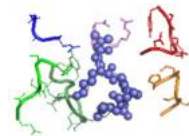**IMGT®, the international ImMunoGeneTics information system®**

Analyse your sequence using IMGT domains

IMGT/DomainGapAlign version: **4.10.3 (../doc/IMGTDomainGapAlign.shtml#version)** (2021-12-06)

Legal notice: In the context of an **INN request (https://www.who.int/teams/health-product-and-policy-standards/inn)** (i.e. determining substem B), IMGT/DomainGapAlign online access and use of data thus obtained
is free for all entities including commercial organizations

Standard parameters and sequence(s)

Put protein sequence(s) (FASTA format (/IMGTindex/Fasta.php)) (sample sequences here (../doc/IMGTDomainGapAlign_testsets.html))

```
>VH_mouse
EVTLKESGPGILQPSQTLSLTCSFSGFSLSTYGMGVGWIRQPSGKGLEWLAHIWWDDVKR
YNPALKSRLTISKDTSGSQVFLKIASVDTSDTATYYCARMGSDYDVWFDYWGQGTLVTVS
>VL_mouse
DIVMSQSPSSLAVSVGEKVTMSCKSSQSLLYNNNQKNYLAWYQQKPGQSPKLLIYWASTR
ESGVPDRFTGSGSGTDFTLTISSVKAEDLAVYYCQQYYSYPFTFGSGTKLEIK
```

Upload a file Выберите файл | Файл не выбран

Domain type V ▾

Species Homo sapiens (human) ▾
☐ English name

Smith-Waterman score above 0 ▾

Displayed alignments 5 ▾

IMGT Colliers de Perles ☐

[Show] [Reset]

Advanced parameters

Alignment

E-value 200

Gap penalty for query -5

Gap penalty for reference -20

Results of IMGT/DomainGapAlign

Your selection:

Domain type: V

Species: *Homo sapiens* (human)

SW score above: 0

Displayed alignments: 5

Number of sequences: 2

> Sequence name: VH_mouse

ℹ Move your mouse over the amino acids below the alignment for the characterization of AA changes

Closest reference gene and allele(s) from the IMGT V domain directory: *Homo sapiens* (human)

Species	Gene and allele	Domain	Domain label	Smith-Waterman score	% identity	Overlap	Show alignment
Homo sapiens	IGHV2-5*09 (/genedb/individualEntry?name=IGHV2-5&species=Homo sapiens)	1	VH	488	71.4	98	○
Homo sapiens	IGHV2-5*02 (/genedb/individualEntry?name=IGHV2-5&species=Homo sapiens)	1	VH	488	70.4	98	○
Homo sapiens	IGHV2-5*05 (/genedb/individualEntry?name=IGHV2-5&species=Homo sapiens)	1	VH	487	70.4	98	○
Homo sapiens	IGHV2-5*06 (/genedb/individualEntry?name=IGHV2-5&species=Homo sapiens)	1	VH	487	70.4	98	○
Homo sapiens	IGHV2-5*08 (/genedb/individualEntry?name=IGHV2-5&species=Homo sapiens)	1	VH	478	70.4	98	○

Species	Gene and allele	Domain	Domain label	Smith-Waterman score	% identity	Overlap
Homo sapiens	IGHJ5*01 (/genedb/individualEntry?name=IGHJ5&species=Homo sapiens)	1		97	92.9	14
Homo sapiens	IGHJ5*02 (/genedb/individualEntry?name=IGHJ5&species=Homo sapiens)	1		96	92.9	14
Homo sapiens	IGHJ4*01 (/genedb/individualEntry?name=IGHJ4&species=Homo sapiens)	1		94	92.9	14
Homo sapiens	IGHJ4*02 (/genedb/individualEntry?name=IGHJ4&species=Homo sapiens)	1		94	92.9	14
Homo sapiens	IGHJ4*03 (/genedb/individualEntry?name=IGHJ4&species=Homo sapiens)	1		94	92.9	14

These matches correspond to the first candidate in the previous table.

Alignment with the closest gene and allele from the IMGT V domain directory: *Homo sapiens* (human)

VH_mouse (Collier-de-Perles.cgi?
type=V&insertions1=&sequence1=EVTLKESGP.GILQPSQTLSLTCSFSGFSLS..TYGMGVGWIRQPSGKGLEWLAHIWWD...DVKRYNPALK.SRLTISK
T11G-L12I-V13L-K14Q-T16S-T20S-T24S-S35Y-V37M-P46S-A49G-L55H-Y57W-D64V-G68N-S70A-T79S-K84G-N85S-V88F-T90K-M91I-T92A-N93S-M94V-P96T-

IGHV2-5*09 (collier_perles_allele.cgi?alleleid=2862&type=V&dom=1)
Homo sapiens

ⓘ Region(s) and domain(s) identified in your sequence (by comparison with the closest genes and alleles *Homo sapiens* IGHV2-5*09 and IGHJ5*01)

```
EVTLKESGPGILQPSQTLSLTCSFSGFSLSTYGMGVGWIRQPSGKGLEWL
AHIWWDDVKRYNPALKSRLTISKDTSGSQVFLKIASVDTSDTATYYCARM
GSDYDVWFDYWGQGTLVTVS
```

