

The Mouse (*Mus musculus*) T Cell Receptor Beta Variable (TRBV), Diversity (TRBD) and Joining (TRBJ) Genes

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Key Words

Mouse genes · IMGT · T cell receptor · Beta variable regions · Beta diversity regions · Beta joining regions

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Abstract

'The Mouse (*Mus musculus*) T cell Receptor Beta Variable (TRBV), Diversity (TRBD), and Joining (TRBJ) Genes', the 14th report of the 'IMGT Locus in Focus' section, comprises 8 tables entitled: (1) 'Number of mouse (*Mus musculus*) germline TRBV genes at 6A–C and potential repertoire'; (2) 'Mouse (*Mus musculus*) germline TRBV genes at 6A–C'; (3) 'Mouse (*Mus musculus*) TRBV allele table'; (4) 'Mouse (*Mus musculus*) germline TRBD genes and alleles'; (5) 'Mouse (*Mus musculus*) germline TRBJ genes'; (6) 'Mouse (*Mus musculus*) TRBJ allele table'; (7) 'Correspondence between the different mouse (*Mus musculus*) TRBV gene nomenclatures'; (8) 'Mouse (*Mus musculus*) TRBV genes and related human TRBV genes'. These tables are

Introduction

'The Mouse (*Mus musculus*) T cell Receptor Beta Variable (TRBV), Diversity (TRBD) and Joining (TRBJ) Genes' is the 14th report of the 'IMGT Locus in Focus' section launched in the April 1998 issue of *Experimental and Clinical Immunogenetics* [1–14]. The complete repertoire of the human germline TRBV, TRBD and TRBJ genes has previously been reported [8, 11, 14]. This 14th report on the mouse (*Mus musculus*) T cell receptor beta variable, diversity and joining genes describes, for the first time, the complete murine germline TRB repertoire, with the same standardized rules of the IMGT scientific chart [15]

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which were used for the description of the human TRB repertoire [8, 11, 14]. This report comprises 8 tables entitled: (1) ‘Number of mouse (*Mus musculus*) germline TRBV genes at 6A-C and potential repertoire’; (2) ‘Mouse (*Mus musculus*) germline TRBV genes at 6A-C’; (3) ‘Mouse (*Mus musculus*) TRBV allele table’; (4) ‘Mouse (*Mus musculus*) germline TRBD genes and alleles’; (5) ‘Mouse (*Mus musculus*) germline TRBJ genes’; (6) ‘Mouse (*Mus musculus*) TRBJ allele table’; (7) ‘Correspondence between the different mouse (*Mus musculus*) TRBV gene nomenclatures’; (8) ‘Mouse (*Mus musculus*) TRBV genes and related human TRBV genes’. These tables are available at the IMGT Marie-Paule page from **IMGT**, the international ImMunoGeneTics database (<http://imgt.cines.fr:8104>) created by Marie-Paule Lefranc, Université Montpellier II, CNRS, Montpellier, France [15, 16].

Table 1. Number of mouse (*Mus musculus*) germline TRBV genes at 6A-C and potential repertoire

35 TRBV genes belonging to 31 subgroups, on 700 kilobases:

21 FUNCTIONAL

1 ORF (Open Reading Frame)

12 PSEUDOGENE

1 FUNCTIONAL or PSEUDOGENE or ORF

Potential repertoire: 21-22 FUNCTIONAL TRBV genes belonging to 19 subgroups

Subgroup	Functional	ORF	Pseudogene	Total
TRBV1	1	-	-	1
TRBV2	1	-	-	1
TRBV3	1	-	-	1
TRBV4	1	-	-	1
TRBV5	1	-	-	1
TRBV6	-	-	1	1
TRBV7	-	-	1	1
TRBV8	-	-	1	1
TRBV9	-	-	1	1
TRBV10	-	-	1	1
TRBV11	-	-	1	1
TRBV12	2	-	1	3
TRBV13	3	-	-	3
TRBV14	1	-	-	1
TRBV15	1	-	-	1
TRBV16	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)*	(1)*	1
TRBV25	-	-	1	1
TRBV26	1	-	-	1
TRBV27	-	-	1	1
TRBV28	-	-	1	1
TRBV29	1	-	-	1
TRBV30	1	-	-	1
TRBV31	1	-	-	1
Total	21(+1)*	1(+1)*	12(+1)*	35

