAC	CAA	GGA	CTC	CAG	CTT	CTC	CTG	AAG	TAC	ACA	TCA	GCG	---
AE000659, TRAV8-4*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X02592, TRAV8-4*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M12423, TRAV8-4*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
D13077, TRAV8-4*03		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M12959, TRAV8-4*04		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X63455, TRAV8-4*05		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
K02777, TRAV8-4*06		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M17665, TRAV8-4*07		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

		61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
		--- <td>---</td> <td>---</td> <td>---</td> <td>---</td> <td>A</td> <td>T</td> <td>L</td> <td>V</td> <td>K</td> <td>G</td> <td>I</td> <td>---</td> <td>N</td> <td>G</td> <td>F</td> <td>E</td> <td>A</td> <td>E</td> <td>F</td>	---	---	---	---	A	T	L	V	K	G	I	---	N	G	F	E	A	E	F
AE000659, TRAV8-4*01		---	---	---	---	---	GCC	ACC	CTG	GTT	AAA	GGC	ATC	---	AAC	GGT	TTT	GAG	GCT	GAA	TTT
X02592, TRAV8-4*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M12423, TRAV8-4*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
D13077, TRAV8-4*03		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M12959, TRAV8-4*04		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X63455, TRAV8-4*05		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
K02777, TRAV8-4*06		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M17665, TRAV8-4*07		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

		81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
		K <td>K</td> <td>S</td> <td>E</td> <td>T</td> <td>S</td> <td>F</td> <td>H</td> <td>L</td> <td>T</td> <td>K</td> <td>P</td> <td>S</td> <td>TCA</td> <td>GCC</td> <td>A</td> <td>H</td> <td>M</td> <td>S</td> <td>D</td>	K	S	E	T	S	F	H	L	T	K	P	S	TCA	GCC	A	H	M	S	D
AE000659, TRAV8-4*01		AAG	AAG	AGT	GAA	ACC	TCC	TTC	CAC	CTG	ACG	AAA	CCC	TCA	GCC	CAT	ATG	AGC	GAC	GCG	GCT
X02592, TRAV8-4*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M12423, TRAV8-4*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
D13077, TRAV8-4*03		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M12959, TRAV8-4*04		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X63455, TRAV8-4*05		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
K02777, TRAV8-4*06		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M17665, TRAV8-4*07		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---



		101	102	103	104	105	106	107	
		E	Y	F	C	A	V	S	
		GAG	TAC	TTC	TGT	GCT	GTG	AGT	GA
AE000659, TRAV8-4*01		---	---	---	---	---	---	---	#c
X02592, TRAV8-4*01		---	---	---	---	---	---	---	#c
M12423, TRAV8-4*02		---	---	---	---	---	---	---	#c
D13077, TRAV8-4*03		---	---	---	---	---	---	---	#c
M12959, TRAV8-4*04		---	---	---	---	---	---	---	#c
X63455, TRAV8-4*05		---	---	---	---	---	---	---	#c
K02777, TRAV8-4*06		---	---	---	---	---	---	---	#c
M17665, TRAV8-4*07		---	---	---	---	R	-GG	---	#c

#c: Rearranged cDNA

Framework and complementarity determining regions

FR1-IMGT: 26

CDR1-IMGT: 6

FR2-IMGT: 17

CDR2-IMGT: 4

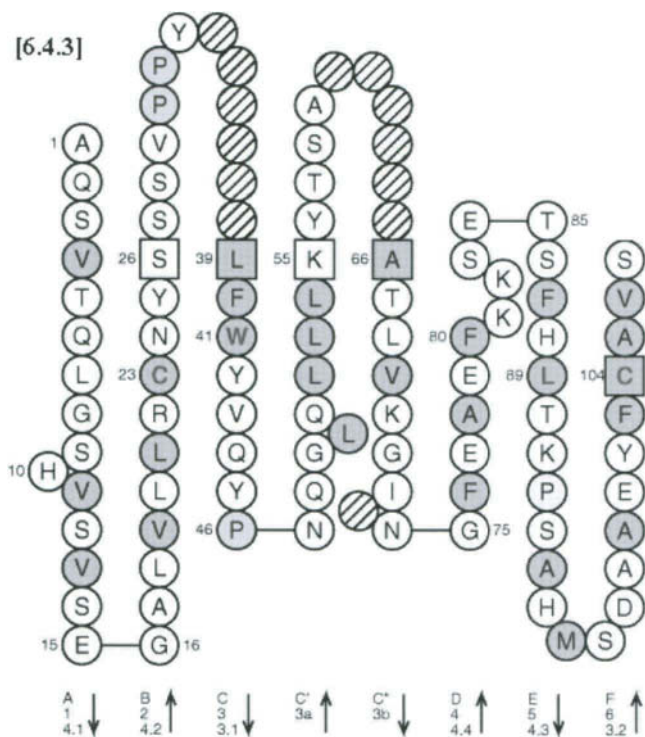
FR3-IMGT: 38 (-1 aa: 73)

CDR3-IMGT: 3

Collier de Perles for human TRAV8-4*01

Accession number: IMGT AE000659

EMBL/GenBank/DDBJ: AE000659



Genome database accession numbers

GDB:9953943

LocusLink: 28682

Nomenclature

TRAV8-6: T cell receptor alpha variable 8-6.

Definition and functionality

TRAV8-6 is one of the six functional genes of the TRAV8 subgroup which comprises seven mapped genes.

Gene location

TRAV8-6 is in the TRA/TRD locus on chromosome 14 at 14q11.2.

Nucleotide and amino acid sequences for human TRAV8-6

[illegible]

#c: Rearranged cDNA

Framework and complementarity determining regions

FR1-IMGT: 26

FR2-IMGT: 17

FR3-IMGT: 38 (-1 aa: 73)

CDR1-IMGT: 6

CDR2-IMGT: 4

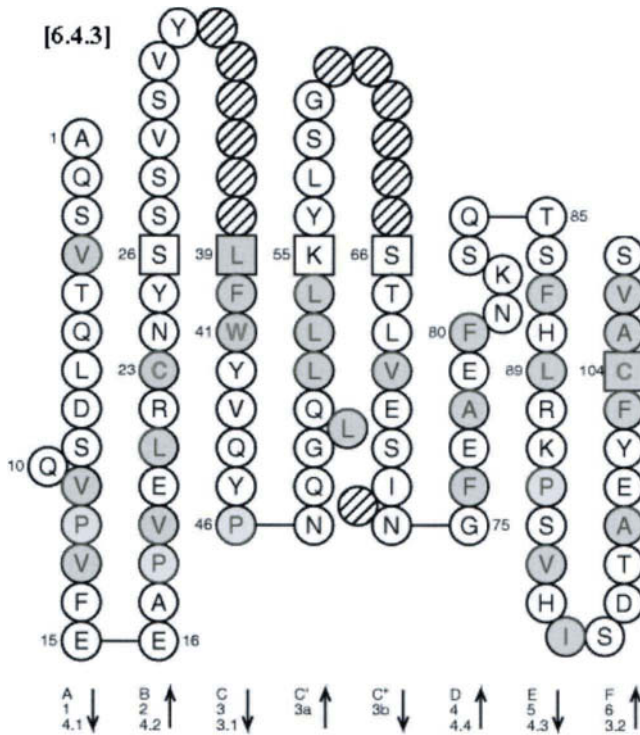
CDR3-IMGT: 3



Collier de Perles for human TRAV8-6*01

Accession number: IMGT X02850

EMBL/GenBank/DBJ: X02850



Genome database accession numbers

GDB:9953947

LocusLink: 28680

Nomenclature

TRAV8-7: T cell receptor alpha variable 8-7.

Definition and functionality

TRAV8-7 is one of the six functional genes of the TRAV8 subgroup which comprises seven mapped genes.

Gene location

TRAV8-7 is in the TRA/TRD locus on chromosome 14 at 14q11.2.

Nucleotide and amino acid sequences for human TRAV8-7

[illegible]

Framework and complementarity determining regions

FR1-IMGT: 26

CDR1-IMGT: 6

FR2-IMGT: 17

CDR2-IMGT: 4

FR3-IMGT: 38 (-1 aa: 73)

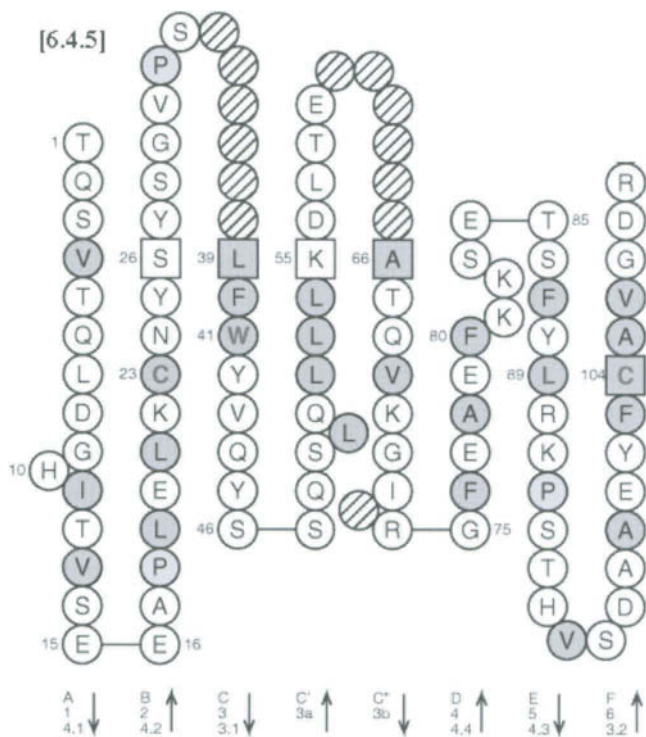
CDR3-IMGT: 5



Collier de Perles for human TRAV8-7*01

Accession number: IMGT AE000660

EMBL/GenBank/DDBJ: AE000660



GDB:9953949

LocusLink: 28679

Nomenclature

TRAV9-1: T cell receptor alpha variable 9-1.

Definition and functionality

TRAV9-1 is one of the two functional genes of the TRAV9 subgroup which comprises two mapped genes.

Gene location

TRAV9-1 is in the TRA/TRD locus on chromosome 14 at 14q11.2.

Nucleotide and amino acid sequences for human TRAV9-1



```

      1  2  3  4  5  6  7  8  9 10 11 12 13 14 15 16 17 18 19 20
AE000659, TRAV9-1*01  [6] GGA GAT TCA GTG GTC CAG ACA GAA GGC CAA GTG CTC CCC TCT GAA GGG GAT TCC CTG ATT
                                G D S V V Q T E G Q V L P S E G D S L I

                                CDR1-IMGT_
      21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40
AE000659, TRAV9-1*01  GTG AAC TGC TCC TAT GAA ACC ACA CAG TAC CCT TCC ... .. CTT TTT
                                V N C S Y E T T Q Y P S L F

                                CDR2-
      41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60
AE000659, TRAV9-1*01  TGG TAG GTC CAA TAT CCT GGA GAA GGT CCA CAG CTC CAC CTG AAA GCC ATG AAG ... ..
                                W Y V Q Y P G E G P Q L H L K A M K

      IMGT_
      61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80
AE000659, TRAV9-1*01  ... .. GCC AAT GAC AAG GGA AGG AAC ... AAA GGT TTT GAA GCC ATG TAC
                                A N D K G R N K G F E A M Y

      81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100
AE000659, TRAV9-1*01  CGT AAA GAA ACC ACT TCT TTC CAC TTG GAG AAA GAC TCA GTT CAA GAG TCA GAC TCC GCT
                                R K E T T S F H L E K D S V Q E S D S A

                                CDR3-IMGT_
      101 102 103 104 105 106 107
AE000659, TRAV9-1*01  V Y F C A L S
                                GTG TAC TTC TGT GCT CTG AGT GA
  
```

Framework and complementarity determining regions

FR1-IMGT: 26

FR2-IMGT: 17

FR3-IMGT: 38 (-1 aa: 73)

CDR1-IMGT: 6

CDR2-IMGT: 3

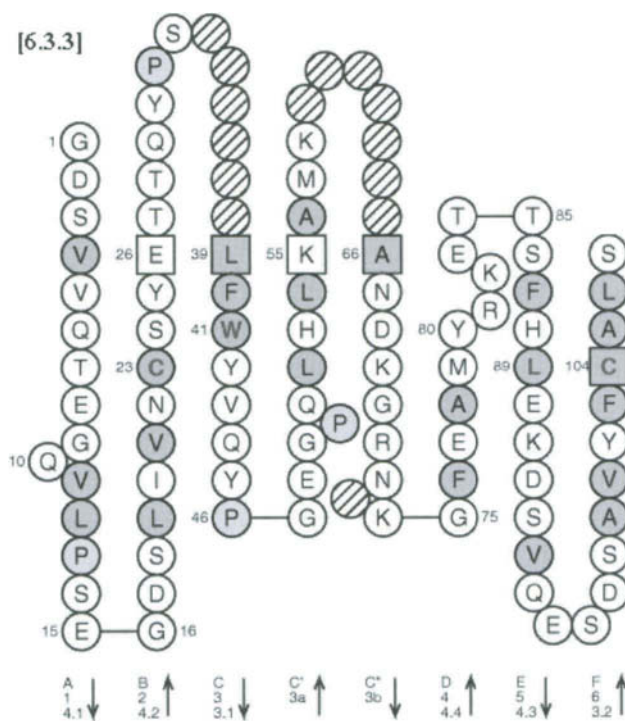
CDR3-IMGT: 3



Collier de Perles for human TRAV9-1*01

Accession number: IMGT AE000659

EMBL/GenBank/DDBJ: AE000659



Genome database accession numbers

GDB:9953951

LocusLink: 28678



Framework and complementarity determining regions

FR1-IMGT: 26

CDR1-IMGT: 6

FR2-IMGT: 17

CDR2-IMGT: 3

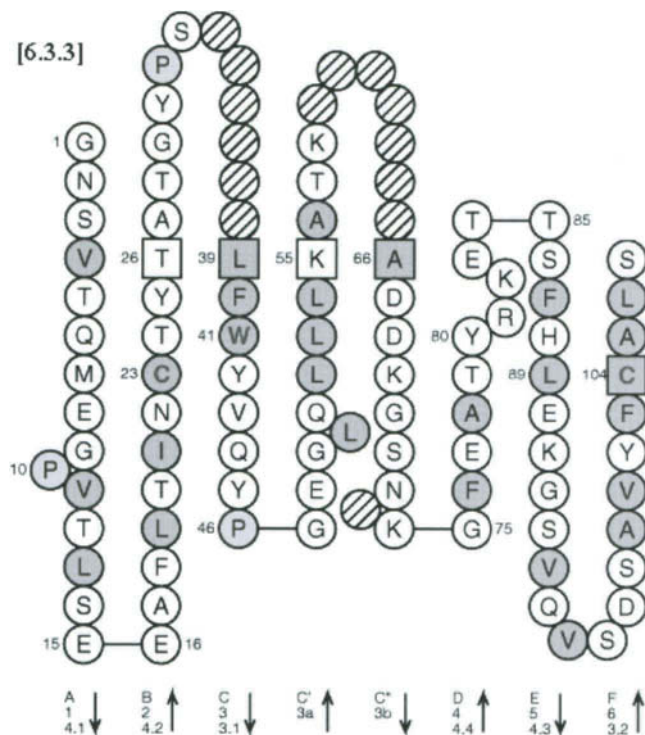
FR3-IMGT: 38 (-1 aa: 73)

CDR3-IMGT: 3

Collier de Perles for human TRAV9-2*01

Accession number: IMGT AE000659

EMBL/GenBank/DDBJ: AE000659



Genome database accession numbers

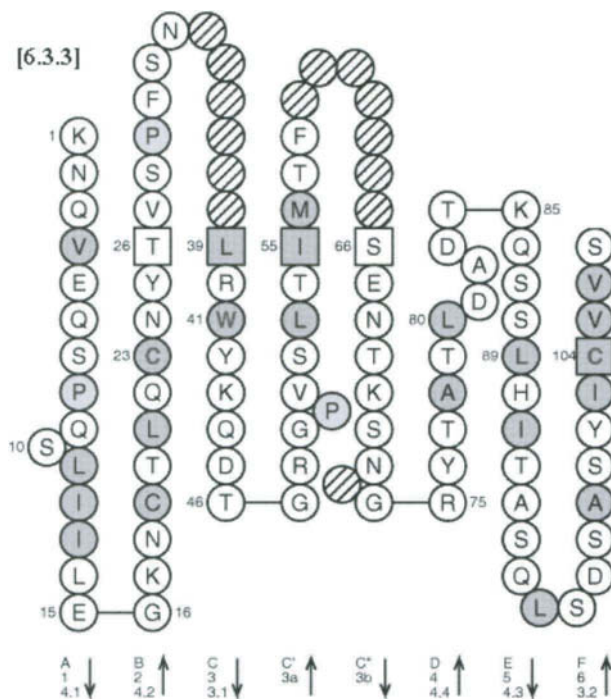
GDB:9953953

LocusLink: 28677

Collier de Perles for human TRAV10*01

Accession number: IMGT AE000659

EMBL/GenBank/DDBJ: AE000659



Genome database accession numbers

GDB:9953955

LocusLink: 28676

Nomenclature

TRAV12-1: T cell receptor alpha variable 12-1.

Definition and functionality

TRAV12-1 is one of the three functional genes of the TRAV12 subgroup which comprises three mapped genes.

Gene location

TRAV12-1 is in the TRA/TRD locus on chromosome 14 at 14q11.2.

Nucleotide and amino acid sequences for human TRAV12-1

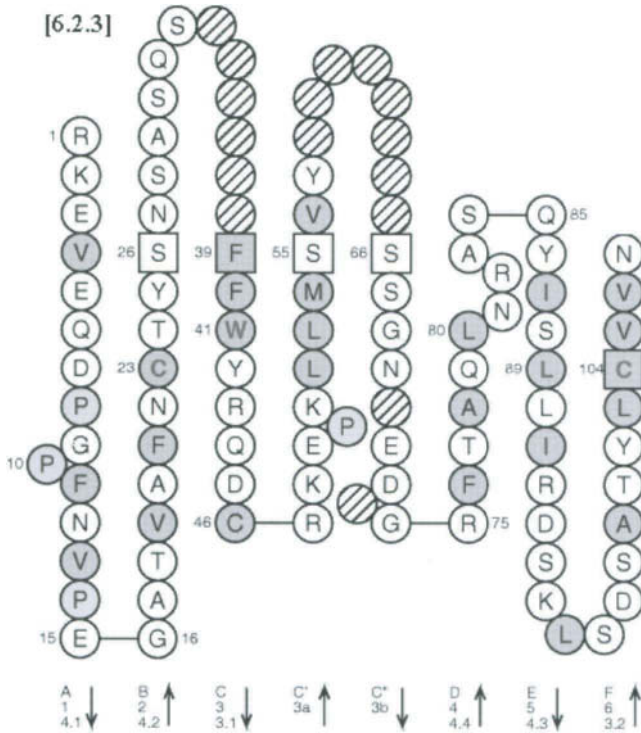
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
AE000659,TRAV12-1*01	[6]	CGG	AAG	GAG	GTG	GAG	CAG	GAT	CCT	GGA	CCC	TTC	AAT	GTT	CCA	GAG	GGA	GCC	ACT	GTC	GCT
D13078 ,TRAV12-1*01	[23]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M17657 ,TRAV12-1*02	[17]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---



Collier de Perles for human TRAV12-1*01

Accession number: IMGT AE000659

EMBL/GenBank/DDBJ: AE000659



Genome database accession numbers

GDB:9953959

LocusLink: 28674

Nomenclature

TRAV12-2: T cell receptor alpha variable 12-2.

Definition and functionality

TRAV12-2 is one of the three functional genes of the TRAV12 subgroup which comprises three mapped genes.

Gene location

TRAV12-2 is in the TRA/TRD locus on chromosome 14 at 14q11.2.

Nucleotide and amino acid sequences for human TRAV12-2



		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
AE000659, TRAV12-2*01	[6]	Q	K	E	V	E	Q	N	S	G	P	L	S	V	P	E	G	A	I	A	S
M27369, TRAV12-2*01	[16]	CAG	AAG	GAG	GTG	GAG	CAG	AAT	TCT	GGA	CCC	CTC	AGT	GTT	CCA	GAG	GGA	GCC	ATT	GCC	TCT
M81774, TRAV12-2*02	[31]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L11159, TRAV12-2*02	[7]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X04946, TRAV12-2*03	[38]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

		21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
AE000659, TRAV12-2*01		L	N	C	T	Y	S	D	R	G	S	Q	S							F	F
M27369, TRAV12-2*01		CTC	AAC	TGC	ACT	TAC	AGT	GAC	GGA	GGT	TCC	CAG	TCC	...	...	...	...	...	...	TTC	TTC
M81774, TRAV12-2*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L11159, TRAV12-2*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X04946, TRAV12-2*03		---	---	---	---	---	---	V	---	---	---	---	---	---	---	---	---	---	---	---	---

		41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
AE000659, TRAV12-2*01		W	Y	R	Q	Y	S	G	K	S	P	E	L	I	M	F	I	Y			
M27369, TRAV12-2*01		TGG	TAC	AGA	CAA	TAT	TCT	GGG	AAA	AGC	CCT	GAG	TTG	ATA	ATG	TTC	ATA	TAC	...	...	...
M81774, TRAV12-2*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	S	---	---	---	---	---
L11159, TRAV12-2*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X04946, TRAV12-2*03		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

		61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
AE000659, TRAV12-2*01		...	...	...	...	...	TCC	AAT	GGT	GAC	AAA	GAA	GAT	...	GGA	AGG	TGT	ACA	GCA	CAG	CTC
M27369, TRAV12-2*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M81774, TRAV12-2*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L11159, TRAV12-2*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X04946, TRAV12-2*03		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

		81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
AE000659, TRAV12-2*01		AAT	AAA	GCC	AGC	CAG	TAT	GTT	TCT	CTG	CTC	ATC	AGA	GAC	TCC	CAG	CCC	AGT	GAT	TCA	GCC
M27369, TRAV12-2*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M81774, TRAV12-2*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L11159, TRAV12-2*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X04946, TRAV12-2*03		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

		101	102	103	104	105	106	107
AE000659, TRAV12-2*01		T	Y	L	C	A	V	N
M27369, TRAV12-2*01		ACC	TAC	CTC	TGT	CCC	GTG	AAC
M81774, TRAV12-2*02		---	---	---	---	---	---	---
L11159, TRAV12-2*02		---	---	---	---	---	---	---
X04946, TRAV12-2*03		---	---	---	---	---	---	---

#c: Rearranged cDNA
 °: Genomic DNA, but not known as being germline or rearranged



Framework and complementarity determining regions

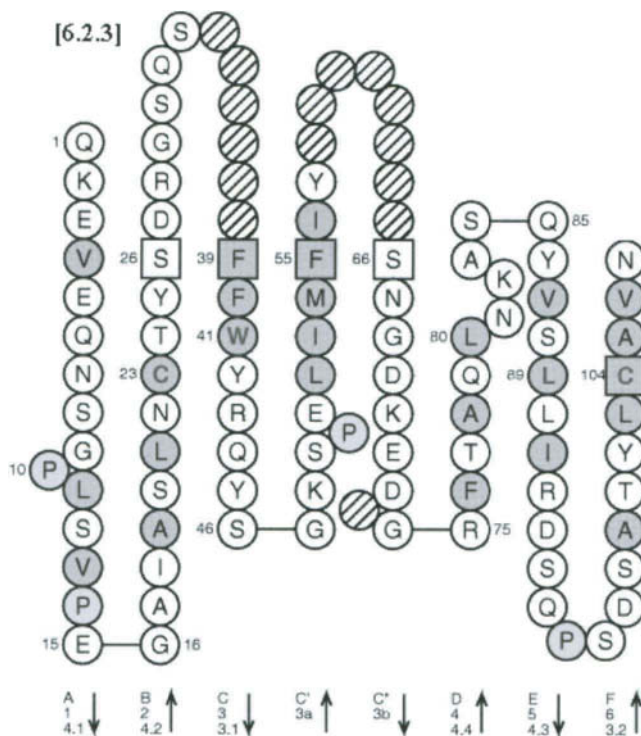
FR1-IMGT: 26
FR2-IMGT: 17
FR3-IMGT: 38 (-1 aa: 73)

CDR1-IMGT: 6
CDR2-IMGT: 2
CDR3-IMGT: 3

Collier de Perles for human TRAV12-2*01

Accession number: IMGT AE000659

EMBL/GenBank/DDBJ: AE000659



Genome database accession numbers

GDB:9953961

LocusLink: 28673

Nomenclature

TRAV12-3: T cell receptor alpha variable 12-3.

Definition and functionality

TRAV12-3 is one of the three functional genes of the TRAV12 subgroup which comprises three mapped genes.

Gene location

TRAV12-3 is in the TRA/TRD locus on chromosome 14 at 14q11.2.

Nucleotide and amino acid sequences for human TRAV12-3

			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
X06193	,TRAV12-3*01	[21]	Q	K	E	V	E	Q	D	P	G	P	L	S	V	P	E	G	A	I	V	S
AE000659	,TRAV12-3*01	[6]	CAG	AAG	GAG	GTG	GAG	CAG	GAT	CCT	GGA	CCA	CTC	AGT	GTT	CCA	GAG	GGA	GCC	ATT	GTT	TCT
U32538	,TRAV12-3*01	[5]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M17656	,TRAV12-3*02	[17]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
			21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
X06193	,TRAV12-3*01		L	N	C	T	Y	S	N	S	A	F	Q	Y							F	M
AE000659	,TRAV12-3*01		CTC	AAC	TGC	ACT	TAC	AGC	AAC	AGT	GCT	TTT	CAA	TAC	...	...	...	...	...	...	TTC	ATG
U32538	,TRAV12-3*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M17656	,TRAV12-3*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
			41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
X06193	,TRAV12-3*01		TGS	TAC	AGA	CAG	TAT	TCC	AGA	AAA	GCC	CCT	GAG	TTG	CTG	ATG	TAC	ACA	TAC	...	...	...
AE000659	,TRAV12-3*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U32538	,TRAV12-3*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M17656	,TRAV12-3*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
			61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
X06193	,TRAV12-3*01		...	...	...	...	...	TCC	AGT	GGT	AAC	AAA	GAA	GAT	...	GGA	AGG	TTT	ACA	GCA	CAG	GTC
AE000659	,TRAV12-3*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U32538	,TRAV12-3*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M17656	,TRAV12-3*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
			81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
X06193	,TRAV12-3*01		D	K	S	S	K	Y	I	S	L	F	I	R	D	S	Q	P	S	D	S	A
AE000659	,TRAV12-3*01		GAT	AAA	TCC	AGC	AAG	TAT	ATC	TCC	TTG	TTC	ATC	AGA	GAC	TCA	CAG	CCC	AGT	GAT	TCA	GCC
U32538	,TRAV12-3*01		--																			
M17656	,TRAV12-3*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
			101	102	103	104	105	106	107	108												
X06193	,TRAV12-3*01		T	Y	L	C	A	M	S													
AE000659	,TRAV12-3*01		ACC	TAC	CTC	TGT	GCA	ATG	AGC	G												
U32538	,TRAV12-3*01		---	---	---	---	---	---	---	---												
M17656	,TRAV12-3*02		---	---	---	---	---	---	---	---	#c											

#c: Rearranged cDNA

°: Genomic DNA, but not known as being rearranged or germline

Framework and complementarity determining regions

FR1-IMGT: 26

FR2-IMGT: 17

FR3-IMGT: 38 (-1 aa: 73)

CDR1-IMGT: 6

CDR2-IMGT: 2

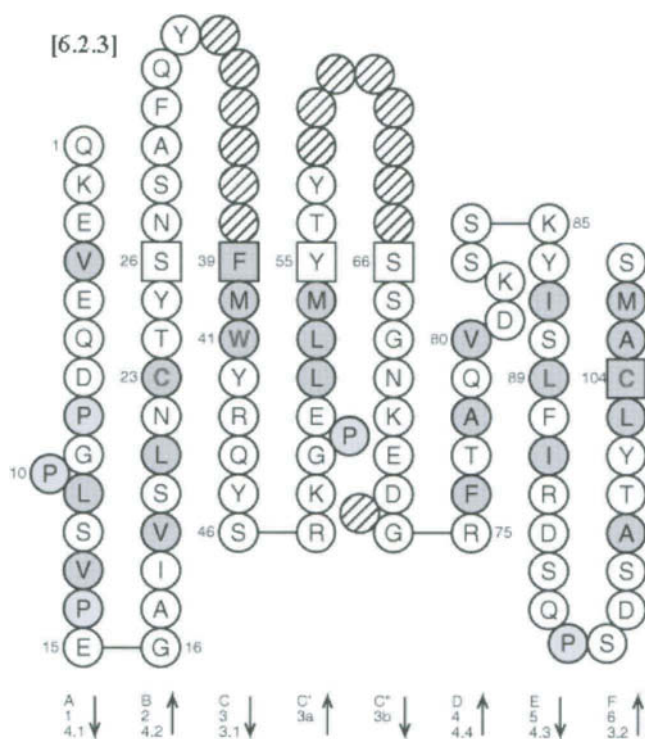
CDR3-IMGT: 3



Collier de Perles for human TRAV12-3*01

Accession number: IMGT X06193

EMBL/GenBank/DBJ: X06193



Genome database accession numbers

GDB:9953963

LocusLink: 28672



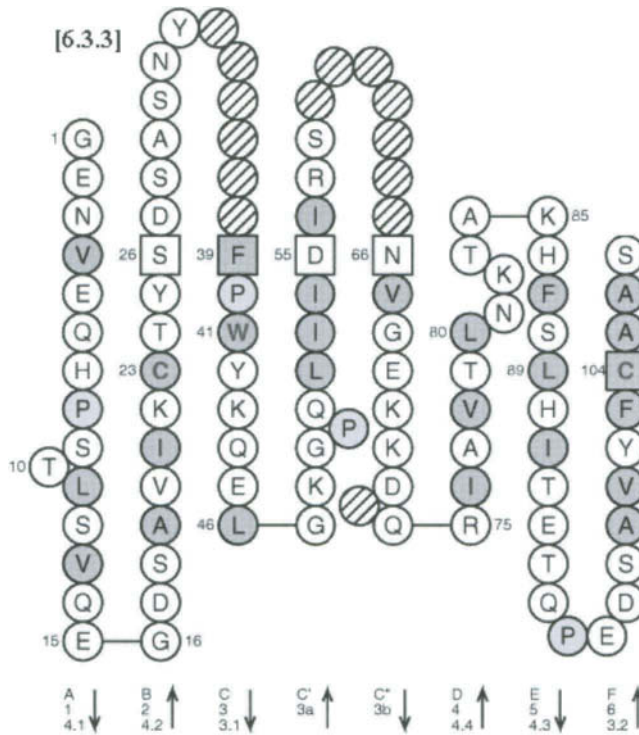
FR1-IMGT: 26
FR2-IMGT: 17
FR3-IMGT: 38 (-1 aa: 73)

CDR1-IMGT: 6
CDR2-IMGT: 3
CDR3-IMGT: 3

Accession number: IMGT AE000659 EMBL/GenBank/DDBJ: AE000659

Accession number: IMGT AE000659

EMBL/GenBank/DDBJ: AE000659



GDB:9953965

LocusLink: 28671

Nomenclature

TRAV13-2: T cell receptor alpha variable 13-2.

Definition and functionality

TRAV13-2 is one of the two functional genes of the TRAV13 subgroup which comprises two mapped genes.

Gene location

TRAV13-2 is in the TRA/TRD locus on chromosome 14 at 14q11.2.



Nucleotide and amino acid sequences for human TRAV13-2

		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
AE000659,TRAV13-2*01	[6]	G	E	S	V	G	L	H	L	P	T	L	S	V	Q	E	G	D	N	S	I
X04956,TRAV13-2*01	[38]	G	A	G	A	G	T	G	G	C	T	G	A	G	T	G	C	A	G	A	G
U32545,TRAV13-2*01	[5]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M17658,TRAV13-2*02	[17]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
AE000659,TRAV13-2*01		A	T	C	A	A	C	A	A	C	A	A	C	A	A	C	A	A	C	A	A
X04956,TRAV13-2*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U32545,TRAV13-2*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M17658,TRAV13-2*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
AE000659,TRAV13-2*01		T	G	G	A	A	G	A	A	G	A	A	G	A	A	G	A	A	G	A	A
X04956,TRAV13-2*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U32545,TRAV13-2*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M17658,TRAV13-2*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
AE000659,TRAV13-2*01		---	---	---	---	---	A	A	T	G	A	A	A	G	A	A	G	A	A	G	A
X04956,TRAV13-2*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U32545,TRAV13-2*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M17658,TRAV13-2*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
AE000659,TRAV13-2*01		A	A	T	A	A	G	A	A	G	A	A	G	A	A	G	A	A	G	A	A
X04956,TRAV13-2*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U32545,TRAV13-2*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M17658,TRAV13-2*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		101	102	103	104	105	106	107													
AE000659,TRAV13-2*01		G	T	C	A	A	G	A	A	G	A	A	G	A	A	G	A	A	G	A	A
X04956,TRAV13-2*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U32545,TRAV13-2*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M17658,TRAV13-2*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

#c: Rearranged cDNA

°: Genomic DNA, but not known as being germline or rearranged

Framework and complementarity determining regions

FR1-IMGT: 26

FR2-IMGT: 17

FR3-IMGT: 38 (-1 aa: 73)

CDR1-IMGT: 6

CDR2-IMGT: 3

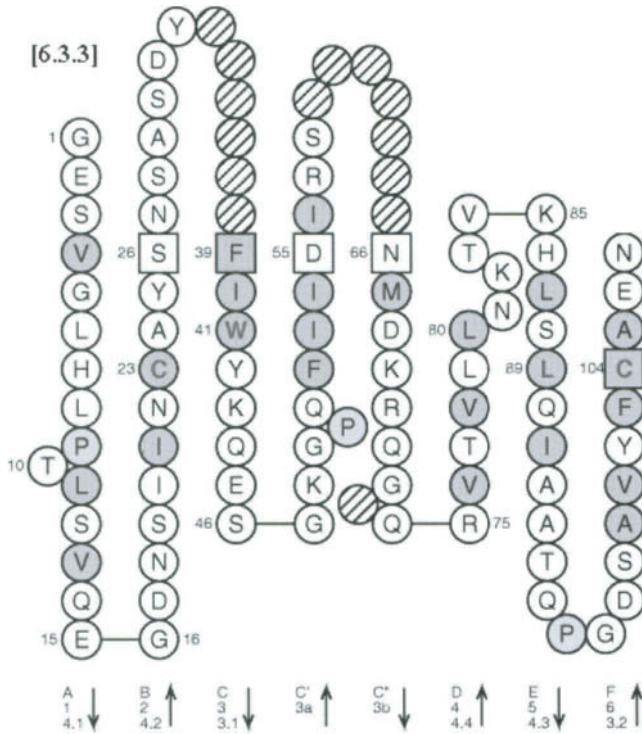
CDR3-IMGT: 3



Collier de Perles for human TRAV13-2*01

Accession number: IMGT AE000659

EMBL/GenBank/DDBJ: AE000659



Genome database accession numbers

GDB:9953967

LocusLink: 28670

TRAV14/DV4

Nomenclature

TRAV14/DV4: T cell receptor alpha variable 14/delta variable 4.

Definition and functionality

TRAV14/DV4 is the unique functional gene of the TRAV14 subgroup which only comprises this mapped gene.

TRAV14/DV4 has been found rearranged to both (D)J genes of the TRD locus and TRAJ genes, the TRD locus being embedded in the TRA locus. This gene can therefore be used for the synthesis of both delta and alpha chains.

Gene location

TRAV14/DV4 is in the TRA/TRD locus on chromosome 14 at 14q11.2.

Nucleotide and amino acid sequences for human TRAV14/DV4



		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	
M21626	,TRAV14*01	[10]	GCC	CAG	AAG	ATA	ACT	CAA	ACC	CAA	CCA	GGA	ATG	TTC	GTG	CAG	GAA	AAG	GAG	GCT	GTG	ACT
AE000659	,TRAV14*02	[6]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
S51029	,TRAV14*02	[36]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M21624	,TRAV14*03	[10]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L09758	,TRAV14*04	[27]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

		21	22	23	24	25	26	CDR1-IMGT										34	35	36	37	38	39	40	
M21626	,TRAV14*01	CTG	GAC	TGC	ACA	TAT	GAC	ACC	AGT	GAT	CCA	AGT	TAT	GGT	---	---	---	---	---	---	---	---	---	CTA	TTC
AE000659	,TRAV14*02	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
S51029	,TRAV14*02	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M21624	,TRAV14*03	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L09758	,TRAV14*04	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

		41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	CDR2-									
M21626	,TRAV14*01	TGG	TAC	AAG	CAG	CCC	AGC	AGT	GGG	GAA	ATG	ATT	TTT	CTT	ATT	TAT	CAG	GGG	TCT	TAT	---	---	---	---	---	---
AE000659	,TRAV14*02	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
S51029	,TRAV14*02	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M21624	,TRAV14*03	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L09758	,TRAV14*04	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

		IMGT										61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	
M21626	,TRAV14*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
AE000659	,TRAV14*02	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
S51029	,TRAV14*02	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M21624	,TRAV14*03	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L09758	,TRAV14*04	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

		81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
M21626	,TRAV14*01	Q	K	A	R	K	S	A	N	L	V	I	S	A	S	Q	L	G	D	S	A
AE000659	,TRAV14*02	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
S51029	,TRAV14*02	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M21624	,TRAV14*03	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L09758	,TRAV14*04	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---



		CDR3-IMGT									
		101	102	103	104	105	106	107	108	109	
M21626	,TRAV14*01	M	Y	F	C	A	M	R	E		
AE000659	,TRAV14*02	ATG	TAC	TTC	TGT	GCA	ATG	AGA	GAG	GG	
S51029	,TRAV14*02	---	--T	---	---	---	---	---	---	---	#c
M21624	,TRAV14*03	---	--T	---	---	---	---	---	---	---	#c
L09758	,TRAV14*04	---	---	---	---	---	---	---	---	---	o

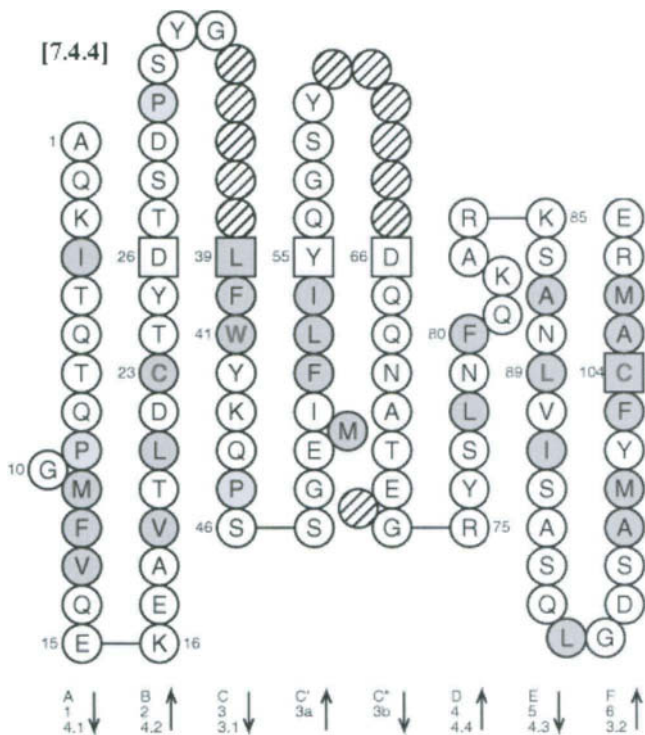
#c:Rearranged cDNA
o: Genomic DNA, but not known as being germline or rearranged

Framework and complementarity determining regions

FR1-IMGT: 26	CDR1-IMGT: 7
FR2-IMGT: 17	CDR2-IMGT: 4
FR3-IMGT: 38 (-1 aa: 73)	CDR3-IMGT: 4

Collier de Perles for human TRAV14/DV4*01

Accession number: IMGT M21626 EMBL/GenBank/DDBJ: M21626



Genome database accession numbers
GDB:9953969 LocusLink: 28669

Nomenclature

TRAV16: T cell receptor alpha variable 16.

Definition and functionality

TRAV16 is the unique functional gene of the TRAV16 subgroup which only comprises this mapped gene.

Gene location

TRAV16 is in the TRA/TRD locus on chromosome 14 at 14q11.2.



Nucleotide and amino acid sequences for human TRAV16

		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
		A	Q	R	V	T	Q	P	E	K	L	L	S	V	F	K	G	A	P	V	E
AE000659, TRAV16*01	[6]	GCC	CAG	AGA	GTG	ACT	CAG	CCC	GAG	AAG	CTC	CTC	TCT	GTC	TTT	AAA	GGG	GCC	CCA	GTG	GAG
X04942, TRAV16*01	[38]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U32546, TRAV16*01	[5]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
		L	K	C	N	Y	S	Y	S	G	S	P	E							L	F
AE000659, TRAV16*01		CTG	AAG	TGC	AAC	TAT	TCC	TAT	TCT	GGG	AGT	CCT	GAA	...	...	...	...	...	...	CTC	TTC
X04942, TRAV16*01		---	---	---	---	---	---	---	---	---	---	---	---	...	...	...	...	...	...	---	---
U32546, TRAV16*01		---	---	---	---	---	---	---	---	---	---	---	---	...	...	...	...	...	...	---	---
		41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
		T	G	G	T	A	T	C	A	G	A	C	A	G	A	G	A	G	A	G	A
AE000659, TRAV16*01		TGG	TAT	GTC	CAG	TAC	TCC	AGA	CAA	CGC	CTC	CAG	TTA	CTC	TTG	AGA	...	...	...	...	...
X04942, TRAV16*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U32546, TRAV16*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
		H	I	S	R	E	S	I						K	G	F	T	A	D	L	
AE000659, TRAV16*01		...	...	...	...	...	CAC	ATC	TCT	AGA	GAG	AGC	ATC	...	...	...	...	...	...	...	...
X04942, TRAV16*01		---	---	---	---	---	---	---	---	---	---	---	---	...	...	...	...	...	...	---	---
U32546, TRAV16*01		---	---	---	---	---	---	---	---	---	---	---	---	...	...	...	...	...	---	---	---
		81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
		N	K	G	E	T	S	F	H	L	K	K	P	F	A	Q	E	E	D	S	A
AE000659, TRAV16*01		AAC	AAA	GGC	GAG	ACA	TCT	TTC	CAC	CTG	AAG	AAA	CCA	TTT	GCT	CAA	GAG	GAA	GAC	TCA	GCC
X04942, TRAV16*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U32546, TRAV16*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		101	102	103	104	105	106	107													
		M	Y	Y	C	A	L	S													
AE000659, TRAV16*01		ATG	TAT	TAC	TGT	GCT	CTA	AGT	GG												
X04942, TRAV16*01		---	---	---	---	---	---	---	---												
U32546, TRAV16*01		---	---	---	---	---	---	---	---												

#c: Rearranged cDNA
°: Genomic DNA, but not known as being germline or rearranged

Framework and complementarity determining regions

FR1-IMGT: 26

FR2-IMGT: 17

FR3-IMGT: 38 (-1 aa: 73)

CDR1-IMGT: 6

CDR2-IMGT: 0

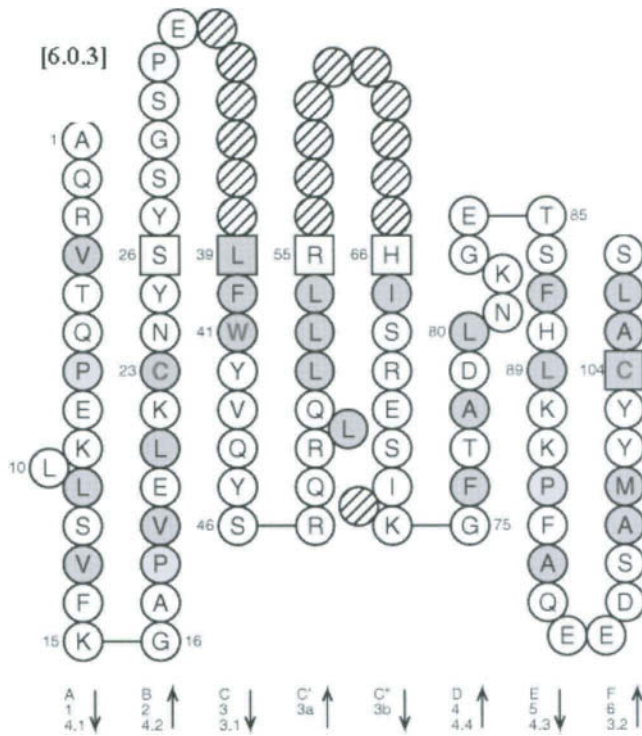
CDR3-IMGT: 3



Collier de Perles for human TRAV16*01

Accession number: IMGT AE000659

EMBL/GenBank/DDBJ: AE000659



Nomenclature

TRAV17: T cell receptor alpha variable 17.

Definition and functionality

TRAV17 is the unique functional gene of the TRAV17 subgroup which only comprises this mapped gene.

Gene location

TRAV17 is in the TRA/TRD locus on chromosome 14 at 14q11.2.



Nucleotide and amino acid sequences for human TRAV17

		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
		S	Q	Q	G	E	E	D	P	Q	A	L	S	I	Q	E	G	E	N	A	T
AE000660,TRAV17*01	[6]	AGT	CAA	CAG	GGA	GAA	GAG	GAT	CCT	CAG	GCC	TTG	AGC	ATC	CAG	GAG	GGT	GAA	AAT	GCC	ACC
X04955 ,TRAV17*01	[38]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U32540 ,TRAV17*01	[5]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		CDR1-IMGT																			
		21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
		M	N	C	S	Y	K	T	S	I	N	N	---	---	---	---	---	---	---	L	Q
AE000660,TRAV17*01		ATG	AAC	TGC	AGT	TAC	AAA	ACT	AGT	ATA	AAC	AAT	---	---	---	---	---	---	---	TTA	CAG
X04955 ,TRAV17*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U32540 ,TRAV17*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		CDR2-																			
		41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
		W	Y	R	Q	N	S	G	R	G	L	V	H	L	I	L	I	R	S	---	---
AE000660,TRAV17*01		TGG	TAT	AGA	CAA	AAT	TCA	GGT	AGA	GGC	CTT	GTC	CAC	CTA	ATT	TTA	ATA	CGT	TCA	---	---
X04955 ,TRAV17*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U32540 ,TRAV17*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		IMGT																			
		61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
		---	---	---	---	---	N	E	R	E	K	H	S	---	G	R	L	R	V	T	L
AE000660,TRAV17*01		---	---	---	---	---	AAT	GAA	AGA	GAG	AAA	CAC	AGT	---	GGA	AGA	TTA	AGA	GTC	ACG	CTT
X04955 ,TRAV17*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U32540 ,TRAV17*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
		D	T	S	K	K	S	S	S	L	L	I	T	A	S	R	A	A	D	T	A
AE000660,TRAV17*01		GAC	ACT	TCC	AAG	AAA	AGC	AGT	TCC	TTG	TTG	ATC	ACG	GCT	TCC	CGG	GCA	GCA	GAC	ACT	GCT
X04955 ,TRAV17*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U32540 ,TRAV17*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		CDR3-IMGT																			
		101	102	103	104	105	106	107													
		S	Y	P	C	A	T	D													
AE000660,TRAV17*01		TCT	TAC	TTC	TGT	GCT	ACG	GAC	G												
X04955 ,TRAV17*01		---	---	---	---	---	---	---	---	#c											
U32540 ,TRAV17*01		---	---	---	---	---	---	---	---	o											

#c: Rearranged cDNA

o: Genomic DNA, but not known as being germline or rearranged

Framework and complementarity determining regions

FR1-IMGT: 26

FR2-IMGT: 17

FR3-IMGT: 38 (-1 aa: 73)

CDR1-IMGT: 5

CDR2-IMGT: 3

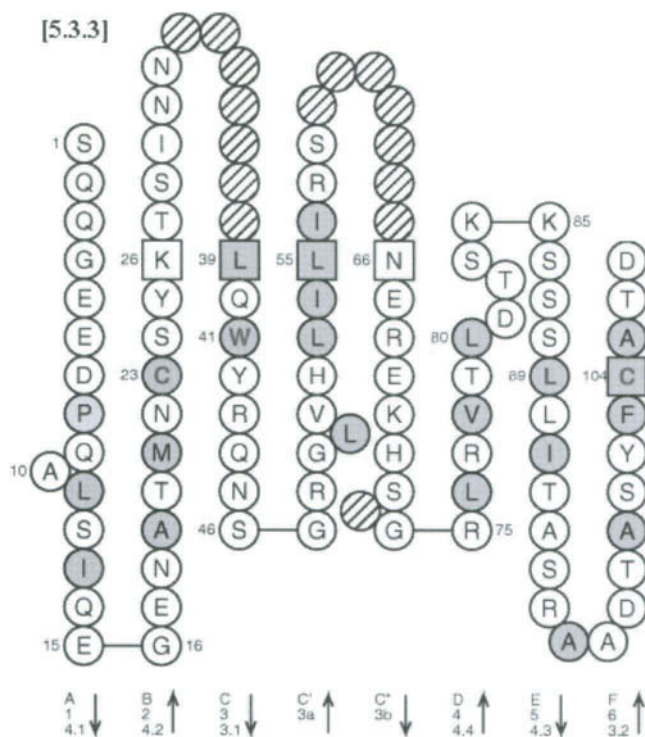
CDR3-IMGT: 3



Collier de Perles for human TRAV17*01

Accession number: IMGT AE000660

EMBL/GenBank/DDBJ: AE000660



Genome database accession numbers

GDB:9953975

LocusLink: 28666

Nomenclature

TRAV18: T cell receptor alpha variable 18.

Definition and functionality

TRAV18 is the unique functional gene of the TRAV18 subgroup which only comprises this mapped gene.

Gene location

TRAV18 is in the TRA/TRD locus on chromosome 14 at 14q11.2.

Nucleotide and amino acid sequences for human TRAV18

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20
 G D S V T Q T E G F V T L P E R A A L T
 AE000660, TRAV18*01 [6] GGA GAC TCG GTT ACC CAG ACA GAA GGC CCA GTT ACC CTC CCT GAG AGG GCA GCT CTG ACA

21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40
 L N C T Y Q S S Y S T F L F
 AE000660, TRAV18*01 TTA AAC TGC ACT TAT CAG TCC AGC TAT TCA ACT TTT ... CTA TTC

41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60
 W Y V Q Y L N K E P E L L L K S S
 AE000660, TRAV18*01 TGG TAT GTC CAG TAT CTA AAC AAA GAG CCT GAG CTC CTC CTG AAA AGT TCA ... CTA TTC

IMGT
 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80
 E N Q E T D S R G F Q A S P
 AE000660, TRAV18*01 ... GAA AAC CAG GAG ACG GAC AGC ... AGA GGT TTT CAG GCC ACT CCT

81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100
 I K S D S S F H L E K P S V Q L S D S A
 AE000660, TRAV18*01 ATC AAG AGT GAC AGT TCC TTC CAC CTG GAG AAG CCC TCG GTG CAG CTG TCG GAC TCT GCC

101 102 103 104 105 106 107
 V Y Y C A L R
 AE000660, TRAV18*01 GTG TAC TAC TGC GCT CTG AGA GA

CDR1-IMGT
 27 28 29 30 31 32 33 34 35 36 37 38 39 40
 TCC AGC TAT TCA ACT TTT ... CTA TTC

CDR2-
 56 57 58 59 60
 AAA AGT TCA ... CTA TTC

CDR3-IMGT
 101 102 103 104 105 106 107
 V Y Y C A L R

Framework and complementarity determining regions

FR1-IMGT: 26

FR2-IMGT: 17

FR3-IMGT: 38 (-1 aa: 73)

CDR1-IMGT: 6

CDR2-IMGT: 2

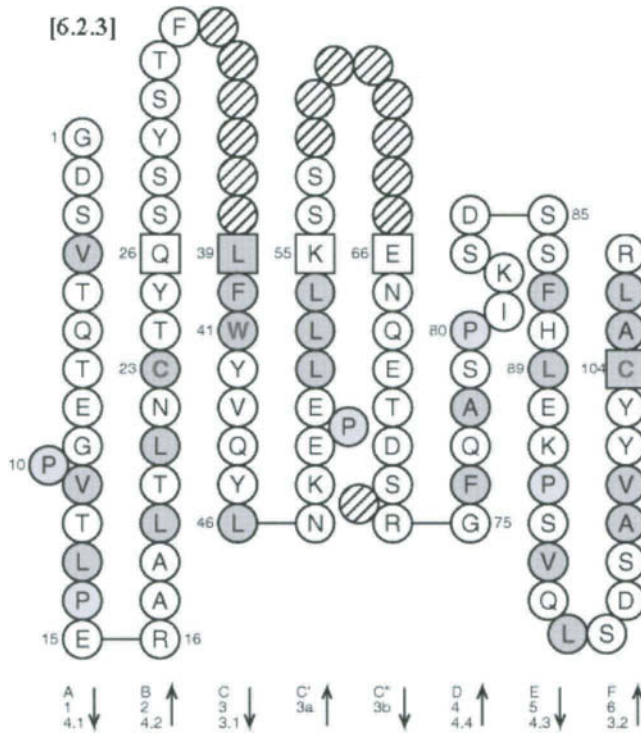
CDR3-IMGT: 3



Collier de Perles for human TRAV18*01

Accession number: IMGT AE000660

EMBL/GenBank/DDBJ: AE000660



Genome database accession numbers

GDB:9953977

LocusLink: 28665

Nomenclature

TRAV19: T cell receptor alpha variable 19.

Definition and functionality

TRAV19 is the unique functional gene of the TRAV19 subgroup which only comprises this mapped gene.

Gene location

TRAV19 is in the TRA/TRD locus on chromosome 14 at 14q11.2.

Nucleotide and amino acid sequences for human TRAV19

		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
AE000660, TRAV19*01	[6]	GCT	CAG	AAG	GTA	ACT	CAA	GCG	CAG	ACT	GAA	ATT	TCT	GTG	GTG	GAG	AAG	GAG	GAT	GTG	ACC
X01403 ,TRAV19*01	[32]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
AE000660, TRAV19*01		TTG	GAC	TGT	GTG	TAT	GAA	ACC	CGT	GAT	ACT	ACT	TAT	TAC	...	...	...	...	...	...	TTA
X01403 ,TRAV19*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
AE000660, TRAV19*01		TGG	TAC	AAG	CAA	CCA	CCA	AGT	GGA	GAA	TTG	GTT	TTC	CTT	ATT	CGT	CGG	AAC	TCT	TTT	...
X01403 ,TRAV19*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
AE000660, TRAV19*01		...	...	...	...	...	GAT	GAG	CAA	AAT	GAA	ATA	AGT	...	GGT	CGG	TAT	TCT	TGG	AAC	TTC
X01403 ,TRAV19*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
AE000660, TRAV19*01		CAG	AAA	TCC	ACC	AGT	TCC	TTC	AAC	TTC	ACC	ATC	ACA	GCC	TCA	CAA	GTC	GTG	GAC	TCA	GCA
X01403 ,TRAV19*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		101	102	103	104	105	106	107	108												
AE000660, TRAV19*01		V	Y	F	C	A	L	S	E												
X01403 ,TRAV19*01		---	---	---	---	---	---	---	---												

#c: Rearranged cDNA

Framework and complementarity determining regions

FR1-IMGT: 26

FR2-IMGT: 17

FR3-IMGT: 38 (-1 aa: 73)

CDR1-IMGT: 7

CDR2-IMGT: 4

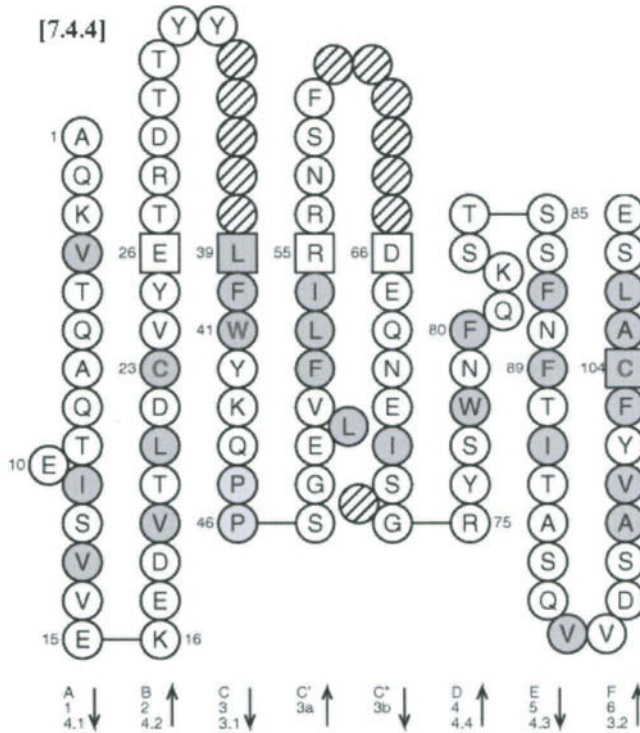
CDR3-IMGT: 4



Collier de Perles for human TRAV19*01

Accession number: IMGT AE000660

EMBL/GenBank/DDBJ: AE000660



Genome database accession numbers

GDB:9953979

LocusLink: 28664

Nomenclature

TRAV20: T cell receptor alpha variable 20.

Definition and functionality

TRAV20 is the unique functional gene of the TRAV20 subgroup which only comprises this mapped gene.

Gene location

TRAV20 is in the TRA/TRD locus on chromosome 14 at 14q11.2.

Nucleotide and amino acid sequences for human TRAV20

		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
AE000660, TRAV20*01	[6]	E	D	Q	V	T	Q	S	P	E	A	L	R	L	Q	R	G	E	S	S	S
X68696, TRAV20*02	[26]	GAA	GAC	CAG	GTG	ACG	CAG	AGT	CCC	GAG	GCC	CTG	AGA	CTC	CAG	GAG	GGA	GAG	AGT	AGC	AGT
S60789, TRAV20*03	[33]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X70305, TRAV20*04	[24]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
AE000660, TRAV20*01		21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
X68696, TRAV20*02		L	N	C	S	Y	T	V	S	G	L	R	G								
S60789, TRAV20*03		CTT	AAC	TGC	AGT	TAC	ACA	GTC	AGC	GGT	TTA	AGA	GGG	...	...	...	...	...	...	CTG	TTC
X70305, TRAV20*04		--C	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
AE000660, TRAV20*01		41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
X68696, TRAV20*02		W	Y	R	Q	D	P	G	K	G	P	E	F	L	F	T	C	Y	S		
S60789, TRAV20*03		TGG	TAT	AGG	CAA	GAT	CCT	GGG	AAA	GCC	CCT	GAA	TTC	CTC	TTC	ACC	CTG	TAT	TCA	...	...
X70305, TRAV20*04		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
AE000660, TRAV20*01		61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
X68696, TRAV20*02		...	...	...	...	...	GCT	GGG	GAA	GAA	AAG	GAG	AAA	...	...	GAA	AGC	CTA	AAA	GCC	ACA
S60789, TRAV20*03		...	...	...	...	...	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X70305, TRAV20*04		...	...	...	...	...	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
AE000660, TRAV20*01		81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
X68696, TRAV20*02		...	...	...	ACA	AAG	AAG	GAA	AGC	TTT	CTG	CAC	ATC	ACA	GCC	CCT	AAA	CCT	GAA	GAC	TCA
S60789, TRAV20*03		...	...	...	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X70305, TRAV20*04		...	...	...	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
AE000660, TRAV20*01		101	102	103	104	105	106	107													
X68696, TRAV20*02		T	Y	L	C	A	V	Q													
S60789, TRAV20*03		ACT	TAT	CTC	TGT	GCT	GTG	CAG	G												
X70305, TRAV20*04		---	---	---	---	---	---	---													

#c: Rearranged cDNA

Framework and complementarity determining regions

FR1-IMGT: 26

FR2-IMGT: 17

FR3-IMGT: 36 (-3 aa: 73,81,82)

CDR1-IMGT: 6

CDR2-IMGT: 3

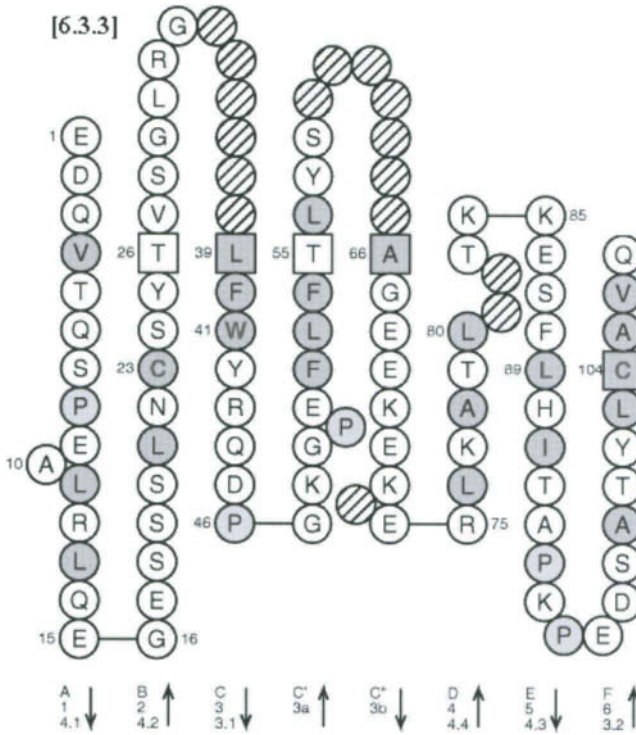
CDR3-IMGT: 3



Collier de Perles for human TRAV20*01

Accession number: IMGT AE000660

EMBL/GenBank/DDBJ: AE000660



Genome database accession numbers

GDB:9953981

LocusLink: 28663

Nomenclature

TRAV21: T cell receptor alpha variable 21.

Definition and functionality

TRAV21 is the unique functional gene of the TRAV21 subgroup which only comprises this mapped gene.

Gene location

TRAV21 is in the TRA/TRD locus on chromosome 14 at 14q11.2.

Nucleotide and amino acid sequences for human TRAV21



```

      1  2  3  4  5  6  7  8  9 10 11 12 13 14 15 16 17 18 19 20
AE000660,TRAV21*01   [6] AAA CAG GAG GTG ACG CAG ATT CCT GCA GCT CTG AGT GTC CCA GAA GGA GAA AAC TTG GTT
X58736 ,TRAV21*02    [28] -----A-----

                                CDR1-IMGT
      21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40
AE000660,TRAV21*01   CTC AAC TGC AGT TTC ACT GAT AGC GCT ATT TAC AAC ... .. CTC CAG
X58736 ,TRAV21*02    -----

                                CDR2-
      41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60
AE000660,TRAV21*01   TGG TTT AGG CAG GAC CCT GGG AAA GGT CTC ACA TCT CTG TTG CTT ATT CAG TCA ... ..
X58736 ,TRAV21*02    -----

      IMGT_
      61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80
AE000660,TRAV21*01   ... .. AGT CAG AGA GAG CCA ACA AGT ... GGA AGA CTT AAT GCC TCG CTG
X58736 ,TRAV21*02    -----

      81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100
AE000660,TRAV21*01   GAT AAA TCA TCA GGA CGT AGT ACT TTA TAC ATT GCA GCT TCT CAG CCT GGT GAC TCA GCC
X58736 ,TRAV21*02    -----

                                _CDR3-IMGT_
      101 102 103 104 105 106 107
AE000660,TRAV21*01   T Y L C A V R
X58736 ,TRAV21*02    ACC TAC CTC TGT GCT GTG AGG
#C
#C: Rearranged cDNA

```

Framework and complementarity determining regions

FR1-IMGT: 26

FR2-IMGT: 17

FR3-IMGT: 38 (-1 aa: 73)

CDR1-IMGT: 6

CDR2-IMGT: 3

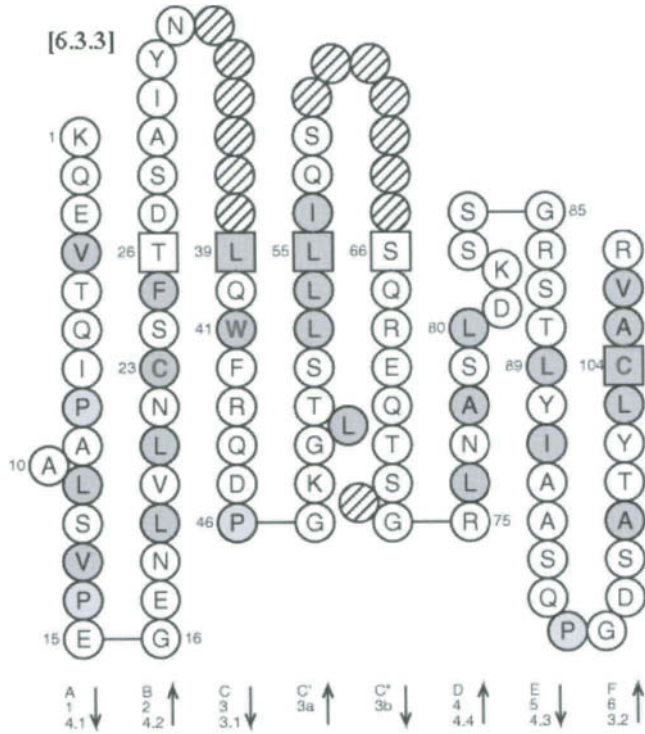
CDR3-IMGT: 3



Collier de Perles for human TRAV21*01

Accession number: IMGT AE000660

EMBL/GenBank/DDBJ: AE000660



Genome database accession numbers

GDB:9953983

LocusLink: 28662

Nomenclature

TRAV22: T cell receptor alpha variable 22.

Definition and functionality

TRAV22 is the unique functional gene of the TRAV22 subgroup which only comprises this mapped gene.

Gene location

TRAV22 is in the TRA/TRD locus on chromosome 14 at 14q11.2.

Nucleotide and amino acid sequences for human TRAV22

		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
AE000660,TRAV22*01	[6]	G	I	Q	V	E	Q	S	P	P	D	L	I	L	Q	E	G	A	N	S	T
		L	R	C	N	F	S	D	S	V	N	N	C	T	G	A	G	G	A	T	C
M27374 ,TRAV22*01	[16]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		CDR1-IMGT																			
AE000660,TRAV22*01		21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
		CTG	CGG	TGC	AAT	TTT	TCT	GAC	TCT	GTG	AAC	AAT	...	...	...	...	...	...	...	TTG	CAG
M27374 ,TRAV22*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		CDR2-																			
AE000660,TRAV22*01		41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
		W	F	H	Q	N	P	W	G	Q	L	I	N	L	F	Y	I	...	...	...	...
M27374 ,TRAV22*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		IMGT																			
AE000660,TRAV22*01		61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
		...	...	...	...	...	CCC	TCA	GGG	ACA	AAA	CAG	AAT	...	GGA	AGA	TTA	AGC	GCC	ACG	ACT
M27374 ,TRAV22*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		CDR3-IMGT																			
AE000660,TRAV22*01		101	102	103	104	105	106	107	...	...	...	...	...	...	...	...	...	...	...	...	...
		V	Y	F	C	A	V	E	...	...	...	...	...	...	...	...	...	...	...	...	...
M27374 ,TRAV22*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

#c: Rerranged cDNA

Framework and complementarity determining regions

FR1-IMGT: 26

FR2-IMGT: 17

FR3-IMGT: 38 (-1 aa: 73)

CDR1-IMGT: 5

CDR2-IMGT: 1

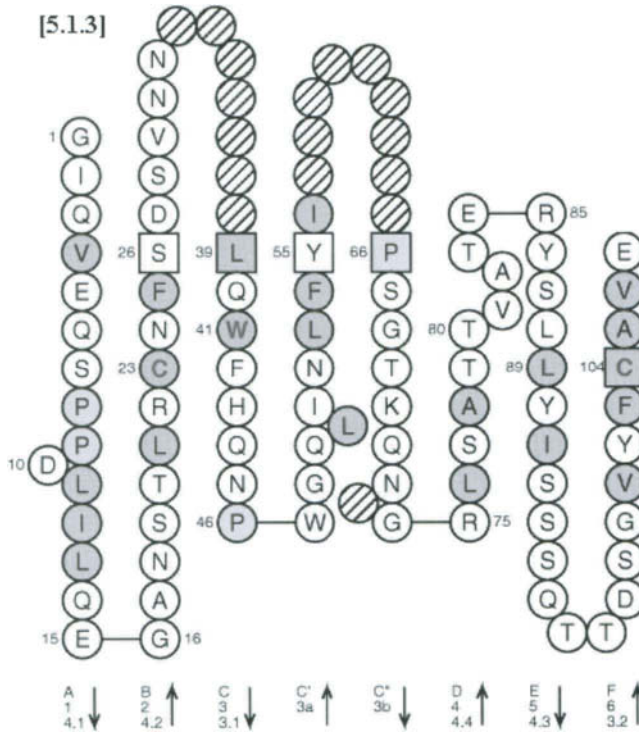
CDR3-IMGT: 3



Collier de Perles for human TRAV22*01

Accession number: IMGT AE000660

EMBL/GenBank/DDBJ: AE000660



Genome database accession numbers

GDB:9953985

LocusLink: 28661

Nomenclature

TRAV23/DV6: T cell receptor alpha variable 23/delta variable 6.

Definition and functionality

TRAV23/DV6 is the unique functional gene of the TRAV23 subgroup which only comprises this mapped gene.

TRAV23/DV6 has been found rearranged to both (D)J genes of the TRD locus and TRAJ genes, the TRD locus being embedded in the TRA locus. This gene can therefore be used for the synthesis of both delta and alpha chains.

Gene location

TRAV23/DV6 is in the TRA/TRD locus on chromosome 14 at 14q11.2.

Nucleotide and amino acid sequences for human TRAV23/DV6



		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
AE000660, TRAV23*01	[6]	CAG	CAG	CAG	GTG	AAA	CAA	AGT	CCT	CAA	TCT	TTG	ATA	GTC	CAG	AAA	GGA	GGG	ATT	TCA	ATT
X70309, TRAV23*01	[24]	---	---	---	---	---	---	---	---	---	---	TTG	---	---	---	---	---	---	---	---	---
U32526, TRAV23*01	[5]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M17660, TRAV23*02	[17]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	P
M22936, TRAV23*01/*02 (1)	[30]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	C
M97704, TRAV23*03	[12]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
Z49057, TRAV23*03	[13]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
Y10411, TRAV23*04	[14]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

		21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
AE000660, TRAV23*01		I	N	C	A	Y	E	N	T	A	F	D	Y							F	P
X70309, TRAV23*01		ATA	AAC	TGT	GCT	TAT	GAG	AAC	ACT	GCG	TTT	GAC	TAC	...	...	...	...	...	...	TTT	CCA
U32526, TRAV23*01		---	---	---	---	---	---	---	---	---	---	---	---	...	...	...	...	...	...	---	---
M17660, TRAV23*02		---	---	---	---	---	---	---	---	---	---	---	---	...	...	...	...	...	...	---	---
M22936, TRAV23*01/*02 (1)		---	---	---	---	---	---	---	---	---	---	---	---	...	...	...	...	...	...	---	---
M97704, TRAV23*03		---	---	---	---	---	---	---	---	---	---	---	---	...	...	...	...	...	...	---	---
Z49057, TRAV23*03		---	---	---	---	---	---	---	---	---	---	---	---	...	...	...	...	...	...	---	---
Y10411, TRAV23*04		---	---	---	---	---	---	---	---	---	---	---	---	...	...	...	...	...	...	---	---

		41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
AE000660, TRAV23*01		W	Y	Q	Q	F	P	G	K	G	P	A	L	L	I	A	I	R	P		
X70309, TRAV23*01		TGG	TAC	CAA	CAA	TTC	CCT	GGG	AAA	GGC	CCT	GCA	TTA	TTG	ATA	GCC	ATA	CGT	CCA	...	...
U32526, TRAV23*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M17660, TRAV23*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M22936, TRAV23*01/*02 (1)		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M97704, TRAV23*03		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
Z49057, TRAV23*03		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
Y10411, TRAV23*04		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---



		IMGT																																	
		61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80														
AE000660	,TRAV23*01	...	...	...	...	...	D	GAT	GTG	AGT	GAA	K	K	E	...	G	A	R	F	T	I	S	F												
X70309	,TRAV23*01	...	...	...	...	...	GAT	GTG	AGT	GAA	AAG	AAA	GAA	...	GGA	AGA	TTC	ACA	ATC	TTC	TTC	...													
U32526	,TRAV23*01	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...													
M17660	,TRAV23*02	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...													
M22936	,TRAV23*01/*02 (1)	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...													
M97704	,TRAV23*03	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...													
Z49057	,TRAV23*03	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...													
Y10411	,TRAV23*04	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...													