*FUNCTIONAL or PSEUDOGENE or ORF (TRBV24)

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Table 2. Mouse (*Mus musculus*) germline TRBV genes at 6A-C

Fct: FUNCTIONALITY

F: Functional

P: Pseudogene

ORF: Open Reading Frame

vg: Vestigial

R: Rearranged

T: Transcribed

Pr: Translated into protein

+ or "-" indicates if the gene sequences have been found (+) or not been found (-) rearranged (R), transcribed (T), and/or translated into protein (Pr).

Arbitrariness that information is shown on the first line of each gene when the data have been confirmed by several studies.

Functionality is shown between:

- parentheses when the accession number refers to rearranged genomic DNA or cDNA and the corresponding germline gene has not yet been isolated.

- brackets when the accession number refers to genomic DNA, but not known as being germline or rearranged.

Reference sequences in bold have been mapped: "mapped" refers to sequences which have been obtained from clones (phages, cosmids, YACs,...) either by subcloning or PCR, and does not apply to sequences obtained directly from genomic DNA.
 In the "Sequences from the literature" column, names of the sequences are preceded by the designation of the mouse strain.

TRBV subgroup	TRBV gene name	Fct	R	T	Pr	Strain	Reference sequences	Accession numbers	Sequences from the literature
1	1	F	+	+		BALB/c	V2S1	AE000663 [22]	
	(F)	+	+	+		BALB/c		X01642 [19]#c	
2	2	F	+	+		BALB/c	V4S1	AE000663 [22]	
	(F)	+	+	+		BALB/c	V16S1	AE000663 [22]	
3	3	F	+	+		B10.A (19)	Vbeta10	X03865 [9]#c	
	(F)	+	+	+		C57BL/6	Vbeta10	X56725 [11]#c	BALB/c, V10S1 [AE000663] [22]
4	4	F	+	+		SV40RJ	Vbeta10	AJ249819 [25]#c	
	(F)	+	+	+		BALB/c	V1S1	AE000663 [22]	
5	5	F	+	+		BALB/c		X00438 [10]#c	
	(F)	+	+	+		AKR	Vbeta1	X02779 [1]#c	
	(F)	+	+	+		B10.SI(9R)(19)	Vbeta1	M20878 [17]#c	
	(F)	+	+	+		SV40RJ	Vbeta1	AJ249820 [25]#c	
6	6	P(2)				BALB/c	V26S1P	AE000663 [22]	
7	7	P(3)				BALB/c	V27S1P	AE000663 [22]	
8	8	P(4)				BALB/c	V28S1P	AE000663 [22]	
9	9	P(5)				BALB/c	VbetaN8	X16693 [6]#c	BALB/c, V24S1P [AE000663] [22]
10	10	P(7)				BALB/c	VbetaN9	X16694 [6]#c	BALB/c, V25S1P [AE000663] [22]
11	11	P(8)				BALB/c	V29S1P	AE000663 [22]	
12	12-1	F	+	+		C57BL/6	Vbeta5.2	M15614 [7]	BALB/c, V5S2 [AE000663] [22]
	(F)	+	+	+		NZW	Vbeta5.2	M30881 [3]#c	
	(F)	+	+	+		C57BL/6	Vbeta5.1	M15613 [7]	BALB/c, V5S1 [AE000663] [22]
	(F)	+	+	+		BALB/c	Vbeta5.1	X02782 [1]#c	
	P(9)					C57BL/6	Vbeta5.3	M15615 [7]	BALB/c, V5S3P [AE000663] [22]
	12-3								

13	13-1	F	+	+	C57BL/6	Vbeta8.3	M15618 [7]
	13-2	F	+	+	BALB/c C57BL/6	Vbeta8.2	AE000663 [22]
		(F)	+	+	BALB/c nu/nu	Vbeta8.2	M15617 [7]
		(F)	+	+	CBA/J	Vbeta8.2	M27350[14](10)#c
		(F)	+	+	C127 (20)	Vbeta8.2	M26417 [12]#c
		(F)	+	+	EF34 (20)	Vbeta8.2	AJ249823 [20](11)#c
		(F)	+	+	C57BL/6	Vbeta8.1	AJ250103 [20](11)#c
14	14	F	+	+	BALB/c	V13S1	M15616 [7]
15	15	F	+	+	BALB/c	V12S1	AE000664 [22]
16	16	F	+	+	C57BL/6		L29434 [8]
		(F)	+	+	C57BL/6	Vbeta5	BALB/c, V11S1 [AE000664][22]
		(F)	+	+	C57BL/6		M13670 [2]#c
		(F)	+	+	C57BL/6		M15459[21]#c
		(F)	+	+	C57BL/6	Vbeta11	X14388 [18]#c
17	17	F	+	+	BALB/c	V9S1	AE000664 [22]
18	18	P(12)	+	+	BALB/c	Vbeta15	X16692 [15]
19	19	F	+	+	BALB/c	V6S1	AE000664 [22]
		(F)	+	+	C57BL/6		X01643 [19]#c
		(F)	+	+	SWR/J	Vbeta6	AJ249821 [25]#c
20	20	F	+	+	BALB/c	V15S1	AE000664 [22]
		(F)	+	+	SJL	Vbeta15	M11859 [4]#c
21	21	ORF(13)	+	+	BALB/c	Vbeta19	X16691 [15](14)
22	22	P(15)	+	+	BALB/c	Vbeta3.3P	X16690 [15](14)
23	23	F	+	+	BALB/c	V20S1	AE000664 [22]
24	24	F	+	+	PKW	Vbeta17a2	M61184 [5]
		P(16)	+	+	BALB/c	V17S1	AE000664 [22]
		(ORF)(17)	+	+	BALB/c	Vbeta17a1	M16203 [13]#g
		(F)	+	+	Czech II	VB17a	L48997 [26]#g
25	25	P(12)	+	+	BALB/c	Vbeta1N1	X16689 [15]
26	26	F	+	+	B10.A		K02548 [6]
		(F)	+	+	SWR/J	Vbeta3	AJ249822 [25]#c
27	27	P(8)	+	+	BALB/c	V30S1P	AE000664 [22]
28	28	P(8)	+	+	BALB/c	V31S1P	AE000664 [22]
29	29	F	+	+	BALB/c	V7S1	AE000664 [22]
30	30	F	+	+	BALB/c	Vbeta18	X00695 [15](14)
31	31	F	+	+	BALB/c	Vbeta14	BALB/c, V18S1 [AE000664][22]
		(F)	+	+	B10.A	Vbeta14	X03277[16]
							M26418[12]#c

#c: rearranged cDNA, #g: rearranged genomic DNA, : DNA genomic sequence, but not known as being germline or rearranged.

TRBV genes are designated by a number for the subgroup followed, whenever there are several genes belonging to the same subgroup, by a dash and a number for their relative localisation in the locus at 6A-C. Numbers increase from 5' to 3' in the locus.