		81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100												
		N	K	S	A	K	Q	F	S	L	H	I	M	D	S	Q	P	G	D	S	A												
AE000660	,TRAV23*01	AAT	AAA	AGT	GCC	AAG	CAG	TTC	TCA	TTG	CAT	ATC	ATG	GAT	TCC	CAG	CCT	GGA	GAC	TCA	GCC												
X70309	,TRAV23*01	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...												
U32526	,TRAV23*01	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...												
M17660	,TRAV23*02	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...												
M22936	,TRAV23*01/*02 (1)	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...												
M97704	,TRAV23*03	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...												
Z49057	,TRAV23*03	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...												
Y10411	,TRAV23*04	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...												

		CDR3-IMGT																																																	
		101	102	103	104	105	106	107																																											
		T	Y	F	C	A	A	S																																											
AE000660	,TRAV23*01	ACC	TAC	TTC	TGT	GCA	GCA	AGC	A																																										
X70309	,TRAV23*01	---	---	---	---	---	---	---	---																																										
U32526	,TRAV23*01	---	---	---	---	---	---	---	---																																										
M17660	,TRAV23*02	---	---	---	---	---	---	---	---																																										
M22936	,TRAV23*01/*02 {1}	---	---	---	---	---	---	---	---																																										
M97704	,TRAV23*03	---	---	---	---	---	---	---	---																																										
Z49057	,TRAV23*03	---	---	---	---	---	---	---	---																																										
Y10411	,TRAV23*04	---	---	---	---	---	---	---	---																																										

#c: Rearranged cDNA
°: Genomic DNA, but not known to be germline or rearranged

Note:
(1) Partial sequence which could not be assigned to a given allele.

Framework and complementarity determining regions

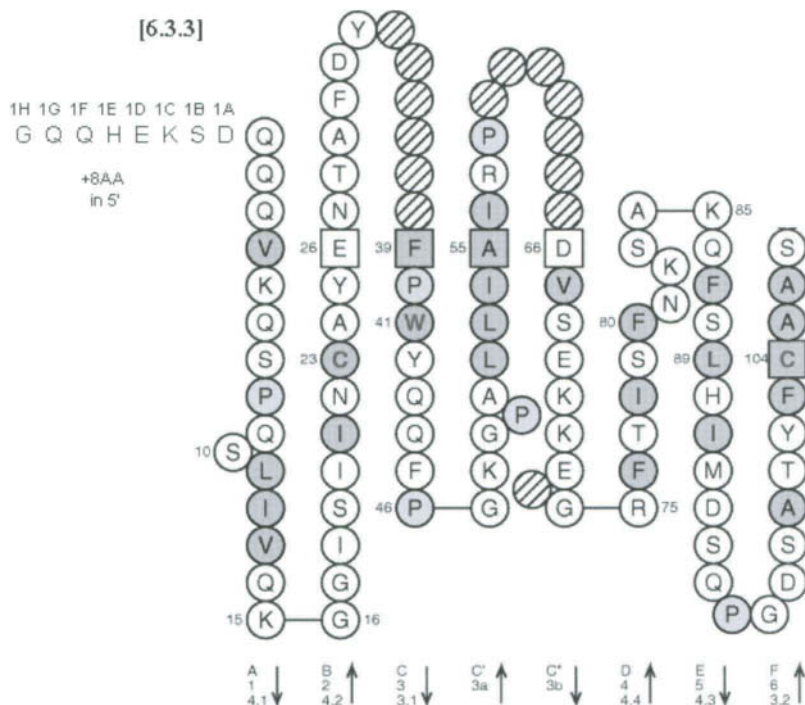
FR1-IMGT: 26	CDR1-IMGT: 6
FR2-IMGT: 17	CDR2-IMGT: 3
FR3-IMGT: 38 (-1 aa: 73)	CDR3-IMGT: 3



Collier de Perles for human TRAV23/DV6*01

Accession number: IMGT AE000660

EMBL/GenBank/DDBJ: AE000660



Note:

The 8 additional amino acids, predicted by the program SIGSEQ2 and described by Wülfing, C. and Plückthun, A. (1995) Immunology Today 16, 405–406, are numbered 1A to 1H.



Genome database accession numbers

GDB:9953987

LocusLink: 28660

Nomenclature

TRAV24: T cell receptor alpha variable 24.

Definition and functionality

TRAV24 is the unique functional gene of the TRAV24 subgroup which only comprises this mapped gene.

Gene location

TRAV24 is in the TRA/TRD locus on chromosome 14 at 14q11.2.

Nucleotide and amino acid sequences for human TRAV24

[illegible]

#c: Rearranged cDNA

Framework and complementarity determining regions

FR1-IMGT: 26

FR2-IMGT: 17

FR3-IMGT: 38 (-1 aa: 73)

CDR1-IMGT: 6

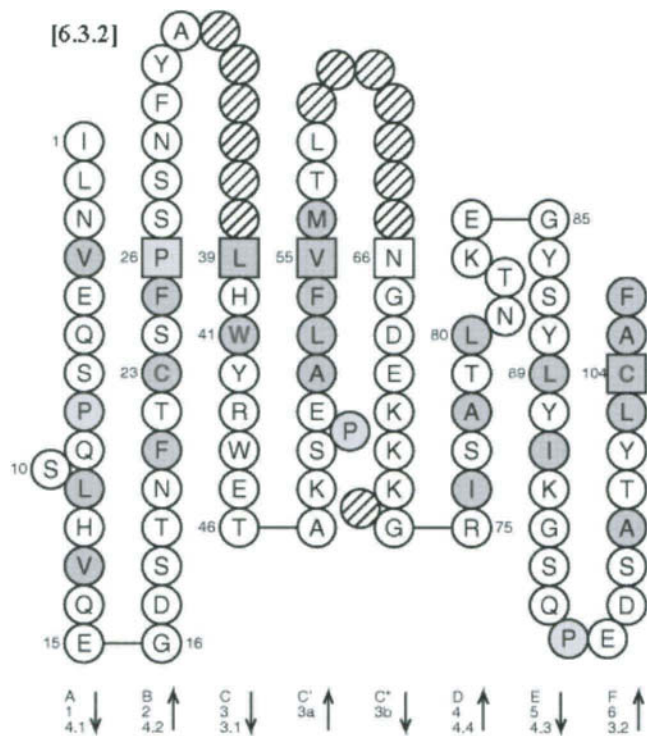
CDR2-IMGT: 3

CDR3-IMGT: 2



Collier de Perles for human TRAV24*01

Accession number: IMGT AE000660 EMBL/GenBank/DDBJ: AE000660



Genome database accession numbers

GDB:9953989 LocusLink: 28659

Nomenclature

TRAV25: T cell receptor alpha variable 25.

Definition and functionality

TRAV25 is the unique functional gene of the TRAV25 subgroup which only comprises this mapped gene.

Gene location

TRAV25 is in the TRA/TRD locus on chromosome 14 at 14q11.2.

Nucleotide and amino acid sequences for human TRAV25



```

      1  2  3  4  5  6  7  8  9 10 11 12 13 14 15 16 17 18 19 20
AE000660, TRAV25*01  [6]  GGA CAA CAG GTA ATG CAA ATT CCT CAG TAC CAG CAT GTA CAA GAA GGA GAG GAC TTC ACC
M64350 ,TRAV25*01    [4]  ---

                                CDR1-IMGT
      21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40
AE000660, TRAV25*01  ACG TAC TGC AAT TCC TCA ACT ACT TTA AGC AAT ... ATA CAG
M64350 ,TRAV25*01    ---

                                CDR2-
      41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60
AE000660, TRAV25*01  TGG TAT TGC CAA AGG CCT GGT GGA CAT CCC GTT TTT TTG ATA CAG TTA GTG AAG ...
M64350 ,TRAV25*01    ---

                                IMGT
      61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80
AE000660, TRAV25*01  ... ACT GGA GAA GTG AAG AAG CAG ... AAA AGA CTG ACA TTT CAG TTT
M64350 ,TRAV25*01    ---

      81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100
AE000660, TRAV25*01  GGA GAA GCA AAA AAG AAC AGC TCC CTG CAC ATC ACA GCC ACC CAG ACT ACA GAT GTA GGA
M64350 ,TRAV25*01    ---

                                CDR3-IMGT_
      101 102 103 104 105 106
AE000660, TRAV25*01  ACC TAC TTC TGT GCA GGG
M64350 ,TRAV25*01    --- #c

#c: Rearranged cDNA

```

Framework and complementarity determining regions

FR1-IMGT: 26

FR2-IMGT: 17

FR3-IMGT: 38 (-1 aa: 73)

CDR1-IMGT: 5

CDR2-IMGT: 3

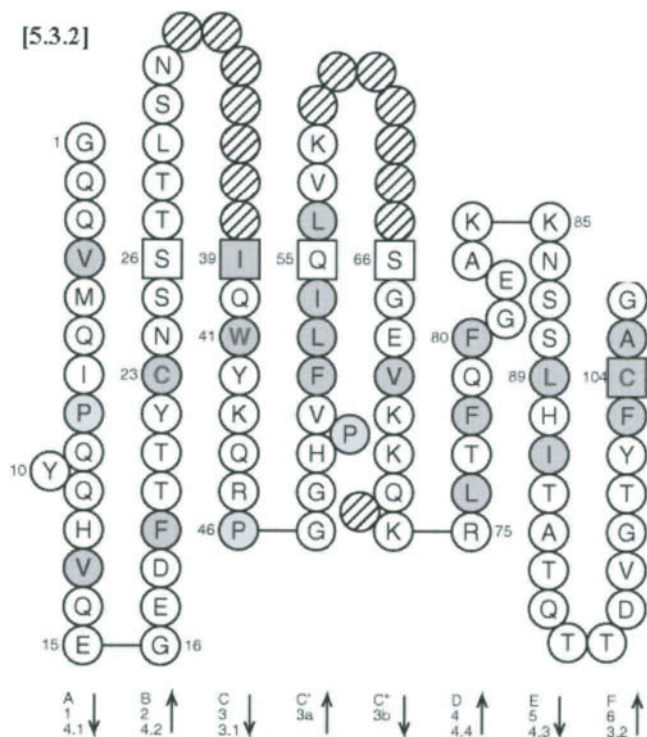
CDR3-IMGT: 2



Collier de Perles for human TRAV25*01

Accession number: IMGT AE000660

EMBL/GenBank/DDBJ: AE000660



Genome database accession numbers

GDB:9953991

LocusLink: 28658



Framework and complementarity determining regions

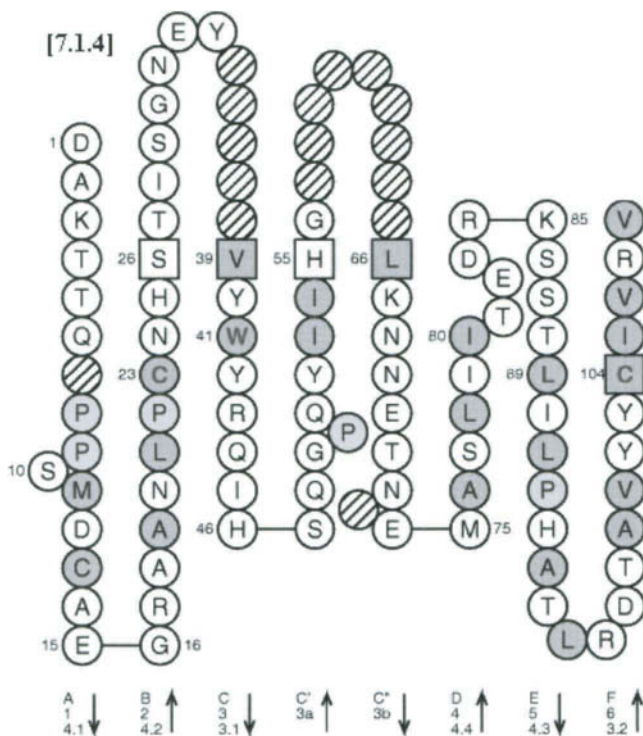
FR1-IMGT: 25 (-1 aa: 7)
FR2-IMGT: 17
FR3-IMGT: 38 (-1 aa: 73)

CDR1-IMGT: 7
CDR2-IMGT: 1
CDR3-IMGT: 4

Collier de Perles for human TRAV26-1*01

Accession number: IMGT AE000660

EMBL/GenBank/DDBJ: AE000660



Genome database accession numbers

GDB:9953993

LocusLink: 28657

Nomenclature

TRAV26-2: T cell receptor alpha variable 26-2.

Definition and functionality

TRAV26-2 is one of the two functional genes of the TRAV26 subgroup which comprises two mapped genes.

Gene location

TRAV26-2 is in the TRA/TRD locus on chromosome 14 at 14q11.2.

Nucleotide and amino acid sequences for human TRAV26-2

		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
AB000660, TRAV26-2*01	[6]	D	A	K	T	T	O	...	P	N	S	M	E	S	N	E	E	P	V	H	
X04937, TRAV26-2*01	[38]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L11160, TRAV26-2*02	[7]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
AB000660, TRAV26-2*01		L	P	C	N	H	S	T	I	S	G	T	D	Y	...	...	...	...	...	I	H
X04937, TRAV26-2*01		TTG	CCT	TGT	AAC	CAC	TCC	ACA	ATC	AGT	GGA	ACT	GAT	TAC	...	...	...	...	...	ATA	CAT
L11160, TRAV26-2*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
AB000660, TRAV26-2*01		M	Y	R	Q	L	P	S	Q	G	P	E	Y	V	I	H	G	...	...	...	...
X04937, TRAV26-2*01		TGG	TAT	CGA	CAG	CTT	CCC	TCC	CAG	GGT	CCA	GAG	TAC	GTG	ATT	CAT	GGT	...	...	...	...
L11160, TRAV26-2*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
AB000660, TRAV26-2*01		...	...	...	...	...	CTT	ACA	AGC	AAT	GTG	AAC	AAC	...	R	M	A	S	L	A	I
X04937, TRAV26-2*01		---	---	---	---	---	---	---	---	---	---	---	---	---	...	...	...	...	...	...	...
L11160, TRAV26-2*02		---	---	---	---	---	---	---	---	---	---	---	---	---	...	...	...	...	...	...	...
		81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
AB000660, TRAV26-2*01		A	E	D	R	K	S	S	T	L	I	L	H	R	A	T	L	R	D	A	A
X04937, TRAV26-2*01		GCT	GAA	GAC	AGA	AAG	TCC	AGT	ACC	TTG	ATC	CTG	CAC	CGT	GCT	ACC	TTG	AGA	GAT	GCT	GCT
L11160, TRAV26-2*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		101	102	103	104	105	106	107	108												
AB000660, TRAV26-2*01		V	V	V	C	I	L	P	D												
X04937, TRAV26-2*01		GTG	TAC	TAC	TGC	ATC	CTG	AGA	GAC												
L11160, TRAV26-2*02		---	---	---	---	---	---	---	---												

#c: Rearranged cDNA

°: Genomic DNA, but not known as being germline or rearranged

Framework and complementarity determining regions

FR1-IMGT: 25 (-1 aa: 7)

FR2-IMGT: 17

FR3-IMGT: 38 (-1 aa: 73)

CDR1-IMGT: 7

CDR2-IMGT: 1

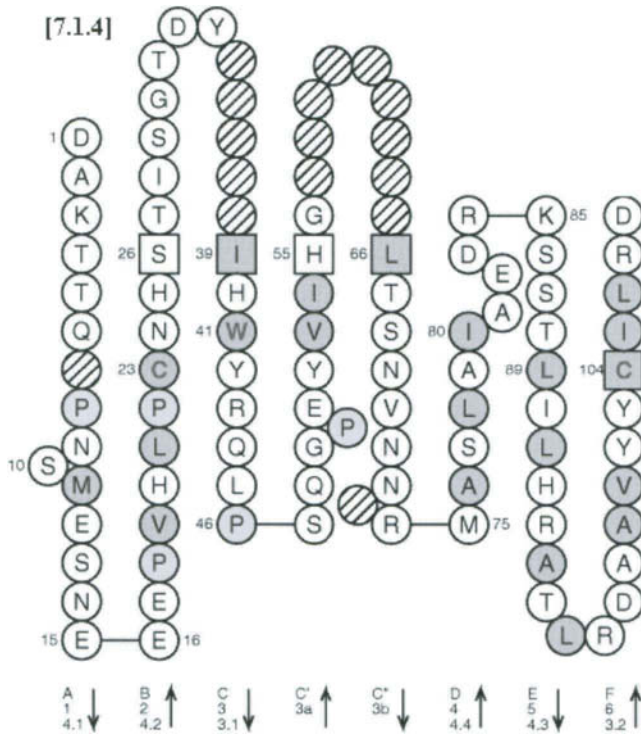
CDR3-IMGT: 4



Collier de Perles for human TRAV26-2*01

Accession number: IMGT AE000660

EMBL/GenBank/DDBJ: AE000660



Genome database accession numbers

GDB:9953995

LocusLink: 28656

Nomenclature

TRAV27: T cell receptor alpha variable 27.

Definition and functionality

TRAV27 is the unique functional gene of the TRAV27 subgroup which only comprises this mapped gene.

Gene location

TRAV27 is in the TRA/TRD locus on chromosome 14 at 14q11.2.

Nucleotide and amino acid sequences for human TRAV27

		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
AE000660, TRAV27*01	[6]	T	Q	L	L	E	Q	S	P	Q	F	L	S	I	Q	E	G	E	N	L	T
		ACC	CAG	CTG	CTG	GAG	CAG	AGC	CCT	CAG	TTT	CTA	AGC	ATC	CAA	GAG	GGA	GAA	AAT	CTC	ACT
L09760, TRAV27*01	[27]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X04957, TRAV27*02	[38]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
D13075, TRAV27*03	[23]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L09759, TRAV27*03	[27]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U32521, TRAV27*02/*03 (1)	[5]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

		21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
AE000660, TRAV27*01		V	Y	C	N	S	S	S	V	F	S	S	L	L	L	V	T	V	V	T	Q
		TGG	TAC	TGC	AAC	TCC	TCA	AGT	GTT	TTT	TCC	AGC	...	...	...	...	...	...	...	TTA	CAA
L09760, TRAV27*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X04957, TRAV27*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
D13075, TRAV27*03		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L09759, TRAV27*03		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U32521, TRAV27*02/*03 (1)		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

		41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
AE000660, TRAV27*01		W	Y	R	Q	E	P	G	E	G	P	V	L	L	V	T	V	V	T	...	...
		TGG	TAC	AGA	CAG	GAG	CCT	GGG	GAA	GGT	CCT	GTC	CTC	CTG	GTG	ACA	GTA	ATC	ACG	...	...
L09760, TRAV27*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X04957, TRAV27*02		---	---	-G	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
D13075, TRAV27*03		---	---	-G	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L09759, TRAV27*03		---	---	-G	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U32521, TRAV27*02/*03 (1)		---	---	-G	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

		61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
AE000660, TRAV27*01		...	...	...	...	...	GGT	GGA	GAA	GTG	AAG	AAG	CTG	...	...	...	...	...	...	...	...
		...	...	...	...	...	G	G	E	V	K	K	L	...	K	R	L	T	F	Q	F
L09760, TRAV27*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X04957, TRAV27*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
D13075, TRAV27*03		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L09759, TRAV27*03		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U32521, TRAV27*02/*03 (1)		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

		81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
AE000660, TRAV27*01		G	D	A	R	K	D	S	S	L	H	I	T	A	A	Q	P	G	D	T	G
		GGT	GAT	GCA	AGA	AAG	GAC	AGT	TCT	CTC	CAC	ATC	ACT	GCA	GGC	CAG	CCT	GCT	GAT	ACA	GGC
L09760, TRAV27*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X04957, TRAV27*02		---	---	---	---	---	---	---	---	---	---	---	---	---	-G	---	---	---	---	---	---
D13075, TRAV27*03		---	---	---	---	---	---	---	---	---	---	---	---	---	-G	---	A	---	---	---	---
L09759, TRAV27*03		---	---	---	---	---	---	---	---	---	---	---	---	---	-G	---	T	---	---	---	---
U32521, TRAV27*02/*03 (1)		---	---	---	---	---	---	---	---	---	---	---	---	---	-G	---	A	---	---	---	---

#c: Rearranged cDNA sequence
°: Genomic DNA, but not known as being germline or rearranged

(1) Partial sequence which could not be assigned to a given allele.

CDR3-IMGT: 2

Accession number: IMGT AE000660 EMBL/GenBank/DDBJ: AE000660



LocusLink: 28655

TRAV29/DV5

Nomenclature

TRAV29/DV5: T cell receptor alpha variable 29/delta variable 5.

Definition and functionality

TRAV29/DV5 is a functional gene (alleles *01 and *02) or a pseudogene (allele *03). TRAV29/DV5 belongs to the TRAV29 subgroup which only comprises this mapped gene.

TRAV29/DV5*03 is a pseudogene due to a 1 nt DELETION in codon 42 leading to a frameshift in FR2-IMGT.

TRAV29/DV5 has been found rearranged to both (D)J genes of the TRD locus and TRAJ genes, the TRD locus being embedded in the TRA locus. This gene can therefore be used for the synthesis of both delta and alpha chains.

Gene location

TRAV29/DV5 is in the TRA/TRD locus on chromosome 14 at 14q11.2.

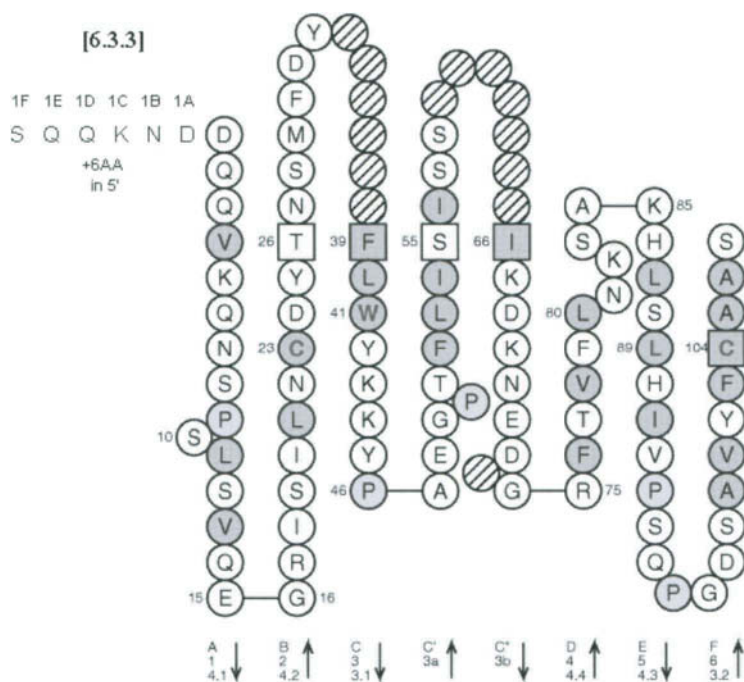
Nucleotide and amino acid sequences for human TRAV29/DV5

		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
AE000660, TRAV29*01	[6]	D	Q	Q	V	K	Q	N	S	P	S	L	S	V	Q	E	G	R	I	S	I
M15565, TRAV29*01	[20]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
S81645, TRAV29*02	[34]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
AJ245565, TRAV29*03	[34]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		CDR1-IMGT																			
AE000660, TRAV29*01		21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
		L	N	C	D	Y	T	A	N	S	M	F	D	Y	---	---	---	---	---	F	L
M15565, TRAV29*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
S81645, TRAV29*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
AJ245565, TRAV29*03		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		CDR2-																			
AE000660, TRAV29*01		41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
		W	Y	K	K	Y	P	A	E	G	P	P	L	I	S	---	I	S	S	---	---
M15565, TRAV29*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
S81645, TRAV29*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
AJ245565, TRAV29*03		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		IMGT																			
AE000660, TRAV29*01		61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
		---	---	---	---	---	I	K	D	K	N	E	D	---	G	R	F	T	V	F	L
M15565, TRAV29*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
S81645, TRAV29*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
AJ245565, TRAV29*03		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
AE000660, TRAV29*01		N	K	S	A	K	H	L	S	L	H	I	V	P	S	Q	P	G	D	S	A
M15565, TRAV29*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
S81645, TRAV29*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
AJ245565, TRAV29*03		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		CDR3-IMGT																			
AE000660, TRAV29*01		101	102	103	104	105	106	107	108												
		V	Y	F	C	A	A	S	---												
M15565, TRAV29*01		---	---	---	---	---	---	---	---												
S81645, TRAV29*02		---	---	---	---	---	---	---	---												
AJ245565, TRAV29*03		---	---	---	---	---	---	---	---												

(in the sequence): Frameshift
#c: Rearranged cDNA

CDR1-IMGT: 6
CDR2-IMGT: 3
CDR3-IMGT: 3

Accession number: IMGT AE000660 EMBL/GenBank/DDBJ: AE000660



The 6 additional amino acids, predicted by the program SIGSEQ2 and described by Wülfing, C. and Plückthun, A. (1995) Immunology Today 16, 405-406, are numbered 1A to 1F.

GDB:9954001 LocusLink: 28653

Nomenclature

TRAV30: T cell receptor alpha variable 30.

Definition and functionality

TRAV30 is the unique functional gene of the TRAV30 subgroup which only comprises this mapped gene.

Gene location

TRAV30 is in the TRA/TRD locus on chromosome 14 at 14q11.2.

Nucleotide and amino acid sequences for human TRAV30

AE000660, TRAV30*01	[6]	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
		Q	Q	P	V		Q	S	P	Q	A	V	I	L	R	E	G	E	D	A	V
S63879, TRAV30*01	[20]	---	---	---	---	---	CAG	AGT	CCT	CAA	GCC	GTG	ATC	CTC	GSA	GAA	GGS	GAA	GAT	GCT	GTC
X58768, TRAV30*02	[28]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L06883, TRAV30*03	[29]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U32537, TRAV30*04	[5]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
AE000660, TRAV30*01		21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
		I	N	C	S	S	S	K	A	L	Y	S								V	H
S63879, TRAV30*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X58768, TRAV30*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L06883, TRAV30*03		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U32537, TRAV30*04		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
AE000660, TRAV30*01		41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
		TGG	TRC	AGG	CAG	AAG	CAT	GGT	GAA	GCA	CCC	GTC	TTG	CTG	ATG	ATA	TTA	CTG	AAG		
S63879, TRAV30*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X58768, TRAV30*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L06883, TRAV30*03		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U32537, TRAV30*04		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
AE000660, TRAV30*01		61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
							GGT	GGA	GAA	CAG	AAG	GGT	CAT		E	K	I	S	A	S	F
S63879, TRAV30*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X58768, TRAV30*02		---	---	---	---	---	---	---	---	---	M	R	R	---	---	---	---	---	---	---	---
L06883, TRAV30*03		---	---	---	---	---	---	---	---	---	C-	-G-	---	---	---	---	---	---	---	---	---
U32537, TRAV30*04		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
AE000660, TRAV30*01		81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
		ATG	GAA	AAA	AAG	CAG	CAA	AGC	TCC	CTG	CTT	ACG	GCC	TCC	CAG	CTC	AGT	TAC	TCA	GGA	
S63879, TRAV30*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X58768, TRAV30*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L06883, TRAV30*03		---	---	---	---	---	R	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U32537, TRAV30*04		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
AE000660, TRAV30*01		101	102	103	104	105	106	107	108												
		T	Y	F	C	G	T	E													
S63879, TRAV30*01		---	---	---	---	---	---	---	---	#g											
X58768, TRAV30*02		---	---	---	---	---	---	---	---	#c											
L06883, TRAV30*03		---	---	---	---	---	---	---	---	#c											
U32537, TRAV30*04		---	---	---	---	---	---	---	---	o											

#c: Rearranged cDNA

#g: Rearranged genomic DNA

o: Genomic DNA, but not known as being germline or rearranged



Framework and complementarity determining regions

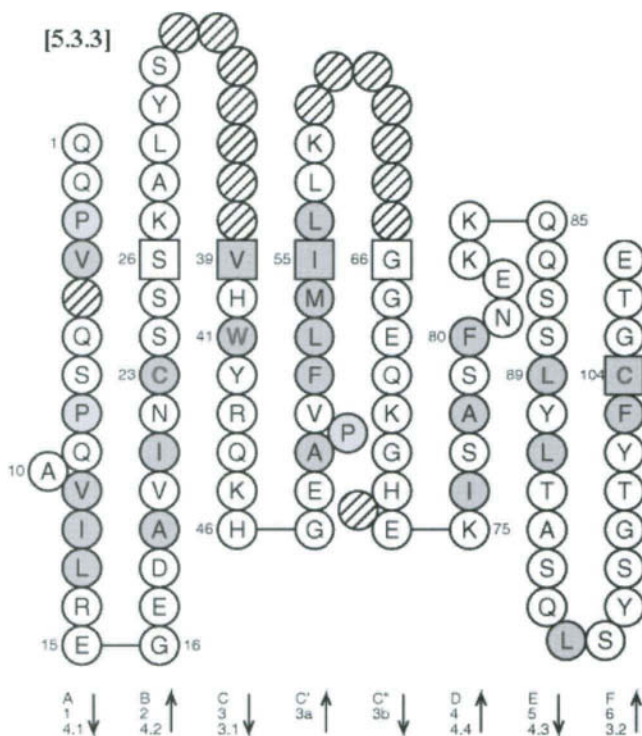
FR1-IMGT: 25 (-1 aa: 5)
FR2-IMGT: 17
FR3-IMGT: 38 (-1 aa: 73)

CDR1-IMGT: 5
CDR2-IMGT: 3
CDR3-IMGT: 3

Collier de Perles for human TRAV30*01

Accession number: IMGT AE000660

EMBL/GenBank/DDBJ: AE000660



Genome database accession numbers

GDB:9954003

LocusLink: 28652

Nomenclature

TRAV34: T cell receptor alpha variable 34.

Definition and functionality

TRAV34 is the unique functional gene of the TRAV34 subgroup which only comprises this mapped gene.

Gene location

TRAV34 is in the TRA/TRD locus on chromosome 14 at 14q11.2.

Nucleotide and amino acid sequences for human TRAV34

		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
AE000660, TRAV34*01	[6]	AGC	CAA	GAA	CTG	GAG	CAG	AGT	CCT	CAG	TCC	TTG	ATC	GTC	CAA	GAG	GGA	AAG	AAT	CTC	ACC
X58739 , TRAV34*01	[28]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U32534 , TRAV34*01	[5]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		CDR1-IMGT																			
AE000660, TRAV34*01		21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
X58739 , TRAV34*01		ATA	AAC	TGC	ACG	TCA	TCA	AAG	ACG	TTA	TAT	GGC	...	...	...	...	...	...	...	TTA	TAC
U32534 , TRAV34*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		CDR2-																			
AE000660, TRAV34*01		41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
X58739 , TRAV34*01		TGG	TAT	AAG	CAA	AAG	TAT	GGT	GAA	GGT	CTT	ATC	TTG	TTG	ATG	ATG	CTA	CAG	AAA	...	...
U32534 , TRAV34*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		IMGT																			
AE000660, TRAV34*01		61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
X58739 , TRAV34*01		...	...	...	...	...	GGT	GGG	GAA	GAG	AAA	AGT	CAT	...	GAA	AAG	ATA	ACT	GCC	AAG	TTG
U32534 , TRAV34*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		CDR3-IMGT																			
AE000660, TRAV34*01		81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
X58739 , TRAV34*01		GAT	GAG	AAA	AAG	CAG	CAA	AGT	TCC	CTG	CAT	ATC	ACA	GCC	TCC	CAG	CCC	AGC	CAT	GCA	GGC
U32534 , TRAV34*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		CDR3-IMGT																			
AE000660, TRAV34*01		101	102	103	104	105	106	107													
X58739 , TRAV34*01		ATC	TAC	CTC	TGT	GGA	GCA	GAC	A												
U32534 , TRAV34*01		---	---	---	---	---	---	---	---												

#: Rearranged cDNA

°: Genomic DNA, but not known as being germline or rearranged

Framework and complementarity determining regions

FR1-IMGT: 26

FR2-IMGT: 17

FR3-IMGT: 38 [-1 aa: 73]

CDR1-IMGT: 5

CDR2-IMGT: 3

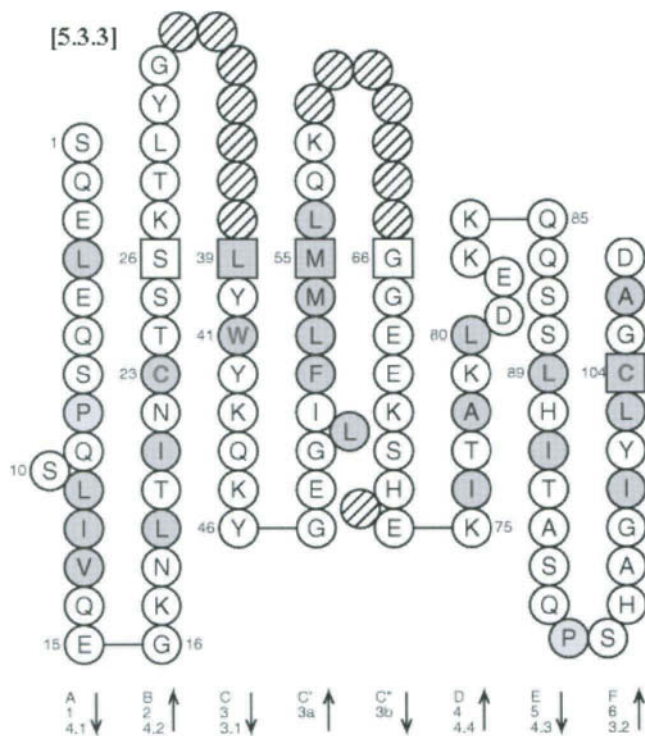
CDR3-IMGT: 3



Collier de Perles for human TRAV34*01

Accession number: IMGT AE000660

EMBL/GenBank/DDBJ: AE000660



Genome database accession numbers

GDB:9954011

LocusLink: 28648

Nomenclature

TRAV35: T cell receptor alpha variable 35.

Definition and functionality

TRAV35 is the unique functional gene of the TRAV35 subgroup which only comprises this mapped gene.

Gene location

TRAV35 is in the TRA/TRD locus on chromosome 14 at 14q11.2.

Nucleotide and amino acid sequences for human TRAV35

		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
AE000660,TRAV35*01	[6]	G	Q	Q	L	N	Q	S	P	Q	S	M	F	I	Q	E	G	E	D	V	S
X58738 ,TRAV35*02	[28]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U32533 ,TRAV35*02	[5]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
AE000660,TRAV35*01		M	N	C	T	S	S	S	I	F	N	T								W	L
X58738 ,TRAV35*02		ATG	AAC	TGC	ACT	TCT	TCA	AGC	ATA	TTT	AAC	ACC	...	...	...	...	...	...	...	TGG	CTA
U32533 ,TRAV35*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
AE000660,TRAV35*01		W	Y	K	Q	E	P	G	E	G	P	V	L	L	I	A	L	Y	K		
X58738 ,TRAV35*02		TGG	TAC	AAG	CAG	GAA	CCT	GGG	GAA	GGT	CCT	GTC	CTC	TTG	ATA	GCC	TTA	TAT	AAG	...	...
U32533 ,TRAV35*02		---	---	---	---	D	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
AE000660,TRAV35*01							A	G	E	L	T	S	N							Q	F
X58738 ,TRAV35*02		...	...	...	...	...	GCT	GGT	GAA	TTG	ACC	TCA	AAT	...	GGA	AGA	CTG	ACT	GCT	CAG	TTT
U32533 ,TRAV35*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
AE000660,TRAV35*01		G	I	T	R	K	D	S	F	L	N	I	S	A	S	I	P	S	D	V	G
X58738 ,TRAV35*02		GGT	ATA	ACC	AGA	AAG	GAC	AGC	TTC	CTG	AAT	ATC	TCA	GCA	TCC	ATA	CCT	AGT	GAT	GTA	GGC
U32533 ,TRAV35*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		101	102	103	104	105	106	107													
AE000660,TRAV35*01		I	Y	F	C	A	C	Q													
X58738 ,TRAV35*02		ATC	TAC	TTC	TGT	GCT	GGG	CAG													
U32533 ,TRAV35*02		---	---	---	---	---	---	---													

#c Rearranged cDNA
%: Genomic DNA, but not known as being germline or rearranged

Framework and complementarity determining regions

FR1-IMGT: 26

FR2-IMGT: 17

FR3-IMGT: 38 (-1 aa: 73)

CDR1-IMGT: 5

CDR2-IMGT: 3

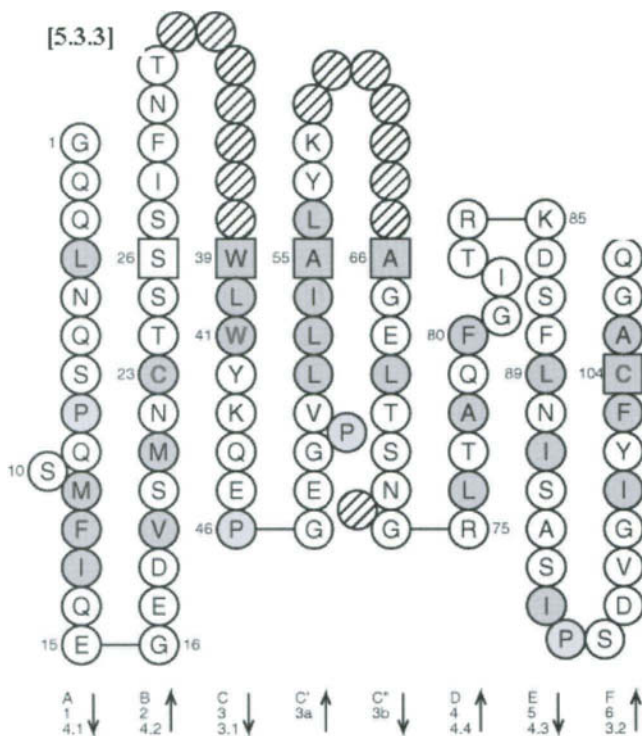
CDR3-IMGT: 3



Collier de Perles for human TRAV35*01

Accession number: IMGT AE000660

EMBL/GenBank/DDBJ: AE000660



Genome database accession numbers

GDB:9954013

LocusLink: 28647



CDR3-IMGT

	101	102	103	104	105	106	107	
	I	Y	L	C	A	V	E	
AE000660, TRAV36*01	ATC	TAC	CTC	TGT	GCT	GTG	GAG	G
	V							
X61070 ,TRAV36*02	G	---	---	---	---	---	---	#c
	V							
X58767 ,TRAV36*03	G	---	---	---	---	---	---	#c
	V							
Z46643 ,TRAV36*04	G	---	---	---	---	---	---	#c
U32536 ,TRAV36*04								o

#c: Rearranged cDNA

o: Genomic DNA, but not known as being germline or rearranged

Framework and complementarity determining regions

FR1-IMGT: 26

CDR1-IMGT: 6

FR2-IMGT: 16 (-1 aa: 50)

CDR2-IMGT: 3

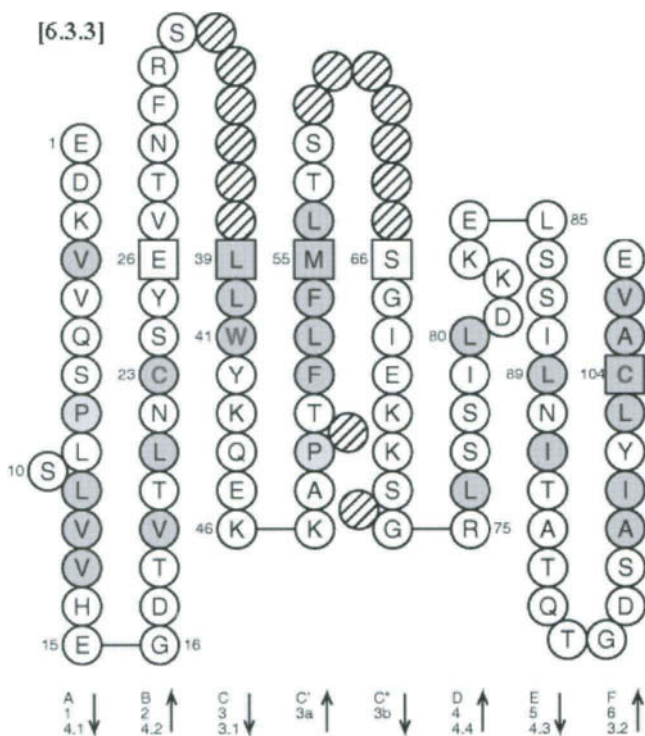
FR3-IMGT: 38 (-1 aa: 73)

CDR3-IMGT: 3

Collier de Perles for human TRAV36/DV7*01

Accession number: IMGT AE000660

EMBL/GenBank/DDBJ: AE000660



Genome database accession numbers

GDB:9954015

LocusLink: 28646

Nomenclature

TRAV38-1: T cell receptor alpha variable 38-1.

Definition and functionality

TRAV38-1 is one of the two functional genes of the TRAV38 subgroup which comprises two mapped genes.

Gene location

TRAV38-1 is in the TRA/TRD locus on chromosome 14 at 14q11.2.

Nucleotide and amino acid sequences for human TRAV38-1



		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
		A	G	T	V	T	Q	S	Q	P	E	M	S	V	Q	E	A	E	T	V	T
AE000661, TRAV38-1*01	[6]	GCC	CAG	ACA	GTC	ACT	CAG	TCT	CAA	CCA	GAG	ATG	TCT	GTG	CAG	GAG	GCA	GAG	ACT	GTG	ACC
D13074, TRAV38-1*01	[23]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M64355, TRAV38-1*02	[41]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M95394, TRAV38-1*03	[19]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L06880, TRAV38-1*04	[29]	---	---	---	---	---	---	CC	GG	---	---	---	---	---	---	---	---	---	---	---	---

		21	22	23	24	25	26	CDR1-IMGT										31	32	33	34	35	36	37	38	39	40
		L	S	C	T	Y	D	L	S	E	N	N	Y	Y	--- <td>---</td> <td>---</td> <td>---</td> <td>---</td> <td>---</td> <td>---</td> <td>---</td> <td>---</td> <td>---</td> <td>---</td>	---	---	---	---	---	---	---	---	---	---		
AE000661, TRAV38-1*01		CTG	AGT	TGC	ACA	TAT	GAC	ACC	AGT	GAG	AAT	AAT	TAT	TAT	---	---	---	---	---	---	---	---	---	---	TTG	TTC	
D13074, TRAV38-1*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
M64355, TRAV38-1*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
M95394, TRAV38-1*03		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
L06880, TRAV38-1*04		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		

		41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	CDR2-				
		W	Y	K	Q	P	P	S	R	Q	M	I	L	V	I	R	Q	E	A	Y	
AE000661, TRAV38-1*01		TGG	TAC	AAG	CAG	CCT	CCC	AGC	AGG	CAG	ATG	ATC	CTC	GTT	ATT	CGC	CAA	GAA	GCT	TAT	
D13074, TRAV38-1*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
M64355, TRAV38-1*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
M95394, TRAV38-1*03		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
L06880, TRAV38-1*04		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	

		IMGT										61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
		K	Q	Q	N	A	T	E	N	R	F	S	V	N	F	--- <td>---</td> <td>---</td> <td>---</td> <td>---</td> <td>---</td> <td>---</td> <td>---</td> <td>---</td> <td>---</td> <td>---</td> <td>---</td> <td>---</td> <td>---</td> <td>---</td> <td>---</td>	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
AE000661, TRAV38-1*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
D13074, TRAV38-1*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M64355, TRAV38-1*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M95394, TRAV38-1*03		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L06880, TRAV38-1*04		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

		81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
		Q	K	A	A	K	S	F	S	L	K	I	S	D	S	Q	L	G	D	T	A
AE000661, TRAV38-1*01		CAG	AAA	GCA	GCC	AAA	TCC	TTC	AGT	CTC	AAG	ATC	TCA	GAC	TCA	CAG	CTG	GGG	GAC	ACT	GCG
D13074, TRAV38-1*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M64355, TRAV38-1*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M95394, TRAV38-1*03		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L06880, TRAV38-1*04		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

		CDR3-IMGT							
		101	102	103	104	105	106	107	108
AE000661, TRAV38-1*01		ATG	TAT	TTC	TGT	GCT	TTC	ATG	AAG
D13074, TRAV38-1*01		---	---	---	---	---	---	---	#c
M64355, TRAV38-1*02		---	---	---	---	---	---	---	#c
M95394, TRAV38-1*03		---	---	---	---	---	---	---	#c
L06880, TRAV38-1*04		---	---	---	---	---	---	---	#c

#c: Rearranged cDNA



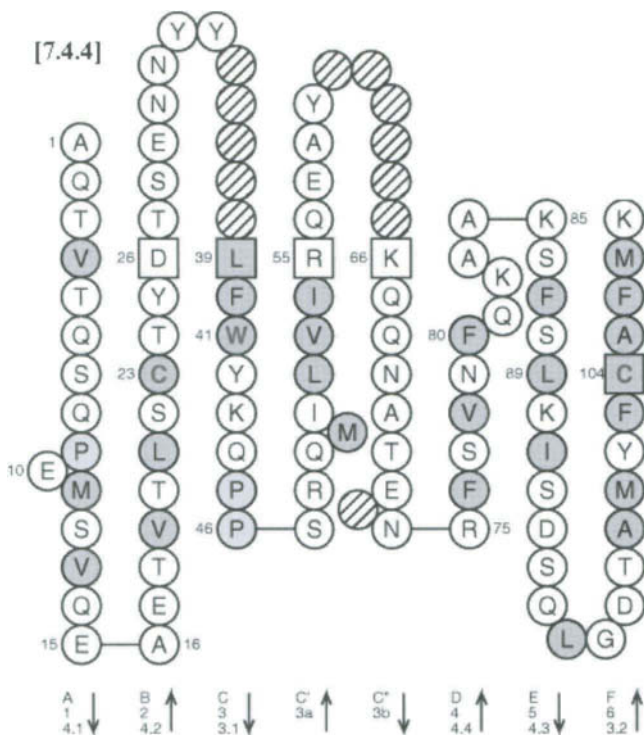
Framework and complementarity determining regions

FR1-IMGT: 26
FR2-IMGT: 17
FR3-IMGT: 38 (-1 aa: 73)

CDR1-IMGT: 7
CDR2-IMGT: 4
CDR3-IMGT: 4

Collier de Perles for human TRAV38-1*01

Accession number: IMGT AE000661 EMBL/GenBank/DDBJ: AE000661



Genome database accession numbers

GDB:9954019 LocusLink: 28644

TRAV38-2/DV8

Nomenclature

TRAV38-2/DV8: T cell receptor alpha variable 38-2/delta variable 8.

Definition and functionality

TRAV38-2/DV8 is one of the two functional genes of the TRAV38 subgroup which comprises two mapped genes.

TRAV38-2/DV8 has been found rearranged to both (D)J genes of the TRD locus and TRAJ genes, the TRD locus being embedded in the TRA locus. This gene can therefore be used for the synthesis of both delta and alpha chains.

Gene location

TRAV38-2/DV8 is in the TRA/TRD locus on chromosome 14 at 14q11.2.

Nucleotide and amino acid sequences for human TRAV38-2/DV8



		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
AE000661, TRAV38-2*01	[6]	GCT	CAG	ACA	GTC	ACT	CAG	TCT	CAA	CCA	GAG	ATG	TCT	GTG	CAG	GAG	GCA	GAG	ACC	GTG	ACC
Z29614, TRAV38-2*01	[15]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
Z46644, TRAV38-2*01	[22]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U32524, TRAV38-2*01	[5]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X58158, TRAV38-2*01	[25]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

		21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
AE000661, TRAV38-2*01		CTG	AGC	TGC	ACA	TAT	GAC	ACC	AGT	GAG	AGT	GAT	TAT	TAT	...	...	...	...	...	TTA	TTC
Z29614, TRAV38-2*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
Z46644, TRAV38-2*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U32524, TRAV38-2*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X58158, TRAV38-2*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

		41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
AE000661, TRAV38-2*01		TGG	TAC	AAG	CAG	CCT	CCC	AGC	AGG	CAG	ATG	ATT	CTC	GTT	ATT	CGC	CAA	GAA	GCT	TAT	...
Z29614, TRAV38-2*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
Z46644, TRAV38-2*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U32524, TRAV38-2*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X58158, TRAV38-2*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

		61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
AE000661, TRAV38-2*01		...	...	...	...	...	AAG	CAA	CAG	AAT	GCA	ACA	GAG	...	AAT	CGT	TTC	TCT	GTG	AAC	TTC
Z29614, TRAV38-2*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
Z46644, TRAV38-2*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U32524, TRAV38-2*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X58158, TRAV38-2*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

		81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
AE000661, TRAV38-2*01		CAG	AAA	GCA	GCC	AAA	TCC	TTC	AGT	CTC	AAG	ATC	TCA	GAC	TCA	CAG	CTG	GGG	GAT	GCC	GCG
Z29614, TRAV38-2*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
Z46644, TRAV38-2*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U32524, TRAV38-2*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X58158, TRAV38-2*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---



CDR3-IMGT
101 102 103 104 105 106 107 108
M Y F C A Y R S
ATG TAT TTC TGT GCT TAT AGG AGC G
T
-CG #c
#g
°
X58158 ,TRAV38-2*01

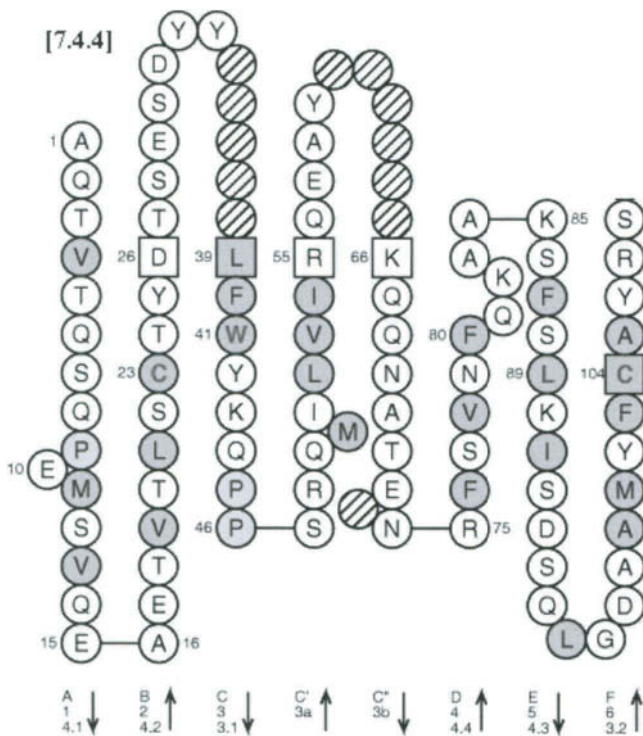
#c: Rearranged cDNA
#g: Rearranged genomic DNA
°: Genomic DNA sequence but not known as being germline or rearranged

Framework and complementarity determining regions

FR1-IMGT: 26 CDR1-IMGT: 7
FR2-IMGT: 17 CDR2-IMGT: 4
FR3-IMGT: 38 (-1 aa: 73) CDR3-IMGT: 4

Collier de Perles for human TRAV38-2/DV8*01

Accession number: IMGT AE000661 EMBL/GenBank/DDBJ: AE000661



Genome database accession numbers
GDB:9954021 LocusLink: 28643

Nomenclature

TRAV39: T cell receptor alpha variable 39.

Definition and functionality

TRAV39 is the unique functional gene of the TRAV39 subgroup which only comprises this mapped gene.

Gene location

TRAV39 is in the TRA/TRD locus on chromosome 14 at 14q11.2.

Nucleotide and amino acid sequences for human TRAV39

		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
		E	L	K	V	E	Q	N	P	L	F	L	S	M	Q	E	G	K	N	Y	T
AE000661, TRAV39*01	[6]	GAG	CTG	AAA	GTG	GAA	CAA	AAC	CCT	CTG	CTC	CTG	AGC	ATG	CAG	GAG	GGA	AAA	AAC	TAT	ACC
X58740, TRAV39*01	[28]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
		A	T	C	T	A	C	C	A	C	T	C	A	G	A	...	...	...	...	...	...
AE000661, TRAV39*01		ATC	TAC	TGC	AAT	TAT	TCA	ACC	ACT	TCA	GAC	AGA	...	...	...	...	...	...	...	CTG	TAT
X58740, TRAV39*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
		W	Y	R	Q	D	P	G	K	S	L	E	S	L	F	V	L	L	S	...	...
AE000661, TRAV39*01		TGG	TAC	AGG	CAG	GAT	CCT	GGG	AAA	AGT	CTG	GAA	TCT	CTG	TTT	GTG	TTG	CTA	TCA	...	...
X58740, TRAV39*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
		N	G	A	V	K	Q	E	...	G	R	L	M	A	S	L	...	...	...	...	...
AE000661, TRAV39*01		...	...	...	...	AAT	GGA	GCA	GTG	AAG	CAG	GAG	...	GGA	GGA	TTA	ATG	GCC	TCA	CTT	...
X58740, TRAV39*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
		D	T	K	A	R	L	S	T	L	H	I	T	A	A	V	H	D	L	S	A
AE000661, TRAV39*01		GAT	ACC	AAA	GCC	CGT	CTC	AGC	ACC	CTC	CAC	ATC	ACA	GCT	GCC	GTG	CAT	GAC	CTC	TCT	GCC
X58740, TRAV39*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		101	102	103	104	105	106	107	...	...	...	...	...	...	...	...	...	...	...	...	...
		T	Y	F	C	A	V	D	...	...	...	...	...	...	...	...	...	...	...	...	...
AE000661, TRAV39*01		ACC	TAC	TTT	TGT	GCC	GTG	GAC	A	...	...	...	...	...	...	...	...	...	...	...	...
X58740, TRAV39*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

#c: Rearranged cDNA

Framework and complementarity determining regions

FR1-IMGT: 26

FR2-IMGT: 17

FR3-IMGT: 38 (-1 aa: 73)

CDR1-IMGT: 5

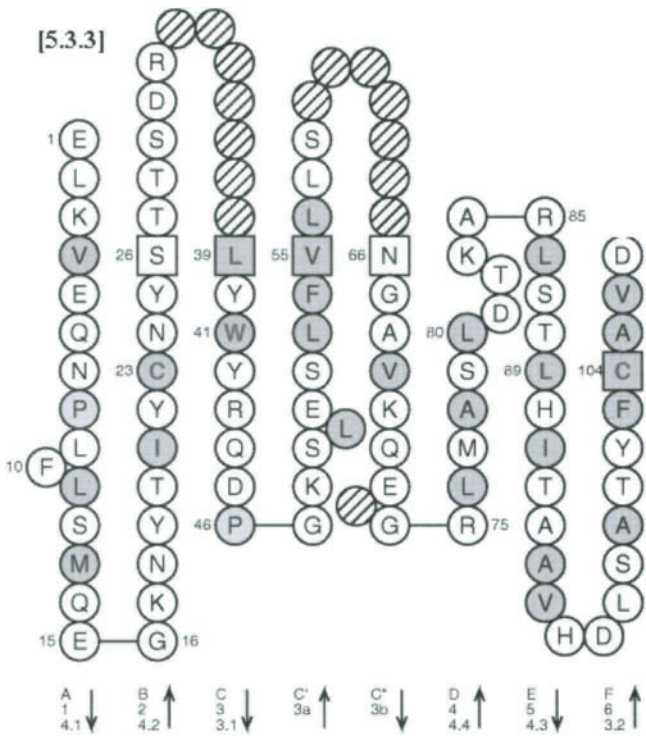
CDR2-IMGT: 3

CDR3-IMGT: 3



Collier de Perles for human TRAV39*01

Accession number: IMGT AE000661 EMBL/GenBank/DDBJ: AE000661



Genome database accession numbers

GDB:9954023 LocusLink: 28642

Nomenclature

TRAV40: T cell receptor alpha variable 40.

Definition and functionality

TRAV40 is the unique functional gene of the TRAV40 subgroup which only comprises this mapped gene.

Gene location

TRAV40 is in the TRA/TRD locus on chromosome 14 at 14q11.2.

Nucleotide and amino acid sequences for human TRAV40



```

      1   2   3   4   5   6   7   8   9  10  11  12  13  14  15  16  17  18  19  20
X73521 ,TRAV40*01 [3] AGC AAT TCA GTC AAG CAG ACG ... GGC CAA ATA ACC GTC TCG GAG GGA GCA TCT GTG ACT
AE000661,TRAV40*01 [6] ---

      21  22  23  24  25  26  27  28  29  30  31  32  33  34  35  36  37  38  39  40
X73521 ,TRAV40*01      CDR1-IMGT
M   N   S   V   K   Q   T   G   Q   I   T   V   S   E   G   A   S   V   T
ATG AAC TGC ACA TAC ACA TCC ACG GGG TAC CCT ACC ... CTT TTC
AE000661,TRAV40*01

      41  42  43  44  45  46  47  48  49  50  51  52  53  54  55  56  57  58  59  60
X73521 ,TRAV40*01      CDR2-
M   Y   V   E   Y   P   S   K   P   L   Q   L   L   Q   R   ...
TGG TAT GTG GAA TAC CCC AGC AAA CCT CTG CAG CTT CTT CAG AGA ...
AE000661,TRAV40*01

      61  62  63  64  65  66  67  68  69  70  71  72  73  74  75  76  77  78  79  80
X73521 ,TRAV40*01      IMGT
...   ...   ...   ...   ...   ...   E   T   M   E   N   S   K   N   F   G   G   N
...   ...   ...   ...   ...   ...   GAG ACA ATG GAA AAC AGC ... AAA AAC TTC GGA GGC GGA AAT
AE000661,TRAV40*01

      81  82  83  84  85  86  87  88  89  90  91  92  93  94  95  96  97  98  99  100
X73521 ,TRAV40*01      I   K   D   K   N   S   P   I   V   K   Y   S   V   Q   V   S   D   S   A
ATT ... AAA GAC AAA AAC TCC CCC ATT GTG AAA TAT TCA GTC CAG GTA TCA GAC TCA GCC
AE000661,TRAV40*01

      101 102 103 104 105 106 107 108
X73521 ,TRAV40*01      CDR3-IMGT
GTC TAC TAC TGT CTT CTG GGA GA
AE000661,TRAV40*01
    
```

Framework and complementarity determining regions

FR1-IMGT: 25 (-1 aa: 8)

FR2-IMGT: 17

FR3-IMGT: 36 (-3 aa: 66,73,82)

CDR1-IMGT: 6

CDR2-IMGT: 0

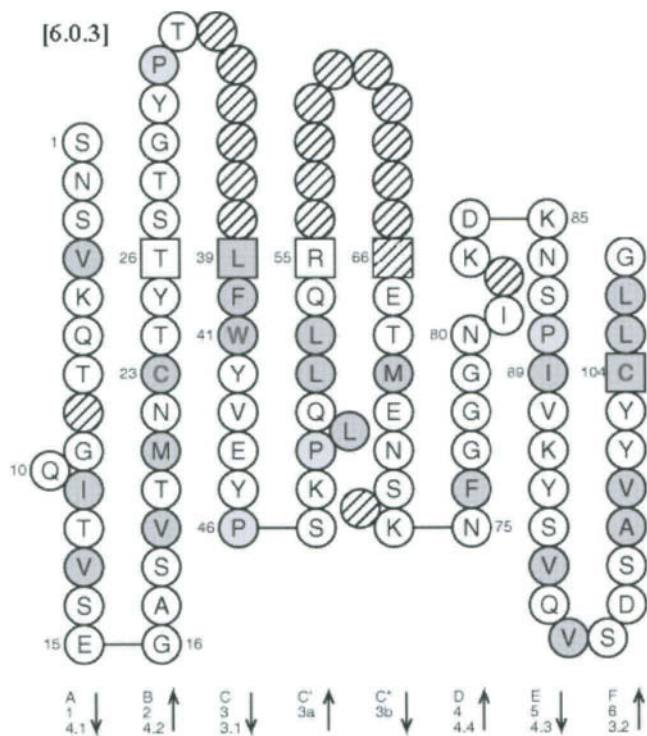
CDR3-IMGT: 3



Collier de Perles for human TRAV40*01

Accession number: IMGT X73521

EMBL/GenBank/DDBJ: X73521



Genome database accession numbers

GDB:9954025

LocusLink: 28641

Nomenclature

TRAV41: T cell receptor alpha variable 41.

Definition and functionality

TRAV41 is the unique functional gene of the TRAV41 subgroup which only comprises this mapped gene.

Gene location

TRAV41 is in the TRA/TRD locus on chromosome 14 at 14q11.2.

Nucleotide and amino acid sequences for human TRAV41

		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
AE000661,TRAV41*01	[6]	AAA	AAT	GAA	GTG	GAG	CAG	AGT	CCT	CAG	AAC	CTG	ACT	GCC	CAG	GAA	GGA	GAA	TTT	ATC	ACA
M17662 ,TRAV41*01	[17]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U32528 ,TRAV41*01	[5]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		CDR1-IMGT																			
AE000661,TRAV41*01		21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
		I	N	C	S	Y	S	V	G	I	S	A								L	H
M17662 ,TRAV41*01		ATC	AAC	TGC	AGT	TAC	TCG	GTA	GGA	ATA	AGT	GCC								TTA	CAC
U32528 ,TRAV41*01		---	---	---	---	---	---	---	---	---	---	---								---	---
		CDR2-																			
AE000661,TRAV41*01		41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
		W	L	Q	Q	H	P	G	G	G	I	V	S	L	F	M	L				
M17662 ,TRAV41*01		TCG	CTG	CAA	CAG	CAT	CCA	GGA	GGA	GGC	ATT	GTT	TCC	TGG	TTT	ATG	CTG				
U32528 ,TRAV41*01		---	---	---	---	---	---	---	---	---	---	---									
		IMGT																			
AE000661,TRAV41*01		61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
							S	S	G	K	K	K	H		G	R	L	I	A	T	I
M17662 ,TRAV41*01							AGC	TCA	GGG	AAG	AAG	CAT			GGA	AGA	TTA	ATT	GCC	ACA	ATA
U32528 ,TRAV41*01							---	---	---	---	---	---									
AE000661,TRAV41*01		81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
		N	I	Q	E	K	H	S	S	L	H	I	T	A	S	H	P	R	D	S	A
M17662 ,TRAV41*01		AAC	ATA	CAG	GAA	AAG	CAC	AGC	TCC	CTG	CAC	ATC	ACA	GCC	TCC	CAT	CCC	AGA	GAC	TCT	GCC
U32528 ,TRAV41*01		---	---	---	---	---	---	---	---	---	---	---									
		CDR3-IMGT																			
AE000661,TRAV41*01		101	102	103	104	105	106	107													
		V	Y	I	C	A	V	R													
M17662 ,TRAV41*01		GTC	TAC	ATC	TGT	GCT	GTC	ACA													
U32528 ,TRAV41*01		---	---	---	---	---	---	T													

#c: Rearranged cDNA

°: Genomic DNA, but not known as being germline or rearranged

Framework and complementarity determining regions

FR1-IMGT: 26

FR2-IMGT: 17

FR3-IMGT: 38 [-1 aa: 73]

CDR1-IMGT: 5

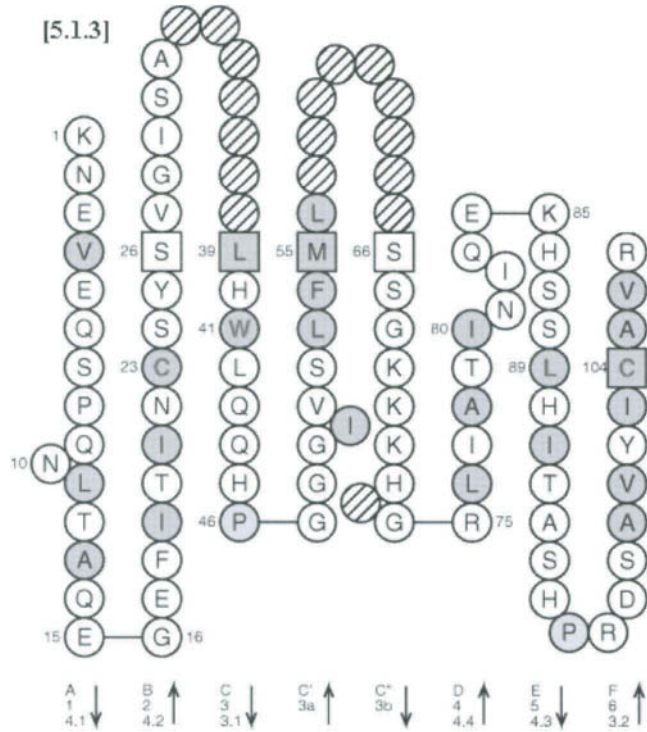
CDR2-IMGT: 1

CDR3-IMGT: 3



Collier de Perles for human TRAV41*01

Accession number: IMGT AE000661 EMBL/GenBank/DDBJ: AE000661



Genome database accession numbers

GDB:9954027 LocusLink: 28640

TRAV gene	FR1-IMGT (1-26)					CDR1-IMGT (27-38)					FR2-IMGT (39-55)					CDR2-IMGT (56-65)					FR3-IMGT (66-104)					CDR3-IMGT (105-115)				
	1	20				30					40	50			60			70	80	90	100			110						
AE000658, TRAV1-1	GQSLEQ.	PSEVTAVEGAIVQIN	CTYQ			TSGFYG.					LSWYQQHDCGAPTFLSY	NA						LDGLEET.	GRFSSFLRSRSDSYGYLLQLQ	MKDASASYFC			AVR							
AE000658, TRAV1-2	GQNIDQ.	PTEMTEGAIVQIN	CTYQ			TSGFNG.					LFWYQQHAGEAPTFLSY	NV						LDGLEEK.	GRFSSFLRSRSGYSYLLKLQ	MKDASASYLC			AVR							
AE000658, TRAV2	KDQVFQ.	PSTVASSEGAVVEIFCNHS				VSNAYN.					FFWYLHFPGCAPRLLVK							GSKPSQQ.	GRYNNMTY.	ERFSSSLLILQVREADAAVYYC			AVE							
AE000658, TRAV3	AQSVAPQEDQVNVAAEGNPLTVKCTYS					VSGNPY.					LFWYVQYPNRLGLQLLK	YITG.						DNLVKGGS.	YGFEAEFNKSGTSPHLKKPSALVSDSALYFC			AVRD								
AE000658, TRAV4	LAKTTQ.	PISMDSEYEGQEVNITCSHN				NIATNDY.					ITWYQQFPSPQGRPIIQ	G						YKTKVTN.	EVASLFIPADRKSTLSLPRVSLSDTAIVYYC			LVGD								
AE000659, TRAV5	GEDVEQS.	LFLSVREGDSSVIN	CTYT			DSSSTY.					LYWYKQEPGAGLQLLTY	IFS						NMDMKQD.	QRLTVLLNKKDKHLSLRADTQTGDSAIYFC			AES								
AE000659, TRAV6	SQKIEQNSEALNIQEGKTAITLTCTNYT					NYSPAY.					LQWYRQDPGRGPVFFLL	IRE						NEREKRK.	ERLKVTFDTTLKQSLPHITASQPADSATYLC			ALD								
AE000659, TRAV7	ENQVEHSPHFLPGPQGDVASMSTCTYS					VSRFNN.					LQWYRQNTGMGPKHLLS	MYS						AGYEKQK.	GRLNATL.	LKNGSSLYITAVQPEDSATYFC			AVD							
AE000659, TRAV8-1	AQSVSQHNHHVILSEAAASLELGCNYS					YGGTVN.					LFWYVQYPGQHLQLLLK	YFSG						DPLVKGI.	KGFEAEFIKSFSPNLRKPSVQWSDTAIEYFC			AVN								
AE000659, TRAV8-2	AQSVITQLDHSVSVSEGTVPVLLRCNYS					SSVSPS.					LFWYVQHNPKNGLQLLLK	YTSA						ATLVKGI.	NGFEAEFFKSGTSPHLTKPSAHMSDAAIEYFC			VVS								
AE000659, TRAV8-3	AQSVITQPDIIHITVSEGAASLELRCNYS					YGATPY.					LFWYVQSPGQGLQLLLK	YFSG						DTLVQGI.	KGFEAEFKRSQSSFPNLRKPSVHWSDAAEYFC			AVG								
AE000659, TRAV8-4	AQSVITQLGSHVSVSEGAALVLLRCNYS					SSVPPY.					LFWYVQYPNQGLQLLLK	YTSA						ATLVKGI.	NGFEAEFFKSGTSPHLTKPSAHMSDAAIEYFC			AVS								
X02850 , TRAV8-6	AQSVITQLDHSVVPFEAAPVELRCNYS					SSVSIV.					LFWYVQYPNQGLQLLLK	YLSG						STLVESI.	NGFEAEFFKSGTSPHLRKPSHTVSDTAIEYFC			AVS								
AE000660, TRAV8-7	TQSVITQLDGHITVSEEAPELLEKNYS					YSGVPS.					LFWYVQYSSQSLQLLLK	DLTE						ATQVQGI.	RGFEAEFFKSGTSPFLRKPSHTVSDAAEYFC			AVGDR								
AE000659, TRAV9-1	GDSVVQTEGQVLPSSEGDSLIVNCSYE					TTQYPS.					LFWYVQYPCGEPQLHLK	AMK						ANKKGRN.	KGFEAMYRKETTSPFHLEKDSVQESDSAVYFC			ALS								
AE000659, TRAV9-2	GNSVTQMEGPVTLSEAEFLITNCTYT					ATGYPS.					LFWYVQYPCGELQLLLK	ATK						ADDKGSN.	KGFEATYRKETTSPFHLEKGSVQVSDSAVYFC			ALS								
AE000659, TRAV10	KNQVEQSPQGLIILEGKNCTLCQNTYT					VSPFSN.					LRWYKQDTRGRGPVSLTI	MTF						SENTKSN.	GRYTAQLKDDTQKSSLLHITASQLSDASAYIC			VVS								
AE000659, TRAV12-1	RKEVEQDPQGLPFNVPEGATVAFNCTYS					NSASQS.					FFWYRQDCKREKPKLLMS	YV						SSGN.	ED.	GRFTAQLNRAQYSILLIRDSKLSDSATYLC			VVN							
AE000659, TRAV12-2	QKEVEQNSGPLSVPEGAIASLNCCTYS					DRGSQS.					FFWYRQYSGKSPELIMF	IY						SNQKED.	GRFTAQLNKASQYVSLIRDSQPSDSATYLC			AVN								
X06193 , TRAV12-3	QKEVEQDPGPLSVPEGAIVSLNCTYS					NSAFQY.					FMWYRQYSRKGPPELLMY	TY						SSGNKED.	GRFTAQVDKSSKYISLIRDSQPSDSATYLC			AMS								
AE000659, TRAV13-1	GENVEQHPSTLSVQEGDSAVIKCTYS					DSASNY.					FWWYKQELGKGPQLIID	IRS						NVGEKKD.	QRIAVTLNKTAKHFSLHITETQPEDSATYFC			AAS								
AE000659, TRAV13-2	GESVGLHLPLTSLVQEGDINSIINCAYS					NSASDY.					FIWYKQESGKGPPQFIID	IRS						NMDKRGQ.	QRVTVLLNKTVKHLSLQIAATQPGDSAVYFC			AEN								
M21626 , TRAV14/DV4	AQKITQTPQGMFVQKEAVFLDCTDY					TSDPSYG.					LFWYKQPSGSEMIFLIY	QGSY						DQONATE.	GRYSLNFOKARKSANLVISASQLGDSAMYFC			AMRE								
AE000660, TRAV17	SQQGEDPQALSIQEGENATMNCYSK					TSINN.					LQWYRQNSGRGLVHLIL	IRS						NEREKHS.	GRRLVTLDTSKSSSLLITASRAADTAASYFC			ALT								
AE000659, TRAV16	AORVTOPEKLLSVFEEAPVELKCNYS					YSGSP.					LFWYVOYSRORLOLLRL							HIRESEI.	KGFTA DLNKGSTSPHLKKPFAEEDSAMYYC			ADS								

TRAV gene	FR1-IMGT (1-26)			CDR1-IMGT (27-38)		FR2-IMGT (39-55)		CDR2-IMGT (56-65)		FR3-IMGT (66-104)			CDR3-IMGT (105-115)	
	1	10	20	30	40	50	60	70	80	90	100	110		
AE000660, TRAV17	SQQGEEDPQALSIQEGENATMNC	SYK	TSINN		LQWYRQNSGRGLVHLIL	IRS		NEREKHS	GRLRVTLDTSKKSSSLITASRAADTASYFC	ATD		ALR		
AE000660, TRAV18	GDSVTQTGEPVTLPERAALT	LNCTYQ	SSYSTF		LFWYVQYLNKEPELLLK	SS		ENQETDS	RGFQASPIKSDSSFHLEKPSVQLSDSAVYYC	ALR		ALR		
AE000660, TRAV19	AQKVTQAQTEISVVEKEDVTLD	CVYE	TRDTTTY		LFWYKQPPSGELVFLIR	RNSF		DEQNEIS	GRYSWNFQKSTSSFN	NTITASQVVD	SAVYFC	ALSE		
AE000660, TRAV20	EDQVTSPEALRLQEGESS	LNCSYT	VSGLRG		LFWYRQDPGKGPEFLFT	LYS		AGEEKEK	ERLKATL	..TKKESPLHITAPKPEDS	SATYLC	AVQ		
AE000660, TRAV21	KQEVTPIPAALSVPEGENLV	LNCSFT	DSAIYN		LQWFRQDPGKGLTSLLL	IQS		SQREQTS	GRNLASLDKSSGRSTLYIAASQPGDS	SATYLC	AVR			
AE000660, TRAV22	GIQVEQSPDLILQEGAN	STLRCNFS	DSVNN		LQWFHQNFQGLINLFY	I		PSGTKQN	GRLSATTVATERYSLLYISSQT	TD	SGVYFC	AVE		
AE000660, TRAV23/DV6	QQQVKQSPQSLIVQKGGISI	INCAYE	NTAFDY		FPWYQQFPFGKGPALLIA	IRP		DVSEKKE	GRFTISFNKSAKQFSLHIMDSQPGDS	SATYFC	AAS			
AE000660, TRAV24	ILNVEQSPQSLHVQEGD	STNETCSFP	SSNFYA		LHWYRWETAKSPEALFV	MTL		NGDEKKK	GRISATLNTKEGYSYLYIKGSQPEDS	SATYLC	AF			
AE000660, TRAV25	GQQVMQIPQYQHVQEGED	FTTYCNSS	TTLN		IQWYKQRFPGHPVFLIQ	LVK		SGEVKKQ	KRLTFQFGEAKNSSLHITATQTTD	DVGT	TYFC	AG		
AE000660, TRAV26-1	DAKTQ	PPSMDCAEGRAANLPCNHS	TISGNEY		VYWYRQIHSQGPQYIIH	G		LKNNETN	EMASLIITEDRKSSLTILPHATLRD	TAVYYC	IVRV			
AE000660, TRAV26-2	DAKTQ	PNSMESNEEPEVHLPCNHS	TISGTDY		IHWYRQLPSQGPYVVIH	G		LTSNVNN	RMASLAIADRKSSLTILHRATLRDA	AVYYC	ILRD			
AE000660, TRAV27	TQLLEQSPQLSTIQEGEN	LTVCNNS	SVFSS		LQWYRQEPQEGPVLLVT	VVT		GGEVKKL	KRLTFQFGDARKDSSSLHITAAQPGD	TGLYLC	AG			
AE000660, TRAV29/DV5	DQQVKQNSPQSLVQEGRI	SLNCDYT	NSMPDY		FLWYKKYPAEGPTFLIS	ISS		IKDKNED	GRFTVFLNKS	SAKHLSHIVPSQPGDS	SAVYFC	AAS		
AE000660, TRAV30	QQPV	QSPQAVILREGEDAVINCSS	KALYS		VHWYRQKHGEAPVFLMI	LLK		GGEQKGH	EKISASFNEKKQQSSSLYLTASQLSYSGTYFC	GTE				
AE000660, TRAV34	SQELEQSPQSLIVQEGK	NLTINCTSS	KTLVG		LYWYKQKYEGELIFLMM	LQK		GGEKSH	EKITAKLDEKQKQSSSLHITASQPSHAGI	YLC	GAD			
AE000660, TRAV35	GQQLNQSPQSMFIQEGED	VSMTCTSS	SIFNT		WLWYKQEPGEGPVLLIA	LYK		AGELTSN	GRLTAQFGITRKDSFLN	ISASIPSDVGI	YFC	AGQ		
AE000660, TRAV36/DV7	EDKVVQSPQLSVVHEG	DIVTLNCSYE	VTNFRS		LLWYKQEKAP	TFLFM		SGIEKKS	GRLLSILDKKELSSILNITATQTGDS	AIYLC	AVE			
AE000661, TRAV38-1	AQTVTQSQPEMSVQEAET	VTLSCTYD	TSENNYY		LFWYKQPPSRQMILVIR	QEAY		KQONATE	NRFSVNFQAKAASFSLKISDSQLGDT	AMYFC	AFMK			
AE000661, TRAV38-2/DV8	AQTVTQSQPEMSVQEAET	VTLSCTYD	TSESDYY		LFWYKQPPSRQMILVIR	QEAY		KQONATE	NRFSVNFQAKAASFSLKISDSQLGDA	AMYFC	AYRS			
AE000661, TRAV39	ELKVEQNPLFLSMQEGK	NYTIYCNYS	TTSR		LYWYRQDPGKSLESFLV	LLS		NGAVKQE	GRLMASLDTKARLSTLHITAAVHDL	SATYFC	AVD			
X73521, TRAV40	SNSVKQT	GQITVSEGASVTMNTY	STGYPT		LFWYVEYPSKPLQLLQR			ETMENS	KNFGGNI	KDKNSPIVKYSVQVSDS	SAVYYC	LLG		
AE000661, TRAV41	KNEVEQSPQNLTAQEGE	FITINCYS	VGISA		LHWLQQHPGGGIVSLFM			SSGKKKH	GRLIATINIQEKHSSSLHITASHPRDS	SAVYYC	AVR			

TRAV recombination signals

Recombination signals

Only the recombination signals of the allele *01 of each functional TRA V-REGION are shown.

TRAV gene name	V Recombination Signal (V-RS)		
	V-HEPTAMER	(bp)	V-NONAMER
TRAV1-1	CACAGTG	23	CCAAAATTC
TRAV1-2	CACGGTG	23	CCAAAATTC
TRAV2	CACAGAG	23	ACAGAAACA
TRAV3	CACACTG	23	ACACAAACT
TRAV4	CACAGTG	23	CCGTTTTC
TRAV5	CACATTG	23	ACCCAAACC
TRAV6	CACAGTA	23	ACCCAAACT
TRAV7	CACAGTA	23	ATCCAAACA
TRAV8-1	CACAGTG	23	ACACAAACT
TRAV8-2	CACAGTG	22	ACACAAGCC
TRAV8-3	CACAGTG	23	ACACAAACT
TRAV8-4	CACAGTG	22	ACATAAACC
TRAV8-6	CACAGTG	22	ACACAAACT
TRAV8-7	GACTGTG	23	ACACAAACT
TRAV9-1	CACAGTG	23	GCACAAACT
TRAV9-2	CACAGTG	23	GCACAAACT
TRAV10	CACTGTG	23	ATGCAAACC
TRAV12-1	CACAGTG	23	ACCCAAACC
TRAV12-2	CACAGTG	23	ACCCAAACC
TRAV12-3	CACAGTG	27/23	ACCCAAACC
TRAV13-1	CACATTG	23	ACACAAACC
TRAV13-2	CACATTG	23	ACCCAAACC
TRAV14/DV4	CACAGTG	23	ACAAAAGCC
TRAV16	CACAGTA	22	ACACAAACC
TRAV17	CACAGTG	23	ACGCAAACC
TRAV18	CAGAGTG	23	GCACAAACC
TRAV19	CACAGTG	23	ACAAAAACC
TRAV20	CACAGCG	23	ATCAAAACC
TRAV21	CACAGTG	23	ACCCAAACT
TRAV22	CACAGTG	23	ACACAAACC
TRAV23/DV6	CACAGTG	23	ACCCAAACC
TRAV24	CACAGTG	23	ACGCAAACC
TRAV25	CACAGTG	23	CTCCAAATC
TRAV26-1	CACACTG	23	CAATATCTC
TRAV26-2	CACAGTG	23	CAATATCTC
TRAV27	CACAGTG	23	ACCCAAACC
TRAV29/DV5	CACAGTG	23	ACTCAAACC
TRAV30	CACAGTG	23	ACTCAAACC
TRAV34	CACAGCG	23	CTCCAAACC
TRAV35	CACAGTG	23	ACTCAAAC
TRAV36/DV7	CACAGTG	23	ACTCAAATT
TRAV38-1	CACAATG	23	ACAGAAACC
TRAV38-2/DV8	CACAGTG	23	ACAGAAACC
TRAV39	CACAGTG	23	ACCCAAACC
TRAV40	CACTGTG	22	ACAAAACC
TRAV41	CACAGTG	23	ACCTAAACT

References

- ¹ Baer, R. et al. (1985) *Cell* 43, 705–713.
- ² Baer, R. et al. (1988) *EMBO J.* 7, 1661–1668.
- ³ Bernard, O. et al. (1993) *Leukemia* 7, 1645–1653.
- ⁴ Bortel, B. et al. (1992) *J. Exp. Med.* 175, 765–777.
- ⁵ Boysen, C. et al. (1996) *Immunogenetics* 44, 121–127.
- ⁶ Boysen, C. et al. (1997) unpublished.
- ⁷ Charmley, P. et al. (1994) *Immunogenetics* 39, 138–145.
- ⁸ Cornelis, F. (1992) unpublished.
- ⁹ Croce, C.M. et al. (1985) *Science* 227, 1044–1047.
- ¹⁰ Guglielmi, P. et al. (1988) *Proc. Natl Acad. Sci. USA* 85, 5634–5638.
- ¹¹ Hewitt, C.R.A. et al. (1992) *J. Exp. Med.* 175, 1493–1499.
- ¹² Hurley, C.K. et al. (1993) *J. Immunol.* 150, 1314–1324.
- ¹³ Ibberson, M.R. et al. (1995) *Genomics* 28, 131–139.
- ¹⁴ Ibberson, M.R. et al. (1998) *Immunogenetics* 47, 124–130.
- ¹⁵ Kalams, S.A. et al. (1994) *J. Exp. Med.* 179, 1261–1271.
- ¹⁶ Kimura, N. et al. (1987) *Eur. J. Immunol.* 17, 375–383.
- ¹⁷ Klein, M.H. et al. (1987) *Proc. Natl Acad. Sci. USA* 84, 6884–6888.
- ¹⁸ Korthäuer, U. et al. (1992) *Scand. J. Immunol.* 36, 855–863.
- ¹⁹ Lauzurica, P. et al. (1992) unpublished.
- ²⁰ Leiden, J.M. et al. (1986) *Immunogenetics* 24, 17–23.
- ²¹ Luria, S. et al. (1987) *EMBO J.* 6, 3307–3312.
- ²² Migone, N. et al. (1995) *Immunogenetics* 42, 323–332.
- ²³ Obata, F. et al. (1993) *Immunogenetics* 38, 67–70.
- ²⁴ Plaza, P. et al. (1993) unpublished.
- ²⁵ Pluschke, G. et al. (1991) *Eur. J. Immunol.* 21, 2749–2754.
- ²⁶ Rabbitts, T.H. et al. (1985) *EMBO J.* 4, 1461–1465.
- ²⁷ Reyburn, H. et al. (1993) *Immunogenetics* 38, 287–291.
- ²⁸ Roman-Roman, S. et al. (1991) *Eur. J. Immunol.* 21, 927–933.
- ²⁹ Santamaria, P. et al. (1993) *Immunogenetics* 38, 163–163.
- ³⁰ Satyanarayana, K. et al. (1988) *Proc. Natl Acad. Sci. USA* 85, 8166–8170.
- ³¹ Sensi, M. et al. (1991) *Melanoma Res.* 1, 261–271.
- ³² Sim, G. K. et al. (1984) *Nature* 312, 771–775.
- ³³ Tsuruta, Y. et al. (1993) *J. Immunol. Methods* 161, 721–721.
- ³⁴ Wright, J.A. et al. (1991) *Hum. Immunol.* 32, 277–283.
- ³⁵ Yanagi, Y. et al. (1985) *Proc. Natl Acad. Sci. USA* 82, 3430–3434.
- ³⁶ Yassai, M. et al. (1992) *Hum. Immunol.* 34, 279–283.
- ³⁷ Yoshikai, Y. et al. (1985) *Nature* 316, 837–840.
- ³⁸ Yoshikai, Y. et al. (1986) *J. Exp. Med.* 164, 90–103.

**THE HUMAN
T CELL RECEPTOR
TRB GENES**

This Page Intentionally Left Blank

Part 1

TRBC

Nomenclature

TRBC1: T cell receptor beta constant 1.

Definition and functionality

TRBC1 is one of the two functional genes of the TRBC group which comprises two mapped genes. TRBC1 and TRBC2 result from a recent duplication.

Gene location

TRBC1 is in the TRB locus on chromosome 7 at 7q34.

Nucleotide and amino acid sequences for human TRBC1

The nucleotide between parentheses at the beginning of exons comes from a DONOR-SPLICE (n from ngt).

The Cysteines involved in the intrachain disulfide bridges are shown with their number and letter C in bold.

N-Glycosylation sites (NXS/T, where X is different from P) are underlined.

			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
M12887 ,TRBC1*01, (EX1)	[1]	(G)AG	GAC	CTG	AAC	AGG	GTG	TTT	CCA	CCC	GAG	GTC	GCT	GTG	TTT	GAG	CCA	TCA	GAA	GCA	GAG	
M14157 ,TRBC1*01	[2]	(-)	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
(1)L36092,U66061,TRBC1*02	[3]	(-)	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
			21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
M12887 ,TRBC1*01			ATC	TCC	CAC	ACC	CAA	AAG	GCC	ACA	CTG	GTG	TGC	CTG	GCC	ACA	CTG	TTT	CCC	GAC	CAC	
M14157 ,TRBC1*01			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
(1)L36092,U66061,TRBC1*02			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
			41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
M12887 ,TRBC1*01			GTG	GAG	CTG	AGC	TGG	TGG	GTG	AAT	GGG	AAG	GAG	GTG	CAC	AGT	GGG	GTG	AGC	ACG	GAC	CCG
M14157 ,TRBC1*01			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
(1)L36092,U66061,TRBC1*02			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
			61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
M12887 ,TRBC1*01			CAG	CCC	CTC	AAG	GAG	CAG	CCC	GCC	CTC	AAT	GAC	TCC	AGA	TAC	TCG	CTG	AGC	AGC	CGC	CTG
M14157 ,TRBC1*01			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
(1)L36092,U66061,TRBC1*02			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
			81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
M12887 ,TRBC1*01			AGG	GTC	TCG	GCC	ACC	TTC	TGG	CAG	AAC	CCC	CGC	AAC	CAC	TTC	CGC	TGT	CAA	GTC	CAG	TTC
M14157 ,TRBC1*01			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
(1)L36092,U66061,TRBC1*02			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
			101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120
M12887 ,TRBC1*01			TAC	GGG	CTC	TCG	GAG	AAT	GAC	GAG	TGG	ACC	CAG	GAT	AGG	GCC	AAA	CCC	GTC	ACC	CAG	ATC
M14157 ,TRBC1*01			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
(1)L36092,U66061,TRBC1*02			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
			121	122	123	124	125	126	127	128	129											
M12887 ,TRBC1*01			GTC	AGC	GCC	GAG	GCC	TGG	GGT	AGA	GCA	G										
M14157 ,TRBC1*01			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
(1)L36092,U66061,TRBC1*02			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
			1	2	3	4	5	6														
M12887 ,TRBC1*01, (EX2)			AC	TGT	GGC	TTT	ACC	TCG	G													
M14157 ,TRBC1*01			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
(1)L36092,U66061,TRBC1*01			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---



M12887 ,TRBC1*01, (EX3)	1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20
M14157 ,TRBC1*01	V S Y Q Q G V L S A T I L Y E I L L G K
(1)L36092,U66061,TRBC1*01	TG TCC TAC CAG CAA GGG GTC CTG TCT GCC ACC ATC CTC TAT GAG ATC CTG CTA GGG AAG

M12887 ,TRBC1*01	21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36
M14157 ,TRBC1*01	A T L Y A V L V S A L V L M A M
(1)L36092,U66061,TRBC1*01	GCC ACC CTG TAT GCT GTG CTG GTC AGC GCC CTT GTG TTG ATG GCC ATG

M12887 ,TRBC1*01, (EX4)	1 2 3 4 5 6
M14157 ,TRBC1*01	V K R K D F *
(1)L36092,U66061,TRBC1*01	GTC AAG AGA AAG GAT TTC

Note:
(1) The original L36092 sequence (684 973 bp) has been split in EMBL into three sequences of 267 156 bp (U66059), 215 422 bp (U66060), and 232 650 bp (U66061); L36092 has become the 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.



Genome database accession numbers
GDB:9954029 LocusLink: 28639



References
¹ Tunnacliffe, A. et al. (1985) Proc. Natl Acad. Sci. USA 82, 5068–5072.
² Toyonaga, B. et al. (1985) Proc. Natl Acad. Sci. USA 82, 8624–8628.
³ Rowen, L. et al. (1996) Science 272, 1755–1762.



Protein display
Protein display of the TRBC1 gene is shown on page 372.

Nomenclature

TRBC2: T cell receptor beta constant 2.

Definition and functionality

TRBC2 is one of the two functional genes of the TRBC group which comprises two mapped genes. TRBC1 and TRBC2 result from a recent duplication.

Gene location

TRBC2 is in the TRB locus on chromosome 7 at 7q34.

Nucleotide and amino acid sequences for human TRBC2

The nucleotide between parentheses at the beginning of exons comes from a DONOR-SPLICE (n from ngT).

The Cysteines involved in the intrachain disulfide bridges are shown with their number and letter **C** in bold.

N-Glycosylation sites (NXS/T, where X is different from P) are underlined.

		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	
M12888	,TRBC2*01, (EX1)	[1]	(G)AG	GAC	CTG	AAA	AAC	GTG	TTC	CCA	CCC	GAG	GTC	GCT	GTG	TTT	GAG	CCA	TCA	GAA	GCA	GAG
M12510	,TRBC2*01	[2]	(-)-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
(1)L36092,U66061,TRBC2*02	[3]	(-)-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
		21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	
M12888	,TRBC2*01	ATC	TCC	CAC	ACC	CAA	AAG	GCC	ACA	CTG	GTG	TGC	CTG	GCC	ACA	GGC	TTC	TAC	CCC	GAC	CAC	
M12510	,TRBC2*01	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
(1)L36092,U66061,TRBC2*02	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
		41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	
M12888	,TRBC2*01	GTG	GAG	CTG	AGC	TGG	TGG	GTG	AAT	GGG	AAG	GAG	GTG	CAC	AGT	GGG	GTG	AGC	ACA	GAC	CCG	
M12510	,TRBC2*01	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
(1)L36092,U66061,TRBC2*02	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
		61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	
M12888	,TRBC2*01	CAG	CCC	CTC	AAG	GAG	CAG	CCC	GCC	CTC	AAT	GAC	TCC	AGA	TAC	TGC	CTG	AGC	AGC	CGC	CTG	
M12510	,TRBC2*01	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
(1)L36092,U66061,TRBC2*02	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
		81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	
M12888	,TRBC2*01	AGG	GTC	TGG	GCC	ACC	TTC	TGG	CAG	AAC	CCC	CGC	AAC	CAC	TTC	CGC	TGT	CAA	GTC	CAG	TTC	
M12510	,TRBC2*01	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
(1)L36092,U66061,TRBC2*02	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
		101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	
M12888	,TRBC2*01	TAC	GGG	CTC	TCG	GAG	AAT	GAC	GAG	TGG	ACC	CAG	GAT	AGG	GCC	AAA	CCT	GTC	ACC	CAG	ATC	
M12510	,TRBC2*01	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
(1)L36092,U66061,TRBC2*02	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
		121	122	123	124	125	126	127	128	129												
M12888	,TRBC2*01	GTC	AGC	GCC	GAG	GCC	TGG	GGT	AGA	GCA	G											
M12510	,TRBC2*01	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
(1)L36092,U66061,TRBC2*02	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
		1	2	3	4	5	6															
M12888	,TRBC2*01, (EX2)	D	C	G	F	T	S															
M12510	,TRBC2*01	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
(1)L36092,U66061,TRBC2*01	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	



```

      1  2  3  4  5  6  7  8  9 10 11 12 13 14 15 16 17 18 19 20
M12888 ,TRBC2*01, (EX3)  E  S  Y  Q  Q  G  V  L  S  A  T  I  L  Y  E  I  L  L  G  K
AG TCT TAC CAG CAA GGG GTC CTG TCT GCC ACC ATC CTC TAT GAG ATC TTG CTA GGG AAG
M12510 ,TRBC2*01      -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- --
(1)L36092,U66061,TRBC2*01      -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- --

      21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36
M12888 ,TRBC2*01      A  T  L  Y  A  V  L  V  S  A  L  V  L  M  A  M
GCC ACC TTG TAT GCC GTG CTG AGT GCC CTC GTG CTG ATG GCC ATG
M12510 ,TRBC2*01      -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- --
(1)L36092,U66061,TRBC2*01      -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- --

      1  2  3  4  5  6  7  8
M12888 ,TRBC2*01, (EX4)  V  K  R  K  D  S  R  G  *
GTC AAG AGA AAG GAT TCC AGA GGC
M12510 ,TRBC2*01      -- -- -- -- -- -- -- --
(1)L36092,U66061,TRBC2*01      -- -- -- -- -- -- -- --
```

Note:
(1) The original L36092 sequence (684973 bp) has been split in EMBL into three sequences of 267 156 bp (U66059), 215 422 bp (U66060) and 232 650 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.



Genome database accession numbers
GDB:9954031 LocusLink: 28638



References
¹ Tunnacliffe, A. et al. (1985) Proc. Natl Acad. Sci. USA 82, 5068–5072.
² Toyonaga, B. et al. (1985) Proc. Natl Acad. Sci. USA 82, 8624–8628.
³ Rowen, L. et al. (1996) Science 272, 1755–1762.



Protein display
Protein display of the TRBC2 gene is shown on page 372.

This Page Intentionally Left Blank

Part 2

TRBD

Nomenclature

T cell receptor beta diversity group.

Definition and functionality

The human TRBD group comprises two functional mapped genes, TRBD1 and TRBD2. The TRBD1 and TRBD2 genes have two or three open reading frames in both the direct and inverted orientations.

Gene location

The human TRBD genes are located in the TRB locus on chromosome 7 at 7q34. TRBD1 is upstream from the TRBJ1-1 to TRBJ1-6 gene cluster. TRBD2 is upstream from the TRBJ2-1 to TRBJ2-7 gene cluster.

Nucleotide and amino acid sequences for the human TRBD genes with nomenclature

	Direct 5' - 3' orientation	Inverted orientation
TRBD1		
T cell receptor beta diversity 1		
	<pre> G T G G G Q G D R G [1] gggacagggggc </pre>	<pre> A P C P P P V P L S gcccctgtccc </pre>
X00936 ,TRBD1*01		
TRBD2		
T cell receptor beta diversity 2		
	<pre> G T S G G G L A G G D * R G [3] gggactagcggggggg </pre>	<pre> P P R * S P P A S P P P L V ccccccgtagtccc </pre>
X02987 ,TRBD2*01		
	<pre> G T S G R G L A G G D * R E [2] gggactagcgggaagg </pre>	<pre> P S R * S P P A S P L P L V cctcccgtagtccc </pre>
M14159 ,TRBD2*02		

Recombination signals

5'D Recombination Signal (5'D-RS)			TRBD gene and allele name	3'D Recombination Signal (3'D-RS)		
5'D-NONAMER	(bp)	5'D-HEPTAMER		3'D-HEPTAMER	(bp)	3'D-NONAMER
TGTTTTTGT	12	CATTGTG	TRBD1*01	CACAATG	23	ACAAAAACC
CATTTTTGT	12	CATTGTG	TRBD2*01	CACGATG	23	ACAAAAAAC
CATTTTTGT	12	CATTGTG	TRBD2*02	CACGATG	23	ACAAAAAAC

References

- Clark, S.P. et al. (1984) Nature 311, 387-389.
- Toyonaga, B. et al. (1985) Proc. Natl Acad. Sci. USA 82, 8624-8628.
- Tunnacliffe, A. et al. (1985) Nucleic Acids Res. 13, 6651-6661.

Part 3

TRBJ

Nomenclature

T cell receptor beta joining group.

Definition and functionality

The human TRBJ group comprises 14 mapped genes of which 12-13 are functional, and 1-2 are ORF.

TRBJ2-2P is an ORF due to J-PHE replaced by Leucine in J-SEGMENT and to missing J-NONAMER.

TRBJ2-7*02 is an ORF due to J-PHE replaced by Valine in J-SEGMENT.

Gene location

The human TRBJ genes are located in the TRB locus on chromosome 7 at 7q34, upstream from the TRBC genes. Six functional TRBJ (TRBJ1-1 to TRBJ1-6) are located upstream from TRBC1, and eight TRBJ (TRBJ2-1 to TRBJ2-7) of which 6-7 are functional, are located upstream from TRBC2.

Nucleotide and amino acid sequences for the human functional or ORF TRBJ genes with nomenclature

The conserved **FGXG** motif, characteristic of the TRB J-REGION is underlined.

TRBJ1-1 T cell receptor beta 1-1		
X00936 ,TRBJ1-1*01	[1]	N T E A F <u>F G O G</u> T R L T V V TG AAC ACT GAA GCT TTC TTT GGA CAA GGC ACC AGA CTC ACA GTT GTA G
TRBJ1-2 T cell receptor beta 1-2		
X00936 ,TRBJ1-2*01	[1]	N Y G Y T <u>F G S G</u> T R L T V V CT AAC TAT GGC TAC ACC TTC GGT TCG GGG ACC AGG TTA ACC GTT GTA G
TRBJ1-3 T cell receptor beta 1-3		
M14158 ,TRBJ1-3*01	[3]	S G N T I Y <u>F G E G</u> S W L T V V C TCT GGA AAC ACC ATA TAT TTT GGA GAG GGA ACT TGG CTC ACT GTT GTA G
TRBJ1-4 T cell receptor beta 1-4		
M14158 ,TRBJ1-4*01	[3]	T N E K L F <u>F G S G</u> T Q L S V L GA ACT AAT GAA AAA CTG TTT TTT GGC AGT GGA ACC CAG CTC TCT GTC TTG G
TRBJ1-5 T cell receptor beta 1-5		
M14158 ,TRBJ1-5*01	[3]	S N Q P Q H <u>F G D G</u> T R L S I L T AGC AAT CAG CCC CAG CAT TTT GGT GAT GGG ACT CGA CTC TCC ATC CTA G
TRBJ1-6 T cell receptor beta 1-6		
M14158 ,TRBJ1-6*01	[3]	S Y N S P L H <u>F G N G</u> T R L T V T C TCC TAT AAT TCA CCC CTC CAC TTT GGG AAT GGG ACC AGG CTC ACT GTG ACA G
L36092,U66061,TRBJ1-6*02	[1,2]	-----C-----
TRBJ2-1 T cell receptor beta 2-1		
X02987 ,TRBJ2-1*01	[4]	S Y N E Q F <u>F G P G</u> T R L T V L C TCC TAC AAT GAG CAG TTC TTC GGG CCA GGG ACA CGG CTC ACC GTG CTA G
TRBJ2-2 T cell receptor beta 2-2		
X02987 ,TRBJ2-2*01	[4]	N T G E L F <u>F G E G</u> S R L T V L CG AAC ACC GGG GAG CTG TTT TTT GGA GAA GGC TCT AGG CTG ACC GTA CTG G
TRBJ2-2P T cell receptor beta 2-2P		
X02987 ,TRBJ2-2P*01	[4]	L R G A A G R <u>L G G G</u> L L V L CTG AGA GGC GCT GCT GGG CGT CTG GGC GGA GGA CTC CTG GTT CTG G
TRBJ2-3 T cell receptor beta 2-3		
X02987 ,TRBJ2-3*01	[4]	S T D T Q Y <u>F G P G</u> T R L T V L AGC ACA GAT ACG CAG TAT TTT GGC CCA GGC ACC CGG CTG ACA CTG CTC G


TRBJ2-4
T cell receptor beta 2-4

X02987 ,TRBJ2-4*01 [4] A K N I Q Y F G A G T R L S V L
A GCC AAA AAC ATT CAG TAC TTC GGC GCC GGG ACC CGG CTC TCA GTG CTG G

TRBJ2-5
T cell receptor beta 2-5

X02987 ,TRBJ2-5*01 [4] Q E T Q Y F G P G T R L L V L
AC CAA GAG ACC CAG TAC TTC GGG CCA GGC ACG CGG CTC CTG GTG CTC G

TRBJ2-6
T cell receptor beta 2-6

X02987 ,TRBJ2-6*01 [4] S G A N V L T F G A G S R L T V L
C TCT GGG GCC AAC GTC CTG ACT TTC GGG GCC GGC AGC AGG CTG ACC GTG CTG G

TRBJ2-7
T cell receptor beta 2-7

M14159 ,TRBJ2-7*01 [3] S Y E Q Y F G P G T R L T V T
C TCC TAC GAG CAG TAC TTC GGG CCG GGC ACC AGG CTC ACG GTC ACA G
X02987 ,TRBJ2-7*02 [4] - - - - - G - - - - - - - - - - - - - - -

Note:

(1) The original L36092 sequence (684 973 bp) has been split in EMBL into three sequences of 267 156 bp [U66059], 215 422 bp [U66060], and 232 650 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.

Recombination signals

J Recombination Signal (J-RS)

			TRBJ gene and allele name
J-NONAMER	(bp)	J-HEPTAMER	
GATTTTCAC	12	CACTGTG	TRBJ1-1*01
CCTTTTAGA	12	TTATGTG	TRBJ1-2*01
GGTTTGA	12	GGCTGTG	TRBJ1-3*01
GGTTTCCCT	12	TGTTGTG	TRBJ1-4*01
GGGTTTGCC	12	CACTGTG	TRBJ1-5*01
GGGTTTAT	12	AGCTGTG	TRBJ1-6*01
GGGTTTAT	12	AGCTGTG	TRBJ1-6*02
GAATTCTGG	12	CACTGTG	TRBJ2-1*01
GGTTTGCGC	12	GGCTGTG	TRBJ2-2*01
del	del	GGCTGTG	TRBJ2-2P*01 (ORF)
GGTTTTTGT	12	GGCTGTG	TRBJ2-3*01
AGTTTCTGT	12	GGCTGTG	TRBJ2-4*01
GGTTTTTGT	12	GGCCGTG	TRBJ2-5*01
GGTTTTTGC	12	GGCTGTG	TRBJ2-6*01
GGTTTGCAT	12	CTCCGTG	TRBJ2-7*01
GGTTTGCAT	12	CTCCGTG	TRBJ2-7*02 (ORF)

del: deleted

References

- Clark, S.P. et al. (1984) Nature 311, 387-389.
- Rowen, L. et al. (1996) Science 272, 1755-1762.
- Toyonaga, B. et al. (1985) Proc. Natl Acad. Sci. USA 82, 8624-8628.
- Tunnaccliffe, A. et al. (1985) Nucleic Acids Res. 13, 6651-6661.

This Page Intentionally Left Blank

Part 4

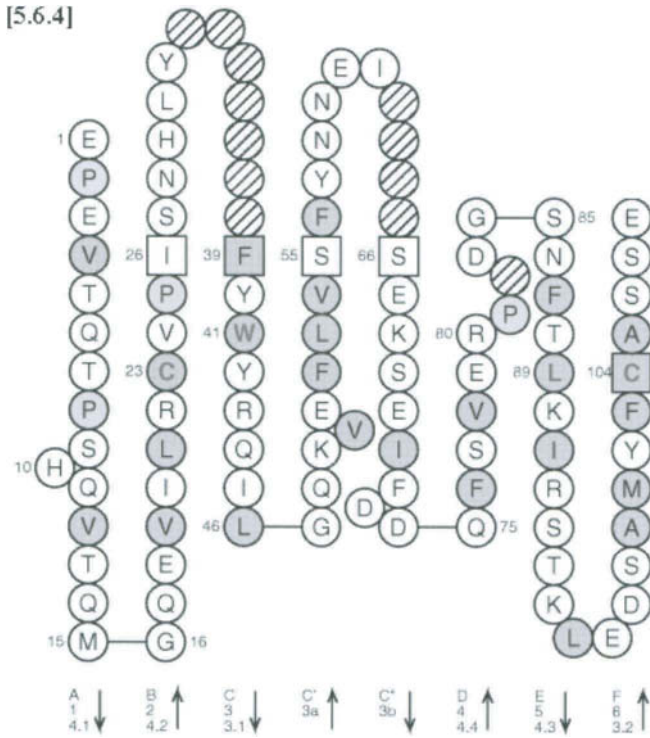
TRBV



Collier de Perles for human TRBV2*01

Accession number: IMGT L36092

EMBL/GenBank/DDBJ: L36092



Genome database accession numbers

GDB:9954067

LocusLink: 28620

Nomenclature

TRBV3-1: T cell receptor beta variable 3-1.

Definition and functionality

TRBV3-1 is the unique functional gene of the TRBV3 subgroup which comprises one or two mapped genes, depending on the haplotypes, in the TRB locus.

Gene location

TRBV3-1 is in the TRB locus on chromosome 7 at 7q34.



Nucleotide and amino acid sequences for human TRBV3-1

			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																
U07977	,TRBV3-1*01	[47]	G	A	C	A	G	C	T	T	C	C	A	A	A	T	A	C	A	G	A	A	G																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																															
L36092,U66059,TRBV3-1*01	[34]		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																
L06889	,TRBV3-1*02	[36]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																
			21	22	23	24	25	26	CDR1-IMGT										31	32	33	34	35	36	37	38	39	40																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																										
U07977	,TRBV3-1*01		A	T	T	G	A	A	A	T	C	T	G	G	C	A	T	G	A	T	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...</

#c: Rearranged cDNA

Framework and complementarity determining regions

FR1-IMGT: 26

FR2-IMGT: 17

FR3-IMGT: 37 (-2 aa: 73, 82)

CDR1-IMGT: 5

CDR2-IMGT: 6

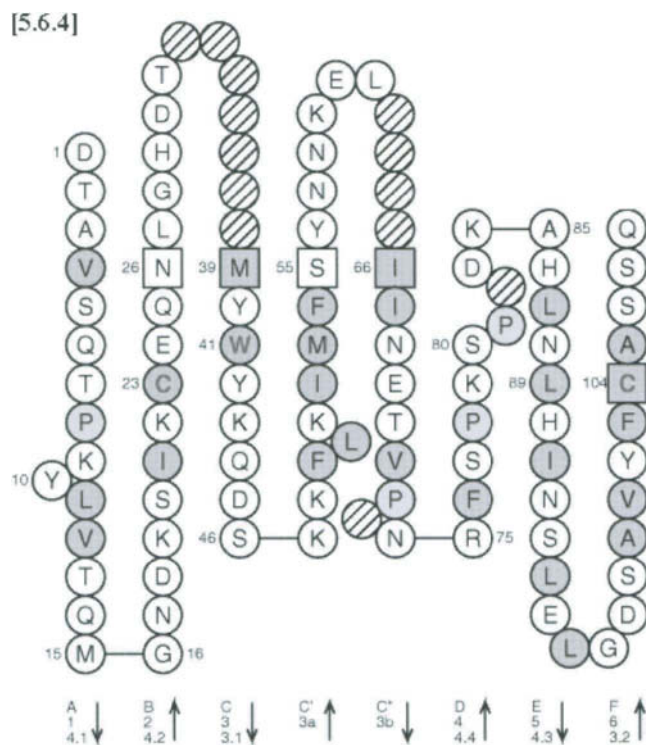
CDR3-IMGT: 4



Collier de Perles for human TRBV3-1*01

Accession number: IMGT U07977

EMBL/GenBank/DDBJ: U07977



Genome database accession numbers

GDB:9954069

LocusLink: 28619

Nomenclature

TRBV4-1: T cell receptor beta variable 4-1.

Definition and functionality

TRBV4-1 is one of the 2–3 functional genes of the TRBV4 subgroup which comprises two or three mapped genes, depending on the haplotypes, in the TRB locus.

Gene location

TRBV4-1 is in the TRB locus on chromosome 7 at 7q34.



Nucleotide and amino acid sequences for human TRBV4-1

			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	
U07977	,TRBV4-1*01	(47)	G	A	C	A	C	T	G	A	C	C	A	A	C	T	G	T	A	T	G	A	G
L36092,U66059,TRBV4-1*01	[34]																						
M13855	,TRBV4-1*02	[5]																					
			21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	
U07977	,TRBV4-1*01		L	K	C	E	Q	H	M	G	H	R	A								M	Y	
L36092,U66059,TRBV4-1*01			T	T	G	A	A	C	A	T	G	G	G	C	A	G	G	C	T		A	T	
M13855	,TRBV4-1*02																						
			41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	
U07977	,TRBV4-1*01		W	Y	K	Q	K	A	K	K	P	P	E	L	M	F	V	Y	S	Y	E	K	
L36092,U66059,TRBV4-1*01			T	G	T	A	G	C	A	A	A	C	C	G	A	G	T	C	T	A	G	A	
M13855	,TRBV4-1*02																						
			61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	
U07977	,TRBV4-1*01		C	T				S	I	N	E	S	V	P			S	R	P	S	P	C	
L36092,U66059,TRBV4-1*01																							
M13855	,TRBV4-1*02																						
			81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	
U07977	,TRBV4-1*01		P	N	S	S	L	L	N	L	H	L	H	A	L	Q	P	E	D	S	A		
L36092,U66059,TRBV4-1*01			C	C		A	A	C	T	T	A	A	C	T	C	A	C	G	C	A	G	A	
M13855	,TRBV4-1*02																						
			101	102	103	104	105	106	107	108	109												
U07977	,TRBV4-1*01		L	Y	L	C	A	S	S	Q													
L36092,U66059,TRBV4-1*01			C	T	G	T	C	G	C	A	G	A											
M13855	,TRBV4-1*02																						

#c: Rearranged cDNA

Framework and complementarity determining regions

FR1-IMGT: 26

FR2-IMGT: 17

FR3-IMGT: 37 (-2 aa: 73, 82)

CDR1-IMGT: 5

CDR2-IMGT: 6

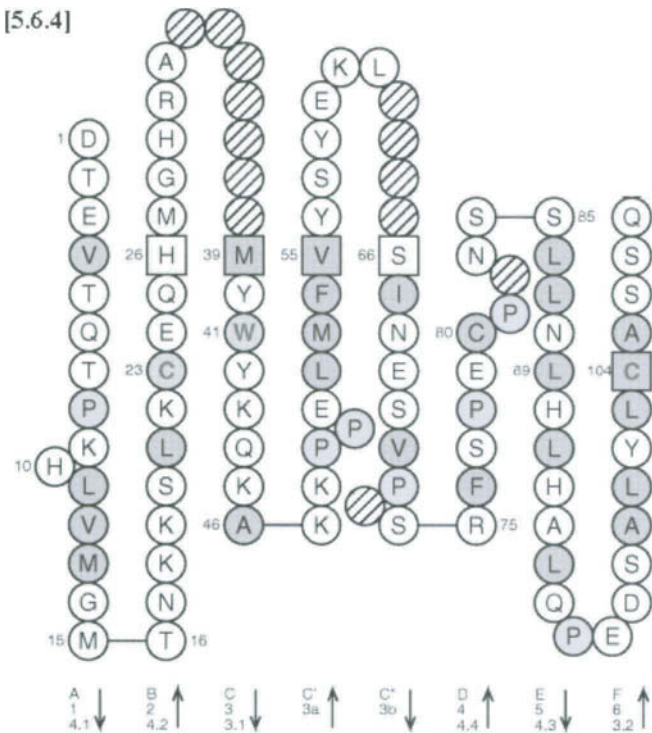
CDR3-IMGT: 4



Collier de Perles for human TRBV4-1*01

Accession number: IMGT U07977

EMBL/GenBank/DDBJ: U07977



Genome database accession numbers

GDB:9954073

LocusLink: 28617

Nomenclature

TRBV4-2: T cell receptor beta variable 4-2.

Definition and functionality

TRBV4-2 is one of the 2-3 functional genes of the TRBV4 subgroup which comprises two or three mapped genes, depending on the haplotypes, in the TRB locus.

Gene location

TRBV4-2 is in the TRB locus on chromosome 7 at 7q34.

Nucleotide and amino acid sequences for human TRBV4-2

			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20			
U07975	,TRBV4-2*01	[47]	GAA	ACG	GGA	GTT	ACG	CAG	ACA	CCA	AGA	CAC	CTG	GTC	ATG	GGA	ATG	ACA	AAT	AAG	AAG	TCT			
U07976	,TRBV4-2*01	[47]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---			
U07978	,TRBV4-2*01	[47]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---			
L36092,U66059,TRBV4-2*01	[34]		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---			
L36190	,TRBV4-2*01	[34]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---			
AF009660,TRBV4-2*01	[35]		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---			
X58811	,TRBV4-2*02	[10]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---			
			21	22	23	24	25	26	CDR1-IMGT																
U07975	,TRBV4-2*01		L	K	C	E	S	A	K	K	P	N	A												
U07976	,TRBV4-2*01		TTG	AAA	TGT	GAA	CAA	CAT	CTG	GGG	CAT	AAC	GCT	---	---	---	---	---	---	---	ATG	TAT			
U07978	,TRBV4-2*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---			
L36092,U66059,TRBV4-2*01			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---			
L36190	,TRBV4-2*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---			
AF009660,TRBV4-2*01			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---			
X58811	,TRBV4-2*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---			
			41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60			
U07975	,TRBV4-2*01		TGG	TAC	AAG	CAA	AGT	GCT	AAG	AAG	CCA	CTG	GAG	CTC	ATG	TTT	GTC	TAC	AAC	TTT	AAA	GAA			
U07976	,TRBV4-2*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---			
U07978	,TRBV4-2*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---			
L36092,U66059,TRBV4-2*01			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---			
L36190	,TRBV4-2*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---			
AF009660,TRBV4-2*01			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---			
X58811	,TRBV4-2*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---			
			61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80			
U07975	,TRBV4-2*01		Q					T	E	N	N	S	V	P		S	R	F	S	P	E	C			
U07976	,TRBV4-2*01		CAG	---	---	---	---	ACT	GAA	AAC	AAC	AGT	GTG	CCA	---	AGT	CGC	TTC	TCA	CCT	GAA	TGC			
U07978	,TRBV4-2*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---			
L36092,U66059,TRBV4-2*01			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---			
L36190	,TRBV4-2*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---			
AF009660,TRBV4-2*01			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---			
X58811	,TRBV4-2*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---			
			81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100			
U07975	,TRBV4-2*01		P					S	H	L	F	L	H	L	H	T	L	Q	P	E	D	S			
U07976	,TRBV4-2*01		CCC	---	---	AAC	AGC	TCT	CAC	TTA	TTC	CTT	CAC	CTA	CAC	ACC	CTG	CAG	CCA	GAA	GAC	TCG			
U07978	,TRBV4-2*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---			
L36092,U66059,TRBV4-2*01			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---			
L36190	,TRBV4-2*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---			
AF009660,TRBV4-2*01			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---			
X58811	,TRBV4-2*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---			



		CDR3-IMGT									
		101	102	103	104	105	106	107	108	109	
		L	Y	L	C	A	S	S	Q		
		CTG	TAT	CTC	TGT	GCC	AGC	AGC	CAA	GA	
U07975	,TRBV4-2*01										
U07976	,TRBV4-2*01										
U07978	,TRBV4-2*01										
L36092,U66059,TRBV4-2*01											
L36190	,TRBV4-2*01										
AF009660,TRBV4-2*01											
X59811	,TRBV4-2*02						T				#c
							C				

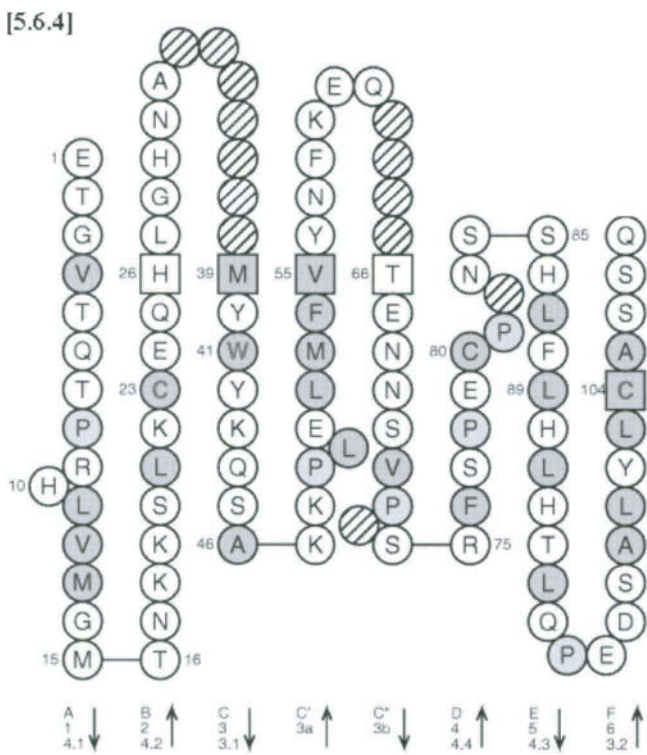
#c: Rearranged cDNA

Framework and complementarity determining regions

FR1-IMGT: 26	CDR1-IMGT: 5
FR2-IMGT: 17	CDR2-IMGT: 6
FR3-IMGT: 37 (-2 aa: 73, 82)	CDR3-IMGT: 4

Collier de Perles for human TRBV4-2*01

Accession number: IMGT U07975 EMBL/GenBank/DDBJ: U07975



Genome database accession numbers

GDB:9954075 LocusLink: 28616



Framework and complementarity determining regions

FR1-IMGT: 26

CDR1-IMGT: 5

FR2-IMGT: 17

CDR2-IMGT: 6

FR3-IMGT: 37 (-2 aa: 73, 82)

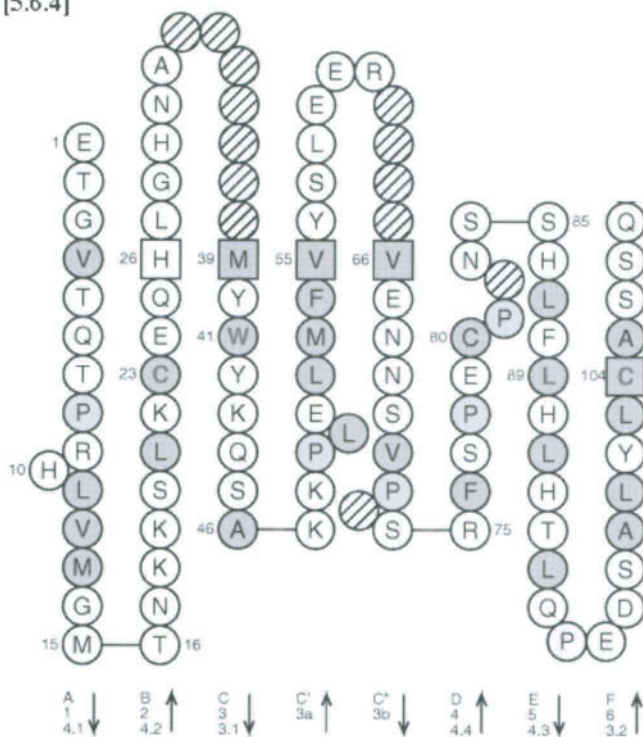
CDR3-IMGT: 4

Collier de Perles for human TRBV4-3*01

Accession number: IMGT U07978

EMBL/GenBank/DDBJ: U07978

[5.6.4]



Genome database accession numbers

GDB:9954077

LocusLink: 28615

Nomenclature

TRBV5-1: T cell receptor beta variable 5-1.

Definition and functionality

TRBV5-1 is one of the five functional genes of the TRBV5 subgroup which comprises eight mapped genes in the TRB locus.

Gene location

TRBV5-1 is in the TRB locus on chromosome 7 at 7q34.

Nucleotide and amino acid sequences for human TRBV5-1



```

1   2   3   4   5   6   7   8   9   10  11  12  13  14  15  16  17  18  19  20
L36092,U66059,TRBV5-1*01 [34] K A G V T Q T P R Y L I K T R G Q Q V T
AAG GCT GGA GTC ACT CAA ACT CCA AGA TAT CTG ATC AAA ACG AGA GGA CAG CAA GTG ACA
R                                     H
M14271 ,TRBV5-1*02  -G- --- --G- --- --- --- C- --- --- ---

                                CDR1-IMGT
21  22  23  24  25  26  27  28  29  30  31  32  33  34  35  36  37  38  39  40
L36092,U66059,TRBV5-1*01 L S C S P I S G H R S
CTG AGC TGC TCC CCT ATC TCT GGG CAT AGG AGT ... .. . GTA TCC
G
M14271 ,TRBV5-1*02  --- G- --- --- --- --- --- --- --- ---

                                CDR2-
41  42  43  44  45  46  47  48  49  50  51  52  53  54  55  56  57  58  59  60
L36092,U66059,TRBV5-1*01 W Y Q Q T P G Q G L Q F L F E Y F S R T
TGG TAC CAA CAG ACC CCA GGA CAG GGC CTT CAG TTC CTC TTT GAA TAC TTC AGT GAG ACA
L
M14271 ,TRBV5-1*02  --- T- --- --- --- --- --- --- --- ---

IMGT
61  62  63  64  65  66  67  68  69  70  71  72  73  74  75  76  77  78  79  80
L36092,U66059,TRBV5-1*01 Q R N K G N F P G R F S G R Q
CAG ... .. . AGA AAC AAA GGA AAC TTC CCT ... GST CGA TTC TCA GGG CGC CAG
L
M14271 ,TRBV5-1*02  --- ... .. . --- --- --- T- ... .. .

81  82  83  84  85  86  87  88  89  90  91  92  93  94  95  96  97  98  99  100
L36092,U66059,TRBV5-1*01 F S N S R S E M N V S T L E L G D S A
TTC ... TCT AAC TCT CGC TCT GAG ATG AAT GTG AGC ACC TTG CAG GTG GGG GAC TCG GCC
... .. .

                                CDR3-IMGT
101 102 103 104 105 106 107 108 109
L36092,U66059,TRBV5-1*01 L Y L C A S S L
CTT TAT CTT TGC GCC AGC AGC TTG G
A
M14271 ,TRBV5-1*02  --- ... .. . GCT TGC #c

```

#c: Rearranged cDNA

Framework and complementarity determining regions

FR1-IMGT: 26

FR2-IMGT: 17

FR3-IMGT: 37 [-2 aa: 73, 82]

CDR1-IMGT: 5

CDR2-IMGT: 6

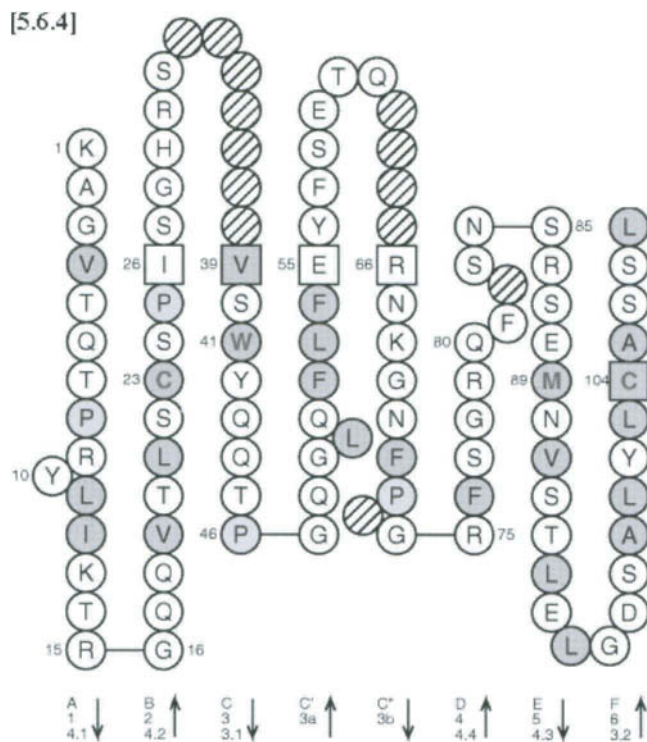
CDR3-IMGT: 4



Collier de Perles for human TRBV5-1*01

Accession number: IMGT L36092

EMBL/GenBank/DDBJ: L36092

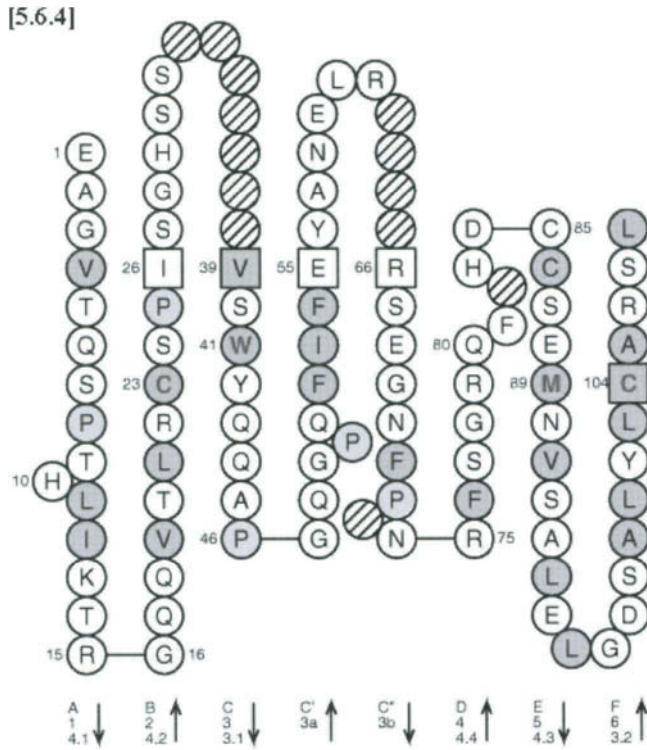


Genome database accession numbers

GDB:9954079

LocusLink: 28614

EMBL/GenBank/DDBJ: X61439



Genome database accession numbers

GDB:9954083

LocusLink: 28612

Nomenclature

TRBV5-4: T cell receptor beta variable 5-4.

Definition and functionality

TRBV5-4 is one of the five functional genes of the TRBV5 subgroup which comprises eight mapped genes in the TRB locus.

Gene location

TRBV5-4 is in the TRB locus on chromosome 7 at 7q34.



Nucleotide and amino acid sequences for human TRBV5-4

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
L36092,U66060,TRBV5-4*01	E	T	G	V	T	Q	S	P	T	H	L	I	K	T	R	G	D	Q	V	T
AF009663,TRBV5-4*01	GAG	ACT	GGA	GTC	ACC	CAA	AGT	CCC	ACA	CAC	CTG	ATC	AAA	ACG	AGA	GGA	CAG	CAA	GTG	ACT
AF009662,TRBV5-4*01	[35]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X57615,TRBV5-4*02	[35]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
S50547,TRBV5-4*03	[43]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X58804,TRBV5-4*04	[10]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
L36092,U66060,TRBV5-4*01	L	R	C	S	S	Q	S	G	H	N	T	...	...	...	...	...	...	...	V	S
AF009663,TRBV5-4*01	CTG	AGA	TGC	TCT	TCT	CAG	TCT	GGG	CAC	AAC	ACT	...	...	...	...	...	...	...	GTG	TCC
AF009662,TRBV5-4*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X57615,TRBV5-4*02	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
S50547,TRBV5-4*03	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X58804,TRBV5-4*04	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
L36092,U66060,TRBV5-4*01	W	Y	Q	Q	A	L	G	Q	G	P	Q	P	I	F	Q	Y	Y	R	E	E
AF009663,TRBV5-4*01	TGG	TAC	CAA	CAG	GCC	CTG	GGT	CAG	GGA	CCC	CAG	TTT	ATC	TTT	CAG	TAT	TAT	AGG	GAG	GAA
AF009662,TRBV5-4*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X57615,TRBV5-4*02	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
S50547,TRBV5-4*03	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X58804,TRBV5-4*04	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
L36092,U66060,TRBV5-4*01	E	G	...	...	...	AAT	GCC	AGA	GGA	AAC	TTC	CCT	...	CCT	AGA	TTC	TCA	GGT	CTC	CAG
AF009663,TRBV5-4*01	GAG	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
AF009662,TRBV5-4*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X57615,TRBV5-4*02	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
S50547,TRBV5-4*03	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X58804,TRBV5-4*04	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
L36092,U66060,TRBV5-4*01	F	P	N	Y	S	S	E	L	N	V	N	N	A	L	E	L	D	P	S	A
AF009663,TRBV5-4*01	TTC	...	CCT	AAT	TAT	AGC	TCT	GAG	CTG	AAT	GTC	AAC	GCC	TTG	GAG	CTG	GAC	GAC	TCG	GCC
AF009662,TRBV5-4*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X57615,TRBV5-4*02	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
S50547,TRBV5-4*03	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X58804,TRBV5-4*04	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---



	CDR3-IMGT									
	101	102	103	104	105	106	107	108	109	
L36092,U66060,TRBV5-4*01	L	Y	L	C	A	S	S	L		
AF009663,TRBV5-4*01	CTG	TAT	CTC	TGT	GCC	AGC	AGC	TTG	G	
AF009662,TRBV5-4*01	---	---	---	---	---	---	---	---	---	
X57615,TRBV5-4*02	---	---	---	---	---	---	---	---	---	#c
S50547,TRBV5-4*03	---	---	---	---	---	---	---	---	---	#
X58804,TRBV5-4*04	---	---	---	---	---	---	---	---	---	#c

#: Rearranged
#c: Rearranged cDNA

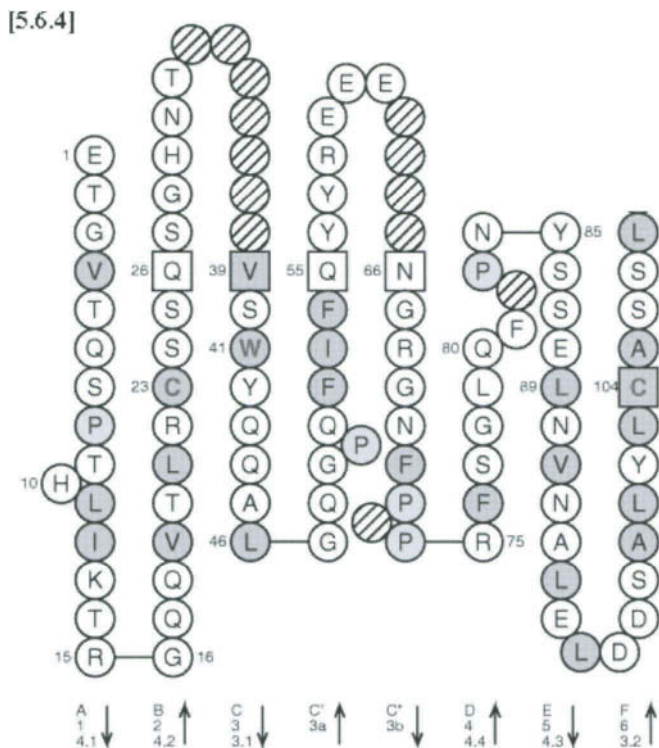
Framework and complementarity determining regions

FR1-IMGT: 26
FR2-IMGT: 17
FR3-IMGT: 37 (-2 aa: 73, 82)

CDR1-IMGT: 5
CDR2-IMGT: 6
CDR3-IMGT: 4

Collier de Perles for human TRBV5-4*01

Accession number: IMGT L36092 EMBL/GenBank/DBJ: L36092



Genome database accession numbers

GDB:9954085 LocusLink: 28611

Nomenclature

TRBV5-5: T cell receptor beta variable 5-5.

Definition and functionality

TRBV5-5 is one of the five functional genes of the TRBV5 subgroup which comprises eight mapped genes in the TRB locus.

Gene location

TRBV5-5 is in the TRB locus on chromosome 7 at 7q34.

Nucleotide and amino acid sequences for human TRBV5-5



		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
L36092,U66060,TRBV5-5*01	[34]	D	A	G	V	T	Q	S	P	T	H	L	I	K	T	R	G	Q	Q	V	T
		GAC	GCT	GGA	GTC	ACC	CAA	AGT	CCC	ACA	CAC	CTG	ATC	AAA	ACG	AGA	GGA	CAG	CAA	GTG	ACT
AF009663,TRBV5-5*01	[35]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X57611,TRBV5-5*02	[31]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	H	---
X58801,TRBV5-5*03	[10]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	C	---

		21	22	23	24	25	26	CDR1-IMGT										39	40
		L	R	C	S	P	I	S	G	H	K	S	...	...	...	...	V	S	
L36092,U66060,TRBV5-5*01		CTG	AGA	TGC	TCT	CCT	ATC	TCT	GGG	CAC	AAG	AGT	...	...	...	...	GTG	TCC	
AF009663,TRBV5-5*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
X57611,TRBV5-5*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
X58801,TRBV5-5*03		---	---	---	---	---	---	E	---	---	---	---	---	---	---	---	---	---	

		41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	CDR2-				
		W	Y	Q	Q	V	L	G	G	G	P	Q	F	I	F	Q	Y	Y	E	K	E
L36092,U66060,TRBV5-5*01		TGG	TAC	CAA	CAG	GTC	CTG	GGT	CAG	GGG	CCC	CAG	TTT	ATC	TTT	CAG	TAT	TAT	GAG	AAA	GAA
AF009663,TRBV5-5*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X57611,TRBV5-5*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X58801,TRBV5-5*03		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

		IMGT										61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
		E	R	G	R	G	N	F	P	P	...	D	R	F	S	A	R	Q	...	...	...	...	...	...	...	...	...	...	...	...	
L36092,U66060,TRBV5-5*01		GAG	...	...	...	...	AGA	GGA	AGA	GGA	AAC	TTC	CCT	...	GAT	CGA	TTC	TCA	GCT	CGC	CAG	...	...	...	...	...	...	...	...	...	
AF009663,TRBV5-5*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X57611,TRBV5-5*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X58801,TRBV5-5*03		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

		81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
		P	P	N	Y	S	S	E	L	N	V	N	A	L	L	L	G	D	S	A	
L36092,U66060,TRBV5-5*01		TTC	...	CCT	AAC	TAT	AGC	TCT	GAG	CTG	AAT	GTG	AAC	GCC	TTC	TTG	CTG	GGG	GAC	TGC	GCC
AF009663,TRBV5-5*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X57611,TRBV5-5*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X58801,TRBV5-5*03		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

		CDR3-IMGT										101	102	103	104	105	106	107	108	109
		L	Y	L	C	A	S	S	L	...	...	...	...	...	...	...	...	...	...	...
L36092,U66060,TRBV5-5*01		CTG	TAT	CTC	TGT	GCC	AGC	AGC	TTC	G	...	...	...	...	...	...	...	...	...	...
AF009663,TRBV5-5*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X57611,TRBV5-5*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X58801,TRBV5-5*03		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

#c: Rearranged cDNA

Framework and complementarity determining regions

FR1-IMGT: 26

FR2-IMGT: 17

FR3-IMGT: 37 (-2 aa: 73, 82)

CDR1-IMGT: 5

CDR2-IMGT: 6

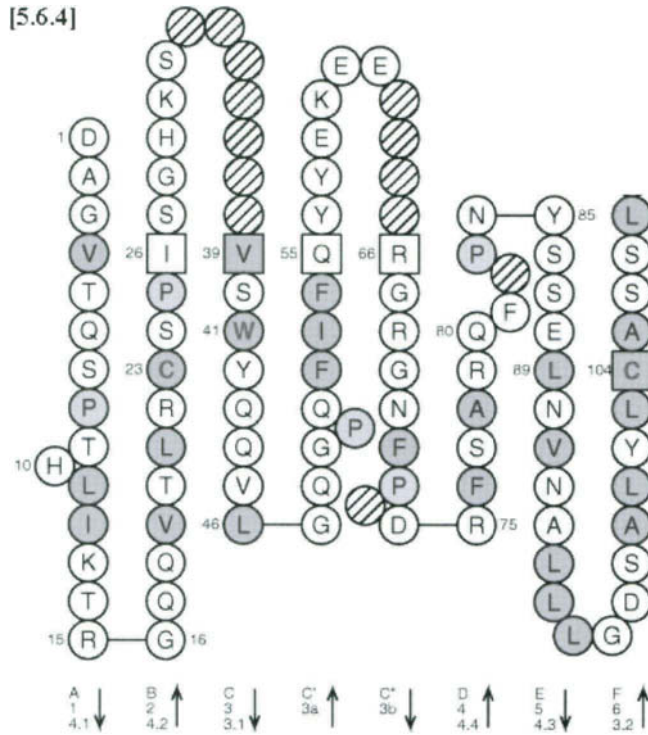
CDR3-IMGT: 4



Collier de Perles for human TRBV5-5*01

Accession number: IMGT L36092

EMBL/GenBank/DDBJ: L36092



Genome database accession numbers

GDB:9954087

LocusLink: 28610

Nomenclature

TRBV5-6: T cell receptor beta variable 5-6.

Definition and functionality

TRBV5-6 is one of the five functional genes of the TRBV5 subgroup which comprises eight mapped genes in the TRB locus.

Gene location

TRBV5-6 is in the TRB locus on chromosome 7 at 7q34.

Nucleotide and amino acid sequences for human TRBV5-6

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
L36092.U66060,TRBV5-6*01 [34]	D	A	G	V	T	Q	S	P	T	H	L	I	R	T	R	G	Q	Q	V	T
AF009663,TRBV5-6*01 [35]	GAC	GCT	GGA	GTC	ACC	CAA	AGT	CCC	ACA	CAC	CTG	ATC	AAA	ACG	AGA	GGA	CAG	CAA	GTG	ACT
	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
L36092.U66060,TRBV5-6*01	L	R	C	S	P	K	S	G	H	D	T								V	S
AF009663,TRBV5-6*01	CTG	AGA	TGC	TCT	CCT	AAG	TCT	GGG	CAT	GAC	ACT	...	...	...	...	...	...	...	GTG	TCC
	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
L36092.U66060,TRBV5-6*01	W	Y	Q	Q	A	L	G	Q	G	P	Q	F	I	F	Q	Y	Y	E	E	E
AF009663,TRBV5-6*01	TGG	TAC	CAA	CAG	GCC	CTG	GGT	CAG	GGG	CCC	CAG	TTT	ATC	TTF	CAG	TAT	TAT	GAG	GAG	GAA
	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
L36092.U66060,TRBV5-6*01	E					R	Q	R	G	N	F	P		D	R	F	S	G	H	Q
AF009663,TRBV5-6*01	GAG	...	...	...	...	AGA	CAG	AGA	GGC	AAC	TTC	CCT	...	GAT	CGA	TTC	TCA	GGT	CAC	CAG
	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
L36092.U66060,TRBV5-6*01	F		P	N	Y	S	S	E	L	N	V	N	A	L	L	L	G	D	S	A
AF009663,TRBV5-6*01	TTC	...	CCT	AAC	TAT	AGC	TCT	GAG	CTG	AAT	GTG	AAC	GCC	TTG	TTG	CTG	GGG	GAC	TCG	GCC
	101	102	103	104	105	106	107	108	109											
L36092.U66060,TRBV5-6*01	L	Y	L	C	A	S	S	L												
AF009663,TRBV5-6*01	CTC	TAT	CTC	TGT	GCC	AGC	AGC	TTG	G											

Framework and complementarity determining regions

FR1-IMGT: 26

FR2-IMGT: 17

FR3-IMGT: 37 (-2 aa: 73, 82)

CDR1-IMGT: 5

CDR2-IMGT: 6

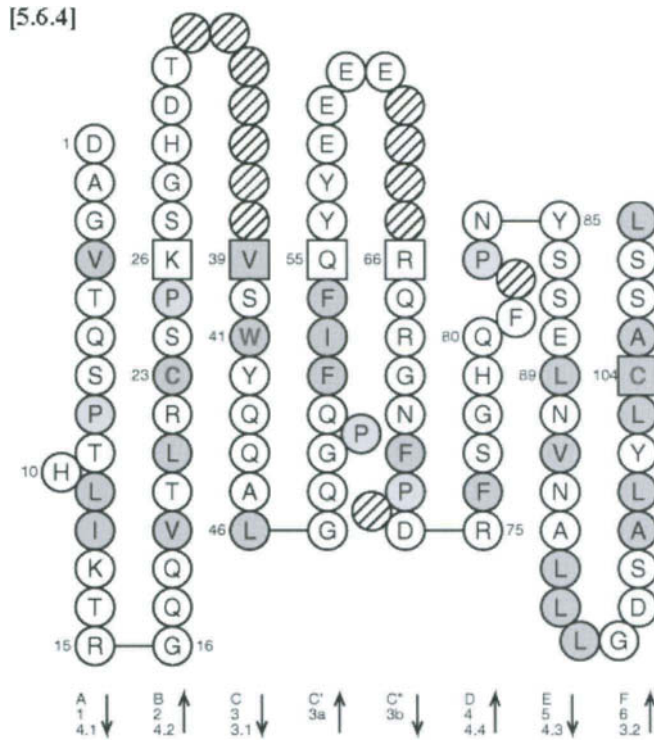
CDR3-IMGT: 4



Collier de Perles for human TRBV5-6*01

Accession number: IMGT L36092

EMBL/GenBank/DDBJ: L36092



Genome database accession numbers

GDB:9954089

LocusLink: 28609

Nomenclature

TRBV5-7: T cell receptor beta variable 5-7.

Definition and functionality

TRBV5-7 is an ORF due to the CONSERVED-TRP (tgg) of the V-EXON, being replaced by a Serine (tcg). TRBV5-7 belongs to the TRBV5 subgroup which comprises eight mapped genes, of which five are functional in the TRB locus.

Gene location

TRBV5-7 is in the TRB locus on chromosome 7 at 7q34.