Table 2 (continued)**IMGT notes:**

- (1) The last codon of the IMGT-CDR3 of the germline V-REGION is a STOP-CODON which may disappear during rearrangements.
- (2) No L-PART1, frameshift in V-REGION.
- (3) STOP-CODON in L-PART1, GAT replaced by GGT in DONOR_SPlice, frameshift in V-EXON.
- (4) STOP-CODON in FR2-IMGT.
- (5) No L-PART1, STOP-CODON in V-REGION.
- (6) V-EXON is partial: no L-PART12.
- (7) No L-PART1, no 1st_CYS, no 2nd_CYS.
- (8) Frameshift in V-EXON.
- (9) INSERTION of 2 bp in position 290 to 291 leading to a frameshift in FR1-IMGT, STOP-CODON in FR3-IMGT.
- (10) V-REGION is partial: AA 1 to 3 are absent (partial FR1-IMGT).
- (11) V-REGION is partial: AA 1 and 2 are absent (partial FR1-IMGT).
- (12) STOP-CODON in V-REGION, frameshift in V-REGION.
- (13) Unexpected position of DONOR_SPlice.
- (14) V-GENE is partial: no L-PART1, no L-PART2.
- (15) STOP-CODON in FR1-IMGT and FR3-IMGT, DELETION of 1 pb in codon 58 leading to a frameshift in CDR2-IMGT.
- (16) STOP-CODON in FR3-IMGT.
- (17) Unexpected position of ACCEPTOR_SPlice.
- (18) In the TRB locus the TRBV14 gene is localised 3' from the TRBC2 gene and is in an inverted orientation of transcription.
- (19) B10.A and B10.S[9R] are congenic strains (see MGD for Strain Nomenclature Guidelines), B10 is the abbreviated symbol of C57BL/10.
- (20) C127 and ER34 are wild mice.

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Table 3. Mouse (*Mus musculus*) TRBV allele table

TRBV	TRBV sub group name	TRBV allelic name	Strain	Accession number	Confirmed by genetics and/or data		Description of mutations
					Fct	V-gene	
1	1	F V1'01	BALB/c	AE000663	+	q178 G60 [q294]	
		(F) V1'02	BALB/c	X01642		q178>a G60>R q294>a	
2	2	F V2'01	BALB/c	AE000663	+	q176 G59	
3	3	F V3'01	BALB/c	AE000663	+	q176>c G59>y	
4	4	(F) V4'02	B10.A	X03865	+	a32 ,q11 ,a1 ,q42 ,q14 ,a70 ,K24 t78 ,q83 ,G28 ,q88 ,D10 ,t120 c287 ,P96	
		(F) V4'02	C57BL/6	X56725(1)	+	a32 ,q11 ,a1 ,q42 ,q14 ,a70 ,K24 t78 ,q83 ,G28 ,q88 ,D10 ,N1 t120 c287 ,P96	
5	5	F V5'01	BALB/c	AE000663	+	c37 ,q49 H1>R a1>a q42>t Q14>R t78>c G83>t R24>E a70>t a170 ,N57 C172 ,L58 G180 a271 ,I31 c287 ,P96	
		(F) V5'02	BALB/c	X00438	+	c37 ,q49 H1>R a1>a q42>t Q14>R t78>c G83>t R24>E a70>t a170 ,N57 C172 ,L58 G180 a271 ,I31 c287 ,P96	
		(F) V5'03	AKR	X02779	+	[q49>a A17>t]	
		(F) V5'04	B10.SWIR	M20878		c37>t [q49>a A17>t]	
		(F) V5'05	SWIR	A2469820	+	a41 ,E14	
12	12-1	F V12'101	C57BL/6	M15614	+	a41 ,E14	
12-2	F V12'102	NZW	M30881		a41>t; E1>G		
		(F) V12'201	C57BL/6	M15613	+	t71 ,a24	
		(F) V12'202	BALB/c	X02782		t71>c ,L24>t	
13	13-1	F V13'101	C57BL/6	M15618		s200>a R67>q	
		(F) V13'102	BALB/c	AE000663	+	a1 ,E1 [a29 ,N10 a70 ,N24 q147 ,q147>t] q147>q147>t	
13-2	F V13'201	C57BL/6	M15617	+	a1 ,E1 [a29 ,N10 a70 ,N24 q147 ,q147>t] q147>q147>t		
		(F) V13'202	BALB/c/nu	M27350		[q19>c ,L67>q G56>c G59>a]	
		(F) V13'203	CBAL	M15617		[q19>c ,L67>q G56>c G59>a]	
		(F) V13'204	C127	A248823		a70>t N24>d	
		(F) V13'205	ER34	A25013		a29>q N10>s a70>q N24>d	
13-3	F V13'301	C57BL/6	M15616	+	a29>q N10>s a70>q N24>d		
14	14	F V14'01	BALB/c	AE000664	+	t165>c [q179>a ,d60>d] t198>q	
15	15	F V15'01	BALB/c	AE000664	+	t165>c [q179>a ,d60>d] t198>q	
16	16	F V16'01	C57BL/6	A29434	+	c74 ,P25 ,a84 t137 ,I46 L155 ,Y52 c161 ,t162 ,T54	
		(F) V16'02	C57BL/6	M13970		c74>q P25>r a84>t t137>q I46>s	
		(F) V16'03	C57BL/6	M15459		c161>t t162>c ,T54>t	
		(F) V16'04	C57BL/6	X14388			
17	17	F V17'01	BALB/c	AE000664	+	t63>c a91>t T11>s	
19	19	F V19'01	BALB/c	AE000664	+	t63>c a91>t T11>s	
		(F) V19'03	C57BL/6	X01643		[q298>a ,A100>t]	
20	20	F V20'01	BALB/c	AE000664	+	t96 ,a135 ,T49	
		(F) V20'02	SJL	M11059		t96>c a135>q ,T49>a	
21	21	ORF V21'01	BALB/c	X16691	+		
23	23	F V23'01	BALB/c	AE000664	+		