Nucleotide and amino acid sequences for human TRBV5-7



		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
L36092,U66060,TRBV5-7*01	[34]	D	A	G	V	T	Q	S	P	T	H	L	I	K	T	R	G	Q	H	V	T
		GAC	GCT	GGA	GTG	ACC	CAA	AGT	CCC	ACA	CAC	CTG	ATC	AAA	ACG	AGA	GGA	CAG	CAC	GTG	ACT
AF009663,TRBV5-7*01	[35]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L26226,TRBV5-7*01	[44]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
L36092,U66060,TRBV5-7*01		L	R	C	S	P	I	S	G	H	T	S								V	S
		CTG	AGA	TGC	TCT	CCT	ATC	TCT	GGG	CAC	ACC	AGT	...	...	...	...	...	...	...	GTG	TCC
AF009663,TRBV5-7*01		---	---	---	---	---	---	---	---	---	---	---	...	...	...	...	...	...	...	---	---
L26226,TRBV5-7*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
L36092,U66060,TRBV5-7*01		S	Y	Q	Q	A	L	G	Q	G	P	Q	F	T	F	Q	Y	V	E	K	E
		TGG	TAC	CAA	CAG	GCC	CTG	GGT	CAG	GGG	CCC	CAG	TTT	ATC	TTT	CAG	TAT	TAT	GAG	AAA	GAA
AF009663,TRBV5-7*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L26226,TRBV5-7*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
L36092,U66060,TRBV5-7*01		E					R	G	R	G	N	F	P		D	Q	F	S	G	H	Q
		GAG	...	...	...	...	AGA	GGA	AGA	GGA	AAC	TTC	CCT	...	GAT	CAA	TTC	TCA	GGT	CAC	CAG
AF009663,TRBV5-7*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L26226,TRBV5-7*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
L36092,U66060,TRBV5-7*01		F		P	N	Y	S	S	E	L	N	V	N	A	L	L	G	D	S	A	
		TTC	...	CCT	AAC	TAT	AGC	TCT	GAG	CTG	AAT	GTG	AAC	GCC	TTG	TTG	CTA	GGG	GAC	TCG	GCC
AF009663,TRBV5-7*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L26226,TRBV5-7*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		101	102	103	104	105	106	107	108	109											
L36092,U66060,TRBV5-7*01		L	Y	L	C	A	S	S													
		CTC	TAT	CTC	TGT	GCC	AGC	AGC	TTG	G											
AF009663,TRBV5-7*01		---	---	---	---	---	---	---	---	---											
L26226,TRBV5-7*01		---	---	---	---	---	---	---	---	---											

°: Genomic DNA, but not known as being germline or rearranged

Framework and complementarity determining regions

FR1-IMGT: 26

FR2-IMGT: 17

FR3-IMGT: 37 (-2 aa: 73, 82)

CDR1-IMGT: 5

CDR2-IMGT: 6

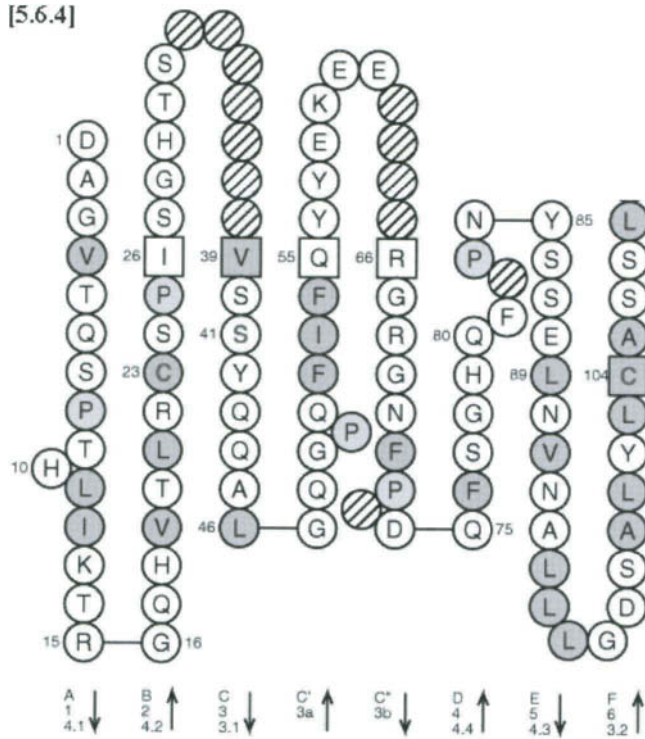
CDR3-IMGT: 4



Collier de Perles for human TRBV5-7*01

Accession number: IMGT L36092

EMBL/GenBank/DDBJ: L36092



Genome database accession numbers

GDB:9954091

LocusLink: 28608

Nomenclature

TRBV5-8: T cell receptor beta variable 5-8.

Definition and functionality

TRBV5-8 is one of the five functional genes of the TRBV5 subgroup which comprises eight mapped genes in the TRB locus.

Gene location

TRBV5-8 is in the TRB locus on chromosome 7 at 7q34.

Nucleotide and amino acid sequences for human TRBV5-8

[illegible]

#c: Rearranged cDNA

Framework and complementarity determining regions

FR1-IMGT: 26
FR2-IMGT: 17
FR3-IMGT: 37 (-2 aa: 73.82)

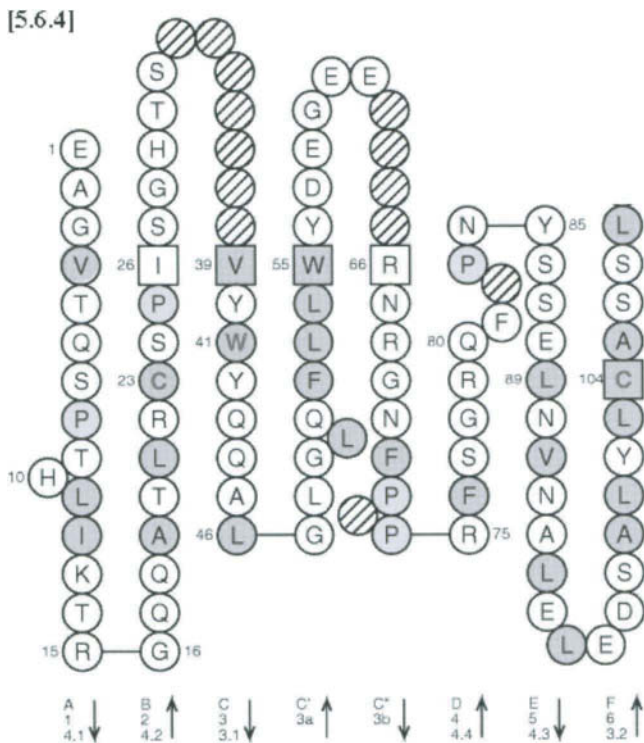
CDR1-IMGT: 5
CDR2-IMGT: 6
CDR3-IMGT: 4



Collier de Perles for human TRBV5-8*01

Accession number: IMGT L36092

EMBL/GenBank/DDBJ: L36092



Genome database accession numbers

GDB:9954093

LocusLink: 28607

Nomenclature

TRBV6-1: T cell receptor beta variable 6-1.

Definition and functionality

TRBV6-1 is one of the 5–7 functional genes of the TRBV6 subgroup which comprises 8–9 mapped genes, depending on the haplotypes, in the TRB locus.

Gene location

TRBV6-1 is in the TRB locus on chromosome 7 at 7q34.

Nucleotide and amino acid sequences for human TRBV6-1

[illegible]

Framework and complementarity determining regions

FR1-IMGT: 26

FR2-IMGT: 17

FR3-IMGT: 37 (-2 aa: 73, 82)

CDR1-IMGT: 5

CDR2-IMGT: 6

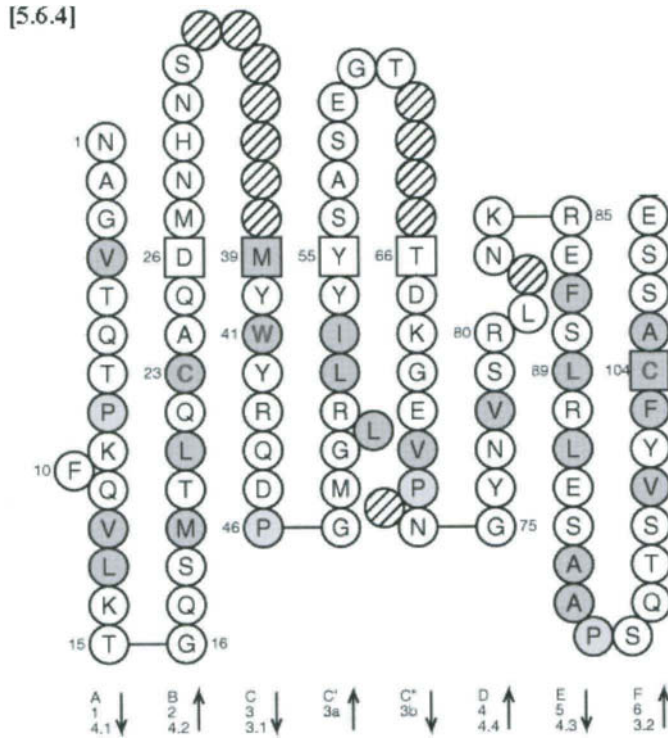
CDR3-IMGT: 4



Collier de Perles for human TRBV6-1*01

Accession number: IMGT X61446

EMBL/GenBank/DDBJ: X61446



Genome database accession numbers

GDB:9954095

LocusLink: 28606

Nomenclature

TRBV6-2: T cell receptor beta variable 6-2.

Definition and functionality

TRBV6-2 is a functional gene (allele *01) or a pseudogene (alleles *02 and *03). TRBV6-2 belongs to the TRBV6 subgroup which comprises 8–9 mapped genes, of which 5–7 are functional, depending on the haplotypes, in the TRB locus.

TRBV6-2*02 and TRBV6-2*03 are pseudogenes due to a 1 nt DELETION in codon 49, leading to a frameshift.

Gene location

TRBV6-2 is in the TRB locus on chromosome 7 at 7q34.

Nucleotide and amino acid sequences for human TRBV6-2



		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	
		N	A	G	V	T	Q	T	P	K	F	R	G	V	L	K	T	G	Q	S	M	T
X61445	,TRBV6-2*01	[26]	AAT	GCT	GGT	GTC	ACT	CAG	ACC	CCA	AAA	TTC	CGG	GTC	CTG	AAG	ACA	GGA	CAG	AGC	ATG	ACA
U07975	,TRBV6-2*01	[47]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U07976	,TRBV6-2*01	[47]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U07978	,TRBV6-2*01	[47]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L36092,U66059,TRBV6-2*01	[34]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L36190	,TRBV6-2*01	[34]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
AF009660,TRBV6-2*01	[35]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X75418	,TRBV6-2*01	[20]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X75419	,TRBV6-2*01	[20]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M31347	,TRBV6-2*02	[17]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
[45]	,TRBV6-2*03	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

		21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
		L	L	C	A	Q	D	M	N	H	E	Y								M	Y
X61445	,TRBV6-2*01	CTG	CTG	TGT	GCC	CAG	GAT	ATG	AAC	CAT	GAA	TAC	...	...	...	...	...	...	...	ATG	TAC
U07975	,TRBV6-2*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U07976	,TRBV6-2*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U07978	,TRBV6-2*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L36092,U66059,TRBV6-2*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L36190	,TRBV6-2*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
AF009660,TRBV6-2*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X75418	,TRBV6-2*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X75419	,TRBV6-2*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M31347	,TRBV6-2*02	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
[45]	,TRBV6-2*03	---	---	---	---	A	---	---	---	---	---	G	---	---	---	---	---	---	---	C	---

		41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
		W	Y	R	Q	D	P	G	M	G	L	R	L	I	H	Y	S	V	G	E	G
X61445	,TRBV6-2*01	TGG	TAT	CGA	CAA	GAC	CCA	GGC	ATG	GGG	CTG	AGG	CTG	ATT	CAT	TAC	TCA	GTT	GGT	GAG	GGT
U07975	,TRBV6-2*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U07976	,TRBV6-2*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U07978	,TRBV6-2*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L36092,U66059,TRBV6-2*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L36190	,TRBV6-2*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
AF009660,TRBV6-2*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X75418	,TRBV6-2*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X75419	,TRBV6-2*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M31347	,TRBV6-2*02	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
[45]	,TRBV6-2*03	---	---	---	---	---	---	A	---	---	---	---	---	---	---	---	---	---	---	---	---



		IMGT																															
		61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80												
		T	A	K	G	E	V	P	D	G	Y	N	V	S	R																		
X61445	,TRBV6-2*01	ACA	...	...	...	...	ACT	GCC	AAA	GGA	GAG	GTC	CCT	...	GAT	GGC	TAC	AAT	GTC	TCC	AGA												
U07975	,TRBV6-2*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---												
U07976	,TRBV6-2*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---												
U07978	,TRBV6-2*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---												
L36092,U66059,TRBV6-2*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---												
L36190	,TRBV6-2*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---												
AF009660,TRBV6-2*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---												
X75418	,TRBV6-2*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---												
X75419	,TRBV6-2*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---												
M31347	,TRBV6-2*02	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---												
[45]	,TRBV6-2*03	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---												
		81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100												
		L	K	K	Q	N	F	L	L	G	L	E	S	S	A	A	P	S	Q	T	S												
X61445	,TRBV6-2*01	TTA	...	AAA	AAA	CAG	AAT	TTC	CTG	CTG	GGG	TTG	GAG	TCG	GCT	GCT	CCC	TCC	CAA	ACA	TCT												
U07975	,TRBV6-2*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---												
U07976	,TRBV6-2*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---												
U07978	,TRBV6-2*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---												
L36092,U66059,TRBV6-2*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---												
L36190	,TRBV6-2*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---												
AF009660,TRBV6-2*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---												
X75418	,TRBV6-2*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---												
X75419	,TRBV6-2*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---												
M31347	,TRBV6-2*02	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---												
[45]	,TRBV6-2*03	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---												

(in the sequence): Frameshift
#: Rearranged
#g: Rearranged genomic DNA

Framework and complementarity determining regions

FR1-IMGT: 26

FR2-IMGT: 17

FR3-IMGT: 37 (-2 aa: 73, 82)

CDR1-IMGT: 5

CDR2-IMGT: 6

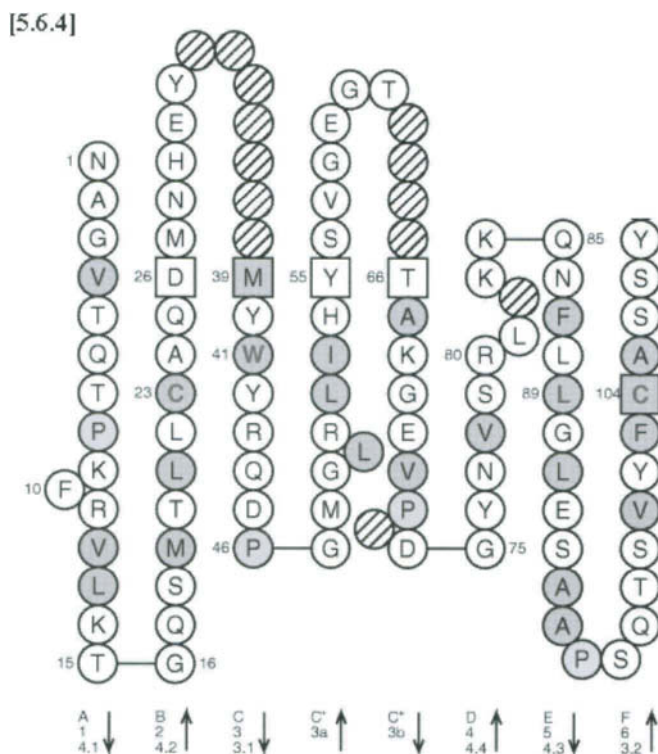
CDR3-IMGT: 4



Collier de Perles for human TRBV6-2*01

Accession number: IMGT X61445

EMBL/GenBank/DDBJ: X61445



Nomenclature

TRBV6-3: T cell receptor beta variable 6-3.

Definition and functionality

TRBV6-3 is one of the 5–7 functional genes which may or may not be present due to a polymorphism by insertion/deletion. TRBV6-3 belongs to the TRBV6 subgroup which comprises 8–9 mapped genes, depending on the haplotypes, in the TRB locus.

Gene location

TRBV6-3 is in the TRB locus on chromosome 7 at 7q34.

Nucleotide and amino acid sequences for human TRBV6-3

U07978 ,TRBV6-3*01	[47]	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
		N	A	G	V	T	Q	T	P	K	F	R	V	L	K	T	G	Q	S	M	T
L36092,U66059,TRBV6-3*01	[34]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L26229 ,TRBV6-3*01	[44]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U07978 ,TRBV6-3*01		21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
		L	L	C	A	Q	D	M	N	H	E	Y	...	...	...	...	...	...	...	M	Y
L36092,U66059,TRBV6-3*01		CTG	CTG	TGT	GCC	CAG	GAT	ATG	AAC	CAT	GAA	TAC	...	...	...	...	...	...	...	ATG	TAC
L26229 ,TRBV6-3*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U07978 ,TRBV6-3*01		41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
		W	Y	R	Q	D	P	G	M	G	L	R	L	I	H	Y	S	V	G	E	G
L36092,U66059,TRBV6-3*01		TGG	TAT	CGA	CAA	GAC	CCA	GGC	ATG	GGG	CTG	AGG	CTG	ATT	CAT	TAC	TCA	GTT	GGT	GAG	GGT
L26229 ,TRBV6-3*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U07978 ,TRBV6-3*01		61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
		T	A	K	G	E	V	P	P	D	G	Y	N	V	S	R	...	...	...	...	...
L36092,U66059,TRBV6-3*01		ACA	...	...	...	...	ACT	GCC	AAA	GGA	GAG	GTC	CCT	...	GAT	GGC	TAC	AAT	GTC	TCC	AGA
L26229 ,TRBV6-3*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U07978 ,TRBV6-3*01		81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
		L	K	K	Q	N	F	L	L	L	G	L	E	S	A	A	P	S	Q	T	S
L36092,U66059,TRBV6-3*01		TTA	...	AAA	AAA	CAG	AAT	TTC	CTG	CTG	GGG	TGG	GAG	TCG	GCT	GCT	CCC	TCC	CAA	ACA	TCT
L26229 ,TRBV6-3*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U07978 ,TRBV6-3*01		101	102	103	104	105	106	107	108	109											
		V	V	F	C	A	S	S	V	...											
L36092,U66059,TRBV6-3*01		GTG	TAC	TTC	TGT	GCC	AGC	AGT	TAC	TC											
L26229 ,TRBV6-3*01		---	---	---	---	---	---	---	---	---											

◊: Genomic DNA, but not known as being germline or rearranged

Framework and complementarity determining regions

FR1-IMGT: 26

FR2-IMGT: 17

FR3-IMGT: 37 [-2 aa: 73, 82]

CDR1-IMGT: 5

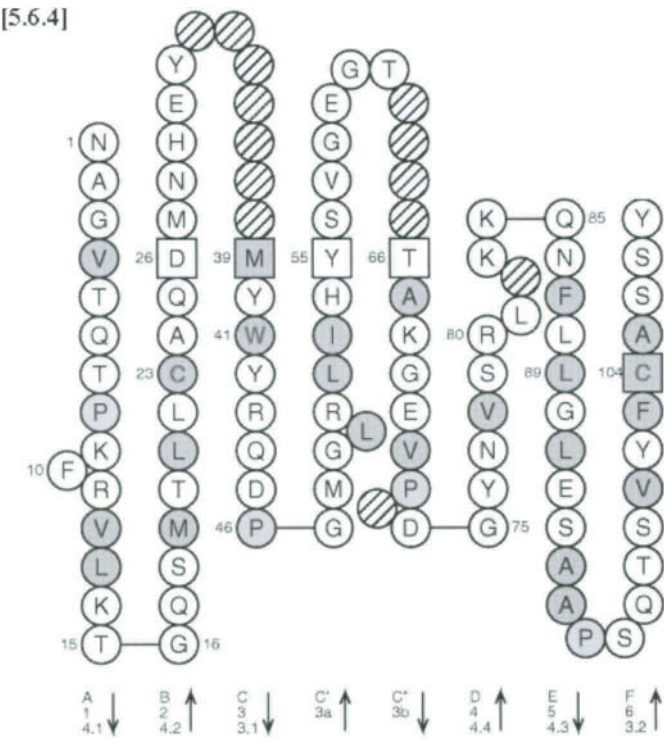
CDR2-IMGT: 6

CDR3-IMGT: 4



Collier de Perles for human TRBV6-3*01

Accession number: IMGT U07978 EMBL/GenBank/DDBJ: U07978



Genome database accession numbers

GDB:9954099 LocusLink: 28604

Nomenclature

TRBV6-4: T cell receptor beta variable 6-4.

Definition and functionality

TRBV6-4 is one of the 5–7 functional genes of the TRBV6 subgroup which comprises 8–9 mapped genes, depending on the haplotypes, in the TRB locus.

Gene location

TRBV6-4 is in the TRB locus on chromosome 7 at 7q34.

Nucleotide and amino acid sequences for human TRBV6-4



		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	
X61653	,TRBV6-4*01	[26]	ATT	GCT	GGG	ATC	ACC	CAG	GCA	CCA	ACA	TCT	CAG	ATC	CTG	GCA	GCA	GGA	CGG	CGC	ATG	ACA
L36092,U66059,TRBV6-4*01	[34]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
AF009660,TRBV6-4*02	[35]	-C-	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	A-	---	---	---
		CDR1-IMGT																				
		21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	
X61653	,TRBV6-4*01	L	R	C	T	Q	D	M	R	H	N	A								M	Y	
		CTG	AGA	TGT	ACC	CAG	GAT	ATG	AGA	CAT	AAT	GCC	...	...	...	...	...	...	...	ATG	TAC	
L36092,U66059,TRBV6-4*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
AF009660,TRBV6-4*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
		CDR2-																				
		41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	
X61653	,TRBV6-4*01	W	Y	R	Q	D	L	G	L	G	L	R	L	I	H	Y	S	N	T	A	G	
		TGG	TAT	AGA	CAA	GAT	CTA	GGA	CTG	GGG	CTA	AGG	CTC	ATC	CAT	TAT	TCA	AAT	ACT	GCA	GGT	
L36092,U66059,TRBV6-4*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
AF009660,TRBV6-4*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
		IMGT																				
		61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	
X61653	,TRBV6-4*01	T					T	G	K	G	E	V	P		D	G	Y	S	V	S	R	
		ACC	...	...	...	...	ACT	GGC	AAA	GGA	GAA	GTC	CCT	...	GAT	GGT	TAT	AGT	GTC	TCC	AGA	
L36092,U66059,TRBV6-4*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
AF009660,TRBV6-4*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
		CDR3-IMGT																				
		101	102	103	104	105	106	107	108	109												
X61653	,TRBV6-4*01	V	Y	F	C	A	S	S	D													
		GTG	TAC	TTC	TGT	GCC	AGC	AGT	GAC	TC												
L36092,U66059,TRBV6-4*01		---	---	---	---	---	---	---	---	---												
AF009660,TRBV6-4*02		---	---	---	---	---	---	---	---	---												

Framework and complementarity determining regions

FR1-IMGT: 26

FR2-IMGT: 17

FR3-IMGT: 37 [-2 aa: 73, 82]

CDR1-IMGT: 5

CDR2-IMGT: 6

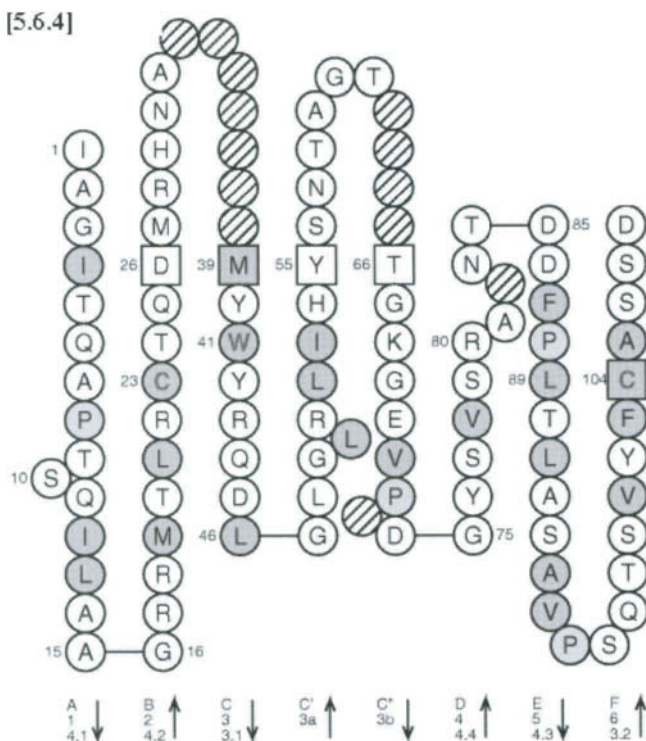
CDR3-IMGT: 4



Collier de Perles for human TRBV6-4*01

Accession number: IMGT X61653

EMBL/GenBank/DDBJ: X61653



Genome database accession numbers

GDB:9954101

LocusLink: 28603

Nomenclature

TRBV6-5: T cell receptor beta variable 6-5.

Definition and functionality

TRBV6-5 is one of the 5–7 functional genes of the TRBV6 subgroup which comprises 8–9 mapped genes, depending on the haplotypes, in the TRB locus.

Gene location

TRBV6-5 is in the TRB locus on chromosome 7 at 7q34.

Nucleotide and amino acid sequences for human TRBV6-5

L36092, U66059, U66060, TRBV6-5*01 [34]	1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 N A G V T Q T P K F Q V L K T G Q S W T AAT GCT GGT GTC ACT CAG ACC CCA AAA TTC CAG GTC CTG AAG ACA GGA CAG AGC ATG ACA																			
AF009662, TRBV6-5*01 [35]	-----																			
AF009663, TRBV6-5*01 [35]	-----																			
L36092, U66059, U66060, TRBV6-5*01	CDR1-IMGT 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 L Q C A Q D M N H E Y CTG CAG TGT GCC CAG GAT ATG AAC CAT GAA TAC ATG TCC																			
AF009662, TRBV6-5*01	-----																			
AF009663, TRBV6-5*01	-----																			
L36092, U66059, U66060, TRBV6-5*01	CDR2- 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 W Y R Q D P G M G L R L I H Y S V G A G TGG TAT CGA CAA GAC CCA GGC ATG GGG CTG AGG CTG ATT CAT TAC TCA GTT GGT GCT GGT																			
AF009662, TRBV6-5*01	-----																			
AF009663, TRBV6-5*01	-----																			
L36092, U66059, U66060, TRBV6-5*01	IMGT 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 I T D Q G E V P N G Y N V S R ATC ACT GAC CAA GGA GAA GTC CCC ... AAT GGC TAC AAT GTC TCC AGA																			
AF009662, TRBV6-5*01	-----																			
AF009663, TRBV6-5*01	-----																			
L36092, U66059, U66060, TRBV6-5*01	81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 S T T E D F P L R L L S A A P S Q T S TCA ... ACC ACA GAG GAT TTC CCG CTC AGG CTG CTG TCG GCT GCT CCC TCC CAG ACA TCT																			
AF009662, TRBV6-5*01	-----																			
AF009663, TRBV6-5*01	-----																			
L36092, U66059, U66060, TRBV6-5*01	CDR3-IMGT 101 102 103 104 105 106 107 108 109 V Y F C A S S Y GTG TAC TTC TGT GCC AGC AGT TAC TC																			
AF009662, TRBV6-5*01	-----																			
AF009663, TRBV6-5*01	-----																			

Framework and complementarity determining regions

FR1-IMGT: 26

FR2-IMGT: 17

FR3-IMGT: 37 (-2 aa: 73, 82)

CDR1-IMGT: 5

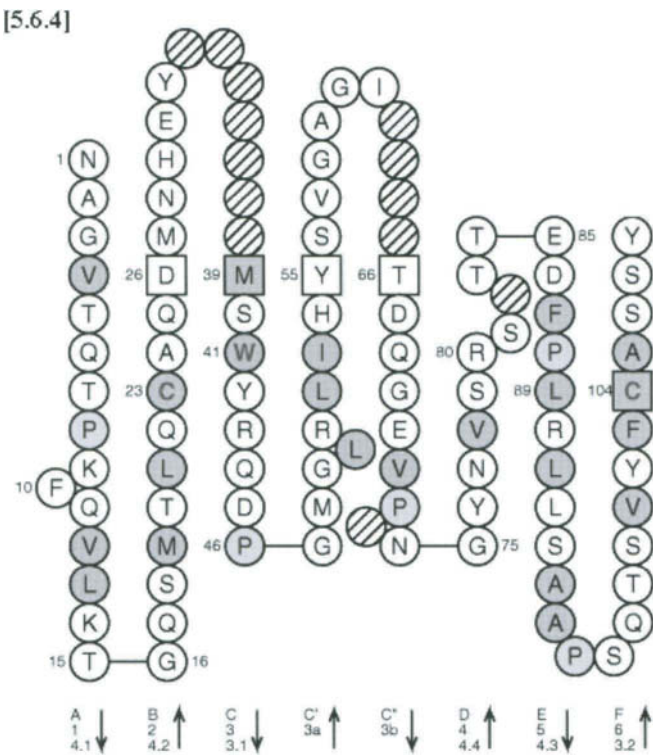
CDR2-IMGT: 6

CDR3-IMGT: 4



Collier de Perles for human TRBV6-5*01

Accession number: IMGT L36092 EMBL/GenBank/DDBJ: L36092



Genome database accession numbers

GDB:9954103 LocusLink: 28602

Nomenclature

TRBV6-6: T cell receptor beta variable 6-6.

Definition and functionality

TRBV6-6 is one of the 5–7 functional genes of the TRBV6 subgroup which comprises 8–9 mapped genes, depending on the haplotypes, in the TRB locus.

Gene location

TRBV6-6 is in the TRB locus on chromosome 7 at 7q34.

Nucleotide and amino acid sequences for human TRBV6-6

		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
L36092,U66060,TRBV6-6*01	[34]	N	A	G	V	T	Q	T	P	K	F	R	I	L	R	I	G	Q	S	M	T
AF009663,TRBV6-6*01	[35]	AAT	GCT	GGT	OTC	ACT	CAG	ACC	CCA	AAA	TTC	CGC	ATC	CTG	AAG	ATA	GSA	CAG	AGC	ATG	ACA
AF009662,TRBV6-6*02	[35]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X58815,TRBV6-6*03	[10]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X74848,TRBV6-6*04	[19]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L06892,TRBV6-6*05	[36]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

		21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
L36092,U66060,TRBV6-6*01		L	Q	C	T	Q	D	M	N	H	N	Y								M	Y
AF009663,TRBV6-6*01		CTG	CAG	TGT	ACC	CAG	GAT	ATG	AAC	CAT	AAC	TAC	...	...	...	...	...	...	...	ATG	TAC
AF009662,TRBV6-6*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X58815,TRBV6-6*03		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X74848,TRBV6-6*04		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L06892,TRBV6-6*05		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

		41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
L36092,U66060,TRBV6-6*01		W	Y	R	Q	D	F	G	M	G	L	K	L	I	Y	Y	S	V	G	A	G
AF009663,TRBV6-6*01		TGG	TAT	CCA	CAA	GAC	CCA	GGC	ATG	GGG	CTG	AAG	CTG	ATT	TAT	TAT	TCA	GTT	GGT	GCT	GGT
AF009662,TRBV6-6*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X58815,TRBV6-6*03		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X74848,TRBV6-6*04		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L06892,TRBV6-6*05		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

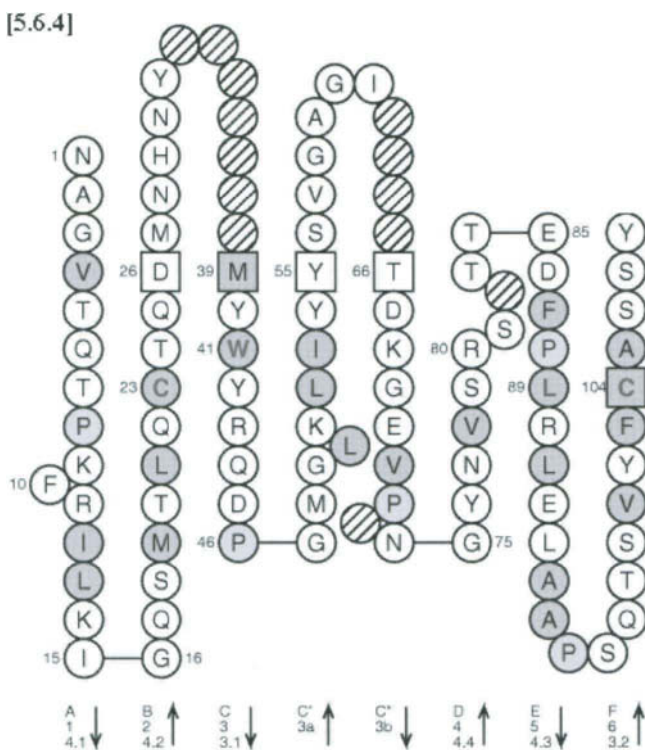
		61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
L36092,U66060,TRBV6-6*01		I	...	...	...	...	T	D	K	G	E	V	P	...	N	G	Y	N	V	S	R
AF009663,TRBV6-6*01		ATC	...	...	...	...	ACT	GAT	AAA	GGA	GAA	GTC	CCG	...	AAT	GGC	TAC	AAC	OTC	TCC	AGA
AF009662,TRBV6-6*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X58815,TRBV6-6*03		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X74848,TRBV6-6*04		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L06892,TRBV6-6*05		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

		81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
L36092,U66060,TRBV6-6*01		S	...	...	...	...	T	E	D	F	P	L	R	L	E	I	A	A	P	S	O
AF009663,TRBV6-6*01		TCA	...	ACC	ACA	GAG	GAT	TTC	CCG	CTC	AGG	CTG	GAG	TTG	GCT	GCT	CCC	TCC	CAG	ACA	TCT
AF009662,TRBV6-6*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X58815,TRBV6-6*03		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X74848,TRBV6-6*04		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L06892,TRBV6-6*05		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

#c: Rearranged cDNA

CDR3-IMGT: 4

EMBL/GenBank/DDBJ: L36092



LocusLink: 28601

Nomenclature

TRBV6-7: T cell receptor beta variable 6-7.

Definition and functionality

TRBV6-7 is an ORF due to the CONSERVED-TRP (tgg) of the V-EXON, being replaced by an Arginine (cgg). TRBV6-7 belongs to the TRBV6 subgroup which comprises 8–9 mapped genes, of which 5–7 are functional, depending on the haplotypes, in the TRB locus.

Gene location

TRBV6-7 is in the TRB locus on chromosome 7 at 7q34.

Nucleotide and amino acid sequences for human TRBV6-7

		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
L36092,U66060,TRBV6-7*01	[34]	AAT	GCT	GGT	GTC	ACT	CAG	ACC	CCA	AAA	TTC	CAC	GTC	CTG	AAG	ACA	GGA	CAG	AGC	ATG	ACT
AF009663,TRBV6-7*01	[35]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L26227,TRBV6-7*01	[44]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		CDR1-IMGT																			
		21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
L36092,U66060,TRBV6-7*01		L	L	C	A	Q	D	M	N	H	E	Y								M	Y
AF009663,TRBV6-7*01		CTG	CTG	TGT	GCC	CAG	GAT	ATG	AAC	CAT	GAA	TAC								ATG	TAT
L26227,TRBV6-7*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		CDR2-																			
		41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
L36092,U66060,TRBV6-7*01		R	Y	R	Q	D	P	G	K	G	L	R	L	I	Y	Y	S	V	A	A	A
AF009663,TRBV6-7*01		CGG	TAT	CGA	CAA	GAC	CCA	GGC	AAG	GGG	CTG	AGG	CTG	ATT	TAC	TAC	TCA	GTT	GCT	GCT	GCT
L26227,TRBV6-7*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		IMGT																			
		61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
L36092,U66060,TRBV6-7*01		L					T	D	K	G	E	V	P		N	G	Y	N	V	S	R
AF009663,TRBV6-7*01		CTC	---	---	---	---	ACT	GAC	AAA	GGA	GAA	GTT	CCC	---	AAT	GGC	TAC	AAT	GTC	TCC	AGA
L26227,TRBV6-7*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
L36092,U66060,TRBV6-7*01		S		N	T	E	D	F	P	L	X	L	E	S	A	A	P	S	Q	T	S
AF009663,TRBV6-7*01		TCA	---	AAC	ACA	GAG	GAT	TTC	CCC	CTC	AAG	CTG	GAG	TCA	GCT	GCT	CCC	TCT	CAG	ACT	TCT
L26227,TRBV6-7*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		CDR3-IMGT																			
		101	102	103	104	105	106	107	108	109											
L36092,U66060,TRBV6-7*01		V	Y	F	C	A	S	S	Y												
AF009663,TRBV6-7*01		GTT	TAC	TTC	TGT	GCC	AGC	AGT	TAC	TC											
L26227,TRBV6-7*01		---	---	---	---	---	---	---	---	---											

°: Genomic DNA, but not known as being germline or rearranged

Framework and complementarity determining regions

FR1-IMGT: 26

FR2-IMGT: 17

FR3-IMGT: 37 (-2 aa: 73, 82)

CDR1-IMGT: 5

CDR2-IMGT: 6

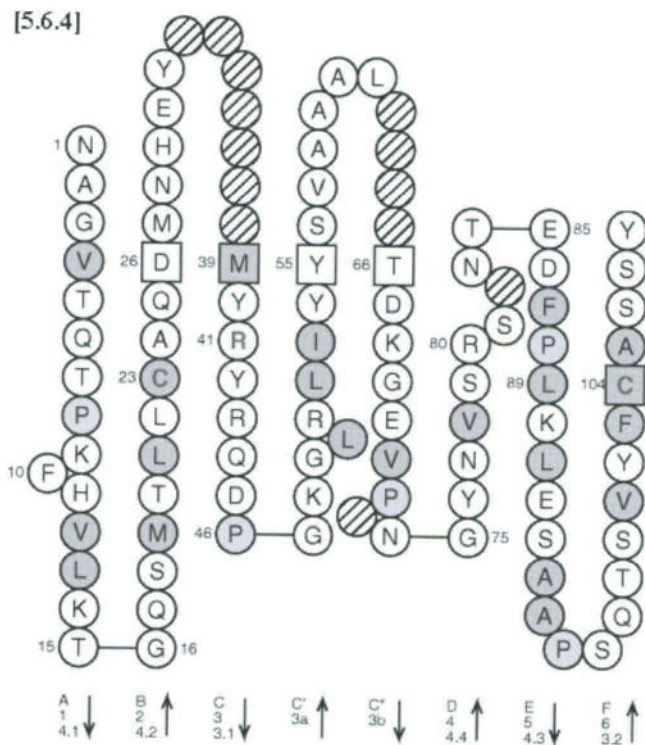
CDR3-IMGT: 4



Collier de Perles for human TRBV6-7*01

Accession number: IMGT L36092

EMBL/GenBank/DDBJ: L36092



Genome database accession numbers

GDB:9954107

LocusLink: 28600

Nomenclature

TRBV6-8: T cell receptor beta variable 6-8.

Definition and functionality

TRBV6-8 is one of the 5–7 functional genes of the TRBV6 subgroup which comprises 8–9 mapped genes, depending on the haplotypes, in the TRB locus.

Gene location

TRBV6-8 is in the TRB locus on chromosome 7 at 7q34.

Nucleotide and amino acid sequences for human TRBV6-8

		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
		N	A	G	V	T	Q	T	P	K	F	H	I	L	K	T	G	D	S	N	T
L36092,U66060,TRBV6-8*01	[34]	AAT	GCT	GCT	GTC	ACT	CAG	ACC	CCA	AAA	TTC	CAC	ATC	CTG	AAG	ACA	GGA	CAG	AGC	ATG	ACA
AF009663,TRBV6-8*01	[35]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L26228	,TRBV6-8*01	[44]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
		L	Q	C	A	Q	D	M	N	H	G	Y	---	---	---	---	---	---	---	M	S
L36092,U66060,TRBV6-8*01		CTG	CAG	TGT	GCC	CAG	GAT	ATG	AAC	CAT	GGA	TAC	---	---	---	---	---	---	---	ATG	TCC
AF009663,TRBV6-8*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L26228	,TRBV6-8*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
		W	Y	R	Q	D	P	G	M	G	L	R	L	I	Y	Y	S	A	A	A	G
L36092,U66060,TRBV6-8*01		TGG	TAT	CGA	CAA	GAC	CCA	GGC	ATC	GCG	CTG	AGA	CTG	ATT	TAC	TAC	TCA	GCT	GCT	GCT	GCT
AF009663,TRBV6-8*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L26228	,TRBV6-8*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
		T	---	---	---	---	T	D	K	---	E	V	P	---	N	G	Y	N	V	S	R
L36092,U66060,TRBV6-8*01		ACT	---	---	---	---	ACT	GAC	AAA	---	GAA	CTC	CCC	---	AAT	GGC	TAC	AAT	GTC	TCT	AGA
AF009663,TRBV6-8*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L26228	,TRBV6-8*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
		L	N	T	E	D	F	P	P	L	R	L	V	S	A	A	P	S	Q	T	S
L36092,U66060,TRBV6-8*01		TTA	---	AAC	ACA	GAG	GAT	TTC	CCA	CTC	AGG	CTG	GTG	TCG	GCT	GCT	CCC	TCC	CAG	ACA	TCT
AF009663,TRBV6-8*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L26228	,TRBV6-8*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		101	102	103	104	105	106	107	108	109											
		V	Y	L	C	A	S	S	Y	---											
L36092,U66060,TRBV6-8*01		GTG	TAC	TTG	TGT	GCC	AGC	ACT	TAC	TC											
AF009663,TRBV6-8*01		---	---	---	---	---	---	---	---	---											
L26228	,TRBV6-8*01	---	---	---	---	---	---	---	---	---											

°: Genomic DNA, but not known as being germline or rearranged

Framework and complementarity determining regions

FR1-IMGT: 26

FR2-IMGT: 17

FR3-IMGT: 36 (-3 aa: 69, 73, 82)

CDR1-IMGT: 5

CDR2-IMGT: 6

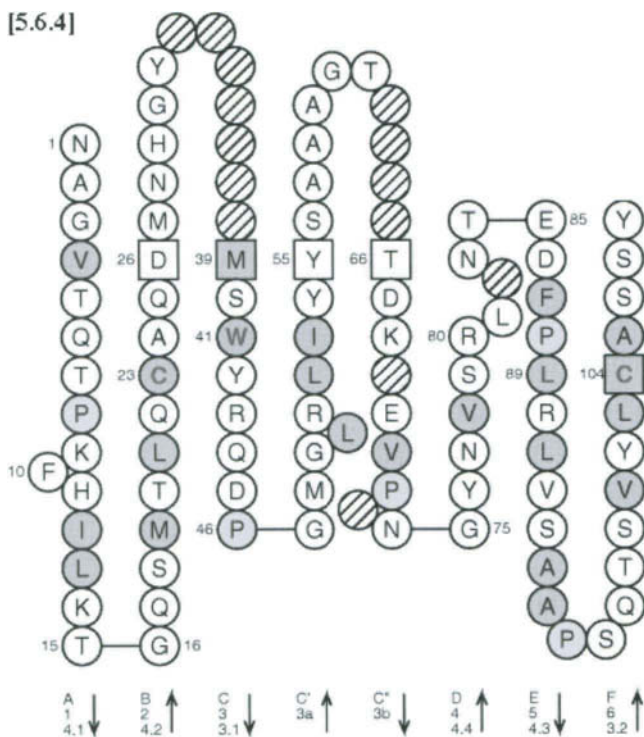
CDR3-IMGT: 4



Collier de Perles for human TRBV6-8*01

Accession number: IMGT L36092

EMBL/GenBank/DDBJ: L36092



Genome database accession numbers

GDB:9954109

LocusLink: 28599

Nomenclature

TRBV6-9: T cell receptor beta variable 6-9.

Definition and functionality

TRBV6-9 is one of the 5–7 functional genes of the TRBV6 subgroup which comprises 8–9 mapped genes, depending on the haplotypes, in the TRB locus.

Gene location

TRBV6-9 is in the TRB locus on chromosome 7 at 7q34.

Nucleotide and amino acid sequences for human TRBV6-9

			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
			N	A	G	V	T	Q	T	P	K	F	H	I	L	K	T	G	Q	S	M	T
X61447	,TRBV6-9*01	[26]	AAT	GCT	GGT	GTC	ACT	CAG	ACC	CCA	AAA	TTC	CAC	ATC	CTG	AAG	ACA	GGA	CAG	AGC	ATG	ACA
L36092,U66060,TRBV6-9*01	[34]		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
AF009663,TRBV6-9*01	[35]		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
			CDR1-IMGT																			
			21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
			L	Q	C	A	Q	D	M	N	H	G	Y								L	S
X61447	,TRBV6-9*01		CTC	CAG	TGT	GCC	CAG	GAT	ATG	AAC	CAT	GGA	TAC	---	---	---	---	---	---	---	TTG	TCC
L36092,U66060,TRBV6-9*01			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
AF009663,TRBV6-9*01			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
			CDR2-																			
			41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
			W	Y	R	Q	D	P	G	M	G	L	R	R	I	H	Y	S	V	A	A	G
X61447	,TRBV6-9*01		TGG	TAT	CGA	CAA	GAC	CCA	GGC	ATG	GGG	CTG	AGG	CGC	ATT	CAT	TAC	TCA	GTT	GCT	GCT	GGT
L36092,U66060,TRBV6-9*01			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
AF009663,TRBV6-9*01			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
			IMGT																			
			61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
			I					T	D	K	G	E	V	P		D	G	Y	N	V	S	R
X61447	,TRBV6-9*01		ATC	---	---	---	---	ACT	GAC	AAA	GGA	GAA	GTC	CCC	---	GAT	GGC	TAC	AAT	GTA	TCC	AGA
L36092,U66060,TRBV6-9*01			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
AF009663,TRBV6-9*01			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
			81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
			S	N	T	E	D	F	P	L	R	L	E	S	A	A	P	S	Q	T	S	
X61447	,TRBV6-9*01		TCA	---	AAC	ACA	GAG	GAT	TTC	CCG	CTC	AGG	CTG	GAG	TCA	GCT	GCT	CCC	TCC	CAG	ACA	TCT
L36092,U66060,TRBV6-9*01			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
AF009663,TRBV6-9*01			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
			CDR3-IMGT																			
			101	102	103	104	105	106	107	108	109											
			V	Y	F	C	A	S	S	Y												
X61447	,TRBV6-9*01		GTA	TAC	TTC	TGT	GCC	AGC	AGT	TAT	TC	---	---	---	---	---	---	---	---	---	---	---
L36092,U66060,TRBV6-9*01			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
AF009663,TRBV6-9*01			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

Framework and complementarity determining regions

FR1-IMGT: 26

FR2-IMGT: 17

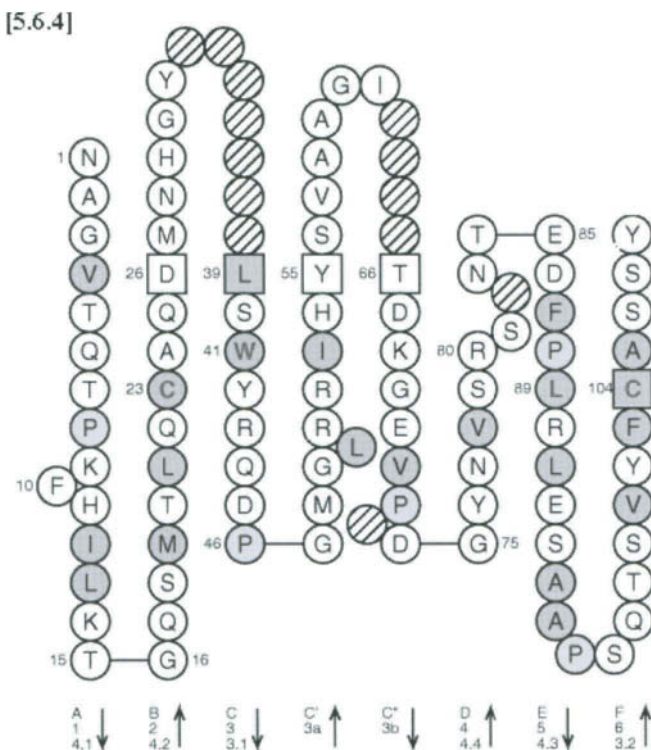
FR3-IMGT: 37 (-2 aa: 73, 82)

CDR1-IMGT: 5

CDR2-IMGT: 6

CDR3-IMGT: 4

EMBL/GenBank/DDDBJ: X61447



LocusLink: 28598

Nomenclature

TRBV7-1: T cell receptor beta variable 7-1.

Definition and functionality

TRBV7-1 is an ORF due to the 1st-CYS of FR1-IMGT, being replaced by a Tyrosine (tat) and, missing V-SPACER and V-NONAMER. TRBV7-1 belongs to the TRBV7 subgroup which comprises nine mapped genes, of which 5-6 are functional in the TRB locus.

Gene location

TRBV7-1 is in the TRB locus on chromosome 7 at 7q34.

Nucleotide and amino acid sequences for human TRBV7-1

			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
X61444	,TRBV7-1*01	[26]	G	A	G	V	S	O	S	L	R	H	K	V	A	K	G	K	D	V	A	
			GGT	GCT	GGA	GTG	TCC	CAG	TCC	CTG	AGA	CAC	AAG	GTA	GCA	AAG	AAG	GGA	AAG	GAT	GTA	GCT
L36092,U66059,TRBV7-1*01	[34]		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
			CDR1-IMGT																			
			21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
X61444	,TRBV7-1*01		L	R	V	D	P	I	S	G	H	N	A								L	Y
			CTC	AGA	TAT	GAT	CCA	ATT	TCA	GGT	CAT	AAT	GCC	...	...	...	...	...	...	...	CTT	TAT
L36092,U66059,TRBV7-1*01			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
			CDR2-																			
			41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
X61444	,TRBV7-1*01		W	V	R	Q	S	L	G	Q	G	L	E	F	P	I	V	F	Q	G	K	D
			TGG	TAC	CGA	CAG	AGC	CTG	GGG	CAG	GGC	CTG	GAG	TTT	CCA	ATT	TAC	TTC	CAA	GGC	AAG	GAT
L36092,U66059,TRBV7-1*01			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
			IMGT																			
			61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
X61444	,TRBV7-1*01		A					A	D	K	S	G	L	P	R	D	R	F	S	A	Q	R
			GCA	...	...	...	...	GCA	GAC	AAA	TCG	GGG	CTT	CCC	CGT	GAT	CGG	TTC	TCT	GCA	CAG	AGG
L36092,U66059,TRBV7-1*01			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
			81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
X61444	,TRBV7-1*01		S		E	G	S	I	S	T	L	K	F	Q	R	T	Q	Q	G	D	L	A
			TCT	...	GAG	GGA	TCC	ATC	TCC	ACT	CTG	AAG	TTC	CAG	CGC	ACA	CAG	CAG	GGG	GAC	TTG	GCT
L36092,U66059,TRBV7-1*01			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
			CDR3-IMGT																			
			101	102	103	104	105	106	107	108	109											
X61444	,TRBV7-1*01		V	Y	L	C	A	S	S	S												
			GTC	TAT	CTC	TGT	GCC	AGC	AGC	TCA	GC											
L36092,U66059,TRBV7-1*01			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

Framework and complementarity determining regions

FR1-IMGT: 26

FR2-IMGT: 17

FR3-IMGT: 38 (-1 aa: 82)

CDR1-IMGT: 5

CDR2-IMGT: 6

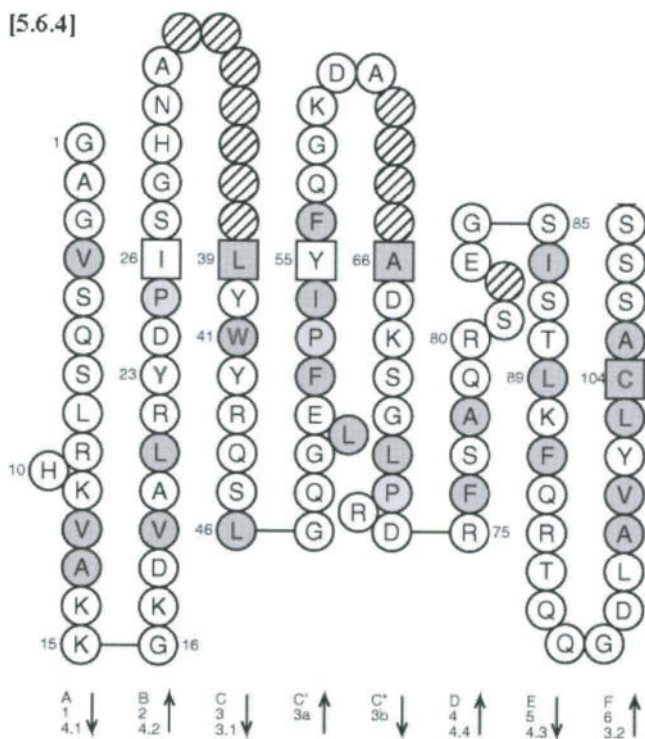
CDR3-IMGT: 4



Collier de Perles for human TRBV7-1*01

Accession number: IMGT X61444

EMBL/GenBank/DDBJ: X61444



Genome database accession numbers

GDB:9954113

LocusLink: 28597

Nomenclature

TRBV7-2: T cell receptor beta variable 7-2.

Definition and functionality

TRBV7-2 is one of the 5–6 functional genes of the TRBV7 subgroup which comprises nine mapped genes, in the TRB locus.

Gene location

TRBV7-2 is in the TRB locus on chromosome 7 at 7q34.

Nucleotide and amino acid sequences for human TRBV7-2



			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
X61442	, TRBV7-2*01	[26]	G	A	G	V	S	Q	S	P	S	N	K	V	T	E	K	G	K	D	V	E
U07976	, TRBV7-2*01	[47]	GGA	GCT	GGA	GTC	TCC	CAG	TCC	CCC	AGT	AAC	AAG	GTC	ACA	GAG	AAG	GGA	AAG	GAT	GTA	GAG
U07978	, TRBV7-2*01	[47]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L36092	, U66059, TRBV7-2*01	[34]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X61443	, TRBV7-2*02	[26]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L36190	, TRBV7-2*02	[34]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
AF009660	, TRBV7-2*02	[35]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U07975	, TRBV7-2*03	[47]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M27387	, TRBV7-2*04	[21]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

			21	22	23	24	25	26	CDR1-IMGT										31	32	33	34	35	36	37	38	39	40
X61442	, TRBV7-2*01	[26]	L	R	C	D	P	I	S	G	H	T	A	A	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U07976	, TRBV7-2*01		CTC	AGG	TGT	GAT	CCA	ATT	TCA	GGT	CAT	ACT	GCC	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U07978	, TRBV7-2*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L36092	, U66059, TRBV7-2*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X61443	, TRBV7-2*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L36190	, TRBV7-2*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
AF009660	, TRBV7-2*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U07975	, TRBV7-2*03		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M27387	, TRBV7-2*04		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

			41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
X61442	, TRBV7-2*01		W	Y	R	Q	S	L	G	Q	G	L	E	F	L	I	Y	F	Q	G	N	S
U07976	, TRBV7-2*01		TGG	TAC	CGA	CAG	AGC	CTG	GGG	CAG	GGC	CTG	GAG	TTT	TTA	ATT	TAC	TTC	CAA	GGC	AAC	AGT
U07978	, TRBV7-2*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L36092	, U66059, TRBV7-2*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X61443	, TRBV7-2*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L36190	, TRBV7-2*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
AF009660	, TRBV7-2*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U07975	, TRBV7-2*03		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M27387	, TRBV7-2*04		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

		IMGT																				
		61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	
		A					P	D	K	S	G	L	P	S	D	R	F	S	A	E	R	
X61442	,TRBV7-2*01	GCA	...	...	...	...	CCA	GAC	AAA	TCA	GGG	CTG	CCC	AGT	GAT	CGC	TTC	TCT	GCA	GAG	AGG	
U07976	,TRBV7-2*01		...	...	...	...																
U07978	,TRBV7-2*01		...	...	...	...																
L36092,U66059,TRBV7-2*01			...	...	...	...																
X61443	,TRBV7-2*02		...	...	...	...																
L36190	,TRBV7-2*02		...	...	...	...																
AF009660,TRBV7-2*02			...	...	...	...																
U07975	,TRBV7-2*03		...	...	...	...																
M27387	,TRBV7-2*04		...	...	...	...																



		81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
		T	G	G	S	S	V	S	T	L	T	I	Q	R	T	Q	Q	E	D	S	A
X61442	,TRBV7-2*01	ACT	...	GGG	GGA	TCC	GTC	TCC	ACT	CTG	ACG	ATC	CAG	CGC	ACA	CAG	CAG	GAG	GAC	TCG	GCC
U07976	,TRBV7-2*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U07978	,TRBV7-2*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L36092,U66059,TRBV7-2*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X61443	,TRBV7-2*02	---	---	---	E	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L36190	,TRBV7-2*02	---	---	---	A	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
AF009660,TRBV7-2*02		---	---	---	E	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U07975	,TRBV7-2*03	---	---	---	A	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M27387	,TRBV7-2*04	---	---	---	A	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
</																					

Nomenclature

TRBV7-3: T cell receptor beta variable 7-3.

Definition and functionality

TRBV7-3 is a functional gene (alleles *01, *04 and *05) or an ORF (alleles *02 and *03). TRBV7-3 belongs to TRBV7 subgroup which comprises nine mapped genes, of which 5–6 are functional, in the TRB locus.

TRBV7-3*02 and TRBV7-3*03 are ORF due to the 2nd-CYS (tgt) of FR3-IMGT being replaced by an Arginine (cgt).

Gene location

TRBV7-3 is in the TRB locus on chromosome 7 at 7q34.

Nucleotide and amino acid sequences for human TRBV7-3

			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
			G	A	G	V	S	Q	T	P	S	N	K	V	T	E	K	G	K	Y	V	E
X61440	, TRBV7-3*01	[26]	GGT	GCT	GGA	GTC	TCC	CAG	ACC	CCC	AGT	AAC	AAG	GTC	ACA	GAG	AAG	GGA	AAA	TAT	CTA	GAG
L33104	, TRBV7-3*01	[1]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L36092	U66059, TRBV7-3*01	[34]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M67511	, TRBV7-3*01	[28]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M67512	, TRBV7-3*01	[28]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M97943	, TRBV7-3*02	[27]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	D	---
L33103	, TRBV7-3*02	[1]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	G	---
L33105	, TRBV7-3*03	[1]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	D	---
AF009660	, TRBV7-3*03	[35]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	G	---
X74843	, TRBV7-3*04	[19]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M13550	, TRBV7-3*05	[24]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	W	---
																					TGG	---

			21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
			L	R	C	D	P	I	S	G	H	T	A								L	Y
X61440	, TRBV7-3*01		CTC	AGG	TGT	GAT	CCA	ATT	TCA	GGT	CAT	ACT	GCC	...	...	...	...	...	...	...	CTT	TAC
L33104	, TRBV7-3*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L36092	U66059, TRBV7-3*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M67511	, TRBV7-3*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M67512	, TRBV7-3*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M97943	, TRBV7-3*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L33103	, TRBV7-3*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L33105	, TRBV7-3*03		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
AF009660	, TRBV7-3*03		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X74843	, TRBV7-3*04		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M13550	, TRBV7-3*05		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

			41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
			W	Y	R	Q	S	L	G	Q	G	P	E	F	L	I	Y	P	Q	G	T	G
X61440	, TRBV7-3*01		TGG	TAC	CGA	CAA	AGC	CTG	GGG	CAG	GGC	CCA	GAG	TTT	CTA	ATT	TAC	CTC	CAA	GGC	ACG	GGT
L33104	, TRBV7-3*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L36092	U66059, TRBV7-3*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M67511	, TRBV7-3*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M67512	, TRBV7-3*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M97943	, TRBV7-3*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L33103	, TRBV7-3*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L33105	, TRBV7-3*03		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
AF009660	, TRBV7-3*03		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X74843	, TRBV7-3*04		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M13550	, TRBV7-3*05		---	---	---	---	---	---	---	---	---	---	---	---	---	L	C	---	---	---	---	---



		IMGT																															
		61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80												
X61440	,TRBV7-3*01	A	F	A	F	A	A	D	D	S	G	L	P	N	D	R	F	F	A	V	R												
L33104	,TRBV7-3*01	GCG	...	...	...	...	GCA	GAT	GAC	TCA	GGG	CTG	CCC	AAC	GAT	CGG	TTC	TTT	GCA	GTC	AGG												
L36092,U66059,TRBV7-3*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---												
M67511	,TRBV7-3*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---												
M67512	,TRBV7-3*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---												
M97943	,TRBV7-3*02	---	---	---	---	---	---	---	---	---	---	---	---	---	K	---	---	---	---	---	---												
L33103	,TRBV7-3*02	---	---	---	---	---	---	---	---	---	---	---	---	---	A	---	---	---	---	---	---												
L33105	,TRBV7-3*03	---	---	---	---	---	---	---	---	---	---	---	---	---	K	---	---	---	---	---	---												
AF009660,TRBV7-3*03		---	---	---	---	---	---	---	---	---	---	---	---	---	K	---	---	---	---	---	---												
X74843	,TRBV7-3*04	---	---	---	---	---	---	---	---	---	---	---	---	---	A	---	---	---	---	---	---												
M13550	,TRBV7-3*05	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---												
X61440	,TRBV7-3*01	P	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100											
L33104	,TRBV7-3*01	E	G	S	V	S	T	L	K	I	Q	R	T	E	R	G	D	S	A														
L36092,U66059,TRBV7-3*01		CCT	...	GAG	GGA	TCC	GTC	TCT	ACT	CTG	AAG	ATC	CAG	CGC	ACA	GAG	CGG	GGG	GAC	TCA	GCC												
M67511	,TRBV7-3*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---												
M67512	,TRBV7-3*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---												
M97943	,TRBV7-3*02	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	Q	---	---												
L33103	,TRBV7-3*02	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	A	---	---												
L33105	,TRBV7-3*03	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	A	---	---												
AF009660,TRBV7-3*03		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	A	---	---												
X74843	,TRBV7-3*04	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	A	---	---												
M13550	,TRBV7-3*05	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	A	---	---												
		CDR3-IMGT																															
X61440	,TRBV7-3*01	101	102	103	104	105	106	107	108	109																							
L33104	,TRBV7-3*01	V	Y	L	C	A	S	S	L																								
L36092,U66059,TRBV7-3*01		GTG	TAT	CTC	TGT	CCC	AGC	AGC	TTA	AC																							
M67511	,TRBV7-3*01	---	---	---	---	---	---	---	---	---																							
M67512	,TRBV7-3*01	---	---	---	---	---	---	---	---	---																							
M97943	,TRBV7-3*02	---	---	---	R	---	---	---	---	---																							
L33103	,TRBV7-3*02	---	---	---	C	---	---	---	---	---																							
L33105	,TRBV7-3*03	---	---	---	R	---	---	---	---	---																							
AF009660,TRBV7-3*03		---	---	---	A	---	---	---	---	---																							
X74843	,TRBV7-3*04	---	---	---	C	---	---	---	---	---																							
M13550	,TRBV7-3*05	---	---	---	R	---	---	---	---	---																							

#c: Rearranged cDNA
°: Genomic DNA, but not known as being germline or rearranged

Framework and complementarity determining regions

FR1-IMGT: 26

FR2-IMGT: 17

FR3-IMGT: 38 (-1 aa: 82)

CDR1-IMGT: 5

CDR2-IMGT: 6

CDR3-IMGT: 4

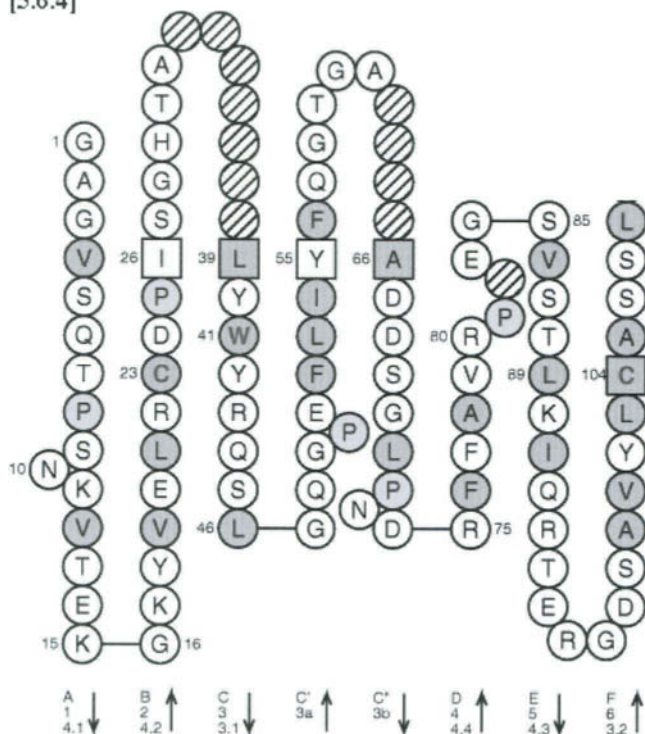


Collier de Perles for human TRBV7-3*01

Accession number: IMGT X61440

EMBL/GenBank/DDBJ: X61440

[5.6.4]



Genome database accession numbers

GDB:9954117

LocusLink: 28595

Nomenclature

TRBV7-4: T cell receptor beta variable 7-4.

Definition and functionality

TRBV7-4 is a functional gene (allele *01) or a pseudogene (allele *02). TRBV7-4 belongs to TRBV7 subgroup which comprises nine mapped genes, of which 5-6 are functional, in the TRB locus.

TRBV7-4*02 is a pseudogene due to 1 nt DELETION in codon 85 leading to a frameshift in FR3-IMGT.

Gene location

TRBV7-4 is in the TRB locus on chromosome 7 at 7q34.

Nucleotide and amino acid sequences for human TRBV7-4



	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
L36092.U66060,TRBV7-4*01 [34]	G	A	G	V	S	Q	S	P	R	Y	K	V	A	K	R	G	R	D	V	A
AF009662,TRBV7-4*01 [35]	GGT	GCT	GGA	GTC	TCC	CAG	TCC	CCA	AGG	TAC	AAA	GTC	GCA	AAG	AGG	GGA	CGG	GAT	GTA	GCT
AF009663,TRBV7-4*01 [35]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L14432,TRBV7-4*01 [11]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L14459,TRBV7-4*01 [11]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L13762,TRBV7-4*02 [11]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L14431,TRBV7-4*02 [11]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
L36092.U66060,TRBV7-4*01	L	R	C	D	S	I	S	G	H	V	T	...	...	...	...	...	...	...	L	Y
AF009662,TRBV7-4*01	CTC	AGG	TGT	GAT	TCA	ATC	TCG	GGT	CAT	GTA	ACC	...	...	...	...	...	...	...	CTT	TAT
AF009663,TRBV7-4*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L14432,TRBV7-4*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L14459,TRBV7-4*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L13762,TRBV7-4*02	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L14431,TRBV7-4*02	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
L36092.U66060,TRBV7-4*01	W	Y	R	Q	T	L	G	Q	Q	S	E	V	L	T	Y	S	Q	S	D	A
AF009662,TRBV7-4*01	TGG	TAC	CGA	CAG	ACC	CTG	GGG	CAG	GGC	TCA	GAG	GTT	CTG	ACT	TAC	TCC	CAG	AGT	GAT	GCT
AF009663,TRBV7-4*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L14432,TRBV7-4*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L14459,TRBV7-4*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L13762,TRBV7-4*02	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L14431,TRBV7-4*02	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
L36092.U66060,TRBV7-4*01	Q	...	...	...	...	R	D	K	S	G	R	P	S	G	R	F	S	A	E	R
AF009662,TRBV7-4*01	CAA	...	...	...	...	CGA	GAC	AAA	TCA	GGG	CGG	CCC	AGT	GGT	CGG	TTC	TCT	GCA	GAG	AGG
AF009663,TRBV7-4*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L14432,TRBV7-4*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L14459,TRBV7-4*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L13762,TRBV7-4*02	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L14431,TRBV7-4*02	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
L36092.U66060,TRBV7-4*01	P	E	R	S	V	S	T	L	K	I	Q	R	T	E	Q	G	D	S	A	...
AF009662,TRBV7-4*01	CCT	...	GAG	AGA	TCC	GTC	TCC	ACT	CTG	AAG	ATC	CAG	CGC	ACA	GAG	CAG	GAG	GAC	TCA	GCT
AF009663,TRBV7-4*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L14432,TRBV7-4*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L14459,TRBV7-4*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L13762,TRBV7-4*02	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L14431,TRBV7-4*02	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---



L36092.U66060,TRBV7-4*01

AF009662,TRBV7-4*01

AF009663,TRBV7-4*01

L14432 ,TRBV7-4*01

L14459 ,TRBV7-4*01

L13762 ,TRBV7-4*02

L14431 ,TRBV7-4*02

101 102 103 104 105 106 107 108 109

V Y L C A S S L

GTG TAT CTC TGT GCC AGC AGC TTA GC

(in the sequence): Frameshift

°: Genomic DNA, but not known as being germline or rearranged

Framework and complementarity determining regions

FR1-IMGT: 26

FR2-IMGT: 17

FR3-IMGT: 38 (-1 aa: 82)

CDR1-IMGT: 5

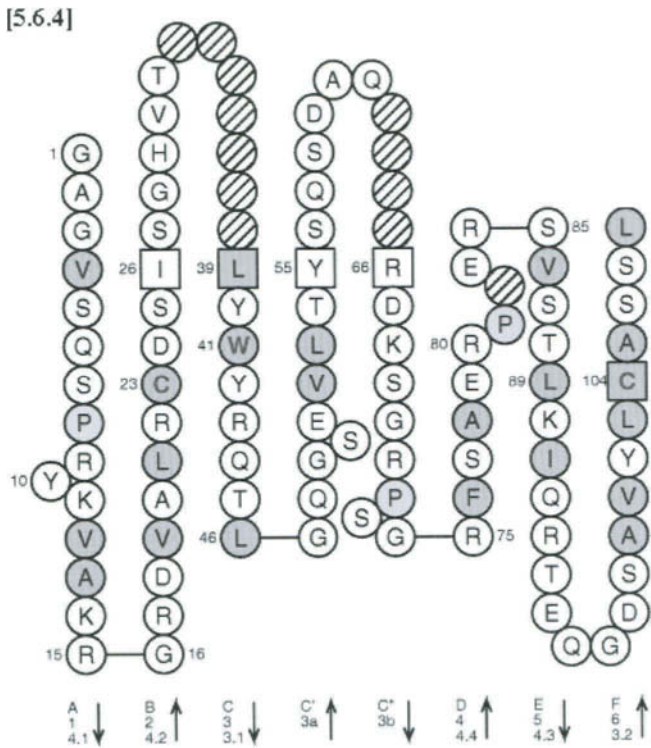
CDR2-IMGT: 6

CDR3-IMGT: 4

Collier de Perles for human TRBV7-4*01

Accession number: IMGT L36092

EMBL/GenBank/DDBJ: L36092



Genome database accession numbers

GDB:9954119 LocusLink: 28594

Nomenclature

TRBV7-6: T cell receptor beta variable 7-6.

Definition and functionality

TRBV7-6 is one of the 5–6 functional genes of the TRBV7 subgroup which comprises nine mapped genes, in the TRB locus.

Gene location

TRBV7-6 is in the TRB locus on chromosome 7 at 7q34.