Table 3 (continued)

24	24	F	V24*01	PWK	M6184	c66 c66>t c66>t c66>t c66>t c66>t c66>t c66>t	t90 t90>t t90>t t90>t t90>t t90>t t90>t t90>t	c152 c152>c c152>c c152>c c152>c c152>c c152>c c152>c	t51 g91>a g91>a g91>a g91>a g91>a g91>a g91>a g91>a	s55 g95>n g95>n g95>n g95>n g95>n g95>n g95>n g95>n	g258 g258>q g258>q g258>q g258>q g258>q g258>q g258>q	r86 r86>q r86>q r86>q r86>q r86>q r86>q r86>q	c306 c306>q c306>q c306>q c306>q c306>q c306>q c306>q	y102 y102*
	(ORF)	P	V24*02	BALB/c	AE000654									
	V24*03	BALB/c	M16203											
	(F)	V24*04	Czechii	L48597										
26	26	F	V26*01	B10 A	K022448	+	g91 c22>t c22>t c22>t	-V31 ,V31 IF ,P8 ,P8>s	[c155 c155>t c155>t c155>t]					
27	26	(F)	V26*02	SWR/J	A1246822	+	g91>t c22>t c22>t	-V31 IF c155>t						
29	29	F	V29*01	BALB/c	AE000654	+								
	(F)	V29*02	BALB/c	X00696										
30	30	F	V30*01	BALB/c	X16895	+								
31	31	F	V31*01	BALB/c	X03277	+	g50 g50>s	,S17						
	(F)	V31*02	B10 A	M66118										

IMGT note:

(1) The last codon of the IMGT-CDR3 of the germline V-REGION is a STOP-CODON which may disappear during rearrangements.

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Table 4. Mouse (*Mus musculus*) germline TRBD genes and alleles**Fct:** FUNCTIONALITY**F:** Functional

D-REGION alleles are only described at the nucleotide level since D-REGION can be used in the three reading frames. The numbering starts with the first nucleotide downstream the 5D-HEPTAMER. The accession number of a reference sequence is given for each allele.

TRBD name	Fct	TRBD allele name	Strain	Reference sequences	Accession number	Confirmed by genetics and/or data	Sequences from the literature
TRBD1	F	TRBD1*01	BALB/c	Dbeta1-1	X00933 [3]	+	D1[AE000665][2], Dbeta1[U77843][1]
TRBD2	F	TRBD2*01	BALB/c	Dbeta1-2	X00934 [3]	+	D2[AE000665][2]

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Table 5. Mouse (*Mus musculus*) germline TRBJ genes

Fct: FUNCTIONALITY
F: Functional
P: Pseudogene
ORF: Open Reading Frame
vg: Vestigial
R: Rearranged
T: Transcribed
Pr: Translated into protein

+ or "-" indicates if the gene sequences have been found (+) or not been found (-) rearranged (R), transcribed (T), and/or translated into protein (Pr). Arbitrarily that information is shown on the first line of each gene when the data have been confirmed by several studies. Functionality is shown between **parentheses** when the accession number refers to rearranged genomic DNA or cDNA and the corresponding germline gene has not yet been isolated.
Reference sequences in bold have been mapped: "mapped" refers to sequences which have been obtained from clones (phages, cosmids, YACs...) either by subcloning or PCR, and does not apply to sequences obtained directly from genomic DNA.
In the "Sequences from the literature" column, names of the sequences are preceded by the designation of the mouse strain.

TRBJ name	Fct	R	T	P	Strains	References sequences	Accession numbers	Sequences from the literature
TRBJ1-1	F				B10.A (1)	JT1	X01018 [2]	BALB/c, J1S1 [AE000665][5], SJL/J, Jbeta1.1 [U77843][1]
	(F)				BALB/c x C56BL/6 (F1)	Jbeta1	M11456 [4]#C	BALB/c, J1S2 [AE000665][5], SJL/J, Jbeta1.2 [U77843][1]
TRBJ1-2	F				B10.A	JT2	X01018 [2]	BALB/c, J1S3 [AE000665][5], SJL/J, Jbeta1.3 [U77843][1]
								BALB/c, J1S4 [AE000665][5], SJL/J, Jbeta1.4 [U77843][1]
TRBJ1-3	F				B10.A	JT3	X01018 [2]	BALB/c, J1S5 [AE000665][5], SJL/J, Jbeta1.5 [U77843][1]
					BALB/c			
TRBJ1-4	F				B10.A	JT4	X01018 [2]	BALB/c, J1S6 [AE000665][5], SJL/J, Jbeta1.6 [U77843][1]
					BALB/c			
TRBJ1-5	F(2)				B10.A	JT5	X01018 2	BALB/c, J1S7 [AE000665][5], SJL/J, Jbeta2.1 [K02802][3]
	(F2)				SJL/J			
TRBJ1-6	ORF(3)				B10.A	JT6	X01018 [2]	BALB/c, J1S8 [AE000665][5], SJL/J, Jbeta2.2 [K02802][3]
					B10.A			
TRBJ1-7	ORF(4)				B10.A	JT7	X01018 [2]	BALB/c, J1S9 [AE000665][5], SJL/J, Jbeta2.3 [K02802][3]
					B10.A			
TRBJ2-1	F					Jbeta2.1	K02802 [3]	BALB/c, J2S1 [AE000665][5], SJL/J, Jbeta2-1 [X00934][7]
TRBJ2-2	F				B10.A	Jbeta2.2	K02802 [3]	BALB/c, J2S2 [AE000665][5], SJL/J, Jbeta2-2 [K02802][3]
					B10.A	Jbeta2.3	K02802 [3]	BALB/c, J2S3 [AE000665][5], SJL/J, Jbeta2-3 [K02802][3]
TRBJ2-3	F				B10.A	Jbeta2.4	K02802 [3]	BALB/c, J2S4 [AE000665][5], SJL/J, Jbeta2-4 [K02802][3]
					B10.A	Jbeta2.5	K02802 [3]	BALB/c, J2S5 [AE000665][5], SJL/J, Jbeta2-5 [K02802][3]