Nucleotide and amino acid sequences for human TRBV7-6

[illegible]

#c: Rearranged cDNA

°: Genomic DNA, but not known as being germline or rearranged



Framework and complementarity determining regions

FR1-IMGT: 26

CDR1-IMGT: 5

FR2-IMGT: 17

CDR2-IMGT: 6

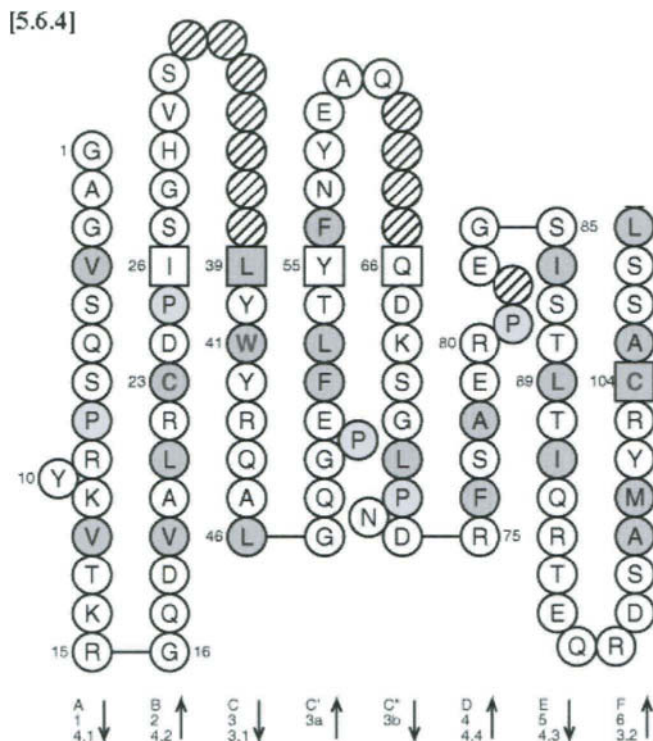
FR3-IMGT: 38 [-1 aa: 82]

CDR3-IMGT: 4

Collier de Perles for human TRBV7-6*01

Accession number: IMGT L36092

EMBL/GenBank/DBJ: L36092



Genome database accession numbers

GDB:9954123

LocusLink: 28592

Nomenclature

TRBV7-7: T cell receptor beta variable 7-7.

Definition and functionality

TRBV7-7 is one of the 5–6 functional genes of the TRBV7 subgroup which comprises nine mapped genes, in the TRB locus.

Gene location

TRBV7-7 is in the TRB locus on chromosome 7 at 7q35.

Nucleotide and amino acid sequences for human TRBV7-7

		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
L36092,U66060,TRBV7-7*01	[34]	G	A	G	V	S	Q	S	P	R	Y	K	V	T	K	R	G	Q	D	V	T
AF009663,TRBV7-7*01	[35]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L14483,TRBV7-7*01	[11]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M97505,TRBV7-7*01	[11]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X57607,TRBV7-7*02	[31]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		CDR1-IMGT																			
		21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
		L	R	C	D	P	I	S	S	H	A	T	---	---	---	---	---	---	---	L	Y
L36092,U66060,TRBV7-7*01		CTC	AGG	TGT	GAT	CCA	ATT	TCG	AGT	CAT	GCA	ACC	---	---	---	---	---	---	---	CTT	TAT
AF009663,TRBV7-7*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L14483,TRBV7-7*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M97505,TRBV7-7*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X57607,TRBV7-7*02		---	---	---	---	---	---	---	---	V	---	---	---	---	---	---	---	---	---	---	---
		CDR2-																			
		41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
		W	Y	Q	Q	A	L	G	Q	G	P	E	F	L	T	Y	F	N	Y	E	A
L36092,U66060,TRBV7-7*01		TGG	TAT	CAA	CAG	GCC	CTG	GGG	CAG	GGC	CCA	GAG	TTT	CTG	ACT	TAC	TTC	AAT	TAT	GAA	GCT
AF009663,TRBV7-7*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L14483,TRBV7-7*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M97505,TRBV7-7*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X57607,TRBV7-7*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		IMGT																			
		61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
		Q	---	---	---	---	P	D	K	S	G	L	P	S	D	R	F	S	A	E	R
L36092,U66060,TRBV7-7*01		CAA	---	---	---	---	CCA	GAC	AAA	TCA	GGG	CTG	CCC	AGT	GAT	CGG	TTC	TCT	GCA	GAG	AGG
AF009663,TRBV7-7*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L14483,TRBV7-7*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M97505,TRBV7-7*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X57607,TRBV7-7*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		IMGT																			
		81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
		P	E	G	S	I	S	T	L	T	I	Q	R	T	E	Q	R	D	S	A	
L36092,U66060,TRBV7-7*01		CGT	---	GAG	GGA	TCC	ATC	TCC	ACT	CTG	ACG	ATT	CAG	CGC	ACA	GAG	CAG	CGG	GAC	TCA	GCC
AF009663,TRBV7-7*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L14483,TRBV7-7*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M97505,TRBV7-7*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X57607,TRBV7-7*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		CDR3-IMGT																			
		101	102	103	104	105	106	107	108	109											
		M	Y	R	C	A	S	S	L	---											
L36092,U66060,TRBV7-7*01		ATG	TAT	CGC	TGT	GCC	AGC	AGC	TTA	GC											
AF009663,TRBV7-7*01		---	---	---	---	---	---	---	---	---											
L14483,TRBV7-7*01		---	---	---	---	---	---	---	---	---											
M97505,TRBV7-7*01		---	---	---	---	---	---	---	---	---											
X57607,TRBV7-7*02		---	---	---	---	---	---	---	---	---											

#c: Rearranged cDNA

°: Genomic DNA, but not known as being germline or rearranged



Framework and complementarity determining regions

FR1-IMGT: 26

CDR1-IMGT: 5

FR2-IMGT: 17

CDR2-IMGT: 6

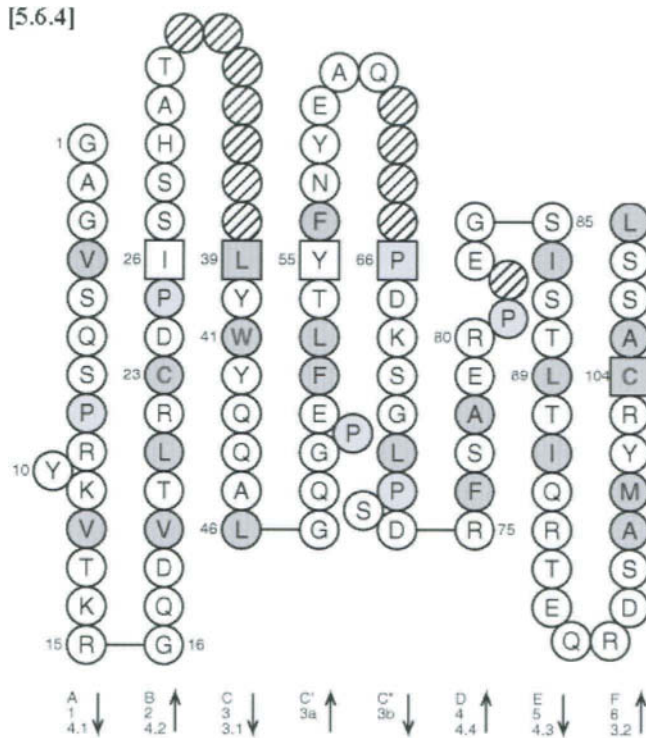
FR3-IMGT: 38 (-1 aa: 82)

CDR3-IMGT: 4

Collier de Perles for human TRBV7-7*01

Accession number: IMGT L36092

EMBL/GenBank/DBJ: L36092



Genome database accession numbers

GDB:9954125

LocusLink: 28591

Nomenclature

TRBV7-8: T cell receptor beta variable 7-8.

Definition and functionality

TRBV7-8 is one of the 5-6 functional genes of the TRBV7 subgroup which comprises nine mapped genes, in the TRB locus.

Gene location

TRBV7-8 is in the TRB locus on chromosome 7 at 7q34.

Nucleotide and amino acid sequences for human TRBV7-8

			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
			G	A	G	V	S	Q	S	F	F	Y	X	V	A	K	R	G	Q	D	V	A
M11953	,TRBV7-8*01	[18]	GGT	GCT	GGA	GTC	TCC	CAG	TCC	CCT	AGG	TAC	AAA	GTC	GCA	AAG	AGA	GGA	CAG	GAT	GTA	GCT
L36092,U66060,TRBV7-8*01	[34]		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
AF009663,TRBV7-8*01	[35]		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X61441	,TRBV7-8*02	[13]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M27384	,TRBV7-8*03	[21]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
			CDR1-IMGT																			
			21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
			L	R	C	D	P	I	S	G	H	V	S								L	F
M11953	,TRBV7-8*01		CTC	AGG	TGT	GAT	CCA	ATT	TCG	GGT	CAT	GTA	TCC	...	...	...	...	...	...	...	CTT	TTT
L36092,U66060,TRBV7-8*01			---	---	---	---	---	---	---	---	---	---	---	...	...	...	...	...	...	---	---	---
AF009663,TRBV7-8*01			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X61441	,TRBV7-8*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M27384	,TRBV7-8*03		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
			CDR2-																			
			41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
			W	Y	Q	Q	A	L	G	O	G	P	E	F	L	T	Y	F	O	N	E	A
M11953	,TRBV7-8*01		TGG	TAC	CAA	CAG	GCC	CTG	GCG	CAG	GCG	CCA	GAG	TTT	CTG	ACT	TAT	TTC	CAG	AAT	GAA	GCT
L36092,U66060,TRBV7-8*01			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
AF009663,TRBV7-8*01			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X61441	,TRBV7-8*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M27384	,TRBV7-8*03		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
			IMGT																			
			61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
			Q					L	D	K	S	G	L	P	S	D	R	F	F	A	E	R
M11953	,TRBV7-8*01		CAA	...	...	...	...	CTA	GAC	AAA	TCG	GCG	CTG	CCC	AGT	GAT	CGC	TTC	TTT	GCA	GAA	AGG
L36092,U66060,TRBV7-8*01			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
AF009663,TRBV7-8*01			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X61441	,TRBV7-8*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M27384	,TRBV7-8*03		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
			IMGT																			
			81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
			P	E	G	S	V	S	T	L	K	I	Q	R	T	Y	P	O	E	D	S	A
M11953	,TRBV7-8*01		CCT	...	GAG	GGA	TCC	GTC	TCC	ACT	CTG	AAG	ATC	CAG	CGC	ACA	CAG	CAG	GAG	GAC	TCC	GCC
L36092,U66060,TRBV7-8*01			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
AF009663,TRBV7-8*01			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X61441	,TRBV7-8*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M27384	,TRBV7-8*03		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
			CDR3-IMGT																			
			101	102	103	104	105	106	107	108	109											
			V	Y	L	C	A	S	S	L												
M11953	,TRBV7-8*01		GTG	TAT	CTC	TGT	GCC	AGC	AGC	TTA	GC											
L36092,U66060,TRBV7-8*01			---	---	---	---	---	---	---	---	---											
AF009663,TRBV7-8*01			---	---	---	---	---	---	---	---	---											
X61441	,TRBV7-8*02		---	---	---	---	---	---	---	---	---											
M27384	,TRBV7-8*03		---	---	---	---	---	---	---	---	---											
			R																			
			CG-																			
			#c																			

#c: Rearranged cDNA



Framework and complementarity determining regions

FR1-IMGT: 26

CDR1-IMGT: 5

FR2-IMGT: 17

CDR2-IMGT: 6

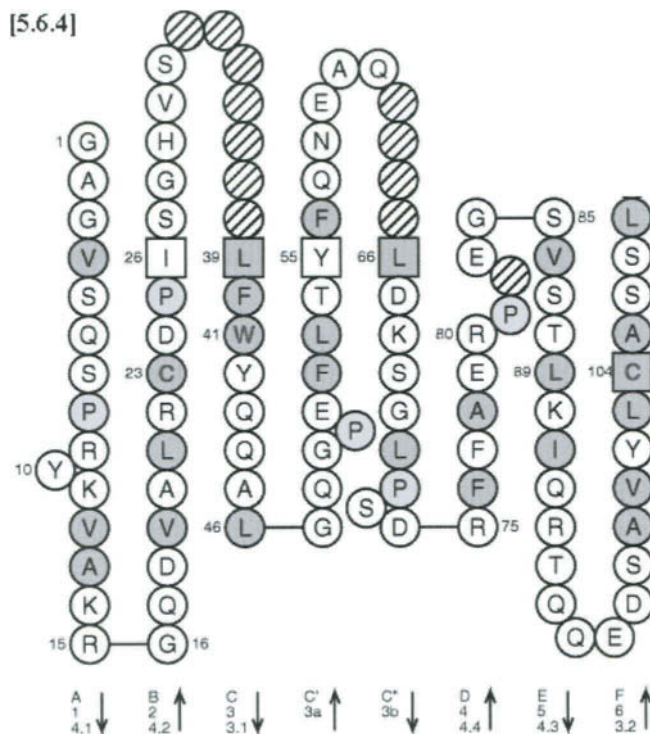
FR3-IMGT: 38 (-1 aa: 82)

CDR3-IMGT: 4

Collier de Perles for human TRBV7-8*01

Accession number: IMGT M11953

EMBL/GenBank/DBJ: M11953



Genome database accession numbers

GDB:9954127

LocusLink: 28590

Nomenclature

TRBV7-9: T cell receptor beta variable 7-9.

Definition and functionality

TRBV7-9 is one of the 5–6 functional genes of the TRBV7 subgroup which comprises nine mapped genes, in the TRB locus.

Gene location

TRBV7-9 is in the TRB locus on chromosome 7 at 7q34.



Nucleotide and amino acid sequences for human TRBV7-9

		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
		D	T	G	V	S	Q	N	P	R	H	K	I	T	K	R	G	Q	N	V	T
L36092, U66060, TRBV7-9*01	{34}	GAT	ACT	GGA	GTC	TCC	CAG	AAC	CCC	AGA	CAC	AAG	ATC	ACA	AAG	AGG	GGA	CAG	AAT	GTA	ACT
AF009661, TRBV7-9*01	{35}	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U03115, TRBV7-9*01	{39}	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X64741, TRBV7-9*01	{13}	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M15564, TRBV7-9*02	{23}	---	---	---	---	---	---	---	---	---	---	---	N	---	---	---	---	---	---	---	---
AF009663, TRBV7-9*03	{35}	---	---	---	---	---	D	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M14261, TRBV7-9*04	{41}	I	S	---	---	---	H	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M27385, TRBV7-9*05	{21}	ATA	T	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X74844, TRBV7-9*06	{19}	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L14854, TRBV7-9*07	{15}	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

		21	22	23	24	25	26	CDR1-IMGT														39	40
		T	T	A	G	G	T	T	C	T	G	A	A	C	A	C	C	...	...	...	...	...	...
L36092, U66060, TRBV7-9*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
AF009661, TRBV7-9*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U03115, TRBV7-9*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X64741, TRBV7-9*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M15564, TRBV7-9*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
AF009663, TRBV7-9*03		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M14261, TRBV7-9*04		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M27385, TRBV7-9*05		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X74844, TRBV7-9*06		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L14854, TRBV7-9*07		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

		41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
		W	Y	R	Q	T	L	G	Q	G	P	E	F	L	T	Y	F	Q	N	E	A
L36092, U66060, TRBV7-9*01		TGG	TAC	CGA	CAG	ACC	CTG	GGG	CAG	GGC	CCA	GAG	TTT	CTG	ACT	TAC	TTC	CAG	AAT	GAA	GCT
AF009661, TRBV7-9*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U03115, TRBV7-9*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X64741, TRBV7-9*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M15564, TRBV7-9*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
AF009663, TRBV7-9*03		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M14261, TRBV7-9*04		---	---	---	---	N	P	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M27385, TRBV7-9*05		---	---	---	---	-CT	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X74844, TRBV7-9*06		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L14854, TRBV7-9*07		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---



	IMGT																			
	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
L36092,U66060,TRBV7-9*01	Q	...	...	...	...	L	E	K	S	R	L	L	S	D	R	F	S	A	E	R
AF009661,TRBV7-9*01	CAA	...	...	...	...	CTA	GAA	AAA	TCA	AGG	CTG	CTC	AGT	GAT	CGG	TTC	TCT	GCA	GAG	AGG
U03115 ,TRBV7-9*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X64741 ,TRBV7-9*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M15564 ,TRBV7-9*02	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
AF009663,TRBV7-9*03	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M14261 ,TRBV7-9*04	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M27385 ,TRBV7-9*05	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X74844 ,TRBV7-9*06	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L14854 ,TRBV7-9*07	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
L36092,U66060,TRBV7-9*01	P	K	G	S	F	S	T	L	E	I	Q	R	T	E	Q	G	D	S	A	
AF009661,TRBV7-9*01	CCT	...	AAG	GGA	TCT	CTC	TCC	ACC	TTG	GAG	ATC	CAG	CGC	ACA	GAG	CAG	GGG	GAC	TCG	GCC
U03115 ,TRBV7-9*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X64741 ,TRBV7-9*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M15564 ,TRBV7-9*02	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
AF009663,TRBV7-9*03	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M14261 ,TRBV7-9*04	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M27385 ,TRBV7-9*05	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X74844 ,TRBV7-9*06	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L14854 ,TRBV7-9*07	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

	CDR3-IMGT									
	101	102	103	104	105	106	107	108	109	
L36092,U66060,TRBV7-9*01	M	Y	L	C	A	S	S	L		
AF009661,TRBV7-9*01	ATG	TAT	CTC	TGT	GCC	AGC	AGC	TTA	GC	
U03115 ,TRBV7-9*01	---	---	---	---	---	---	---	---	---	
X64741 ,TRBV7-9*01	---	---	---	---	---	---	---	---	---	°
M15564 ,TRBV7-9*02	---	---	---	---	---	---	---	---	---	#c
AF009663,TRBV7-9*03	---	---	---	---	---	---	---	---	---	#c
M14261 ,TRBV7-9*04	---	---	---	---	---	---	---	---	---	#c
M27385 ,TRBV7-9*05	---	---	---	---	---	---	---	---	---	#c
X74844 ,TRBV7-9*06	---	---	---	---	---	---	---	---	---	#c
L14854 ,TRBV7-9*07	---	---	---	---	---	---	---	---	---	#c

#c: Rearranged cDNA
°: Genomic DNA, but not known as being germline or rearranged

Framework and complementarity determining regions

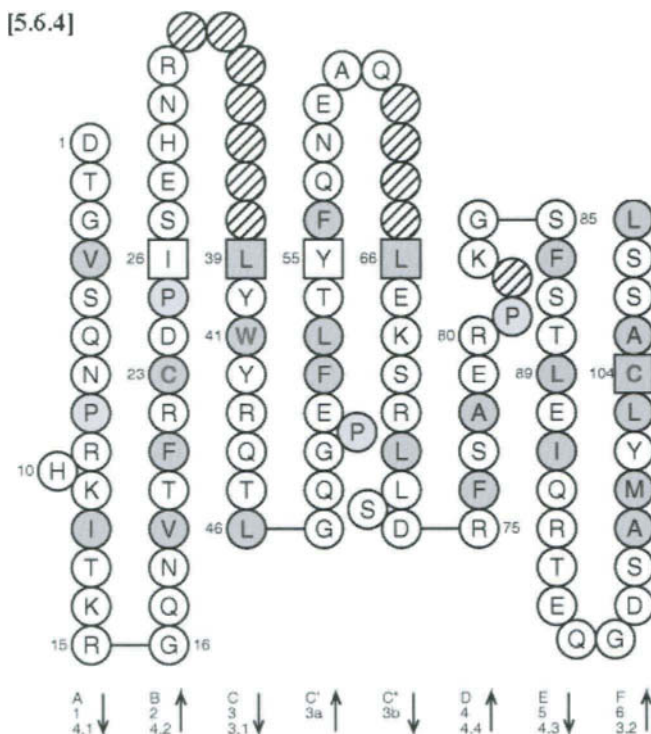
FR1-IMGT: 26	CDR1-IMGT: 5
FR2-IMGT: 17	CDR2-IMGT: 6
FR3-IMGT: 38 (-1 aa: 82)	CDR3-IMGT: 4



Collier de Perles for human TRBV7-9*01

Accession number: IMGT L36092

EMBL/GenBank/DDBJ: L36092



Genome database accession numbers

GDB:9954129

LocusLink: 28589

Nomenclature

TRBV9: T cell receptor beta variable 9.

Definition and functionality

TRBV9 is the unique functional gene of the TRBV9 subgroup which only comprises this mapped gene, in the TRB locus.

Gene location

TRBV9 is in the TRB locus on chromosome 7 at 7q34.

Nucleotide and amino acid sequences for human TRBV9

		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
L36092, U66059, TRBV9*01	[34]	D	S	G	V	T	Q	T	P	K	H	L	I	T	A	T	G	Q	R	V	T
AF009660, TRBV9*02	[35]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M27380, TRBV9*03	[21]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
L36092, U66059, TRBV9*01		L	R	C	S	F	R	S	G	D	L	S	---	---	---	---	---	---	---	V	Y
AF009660, TRBV9*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M27380, TRBV9*03		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
L36092, U66059, TRBV9*01		W	Y	Q	Q	S	L	D	Q	G	L	Q	F	L	I	Q	Y	Y	N	G	E
AF009660, TRBV9*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M27380, TRBV9*03		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
L36092, U66059, TRBV9*01		E	---	---	---	---	R	A	K	G	N	I	L	---	---	---	---	---	---	---	---
AF009660, TRBV9*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M27380, TRBV9*03		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
L36092, U66059, TRBV9*01		F	P	D	L	H	S	E	L	N	L	S	S	L	E	L	G	D	S	A	---
AF009660, TRBV9*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M27380, TRBV9*03		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		101	102	103	104	105	106	107	108	109											
L36092, U66059, TRBV9*01		L	Y	F	C	A	S	S	V	---											
AF009660, TRBV9*02		---	---	---	---	---	---	---	---	---											
M27380, TRBV9*03		---	---	---	---	---	---	---	---	---											

#c: Rearranged cDNA

Framework and complementarity determining regions

FR1-IMGT: 26

FR2-IMGT: 17

FR3-IMGT: 37 (-2 aa: 73, 82)

CDR1-IMGT: 5

CDR2-IMGT: 6

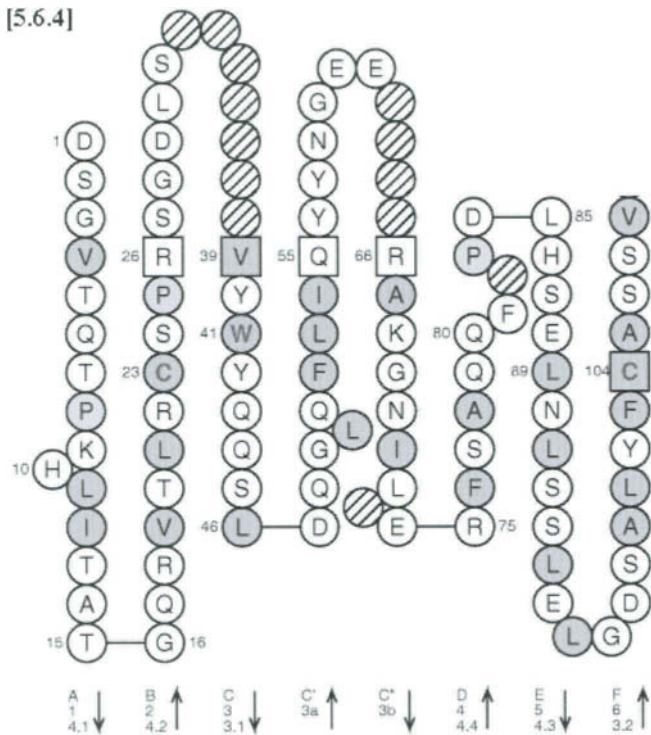
CDR3-IMGT: 4



Collier de Perles for human TRBV9*01

Accession number: IMGT L36092

EMBL/GenBank/DDBJ: L36092



Genome database accession numbers

GDB:9954135

LocusLink: 28586

Nomenclature

TRBV10-1: T cell receptor beta variable 10-1.

Definition and functionality

TRBV10-1 is a functional gene (alleles *01 and *02) or a pseudogene (allele *03). TRBV10-1 belongs to TRBV10 subgroup which comprises three mapped genes, of which 2–3 are functional, in the TRB locus.

TRBV10-1*03 is a pseudogene due to Glutamic acid (gag) 92 replaced by a STOP-CODON (tag), in the FR3-IMGT.

Gene location

TRBV10-1 is in the TRB locus on chromosome 7 at 7q34.

Nucleotide and amino acid sequences for human TRBV10-1

			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
U17050	,TRBV10-1*01	[9]	D	A	E	I	T	Q	S	P	R	H	K	I	T	E	T	G	R	Q	V	T
L36092,U66059,TRBV10-1*01	[34]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L26230	,TRBV10-1*01	[44]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
AF009660,TRBV10-1*02	[35]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U17051	,TRBV10-1*03	[9]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

			21	22	23	24	25	26	27	28	29	30	31	CDR1-IMGT										39	40
U17050	,TRBV10-1*01		L	A	C	H	Q	T	W	N	H	N	N	32	33	34	35	36	37	38	39	40			
L36092,U66059,TRBV10-1*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---			
L26230	,TRBV10-1*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---			
AF009660,TRBV10-1*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---			
U17051	,TRBV10-1*03		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---			

			41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
U17050	,TRBV10-1*01		W	Y	R	Q	D	L	G	H	C	L	R	L	I	H	Y	S	Y	G	V	Q
L36092,U66059,TRBV10-1*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L26230	,TRBV10-1*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
AF009660,TRBV10-1*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U17051	,TRBV10-1*03		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

			IMGT										61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
U17050	,TRBV10-1*01		G	A	C	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
L36092,U66059,TRBV10-1*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L26230	,TRBV10-1*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
AF009660,TRBV10-1*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U17051	,TRBV10-1*03		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

			81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
U17050	,TRBV10-1*01		S	N	T	E	D	L	P	L	T	L	E	S	A	A	S	S	Q	T	S	
L36092,U66059,TRBV10-1*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L26230	,TRBV10-1*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
AF009660,TRBV10-1*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U17051	,TRBV10-1*03		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

		CDR3-IMGT									
		101	102	103	104	105	106	107	108	109	
		V	F	C	A	S	A	S	G	E	
		GTA	TAT	FTT	TGC	GCC	AGC	AGT	GAG	TC	
U17050	,TRBV10-1*01										
L36092,U66059,TRBV10-1*01		---	---	---	---	---	---	---	---	---	
L26230	,TRBV10-1*01										
AFG09660,TRBV10-1*02		---	---	---	---	---	---	---	---	---	
U17051	,TRBV10-1*03	--									

*: STOP-CODON mutation
 °: Genomic DNA, but not known as being germline or rearranged

Framework and complementarity determining regions

FR1-IMGT: 26

CDR1-IMGT: 5

FR2-IMGT: 17

CDR2-IMGT: 6

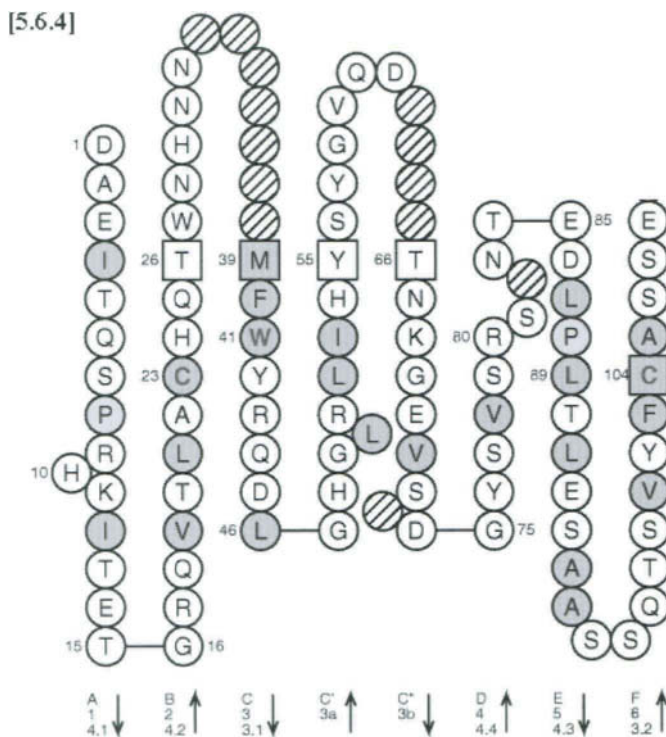
FR3-IMGT: 37 (-2 aa: 73, 82)

CDR3-IMGT: 4

Collier de Perles for human TRBV10-1*01

Accession number: IMGT U17050

EMBL/GenBank/DDDBJ: U17050



Genome database accession numbers

GDB:9954137

LocusLink: 28585

Nomenclature

TRBV10-2: T cell receptor beta variable 10-2.

Definition and functionality

TRBV10-2 is one of the 2–3 functional genes of the TRBV10 subgroup which comprises three mapped genes, in the TRB locus.

Gene location

TRBV10-2 is in the TRB locus on chromosome 7 at 7q34.

Nucleotide and amino acid sequences for human TRBV10-2

			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
U17049	,TRBV10-2*01	[9]	D	A	G	I	T	Q	S	P	R	Y	K	I	T	E	G	R	Q	V	T	
			GAT	GCT	GGA	ATC	ACC	CAG	AGC	CCA	AGA	TAC	AAG	ATC	ACA	GAG	ACA	GGA	AGG	CAG	GTG	ACC
L36092,U66059,TRBV10-2*01	[34]		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U17048	,TRBV10-2*02	[9]																				

°: Genomic DNA, but not known as being germline or rearranged

Framework and complementarity determining regions

FR1-IMGT: 26

FR2-IMGT: 17

FR3-IMGT: 37 (-2 aa: 73, 82)

CDR1-IMGT: 5

CDR2-IMGT: 6

CDR3-IMGT: 4

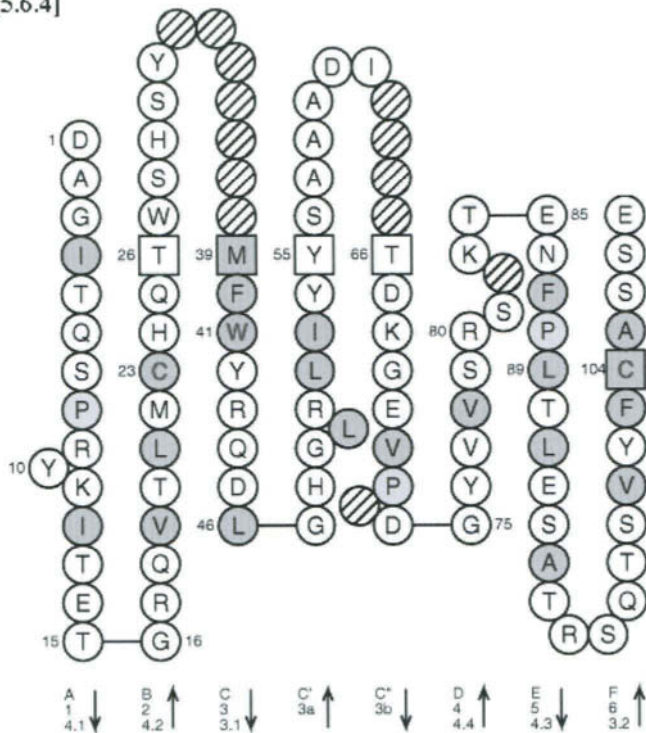


Collier de Perles for human TRBV10-2*01

Accession number: IMGT U17049

EMBL/GenBank/DDBJ: U17049

[5.6.4]



Genome database accession numbers

GDB:9954139

LocusLink: 28584

Nomenclature

TRBV10-3: T cell receptor beta variable 10-3.

Definition and functionality

TRBV10-3 is one of the 2-3 functional genes of the TRBV10 subgroup which comprises three mapped genes, in the TRB locus.

Gene location

TRBV10-3 is in the TRB locus on chromosome 7 at 7q34.

Nucleotide and amino acid sequences for human TRBV10-3



			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20		
U03115	,TRBV10-3*01	[39]	GAT	GCT	GGA	ATC	ACC	CAG	AGC	CCA	AGA	CAC	AAG	GTC	ACA	GAG	ACA	GGA	ACA	CCA	GTG	ACT		
L36092,U66060,TRBV10-3*01	[34]		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
AF009661,TRBV10-3*01	[35]		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
AF009663,TRBV10-3*01	[35]		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
L33100 ,TRBV10-3*01	[8]		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
U17047 ,TRBV10-3*02	[9]		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
L33101 ,TRBV10-3*03	[8]		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
L33102 ,TRBV10-3*04	[8]		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
U03115	,TRBV10-3*01		21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40		
L36092,U66060,TRBV10-3*01			CTG	AGA	TGT	CAC	CAG	ACT	GAG	AAC	CAC	CGC	TAT	...	...	...	...	...	...	...	ATG	TAC		
AF009661,TRBV10-3*01			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
AF009663,TRBV10-3*01			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
L33100 ,TRBV10-3*01			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
U17047 ,TRBV10-3*02			---	---	---	-T	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
L33101 ,TRBV10-3*03			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
L33102 ,TRBV10-3*04			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
U03115	,TRBV10-3*01		41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60		
L36092,U66060,TRBV10-3*01			TGG	TAT	CGA	CAA	GAC	CCG	GGG	CAT	GGG	CTG	AGG	CTG	ATC	CAT	TAC	TCA	TAT	GGT	GTT	AAA		
AF009661,TRBV10-3*01			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
AF009663,TRBV10-3*01			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
L33100 ,TRBV10-3*01			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
U17047 ,TRBV10-3*02			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
L33101 ,TRBV10-3*03			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
L33102 ,TRBV10-3*04			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
U03115	,TRBV10-3*01		IMGT	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	
L36092,U66060,TRBV10-3*01			D	...	...	...	...	...	T	D	K	G	E	V	S	...	D	G	Y	S	V	S	R	
AF009661,TRBV10-3*01			GAT	...	...	...	...	...	ACT	GAC	AAA	GGA	GAA	GTC	TCA	...	GAT	GGC	TAT	AGT	GTC	TCT	AGA	
AF009663,TRBV10-3*01			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
L33100 ,TRBV10-3*01			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
U17047 ,TRBV10-3*02			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
L33101 ,TRBV10-3*03			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
L33102 ,TRBV10-3*04			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
U03115	,TRBV10-3*01		81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100		
L36092,U66060,TRBV10-3*01			S	...	...	...	...	...	T	E	D	F	L	L	T	L	E	S	A	T	S	S		
AF009661,TRBV10-3*01			TCA	...	...	...	...	...	AA	G	ACA	GAG	GAT	ITC	CTC	CTC	GAG	TCC	GCT	ACC	AGC	TCC	ACA	TCT
AF009663,TRBV10-3*01			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
L33100 ,TRBV10-3*01			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
U17047 ,TRBV10-3*02			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
L33101 ,TRBV10-3*03			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
L33102 ,TRBV10-3*04			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	

[illegible]^o: Genomic DNA, but not known as being germline or rearranged

Framework and complementarity determining regions

FR1-IMGT: 26

CDR1-IMGT: 5

FR2-IMGT: 17

CDR2-IMGT: 6

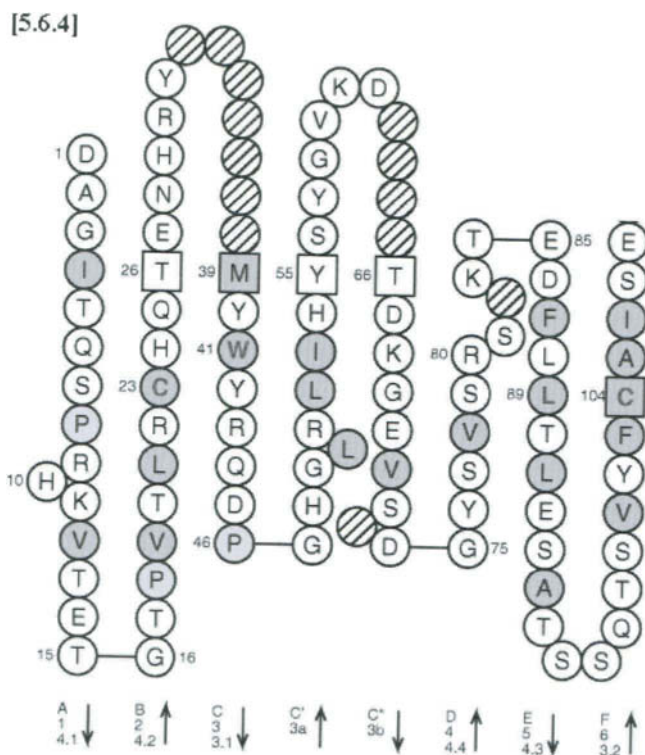
FR3-IMGT: 37 (-2 aa: 73, 82)

CDR3-IMGT: 4

Collier de Perles for human TRBV10-3*01

Accession number: IMGT U03115

EMBL/GenBank/DDDBJ: U03115



Genome database accession numbers

GDB:9954141

LocusLink: 28583

Nomenclature

TRBV11-1: T cell receptor beta variable 11-1.

Definition and functionality

TRBV11-1 is one of the three functional genes of the TRBV11 subgroup which comprises three mapped genes, in the TRB locus.

Gene location

TRBV11-1 is in the TRB locus on chromosome 7 at 7q34.

Nucleotide and amino acid sequences for human TRBV11-1



```

      1   2   3   4   5   6   7   8   9  10  11  12  13  14  15  16  17  18  19  20
M33233 ,TRBV11-1*01 [46] GAA GCT GAA GTT GCC CAG TCC CCC AGA TAT AAG ATT ACA GAG AAA AGC CAG GCT GTG GCT
L36092,U66059,TRBV11-1*01 [34] -----

      21  22  23  24  25  26  27  28  29  30  31  32  33  34  35  36  37  38  39  40
M33233 ,TRBV11-1*01      F W C D P I S G H A T      L Y
TTT TGG TGT GAT CCT ATT TCT GGC CAT GCT ACC      CTT TAC
L36092,U66059,TRBV11-1*01 -----

      41  42  43  44  45  46  47  48  49  50  51  52  53  54  55  56  57  58  59  60
M33233 ,TRBV11-1*01      W Y R Q I L G Q G P E L L V Q F Q D E S
TTG TAC CGG CAG ATC CTG GGA CAG GGC CCG GAG CTT CTG GTT CAA TTT CAG GAT GAG AGT
L36092,U66059,TRBV11-1*01 -----

      61  62  63  64  65  66  67  68  69  70  71  72  73  74  75  76  77  78  79  80
M33233 ,TRBV11-1*01      V      V D D S Q L P K D R F S A E R
GTA ... .. . GTA GAT GAT TCA CAG TTG CCT AAG GAT CGA TTT TCT GCA GAG AGG
L36092,U66059,TRBV11-1*01 -----

      81  82  83  84  85  86  87  88  89  90  91  92  93  94  95  96  97  98  99 100
M33233 ,TRBV11-1*01      L      K G V D S T L K I Q P A E L G D S A
CTC ... AAA GSA GTA GAC TCC ACT CTC AAG ATC CAG CCT GCA GAG CTT GGG GAC TCG GCC
L36092,U66059,TRBV11-1*01 -----

      101 102 103 104 105 106 107 108 109
M33233 ,TRBV11-1*01      W Y L C A S S L
ATG TAT CTC TGT GCC AGC AGC TTA GC
L36092,U66059,TRBV11-1*01 -----

```

Framework and complementarity determining regions

FR1-IMGT: 26

FR2-IMGT: 17

FR3-IMGT: 38 (-1 aa: 82)

CDR1-IMGT: 5

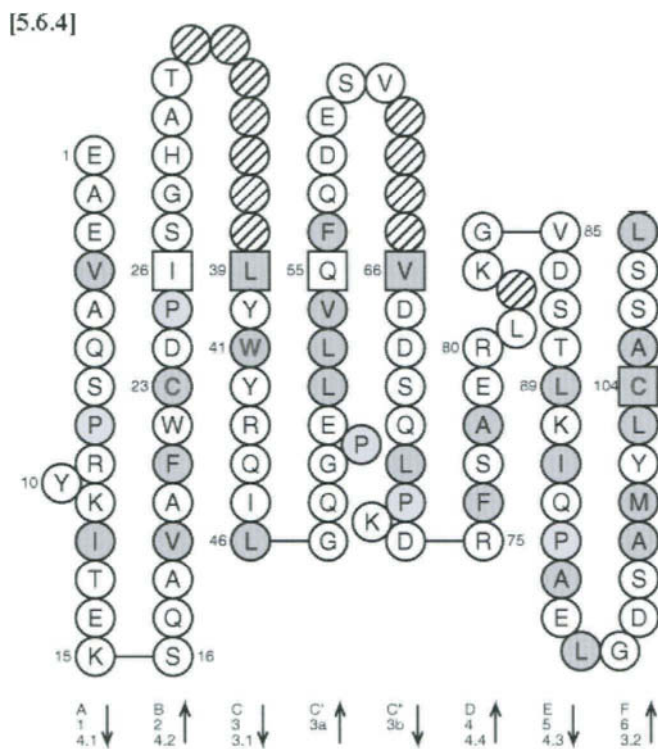
CDR2-IMGT: 6

CDR3-IMGT: 4



Accession number: IMGT M33233

EMBL/GenBank/DDBJ: M33233



1. *Journal of the American Medical Association*, 1997; 277: 103-107.

GDB:9954143

LocusLink: 28582

Nomenclature

TRBV11-2: T cell receptor beta variable 11-2.

Definition and functionality

TRBV11-2 is one of the three functional genes of the TRBV11 subgroup which comprises three mapped genes, in the TRB locus.

Gene location

TRBV11-2 is in the TRB locus on chromosome 7 at 7q34.

Nucleotide and amino acid sequences for human TRBV11-2

		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
L36092,U66059,TRBV11-2*01	[34]	GAA	GCT	GGA	GTT	GCC	CAG	TCT	CCC	AGA	TAT	AAG	ATT	ATA	GAG	AAA	AGG	CAG	AGT	GTG	GCT
M33235	,TRBV11-2*02	[46]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X58796	,TRBV11-2*03	[10]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
L36092,U66059,TRBV11-2*01		TTT	TGG	TGC	AAT	CCT	ATA	TCT	GGC	CAT	GCT	ACC	...	...	...	...	...	...	...	CTT	TAC
M33235	,TRBV11-2*02	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X58796	,TRBV11-2*03	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
L36092,U66059,TRBV11-2*01		TGG	TAC	CAG	CAG	ATC	CTG	GGA	CAG	GGC	CCA	AAG	CTT	CTG	ATT	CAG	TTT	CAG	AAT	AAC	GGT
M33235	,TRBV11-2*02	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X58796	,TRBV11-2*03	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
L36092,U66059,TRBV11-2*01		GTA	...	...	...	...	GTG	GAT	GAT	TCA	CAG	TTG	CCT	AAG	GAT	CGA	TTT	TCT	GCA	GAG	AGG
M33235	,TRBV11-2*02	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X58796	,TRBV11-2*03	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
L36092,U66059,TRBV11-2*01		CTC	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
M33235	,TRBV11-2*02	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X58796	,TRBV11-2*03	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		101	102	103	104	105	106	107	108	109											
L36092,U66059,TRBV11-2*01		GTG	TAT	CTC	TGT	GCC	AGC	AGC	TTA	GA											
M33235	,TRBV11-2*02	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X58796	,TRBV11-2*03	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

#c: Rearranged cDNA

?: Genomic DNA, but not known as being germline or rearranged

Framework and complementarity determining regions

FR1-IMGT: 26

FR2-IMGT: 17

FR3-IMGT: 38 (-1 aa: 82)

CDR1-IMGT: 5

CDR2-IMGT: 6

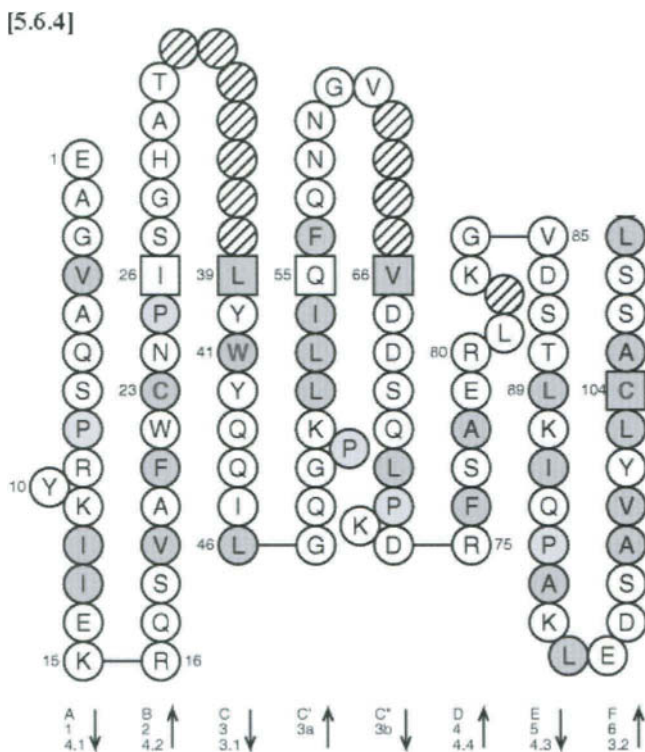
CDR3-IMGT: 4



Collier de Perles for human TRBV11-2*01

Accession number: IMGT L36092

EMBL/GenBank/DDBJ: L36092



Genome database accession numbers

GDB:9954145

LocusLink: 28581

Nomenclature

TRBV11-3: T cell receptor beta variable 11-3.

Definition and functionality

TRBV11-3 is one of the three functional genes of the TRBV11 subgroup which comprises three mapped genes, in the TRB locus.

Gene location

TRBV11-3 is in the TRB locus on chromosome 7 at 7q34.

Nucleotide and amino acid sequences for human TRBV11-3

M33234 , TRBV11-3*01	[46]	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
U03115 , TRBV11-3*01	[39]	E	A	G	V	V	Q	S	P	R	Y	K	I	I	E	K	K	Q	P	V	A
L36092,U66060,TRBV11-3*01	[34]	GAA	GCT	GGA	GTG	GTT	CAG	TCT	CCC	AGA	TAT	AAG	ATT	ATA	GAG	AAA	AAA	CAG	CCT	GTG	GCT
AF009661,TRBV11-3*01	[35]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
AF009663,TRBV11-3*01	[35]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X58797 , TRBV11-3*02	[10]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M62377 , TRBV11-3*03	[33]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
[13] , TRBV11-3*04		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M33234 , TRBV11-3*01		21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
U03115 , TRBV11-3*01		F	W	C	N	P	I	S	G	H	N	T	---	---	---	---	---	---	---	---	---
L36092,U66060,TRBV11-3*01		TTT	TGG	TGC	AAT	CCT	ATT	TCT	GGC	CAC	AAT	ACC	---	---	---	---	---	---	---	---	---
AF009661,TRBV11-3*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
AF009663,TRBV11-3*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X58797 , TRBV11-3*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M62377 , TRBV11-3*03		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
[13] , TRBV11-3*04		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M33234 , TRBV11-3*01		41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
U03115 , TRBV11-3*01		W	Y	L	Q	N	L	G	G	P	E	L	L	I	R	Y	E	N	E	E	E
L36092,U66060,TRBV11-3*01		TGG	TAC	CTG	CAG	AAC	TTG	GGA	CAG	GCC	COG	GAG	CTT	CTG	ATT	CGA	TAT	GAG	AAT	GAG	AGG
AF009661,TRBV11-3*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
AF009663,TRBV11-3*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X58797 , TRBV11-3*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M62377 , TRBV11-3*03		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
[13] , TRBV11-3*04		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M33234 , TRBV11-3*01		61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
U03115 , TRBV11-3*01		A	---	---	---	---	V	D	D	S	Q	L	P	K	D	R	F	S	A	E	R
L36092,U66060,TRBV11-3*01		GCA	---	---	---	---	GTA	GAC	GAT	TCA	CAG	TTG	CCT	ANG	GAT	CGA	TTT	TCT	GCA	GAG	AGG
AF009661,TRBV11-3*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
AF009663,TRBV11-3*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X58797 , TRBV11-3*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M62377 , TRBV11-3*03		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
[13] , TRBV11-3*04		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M33234 , TRBV11-3*01		81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
U03115 , TRBV11-3*01		L	---	---	---	---	K	G	V	D	S	T	L	K	I	Q	P	A	E	L	G
L36092,U66060,TRBV11-3*01		CTC	---	---	AAA	GGA	GTA	GAC	TCC	ACT	CTC	AAG	ATC	CAG	CCT	GCA	GAG	CTT	GGG	GAC	TGC
AF009661,TRBV11-3*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
AF009663,TRBV11-3*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X58797 , TRBV11-3*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M62377 , TRBV11-3*03		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
[13] , TRBV11-3*04		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---



		CDR3-IMGT									
		101	102	103	104	105	106	107	108	109	
M33234	,TRBV11-3*01	V	Y	L	C	A	S	S	L		
U03115	,TRBV11-3*01	GTG	TAT	CTC	TGT	GCC	AGC	AGC	TTA	GA	
L36092,U66060,TRBV11-3*01		---	---	---	---	---	---	---	---	---	
AF009661,TRBV11-3*01		---	---	---	---	---	---	---	---	---	
AF009663,TRBV11-3*01		---	---	---	---	---	---	---	---	---	
X58797	,TRBV11-3*02	---	---	---	---	---	---	---	---	---	#c
M62377	,TRBV11-3*03	M	---	---	---	---	---	---	---	---	#c
[13]	,TRBV11-3*04	A	---	---	---	---	---	---	---	---	#

#: Rearranged
#c: Rearranged cDNA

Framework and complementarity determining regions

FR1-IMGT: 26

CDR1-IMGT: 5

FR2-IMGT: 17

CDR2-IMGT: 6

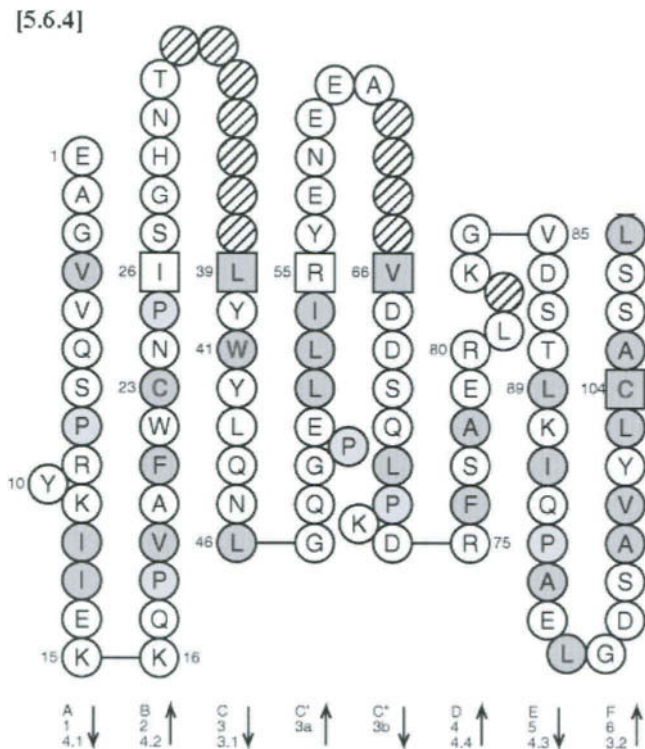
FR3-IMGT: 38 (-1 aa: 82)

CDR3-IMGT: 4

Collier de Perles for human TRBV11-3*01

Accession number: IMGT M33234

EMBL/GenBank/DDBJ: M33234



Genome database accession numbers

GDB:9954147

LocusLink: 28580

Nomenclature

TRBV12-3: T cell receptor beta variable 12-3.

Definition and functionality

TRBV12-3 is one of the three functional genes of the TRBV12 subgroup which comprises five mapped genes, in the TRB locus.

Gene location

TRBV12-3 is in the TRB locus on chromosome 7 at 7q34.

Nucleotide and amino acid sequences for human TRBV12-3

[illegible]

Framework and complementarity determining regions

FR1-IMGT: 26

FR2-IMGT: 17

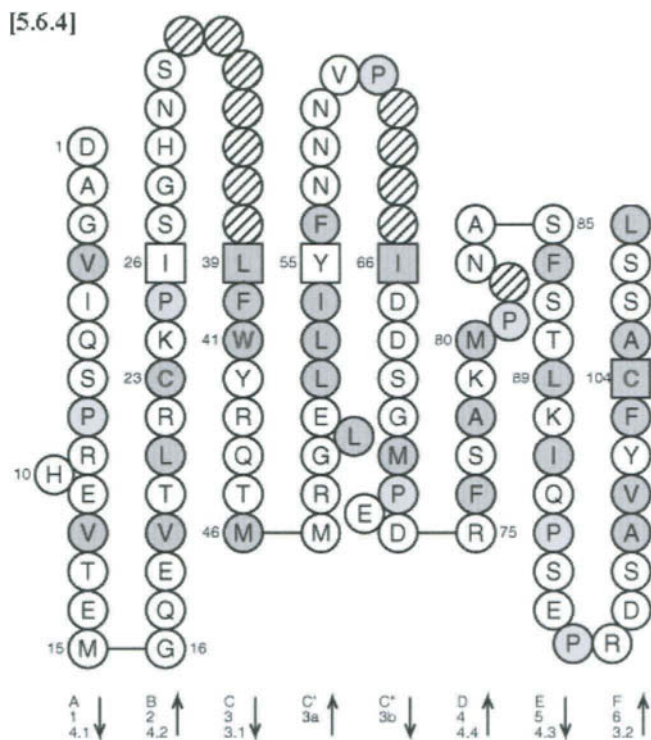
FR3-IMGT: 38 (-1 aa: 82)

CDR1-IMGT: 5

CDR2-IMGT: 6

CDR3-IMGT: 4

EMBL/GenBank/DDBJ: X07192



LocusLink: 28577

TRBV12-4

Nomenclature

TRBV12-4: T cell receptor beta variable 12-4.

Definition and functionality

TRBV12-4 is one of the three functional genes of the TRBV12 subgroup which comprises five mapped genes, in the TRB locus.

Gene location

TRBV12-4 is in the TRB locus on chromosome 7 at 7q34.

Nucleotide and amino acid sequences for human TRBV12-4

		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	
K02546	,TRBV12-4*01	[37]	D	A	G	V	I	Q	S	P	R	H	E	V	T	E	M	G	Q	E	V	T
X07222	,TRBV12-4*01	[38]	GAT	GCT	GGA	GTT	ATC	CAG	TCA	CCC	CGG	CAC	GAG	GTG	ACA	GAG	ATG	GGA	CAA	GAA	GTG	ACT
U03115	,TRBV12-4*01	[39]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L36092,U66060,TRBV12-4*01	[34]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M14264	,TRBV12-4*02	[41]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

		21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
K02546	,TRBV12-4*01	L	R	C	K	P	I	S	G	H	D	Y	---	---	---	---	---	---	---	L	F
X07222	,TRBV12-4*01	CTG	AGA	TGT	AAA	CCA	ATT	TCA	GGA	CAC	GAC	TAC	---	---	---	---	---	---	---	CTT	TTC
U03115	,TRBV12-4*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L36092,U66060,TRBV12-4*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M14264	,TRBV12-4*02	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

		41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
K02546	,TRBV12-4*01	W	Y	R	Q	T	M	M	R	G	L	E	L	L	I	Y	F	N	N	N	V
X07222	,TRBV12-4*01	TGG	TAC	AGA	CAG	ACC	ATG	ATG	CGG	GGA	CTG	GAG	TTG	CTC	ATT	TAC	TTT	AAC	AAC	AAC	GTT
U03115	,TRBV12-4*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L36092,U66060,TRBV12-4*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M14264	,TRBV12-4*02	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

		61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
K02546	,TRBV12-4*01	P	---	---	---	---	I	D	D	S	G	M	P	E	D	R	P	S	A	K	M
X07222	,TRBV12-4*01	CCG	---	---	---	---	ATA	GAT	GAT	TCA	GGG	ATG	CCC	GAG	GAT	CGA	TTC	TCA	GCT	AAG	ATG
U03115	,TRBV12-4*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L36092,U66060,TRBV12-4*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M14264	,TRBV12-4*02	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

		81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
K02546	,TRBV12-4*01	P	N	A	S	P	S	T	L	K	I	Q	P	S	E	P	R	D	S	A	---
X07222	,TRBV12-4*01	CCT	---	AAT	GCA	TCA	TTC	TCC	ACT	CTG	AAG	ATC	CAG	CCC	TCA	GAA	CCC	AGG	GAC	TCA	GCT
U03115	,TRBV12-4*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L36092,U66060,TRBV12-4*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M14264	,TRBV12-4*02	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

		101	102	103	104	105	106	107	108	109
K02546	,TRBV12-4*01	V	Y	F	C	A	S	S	L	---
X07222	,TRBV12-4*01	GTG	TAC	TTC	TGT	GCC	AGC	AGT	TTA	GC
U03115	,TRBV12-4*01	---	---	---	---	---	---	---	---	---
L36092,U66060,TRBV12-4*01	---	---	---	---	---	---	---	---	---	---
M14264	,TRBV12-4*02	---	---	---	---	---	---	---	---	---

#c: Rearranged cDNA



Framework and complementarity determining regions

FR1-IMGT: 26

FR2-IMGT: 17

FR3-IMGT: 38 [-1 aa: 82]

CDR1-IMGT: 5

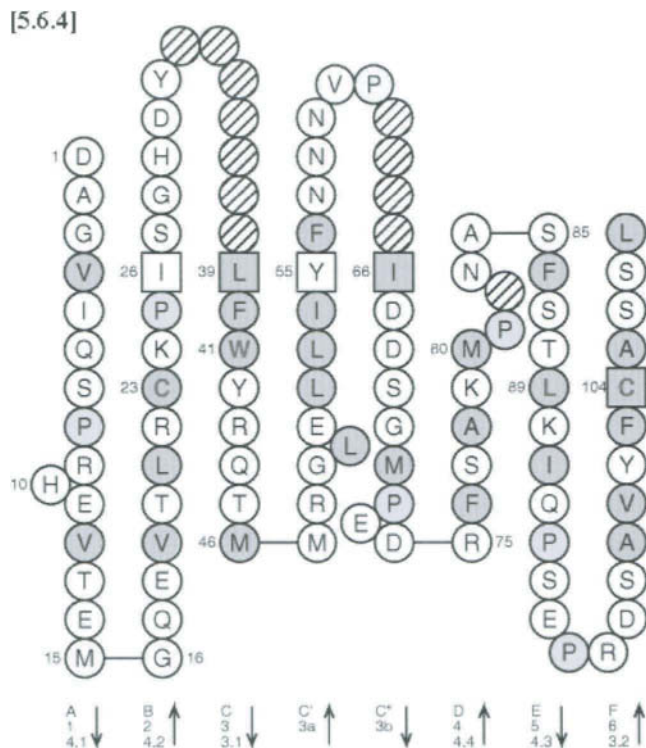
CDR2-IMGT: 6

CDR3-IMGT: 4

Collier de Perles for human TRBV12-4*01

Accession number: IMGT K02546

EMBL/GenBank/DDBJ: K02546



Genome database accession numbers

GDB:9954155

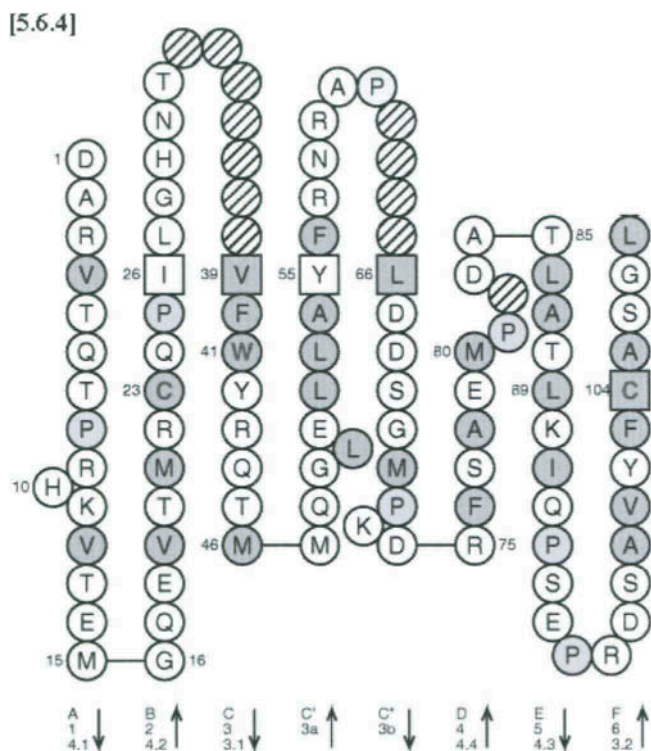
LocusLink: 28576



Collier de Perles for human TRBV12-5*01

Accession number: IMGT X07223

EMBL/GenBank/DDBJ: X07223



Genome database accession numbers

GDB:9954157

LocusLink: 28575

Nomenclature

TRBV13: T cell receptor beta variable 13.

Definition and functionality

TRBV13 is the unique functional gene of the TRBV13 subgroup which only comprises this mapped gene, in the TRB locus.

Gene location

TRBV13 is in the TRB locus on chromosome 7 at 7q34.

Nucleotide and amino acid sequences for human TRBV13

[illegible]



		CDR3-IMGT								
		101	102	103	104	105	106	107	108	109
		L	Y	F		A	S	S	L	
U03115	,TRBV13*01	CTG	TAC	TTC	TGT	GCC	AGC	AGC	TTA	GG
L36092,U66060,TRBV13*01		---	---	---	---	---	---	---	---	---
AF009661,TRBV13*01		---	---	---	---	---	---	---	---	---
AF009663,TRBV13*01		---	---	---	---	---	---	---	---	---
U96844	,TRBV13*01	---	---	---	---	---	---	---	---	---
M62378	,TRBV13*02	---	---	---	---	---	---	---	---	---
#c: Rearranged cDNA		#c								

Framework and complementarity determining regions

FR1-IMGT: 26

FR2-IMGT: 17

FR3-IMGT: 37 (-2 aa: 73, 82)

CDR1-IMGT: 5

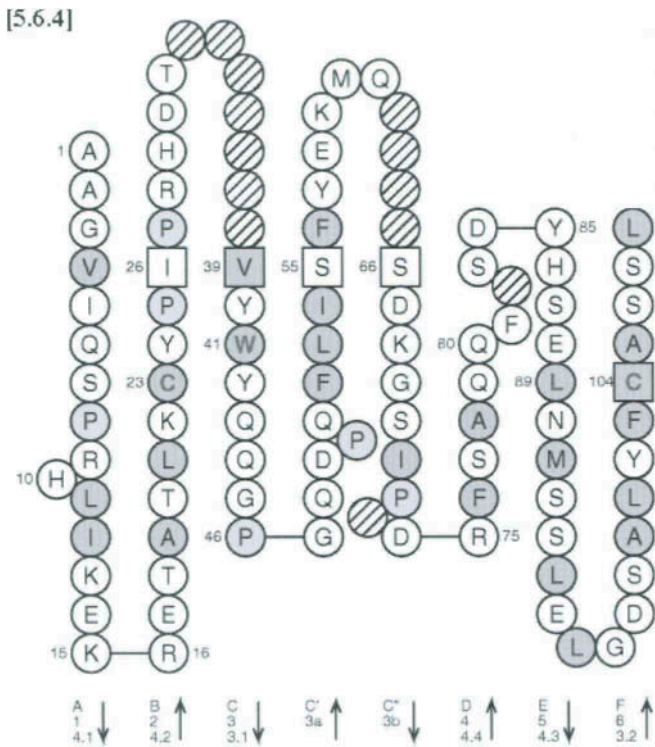
CDR2-IMGT: 6

CDR3-IMGT: 4

Collier de Perles for human TRBV13*01

Accession number: IMGT U03115

EMBL/GenBank/DDBJ: U03115



Genome database accession numbers

GDB:9954159 LocusLink: 28574

Nomenclature

TRBV14: T cell receptor beta variable 14.

Definition and functionality

TRBV14 is the unique functional gene of the TRBV14 subgroup which only comprises this mapped gene, in the TRB locus.

Gene location

TRBV14 is in the TRB locus on chromosome 7 at 7q34.

Nucleotide and amino acid sequences for human TRBV14

			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20									
X06154	,TRBV14*01	[40]	E	A	G	G	V	T	Q	F	P	S	H	S	V	I	E	K	G	Q	T	V	T								
U03115	,TRBV14*01	[39]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---								
L36092	U66060,TRBV14*01	[34]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---								
X57722	,TRBV14*02	[31]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---								
			CDR1-IMGT																												
X06154	,TRBV14*01		21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40									
U03115	,TRBV14*01		L	R	C	D	P	T	S	G	H	D	N	---	---	---	---	---	---	---	L	Y									
L36092	U66060,TRBV14*01		CTG	AGA	TGT	GAC	CCA	ATT	TCT	GGA	CAT	GAT	AAT	---	---	---	---	---	---	---	CTT	TAT									
X57722	,TRBV14*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---									
			CDR2-																												
X06154	,TRBV14*01		41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60									
U03115	,TRBV14*01		W	Y	R	R	V	M	G	K	E	I	K	F	L	L	H	F	V	K	E	S									
L36092	U66060,TRBV14*01		TGG	TAT	CGA	CGT	GTT	ATG	GGA	AAA	GAA	ATA	AAA	TTT	CTG	TTA	CAT	TTT	GTG	AAA	GAG	TCT									
X57722	,TRBV14*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---									
			IMGT																												
X06154	,TRBV14*01		61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80									
U03115	,TRBV14*01		K	---	---	---	---	Q	D	E	S	G	M	P	N	N	R	F	L	A	E	R									
L36092	U66060,TRBV14*01		AAA	---	---	---	---	CAG	GAT	GAG	TCC	GST	ATG	CCC	AAC	AAT	CGA	TTT	TTA	GCT	GAA	AGG									
X57722	,TRBV14*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---									
			IMGT																												
X06154	,TRBV14*01		81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100									
U03115	,TRBV14*01		T	---	G	G	T	Y	S	T	L	K	V	Q	P	A	E	L	E	D	S	G									
L36092	U66060,TRBV14*01		ACT	---	GGA	GGG	ACG	TAT	TCT	ACT	CTG	AAG	GTG	CAG	CCT	GCA	GAA	CTG	GAG	GAT	TCT	GGA									
X57722	,TRBV14*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---									
			CDR3-IMGT																												
X06154	,TRBV14*01		101	102	103	104	105	106	107	108	109																				
U03115	,TRBV14*01		V	Y	F	C	A	S	S	Q	---																				
L36092	U66060,TRBV14*01		GTT	TAT	TTC	TGT	GCC	AGC	AGC	CAA	GA																				
X57722	,TRBV14*02		---	---	---	---	---	---	---	---	---																				

#g: Rearranged genomic DNA

Framework and complementarity determining regions

FR1-IMGT: 26

FR2-IMGT: 17

FR3-IMGT: 38 (-1 aa: 82)

CDR1-IMGT: 5

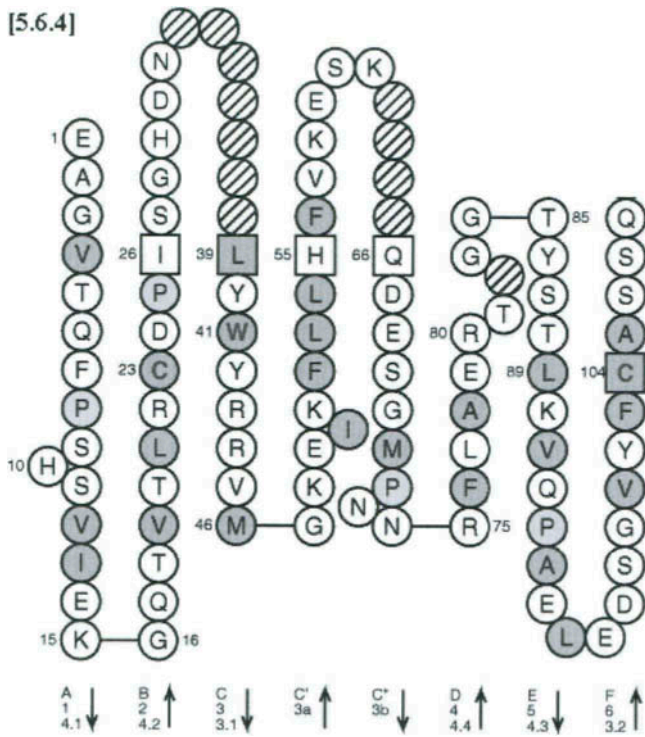
CDR2-IMGT: 6

CDR3-IMGT: 4



Collier de Perles for human TRBV14*01

Accession number: IMGT X06154 EMBL/GenBank/DDBJ: X06154



Genome database accession numbers

GDB:9954161 LocusLink: 28573

Nomenclature

TRBV15: T cell receptor beta variable 15.

Definition and functionality

TRBV15 is the unique functional gene of the TRBV15 subgroup which only comprises this mapped gene, in the TRB locus.

Gene location

TRBV15 is in the TRB locus on chromosome 7 at 7q34.

Nucleotide and amino acid sequences for human TRBV15

[illegible]

#c: Rearranged cDNA

Framework and complementarity determining regions

FR1-IMGT: 26

FR2-IMGT: 17

FR3-IMGT: 37 (-2 aa: 73, 82)

CDR1-IMGT: 5

CDR2-IMGT: 6

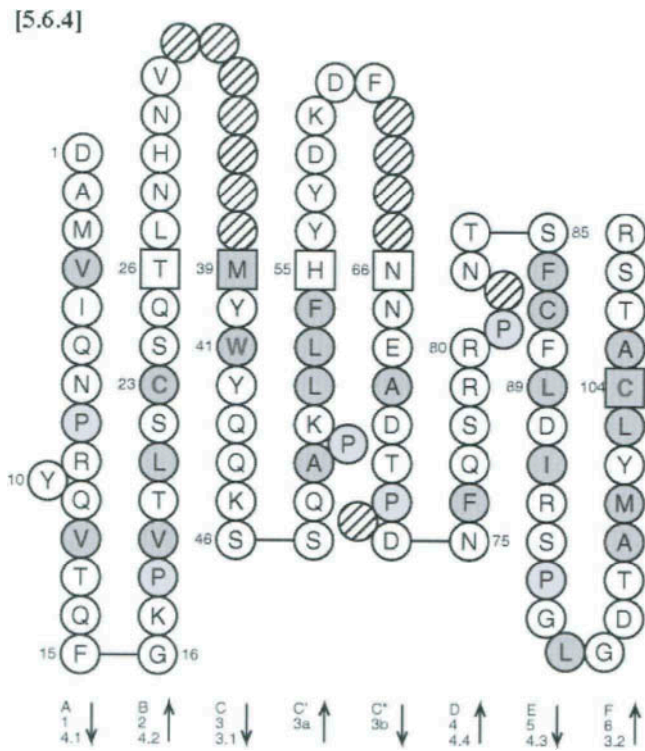
CDR3-IMGT: 4



Collier de Perles for human TRBV15*01

Accession number: IMGT U03115

EMBL/GenBank/DDBJ: U03115



Genome database accession numbers

GDB:9954163

LocusLink: 28572

Nomenclature

TRBV16: T cell receptor beta variable 16.

Definition and functionality

TRBV16 is a functional gene (alleles *01 and *03) or a pseudogene (allele *02). TRBV16 belongs to the TRBV16 subgroup which only comprises this mapped gene, in the TRB locus.

TRBV16*02 is a pseudogene due to Tyrosine (tat) 31 being replaced by a STOP-CODON (tag), in the FR1-IMGT.

Gene location

TRBV16 is in the TRB locus on chromosome 7 at 7q34.

Nucleotide and amino acid sequences for human TRBV16

[illegible]

*: STOP-CODON mutation
#c: Rearranged cDNA



Framework and complementarity determining regions

FR1-IMGT: 26

CDR1-IMGT: 5

FR2-IMGT: 17

CDR2-IMGT: 6

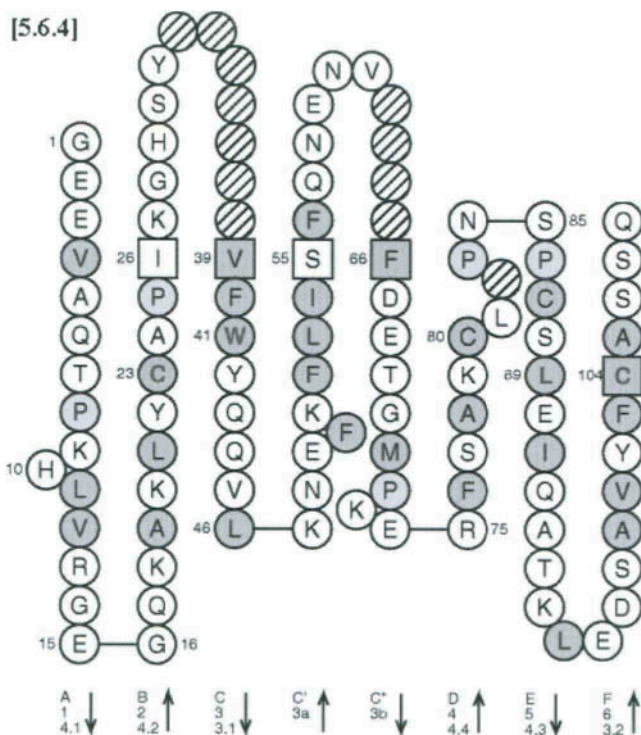
FR3-IMGT: 38 [-1 aa: 82]

CDR3-IMGT: 4

Collier de Perles for human TRBV16*01

Accession number: IMGT L26231

EMBL/GenBank/DBJ: L26231



Genome database accession numbers

GDB:9954165

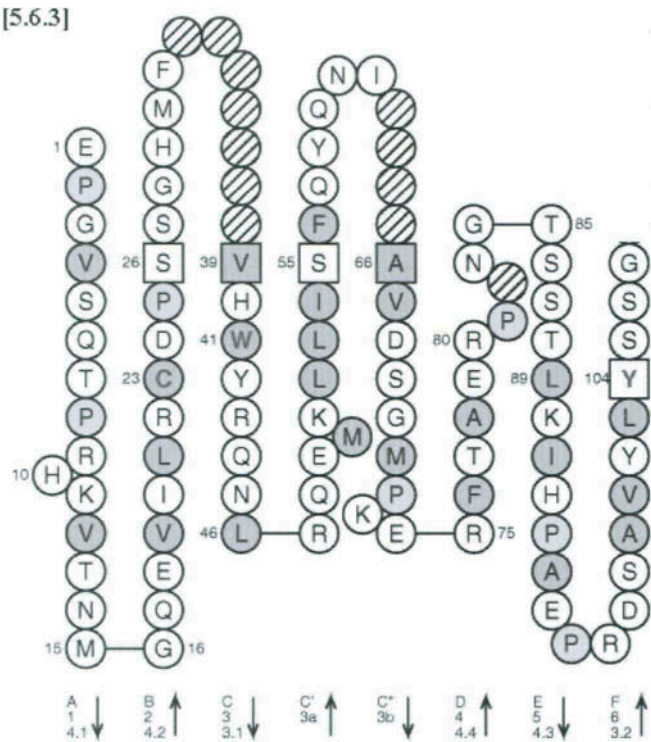
LocusLink: 28571



Collier de Perles for human TRBV17*01

Accession number: IMGT U03115

EMBL/GenBank/DDBJ: U03115



Genome database accession numbers

GDB:9954167

LocusLink: 28570

Nomenclature

TRBV18: T cell receptor beta variable 18.

Definition and functionality

TRBV18 is the unique functional gene of the TRBV18 subgroup which only comprises this mapped gene, in the TRB locus.

Gene location

TRBV18 is in the TRB locus on chromosome 7 at 7q34.

Nucleotide and amino acid sequences for human TRBV18

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20
L36092.U66060,TRBV18*01 [34] AAT GCC GGC GTC ATG CAG AAC CCA AGA CAC CTG GTC AGG AGG AGG GGA CAG GAG GCA AGA
N A G V M Q N P R H L V R R R G Q E A R

21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40
L36092.U66060,TRBV18*01 CTG AGA TGC AGC CCA ATG AAA GGA CAC AGT CAT GTT TAC
L R C S P M K G H S H V Y

41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60
L36092.U66060,TRBV18*01 TGG TAT CGG CAG CTC CCA GAG GAA GGT CTG AAA TTC ATG GTT TAT CTC CAG AAA GAA AAT
W Y R Q L P E E G L K F M V Y L Q K E N

61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80
L36092.U66060,TRBV18*01 ATC ATA GAT GAG TCA GGA ATG CCA AAG GAA CGA TTT TCT GCT GAA TTT
I D E S G M P K E R F S A E F
ATC ATA GAT GAG TCA GGA ATG CCA AAG GAA CGA TTT TCT GCT GAA TTT

81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100
L36092.U66060,TRBV18*01 CCC ... AAA GAG GGC CCC AGC ATC CTG AGG ATC CAG CAG GTA GTG CGA GGA GAT TCG GCA
P K E G P S I L R I Q Q V V R G D S A

101 102 103 104 105 106 107 108 109
L36092.U66060,TRBV18*01 GCT TAT TTC TGT GCC AGC TCA CCA CC
A Y F C A S S P

Framework and complementarity determining regions

FR1-IMGT: 26

FR2-IMGT: 17

FR3-IMGT: 38 (-1 aa: 82)

CDR1-IMGT: 5

CDR2-IMGT: 6

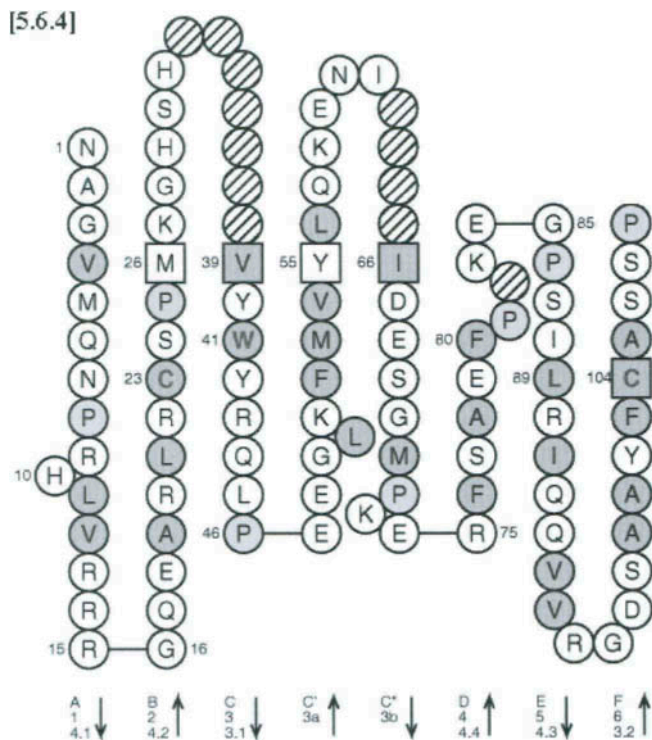
CDR3-IMGT: 4



Collier de Perles for human TRBV18*01

Accession number: IMGT L36092

EMBL/GenBank/DDBJ: L36092



Genome database accession numbers

GDB:9954169

LocusLink: 28569

Nomenclature

TRBV19: T cell receptor beta variable 19.

Definition and functionality

TRBV19 is the unique functional gene of the TRBV19 subgroup which only comprises this mapped gene, in the TRB locus.

Gene location

TRBV19 is in the TRB locus on chromosome 7 at 7q34.

Nucleotide and amino acid sequences for human TRBV19

[illegible]

#c: Rearranged cDNA

Framework and complementarity determining regions

FR1-IMGT: 26

FR2-IMGT: 17

FR3-IMGT: 37 (-2 aa: 73, 82)

CDR1-IMGT: 5

CDR2-IMGT: 6

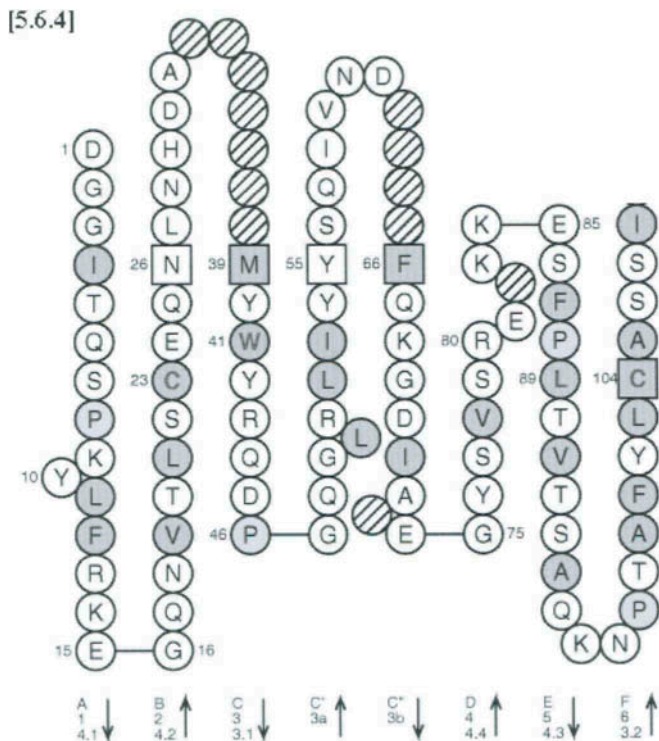
CDR3-IMGT: 4



Collier de Perles for human TRBV19*01

Accession number: IMGT U48260

EMBL/GenBank/DDBJ: U48260



Genome database accession numbers

GDB:9954171

LocusLink: 28568



		101	102	103	104	105	106	107	108	CDR3-IMGT
		F	Y	2	C	S	A	R		
M11955 ,TRBV20-1*01		TTC	TAC	ATC	TGC	AGT	GCT	AGA	GA	
L36092,U66060,U66061,TRBV20-1*01		---	---	---	---	---	---	---	---	
X72719 ,TRBV20-1*02		---	---	---	---	---	---	---	---	
M11954 ,TRBV20-1*03		---	---	---	---	---	---	---	---	#g
M14263 ,TRBV20-1*04		---	---	---	---	---	---	---	---	#c
X57604 ,TRBV20-1*05		---	---	---	---	---	---	---	---	#g
D13088 ,TRBV20-1*06		---	---	---	---	---	---	---	---	#c
X74852 ,TRBV20-1*07		---	---	---	---	---	---	---	---	#c

#c: Rearranged cDNA
#g: Rearranged genomic DNA

Framework and complementarity determining regions

FR1-IMGT: 26

CDR1-IMGT: 6

FR2-IMGT: 17

CDR2-IMGT: 7

FR3-IMGT: 38 (-1 aa: 82)

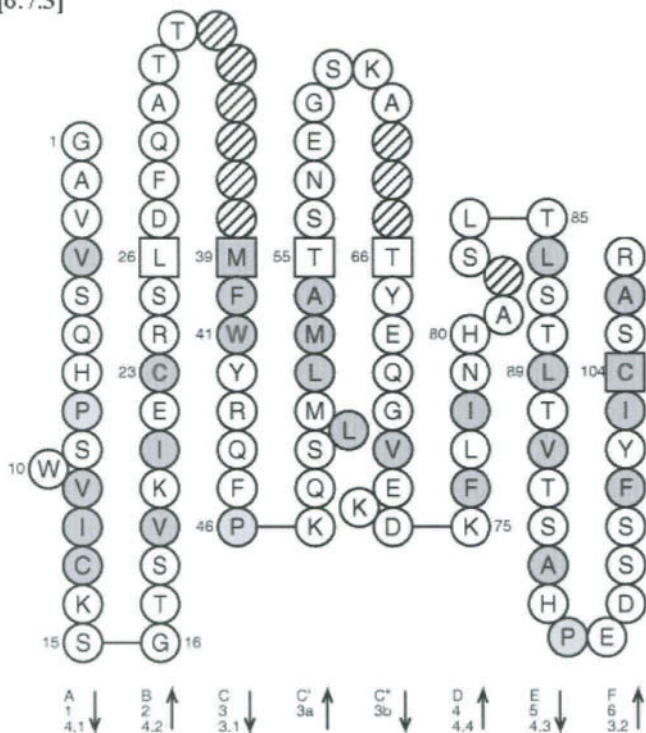
CDR3-IMGT: 3

Collier de Perles for human TRBV20-1*01

Accession number: IMGT M11955

EMBL/GenBank/DDBJ: M11955

[6.7.3]



Genome database accession numbers

GDB:9954173

LocusLink: 28567

Nomenclature

TRBV23-1: T cell receptor beta variable 23-1.

Definition and functionality

TRBV23-1 is an ORF of the TRBV23 subgroup which only comprises this mapped gene, in the TRB locus.

TRBV23-1 is an ORF due to a mutation in the DONOR-SPLICE (ngt being replaced by nat).

Gene location

TRBV23-1 is in the TRB locus on chromosome 7 at 7q34.

Nucleotide and amino acid sequences for human TRBV23-1

		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20			
L36092,U66061,TRBV23-1*01	[34]	CAT	GCC	AAA	GTC	ACA	CAG	ACT	CCA	GGA	CAT	TTG	GTC	AAA	GGA	AAA	GGA	CAG	AAA	ACA	AAG			
L48730	,TRBV23-1*01	[7]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---			
L27614	,TRBV23-1*01	[3]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---			
		21	22	23	24	25	26	CDR1-IMGT														29	30	
L36092,U66061,TRBV23-1*01		ATG	GAT	TGT	ACC	CCC	GAA	AAA	GGA	CAT	ACT	TTT	...	...	...	...	...	...	...	GTT	TAT			
L48730	,TRBV23-1*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---			
L27614	,TRBV23-1*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---			
		41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	CDR2-						59	60
L36092,U66061,TRBV23-1*01		TGG	TAT	CAA	CAG	AAT	CAG	AAT	AAA	GAG	TTT	ATG	CTT	TTG	ATT	TCC	TTT	CAG	AAT	GAA	CAA			
L48730	,TRBV23-1*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---			
L27614	,TRBV23-1*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---			
		IMGT										61	62	63	64	65	66	67	68	69	70	71		
L36092,U66061,TRBV23-1*01												V	L	Q	E	T	E	M	H	K	R	R	72	
L48730	,TRBV23-1*01											---	---	---	---	---	---	---	---	---	---	---	---	
L27614	,TRBV23-1*01											---	---	---	---	---	---	---	---	---	---	---	---	
		81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100			
L36092,U66061,TRBV23-1*01		CCC	...	AAG	AAC	GCA	CCC	TGC	AGC	CTG	GCA	ATC	CTG	TCC	TCA	GAA	CCG	GGA	GAC	ACG	GCA			
L48730	,TRBV23-1*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---			
L27614	,TRBV23-1*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---			
		CDR3-IMGT										101	102	103	104	105	106	107	108	109				
L36092,U66061,TRBV23-1*01												L	Y	L	C	A	S	S	Q					
L48730	,TRBV23-1*01											---	---	---	---	---	---	---	---	---	---	---		
L27614	,TRBV23-1*01											---	---	---	---	---	---	---	---	---	---	---		

°: Genomic DNA, but not known as being germline or rearranged

Framework and complementarity determining regions

FR1-IMGT: 26
FR2-IMGT: 17
FR3-IMGT: 38 (-1 aa: 82)

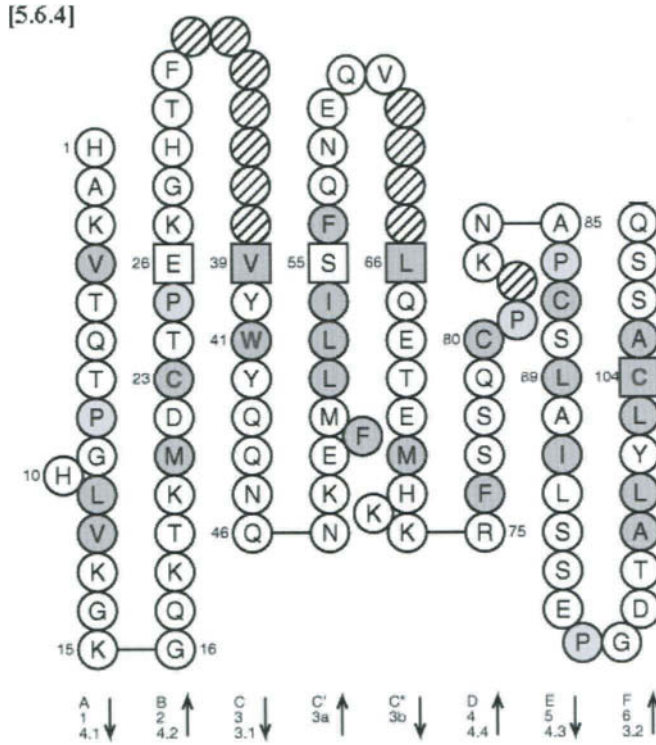
CDR1-IMGT: 5
CDR2-IMGT: 6
CDR3-IMGT: 4



Collier de Perles for human TRBV23-1*01

Accession number: IMGT L36092

EMBL/GenBank/DDBJ: L36092



Genome database accession numbers

GDB:9954179

LocusLink: 28564

Nomenclature

TRBV24-1: T cell receptor beta variable 24-1.

Definition and functionality

TRBV24-1 is the unique functional gene of the TRBV24-1 subgroup which only comprises this mapped gene, in the TRB locus.

Gene location

TRBV24-1 is in the TRB locus on chromosome 7 at 7q34.

Nucleotide and amino acid sequences for human TRBV24-1

			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20			
M11951	,TRBV24-1*01	[18]	D	A	D	V	T	Q	T	P	R	N	R	I	T	K	T	G	K	R	I	M			
L27612	,TRBV24-1*01	[3]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---			
L36092,U66061,TRBV24-1*01	[34]		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---			
			21	22	23	24	25	26	CDR1-IMGT																
M11951	,TRBV24-1*01		L	E	C	S	Q	T	K	G	H	D	R									M	Y		
L27612	,TRBV24-1*01		CTG	GAA	TGT	TCT	CAG	ACT	AAG	GGT	CAT	GAT	AGA	...	...	...	...	...	...	...	...	ATG	TAC		
L36092,U66061,TRBV24-1*01			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
			41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	CDR2-							
M11951	,TRBV24-1*01		W	Y	R	Q	D	P	G	L	G	L	R	L	I	Y	Y	S	F	D	V	K			
L27612	,TRBV24-1*01		TGG	TAT	CGA	CAA	GAC	CCA	GGA	CTG	GGC	CTA	CGG	TTG	ATC	TAT	TAC	TCC	TTT	GAT	GTC	AAA			
L36092,U66061,TRBV24-1*01			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---			
			IMGT			61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
M11951	,TRBV24-1*01		D			I	N	K	G	E	I	S				D	G	Y	S	V	S	R			
L27612	,TRBV24-1*01		GAT	...	...	...	...	...	ATA	AAC	AAA	GGA	GAG	ATC	TCT	...	GAT	GGA	TAC	AGT	GTC	TCT	CGA		
L36092,U66061,TRBV24-1*01			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
			81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100			
M11951	,TRBV24-1*01		Q		A	Q	A	K	F	S	L	S	L	E	S	A	I	P	N	Q	T	A			
L27612	,TRBV24-1*01		GCA	...	GCA	CAG	GCT	AAA	TTC	TCC	CTG	TCC	CTA	GAG	TCT	GCC	ATC	CCC	AAC	CAG	ACA	GCT			
L36092,U66061,TRBV24-1*01			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---			
			CDR3-IMGT			101	102	103	104	105	106	107	108	109											
M11951	,TRBV24-1*01		L	Y	F	C	A	T	S	D	L														
L27612	,TRBV24-1*01		CTT	TAC	TTC	TGT	GCC	ACC	AGT	GAT	TTG														
L36092,U66061,TRBV24-1*01			---	---	---	---	---	---	---	---	---	---	---	---											

Framework and complementarity determining regions

FR1-IMGT: 26

FR2-IMGT: 17

FR3-IMGT: 37 (-2 aa: 73, 82)

CDR1-IMGT: 5

CDR2-IMGT: 6

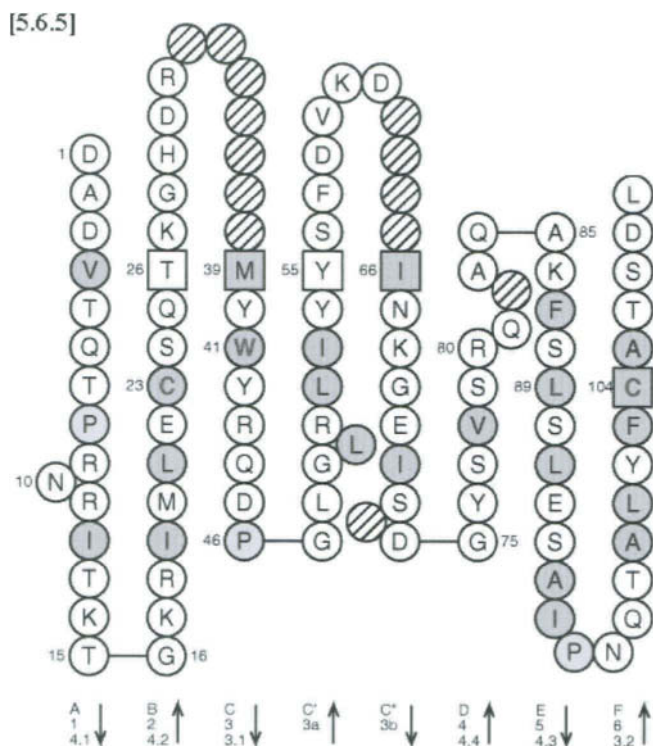
CDR3-IMGT: 5



Collier de Perles for human TRBV24-1*01

Accession number: IMGT M11951

EMBL/GenBank/DDBJ: M11951



Genome database accession numbers

GDB:9954181

LocusLink: 28563

Nomenclature

TRBV25-1: T cell receptor beta variable 25-1.

Definition and functionality

TRBV25-1 is the unique functional gene of the TRBV25-1 subgroup which only comprises this mapped gene, in the TRB locus.

Gene location

TRBV25-1 is in the TRB locus on chromosome 7 at 7q34.

Nucleotide and amino acid sequences for human TRBV25-1

		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
L36092,U66061,TRBV25-1*01	[34]	E	A	D	I	Y	Q	T	P	R	Y	L	V	I	G	T	G	K	K	I	T
L27610	,TRBV25-1*01	[3]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

		21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
L36092,U66061,TRBV25-1*01		L	E	C	S	Q	T	N	G	H	D	K									
L27610	,TRBV25-1*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

		41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
L36092,U66061,TRBV25-1*01		W	Y	Q	Q	D	P	G	M	E	L	H	L	I	H	Y	S	Y	G	V	N
L27610	,TRBV25-1*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

		61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
L36092,U66061,TRBV25-1*01		S					T	E	K	G	D	L	S		S	E	S	T	V	S	R
L27610	,TRBV25-1*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

		81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
L36092,U66061,TRBV25-1*01		I	R	T	E	H	P	P	L	T	L	E	S	A	R	P	S	H	T	S	
L27610	,TRBV25-1*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

		101	102	103	104	105	106	107	108	109
L36092,U66061,TRBV25-1*01		Q	Y	L	C	A	S	S	E	
L27610	,TRBV25-1*01	---	---	---	---	---	---	---	---	---

Framework and complementarity determining regions

FR1-IMGT: 26

FR2-IMGT: 17

FR3-IMGT: 37 (-2 aa: 73, 82)

CDR1-IMGT: 5

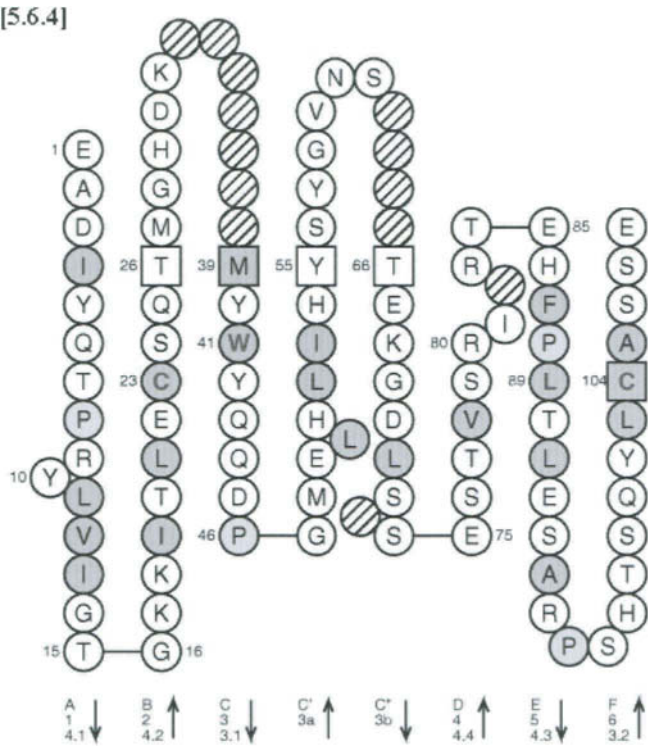
CDR2-IMGT: 6

CDR3-IMGT: 4



Collier de Perles for human TRBV25-1*01

Accession number: IMGT L36092 EMBL/GenBank/DDBJ: L36092



Genome database accession numbers

GDB:9954183 LocusLink: 28562

Nomenclature

TRBV27: T cell receptor beta variable 27.

Definition and functionality

TRBV27 is the unique functional gene of the TRBV27 subgroup which only comprises this mapped gene, in the TRB locus.

Gene location

TRBV27 is in the TRB locus on chromosome 7 at 7q34.



Nucleotide and amino acid sequences for human TRBV27

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
	E	A	Q	V	T	Q	N	P	R	Y	L	I	T	V	T	G	K	K	L	T
L36092,U66061,TRBV27*01 [34]	GAA	GCC	CAA	GTG	ACC	CAG	AAC	CCA	AGA	TAC	CTC	ATC	ACA	GTG	ACT	GGA	AAG	AAG	TTA	ACA
	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
	V	P	C	S	Q	N	M	N	H	E	Y	...	...	...	...	...	...	...	M	S
L36092,U66061,TRBV27*01	GTG	ACT	TGT	TCT	CAG	AAT	ATG	AAC	CAT	GAG	TAT	...	...	...	...	...	...	...	ATG	TCC
	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
	W	Y	R	Q	D	P	G	L	G	L	R	Q	I	Y	Y	S	M	N	V	E
L36092,U66061,TRBV27*01	TGG	TAT	CGA	CAA	GAC	CCA	GGG	CTG	GGC	TTA	AGG	CAG	ATC	TAC	TAT	TCA	ATG	AAT	GTT	GAG
	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
	V	...	...	...	...	T	D	K	G	D	V	P	...	E	G	Y	K	V	S	R
L36092,U66061,TRBV27*01	GTG	...	...	...	...	ACT	GAT	AAG	GGA	GAT	GTT	CCT	...	GAA	GGG	TAC	AAA	GTC	TCT	CGA
	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
	K	...	E	K	R	N	P	P	L	I	L	E	S	P	S	P	N	Q	T	S
L36092,U66061,TRBV27*01	AAA	...	GAG	AAG	AGG	AAT	TTC	CCC	CTG	ATC	CTG	GAG	TCG	CCC	AGC	CCC	AAC	CAG	ACC	TCT
	101	102	103	104	105	106	107	108	109											
	L	Y	F	C	A	S	S	L												
L36092,U66061,TRBV27*01	CTG	TAC	TTC	TGT	GCC	AGC	AGT	TTA	TC											

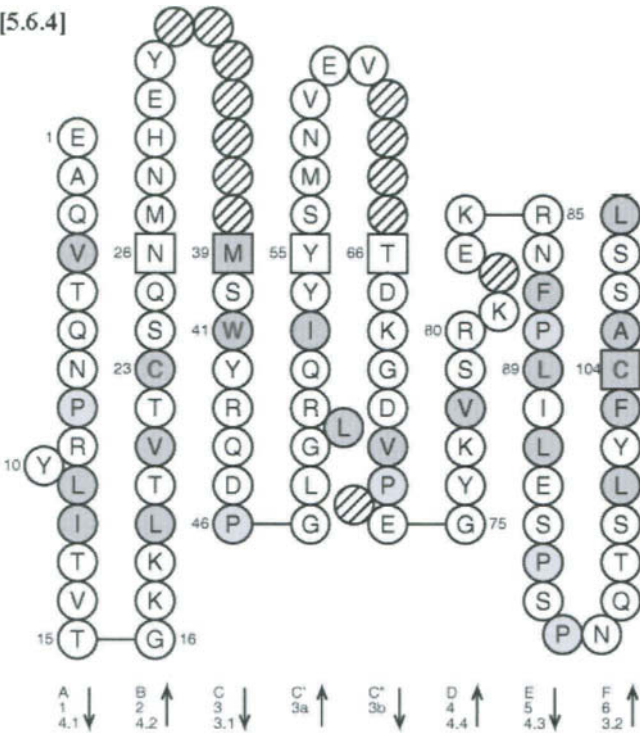
Framework and complementarity determining regions

FR1-IMGT: 26	CDR1-IMGT: 5
FR2-IMGT: 17	CDR2-IMGT: 6
FR3-IMGT: 37 (-2 aa: 73, 82)	CDR3-IMGT: 4



Collier de Perles for human TRBV27*01

Accession number: IMGT L36092 EMBL/GenBank/DDBJ: L36092



Genome database accession numbers

GDB:9954187 LocusLink: 28560

Nomenclature

TRBV28: T cell receptor beta variable 28.

Definition and functionality

TRBV28 is the unique functional gene of the TRBV28 subgroup which only comprises this mapped gene, in the TRB locus.

Gene location

TRBV28 is in the TRB locus on chromosome 7 at 7q34.

Nucleotide and amino acid sequences for human TRBV28

[illegible]

^a: Genomic DNA, but not known as being germline or rearranged

Framework and complementarity determining regions

FR1-IMGT: 26

FR2-IMGT: 17

FR3-IMGT: 37 (-2 aa: 73, 82)

CDR1-IMGT: 5

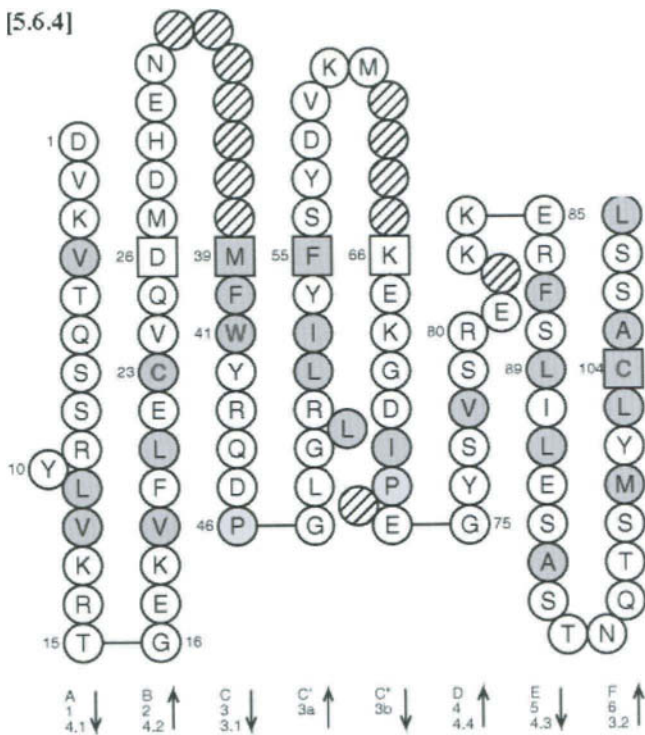
CDR2-IMGT: 6

CDR3-IMGT: 4



Collier de Perles for human TRBV28*01

Accession number: IMGT U08314 EMBL/GenBank/DDBJ: U08314



Genome database accession numbers

GDB:9954189 LocusLink: 28559

TRBV29-1

Nomenclature

TRBV29-1: T cell receptor beta variable 29-1.

Definition and functionality

TRBV29-1 is the unique functional gene of the TRBV29-1 subgroup which only comprises this mapped gene, in the TRB locus.

Gene location

TRBV29-1 is in the TRB locus on chromosome 7 at 7q34.

Nucleotide and amino acid sequences for human TRBV29-1

		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
		S	A	V	I	S	Q	K	P	S	R	D	I	C	Q	R	G	T	S	L	T
L36092,U66061,TRBV29-1*01	[34]	AGT	GCT	GTC	ATC	TCT	CAA	AAG	CCA	AGC	AGG	GAT	ATC	TGT	CAA	CGT	GGA	ACC	TCC	CTG	AGC
L27623,TRBV29-1*01	[3]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M13847,TRBV29-1*02	[5]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X04926,TRBV29-1*03	[22]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
		I	Q	C	Q	V	D	S	Q	V	T	M								M	F
L36092,U66061,TRBV29-1*01		ATC	CAG	TGT	CAA	GTC	GAT	AGC	CAA	GTC	ACC	ATG	...	...	...	...	...	...	...	ATG	TTC
L27623,TRBV29-1*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M13847,TRBV29-1*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X04926,TRBV29-1*03		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	I	A
		41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
		W	Y	R	Q	Q	P	G	A	C	G	A	C	T	G	A	A	N	Q	G	S
L36092,U66061,TRBV29-1*01		TGG	TAC	CGT	CAG	CAA	CCT	GGA	CAG	AGC	CTG	ACA	CTG	ATC	GCA	ACT	GCA	AAT	CAG	GGC	TCT
L27623,TRBV29-1*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M13847,TRBV29-1*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X04926,TRBV29-1*03		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
		E	A				T	Y	E	S	G	F	V	I	D	K	P	P	I	S	R
L36092,U66061,TRBV29-1*01		GAG	GCC	...	...	...	ACA	TAT	GAG	ATG	GGA	TTT	GTC	ATT	GAC	AAG	TTT	CCC	ATC	AGC	CGC
L27623,TRBV29-1*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M13847,TRBV29-1*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X04926,TRBV29-1*03		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
		P	N	L	T	F	S	T	L	T	V	S	N	N	S	P	E	D	S	S	
L36092,U66061,TRBV29-1*01		CCA	...	AAC	CTA	ACA	TTC	TCA	ACT	CTG	ACT	GTG	AGC	AAC	ATG	AGC	CCT	GAA	GAC	AGC	AGC
L27623,TRBV29-1*01		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M13847,TRBV29-1*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X04926,TRBV29-1*03		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		101	102	103	104	105	106	107	108												
		I	Y	L	C	S	V	E													
L36092,U66061,TRBV29-1*01		ATA	TAT	CTC	TGC	AGC	GTT	GAA	GA												
L27623,TRBV29-1*01		---	---	---	---	---	---	---	---												
M13847,TRBV29-1*02		---	---	---	---	---	---	---	---	#c											
X04926,TRBV29-1*03		---	---	---	---	---	---	---	---	A	C										
										-CG	-GC	#c									

#c: Rearranged cDNA

Framework and complementarity determining regions

FR1-IMGT: 26

FR2-IMGT: 17

FR3-IMGT: 38 (-1 aa: 82)

CDR1-IMGT: 5

CDR2-IMGT: 7

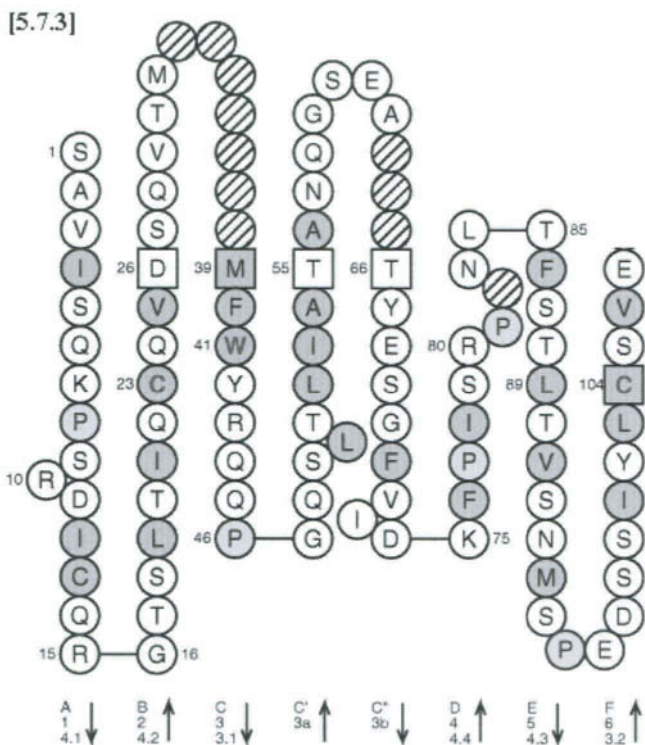
CDR3-IMGT: 3



Collier de Perles for human TRBV29-1*01

Accession number: IMGT L36092

EMBL/GenBank/DDBJ: L36092



Genome database accession numbers

GDB:9954191

LocusLink: 28558

Nomenclature

TRBV30: T cell receptor beta variable 30.

Definition and functionality

TRBV30 is a functional gene (alleles *01, *02, *04, *05) or a pseudogene (allele *03). TRBV30 belongs to the TRBV30 subgroup which only comprises this mapped gene, in the TRB locus.

TRBV30*03 is a pseudogene due to Arginine (cga) 43 being replaced by a STOP-CODON (tga) in the FR2-IMGT.

Gene location

TRBV30 is in the TRB locus on chromosome 7 at 7q34.

Nucleotide and amino acid sequences for human TRBV30



		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
L36092,U66061,TRBV30*01	[34]	TCT	CAG	ACT	ATT	CAT	CAA	TGG	CCA	GCG	ACC	CTG	GTG	CAG	CCT	GTG	GCG	AGC	CCG	CTC	TCT
Z13967	,TRBV30*02	[4]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
[4]	,TRBV30*03		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M13554	,TRBV30*04	[24]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L06893	,TRBV30*05	[36]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

		21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
L36092,U66061,TRBV30*01		L	E	C	T	V	E	G	T	S	N	P	N							L	Y
Z13967	,TRBV30*02	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
[4]	,TRBV30*03	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M13554	,TRBV30*04	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L06893	,TRBV30*05	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

		41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
L36092,U66061,TRBV30*01		TGG	TAC	CGA	CAG	GCT	GCA	GCG	AGG	GCG	CTC	CAG	CTG	CTC	TTC	TAC	TCC	GTT	GGT	ATT	GGC
Z13967	,TRBV30*02	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
[4]	,TRBV30*03	---	---	T--	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M13554	,TRBV30*04	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	I		D	
L06893	,TRBV30*05	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	A-		-A-	

		61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
L36092,U66061,TRBV30*01							Q	I	S	S	E	V	P		Q	N	L	S	A	S	R
Z13967	,TRBV30*02	---	---	---	---	---	CAG	ATC	AGC	TCT	GAG	GTG	CCC	---	CAG	AAT	CTC	TCA	GCC	TCC	AGA
[4]	,TRBV30*03	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M13554	,TRBV30*04	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L06893	,TRBV30*05	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

		81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
L36092,U66061,TRBV30*01		CCC	---	CAG	GAC	CGG	CAG	TTC	ATC	CTG	AGT	TCT	AAG	AAG	CTC	CTT	CTC	AGT	GAC	TCT	GGC
Z13967	,TRBV30*02	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
[4]	,TRBV30*03	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M13554	,TRBV30*04	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L06893	,TRBV30*05	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---



		CDR3-IMGT							
		101	102	103	104	105	106	107	108
L36092,U66C61,TRBV30*01		F	Y	L	C	A	W	S	
		TTC	TAT	CTC	TGT	GCC	TGG	AGT	GT
Z13967,TRBV30*02		---	---	---	---	---	---	---	---
[4],TRBV30*03		---	---	---	---	---	---	---	---
M13554,TRBV30*04		---	---	---	---	---	---	---	#c
		---	---	---	---	G	---	---	
L06893,TRBV30*05		---	---	---	---	G-A	---	---	#c

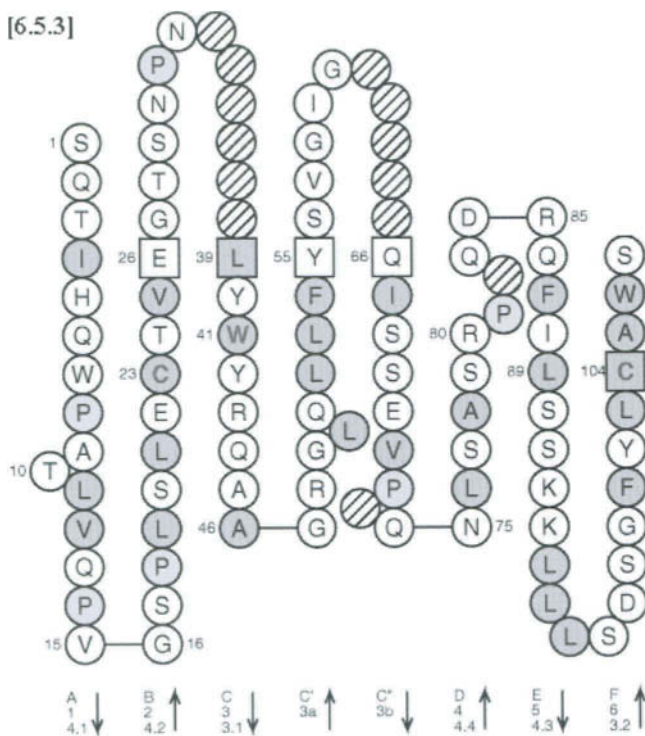
*: STOP-CODON mutation
#c: Rearranged cDNA

Framework and complementarity determining regions

FR1-IMGT: 26	CDR1-IMGT: 6
FR2-IMGT: 17	CDR2-IMGT: 5
FR3-IMGT: 37 (-2 aa: 73, 82)	CDR3-IMGT: 3

Collier de Perles for human TRBV30*01

Accession number: IMGT L36092 EMBL/GenBank/DDBJ: L36092



Genome database accession numbers
GDB:9954193 LocusLink: 28557

Protein display of the human TRB V-REGIONS

Only the *01 allele of each functional or ORF V-REGION is shown. TRBV genes are listed, for each subgroup, according to their position from 5' to 3' in the locus. N-glycosylation sites (NXS/T, where X is different from P) are underlined.

TRBV gene	FR1-IMGT (1-26)	CDR1-IMGT (27-38)	FR2-IMGT (39-55)	CDR2-IMGT (56-65)	FR3-IMGT (66-104)	CDR3-IMGT (105-115)
	1 10 20 30 40 50 60 70 80 90 100 110					
L36092 ,TRBV2	EPEVTQTPSHQVQTQMGQEVILRCVPI	SNHLY.....	FYWYRQILGQKVEFLVS	FYNNEI....	SEKSEIFDDQFSVERP.DGSNFTLKIRSTPKLEDSAMYFC	ASSE.....
U07977 ,TRBV3-1	DTAVSQTPKYLVTQMGNDKSIKCEQN	LGHDT.....	MYWYQDKSKKFLKIMFS	YNNKEL....	IINETVP.NRFSKSPK.DKAHLNLHINSLELGDSAVYFC	ASSQ.....
U07977 ,TRBV4-1	DTEVTQTPKHLVMGMTNNKSLKCEQH	MGHRA.....	MYWYQKAKKPPELMFV	YSYEKL....	SINESVP.SRFSPECP.NSSLLNLHLHALQPEDSALYLC	ASSQ.....
U07975 ,TRBV4-2	ETGVTQTPRHLVMGMTNNKSLKCEQH	LGHNA.....	MYWYQSAKKPPELMFV	YNFKEQ....	TENNSVP.SRFSPECP.NSHLFLHLHTLQPEDSALYLC	ASSQ.....
U07978 ,TRBV4-3	ETGVTQTPRHLVMGMTNNKSLKCEQH	LGHNA.....	MYWYQSAKKPPELMFV	YSLEER....	VENNSVP.SRFSPECP.NSHLFLHLHTLQPEDSALYLC	ASSQ.....
L36092 ,TRBV5-1	KAGVTQTPRYLIKTRGQQVTLSCSPI	SGHRS.....	VSWYQQTGQGLQFLFE	YFSETQ....	RNKGNFP.GRFSGRQF.SNSRSEMNVSTLELGDSALYLC	ASSL.....
X61439 ,TRBV5-3	EAGVTQSPTHLIKTRGQQVTLRCSPI	SGHSS.....	VSWYQQAAGQGQPFIFE	YANELR....	RSEGNFP.NRFSGRQF.HDCSEMNVSALELGDSALYLC	ARSL.....
L36092 ,TRBV5-4	ETGVTQSPTHLIKTRGQQVTLRCSSP	SGHNT.....	VSWYQQAALGQGPQFIFQ	YYREEE....	NGRGNFP.PRFSGLQF.PNYSELNVNALLEDDSDALYLC	ASSL.....
L36092 ,TRBV5-5	DAGVTQSPTHLIKTRGQQVTLRCSPI	SGHKS.....	VSWYQQVLGQGPQFIFQ	YYEKEE....	RGRGNFP.DRFSARQF.PNYSELNVNALLLGDSALYLC	ASSL.....
L36092 ,TRBV5-6	DAGVTQSPTHLIKTRGQQVTLRCSPK	SGHDT.....	VSWYQQAALGQGPQFIFQ	YYEEEE....	RQRGNFP.DRFSGHQF.PNYSELNVNALLLGDSALYLC	ASSL.....
L36092 ,TRBV5-7	DAGVTQSPTHLIKTRGQHVTLRCSPI	SGHTS.....	VSSYQQAALGQGPQFIFQ	YYEKEE....	RGRGNFP.DQFSGHQF.PNYSELNVNALLLGDSALYLC	ASSL.....
L36092 ,TRBV5-8	EAGVTQSPTHLIKTRGQQATLRCSPI	SGHTS.....	VYWYQQAALGLQGLFLW	YDEGEE....	RNRGNFP.PRFSGRQF.PNYSELNVNALLEDDSDALYLC	ASSL.....
X61446 ,TRBV6-1	NAGVTQTPKFQVLKTGQSMTLQCAQD	MNHNS.....	MYWYRQDPCMGLRLIYY	SASEGT....	TDKGEVP.NGYNVSRL.NKREFSLRLESAAPSQTSVYFC	ASSE.....
X61445 ,TRBV6-2	NAGVTQTPKFRVLKTGQSMTLQCAQD	MNHEY.....	MYWYRQDPCMGLRLIHY	SVGEGT....	TAKGEVP.DGYNVSRL.KKQNFLLGLLESAAPSQTSVYFC	ASSY.....
U07978 ,TRBV6-3	NAGVTQTPKFRVLKTGQSMTLQCAQD	MNHEY.....	MYWYRQDPCMGLRLIHY	SVGEGT....	TAKGEVP.DGYNVSRL.KKQNFLLGLLESAAPSQTSVYFC	ASSY.....
X61453 ,TRBV6-4	IAGITQAPTSQLAAGRMTLRCQD	MRHNA.....	MYWYRQDLGLGLRLIHY	SNTAGT....	TGKGEVP.DGYSVSRA.NTDDFPLTLASAVPSQTSVYFC	ASSD.....
L36092 ,TRBV6-5	NAGVTQTPKFRVLKTGQSMTLQCAQD	MNHEY.....	MSWYRQDPCMGLRLIHY	SVGAGI....	TDQGEVP.NGYNVSRL.NTDDFPLRLLSAAPSQTSVYFC	ASSY.....
L36092 ,TRBV6-6	NAGVTQTPKFRVLKTGQSMTLQCAQD	MNHNY.....	MYWYRQDPCMGLRLIHY	SVGAGI....	TDKGEVP.NGYNVSRL.NTDDFPLRLLESAAPSQTSVYFC	ASSY.....
L36092 ,TRBV6-7	NAGVTQTPKFRVLKTGQSMTLQCAQD	MNHEY.....	MYWYRQDPCMGLRLIHY	SVAAL....	TDKGEVP.NGYNVSRL.NTDDFPLKLESAAPSQTSVYFC	ASSY.....
L36092 ,TRBV6-8	NAGVTQTPKFRVLKTGQSMTLQCAQD	MNHGY.....	MSWYRQDPCMGLRLIYY	SAAAGT....	TDK.EVP.NGYNVSRL.NTDDFPLRLVSAAPSQTSVYLC	ASSY.....
X61447 ,TRBV6-9	NAGVTQTPKFRVLKTGQSMTLQCAQD	MNHGY.....	LSWYRQDPCMGLRLIHY	SVAAGI....	TDKGEVP.DGYNVSRL.NTDDFPLRLLESAAPSQTSVYFC	ASSY.....
X61444 ,TRBV7-1	GAGVSQSLRHKVAKKGKDVALRYDPI	SGHNA.....	LYWYRQSLGQGLEFLPIY	FQKKA....	ADKSGLPDRFSAQRS.EGSISTLKQRTQQQDVALYLC	ASSS.....
X61442 ,TRBV7-2	GAGVSQSPSNKVTEKGKDVALRCDDPI	SGHTA.....	LYWYRQSLGQGLEFLPIY	FQGNAS....	PDKSGLPDRFSAERT.GGSVSTLTQRTQQEDSAVYLC	ASSL.....
X61440 ,TRBV7-3	GAGVSQTPSNKVTEKGQVVELRCDDPI	SGHTA.....	LYWYRQSLGQGPFLPIY	FQGTGA....	ADDSGLPNDRFFAVRP.EGSVSTLTKIQRTERGDSAVYLC	ASSL.....
L36092 ,TRBV7-4	GAGVSQSPRYKVAKRGRDVALRCDSI	SGHVT.....	LYWYRQTLGQGSSEVLTY	SQSDAQ....	RDKSGRPSGRFSAERP.ERSVSTLTKIQRTEQQDSAVYLC	ASSL.....
L36092 ,TRBV7-6	GAGVSQSPRYKVTKRGQDVALRCDDPI	SGHVS.....	LYWYRQALGQGPFLTY	FNVEAQ....	QDKSGLPNDRFSAERP.EGSISTLTQRTQEQDSAMYRC	ASSL.....
L36092 ,TRBV7-7	GAGVSQSPRYKVTKRGQDVALRCDDPI	SSHAT.....	LYWYQQAALGQGPFLTY	FNVEAQ....	PDKSGLPNDRFSAERP.EGSISTLTQRTQEQDSAMYRC	ASSL.....
M11953 ,TRBV7-8	GAGVSQSPRYKVAKRGRDVALRCDDPI	SGHVS.....	LFWYQQAALGQGPFLTY	FQNEAQ....	LDKSGLPNDRFFAERP.EGSVSTLTKIQRTEQQDSAVYLC	ASSL.....
L36092 ,TRBV7-9	DTGVSQNPRIKTKRGQNVTFRCDDPI	SEHNR.....	LYWYRQTLGQGPFLTY	FQNEAQ....	LEKSRLLSDRFSAERP.KGSFSTLEIQRTEQQDSAMYLC	ASSL.....

Continued

Continued

TRBV gene	FR1-IMGT (1-26)			CDR1-IMGT (27-38)		FR2-IMGT (39-55)		CDR2-IMGT (56-65)		FR3-IMGT (66-104)			CDR3-IMGT (105-115)	
	1	10	20	30	40	50	60	70	80	90	100	110		
L36092 , TRBV9	DSGVTQTPKHLITATGQRVTLRCS	PR	SPR	SGDLS		VYWYQQSLDQGLQLFIQ	YNGEE		RAKGNIL	ERFSAQQF	PDLHSELNLSLELGDSALYFC	ASSV		
U17050 , TRBV10-1	DAEITQSPRHKITETGRQVTLACHQT	WNHNN		MFWYRQDLGHGLRLIHY	SYGVQD		TNKG	EV	DGYSV	SRS	NTEDLPLTLESAASSQTSVYFC	ASSE		
U17049 , TRBV10-2	DAGITQSPRYKITETGRQVTLMCHQT	WSHSY		MFWYRQDLGHGLRLIYY	SAAADI		TDKGE	VP	DG	VVS	SRS	KTENFPLTLESATRSQTSVYFC	ASSE	
U03115 , TRBV10-3	DAGITQSPRHKVTETGTPVTLRCHQT	ENHRY		MYWYRQDPGHGLRLIHY	SYGVKD		TDKGE	VS	DGYS	VSR	S	KTEDFLLTLESATSSQTSVYFC	AISE	
M33233 , TRBV11-1	EAEVAQSPRYKITEKSAVAFWCDPI	SGHAT		LYWYRQILGQGPELLVQ	FQDES		VDDSQLPKDRFSAERL	KGVD	STLKI	QPAELGDSAMYLC	ASSL			
L36092 , TRBV11-2	EAGVAQSPRYKII EKQSVAFWCNPI	SGHAT		LYWYQQILGQGPPELLIY	FQNGV		VDDSQLPKDRFSAERL	KGVD	STLKI	QPAKLED	SAVYLC	ASSL		
M33234 , TRBV11-3	EAGVVQSPRYKII EKQVPVAFWCNPI	SGHNT		LYWYLQNLGQGPPELLIR	YENEE		VDDSQLPKDRFSAERL	KGVD	STLKI	QPAELGDSAVYLC	ASSL			
X07192 , TRBV12-3	DAGVIQSPRHEVT	EMGQ	EVTLRCKPI	SGHNS		LFWYRQTMGRLELLIY	FNNNVP		IDDSG	MPDRFSAKMP	NASFSTLKI	QPS	EPDR	SAVYFC
K02546 , TRBV12-4	DAGVIQSPRHEVT	EMGQ	EVTLRCKPI	SGHIY		LFWYRQTMGRLELLIY	FNNNVP		IDDSG	MPDRFSAKMP	NASFSTLKI	QPS	EPDR	SAVYFC
X07223 , TRBV12-5	DARVTQTPRHKVT	EMGQ	EVTLRCKPI	LGHNT		LFWYRQTMGRLELLIY	FRNRAP		LD	SGMPKDRFSAEMP	DATLATLKI	QPS	EPDR	SAVYFC
U03115 , TRBV13	AAGVIQSPRHLIKEKRETATLKCYPI	PRHDT		VYWYQQGPGQDPQLIS	FYEKM		SDKGSIP	DRFSAQQF	SDYHSELNMS	SLELGDSALYFC	ASSL			
X06154 , TRBV14	EAGVTQFPSSHVIEKGQVTLRCDPI	SGHDN		LYWYRRVMGKEIKFLH	FVKESK		QDESGMPNNRFLAERT	GGTYSTLKVQPAELED	SGVYFC	ASSQ				
U03115 , TRBV15	DAMVIQNPRYQVTQFGKPVTLSCSQT	LNHN		MYWYQQKSSQAPKLLFH	YYDKDF		NNEADTP	DNFQSR	RP	NTSFCFLDIRSPGLGDTAMYLC	ATSR			
L26231 , TRBV16	GEEVAQTPKHLVRGEGQAKLYCAPI	KGHSY		VFWYQQVLKNEFKFLIS	FQNE	ENV		FDE	TGMPKERFSAKCL	PNSPCSLEI	QATKLED	SAVYFC	ASSQ	
U03115 , TRBV17	EPGVSQTPRHKVNTMGGQEVILRCDPS	SGHMF		VHWYRQNLRQEMKLLIS	FQYQNI		AVDSGMPKERFTAERP	NGTSS	TLKIHPAEPDR	SAVYLY	SSG			
L36092 , TRBV18	NAGVMQNPRHLVRRRGQEARLRCSMP	KGHS		VYWYRQLPEEGLKFMVY	LQKENI		IDESGMPKERFSAEFP	KEGPSILRI	QVVVRGDS	SAAYFC	ASSP			
U48260 , TRBV19	DGGITQSPKYLFRKEGQNVTLSCQEN	LNHDA		MYWYRQDPGQGLRLIYY	SQIVND		FQKGDIA	EGYSV	SRE	KKESFPLTVTSAQKNPTAFYLC	ASSI			
M11955 , TRBV20-1	GAVVSQHPSPWICKSGTSVKIECRSL	DFQATT		MFWYRQFPKQSLMLMAT	SNESKA		TYEQGVEKD	FLINHA	SLTLSTLTVTSAHPED	SSFYIC	SAR			
L36092 , TRBV23-1	HAKVTQTPGHLVKGGQKTKMCDTPE	KGHTF		VYWYQQNQNKEFMLLIS	FQNEQV		LQETEMHKKRFSSQCP	KNAPCSLAIL	SEPGD	TALYLC	ASSQ			
M11951 , TRBV24-1	DADVQTTPRNRIKTGKRIMLECSQT	KGHDR		MYWYRQDPGLGLRLIYY	SFDVKD		INKGEIS	DGYSV	SRS	AQAKFSL	SLESAIPNQ	TALYFC	ATSDL	
L36092 , TRBV25-1	EADIYQTPRYLVIGTGKKITLESQST	MGHDK		MYWYQQDPGMELHLIHY	SYGVNS		TEKGDLS	SESTVSRI	RTEHFPLTLESAR	PSHTSQYLC	ASSE			
L36092 , TRBV27	EAQVTQNPRYLITVTGKKLTVTCSQN	MNHEY		MSWYRQDPGLGLRQIYY	SMNVEV		TDKGDVP	EGYKVS	RK	EKRNFPLILESPSPNQTS	SLYFC	ASSL		
U08314 , TRBV28	DKVKTQSSRYLVKRTGEKVFL	ECVQD	MDHEN		MFWYRQDPGLGLRLIYY	SYDVKM		KEKGDIP	EGYSV	SRE	KKERFSLILE	SASTNQTS	SMYLC	ASSL
L36092 , TRBV29-1	SAVISQKPSRDICQRGTSLTIQ	CQVD	SQVTM		MFWYRQDPGQSLTLIAT	ANQGSEA		TYESG	FVIDKFPISRP	NLTFSTLTVSNMS	SPEDSSI	YLC	SVE	
L36092 , TRBV30	SQTIHQWPATLVQPVGSPLS	LECTVE	GTSNPN		LYWYRQAAGRLQLLFY	SVGIG		QISSEVP	QNLSASRP	QDRQF	ILSSKKLL	LLSDSGFYLC	AWS	

TRBV recombination signals

Recombination signals

Only the recombination signal of the *01 allele of each functional or ORF TRB V-REGION is shown. Non-conserved nucleotides taken into account for the ORF functionality definition are shown in bold and italic.

TRAV gene name	V Recombination Signal (V-RS)		
	V-HEPTAMER	(bp)	V-NONAMER
TRBV2*01	CACAGCC	23	GCAAAATCC
TRBV3-1*01	CACAGCC	23	GCACAAACC
TRBV4-1*01	CACAGCC	23	GCAGAAACC
TRBV4-2*01	CACAGCC	23	GCAGAAACC
TRBV4-3*01	CACAGCC	23	GCAGAAACC
TRBV5-1*01	CACAGCC	23	GCACAAACC
TRBV5-3*01 (ORF)	CACAGCC	23	GCACTAATC
TRBV5-4*01	CACAGCC	23	ACATAAACT
TRBV5-5*01	CACAGCC	23	ATATAAACT
TRBV5-6*01	CACAGCC	23	ATATAAACT
TRBV5-7*01 (ORF)	CACAGCC	23	ATATAAACT
TRBV5-8*01	CACAGCC	23	ATATAAACT
TRBV6-1*01	CACAGCG	23	ACATAAAGG
TRBV6-2*01	CACAGTG	23	ACAGAAAGG
TRBV6-3*01	CACAGTG	23	ACAGAAAGG
TRBV6-4*01	CACAGTG	23	ACATAAATG
TRBV6-5*01	CACAGCG	23	ACATAAAGG
TRBV6-6*01	CACAGCG	23	ACATAAAGG
TRBV6-7*01 (ORF)	CACAGCG	23	ACATAAAGG
TRBV6-8*01	CACAGCG	23	ACATAAAGG
TRBV6-9*01	CACAGCG	23	ACATAAAGG
TRBV7-1*01 (ORF)	CACAGCA	del	del
TRBV7-2*01	CACAGCA	23	TCATAAACC
TRBV7-3*01	CACAGCA	23	TCATAAACC
TRBV7-4*01	CACAGCG	23	TCACAAACC
TRBV7-6*01	CACAGTG	23	TCACAAACC
TRBV7-7*01	CACAGCA	23	TCACAAACC
TRBV7-8*01	CACAGCA	23	TCACAAACC
TRBV7-9*01	CACAGCA	23	TCACAAACC
TRBV9*01	CACAGCC	23	GCAATAACA
TRBV10-1*01	CACAGTG	23	ACATAAAGG
TRBV10-2*01	CACAGTG	23	ACGGAATG
TRBV10-3*01	CACAGTG	23	ACGTAAACA
TRBV11-1*01	CACAGCG	22	GCACAAAAC
TRBV11-2*01	CACAGTG	23	GCAGAAAAC
TRBV11-3*01	CACAGTG	23	GCAGAAAAC
TRBV12-3*01	CACAGCG	23	GCAGAAAAC
TRBV12-4*01	CACAGCG	23	GCAGAAAAC
TRBV12-5*01	CACAGCG	23	GCAGAAAAC
TRBV13*01	CACAGAC	23	ACCCAAAAC
TRBV14*01	CACAGTG	23	GCAAAACCA
TRBV15*01	CACAGAG	23	TCATAAACC
TRBV16*01	CACAGTG	23	CACAGACTC
TRBV17*01 (ORF)	CACAGCA	23	GTGCAAAAC
TRBV18*01	CACATTG	23	CCACAAACA
TRBV19*01	CACAGTG	23	GCATAAATG
TRBV20-1*01	CACAGCG	23	GCAAGAACC
TRBV23-1*01 (ORF)	CACAGCA	23	ACACAAACT
TRBV24-1*01	CACAGTG	23	ACAGAAAGA
TRBV25-1*01	CACAGTG	23	ACAGAAAGG
TRBV27*01	CACAGTG	23	ACAAAAACA
TRBV28*01	CACAGCG	23	ACAAAAAGA
TRBV29-1*01	CACAGTG	23	GCAAGAACC
TRBV30*01	CACACTG	23	GCAAAAACC

del: deleted

References

- ¹ Barron, K.S. et al., unpublished.
- ² Boitel, B. et al. (1992) *J. Exp. Med.* 175, 765–777.
- ³ Charmley, P. et al. (1995) *Genomics* 25, 150–156.
- ⁴ Charmley, P. et al. (1993) *J. Exp. Med.* 177, 135–143.
- ⁵ Concannon, P. et al. (1986) *Proc. Natl Acad. Sci. USA* 83, 6598–6602.
- ⁶ Cornélis, F. et al. (1993) *Eur. J. Immunol.* 23, 1277–1283.
- ⁷ Currier, J.R. et al. unpublished.
- ⁸ Day, C.E. et al. (1992) *Hum. Immunol.* 34, 196–202.
- ⁹ Deulofeut, H. et al. (1995) *Hum. Immunol.* 43, 227–230.
- ¹⁰ Ferradini, L. et al. (1991) *Eur. J. Immunol.* 21, 935–942.
- ¹¹ Gomolka, M. et al. (1993) *Immunogenetics* 37, 257–265.
- ¹² Hall, M.A. et al. (1994) *Eur. J. Immunol.* 24, 641–645.
- ¹³ Hansen, T. et al. (1992) *Scand. J. Immunol.* 36, 285–290.
- ¹⁴ Hansen, T. et al. (1991) *Tissue Antigens* 38, 99–103.
- ¹⁵ Hoffman, R.W. et al. (1993) *J. Immunol.* 151, 6460–6469.
- ¹⁶ Hurley, C.K. et al. (1993) *J. Immunol.* 150, 1314–1324.
- ¹⁷ Ikuta, K. et al. (1986) *Nucleic Acids Res.* 14, 4899–4909.
- ¹⁸ Ikuta, K. et al. (1985) *Proc. Natl Acad. Sci. USA* 82, 7701–7705.
- ¹⁹ Jores, R. et al. (1993) *J. Immunol.* 151, 6110–6122.
- ²⁰ Kay, R.A. et al. (1994) *Eur. J. Immunol.* 24, 2863–2867.
- ²¹ Kimura, N. et al. (1987) *Eur. J. Immunol.* 17, 375–383.
- ²² Kimura, N. et al. (1986) *J. Exp. Med.* 164, 739–750.
- ²³ Leiden, J.M. et al. (1986) *Immunogenetics* 24, 17–23.
- ²⁴ Leiden, J.N. et al. (1986) *Proc. Natl Acad. Sci. USA* 83, 4456–4460.
- ²⁵ Li, Y. et al. (1996) *Hum. Immunol.* 49, 85–95.
- ²⁶ Li, Y. et al. (1991) *J. Exp. Med.* 174, 1537–1547.
- ²⁷ Luyrink, L. et al. (1993) *Proc. Natl Acad. Sci. USA* 90, 4369–4373.
- ²⁸ Maksymowych, W.P. et al. (1992) *Immunogenetics* 35, 257–262.
- ²⁹ Nickerson, D.A. et al., unpublished.
- ³⁰ Obata, F. et al. (1993) *Immunogenetics* 38, 67–70.
- ³¹ Plaza, A. et al. (1992) *J. Immunol.* 147, 4360–4365.
- ³² Posnett, D.N. et al. (1994) *J. Exp. Med.* 179, 1707–1711.
- ³³ Robinson, M.A. et al. (1991) *J. Immunol.* 146, 4392–4397.
- ³⁴ Rowen, L. et al. (1996) *Science* 272, 1755–1762. (see Note)
- ³⁵ Rowen, L. et al., unpublished.
- ³⁶ Santamaria, P. et al. (1993) *Immunogenetics* 38, 163–163.
- ³⁷ Siu, G. et al. (1984) *Cell* 37, 393–401.
- ³⁸ Siu, G. et al. (1986) *J. Exp. Med.* 164, 1600–1614.
- ³⁹ Slightom, J.L. et al. (1994) *Genomics* 20, 146–168.
- ⁴⁰ Smith, W.J. et al. (1987) *Nucleic Acids Res.* 15, 4991–4991.
- ⁴¹ Tillinghast, J.P. et al. (1986) *Science* 233, 879–883.
- ⁴² Triebel, F. et al. (1988) *J. Immunol.* 140, 300–304.
- ⁴³ Van Schooten, W.C. et al. (1992) *Proc. Natl Acad. Sci. USA* 89, 11244–11248.
- ⁴⁴ Wei, S. et al. (1994) *Immunogenetics* 40, 27–36.
- ⁴⁵ Weiss, S. et al., unpublished.
- ⁴⁶ Wilson, R.K. et al. (1990) *Immunogenetics* 32, 406–412.

⁴⁷ Zhao, T.M. et al. (1994) J. Exp. Med. 180, 1405–1414.

Note:

The original L36092 sequence (684 973 bp) has been split in EMBL into three sequences of 267 156 bp (U66059), 215 422 bp (U66060), and 232 650 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.

This Page Intentionally Left Blank

**THE HUMAN
T CELL RECEPTOR
TRG GENES**

This Page Intentionally Left Blank

Part 1

TRGC

[illegible]

GDB:120408 LocusLink: 6966

Abstract—The purpose of this study was to determine the effect of a 12-week training program on the heart rate (HR) and heart rate reserve (HRR) of sedentary middle-aged men. The subjects were divided into two groups: a control group and an exercise group. The exercise group performed a 12-week training program consisting of three sessions per week. The control group did not exercise. The HR and HRR were measured at rest and during exercise at the beginning and end of the 12-week period. The results showed that the exercise group had a significant decrease in HR and HRR at rest and during exercise compared to the control group. The control group had no significant change in HR and HRR. The results suggest that a 12-week training program can improve the cardiovascular fitness of sedentary middle-aged men.

- ¹ Lefranc, M.-P. and Rabbitts T.H. (1985) *Nature* 316, 464–466.
- ² Lefranc, M.-P. et al. (1986) *Proc. Natl Acad. Sci. USA* 83, 9596–9600.
- ³ Pelicci, P.G. et al. (1987) *Science* 237, 1051–1055.
- ⁴ Zhan, M. et al., unpublished.

Protein display of the TRGC1 gene is shown on page 372.

Nomenclature

TRGC2(2x): T cell receptor gamma constant 2 (2x).

Definition and functionality

TRGC2 is one of the two functional genes of the TRGC group which comprises two mapped genes. TRGC1 and TRGC2 result from a recent duplication. The TRGC2 gene has four or five exons due to the duplication or triplication of exon 2. These polymorphic TRGC2 genes are designated as TRGC2(2x) and TRGC2(3x) respectively.

Based on sequence similarity with the TRGC2(3x) exons, and taking into account the evolution of the TRGC2 polymorphism as a result of unequal crossings-over⁴, the duplicated exon 2 of TRGC2(2x) is designated as EX2T or EX2R.

EX2R, but not EX2T, has one N-glycosylation site.

Gene location

TRGC2 is in the TRG locus on chromosome 7 at 7p14. TRGC2 is preceded by two functional joining genes TRGJP2 and TRGJ2.

Nucleotide and amino acid sequences for human TRGC2(2x)

The nucleotide between parentheses at the beginning of exons comes from a DONOR-SPLICE (n from ngt).

The Cysteines involved in the intrachain disulfide bridges are shown with their number and letter C in bold.

N-glycosylation sites (NXS/T, where X is different from P) are underlined.