Table 5 (continued)

TRBJ2-6	vg [5]	B10.A	Jbeta2.psi	K02802 [3]	BA1B/c, J2S6 [AE000665][5]
TRBJ2-7	F (F)	B10.A C57BL/6	Jbeta2.7	K02802 [3] M16122 [6]#c	BA1B/c, J2S6 [AE000665][5]
#c: rearranged cDNA					

IMGT notes:

- (1) B10.A is a congenic strain (see MGD for Strain Nomenclature Guidelines), B10 is the abbreviated symbol of C57BL/10 and A the abbreviated symbol of A/J.
- (2) Nucleotide G, at position 10 (according to the IMGT allele mutation numbering) of TRBJ5 in AE000665, is deleted in X01018. This DELETION leads to a frameshift. However it is not excluded that V-D-J rearrangements allow to reestablish the normal ORF. In those cases, the STOP-CODON needs to be eliminated by the rearrangements. For these reasons the TRBJ1-5'02 is considered as functional.
- (3) Non canonical J-REGION: Phe-Ala-X-Gly instead of Phe-Gly-X-Gly.
- (4) Non canonical J-REGION: His-Gly-X-Gly instead of Phe-Gly-X-Gly. Non canonical DONOR_SPLICE: AGA instead of AGT.
- (5) Vestigial because the germline J-SEGMENT is only identified by the presence of a recombination signal. There is an open reading frame, but without the conserved Phe-Gly-X-Gly motif, and without a donor splicing site in 3'.

References:

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Table 6. Mouse (*Mus musculus*) TRBJ allele table

Fct: FUNCTIONALITY
 F: Functional
 P: Pseudogene
 ORF: Open Reading Frame
 vg: Vestigial

IMGT numbering and description of alleles for germline J-REGIONS start with the first nucleotide of the first codon. The accession number of a reference sequence is given for each allele.

TRBJ name	Fct	TRBJ allele name	Strain	Accession number	Confirmed by genetics and/or data	Description of mutations
TRBJ1-1	F	TRBJ1-1*01	B10.A	X01018	+	G32 , R11
	(F)	TRBJ1-1*02	BALB/c x C56BL/6 (F1)	M11456		G32>C, R11>T
TRBJ1-2	F	TRBJ1-2*01	B10.A	X01018	+	
TRBJ1-3	F	TRBJ1-3*01	B10.A	X01018	+	
TRBJ1-4	F	TRBJ1-4*01	B10.A	X01018	+	t46
	F	TRBJ1-4*02	BALB/c	AE000665		t46>c
TRBJ1-5	F(1)	TRBJ1-5*01	BALB/c	AE000665		g10 c14 , p5 t17 , L6
	F(1)	TRBJ1-5*02	B10.A	X01018	g10>de#	c14>a, p5>q t17>a, L6>H
	F	TRBJ1-5*03	SJL/J	U77843		
TRBJ1-6	ORF	TRBJ1-6*01	B10.A	X01018	+	
TRBJ1-7	ORF	TRBJ1-7*01	B10.A	X01018	+	
TRBJ2-1	F	TRBJ2-1*01	B10.A	K02802	+	
TRBJ2-2	F	TRBJ2-2*01	B10.A	K02802	+	
TRBJ2-3	F	TRBJ2-3*01	B10.A	K02802	+	
TRBJ2-4	F	TRBJ2-4*01	B10.A	K02802	+	
TRBJ2-5	F	TRBJ2-5*01	B10.A	K02802	+	
TRBJ2-7	F	TRBJ2-7*01	B10.A	K02802	+	c30
	(F)	TRBJ2-7*02	C57BL/6	M16122	+	c30>t

IMGT note:

(1) Nucleotide G, at position 10 (according to the IMGT allele mutation numbering) of TRBJ5 in AE000665, is deleted in X01018. This DELETION leads to a frameshift. However it is not excluded that V-D-J rearrangements allow to reestablish the normal ORF. In those cases, the STOP-CODON needs to be eliminated by the rearrangements. For these reasons the TRBJ1-5*02 is considered as functional.