		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
M15002	,TRGC2(2x)*01,lambdadb7 (EX1)	(G)AT	AAA	CAA	CTT	GAT	GCA	GAT	GTT	TCC	CCC	AAG	CCC	ACT	ATT	TTT	CTT	CCT	TCA	ATT	GCT
M13231	,TRGC2(2x)*01,HPB-MLT (cDNA)	(-)	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--
M15001	,TRGC2(2x)*02,lambdadb11	(-)	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--
M17324	,TRGC2(2x)*03,Fgamma7 (cDNA)		--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--
AF159056	,TRGC2(2x)*04	(-)	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--
		21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
M15002	,TRGC2(2x)*01,lambdadb7 (EX1)	GAA	ACA	AAA	CTC	CAG	AAG	GCT	GGA	ACA	TAC	CTT	TGT	CTT	CTT	GAG	AAA	TTT	TTC	CCA	GAT
M13231	,TRGC2(2x)*01,HPB-MLT (cDNA)	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--
M15001	,TRGC2(2x)*02,lambdadb11	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--
M17324	,TRGC2(2x)*03,Fgamma7 (cDNA)	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--
AF159056	,TRGC2(2x)*04	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--
		41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
M15002	,TRGC2(2x)*01,lambdadb7 (EX1)	ATT	ATT	AAG	ATA	CAT	TGG	CAA	GAA	AAG	AGC	AGC	AAC	ACG	ATT	CTG	GGA	TCC	CAG	GAG	GGG
M13231	,TRGC2(2x)*01,HPB-MLT (cDNA)	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--
M15001	,TRGC2(2x)*02,lambdadb11 (EX1)	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--
M17324	,TRGC2(2x)*03,Fgamma7 (cDNA)	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--
AF159056	,TRGC2(2x)*04	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--
		61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
M15002	,TRGC2(2x)*01,lambdadb7 (EX1)	AAC	ACC	ATG	AAG	ACT	AAC	GAC	ACA	TAC	ATG	AAA	TTT	AGC	TGG	TTA	ACG	GTG	CCA	GAA	GAG
M13231	,TRGC2(2x)*01,HPB-MLT (cDNA)	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--
M15001	,TRGC2(2x)*02,lambdadb11	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--
M17324	,TRGC2(2x)*03,Fgamma7 (cDNA)	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--
AF159056	,TRGC2(2x)*04	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--



		81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
		S	L	D	K	E	H	R	C	I	V	R	H	E	N	N	K	N	G	I	D
M15002	,TRGC2(2x)*01,lambdaD7 (EX1)	TCA	CTG	GAC	AAA	GAA	CAC	AGA	TGT	ATC	GTC	AGA	CAT	GAG	AAT	AAT	AAA	AAC	GGA	ATT	GAT
M13231	,TRGC2(2x)*01,HPB-MLT (cDNA)	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M15001	,TRGC2(2x)*02,lambdaD11	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M17324	,TRGC2(2x)*03,Fgamma7 (cDNA)	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
AF159056	,TRGC2(2x)*04	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		101	102	103	104	105	106	107	108	109	110										
		Q	E	I	I	F	P	P	I	K	T										
M15002	,TRGC2(2x)*01,lambdaD7 (EX1)	CAA	GAA	ATT	ATC	TTT	CCT	CCA	ATA	AAG	ACA	G									
M13231	,TRGC2(2x)*01,HPB-MLT (cDNA)	---	---	---	---	---	---	---	---	---	---	---									
M15001	,TRGC2(2x)*02,lambdaD11	---	---	---	---	---	---	---	---	---	---	---									
M17324	,TRGC2(2x)*03,Fgamma7 (cDNA)	---	---	---	---	---	---	---	---	---	---	---									
AF159056	,TRGC2(2x)*04	---	---	---	---	---	---	---	---	---	---	---									
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16				
		D	V	T	T	V	D	P	K	D	S	Y	S	K	D	A	N				
M13231	,TRGC2(2x)*01,HPB-MLT (EX2T)	AT	GTC	ACC	ACA	GTG	GAT	CCC	AAA	GAC	AGT	TAT	TCA	AAA	GAT	GCA	AAT	G			
	cDNA	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---				
M15004	,TRGC2(2x)*02,lambdaS9 (EX2R)	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---				
	(2)	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---				
M17324	,TRGC2(2x)*03,Fgamma7 (EX2R)	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---				
	cDNA	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---				
AF159056	,TRGC2(2x)*04, (EX2R)	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---				
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16				
		D	V	I	T	M	D	P	K	D	N	N	S	K	D	A	N				
M13231	,TRGC2(2x)*01,HPB-MLT cDNA(EX2)	AT	GTC	ATC	ACA	ATG	GAT	CCC	AAA	GAC	AAT	TGG	TCA	AAA	GAT	GCA	AAT	G			
M15005	,TRGC2(2x)*02,lambdaS9	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---				
	(2)	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---				
M17324	,TRGC2(2x)*03,Fgamma7 (cDNA)	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---				
		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---				
AF159056	,TRGC2(2x)*03	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---				
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
		D	T	L	L	L	Q	L	T	N	T	S	A	Y	Y	M	Y	L	L	L	L
M13231	,TRGC2(2x)*01,HPB-MLT cDNA(EX3)	AT	ACA	CTA	CTG	CTG	CAG	CTC	ACA	AAC	ACC	TCT	GCA	TAT	TAC	ATG	TAC	CTC	CTC	CTG	CTC
M15007	,TRGC2(2x)*02,lambdaS9	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	(2)	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M17324	,TRGC2(2x)*03,Fgamma7 (cDNA)	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
AF159056	,TRGC2(2x)*04	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
		L	K	S	V	V	Y	F	A	I	I	T	C	C	L	L	G	R	T	A	F
M13231	,TRGC2(2x)*01,HPB-MLT cDNA(EX3)	CTC	AAG	AGT	GTG	GTC	TAT	TTT	GCC	ATC	ATC	ACC	TGC	TGT	CTG	CTT	GGA	AGA	ACG	GCT	TTC
M15007	,TRGC2(2x)*02,lambdaS9	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M17324	,TRGC2(2x)*03,Fgamma7 (cDNA)	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
AF159056	,TRGC2(2x)*04	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		41	42	43	44	45	46	47													
		C	C	N	G	E	R	S													
M13231	,TRGC2(2x)*01,HPB-MLT cDNA(EX3)	TGC	TGC	AAT	GGA	GAG	AAA	TCA													
M15007	,TRGC2(2x)*02,lambdaS9	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M17324	,TRGC2(2x)*03,Fgamma7 (cDNA)	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
AF159056	,TRGC2(2x)*04	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

Genome database accession numbers

GDB:120409

LocusLink: 6967

References

- ¹ Dialynas, D.P. et al. (1986) Proc. Natl Acad. Sci. USA 83, 2619–2623.
- ² Lefranc, M.-P. et al. (1986) Proc. Natl Acad. Sci. USA 83, 9596–9600.
- ³ Pelicci, P.G. et al. (1987) Science 237, 1051–1055.
- ⁴ Buresi, C. et al. (1989) Immunogenetics 29, 161–172.
- ⁵ Zhan, M. et al., unpublished.

Protein Display

Protein display of the TRGC2(2x) gene is shown on page 372.

**Genome database accession numbers**

GDB:120409

LocusLink: 6967

***References***¹ Pelicci, P.G. et al. (1987) *Science* 237, 1051–1055.² Buresi, C. et al. (1989) *Immunogenetics* 29, 161–172.**Protein display**

Protein display of the TRGC2(3x) gene is shown on page 372.

This Page Intentionally Left Blank

Part 2

TRGJ

Nomenclature

T cell receptor gamma joining group.

Definition and functionality

The human TRGJ group comprises five functional mapped genes: TRGJ1, TRGJ2, TRGJP, TRGJP1, and TRGJP2¹.

Gene location

The human TRGJ genes are located in the TRG locus on chromosome 7 at 7p14. TRGJP1, TRGJP, and TRGJ1 are located upstream from TRGC1. TRGJ2 and TRGJP2 are located upstream from TRGC2. That genomic organization results from a recent duplication. However, there is no equivalent of TRGJP (by far, the most frequently used J gene in the human peripheral $\gamma\delta$ T cells) in the TRGJP2, TRGJ2, TRGC2 cluster.

Nucleotide and amino acid sequences for the human functional TRGJ genes with nomenclature

The conserved FGXG motif, characteristic of the TRG J-REGION is underlined.

TRGJ1
T cell receptor gamma joining 1

M12960 ,TRGJ1*01 [2] N Y Y K K L F G S G T T L V V T
G AAT TAT CAT AAG AAA CTC TTT GGC AGT GGA ACA ACA CTG GTT GTC ACA G
[3][4] ,TRGJ1*02 -----T-----

TRGJ2
T cell receptor gamma joining 2

M12961 ,TRGJ2*01 [2] N Y Y K K L F G S G T T L V V T
G AAT TAT CAT AAG AAA CTC TTT GGC AGT GGA ACA ACT CTT GTT GTC ACA G

TRGJP
T cell receptor gamma joining P

M12950 ,TRGJP*01 [3] G Q E L G K K I K V F G P G T K L I I T
GGG CAA GAG TTG GGC AAA AAA ATC AAG GTA TTT GGT CCC GGA ACA AAG CTT ATC ATT ACA G

TRGJP1
T cell receptor gamma joining P1

X08084 ,TRGJP1*01 [4] T T G W F K I F A E G T K L I V T S P
AT ACC ACT GGT TGG TTC AAG ATA TTT GCT GAA GGG ACT AAG CTC ATA GTA ACT TCA CCT G

TRGJP2
T cell receptor gamma joining P2

M16016 ,TRGJP2*01 [5] S S D W I K T F A K G T R L I V T S P
AT AGT AGT GAT TGG ATC AAG ACG TTT GCA AAA GGG ACT AGG CTC ATA GTA ACT TCG CCT G

Recombination signals

J Recombination Signal (J-RS)			TRGJ gene and allele name
J-NONAMER	(bp)	J-HEPTAMER	
AGTTTTTGA	12	CACTGTG	TRGJ1*01
AGTTTTTGA	12	CACTGTG	TRGJ1*02
AGTTTTTGA	12	CACTGTG	TRGJ2*01
GAGATTCTT	12	CAGGTGG	TRGJP*01
GATTTTTCT	12	CGGTGTG	TRGJP1*01
GATTTTTGT	12	CAGTGTG	TRGJP2*01

References:

- ¹ Lefranc, M.-P. and Rabbitts, T.H. (1986) *Nature* 316, 464–466.
- ² Lefranc, M.-P. et al. (1986) *Nature* 319, 420–422.
- ³ Lefranc, M.-P. et al. (1986) *Cell* 45, 237–246.
- ⁴ Huck, S. and Lefranc, M.-P. (1987) *FEBS Lett.* 224, 291–296.
- ⁵ Quertermous, T. et al. (1987) *J. Immunol.* 138, 2687–2690.

This Page Intentionally Left Blank

Part 3

TRGV

Nomenclature

TRGV1: T cell receptor gamma variable 1.

Definition and functionality

TRGV1 is the unique ORF of the TRGV1 subgroup which comprises 7–9 mapped genes (of which 3–5 are functional) in the TRG locus, depending on the haplotypes^{4,5} TRGV1 is an ORF due to an unusual V-SPACER length: DELETION of 14 nucleotides.

Gene location

TRGV1 is in the TRG locus on chromosome 7 at 7p14.

Nucleotide and amino acid sequences for human TRGV1

		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
M12949 ,TRGV1*01	[8]	TCT	TCC	AAC	TTG	GAA	GGG	AGA	ACG	AAG	TCA	GTC	ACC	AGG	CTG	ACT	GGG	TCA	TCT	GCT	GAA
AF159056,TRGV1*01	(1) [12]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		CDR1-IMGT																			
		21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
M12949 ,TRGV1*01		I	T	C	D	L	P	G	A	S	T	L	Y	...	...	...	...	...	...	I	H
AF159056,TRGV1*01		ATC	ACC	TGT	GAT	CTT	CCT	GGA	GCA	AGT	ACC	TTA	TAC	...	...	...	...	...	...	ATC	CAC
		CDR2-																			
		41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
M12949 ,TRGV1*01		W	Y	L	H	Q	E	G	K	A	P	Q	C	L	L	Y	Y	E	P	Y	Y
AF159056,TRGV1*01		TGG	TAC	CTG	CAC	CAG	GAG	GGG	AAG	GCC	CCA	CAG	TGT	CTT	CTG	TAC	TAT	GAA	CCC	TAC	TAC
		IMGT																			
		61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
M12949 ,TRGV1*01		S	R	V	...	...	V	L	E	S	G	I	T	P	G	K	Y	D	T	...	G
AF159056,TRGV1*01		TTC	AGG	GTT	...	...	GTG	CTG	GAA	TCA	GGA	ATC	ACT	CCA	GGA	AAG	TAT	GAC	ACT	...	GGA
		CDR3-IMGT																			
		101	102	103	104	105	106	107	108	109											
M12949 ,TRGV1*01		F	Y	V	C	A	T	W	D	R											
AF159056,TRGV1*01		TTT	TAT	TAC	TGT	GCC	ACC	TGG	GAC	AGG											

Note:

(1) The allele TRGV1*01 from AF057177 is not reported in this alignment to avoid redundancy, AF057177 being included in AF159056.

Framework and complementarity determining regions

FR1-IMGT: 26

FR2-IMGT: 17

FR3-IMGT: 37 (-2 aa: 79,82)

CDR1-IMGT: 6

CDR2-IMGT: 8

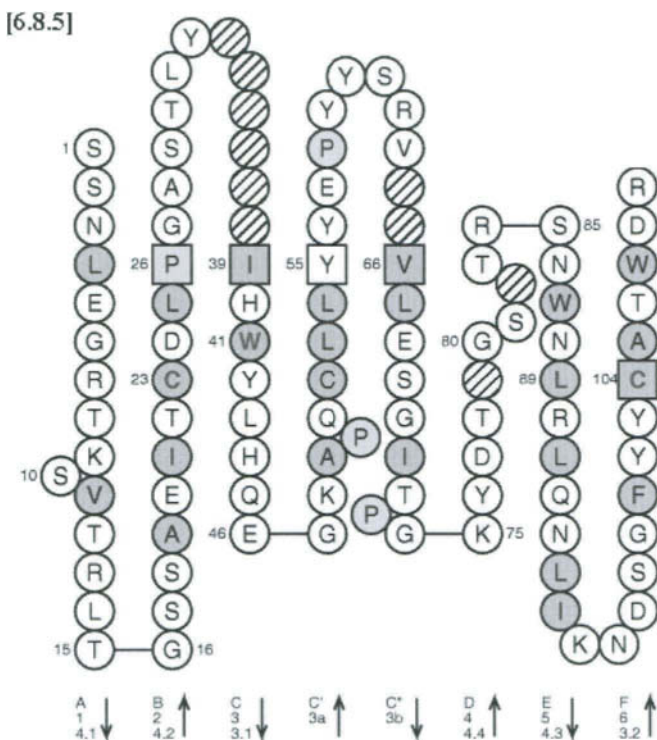
CDR3-IMGT: 5



Collier de Perles for human TRGV1*01

Accession number: IMGT M12949

EMBL/GenBank/DDBJ: M12949



Genome database accession numbers

GDB:120415 LocusLink: 6973

Nomenclature

TRGV2: T cell receptor gamma variable 2.

Definition and functionality

TRGV2 is one of the 3–5 mapped functional genes of the TRGV1 subgroup which comprises 7–9 mapped genes, depending on the haplotypes^{4,5}.

Gene location

TRGV2 is in the TRG locus on chromosome 7 at 7p14.

Nucleotide and amino acid sequences for human TRGV2

			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
M13429	,TRGV2*01	[8]	TCT	TCC	AAC	TTG	GAA	GGG	AGA	ACG	AAG	TCA	GTC	ATC	AGG	CAG	ACT	GGG	TCA	TCT	GCT	GAA
AF159056,TRGV2*01	(1)	[12]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M27337	,TRGV2*02	[11]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
			21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
M13429	,TRGV2*01		ATC	ACT	TGT	GAT	CTT	GCT	GAA	GGA	AGT	AAC	GGC	TAC	...	...	...	...	...	...	ATC	CAC
AF159056,TRGV2*01			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M27337	,TRGV2*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
			41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
M13429	,TRGV2*01		TGG	TAC	CTA	CAC	CAG	GAG	GGG	AAG	GCC	CCA	CAG	CGT	CTT	CAG	TAC	TAT	GAC	TCC	TAC	AAC
AF159056,TRGV2*01			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M27337	,TRGV2*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
			61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
M13429	,TRGV2*01		TCC	AAG	GTT	...	...	GTG	TTG	GAA	TCA	GGA	GTC	AGT	CCA	GGG	AAG	TAT	TAT	ACT	TAC	GCA
AF159056,TRGV2*01			---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M27337	,TRGV2*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
			81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
M13429	,TRGV2*01		AGC	...	T	R	N	N	L	R	L	I	L	R	N	L	I	E	N	D	S	G
AF159056,TRGV2*01			---	---	ACA	AGG	AAC	AAC	TTG	AGA	TTG	ATA	GTC	CGA	AAT	CTA	ATT	GAA	AAT	GAC	TCT	GGG
M27337	,TRGV2*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
			101	102	103	104	105	106	107	108	109											
M13429	,TRGV2*01		V	Y	Y	C	A	T	W	D	G											
AF159056,TRGV2*01			GTC	TAT	TAC	TGT	GCC	ACC	TGG	GAC	GGG											
M27337	,TRGV2*02		---	---	---	---	---	---	---	---	---											

#C: Rearranged cDNA.

Note:

(1) The allele TRGV2*01 from AF057177 is not reported in this alignment to avoid redundancy, AF057177 being included in AF159056.

Framework and complementarity determining regions

FR1-IMGT: 26

FR2-IMGT: 17

FR3-IMGT: 38 (-1 aa: 82)

CDR1-IMGT: 6

CDR2-IMGT: 8

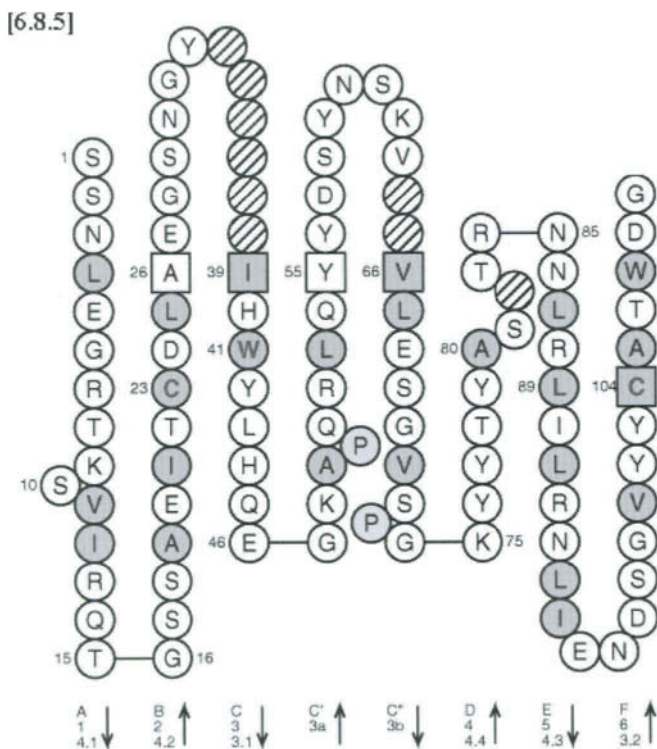
CDR3-IMGT: 5



Collier de Perles for human TRGV2*01

Accession number: IMGT M13429

EMBL/GenBank/DDBJ: M13429



Genome database accession numbers

GDB:120418

LocusLink: 6974

Nomenclature

TRGV3: T cell receptor gamma variable 3.

Definition and functionality

TRGV3 is one of the 3–5 mapped functional genes of the TRGV1 subgroup which comprises 7–9 mapped genes, depending on the haplotypes^{4,5}.

Gene location

TRGV3 is in the TRG locus on chromosome 7 at 7p14.

Nucleotide and amino acid sequences for human TRGV3

			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20			
M13430	,TRGV3*01	{8}	TCT	TCC	AAC	TTG	GAA	GGG	AGA	ACG	AAG	TCA	GTC	ACC	AGG	CAG	ACT	GGG	TCA	TCT	GCT	GAA			
AF159056,TRGV3*01(1)	{12}		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---			
X04038	,TRGV3*02	{10}	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---			
			21	22	23	24	25	26	CDR1-IMGT															39	40
M13430	,TRGV3*01		I	T	C	D	L	T	V	T	N	T	F	Y							I	H			
AF159056,TRGV3*01			ATC	ACT	TGC	GAT	CTT	ACT	GTA	ACA	AAT	ACC	TTC	TAC	...	...	...	...	...	...	ATC	CAC			
X04038	,TRGV3*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---			
			41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	CDR2-							
M13430	,TRGV3*01		W	Y	L	H	Q	E	G	K	A	P	Q	R	L	L	Y	Y	D	V	S	T			
AF159056,TRGV3*01			TGG	TAC	CTA	CAC	CAG	GAG	GGG	AAG	GCC	CCA	CAG	CGT	CTT	CTG	TAC	TAT	GAC	GTC	TCC	ACC			
X04038	,TRGV3*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	-T			
			IMGT																						
M13430	,TRGV3*01		61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80			
AF159056,TRGV3*01			A	R	D									G	L	S	P	G	K	Y	T	H			
X04038	,TRGV3*02		GCA	AGG	GAT	...	...	GTG	TTG	GAA	TCA	GGA	CTC	AGT	CCA	GGA	AAG	TAT	TAT	ACT	CAT	ACA			
			...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...			
X04038	,TRGV3*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---			
			81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100			
M13430	,TRGV3*01		P	R	R	W	S	W	I	L	R	L	A	Q	N	L	I	E	N	D	S	G			
AF159056,TRGV3*01			CCC	...	AGG	AGG	TGG	AGC	TGG	ATA	TTG	AGA	CTG	CAA	AAT	CTA	ATT	GAA	AAT	GAT	TCT	GGG			
X04038	,TRGV3*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---			
			CDR3-IMGT																						
M13430	,TRGV3*01		101	102	103	104	105	106	107	108	109														
AF159056,TRGV3*01			V	Y	C	A	T	W	D	R															
X04038	,TRGV3*02		GTC	TAT	TAC	TGT	GCC	ACC	TGG	GAC	AGG														
AF159056,TRGV3*01			---	---	---	---	---	---	---	---	---														
X04038	,TRGV3*02		---	---	---	---	---	---	---	---	---														

Note:

(1) The allele TRGV3*01 from AF057177 is not reported in this alignment to avoid redundancy, AF057177 being included in AF159056. Note that g181 (codon 61) in AF159056 was undefined (r181, r being a or g) in AF057177.

Framework and complementarity determining regions

FR1-IMGT: 26

FR2-IMGT: 17

FR3-IMGT: 38 (-1 aa: 82)

CDR1-IMGT: 6

CDR2-IMGT: 8

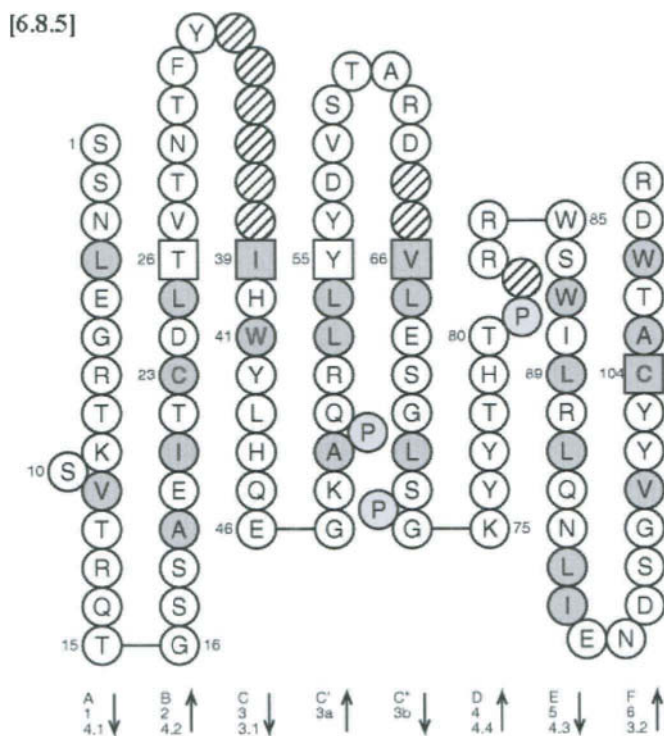
CDR3-IMGT: 5



Collier de Perles for human TRGV3*01

Accession number: IMGT M13430

EMBL/GenBank/DDBJ: M13430



Genome database accession numbers

GDB:120419

LocusLink: 6976

Nomenclature

TRGV4: T cell receptor gamma variable 4.

Definition and functionality

TRGV4 is a mapped functional gene, which may, or may not, be present due to a polymorphism by insertion/deletion^{4,5}. TRGV4 belongs to the TRGV1 subgroup which comprises 7–9 mapped genes (of which 3–5 are functional), depending on the haplotypes^{4,5}.

Gene location

TRGV4 is in the TRG locus on chromosome 7 at 7p14.

Nucleotide and amino acid sequences for human TRGV4

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20		
X15272 ,TRGV4*01	(2)	(8)	S	S	N	L	E	G	R	T	K	S	V	I	R	Q	T	G	S	S	A	E
AF159056,TRGV4*01	(1)	(12)	TCT	TCC	AAC	TTG	GAA	GGG	AGA	ACG	AAG	TCA	GTC	ATC	AGG	CAG	ACT	GGG	TCA	TCT	GCT	GAA
X13354/M36285,TRGV4*02	(3)		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

CDR1-IMGT

	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	
X15272 ,TRGV4*01	I	T	C	D	L	A	E	G	S	T	G	Y							I	H	
AF159056,TRGV4*01	ATC	ACT	TGT	GAT	CTT	GCT	GAA	GGA	AGT	ACC	GGC	TAC	---	---	---	---	---	---	---	ATC	CAC
X13354/M36285,TRGV4*02	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

CDR2-

	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
X15272 ,TRGV4*01	W	Y	L	H	Q	E	G	K	A	P	Q	R	L	L	Y	Y	D	S	Y	T
AF159056,TRGV4*01	TGG	TAC	CTA	CAC	CAG	GAG	GGG	AAG	GCC	CCA	CAG	CGT	CTT	CTG	TAC	TAT	GAC	TCC	TAC	ACC
X13354/M36285,TRGV4*02	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

IMGT

	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
X15272 ,TRGV4*01	S	S	V			V	L	E	S	G	I	S	P	G	K	Y	D	T	Y	G
AF159056,TRGV4*01	TCC	AGC	GTT	---	---	GTG	TTG	GAA	TCA	GGA	ATC	AGC	CCA	GGG	AAG	TAT	GAT	ACT	TAT	GGA
X13354/M36285,TRGV4*02	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

CDR3-IMGT

	101	102	103	104	105	106	107	108	109
X15272 ,TRGV4*01	V	Y	Y	C	A	T	W	D	G
AF159056,TRGV4*01	GTC	TAT	TAC	TGT	GCC	ACC	TGG	GAT	GGG
X13354/M36285,TRGV4*02	---	---	---	---	---	---	---	---	---

Note:

(1) The allele TRGV4*01 from AF057177 is not reported in this alignment to avoid redundancy, AF057177 being included in AF159056. g18>c (codon 6) and t237>c (codon 79) mutations originally in AF057177 are not found in AF159056 and therefore probably resulted from sequencing or typing errors.



Framework and Complementarity Determining Regions

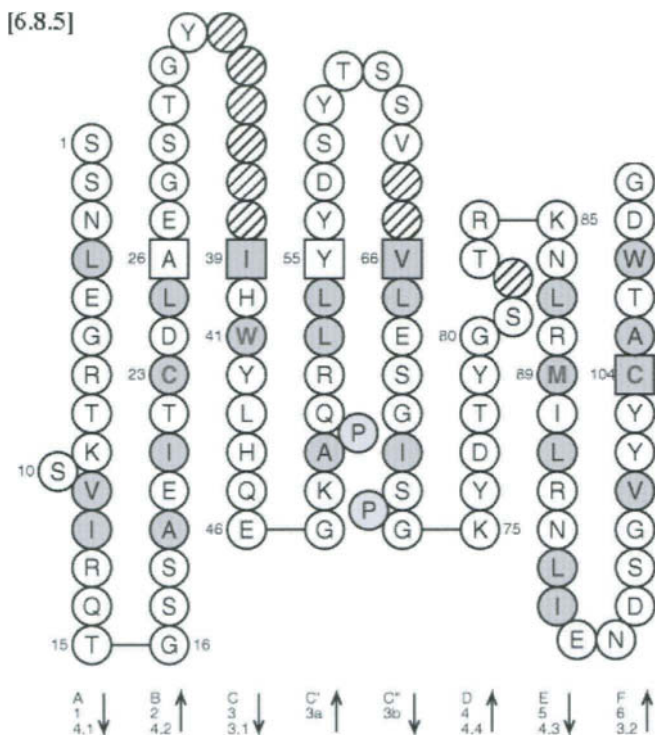
FR1-IMGT: 26
FR2-IMGT: 17
FR3-IMGT: 38 (-1 aa: 82)

CDR1-IMGT: 6
CDR2-IMGT: 8
CDR3-IMGT: 5

Collier de Perles for human TRGV4*01

Accession number: IMGT X15272

EMBL/GenBank/DBJ: X15272



Genome database accession numbers

GDB:120420 LocusLink: 6977

Nomenclature

TRGV5: T cell receptor gamma variable 5.

Definition and functionality

TRGV5 is a mapped functional gene, which may, or may not, be present due to a polymorphism by insertion/deletion^{4,5}. TRGV5 belongs to the TRGV1 subgroup which comprises 7–9 mapped genes (of which 3–5 are functional), depending on the haplotypes^{4,5}.

Gene location

TRGV5 is in the TRG locus on chromosome 7 at 7p14.

Nucleotide and amino acid sequences for human TRGV5

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
X13355/M36286,TRGV5*01 [3]	S	S	N	L	E	G	G	T	K	S	V	T	R	P	T	R	S	S	A	E
AF159056, TRGV5*01 (1) [12]	TCT	TCC	AAC	TTG	GAA	GGG	GGA	ACG	AAG	TCA	GTC	ACG	AGG	CCG	ACT	AGG	TCA	TCT	GCT	GAA
	CDR1-IMGT																			
X13355/M36286,TRGV5*01	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
AF159056, TRGV5*01	I	T	C	D	L	T	V	I	N	A	F	Y							I	H
	ATC	ACT	TGT	GAC	CTT	ACT	GTA	ATA	AAT	GCC	TTC	TAC							ATC	CAC
	CDR2-																			
X13355/M36286,TRGV5*01	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
AF159056, TRGV5*01	W	Y	L	H	Q	E	G	K	A	P	Q	R	L	L	Y	Y	D	V	S	N
	TGG	TAC	CTA	CAC	CAG	GAG	GGG	AAG	GCC	CCA	CAG	CCT	CTT	CTG	TAC	TAT	GAC	GTC	TCC	CAC
	IMGT																			
X13355/M36286,TRGV5*01	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
AF159056, TRGV5*01	S	K	D			V	L	E	S	G	L	S	P	G	K	Y	Y	T	H	T
	TCA	AAG	GAT			GTG	TTG	GAA	TCA	GGA	CTC	AGT	CCA	GGA	AAG	TAT	TAT	ACT	CAT	CAC
	CDR3-IMGT																			
X13355/M36286,TRGV5*01	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
AF159056, TRGV5*01	P	R	R	W	S	W	I	L	I	L	R	N	L	I	E	N	D	S	G	
	CCC			AGG	AGG	TGG	AGC	TGG	ATA	TTG	ATA	CTA	CGA	AAT	CTA	ATT	GAA	AAT	GAT	TCT
	CDR3-IMGT																			
X13355/M36286,TRGV5*01	101	102	103	104	105	106	107	108	109											
AF159056, TRGV5*01	V	Y	Y	C	A	T	W	D	R											
	GTC	TAT	TAC	TGT	GCC	ACC	TGG	GAC	AGG											

Note:

(1) The allele TRGV5*01 from AF057177 is not reported in this alignment to avoid redundancy, AF057177 being included in AF159056.

Framework and complementarity determining regions

FR1-IMGT: 26

FR2-IMGT: 17

FR3-IMGT: 38 (-1 aa: 82)

CDR1-IMGT: 6

CDR2-IMGT: 8

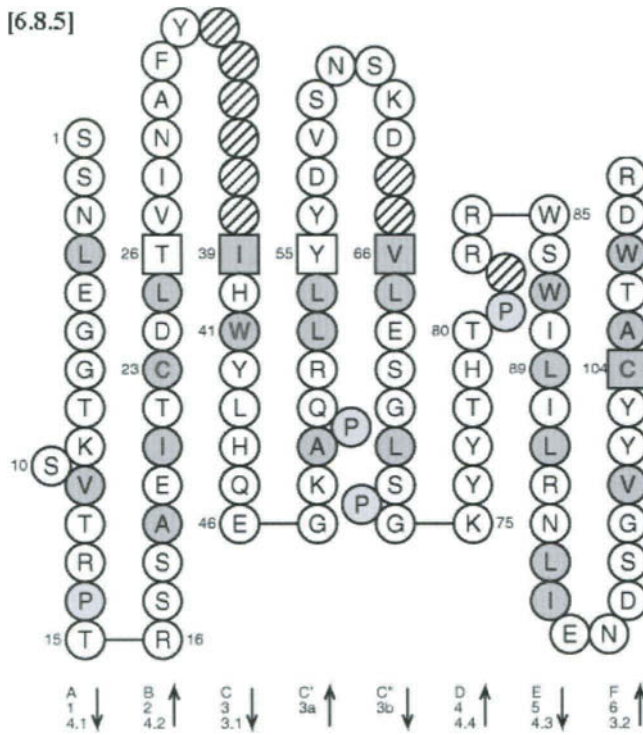
CDR3-IMGT: 5



Collier de Perles for human TRGV5*01

Accession number: IMGT X13355

EMBL/GenBank/DDBJ: X13355



Genome database accession numbers

GDB:120421

LocusLink: 6978

Nomenclature

TRGV8: T cell receptor gamma variable 8.

Definition and functionality

TRGV8 is one of the 3–5 mapped functional genes of the TRGV1 subgroup which comprises 7–9 mapped genes in the TRG locus, depending on the haplotypes^{4,5}.

Gene location

TRGV8 is in the TRG locus on chromosome 7 at 7p14.

Nucleotide and amino acid sequences for human TRGV8

			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
M13434	,TRGV8*01	[8]	TCT	TCC	AAC	TTG	GAA	GGG	AGA	ACA	AAG	TCA	GTC	ACC	AGG	CCA	ACT	GGG	TCA	TCA	GCT	GTA
AF159056	,TRGV8*01	(1) [12]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
</																						

Note:

(1) The allele TRGV8*01 from AF057177 is not reported in this alignment to avoid redundancy, AF057177 being included in AF159056.

Framework and complementarity determining regions

FR1-IMGT: 26

FR2-IMGT: 17

FR3-IMGT: 38 (-1 aa: 82)

CDR1-IMGT: 6

CDR2-IMGT: 8

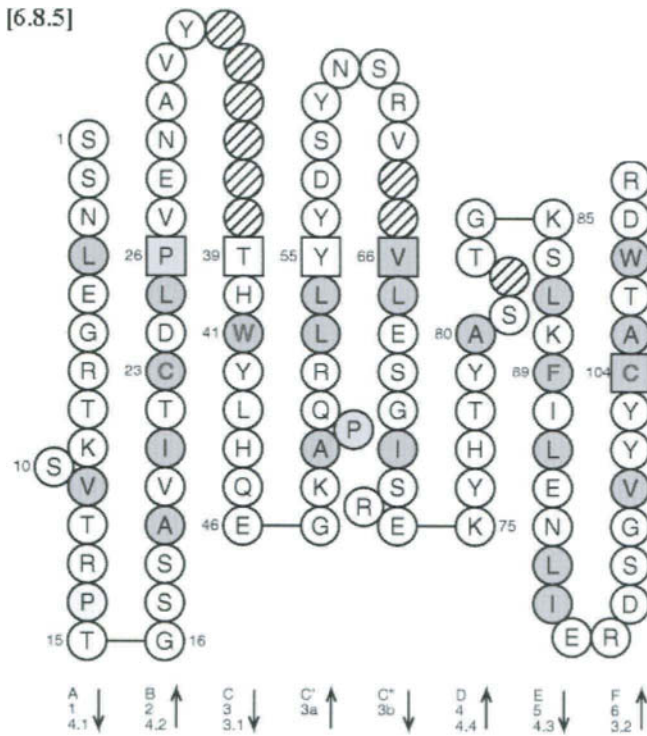
CDR3-IMGT: 5



Collier de Perles for human TRGV8*01

Accession number: IMGT M13434

EMBL/GenBank/DDBJ: M13434

[illegible]

GDB:120425 LocusLink: 6982

Nomenclature

TRGV9: T cell receptor gamma variable 9.

Definition and functionality

TRGV9 is the unique mapped functional gene of the TRGV2 subgroup which only comprises that gene⁷⁻⁹.

Gene location

TRGV9 is in the TRG locus on chromosome 7 at 7p14.

Nucleotide and amino acid sequences for human TRGV9

[illegible]

Framework and complementarity determining regions

FR1-IMGT: 26

FR2-IMGT: 17

FR3-IMGT: 39

CDR1-IMGT: 8

CDR2-IMGT: 7

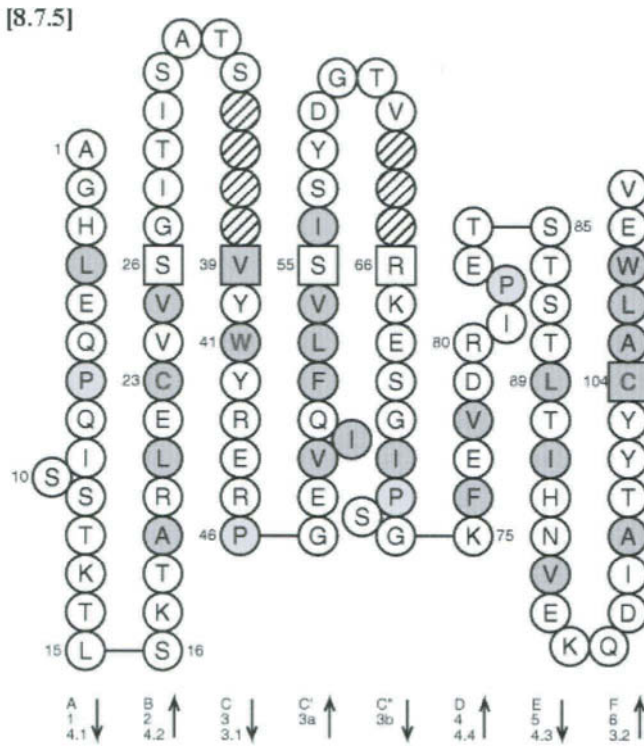
CDR3-IMGT: 5



Collier de Perles for human TRGV9*01

Accession number: IMGT X07205

EMBL/GenBank/DDBJ: X70205



Genome database accession numbers

GDB:120426

LocusLink: 6983

Nomenclature

TRGV10: T cell receptor gamma variable 10.

Definition and functionality

TRGV10 is the unique mapped ORF of the TRGV3 subgroup which only comprises that gene⁶.

TRGV10 is an ORF due to a defective DONOR-SPLICE: nct instead of ngt, and to the absence of splicing of the V10 leader intron^{13,14}.

Gene location

TRGV10 is in the TRG locus on chromosome 7 at 7p14.

Nucleotide and amino acid sequences for human TRGV10

			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20		
X07206	,TRGV10*01	[4]	TTA	TCA	AAA	GTG	GAG	CAG	TTC	CAG	CTA	TCC	ATT	TCC	ACG	GAA	GTC	AAG	AAA	AGT	ATT	GAC		
X74798	,TRGV10*02	[9]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
AF159056	,TRGV10*02	[8]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
			21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40		
X07206	,TRGV10*01		ATA	CCT	TGC	AAG	ATA	TCC	AGC	ACA	AGG	TTT	GAA	ACA	GAT	GTC	...	...	...	...	ATT	CAC		
X74798	,TRGV10*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
AF159056	,TRGV10*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
			41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60		
X07206	,TRGV10*01		TGG	TAC	CGG	CAG	AAA	CCA	AAT	CAG	GCT	TTG	GAG	CAC	CTG	ATC	TAT	ATT	GTC	TCA	ACA	AAA		
X74798	,TRGV10*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
AF159056	,TRGV10*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
			IMGT																					
			61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80		
X07206	,TRGV10*01		S	A	A	A	R	S	M	G	K	T	S	N	K	V	E	A	R	K				
X74798	,TRGV10*02		TCC	GCA	GCT	...	...	CGA	CGC	AGC	ATG	GGT	AAG	ACA	AGC	AAC	AAA	GTG	GAG	GCA	AGA	AAG		
AF159056	,TRGV10*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
			81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100		
X07206	,TRGV10*01		AAT	TCT	CAA	ACT	CTC	ACT	TCA	ATC	CTT	ACC	ATC	AAG	TCC	GTA	GAG	AAA	GAA	GAC	ATG	GCC		
X74798	,TRGV10*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
AF159056	,TRGV10*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
			CDR3-IMGT																					
			101	102	103	104	105	106	107	108	109													
X07206	,TRGV10*01		GTT	TAC	TAC	TGT	GCT	GCG	TGG	TGG	GTG	GC												
X74798	,TRGV10*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
AF159056	,TRGV10*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		

Framework and complementarity determining regions

FR1-IMGT: 26

FR2-IMGT: 17

FR3-IMGT: 39

CDR1-IMGT: 8

CDR2-IMGT: 8

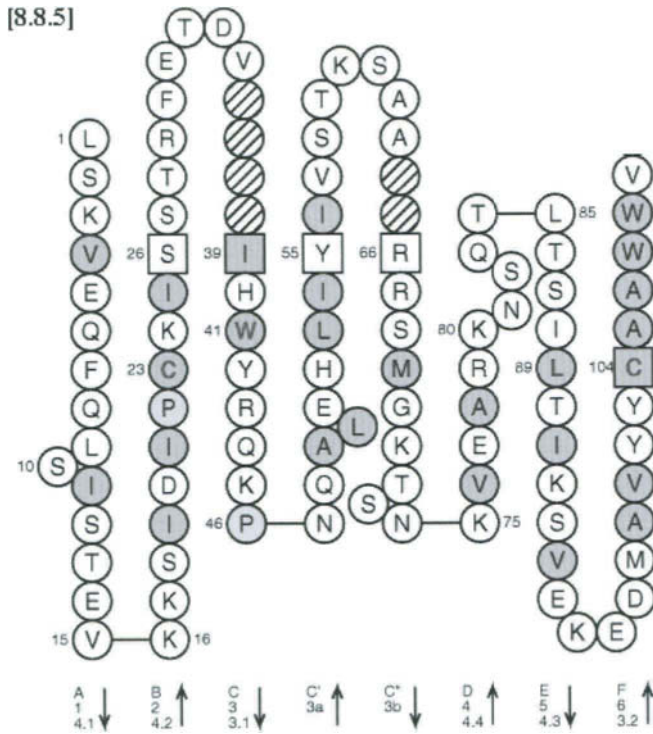
CDR3-IMGT: 5



Collier de Perles for human TRGV10*01

Accession number: IMGT X07206

EMBL/GenBank/DDBJ: X07206



Genome database accession numbers

GDB:120416 LocusLink: 6984

Nomenclature

TRGV11: T cell receptor gamma variable 11

Definition and functionality

TRGV11 is the unique mapped ORF of the TRGV4 subgroup which only comprises that gene^{1,6}.

TRGV11 is an ORF due to a defective DONOR-SPLICE: nct instead of ngt, and to the absence of splicing of the V11 leader intron, and 1st-CYS replaced by Tryptophan (tgg) in FR1-IMGT^{13,14}.

Gene location

TRGV11 is in the TRG locus on chromosome 7 at 7p14.

Nucleotide and amino acid sequences for human TRGV11

			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
Y11227 ,TRGV11*01	[1]	CTT	GGG	CAG	TTG	GAA	CAA	CCT	GAA	ATA	TCT	ATT	TCC	AGA	CCA	GCA	AAT	AAG	AGT	GCC	CAC	
AF159056,TRGV11*02	[8]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
			21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
Y11227 ,TRGV11*01		ATA	TCT	TGG	AAG	GCA	TCC	ATC	CAA	GGC	TTT	AGC	AGT	AAA	ATC	...	...	...	...	ATA	CAC	
AF159056,TRGV11*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
			41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
Y11227 ,TRGV11*01		TGG	TAC	TGG	CAG	AAA	CCA	AAC	AAA	GGC	TTA	GAA	TAT	TTA	TTA	CAT	GTC	TTC	TTG	ACA	ATC	
AF159056,TRGV11*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
			61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
Y11227 ,TRGV11*01		TCT	GCT	...	...	...	...	CAA	GAT	TGC	TCA	GGT	GGG	AAG	ACT	AAG	AAA	CTT	GAG	GTA	AGT	AAA
AF159056,TRGV11*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
			81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
Y11227 ,TRGV11*01		AAT	GCT	CAC	ACT	TCC	ACT	TCC	ACT	TTG	AAA	ATA	AAG	TTT	TTA	GAG	AAA	GAA	GAT	GAG	GTG	
AF159056,TRGV11*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
			101	102	103	104	105	106	107	108	109	110										
Y11227 ,TRGV11*01		GTG	TAC	CAC	TGT	GCC	TGC	TGG	ATT	AGG	CAC											
AF159056,TRGV11*02		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

Framework and complementarity determining regions

FR1-IMGT: 26
FR2-IMGT: 17
FR3-IMGT: 39

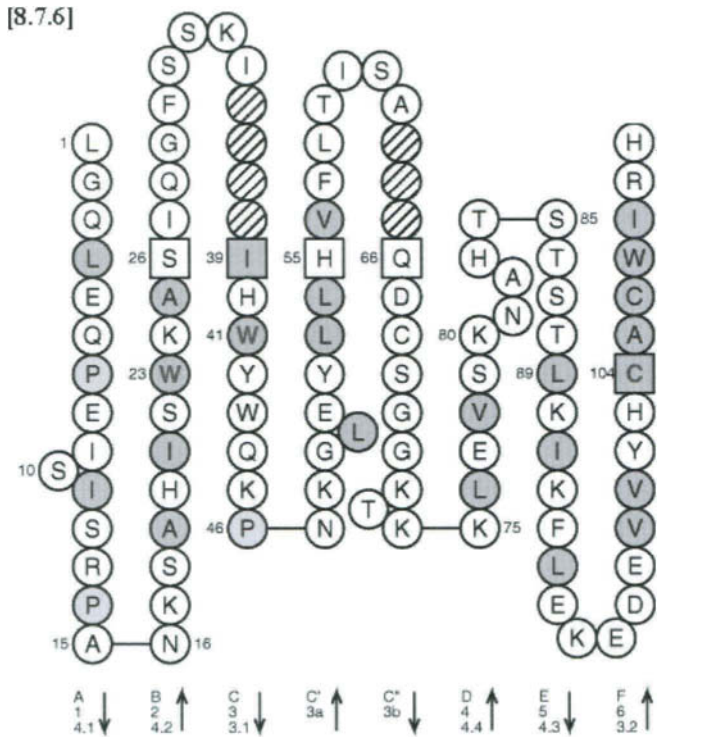
CDR1-IMGT: 8
CDR2-IMGT: 7
CDR3-IMGT: 6



Collier de Perles for human TRGV11*01

Accession number: IMGT Y11227

EMBL/GenBank/DDBJ: Y11227



Genome database accession numbers

GDB:120417 LocusLink: 6985

Protein display of the human TRG V-REGIONS.

Only the *01 allele of each functional or ORF V-REGION is shown. TRGV genes are listed, for each subgroup, according to their position from 5' to 3' in the locus. N-glycosylation sites (NXS/T, where X is different from P) are underlined.

TRGV gene	FR1-IMGT (1-26)	CDR1-IMGT (27-38)	FR2-IMGT (39-55)	CDR2-IMGT (56-65)	FR3-IMGT (66-104)	CDR3-IMGT (105-115)
	1102030405060708090100110					
M12949 ,TRGV1	SSNLEGRTKSVTRLTGSSAEITCDLP	GASTLY.....	IHWYLHQEGKAPQCLLY	YEPYYSRV..	VLESGITPGKYDT.GS.TRSNWNLRLLQNLIKND	SGFYVC ATWDR.....
M13429 ,TRGV2	SSNLEGRTKSVIRQTGSSAEITCDLA	EGSNGY.....	IHWYLHQEGKAPQRLQY	YDSYNSKV..	VLESGVSPGKYITYAS.TRNNLRLLRLNLIEND	SGVYYC ATWDG.....
M13430 ,TRGV3	SSNLEGRTKSVTRQTGSSAEITCDLT	VTNTFY.....	IHWYLHQEGKAPQRLLY	YDVSTARD..	VLESGLSPGKYITHTP.RRWSWILRLQNLIEND	SGVYYC ATWDR.....
X15272 ,TRGV4	SSNLEGRTKSVIRQTGSSAEITCDLA	EGSTGY.....	IHWYLHQEGKAPQRLLY	YDSYTSV..	VLESGISPGKYDTYGS.TRKNLRMILRLNLIEND	SGVYYC ATWDG.....
X13355/M36286,TRGV5	SSNLEGGTKSVTRPTRSSAEITCDLT	VINAFY.....	IHWYLHQEGKAPQRLLY	YDVSNSKD..	VLESGLSPGKYITHTP.RRWSWILRLNLIEND	SGVYYC ATWDR.....
M13434 ,TRGV8	SSNLEGRTKSVTRPTGSSAVITCDLP	VENAVY.....	THWYLHQEGKAPQRLLY	YDSYNSRV..	VLESGISREKYHTYAS.TGKSLKFILENLIERDS	SGVYYC ATWDR.....
X07205 ,TRGV9	AGHLEQPQISSTKTLKSKTARLECVVS	GITISATS....	VYWYRERPGEVIQFLVS	ISYDGTV...	RKESGIPSGKFEVDRIPETSTSTLT	LIHNVEKQDIATYYC ALWEV.....
X07206 ,TRGV10	LSKVEQFQLSISTEVKKSIDIPCKIS	STRFETDV....	IHWYRQKPNQALEHLIY	IVSTKSAA..	RRSMGKTSNKVEARKNSQTLTSLITIKSVEKED	MAVYYC AAWVV.....
Y11227 ,TRGV11	LGQLEQPEISISRPANKSAHISWKAS	IQGFSSKI....	IHWYQKPNRGLEYLLH	VFLTISA...	QDCSGGKTKKLEVSKNAHTSTSTL	KIKFLEKEDEVVYHC ACWIRH.....

TRGV recombination signals and references

Recombination signals

Only the recombination signals of the allele *01 of each functional or ORF V-REGION are shown.

TRGV gene name	V Recombination Signal (V-RS)		
	V-HEPTAMER	(bp)	V-NONAMER
TRGV1*01 (ORF)	CACAGTG	9	CTGAAAATC
TRGV2*01	CACAGTG	23	CTGAAAATC
TRGV3*01	CACAGTG	23	CTGAAAATC
TRGV4*01	CACAGTG	23	CTGAAAATC
TRGV5*01	CACAGTG	23	CTGAAAATC
TRGV8*01	CACAGTG	23	CTGAAAATC
TRGV9*01	CACAGCA	23	TCAATAAAT
TRGV10*01 (ORF)	CACATAC	23	CAAAATCCC
TRGV11*01 (ORF)	CACAGTG	23	ACAGAAACT

References

- ¹ Chen, Z. et al. (1988) Blood 72, 776–783.
- ² Dariavach, P. and Lefranc, M.-P. (1989) FEBS Lett. 256, 185–191.
- ³ Font, M.P. et al. (1988) J. Exp. Med. 168, 1383–1394.
- ⁴ Ghanem, N. et al. (1991) Hum. Genet. 86, 450–456.
- ⁵ Ghanem, N. et al. (1989) Immunogenetics 30, 350–360.
- ⁶ Huck, S. et al. (1988) EMBO J. 7, 719–726.
- ⁷ Lefranc, M.-P. et al. (1985) Nature 316, 464–466.
- ⁸ Lefranc, M.-P. et al. (1986) Cell 45, 237–246.
- ⁹ Lefranc, M.-P. et al. (1989) Eur. J. Immunol. 19, 989–994.
- ¹⁰ Quertermous, T. et al. (1986) Nature 322, 184–187.
- ¹¹ Yoshikai, Y. et al. (1987) Eur. J. Immunol. 17, 119–126.
- ¹² Zhan, M. et al., unpublished.
- ¹³ Zhang, X.M. et al. (1994) Eur. J. Immunol. 24, 571–578.
- ¹⁴ Zhang, X.M. et al. (1996) Immunogenetics 43, 196–203.

This Page Intentionally Left Blank

**THE HUMAN
T CELL RECEPTOR
TRD GENES**

This Page Intentionally Left Blank

Part 1

TRDC

Nomenclature

TRDC: T cell receptor delta constant.

Definition and functionality

TRDC is the functional and unique constant gene in the TRD locus.

Gene location

TRDC is in the TRD locus on chromosome 14 at 14q11.2.

The TRD locus is embedded in the TRA locus, between the TRAV and TRAJ genes.

Nucleotide and amino acid sequences for human TRDC

The nucleotide between parentheses at the beginning of exons comes from a DONOR-SPLICE (n from ngt).

The Cysteines involved in the intrachain disulfide bridges are shown with their number and letter C in bold.

N-Glycosylation sites (NXS/T, where X is different from P) are underlined.

Poly(A) signals are shown in bold and underlined.

A DONOR-SPLICE, located just after the termination codon, uses a downstream ACCEPTOR-SPLICE, placing part of the 3' non-coding sequence on a separate untranslated exon, designated as EX4. Since EX4 is untranslated, nucleotide differences observed in EX4 are not taken into account for the description of alleles, according to IMGT allele nomenclature and sequence polymorphisms.

Note that AE000661 encompasses M94081.

		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	
		R	S	Q	P	H	T	K	P	S	V	F	V	M	K	N	G	T	N	V	A	
M22148	,TRDC*01 (EX1)	[1]	(C)GA	AGT	CAG	CCT	CAT	ACC	AAA	CCA	TCC	GTT	TTT	GTC	ATG	AAA	AAT	GGA	ACA	AAT	GTC	GCT
X07019	,TRDC*01	[2]	(-)-	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	
M94081	,TRDC*01	[4]	(-)-	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	
AE000661	,TRDC*01	[5]	(-)-	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	
M20288	,TRDC*01	[3]	(-)-	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	
		21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	
		T	L	V	K	E	F	D	P	A	I	V	I	R	I	N	L	V	S	S	K	K
M22148	,TRDC*01 (EX1)	C	G	T	C	T	G	T	G	T	A	A	G	A	T	A	A	T	A	A	T	A
X07019	,TRDC*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
M94081	,TRDC*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
AE000661	,TRDC*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
M20288	,TRDC*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
		41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	
		I	T	E	F	D	P	A	I	V	I	S	P	S	G	K	Y	N	A	V	K	
M22148	,TRDC*01 (EX1)	A	T	A	A	C	A	G	A	G	A	G	A	T	A	A	T	A	A	T	A	
X07019	,TRDC*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
M94081	,TRDC*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
AE000661	,TRDC*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
M20288	,TRDC*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	



M22148 ,TRDC*01 (EX1)	61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80
X07019 ,TRDC*01	L G K Y E D S N S V T C S V Q H D N K T
M94081 ,TRDC*01	CTT GGT AAA TAT GAA GAT TCA AAT TCA GTG ACA TGT TCA GTT CAA CAC GAC AAT AAA ACT
AE000661,TRDC*01	-----
M20288 ,TRDC*01	-----
M22148 ,TRDC*01 (EX1)	81 82 83 84 85 86 87 88 89 90 91 92 93
X07019 ,TRDC*01	V H S T D F E V K T D S T
M94081 ,TRDC*01	GTG CAC TCC ACT GAC TTT GAA GTG AAG ACA GAT TCT ACA G
AE000661,TRDC*01	-----
M20288 ,TRDC*01	-----
M22149 ,TRDC*01 (EX2)	1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20
M94081 ,TRDC*01	D H V K P K E T E N T K Q P S K S C H K
AE000661,TRDC*01	AT CAC GTA AAA CCA AAG GAA ACT GAA AAC ACA AAG CAA CCT TCA AAG AGC TGC CAT AAA
M22149 ,TRDC*01 (EX2)	21 22
M94081 ,TRDC*01	P K
AE000661,TRDC*01	CCC AAA G
M22150 ,TRDC*01 (EX3)	1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20
M94081 ,TRDC*01	S I V H T E K V N M M S L T V L G L R M
AE000661,TRDC*01	CC ATA GTT CAT ACC GAG AAG GTG AAC ATG ATG TCC CTC ACA GTG CTT GGG CTA CGA ATG
M22150 ,TRDC*01 (EX3)	21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39
M94081 ,TRDC*01	L F A K T V A V N F L L T A K L F F L
AE000661,TRDC*01	CTG TTT GCA AAG ACT GTT GCC GTC AAT TTT CTC TTG ACT GCC AAG TTA TTT TTC TAA G
M22151 ,TRDC*01 (Untranslated EX4 [1] and 3'UTR)	GCTGACTGGCATGAGGAAGCTACACTCCTGAAGAAACCAAGGCTTACAAAAATGCATCTCCTTGGCTCTGACTCTCTT
M94081 ,TRDC*01	-----
AE000661,TRDC*01	-----
M22151 ,TRDC*01	GTGATTCAAGTTGACCTGTGCATAGCCTTGTAAATGGCTGCTAGCCAACCAATTTTCTTCAAAGACAACAAACCCAGC
M94081 ,TRDC*01	-----C-----
AE000661,TRDC*01	-----C-----
M22151 ,TRDC*01	TCATCTCTCCAGCTTGATGGGAAGACAAAGTCTCTGGGAAGGGGGTTTATGTCTTAAGTCTTTGTATCTGTGTTTATAA
M94081 ,TRDC*01	-----
AE000661,TRDC*01	-----
M22151 ,TRDC*01	AGGGATAGAAAGATATAAAAAAGATATAGGACTCTTTTTTACTCTCAAGTGATACACITTGAAATGATGTTTGTGTC
M94081 ,TRDC*01	-----
AE000661,TRDC*01	-----
M22151 ,TRDC*01	CTTTTGACTTTCTTTACCTTTTGAAGTAGAAAGTGGGAACCAAGGTTACACAGCTTCATCTCATGAGGAAAAATAGGC
M94081 ,TRDC*01	-----C-----
AE000661,TRDC*01	-----C-----
M22151 ,TRDC*01	CTTGGGAGAAGAAGAGCGGGTGCCCTTTTATCTAAACATGGAAGGCTCTGCTCAACTGAGCAGTAGATTTGCTACAAACC
M94081 ,TRDC*01	-----
AE000661,TRDC*01	-----
M22151 ,TRDC*01	AGCATCATCTCTTCTCTCTCTCACGGCTGTGCCACCCCTCTATGTTCACTTCAGGAGCCACACTAGAGATTTCTGCA
M94081 ,TRDC*01	-----
AE000661,TRDC*01	-----
M22151 ,TRDC*01	TGGCGTGAGGAC---AAAGTTTCAGCACTTTCTGCTCTCTTAATACTTTACAAATGAGATTACATTTGAATTTGCTAA
M94081 ,TRDC*01	-----GGA-----
AE000661,TRDC*01	-----GGA-----



M22151	, TRDC*01	TACTTTATGAGCAGGCAATGAGGTTTCCAAAAATCTCATCTAAATACTCTCCAATCTATTAGCAAAAATCAGAGTAAATA
M94081	, TRDC*01	-----
AE000661	, TRDC*01	-----
M22151	, TRDC*01	CAGAGGAAAGGCACCTGCTTTCTGTTAATTGATTTAACATGCATGAATTAGCTCCCTCTGAGTTCAGGCACTATGCTGAG
M94081	, TRDC*01	-----
AE000661	, TRDC*01	-----
M22151	, TRDC*01	AGTACAAAGAGACACAAGTCTGCTTTCAAGCAACTCACTGTGAAAGTGTTTTTGAAGGGAGGAACAGAAATGAGACCCC
M94081	, TRDC*01	-----
AE000661	, TRDC*01	-----
M22151	, TRDC*01	TATCTTTCCCTATAAAAAACAACATTTTACTGTGTTTTTGCCCTGCCAATCTGTATTGAAACGATTGGACACTGATCTCT
M94081	, TRDC*01	-----C-----
AE000661	, TRDC*01	-----C-----
M22151	, TRDC*01	GGCCTGGGACTTTGGCATTGATGGTTTTCTGCCTTCTCTCAGCCTCTGCCTCTATTGCAATTTATTAAACTGCATTGTG
M94081	, TRDC*01	-----
AE000661	, TRDC*01	-----
M22151	, TRDC*01	TGC
M94081	, TRDC*01	---
AE000661	, TRDC*01	---



Genome database accession numbers

GDB:9954211 LocusLink: 28526



References

¹ Takiyara, Y. et al. (1988) Proc. Natl Acad. Sci. USA 85, 6097–6101.
² Boehm, T. et al. (1988) EMBO J. 7, 385–394.
³ Isobe, M. et al. (1988) Proc. Natl Acad. Sci. USA 85, 3933–3937.
⁴ Koop, B.F. et al. (1994) Genomics 19, 478–493.
⁵ Boysen, C. et al., unpublished.



Protein display

Protein display of the TRDC gene is shown on page 372.

Part 2

TRDD

Nomenclature

T cell receptor delta diversity group.

Definition and functionality

The human TRDD group comprises three functional mapped genes, TRDD1, TRDD2, and TRDD3. The TRDD genes have two or three open reading frames in both the direct and inverted orientations.

Gene location

The human TRDD genes are located in the TRA/TRD locus on chromosome 14 at 14q11.2, upstream from the TRDJ genes.



Nucleotide and amino acid sequences for the human TRDD genes with nomenclature

	Direct 5'- 3' orientation		Inverted orientation
TRDD1 T cell receptor delta diversity 1	E I K * N S		T I L F Y F
M23325 ,TRDD1*01	[2]	gaaatagt	actatttc
TRDD2 T cell receptor delta diversity 2	P S Y L P F L		V G R * E R K
M22153 ,TRDD2*01	[1]	ccttcctac	gtagggaagg
TRDD3 T cell receptor delta diversity 3	T G G Y L G D T W G I		R I P Q V S P S Y P P
M22152 ,TRDD3*01	[1]	actgggggatacg	cgtatccccacgt

Recombination signals

5'D Recombination Signal (5'D-RS)		TRDD gene and allele name		3'D Recombination Signal (3'D-RS)	
5'D-NONAMER	(bp)	5'D-HEPTAMER		3'D-HEPTAMER	(bp) 3'D-NONAMER
ATTTTTC	12	CAAAGTG	TRDD1*01	CACTCAA	23 ATTAACCAA
GGTTTTTAT	12	CATTGTG	TRDD2*01	CACACAG	23 CCAAAAACA
AGTTTTTGT	12	CACTGTG	TRDD3*01	CACAGTG	23 ACAAAAAC

References

- ¹ Takihara, Y. et al. (1988) Proc. Natl Acad. Sci. USA 85, 6097-6101.
- ² Loh, M. et al. (1988) Proc. Natl Acad. Sci. USA 85, 9714-9718.

Part 3

TRDJ

Nomenclature

T cell receptor delta joining group.

Definition and functionality

The human TRDJ group comprises four functional mapped genes: TRDJ1, TRDJ2, TRDJ3, and TRDJ4.

Gene location

The human TRDJ genes are located in the TRA/TRD locus on chromosome 14 at 14q11.2, upstream from the TRDC gene.

Nucleotide and amino acid sequences for the human functional TRDJ genes with nomenclature

The conserved FGXG motif, characteristic of the TRD J-REGION is underlined.

TRDJ1 T cell receptor delta joining 1			
M20289 ,TRDJ1*01	[2]	T D K L I <u>F G K G</u> T R V T V E P AC ACC GAT AAA CTC ATC TTT GGA AAA GGA ACC CGT GTG ACT GTG GAA CCA A	
TRDJ2 T cell receptor delta joining 2			
L36386 ,TRDJ2*01	[3]	L T A Q L F <u>F G K G</u> T Q L I V E P CT TTG ACA GCA CAA CTC TTC TTT GGA AAG GGA ACA CAA CTC ATC GTG GAA CCA G	
TRDJ3 T cell receptor delta joining 3			
M21508 ,TRDJ3*01	[4]	S W D T R Q M F <u>F G T G</u> I K L F V E P C TCC TGG GAC ACC CGA CAG ATG TTT TTC GGA ACT GGC ATC AAA CTC TTC GTG GAG CCC C	
TRDJ4 T cell receptor delta joining 4			
AJ249814,TRDJ4*01	[1]	R P L I <u>F G K G</u> T Y L E V Q Q CC AGA CCC CTG ATC TTT GGC AAA GGA ACC TAT CTG GAG GTA CAA CAA C	

Recombination signals

J Recombination Signal (J-RS)			TRDJ gene and allele name
J-NONAMER	[bp]	J-HEPTAMER	
GGTTTTTGG	12	TGCTGTG	TRDJ1*01
GGTTTTTCG	13	GGTAGTG	TRDJ2*01
GTTACCTGT	12	TAATGTG	TRDJ3*01
GGTTTTTCG	13	GGTAGTG	TRDJ4*01

References

- ¹ Davodeau, F. et al. (1994) J. Immunol. 153, 137–142.
- ² Isobe, M. et al. (1988) Proc. Natl Acad. Sci. USA 85, 3933–3937.
- ³ Loh, E.Y. et al. (1988) Proc. Natl Acad. Sci. USA 85, 9714–9718.
- ⁴ Satyanarayana, K. et al. (1988) Proc. Natl Acad. Sci. USA 85, 8166–8170.

Part 4

TRDV

Nomenclature

TRDV1: T cell receptor delta variable 1.

Definition and functionality

TRDV1 is the unique mapped functional gene of the TRDV1 subgroup which only comprises that gene.

Gene location

TRDV1 is in the TRA/TRD locus on chromosome 14 at 14q11.2. TRDV1 is localized at 360 kb upstream of the TRDC gene, among the TRAV genes².

Nucleotide and amino acid sequences for human TRDV1

		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	
M22198	,TRDV1*01	[7]	A	Q	K	V	T	Q	A	Q	S	S	V	S	M	P	V	R	K	A	V	T
U32547	,TRDV1*01	[1]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
AE000660	,TRDV1*01	[2]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	
M22198	,TRDV1*01	CTG	AAC	TGC	CTG	TAT	GAA	ACA	AGT	TGG	TGG	TCA	TAT	TAT	...	...	...	...	...	ATT	TTT	
U32547	,TRDV1*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
AE000660	,TRDV1*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
		41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	
M22198	,TRDV1*01	TGG	TAC	AAG	CAA	CTT	CCC	AGC	AAA	GAG	ATG	ATT	TTC	CTT	ATT	CGC	CAG	GGT	TCT	...	...	
U32547	,TRDV1*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
AE000660	,TRDV1*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
		61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	
M22198	,TRDV1*01	...	...	...	...	...	D	E	Q	N	A	K	S	G	R	Y	S	V	N	F	...	
U32547	,TRDV1*01	---	---	---	---	---	GAT	GAA	CAG	AAT	GCA	AAA	AGT	...	GGT	CGC	TAT	TCT	GTC	AAC	TTT	
AE000660	,TRDV1*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
		81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	
M22198	,TRDV1*01	AAG	AAA	GCA	GCG	AAA	TCC	GTC	GCC	TTA	ACC	ATT	TCA	GCC	TTA	CAG	CTA	GAA	GAT	TCA	GCA	
U32547	,TRDV1*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
AE000660	,TRDV1*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
		101	102	103	104	105	106	107	108													
M22198	,TRDV1*01	K	Y	F	C	A	L	G	E													
U32547	,TRDV1*01	AAG	TAC	TTT	TGT	GCT	CTT	GGG	GAA	CT												
AE000660	,TRDV1*01	---	---	---	---	---	---	---	---													

Framework and complementarity determining regions

FR1-IMGT: 26
FR2-IMGT: 17
FR3-IMGT: 38 (-1 aa: 73)

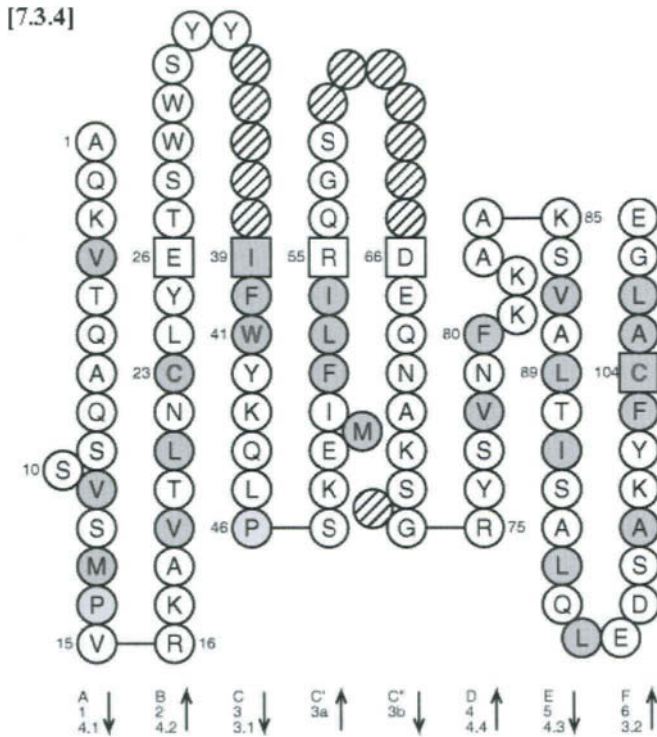
CDR1-IMGT: 7
CDR2-IMGT: 3
CDR3-IMGT: 4



Collier de Perles for human TRDV1*01

Accession number: IMGT M22198

EMBL/GenBank/DDBJ: M22198



Genome database accession numbers

GDB:9953671

LocusLink: 28518

TRDV2 is in the TRA/TRD locus on chromosome 14 at 14q11.2. TRDV2 is localized upstream of the TRD D-J-C-CLUSTER ³.

#c: Rearranged cDNA



Framework and complementarity determining regions

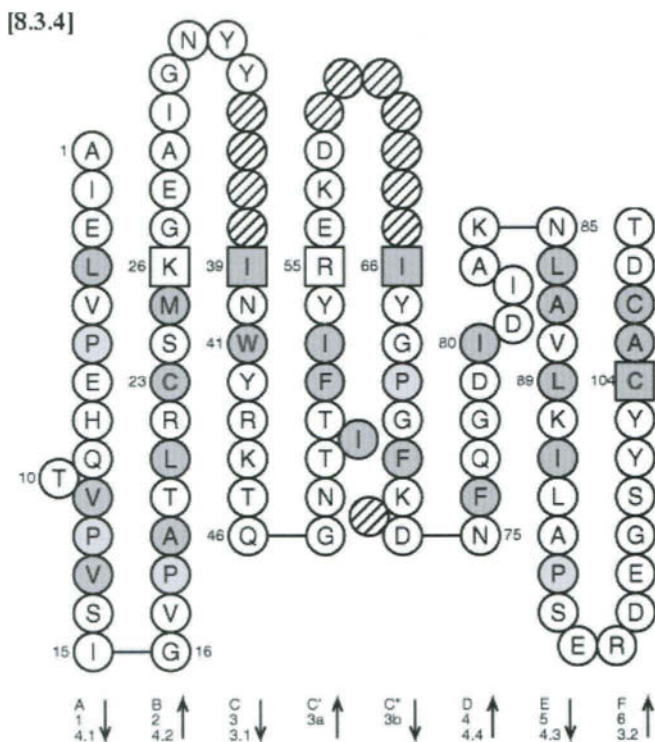
FR1-IMGT: 26
FR2-IMGT: 17
FR3-IMGT: 38 (-1 aa: 73)

CDR1-IMGT: 8
CDR2-IMGT: 3
CDR3-IMGT: 4

Collier de Perles for human TRDV2*01

Accession number: IMGT X15207

EMBL/GenBank/DBJ: X15207



Genome database accession numbers

GDB:9953287

LocusLink: 28517

Nomenclature

TRDV3: T cell receptor delta variable 3.

Definition and functionality

TRDV3 is the unique mapped functional gene of the TRDV3 subgroup which only comprises that gene.

Gene location

TRDV3 is in the TRA/TRD locus on chromosome 14 at 14q11.2. TRDV3 is localized downstream of the TRDC gene, in inverted orientation of trancription, and rearranges by an inversion mechanism^{4,6,8}.