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Table 7. Correspondence between the different mouse (*Mus musculus*) TRBV gene nomenclatures

Mouse TRBV genes are listed from 3' (top of the table) to 5' (bottom of the table) in the TRB locus at 6A-C.

IMGT TRBV gene name 1	Wilson, R.K. et al [2]	Arden, B. et al. [3]
31	14	14S1
30	18 (2)	18S1
29	7	7S1
28		31S1
27		30S1
26	3.1	3S1
25		21S1
24	17	17S1
23	20 (3)	20S1
22		22S1
21	19	19S1
20	15	15S1
19	6	6S1
18		23S1
17	9	9S1
16	11	11S1
15	12	12S1
14	13	13S1
13-3	8.1	8S1
13-2	8.2	8S2
13-1	8.3	8S3
12-3	5.3	5S3
12-2	5.1	5S1
12-1	5.2	5S2
11		29S1
10		25S1
9		24S1
8		28S1
7		27S1
6		26S1
5	1	1S1
4	10	10S1
3	16	16S1
2	4	4S1
1	2	2S1

IMGT notes:

- (1) Mouse TRBV genes are designated by a number for the subgroup followed, whenever there are several genes belonging to the same subgroup, by a dash and a number for their relative localisation in the TRB locus at 6A-C.
- (2) defined in [4]
- (3) defined in [5]

References:

- [1] Bosc, N. and Lefranc, M.-P., In IMGT Repertoire, <http://imgt.cines.fr:8104>, created 22/07/1999, and this paper.
- [2] Wilson, R.K. et al., Immunol. Rev., 101, 149-172 (1988)
- [3] Arden, B. et al., Immunogenetics, 42, 455-500 (1995)
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Table 8. Mouse (*Mus musculus*) TRBV genes and related human TRBV genes

Mouse and humanTRBV genes are listed from 3' (top of the table) to 5' (bottom of the table) in their respective TRB loci at 6A-C, and 7q35.

Mouse IMGT TRBV genes [1] (1)	Related human IMGT TRBV genes [2]
31	30
30	29-1
29	28
	27
	26
	25-1
	24-1
28	
27	
26	23-1
25	
24	
23	
	22
22	
21	21-1
20	20-1
19	19
	18
18	
	17
	16
17	15
	14
	13
16	12-1 to 12-5
15	
14	11-1 to 11-3
13-3	
13-2	10-1 to 10-3
13-1	
12-3	
12-2	
12-1	
	9
	8-1, 8-2
	7-1 to 7-9
11	
10	
9	
8	6-1 to 6-9 5-1 to 5-8
7	
6	4-1 to 4-3
5	
4	3-1, 3-2 2
3	1
2	
1	A B

IMGT notes:

- (1) Mouse and human TRBV genes are designated by a number for the subgroup followed, whenever there are several genes belonging to the same subgroup, by a dash and a number for their relative localisation in their respective loci at 6A-C, and 7q35.

References:

- [1] Bosc, N. and Lefranc, M.-P., In IMGT Repertoire, <http://imgt.cines.fr:8104>, created 22/07/1999, and this paper.
[2] Folch, G. and Lefranc, M.-P., Exp. Clin. Immunogenet., 17, 42-54 (2000)

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- 12 Artéro S, Lefranc MP: The teleostei immunoglobulin heavy IGH genes. *Exp Clin Immunogenet* 2000;17:148-161.
- 13 Artéro S, Lefranc MP: The teleostei immunoglobulin light IGL1 and IGL2 V, J and C genes. *Exp Clin Immunogenet* 2000;17:162-172.
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