Nucleotide and amino acid sequences for human TRDV3

		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	
M23326	,TRDV3*01	[6]	TGT	GAC	AAA	GTA	ACC	CAG	AGT	TCC	CCG	GAC	CAG	ACG	GTG	GCG	AGT	GGC	AGT	GAG	GTG	GTA
X13954	,TRDV3*01	[4]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
U32549	,TRDV3*01	[1]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M94081	,TRDV3*01	[5]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
AE000661	,TRDV3*01	[2]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
X15261	,TRDV3*02	[8]	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
		21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	
		L	L	C	T	Y	D	T	V	Y	S	N	P	D	L	F						
M23326	,TRDV3*01	CTG	CTC	TGC	ACT	TAC	GAC	ACT	GTA	TAT	TCA	AAT	CCA	GAT	---	---	---	---	---	TTA	TTC	
X13954	,TRDV3*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
U32549	,TRDV3*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
M94081	,TRDV3*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
AE000661	,TRDV3*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
X15261	,TRDV3*02	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
		41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	
		W	Y	R	I	R	P	D	Y	S	F	Q	F	V	F	Y	G	D	N	S	R	
M23326	,TRDV3*01	TGG	TAC	CGG	ATA	AGG	CCA	GAT	TAT	TCC	TTT	CAG	TTT	GTC	TTT	TAT	GGG	GAT	AAC	AGC	AGA	
X13954	,TRDV3*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
U32549	,TRDV3*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
M94081	,TRDV3*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
AE000661	,TRDV3*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
X15261	,TRDV3*02	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
		61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	
		S	E	G	A	D	F	T	Q	G	R	F	S	V	K	H						
M23326	,TRDV3*01	---	---	---	---	TCA	GAA	GGT	GCA	GAT	TTT	ACT	CAA	GGA	CGG	TTT	TCT	TTT	GTG	AAA	CAC	
X13954	,TRDV3*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
U32549	,TRDV3*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
M94081	,TRDV3*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
AE000661	,TRDV3*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
X15261	,TRDV3*02	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
		81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	
		I	L	T	Q	K	A	F	H	L	V	I	S	P	V	R	T	E	D	S	A	
M23326	,TRDV3*01	ATT	CTG	ACC	CAG	AAA	GCC	TTT	CAC	TTG	GTG	ATC	TCT	CCA	GTA	AGG	ACT	GAA	GAC	AGT	GCC	
X13954	,TRDV3*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
U32549	,TRDV3*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
M94081	,TRDV3*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
AE000661	,TRDV3*01	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
X15261	,TRDV3*02	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	

		CDR3-1MGT							
		101	102	103	104	105	106	107	
		T	Y	Y	C	A	F		
		ACT	TAC	TAC	TGT	GCC	TTT	AG	
M23326	,TRDV3*01								
X13954	,TRDV3*01	---	---	---	---	---	---	---	
U32549	,TRDV3*01								
M94081	,TRDV3*01	---	---	---	---	---	---	---	
AE000661	,TRDV3*01	---	---	---	---	---	---	---	
X15261	,TRDV3*02								

Framework and complementarity determining regions

FR1-IMGT: 26

CDR1-IMGT: 7

FR2-IMGT: 17

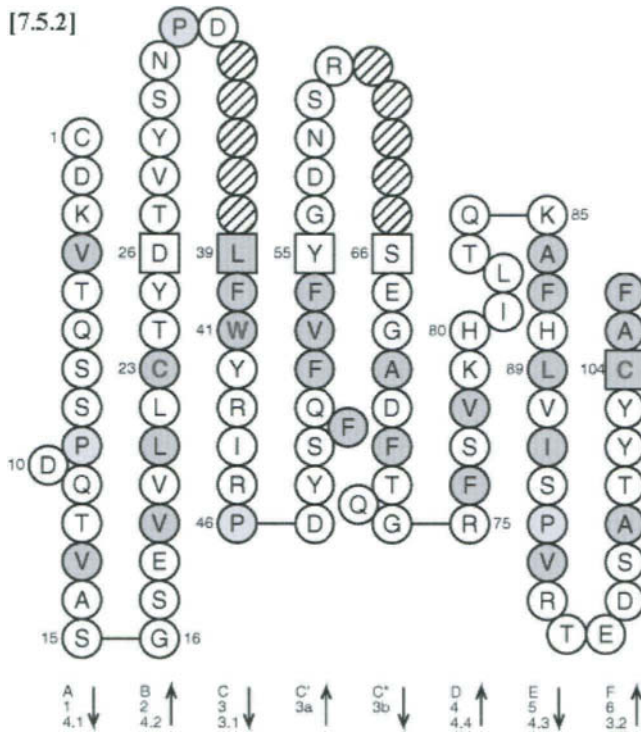
CDR2-IMGT: 5

FR3-IMGT: 39

CDR3-IMGT: 2

Collier de Perles for human TRDV3*01

Accession number: IMGT M23326 EMBL/GenBank/DDBJ: M23326



Genome database accession numbers

GDB:9953273 LocusLink: 28516

Protein display of the human TRD V-REGIONS.

Only the *01 allele of each functional V-REGION is shown. TRDV genes are listed, for each subgroup, according to their position from 5' to 3' in the locus.

TRDV gene	FR1-IMGT (1-26)	CDR1-IMGT (27-38)	FR2-IMGT (39-55)	CDR2-IMGT (56-65)	FR3-IMGT (66-104)	CDR3-IMGT (105-115)
	1 10 20	30	40 50	60	70 80 90 100	110
M22198 ,TRDV1						
	AQKVQTQASSVSMPIRKAVTLNCLYE	TSWWSYY....	IFWYKQLPSKEMIFLIR	QGS.....	DEQNAKS.GRYSVNFKKAASVALTISALQLEDSAKFYC	ALGE.....
X15207 ,TRDV2	AIELVPEHQTVPVSIQVPATLRCSMK	GEAIGNYY....	INWYRKQTQNTITFIYR	EKD.....	IYGPQFK.DNFGQDDIADKNLAVLKILAPSERDEGSYYC	ACDT.....
M23326 ,TRDV3	CDKVTSQSSPDQTVASGSEVLLCTDY	TVYSNPD....	LFWYRIRPDYSQFVFY	GDNSR.....	SEGADFTQGRFSVKHILTQKAFHLVISPVRTEDSATYYC	AF.....

TRDV recombination signals and references

Recombination signals

Only the recombination signals of the allele *01 of each functional V-REGION are shown.

TRDV gene name	V Recombination Signal [V-RS]		
	V-HEPTAMER	(bp)	V-NONAMER
TRDV1*01	CACAGTG	23	ACAAAAACC
TRDV2*01	CACCCTG	23	TCAAAAACC
TRDV3*01	CACTATG	22	AACACAAAC

References

- ¹ Boysen, C. et al. (1996) Immunogenetics 44, 121–127.
- ² Boysen, C. et al., unpublished.
- ³ Dariavach, P. and Lefranc, M.-P. (1989) Nucleic Acids Res. 17, 4880.
- ⁴ Hata, S. et al. (1989) J. Exp. Med. 169, 41–57.
- ⁵ Koop, B.F. et al., unpublished.
- ⁶ Loh, E.Y. et al. (1988) Proc. Natl Acad. Sci. USA 85, 9714–9718.
- ⁷ Satyanarayana, K. et al. (1988) Proc. Natl Acad. Sci. USA 85, 8166–8170.
- ⁸ Takihara, Y. et al. (1989) Eur. J. Immunol. 19, 571–574.
- ⁹ Triebel, F. et al. (1988) Eur. J. Immunol. 18, 2021–2027.
- ¹⁰ Zhang, X.M. and Lefranc, M.-P. (1993) Hum. Genet. 92, 100.

EX1

TRAC (N) IQNPDPVAVYQLRDSK...SSDKSVCLFTDFD.SQTIVSSKDDVYIT.DRTVLDMRSMDP....KNSAVANGIKK.....DFACANAFIN...SLIPEDTFFPSP

TRBC1 (E) DLNKVFPPEVAVFEPSEAEISHTQKATLVCLATGFFPDHVELSWWVNGKEVHSGVSTDPQPLKEQPALNDRYCLSSRLRVSATFWQNPNNHFRCCVQVQFYG...LSENDEWTQDRAKPVTQIVSAEAWGRA

TRBC2 (E) DLNKVFPPEVAVFEPSEAEISHTQKATLVCLATGFFPDHVELSWWVNGKEVHSGVSTDPQPLKEQPALNDRYCLSSRLRVSATFWQNPNNHFRCCVQVQFYG...LSENDEWTQDRAKPVTQIVSAEAWGRA

TRDC (R) SQPHTKPSVFVM....KQTNVACLVKEFYPKDIRINLVSSKIKTEPDPAIVISPS.....GKYNVAVKLGYHD.....SNSVTCVQHDK...KTVHSTDFEVKTDST

TRGC1 (D) KQLDADVSPKPTIFLPSIAETKLQKAGTYLCLLEKFFPDVIRIHWQEKKSNTILSSQEGNTMKTN.....DTVMKFSWLTVPESL...DKEHRCIVRHEN...NKNGVQEIIFPPIKT

TRGC2 (2x) (D) KQLDADVSPKPTIFLPSIAETKLQKAGTYLCLLEKFFPDVIRIHWQEKKSNTILSSQEGNTMKTN.....DTVMKFSWLTVPESL...DKEHRCIVRHEN...NKNGVQEIIFPPIKT

TRGC2 (3x) (D) KQLDADVSPKPTIFLPSIAETKLQKAGTYLCLLEKFFPDVIRIHWQEKKSNTILSSQEGNTMKTN.....DTVMKFSWLTVPESL...DKEHRCIVRHEN...NKNGVQEIIFPPIKT

TRAC **EX2** (E) SSCDVKLVEKSFET

TRBC1 **EX2** (D) CGFTS

TRBC2 **EX2** (D) CGFTS

TRDC **EX2** (D) HVKPKETENTKQPSKSKCHKPK

TRGC1 **EX2** (D) VITMDPKD[N]KDA[N]

TRGC2 (2x) *01 **EX2T** DVTTVDPKDSYSKDN **EX2** (D) VITMDPKD[N]KDA[N]

TRGC2 (2x) *02 **EX2R** DVTTVDPKYNYSKDN **EX2** (D) VITMDPKD[N]KDA[N]

TRGC2 (3x) **EX2T** DVTTVDPKDSYSKDN **EX2R** DVTTVDPKYNYSKDN **EX2** (D) VITMDPKD[N]KDA[N]

EX3

TRAC (D) TNLNFQNLISVIGRILLKLKVGFNLLMTLRL.....WSS

TRBC1 (V) SYQQGVLSATILYEILLGKATLYAVLVSAVLVLMAM VKRKDF **EX4**

TRBC2 (E) SYQQGVLSATILYEILLGKATLYAVLVSAVLVLMAM VKRKDSRG **EX4**

TRDC (S) IVHTEKVNMSLTVLGLRMLFAKTAVAVNPLLAKLFFL

TRGC1 (D) TLLQLQTNMYLLLLTSAYYLKSVVYFAITCCLLRRTAFCCNGEKS

TRGC2 (2x) (D) TLLQLQTNYSAYMYLLLLLSKVYFAITCCLLGRRTAFCCNGEKS

TRGC2 (3x) (D) TLLQLQTNYSAYMYLLLLLSKVYFAITCCLLGRRTAFCCNGEKS

Extracellular region | Transmembrane region | Intracytoplasmic region

Amino acids resulting from the splicing are shown in parentheses.
 N-glycosylation sites (NXS/T, where X is different from P) are boxed.
 Amino acid sequences are deduced from the alleles *01.

TRAC, TRBC, TRGC, and
 TRDC protein displays

Index

- Allele, 5
- Allelic polymorphisms, 38, 62
- Alpha-beta T cell receptors, 16
 - schematic representation, 26
- Alpha-beta T cells, 16–17
 - repertoire, 37
- Alpha chains, 14, 17
 - structural characteristics, 18, 20
 - synthesis of, 25
- Amino acid sequences, 11
 - see also* Collier de Perles; Protein display
- Amino acids, abbreviations, XIV
- Beta chains, 14, 17
 - structural characteristics, 18, 20
 - synthesis of, 25, 30
- CD3 proteins
 - cytoplasmic regions, 21
 - delta chain, 18, 21–2
 - epsilon chain, 18, 21–2
 - eta chain, 18, 22
 - gamma chain, 18, 21–2
 - structural characteristics, 18, 21–2
 - TcR-CD3 complex, 14, 16, 21–3
 - transmembrane regions, 21
 - zeta chain, 18, 22
 - see also* T cell receptor-CD3 complex
- Chain types, 4
 - see also* Alpha chains; Beta chains; Delta chains; Gamma chains
- Chromosomal localization
 - human TRA locus, 47, 69, 70
 - human TRB locus, 54, 55, 69, 70
 - human TRD locus, 64–5, 65, 69, 70
 - human TRG locus, 61, 69, 70
- Chromosome 7, genes on, 54, 61, 69, 70
- Chromosome 14, genes on, 47, 64, 69, 70
- 'CLASSIFICATION' concept, 4–5
- Collier de Perles, 12
- Combinatorial diversity, 29, 31–2, 70
- Complementarity determining region (CDR) lengths
- Configuration, 3
- Constant genes, 33–6
 - characteristics, 36
 - structure, 34–5
 - see also* TRAC; TRBC; TRDC; TRGC
- Correspondence between nomenclatures
 - List of the TRA genes..., and, 48
 - List of the TRB genes..., and, 57
 - List of the TRG genes..., and, 63
 - List of the TRD genes..., and, 67
- Correspondence between V-REGION numberings, 8–10
- Definition, 11
- Deletional rearrangements, 29, 32, 39, 40
- Delta chains, 14, 17
 - structural characteristics, 18
 - synthesis of, 25
- 'DESCRIPTION' concept, 5–6
- Description of data, 5–10
- Enhancers, 42
- Framework (FR) lengths, 11
- Functionality, 4, 11
- Gamma chains, 14, 17
 - structural characteristics, 18, 21
 - synthesis of, 25, 28
- Gamma-delta T cell receptors, 17
 - schematic representation, 26
- Gamma-delta T cells, 17
 - repertoire, 37
- Gene, 5
- Gene location, 11
- Gene type, 3
- Genome database accession numbers, 12

- Genome Database (GDB), 12
 Glycosylation of T cell receptor chains, 20–1
 Group, 5
- 'IDENTIFICATION' concept, 3–4
 IMGT (ImMunoGeneTics) database, 3
 IMGT-ONTOLOGY
 'CLASSIFICATION' concept, 4–5
 'DESCRIPTION' concept, 5–6
 'IDENTIFICATION' concept, 3–4
 IMGT Repertoire, 3, 11
 IMGT Scientific chart, 3
 IMGT standardized labels, xi–xiii
 IMGT unique numbering for V-REGIONS, 7
 correspondence with Kabat numberings, 8–10
 Immunoglobulins, compared with T cell receptors, 14
 Immunoreceptor Tyrosine-based Activation Motifs (ITAMs), in CD3 proteins, 18, 21
 Inversional joinings, 29, 32, 39, 40
- Junctional diversity, 32–3
- Kabat numberings correspondence with the IMGT unique numbering for V-REGIONS, 8–10
- Locus, 4
 LocusLink, 12
- MHC-restricted recognition, 14
 Molecule type, 3
- National Center for Biotechnology Information (NCBI), LocusLink, 12
 Nomenclature, 10–11
 see also Correspondence between nomenclatures
 Nucleotide sequences, 11
 Numbering for V-REGIONS
 correspondence between numberings, 8–10
 IMGT unique numbering, 7
- Online Mendelian Inheritance in Man (OMIM) links, 12
 Organization of data, 10–12
 Orphans, 5, 55, 57, 69
- 'P' (palindromic) nucleotides, 33
 Protein display
 TRAC gene, 372
 TRAV genes, 181–2
 TRBC genes, 372
 TRBV genes, 311–12
 TRDC gene, 372
 TRDV genes, 370
 TRGC genes, 372
 TRGV genes, 350
 see also Amino acid sequences
 Pseudogenes, 5
- Recombinase, 29, 31–2
 Recombination signals, 29
 TRAV genes, 31, 183
 TRAJ genes, 84–5
 TRBD genes, 194
 TRBJ genes, 197
 TRBV genes, 31, 313
 TRDD genes, 360
 TRDJ genes, 362
 TRDV genes, 31, 371
 TRGJ genes, 328
 TRGV genes, 31, 351
 Repertoire of T cells, 37
- Selection of data, 3–5
 'CLASSIFICATION' concept, 4–5
 'IDENTIFICATION' concept, 3–4
 Silencers, 42
 Subgroup, 5
- T cell receptor–CD3 complex, 14, 16, 21–3
 activation of, 22–3
 assembly of, 22
 biosynthesis of, 22
 organization of complex, 21
 T cell receptor chains
 glycosylation of, 20–1
 origins of diversity, 29–33
 structure, 17–20
 synthesis of, 25–44
 see also Alpha chains; Beta chains;

- Delta chains; Gamma chains
- T cell receptor constant genes, 33–6
 - see also* TRAC, TRBC, TRGC, TRDC
- T cell receptor gene expression, transcriptional regulation of, 42
- T cell receptor gene rearrangements
 - analysis of, 41–2, 43
 - chronological order, 27, 37, 39–42
- T cell receptors
 - compared with immunoglobulins, 14
 - structural and biological properties, 14–23
- TcR–CD3 complexes, 14, 16, 18
- TRA genes, 73–184
 - list of functional or ORF human TRA genes, 50–2
 - number per haploid genome, 48, 69, 70
 - potential repertoire, 48
 - rearrangements, 41
- TRA locus, 47–54
 - chromosomal localization, 47, 69, 70
 - organization of human TRA locus, 48, 49
 - somatic V–J rearrangements in, 25
- TRAC
 - amino acid sequences for human TRAC, 76–8, 372
 - characteristics, 36
 - definition and functionality, 50, 76
 - gene location, 76
 - genome database accession number, 78
 - nomenclature, 76
 - nucleotide sequences for human TRAC, 76–8
 - protein display, 372
 - references, 78
 - structure, 34
- TRAJ genes
 - amino acid sequences for human TRAJ genes, 80–3
 - definition and functionality, 80
 - list of functional or ORF human TRAJ genes, 50–1
 - nomenclature, 48, 80
 - nucleotide sequences for human TRAJ genes, 80–3
 - recombination signals, 84–5
 - references, 83
- TRAV genes, 87–184
 - correspondence between numberings, 8–10
 - list of functional or ORF human TRAV genes, 51–2
 - nomenclature, 48, 51–2
 - number of human TRAV germline variable genes, 53
 - potential repertoire, 53–4
 - protein display, 181–2
 - recombination signals, 183
 - references, 184
- TRAV/DV genes
 - nomenclature, 67
 - number of human TRAV/DV germline variable genes, 68
 - potential repertoire, 68
 - see also* TRAV genes, TRDV genes
- TRAV1–1
 - amino acid sequences for human TRAV1–1, 88, 89, 181
 - collier de perles for human TRAV1–1*01, 89
 - complementarity determining region lengths, 89
 - definition and functionality, 88
 - framework lengths, 89
 - gene location, 88
 - genome database accession numbers, 89
 - nomenclature, 88
 - nucleotide sequences for human TRAV1–1, 88
 - protein display, 181
 - recombination signals, 183
- TRAV1–2
 - amino acid sequences for human TRAV1–2, 90, 91, 181
 - collier de perles for human TRAV1–2*01, 91
 - complementarity determining region lengths, 90
 - definition and functionality, 90
 - framework lengths, 90
 - gene location, 90
 - genome database accession numbers,

- 91
- nomenclature, 90
- nucleotide sequences for human
 - TRAV1-2, 90
- protein display, 181
- recombination signals, 183
- TRAV2
 - amino acid sequences for human
 - TRAV2, 92, 93, 181
 - collier de perles for human
 - TRAV2*01, 93
 - complementarity determining region
 - lengths, 92
 - definition and functionality, 92
 - framework lengths, 92
 - gene location, 92
 - genome database accession numbers, 93
 - nomenclature, 92
 - nucleotide sequences for human
 - TRAV2, 92
 - protein display, 181
 - recombination signals, 183
- TRAV3
 - amino acid sequences for human
 - TRAV3, 94, 95, 181
 - collier de perles for human
 - TRAV3*01, 95
 - complementarity determining region
 - lengths, 95
 - definition and functionality, 94
 - framework lengths, 95
 - gene location, 94
 - genome database accession numbers, 95
 - nomenclature, 94
 - nucleotide sequences for human
 - TRAV3, 94
 - protein display, 181
 - recombination signals, 183
- TRAV4
 - amino acid sequences for human
 - TRAV4, 96, 97, 181
 - collier de perles for human
 - TRAV4*01, 97
 - complementarity determining region
 - lengths, 96
 - definition and functionality, 96
 - framework lengths, 96
 - gene location, 96
 - genome database accession numbers, 97
 - nomenclature, 96
 - nucleotide sequences for human
 - TRAV4, 96
 - protein display, 181
 - recombination signals, 183
- TRAV5
 - amino acid sequences for human
 - TRAV5, 98, 99, 181
 - collier de perles for human
 - TRAV5*01, 99
 - complementarity determining region
 - lengths, 98
 - definition and functionality, 98
 - framework lengths, 98
 - gene location, 98
 - genome database accession numbers, 99
 - nomenclature, 98
 - nucleotide sequences for human
 - TRAV5, 98
 - protein display, 181
 - recombination signals, 183
- TRAV6
 - amino acid sequences for human
 - TRAV6, 100, 101, 181
 - collier de perles for human
 - TRAV6*01, 101
 - complementarity determining region
 - lengths, 101
 - definition and functionality, 100
 - framework lengths, 101
 - gene location, 100
 - genome database accession numbers, 101
 - nomenclature, 100
 - nucleotide sequences for human
 - TRAV6, 100
 - protein display, 181
 - recombination signals, 183
- TRAV7
 - amino acid sequences for human
 - TRAV7, 102, 103, 181
 - collier de perles for human
 - TRAV7*01, 103
 - complementarity determining region
 - lengths, 102

- definition and functionality, 102
- framework lengths, 102
- gene location, 102
- genome database accession numbers, 103
- nomenclature, 102
- nucleotide sequences for human TRAV7, 102
- protein display, 181
- recombination signals, 183
- TRAV8-1
 - amino acid sequences for human TRAV8-1, 104, 105, 181
 - collier de perles for human TRAV8-1*01, 105
 - complementarity determining region lengths, 104
 - definition and functionality, 104
 - framework lengths, 104
 - gene location, 104
 - genome database accession numbers, 105
 - nomenclature, 104
 - nucleotide sequences for human TRAV8-1, 104
 - protein display, 181
 - recombination signals, 183
- TRAV8-2
 - amino acid sequences for human TRAV8-2, 106, 107, 181
 - collier de perles for human TRAV8-2*01, 107
 - complementarity determining region lengths, 106
 - definition and functionality, 106
 - framework lengths, 106
 - gene location, 106
 - genome database accession numbers, 107
 - nomenclature, 106
 - nucleotide sequences for human TRAV8-2, 106
 - protein display, 181
 - recombination signals, 183
- TRAV8-3
 - amino acid sequences for human TRAV8-3, 108, 109, 181
 - collier de perles for human TRAV8-3*01, 109
 - complementarity determining region lengths, 108
 - definition and functionality, 108
 - framework lengths, 108
 - gene location, 108
 - genome database accession numbers, 109
 - nomenclature, 108
 - nucleotide sequences for human TRAV8-3, 108
 - protein display, 181
 - recombination signals, 183
- TRAV8-4
 - amino acid sequences for human TRAV8-4, 110-11, 181
 - collier de perles for human TRAV8-4*01, 111
 - complementarity determining region lengths, 111
 - definition and functionality, 110
 - framework lengths, 111
 - gene location, 110
 - genome database accession numbers, 111
 - nomenclature, 110
 - nucleotide sequences for human TRAV8-4, 110-11
 - protein display, 181
 - recombination signals, 183
- TRAV8-6
 - amino acid sequences for human TRAV8-6, 112, 113, 181
 - collier de perles for human TRAV8-6*01, 113
 - complementarity determining region lengths, 112
 - correspondence between numberings, 8-10
 - definition and functionality, 112
 - framework lengths, 112
 - gene location, 112
 - genome database accession numbers, 113
 - nomenclature, 112
 - nucleotide sequences for human TRAV8-6, 112
 - protein display, 181
 - recombination signals, 183
- TRAV8-7

- amino acid sequences for human
 - TRAV8-7, 114, 115, 181
- collier de perles for human
 - TRAV8-7*01, 115
- complementarity determining region
 - lengths, 114
- definition and functionality, 114
- framework lengths, 114
- gene location, 114
- genome database accession numbers, 115
- nomenclature, 114
- nucleotide sequences for human
 - TRAV8-7, 114
- protein display, 181
- recombination signals, 183
- TRAV9-1
 - amino acid sequences for human
 - TRAV9-1, 116, 117, 181
 - collier de perles for human
 - TRAV9-1*01, 117
 - complementarity determining region
 - lengths, 116
 - definition and functionality, 116
 - framework lengths, 116
 - gene location, 116
 - genome database accession numbers, 117
 - nomenclature, 116
 - nucleotide sequences for human
 - TRAV9-1, 116
 - protein display, 181
 - recombination signals, 183
- TRAV9-2
 - amino acid sequences for human
 - TRAV9-2, 118, 119, 181
 - collier de perles for human
 - TRAV9-2*01, 119
 - complementarity determining region
 - lengths, 119
 - definition and functionality, 118
 - framework lengths, 119
 - gene location, 118
 - genome database accession numbers, 119
 - nomenclature, 118
 - nucleotide sequences for human
 - TRAV9-2, 118
 - protein display, 181
 - recombination signals, 183
- TRAV10
 - amino acid sequences for human
 - TRAV10, 120, 121, 181
 - collier de perles for human
 - TRAV10*01, 121
 - complementarity determining region
 - lengths, 120
 - definition and functionality, 120
 - framework lengths, 120
 - gene location, 120
 - genome database accession numbers, 121
 - nomenclature, 120
 - nucleotide sequences for human
 - TRAV10, 120
 - protein display, 181
 - recombination signals, 183
- TRAV12-1
 - amino acid sequences for human
 - TRAV12-1, 122, 123, 181
 - collier de perles for human
 - TRAV12-1*01, 123
 - complementarity determining region
 - lengths, 122
 - definition and functionality, 122
 - framework lengths, 122
 - gene location, 122
 - genome database accession numbers, 123
 - nomenclature, 122
 - nucleotide sequences for human
 - TRAV12-1, 122
 - protein display, 181
 - recombination signals, 183
- TRAV12-2
 - amino acid sequences for human
 - TRAV12-2, 124, 125, 181
 - collier de perles for human
 - TRAV12-2*01, 125
 - complementarity determining region
 - lengths, 125
 - definition and functionality, 124
 - framework lengths, 125
 - gene location, 124
 - genome database accession numbers, 125
 - nomenclature, 124
 - nucleotide sequences for human

- TRAV12-2, 124
 - protein display, 181
 - recombination signals, 183
- TRAV12-3
 - amino acid sequences for human
 - TRAV12-3, 126, 127, 181
 - collier de perles for human
 - TRAV12-3*01, 127
 - complementarity determining region
 - lengths, 126
 - definition and functionality, 126
 - framework lengths, 126
 - gene location, 126
 - genome database accession numbers, 127
 - nomenclature, 126
 - nucleotide sequences for human
 - TRAV12-3, 126
 - protein display, 181
 - recombination signals, 183
- TRAV13-1
 - amino acid sequences for human
 - TRAV13-1, 128, 129, 181
 - collier de perles for human
 - TRAV13-1*01, 129
 - complementarity determining region
 - lengths, 129
 - definition and functionality, 128
 - framework lengths, 129
 - gene location, 128
 - genome database accession numbers, 129
 - nomenclature, 128
 - nucleotide sequences for human
 - TRAV13-1, 128
 - protein display, 181
 - recombination signals, 183
- TRAV13-2
 - amino acid sequences for human
 - TRAV13-2, 130, 131, 181
 - collier de perles for human
 - TRAV13-2*01, 131
 - complementarity determining region
 - lengths, 130
 - definition and functionality, 130
 - framework lengths, 130
 - gene location, 130
 - genome database accession numbers, 131
- nomenclature, 130
 - nucleotide sequences for human
 - TRAV13-2, 130
 - protein display, 181
 - recombination signals, 183
- TRAV14/DV4
 - amino acid sequences for human
 - TRAV14/DV4, 132-3, 181
 - collier de perles for human
 - TRAV14/DV4*01, 133
 - complementarity determining region
 - lengths, 133
 - definition and functionality, 132
 - framework lengths, 133
 - gene location, 132
 - genome database accession numbers, 133
 - nomenclature, 132
 - nucleotide sequences for human
 - TRAV14/DV4, 132-3
 - protein display, 181
 - recombination signals, 183
- TRAV16
 - amino acid sequences for human
 - TRAV16, 134, 135, 182
 - collier de perles for human
 - TRAV16*01, 135
 - complementarity determining region
 - lengths, 134
 - definition and functionality, 134
 - framework lengths, 134
 - gene location, 134
 - genome database accession numbers, 135
 - nomenclature, 134
 - nucleotide sequences for human
 - TRAV16, 134
 - protein display, 182
 - recombination signals, 183
- TRAV17
 - amino acid sequences for human
 - TRAV17, 136, 137, 182
 - collier de perles for human
 - TRAV17*01, 137
 - complementarity determining region
 - lengths, 136
 - definition and functionality, 136
 - framework lengths, 136
 - gene location, 136

- genome database accession numbers, 137
- nomenclature, 136
- nucleotide sequences for human TRAV17, 136
- protein display, 182
- recombination signals, 183
- TRAV18
 - amino acid sequences for human TRAV18, 138, 139, 182
 - collier de perles for human TRAV18*01, 139
 - complementarity determining region lengths, 138
 - definition and functionality, 138
 - framework lengths, 138
 - gene location, 138
 - genome database accession numbers, 139
 - nomenclature, 138
 - nucleotide sequences for human TRAV18, 138
 - protein display, 182
 - recombination signals, 183
- TRAV19
 - amino acid sequences for human TRAV19, 140, 141, 182
 - collier de perles for human TRAV19*01, 141
 - complementarity determining region lengths, 140
 - definition and functionality, 140
 - framework lengths, 140
 - gene location, 140
 - genome database accession numbers, 141
 - nomenclature, 140
 - nucleotide sequences for human TRAV19, 140
 - protein display, 182
 - recombination signals, 183
- TRAV20
 - amino acid sequences for human TRAV20, 142, 143, 182
 - collier de perles for human TRAV20*01, 143
 - complementarity determining region lengths, 142
 - definition and functionality, 142
 - framework lengths, 142
 - gene location, 142
 - genome database accession numbers, 143
 - nomenclature, 142
 - nucleotide sequences for human TRAV20, 142
 - protein display, 182
 - recombination signals, 183
- TRAV21
 - amino acid sequences for human TRAV21, 144, 145, 182
 - collier de perles for human TRAV21*01, 145
 - complementarity determining region lengths, 144
 - definition and functionality, 144
 - framework lengths, 144
 - gene location, 144
 - genome database accession numbers, 145
 - nomenclature, 144
 - nucleotide sequences for human TRAV21, 144
 - protein display, 182
 - recombination signals, 183
- TRAV22
 - amino acid sequences for human TRAV22, 146, 147, 182
 - collier de perles for human TRAV22*01, 147
 - complementarity determining region lengths, 146
 - definition and functionality, 146
 - framework lengths, 146
 - gene location, 146
 - genome database accession numbers, 147
 - nomenclature, 146
 - nucleotide sequences for human TRAV22, 146
 - protein display, 182
 - recombination signals, 183
- TRAV23/DV6
 - amino acid sequences for human TRAV23/DV6, 148–9, 150, 182
 - collier de perles for human TRAV23/DV6*01, 150
 - complementarity determining region

- lengths, 149
- definition and functionality, 148
- framework lengths, 149
- gene location, 148
- genome database accession numbers, 150
- nomenclature, 148
- nucleotide sequences for human TRAV23/DV6, 148–9
- protein display, 182
- recombination signals, 183
- TRAV24
 - amino acid sequences for human TRAV24, 151, 152, 182
 - collier de perles for human TRAV24*01, 152
 - complementarity determining region lengths, 151
 - definition and functionality, 151
 - framework lengths, 151
 - gene location, 151
 - genome database accession numbers, 152
 - nomenclature, 151
 - nucleotide sequences for human TRAV24, 151
 - protein display, 182
 - recombination signals, 183
- TRAV25
 - amino acid sequences for human TRAV25, 153, 154, 182
 - collier de perles for human TRAV25*01, 154
 - complementarity determining region lengths, 153
 - definition and functionality, 153
 - framework lengths, 153
 - gene location, 153
 - genome database accession numbers, 154
 - nomenclature, 153
 - nucleotide sequences for human TRAV25, 153
 - protein display, 182
 - recombination signals, 183
- TRAV26–1
 - amino acid sequences for human TRAV26–1, 155, 156, 182
 - collier de perles for human TRAV26–1*01, 156
 - complementarity determining region lengths, 156
 - definition and functionality, 155
 - framework lengths, 156
 - gene location, 155
 - genome database accession numbers, 156
 - nomenclature, 155
 - nucleotide sequences for human TRAV26–1, 155
 - protein display, 182
 - recombination signals, 183
- TRAV26–2
 - amino acid sequences for human TRAV26–2, 157, 158, 182
 - collier de perles for human TRAV26–2*01, 158
 - complementarity determining region lengths, 157
 - definition and functionality, 157
 - framework lengths, 157
 - gene location, 157
 - genome database accession numbers, 158
 - nomenclature, 157
 - nucleotide sequences for human TRAV26–2, 157
 - protein display, 182
 - recombination signals, 183
- TRAV27
 - amino acid sequences for human TRAV27, 159–60, 182
 - collier de perles for human TRAV27*01, 160
 - complementarity determining region lengths, 159
 - definition and functionality, 159
 - framework lengths, 160
 - gene location, 159
 - genome database accession numbers, 160
 - nomenclature, 159
 - nucleotide sequences for human TRAV27, 159–60
 - protein display, 182
 - recombination signals, 183
- TRAV29/DV5
 - amino acid sequences for human

- TRAV29/DV5, 161, 162, 182
 - collier de perles for human
 - TRAV29/DV5*01, 162
 - complementarity determining region lengths, 162
 - definition and functionality, 161
 - framework lengths, 162
 - gene location, 161
 - genome database accession numbers, 162
 - nomenclature, 161
 - nucleotide sequences for human
 - TRAV29/DV5, 161
 - protein display, 182
 - recombination signals, 183
- TRAV30
 - amino acid sequences for human
 - TRAV30, 163, 164, 182
 - collier de perles for human
 - TRAV30*01, 164
 - complementarity determining region lengths, 164
 - definition and functionality, 163
 - framework lengths, 164
 - gene location, 163
 - genome database accession numbers, 164
 - nomenclature, 163
 - nucleotide sequences for human
 - TRAV30, 163
 - protein display, 182
 - recombination signals, 183
- TRAV34
 - amino acid sequences for human
 - TRAV34, 165, 166, 182
 - collier de perles for human
 - TRAV34*01, 166
 - complementarity determining region lengths, 165
 - definition and functionality, 165
 - framework lengths, 165
 - gene location, 165
 - genome database accession numbers, 166
 - nomenclature, 165
 - nucleotide sequences for human
 - TRAV34, 165
 - protein display, 182
 - recombination signals, 183
- TRAV35
 - amino acid sequences for human
 - TRAV35, 167, 168, 182
 - collier de perles for human
 - TRAV35*01, 168
 - complementarity determining region lengths, 167
 - definition and functionality, 167
 - framework lengths, 167
 - gene location, 167
 - genome database accession numbers, 168
 - nomenclature, 167
 - nucleotide sequences for human
 - TRAV35, 167
 - protein display, 182
 - recombination signals, 183
- TRAV36/DV7
 - amino acid sequences for human
 - TRAV36/DV7, 169–70, 182
 - collier de perles for human
 - TRAV36/DV7*01, 170
 - complementarity determining region lengths, 170
 - definition and functionality, 169
 - framework lengths, 170
 - gene location, 169
 - genome database accession numbers, 170
 - nomenclature, 169
 - nucleotide sequences for human
 - TRAV36/DV7, 169–70
 - protein display, 182
 - recombination signals, 183
- TRAV38–1
 - amino acid sequences for human
 - TRAV38–1, 171, 172, 182
 - collier de perles for human
 - TRAV38–1*01, 172
 - complementarity determining region lengths, 172
 - definition and functionality, 171
 - framework lengths, 172
 - gene location, 171
 - genome database accession numbers, 172
 - nomenclature, 171
 - nucleotide sequences for human
 - TRAV38–1, 171

- protein display, 182
- recombination signals, 183
- TRAV38-2/DV8
 - amino acid sequences for human TRAV38-2/DV8, 173-4, 182
 - collier de perles for human TRAV38-2/DV8*01, 174
 - complementarity determining region lengths, 174
 - definition and functionality, 173
 - framework lengths, 174
 - gene location, 173
 - genome database accession numbers, 174
 - nomenclature, 173
 - nucleotide sequences for human TRAV38-2/DV8, 173-4
 - protein display, 182
 - recombination signals, 183
- TRAV39
 - amino acid sequences for human TRAV39, 175, 176, 182
 - collier de perles for human TRAV39*01, 176
 - complementarity determining region lengths, 175
 - definition and functionality, 175
 - framework lengths, 175
 - gene location, 175
 - genome database accession numbers, 176
 - nomenclature, 175
 - nucleotide sequences for human TRAV39, 175
 - protein display, 182
 - recombination signals, 183
- TRAV40
 - amino acid sequences for human TRAV40, 177, 178, 182
 - collier de perles for human TRAV40*01, 178
 - complementarity determining region lengths, 177
 - definition and functionality, 177
 - framework lengths, 177
 - gene location, 177
 - genome database accession numbers, 178
 - nomenclature, 177
 - nucleotide sequences for human TRAV40, 177
 - protein display, 182
 - recombination signals, 183
- TRAV41
 - amino acid sequences for human TRAV41, 179, 180, 182
 - collier de perles for human TRAV41*01, 180
 - complementarity determining region lengths, 179
 - definition and functionality, 179
 - framework lengths, 179
 - gene location, 179
 - genome database accession numbers, 180
 - nomenclature, 179
 - nucleotide sequences for human TRAV41, 179
 - protein display, 182
 - recombination signals, 183
- TRB genes, 185-315
 - list of functional or ORF human TRB genes, 57-9
 - number per haploid genome, 55, 69, 70
 - potential repertoire, 55
 - rearrangements, 41-2
- TRB locus, 54-60
 - chromosomal localization, 54, 55, 69, 70
 - organization of human TRB locus, 54-6
 - somatic V-D-J rearrangements in, 25
- TRBC genes, 187-91
 - characteristics, 36
 - list of functional or ORF human TRBC genes, 57
 - protein display, 372
 - structure, 34
- TRBC1
 - amino acid sequences for human TRBC1, 188-9, 372
 - characteristics, 36
 - definition and functionality, 188
 - gene location, 188
 - genome database accession numbers, 189
 - nomenclature, 188

- nucleotide sequences for human
 - TRBC1, 188–9
- protein display, 372
- references, 189
- structure, 34
- TRBC2
 - amino acid sequences for human
 - TRBC2, 190–1, 372
 - characteristics, 36
 - definition and functionality, 190
 - gene location, 190
 - genome database accession numbers, 191
 - nomenclature, 190
 - nucleotide sequences for human
 - TRBC2, 190–1
 - protein display, 372
 - references, 191
 - structure, 34
- TRBD genes
 - amino acid sequences for human
 - TRBD genes, 194
 - definition and functionality, 194
 - gene location, 194
 - list of functional or ORF human
 - TRBD genes, 57
 - nomenclature, 194
 - nucleotide sequences for human
 - TRBD genes, 194
 - recombination signals, 194
 - references, 194
- TRBJ genes
 - amino acid sequences for human
 - TRBJ genes, 196–7
 - definition and functionality, 196
 - gene location, 196
 - list of functional or ORF human
 - TRBJ genes, 57–8
 - nomenclature, 196
 - nucleotide sequences for human
 - TRBJ genes, 196–7
 - recombination signals, 197
 - references, 197
- TRBV genes, 199–315
 - correspondence between
 - numberings, 8–10
 - list of functional or ORF human
 - TRBV genes, 58–9
 - nomenclature, 57, 58–9
 - number of human TRBV germline
 - variable genes, 59
 - potential repertoire, 59–60
 - protein display, 311–12
 - recombination signals, 313
 - references, 314–15
- TRBV2
 - amino acid sequences for human
 - TRBV2, 200, 201, 311
 - collier de perles for human
 - TRBV2*01, 201
 - complementarity determining region
 - lengths, 200
 - definition and functionality, 200
 - framework lengths, 200
 - gene location, 200
 - genome database accession numbers, 201
 - nomenclature, 200
 - nucleotide sequences for human
 - TRBV2, 200
 - protein display, 311
 - recombination signals, 313
- TRBV3–1
 - amino acid sequences for human
 - TRBV3–1, 202, 203, 311
 - collier de perles for human
 - TRBV3–1*01, 203
 - complementarity determining region
 - lengths, 202
 - definition and functionality, 202
 - framework lengths, 202
 - gene location, 202
 - genome database accession numbers, 203
 - nomenclature, 202
 - nucleotide sequences for human
 - TRBV3–1, 202
 - protein display, 311
 - recombination signals, 313
- TRBV4–1
 - amino acid sequences for human
 - TRBV4–1, 204, 205, 311
 - collier de perles for human
 - TRBV4–1*01, 205
 - complementarity determining region
 - lengths, 204
 - definition and functionality, 204
 - framework lengths, 204

- gene location, 204
- genome database accession numbers, 205
- nomenclature, 204
- nucleotide sequences for human TRBV4-1, 204
- protein display, 311
- recombination signals, 313
- TRBV4-2
 - amino acid sequences for human TRBV4-2, 206-7, 311
 - collier de perles for human TRBV4-2*01, 207
 - complementarity determining region lengths, 207
 - definition and functionality, 206
 - framework lengths, 207
 - gene location, 206
 - genome database accession numbers, 207
 - nomenclature, 206
 - nucleotide sequences for human TRBV4-2, 206
 - protein display, 311
 - recombination signals, 313
- TRBV4-3
 - amino acid sequences for human TRBV4-3, 208, 209, 311
 - collier de perles for human TRBV4-3*01, 209
 - complementarity determining region lengths, 209
 - definition and functionality, 208
 - framework lengths, 209
 - gene location, 208
 - genome database accession numbers, 209
 - nomenclature, 208
 - nucleotide sequences for human TRBV4-3, 208
 - protein display, 311
 - recombination signals, 313
- TRBV5-1
 - amino acid sequences for human TRBV5-1, 210, 211, 311
 - collier de perles for human TRBV5-1*01, 211
 - complementarity determining region lengths, 210
 - definition and functionality, 210
 - framework lengths, 210
 - gene location, 210
 - genome database accession numbers, 211
 - nomenclature, 210
 - nucleotide sequences for human TRBV5-1, 210
 - protein display, 311
 - recombination signals, 313
- TRBV5-3
 - amino acid sequences for human TRBV5-3, 212, 213, 311
 - collier de perles for human TRBV5-3*01, 213
 - complementarity determining region lengths, 212
 - definition and functionality, 212
 - framework lengths, 212
 - gene location, 212
 - genome database accession numbers, 213
 - nomenclature, 212
 - nucleotide sequences for human, 212
 - protein display, 311
 - recombination signals, 313
- TRBV5-4
 - amino acid sequences for human TRBV5-4, 214, 215, 311
 - collier de perles for human TRBV5-4*01, 215
 - complementarity determining region lengths, 215
 - definition and functionality, 214
 - framework lengths, 215
 - gene location, 214
 - genome database accession numbers, 215
 - nomenclature, 214
 - nucleotide sequences for human TRBV5-4, 214
 - protein display, 311
 - recombination signals, 313
- TRBV5-5
 - amino acid sequences for human, TRBV5-5, 216, 217, 311
 - collier de perles for human TRBV5-5*01, 217

- complementarity determining region lengths, 216
- definition and functionality, 216
- framework lengths, 216
- gene location, 216
- genome database accession numbers, 217
- nomenclature, 216
- nucleotide sequences for human TRBV5-5, 216
- protein display, 311
- recombination signals, 313
- TRBV5-6
 - amino acid sequences for human TRBV5-6, 218, 219, 311
 - collier de perles for human TRBV5-6*01, 219
 - complementarity determining region lengths, 218
 - definition and functionality, 218
 - framework lengths, 218
 - gene location, 218
 - genome database accession numbers, 219
 - nomenclature, 218
 - nucleotide sequences for human TRBV5-6, 218
 - protein display, 311
 - recombination signals, 313
- TRBV5-7
 - amino acid sequences for human TRBV5-7, 220, 221, 311
 - collier de perles for human TRBV5-7*01, 221
 - complementarity determining region lengths, 220
 - definition and functionality, 220
 - framework lengths, 220
 - gene location, 220
 - genome database accession numbers, 221
 - nomenclature, 220
 - nucleotide sequences for human TRBV5-7, 220
 - protein display, 311
 - recombination signals, 313
- TRBV5-8
 - amino acid sequences for human TRBV5-8, 222, 223, 311
 - collier de perles for human TRBV5-8*01, 223
 - complementarity determining region lengths, 222
 - definition and functionality, 222
 - framework lengths, 222
 - gene location, 222
 - genome database accession numbers, 223
 - nomenclature, 222
 - nucleotide sequences for human TRBV5-8, 222
 - protein display, 311
 - recombination signals, 313
- TRBV6-1
 - amino acid sequences for human TRBV6-1, 224, 225, 311
 - collier de perles for human TRBV6-1*01, 225
 - complementarity determining region lengths, 224
 - definition and functionality, 224
 - framework lengths, 224
 - gene location, 224
 - genome database accession numbers, 225
 - nomenclature, 224
 - nucleotide sequences for human TRBV6-1, 224
 - protein display, 311
 - recombination signals, 313
- TRBV6-2
 - amino acid sequences for human, TRBV6-2, 226-7, 228, 311
 - collier de perles for human TRBV6-2*01, 228
 - complementarity determining region lengths, 227
 - definition and functionality, 226
 - framework lengths, 227
 - gene location, 226
 - genome database accession numbers, 228
 - nomenclature, 226
 - nucleotide sequences for human TRBV6-2, 226-7
 - protein display, 311
 - recombination signals, 313
- TRBV6-3

- amino acid sequences for human
 - TRBV6-3, 229, 230, 311
- collier de perles for human
 - TRBV6-3*01, 230
- complementarity determining region
 - lengths, 229
- definition and functionality, 229
- framework lengths, 229
- gene location, 229
- genome database accession numbers, 230
- nomenclature, 229
- nucleotide sequences for human
 - TRBV6-3, 229
- protein display, 311
- recombination signals, 313
- TRBV6-4
 - amino acid sequences for human
 - TRBV6-4, 231, 232, 311
 - collier de perles for human
 - TRBV6-4*01, 232
 - complementarity determining region
 - lengths, 231
 - definition and functionality, 231
 - framework lengths, 231
 - gene location, 231
 - genome database accession numbers, 232
 - nomenclature, 231
 - nucleotide sequences for human
 - TRBV6-4, 231
 - protein display, 311
 - recombination signals, 313
- TRBV6-5
 - amino acid sequences for human
 - TRBV6-5, 233, 234, 311
 - collier de perles for human
 - TRBV6-5*01, 234
 - complementarity determining region
 - lengths, 233
 - correspondence between
 - numberings, 8-10
 - definition and functionality, 233
 - framework lengths, 233
 - gene location, 233
 - genome database accession numbers, 234
 - nomenclature, 233
 - nucleotide sequences for human
 - TRBV6-5, 233
 - protein display, 311
 - recombination signals, 313
- TRBV6-6
 - amino acid sequences for human
 - TRBV6-6, 235, 236, 311
 - collier de perles for human
 - TRBV6-6*01, 236
 - complementarity determining region
 - lengths, 236
 - definition and functionality, 235
 - framework lengths, 236
 - gene location, 235
 - genome database accession numbers, 236
 - nomenclature, 235
 - nucleotide sequences for human
 - TRBV6-6, 235
 - protein display, 311
 - recombination signals, 313
- TRBV6-7
 - amino acid sequences for human
 - TRBV6-7, 237, 238, 311
 - collier de perles for human
 - TRBV6-7*01, 238
 - complementarity determining region
 - lengths, 237
 - definition and functionality, 237
 - framework lengths, 237
 - gene location, 237
 - genome database accession numbers, 238
 - nomenclature, 237
 - nucleotide sequences for human
 - TRBV6-7, 237
 - protein display, 311
 - recombination signals, 313
- TRBV6-8
 - amino acid sequences for human
 - TRBV6-8, 239, 240, 311
 - collier de perles for human
 - TRBV6-8*01, 240
 - complementarity determining region
 - lengths, 239
 - definition and functionality, 239
 - framework lengths, 239
 - gene location, 239
 - genome database accession numbers, 240

- nomenclature, 239
- nucleotide sequences for human
 - TRBV6-8, 239
- protein display, 311
- recombination signals, 313
- TRBV6-9
 - amino acid sequences for human
 - TRBV6-9, 241, 242, 311
 - collier de perles for human
 - TRBV6-9*01, 242
 - complementarity determining region
 - lengths, 241
 - definition and functionality, 241
 - framework lengths, 241
 - gene location, 241
 - genome database accession numbers, 242
 - nomenclature, 241
 - nucleotide sequences for human
 - TRBV6-9, 241
 - protein display, 311
 - recombination signals, 313
- TRBV7-1
 - amino acid sequences for human
 - TRBV7-1, 243, 244, 311
 - collier de perles for human
 - TRBV7-1*01, 244
 - complementarity determining region
 - lengths, 243
 - definition and functionality, 243
 - framework lengths, 243
 - gene location, 243
 - genome database accession numbers, 244
 - nomenclature, 243
 - nucleotide sequences for human
 - TRBV7-1, 243
 - protein display, 311
 - recombination signals, 313
- TRBV7-2
 - amino acid sequences for human
 - TRBV7-2, 245-6, 311
 - collier de perles for human
 - TRBV7-2*01, 246
 - complementarity determining region
 - lengths, 246
 - definition and functionality, 245
 - framework lengths, 246
 - gene location, 245
 - genome database accession numbers, 246
 - nomenclature, 245
 - nucleotide sequences for human
 - TRBV7-2, 245-6
 - protein display, 311
 - recombination signals, 313
- TRBV7-3
 - amino acid sequences for human
 - TRBV7-3, 247-8, 249, 311
 - collier de perles for human
 - TRBV7-3*01, 249
 - complementarity determining region
 - lengths, 248
 - definition and functionality, 247
 - framework lengths, 248
 - gene location, 247
 - genome database accession numbers, 249
 - nomenclature, 247
 - nucleotide sequences for human
 - TRBV7-3, 247-8
 - protein display, 311
 - recombination signals, 313
- TRBV7-4
 - amino acid sequences for human
 - TRBV7-4, 250-1, 311
 - collier de perles for human
 - TRBV7-4*01, 251
 - complementarity determining region
 - lengths, 251
 - definition and functionality, 250
 - framework lengths, 251
 - gene location, 250
 - genome database accession numbers, 251
 - nomenclature, 250
 - nucleotide sequences for human
 - TRBV7-4, 250-1
 - protein display, 311
 - recombination signals, 313
- TRBV7-6
 - amino acid sequences for human
 - TRBV7-6, 252, 253, 311
 - collier de perles for human
 - TRBV7-6*01, 253
 - complementarity determining region
 - lengths, 253
 - definition and functionality, 252

- framework lengths, 253
- gene location, 252
- genome database accession numbers, 253
- nomenclature, 252
- nucleotide sequences for human TRBV7-6, 252
- protein display, 311
- recombination signals, 313
- TRBV7-7
 - amino acid sequences for human TRBV7-7, 254, 255, 311
 - collier de perles for human TRBV7-7*01, 255
 - complementarity determining region lengths, 255
 - definition and functionality, 254
 - framework lengths, 255
 - gene location, 254
 - genome database accession numbers, 255
 - nomenclature, 254
 - nucleotide sequences for human TRBV7-7, 254
 - protein display, 311
 - recombination signals, 313
- TRBV7-8
 - amino acid sequences for human TRBV7-8, 256, 257, 311
 - collier de perles for human TRBV7-8*01, 257
 - complementarity determining region lengths, 257
 - definition and functionality, 256
 - framework lengths, 257
 - gene location, 256
 - genome database accession numbers, 257
 - nomenclature, 256
 - nucleotide sequences for human TRBV7-8, 256
 - protein display, 311
 - recombination signals, 313
- TRBV7-9
 - amino acid sequences for human TRBV7-9, 258-9, 260, 311
 - collier de perles for human TRBV7-9*01, 260
 - complementarity determining region lengths, 259
 - definition and functionality, 258
 - framework lengths, 259
 - gene location, 258
 - genome database accession numbers, 260
 - nomenclature, 258
 - nucleotide sequences for human TRBV7-9, 258-9
 - protein display, 311
 - recombination signals, 313
- TRBV9
 - amino acid sequences for human TRBV9, 261, 262, 312
 - collier de perles for human TRBV9*01, 262
 - complementarity determining region lengths, 261
 - definition and functionality, 261
 - framework lengths, 261
 - gene location, 261
 - genome database accession numbers, 262
 - nomenclature, 261
 - nucleotide sequences for human TRBV9, 261
 - protein display, 312
 - recombination signals, 313
- TRBV10-1
 - amino acid sequences for human TRBV10-1, 263-4, 312
 - collier de perles for human TRBV10-1*01, 264
 - complementarity determining region lengths, 264
 - definition and functionality, 263
 - framework lengths, 264
 - gene location, 263
 - genome database accession numbers, 264
 - nomenclature, 263
 - nucleotide sequences for human TRBV10-1, 263-4
 - protein display, 312
 - recombination signals, 313
- TRBV10-2
 - amino acid sequences for human TRBV10-2, 265, 266, 312
 - collier de perles for human

- TRBV10-2*01, 266
 - complementarity determining region lengths, 265
 - definition and functionality, 265
 - framework lengths, 265
 - gene location, 265
 - genome database accession numbers, 266
 - nomenclature, 265
 - nucleotide sequences for human TRBV10-2, 265
 - protein display, 312
 - recombination signals, 313
- TRBV10-3
 - amino acid sequences for human TRBV10-3, 267-8, 312
 - collier de perles for human TRBV10-3*01, 268
 - complementarity determining region lengths, 268
 - definition and functionality, 267
 - framework lengths, 268
 - gene location, 267
 - genome database accession numbers, 268
 - nomenclature, 267
 - nucleotide sequences for human TRBV10-3, 267-8
 - protein display, 312
 - recombination signals, 313
- TRBV11-1
 - amino acid sequences for human TRBV11-1, 269, 270, 312
 - collier de perles for human TRBV11-1*01, 270
 - complementarity determining region lengths, 269
 - definition and functionality, 269
 - framework lengths, 269
 - gene location, 269
 - genome database accession numbers, 270
 - nomenclature, 269
 - nucleotide sequences for human TRBV11-1, 269
 - protein display, 312
 - recombination signals, 313
- TRBV11-2
 - amino acid sequences for human TRBV11-2, 271, 272, 312
 - collier de perles for human TRBV11-2*01, 272
 - complementarity determining region lengths, 271
 - definition and functionality, 271
 - framework lengths, 271
 - gene location, 271
 - genome database accession numbers, 272
 - nomenclature, 271
 - nucleotide sequences for human TRBV11-2, 271
 - protein display, 312
 - recombination signals, 313
- TRBV11-3
 - amino acid sequences for human, TRBV11-3, 273-4, 312
 - collier de perles for human TRBV11-3*01, 274
 - complementarity determining region lengths, 274
 - definition and functionality, 273
 - framework lengths, 274
 - gene location, 273
 - genome database accession numbers, 274
 - nomenclature, 273
 - nucleotide sequences for human TRBV11-3, 273-4
 - protein display, 312
 - recombination signals, 313
- TRBV12-3
 - amino acid sequences for human TRBV12-3, 275, 276, 312
 - collier de perles for human TRBV12-3*01, 276
 - complementarity determining region lengths, 275
 - definition and functionality, 275
 - framework lengths, 275
 - gene location, 275
 - genome database accession numbers, 276
 - nomenclature, 275
 - nucleotide sequences for human, TRBV12-3, 275
 - protein display, 312
 - recombination signals, 313

- TRBV12-4
 amino acid sequences for human
 TRBV12-4, 277, 278, 312
 collier de perles for human
 TRBV12-4*01, 278
 complementarity determining region
 lengths, 278
 definition and functionality, 277
 framework lengths, 278
 gene location, 277
 genome database accession numbers,
 278
 nomenclature, 277
 nucleotide sequences for human
 TRBV12-4, 277
 protein display, 312
 recombination signals, 313
- TRBV12-5
 amino acid sequences for human
 TRBV12-5, 279, 280, 312
 collier de perles for human
 TRBV12-5*01, 280
 complementarity determining region
 lengths, 279
 definition and functionality, 279
 framework lengths, 279
 gene location, 279
 genome database accession numbers,
 280
 nomenclature, 279
 nucleotide sequences for human
 TRBV12-5, 279
 protein display, 312
 recombination signals, 313
- TRBV13
 amino acid sequences for human
 TRBV13, 281-2, 312
 collier de perles for human
 TRBV13*01, 282
 complementarity determining region
 lengths, 282
 definition and functionality, 281
 framework lengths, 282
 gene location, 281
 genome database accession numbers,
 282
 nomenclature, 281
 nucleotide sequences for human
 TRBV13, 281-2
 protein display, 312
 recombination signals, 313
- TRBV14
 amino acid sequences for human
 TRBV14, 283, 284, 312
 collier de perles for human
 TRBV14*01, 284
 complementarity determining region
 lengths, 283
 definition and functionality, 283
 framework lengths, 283
 gene location, 283
 genome database accession numbers,
 284
 nomenclature, 283
 nucleotide sequences for human
 TRBV14, 283
 protein display, 312
 recombination signals, 313
- TRBV15
 amino acid sequences for human
 TRBV15, 285, 286, 312
 collier de perles for human
 TRBV15*01, 286
 complementarity determining region
 lengths, 285
 definition and functionality, 285
 framework lengths, 285
 gene location, 285
 genome database accession numbers,
 286
 nomenclature, 285
 nucleotide sequences for human
 TRBV15, 285
 protein display, 312
 recombination signals, 313
- TRBV16
 amino acid sequences for human
 TRBV16, 287, 288, 312
 collier de perles for human
 TRBV16*01, 288
 complementarity determining region
 lengths, 288
 definition and functionality, 287
 framework lengths, 288
 gene location, 287
 genome database accession numbers,
 288
 nomenclature, 287

- nucleotide sequences for human
 - TRBV16, 287
- protein display, 312
- recombination signals, 313
- TRBV17
 - amino acid sequences for human
 - TRBV17, 289, 290, 312
 - collier de perles for human
 - TRBV17*01, 290
 - complementarity determining region
 - lengths, 289
 - definition and functionality, 289
 - framework lengths, 289
 - gene location, 289
 - genome database accession numbers,
 - 290
 - nomenclature, 289
 - nucleotide sequences for human
 - TRBV17, 289
 - protein display, 312
 - recombination signals, 313
- TRBV18
 - amino acid sequences for human
 - TRBV18, 291, 292, 312
 - collier de perles for human
 - TRBV18*01, 292
 - complementarity determining region
 - lengths, 291
 - definition and functionality, 291
 - framework lengths, 291
 - gene location, 291
 - genome database accession numbers,
 - 292
 - nomenclature, 291
 - nucleotide sequences for human
 - TRBV18, 291
 - protein display, 312
 - recombination signals, 313
- TRBV19
 - amino acid sequences for human
 - TRBV19, 293, 312
 - collier de perles for human
 - TRBV19*01, 294
 - complementarity determining region
 - lengths, 293
 - definition and functionality, 293
 - framework lengths, 293
 - gene location, 293
 - genome database accession numbers,
 - 294
 - nomenclature, 293
 - nucleotide sequences for human
 - TRBV19, 293
 - protein display, 312
 - recombination signals, 313
- TRBV20-1
 - amino acid sequences for human
 - TRBV20-1, 295-6, 312
 - collier de perles for human
 - TRBV20-1*01, 296
 - complementarity determining region
 - lengths, 296
 - definition and functionality, 295
 - framework lengths, 296
 - gene location, 295
 - genome database accession numbers,
 - 296
 - nomenclature, 295
 - nucleotide sequences for human
 - TRBV20-1, 295-6
 - protein display, 312
 - recombination signals, 313
- TRBV23-1
 - amino acid sequences for human
 - TRBV23-1, 297, 298, 312
 - collier de perles for human
 - TRBV23-1*01, 298
 - complementarity determining region
 - lengths, 297
 - definition and functionality, 297
 - framework lengths, 297
 - gene location, 297
 - genome database accession numbers,
 - 298
 - nomenclature, 297
 - nucleotide sequences for human
 - TRBV23-1, 297
 - protein display, 312
 - recombination signals, 313
- TRBV24-1
 - amino acid sequences for human
 - TRBV24-1, 299, 300, 312
 - collier de perles for human
 - TRBV24-1*01, 300
 - complementarity determining region
 - lengths, 299
 - definition and functionality, 299
 - framework lengths, 299

- gene location, 299
- genome database accession numbers, 300
- nomenclature, 299
- nucleotide sequences for human TRBV24-1, 299
- protein display, 312
- recombination signals, 313
- TRBV25-1
 - amino acid sequences for human TRBV25-1, 301, 302, 312
 - collier de perles for human TRBV25-1*01, 302
 - complementarity determining region lengths, 301
 - definition and functionality, 301
 - framework lengths, 301
 - gene location, 301
 - nomenclature, 301
 - nucleotide sequences for human TRBV25-1, 301
 - protein display, 312
 - recombination signals, 313
- TRBV27
 - amino acid sequences for human TRBV27, 303, 304, 312
 - collier de perles for human TRBV27*01, 304
 - complementarity determining region lengths, 303
 - definition and functionality, 303
 - framework lengths, 303
 - gene location, 303
 - genome database accession numbers, 304
 - nomenclature, 303
 - nucleotide sequences for human TRBV27, 303
 - protein display, 312
 - recombination signals, 313
- TRBV28
 - amino acid sequences for human TRBV28, 305, 306, 312
 - collier de perles for human TRBV28*01, 306
 - complementarity determining region lengths, 305
 - definition and functionality, 305
 - framework lengths, 305
 - gene location, 305
 - genome database accession numbers, 306
 - nomenclature, 305
 - nucleotide sequences for human TRBV28, 305
 - protein display, 312
 - recombination signals, 313
- TRBV29-1
 - amino acid sequences for human TRBV29-1, 307, 308, 312
 - collier de perles for human TRBV29-1*01, 308
 - complementarity determining region lengths, 307
 - definition and functionality, 307
 - framework lengths, 307
 - gene location, 307
 - genome database accession numbers, 308
 - nomenclature, 307
 - nucleotide sequences for human TRBV29-1, 307
 - protein display, 312
 - recombination signals, 313
- TRBV30
 - amino acid sequences for human TRBV30, 309-10, 312
 - collier de perles for human TRBV30*01, 310
 - complementarity determining region lengths, 310
 - definition and functionality, 309
 - framework lengths, 310
 - gene location, 309
 - genome database accession numbers, 310
 - nomenclature, 309
 - nucleotide sequences for human TRBV30, 309-10
 - protein display, 312
 - recombination signals, 313
- TRD genes, 353-72
 - list of functional or ORF human TRD genes, 67
 - number per haploid genome, 69, 70
 - rearrangements, 41
- TRD locus
 - chromosomal localization, 64-5, 69,

- 70
- organization of human TRD locus, 65–6
- somatic V-D-J rearrangements in, 25
- TRDC
 - amino acid sequences for human TRDC, 356–8, 372
 - characteristics, 36
 - definition and functionality, 356
 - gene location, 356
 - genome database accession numbers, 358
 - nomenclature, 356
 - nucleotide sequences for human TRDC, 356–8
 - protein display, 372
 - references, 358
 - structure, 34
- TRDD genes
 - amino acid sequences for human TRDD genes, 360
 - definition and functionality, 360
 - list of functional or ORF human TRDD genes, 67
 - nomenclature, 360
 - nucleotide sequences for human TRDD genes, 360
 - recombination signals, 360
 - references, 360
- TRDJ genes
 - amino acid sequences for human TRDJ genes, 362
 - definition and functionality, 362
 - gene location, 362
 - list of functional or ORF human TRDJ genes, 67
 - nomenclature, 362
 - nucleotide sequences for human TRDJ genes, 362
 - recombination signals, 362
 - references, 362
- TRDV genes, 363–71
 - correspondence between numberings, 8–10
 - list of functional or ORF human TRDV genes, 67
 - nomenclature, 67
 - number of human TRDV germline variable genes, 68
 - potential repertoire, 68
 - protein display, 370
 - recombination signals, 371
 - references, 371
 - see also* TRAV/DV genes
- TRDV1
 - amino acid sequences for human TRDV1, 364, 365, 370
 - collier de perles for human TRDV1*01, 365
 - complementarity determining region lengths, 364
 - definition and functionality, 364
 - framework lengths, 364
 - gene location, 364
 - genome database accession numbers, 365
 - nomenclature, 364
 - nucleotide sequences for human TRDV1, 364
 - protein display, 370
 - recombination signals, 371
- TRDV2
 - amino acid sequences for human TRDV2, 366, 367, 370
 - collier de perles for human TRDV2*01, 367
 - complementarity determining region lengths, 367
 - correspondence between numberings, 8–10
 - definition and functionality, 366
 - framework lengths, 367
 - gene location, 366
 - genome database accession numbers, 367
 - nomenclature, 366
 - nucleotide sequences for human TRDV2, 366
 - protein display, 370
 - recombination signals, 371
- TRDV3
 - amino acid sequences for human TRDV3, 368–9, 370
 - collier de perles for human TRDV3*01, 369
 - complementarity determining region lengths, 369
 - definition and functionality, 368

- framework lengths, 369
- gene location, 368
- genome database accession numbers, 369
- nomenclature, 368
- nucleotide sequences for human TRDV3, 368–9
- protein display, 370
- recombination signals, 371
- TRG genes, 317–51
 - allelic polymorphisms, 38
 - list of functional or ORF human TRG genes, 63
 - number per haploid genome, 69, 70
 - potential repertoire, 62
 - rearrangements, 39, 40, 41–2
- TRG locus, 61–4
 - chromosomal localization, 61, 69, 70
 - organization of human TRG locus, 61–2
 - somatic V-J rearrangements in, 25
- TRGC genes, 319–25
 - allelic polymorphisms, 38, 62
 - list of functional or ORF human TRGC genes, 63
 - protein display, 372
- TRGC1
 - amino acid sequences for human TRGC1, 320–1, 372
 - characteristics, 36
 - definition and functionality, 320
 - gene location, 320
 - genome database accession numbers, 321
 - nomenclature, 320
 - nucleotide sequences for human TRGC1, 320–1
 - protein display, 372
 - references, 321
 - schematic representation, 38
 - structure, 35
- TRGC2(2x)
 - amino acid sequences for human TRGC2(2x), 322–3, 372
 - characteristics, 36
 - definition and functionality, 322
 - gene location, 322
 - genome database accession numbers, 323
 - nomenclature, 322
 - nucleotide sequences for human TRGC2(2x), 322–3
 - protein display, 372
 - references, 323
 - schematic representation, 38
 - structure, 35
- TRGC2(3x)
 - amino acid sequences for human TRGC2(3x), 324, 372
 - characteristics, 36
 - definition and functionality, 324
 - gene location, 324
 - genome database accession numbers, 325
 - nomenclature, 324
 - nucleotide sequences for human TRGC2(3x), 324
 - protein display, 372
 - references, 325
 - schematic representation, 38
 - structure, 35
- TRGJ genes
 - amino acid sequences for human TRGJ genes, 328
 - definition and functionality, 328
 - gene location, 328
 - list of functional or ORF human TRGJ genes, 63
 - nomenclature, 328
 - nucleotide sequences for human TRGJ genes, 328
 - recombination signals, 328
 - references, 329
- TRGV genes, 331–51
 - allelic polymorphisms, 38, 62
 - correspondence between numberings, 8–10
 - list of functional or ORF human TRGV genes, 63
 - number of human TRGV germline variable genes, 64
 - potential repertoire, 64
 - protein display, 350
 - recombination signals, 351
 - references, 351
- TRGV1
 - allelic polymorphisms, 38
 - amino acid sequences for human

- TRGV1, 332, 333, 350
 - collier de perles for human
 - TRGV1*01, 333
 - complementarity determining region
 - lengths, 332
 - definition and functionality, 332
 - framework lengths, 332
 - gene location, 332
 - genome database accession numbers, 333
 - nomenclature, 332
 - nucleotide sequences for human
 - TRGV1, 332
 - protein display, 350
 - recombination signals, 351
- TRGV2
 - amino acid sequences for human
 - TRGV2, 334, 335, 350
 - collier de perles for human
 - TRGV2*01, 335
 - complementarity determining region
 - lengths, 334
 - definition and functionality, 334
 - framework lengths, 334
 - gene location, 334
 - genome database accession numbers, 335
 - nomenclature, 334
 - nucleotide sequences for human
 - TRGV2, 334
 - protein display, 350
 - recombination signals, 351
- TRGV3
 - amino acid sequences for human
 - TRGV3, 336, 337, 350
 - collier de perles for human
 - TRGV3*01, 337
 - complementarity determining region
 - lengths, 336
 - correspondence between
 - numberings, 8–10
 - definition and functionality, 336
 - framework lengths, 336
 - gene location, 336
 - genome database accession numbers, 337
 - nomenclature, 336
 - nucleotide sequences for human
 - TRGV3, 336
 - protein display, 350
 - recombination signals, 351
- TRGV4
 - amino acid sequences for human
 - TRGV4, 338, 339, 350
 - collier de perles for human
 - TRGV4*01, 339
 - complementarity determining region
 - lengths, 339
 - definition and functionality, 338
 - framework lengths, 339
 - gene location, 338
 - genome database accession numbers, 339
 - nomenclature, 338
 - nucleotide sequences for human
 - TRGV4, 338
 - protein display, 350
 - recombination signals, 351
- TRGV5
 - amino acid sequences for human
 - TRGV5, 340, 341, 350
 - collier de perles for human
 - TRGV5*01, 341
 - complementarity determining region
 - lengths, 340
 - definition and functionality, 340
 - framework lengths, 340
 - gene location, 340
 - genome database accession numbers, 341
 - nomenclature, 340
 - nucleotide sequences for human
 - TRGV5, 340
 - protein display, 350
 - recombination signals, 351
- TRGV8
 - amino acid sequences for human
 - TRGV8, 342, 343, 350
 - collier de perles for human
 - TRGV8*01, 343
 - complementarity determining region
 - lengths, 342
 - definition and functionality, 342
 - framework lengths, 342
 - gene location, 342
 - genome database accession numbers, 343
 - nomenclature, 342

- nucleotide sequences for human
 - TRGV8, 342
 - protein display, 350
 - recombination signals, 351
- TRGV9
 - amino acid sequences for human
 - TRGV9, 344, 345, 350
 - collier de perles for human
 - TRGV9*01, 345
 - complementarity determining region
 - lengths, 344
 - definition and functionality, 344
 - framework lengths, 344
 - gene location, 344
 - genome database accession numbers, 345
 - nomenclature, 344
 - nucleotide sequences for human
 - TRGV9, 344
 - protein display, 350
 - recombination signals, 351
- TRGV10
 - amino acid sequences for human
 - TRGV10, 346, 347, 350
 - collier de perles for human
 - TRGV10*01, 347
 - complementarity determining region
 - lengths, 346
 - definition and functionality, 346
 - framework lengths, 346
 - gene location, 346
 - genome database accession numbers, 347
 - nomenclature, 346
 - nucleotide sequences for human
 - TRGV10, 346
 - protein display, 350
 - recombination signals, 351
- TRGV11
 - amino acid sequences for human
 - TRGV11, 348, 349, 350
 - collier de perles for human
 - TRGV11*01, 349
 - complementarity determining region
 - lengths, 348
 - definition and functionality, 348
 - framework lengths, 348
 - gene location, 348
 - genome database accession numbers, 349
 - nomenclature, 348
 - nucleotide sequences for human
 - TRGV11, 348
 - protein display, 350
 - recombination signals, 351
- V-REGIONS
 - correspondence between
 - numberings, 8–10
 - IMGT unique numbering for, 7

This Page Intentionally Left Blank