Sequence without gaps (SeqFasta.cgi?
domtype=V&seq=EVTLKESGPGILQPSQTLSLTCSFSGFSLSTYGMGVGWIRQPSGKGLEWLAHIWWDDVKRYNPALKSRLTISKDTSGSQVFLKIASVDTSDTATYY
5*09&score=71.4&species=Homo sapiens&gaps=no&alleleJ=IGHJ5*01&scoreJ=92.9) 🔖 *(SeqFasta.cgi?*
domtype=V&seq=EVTLKESGPGILQPSQTLSLTCSFSGFSLSTYGMGVGWIRQPSGKGLEWLAHIWWDDVKRYNPALKSRLTISKDTSGSQVFLKIASVDTSDTATYY
5*09&score=71.4&species=Homo sapiens&gaps=no&alleleJ=IGHJ5*01&scoreJ=92.9&download) *Sequence with gaps (SeqFasta.cgi?*
domtype=V&seq=EVTLKESGP.GILQPSQTLSLTCSFSGFSLS..TYGMGVGWIRQPSGKGLEWLAHIWWD...DVKRYNPALK.SRLTISKDTSGSQVFLKIASVDTSDTA
5*09&score=71.4&species=Homo sapiens&gaps=yes&alleleJ=IGHJ5*01&scoreJ=92.9) 🔖 *(SeqFasta.cgi?*
domtype=V&seq=EVTLKESGP.GILQPSQTLSLTCSFSGFSLS..TYGMGVGWIRQPSGKGLEWLAHIWWD...DVKRYNPALK.SRLTISKDTSGSQVFLKIASVDTSDTA
5*09&score=71.4&species=Homo sapiens&gaps=yes&alleleJ=IGHJ5*01&scoreJ=92.9&download)

ⓘ Results summary (by comparison with the closest genes and alleles *Homo sapiens* IGHV2-5*09 and IGHJ5*01)

Sequence name	V-REGION identity percentage	CDR-IMGT lengths	Number of different AA in CDR1- and CDR2-IMGT	FR-IMGT lengths	Number of different AA in FR-IMGT	Total number of AA changes in V-DOMAIN
VH_mouse	71.4%	[10.7.13]	4	[25.17.38.10] = 90 AA	24	28

▶ AA changes in strands and loops

Strands	Number of different AA	AA changes
A (1-15)	5	Q1>E (+ + -) similar T11>G (+ - -) dissimilar L12>I (+ + +) very similar V13>L (+ - +) similar K14>Q (+ - -) dissimilar
B (16-26)	3	T16>S (+ - +) similar T20>S (+ - +) similar T24>S (+ - +) similar
C (39-46)	1	P46>S (+ - -) dissimilar
C' (47-55)	2	A49>G (- + -) dissimilar L55>H (- - -) very dissimilar
C'' (66-74)	2	G68>N (- - -) very dissimilar S70>A (- + -) dissimilar
D (75-84)	2	T79>S (+ - +) similar K84>G (- - -) very dissimilar
E (85-96)	8	N85>S (- - -) very dissimilar V88>F (+ - -) dissimilar T90>K (- - -) very dissimilar M91>I (+ + -) similar T92>A (- - -) very dissimilar N93>S (- - -) very dissimilar M94>V (+ - -) dissimilar P96>T (+ + -) similar
F (97-104)	1	V97>S (- - -) very dissimilar
G (118-128)	0	-

Loops	Number of different AA	AA changes
BC (27-38)	2	S35>Y (+ - -) dissimilar V37>M (+ - -) dissimilar
C'C'' (56-65)	2	Y57>W (- + +) dissimilar D64>V (- - -) very dissimilar
FG (105-117)	2	H106>R (- - +) dissimilar R107>M (- + -) dissimilar

▶ AA changes in FR-IMGT and CDR-IMGT

FR-IMGT	Number of different AA	AA changes
FR1-IMGT (1-26)	8	Q1>E (+ + -) similar T11>G (+ - -) dissimilar L12>I (+ + +) very similar V13>L (+ - +) similar K14>Q (+ - -) dissimilar T16>S (+ - +) similar T20>S (+ - +) similar T24>S (+ - +) similar
FR2-IMGT (39-55)	3	P46>S (+ - -) dissimilar A49>G (- + -) dissimilar L55>H (- - -) very dissimilar
FR3-IMGT (66-104)	13	G68>N (- - -) very dissimilar S70>A (- + -) dissimilar T79>S (+ - +) similar K84>G (- - -) very dissimilar N85>S (- - -) very dissimilar V88>F (+ - -) dissimilar T90>K (- - -) very dissimilar M91>I (+ + -) similar T92>A (- - -) very dissimilar N93>S (- - -) very dissimilar M94>V (+ - -) dissimilar P96>T (+ + -) similar V97>S (- - -) very dissimilar
FR4-IMGT (118-129)	0	-

CDR-IMGT	Number of different AA	AA changes
CDR1-IMGT (27-38)	2	S35>Y (+ - -) dissimilar V37>M (+ - -) dissimilar
CDR2-IMGT (56-65)	2	Y57>W (- + -) dissimilar D64>V (- - -) very dissimilar
CDR3-IMGT (105-117)	2	H106>R (- - +) dissimilar R107>M (- + -) dissimilar

Alignment with other(s) gene(s) and allele(s) from the IMGT V domain directory: *Homo sapiens* **(human)**

VH_mouse (Collier-de-Perles.cgi?
type=V&insertions1=&sequence1=EVTLKESGP.GILQPSQTLSLTCSFSGFSLS..TYGMGVGWIRQPSGKGLEWLAHIWWD...DVKRYNPALK.SRLTISK
I2V-T11G-L12I-V13L-K14Q-T16S-T20S-T24S-S35Y-V37M-P46S-A49G-L55H-Y57W-D64V-S68N-S70A-T79S-K84G-N85S-V88F-T90K-M91I-T92A-N93S-M94V-P9

IGHV2-5*02 (collier_perles_allele.cgi?alleleid=2855&type=V&dom=1)
Homo sapiens

VH_mouse (Collier-de-Perles.cgi?
type=V&insertions1=&sequence1=EVTLKESGP.GILQPSQTLSLTCSFSGFSLS..TYGMGVGWIRQPSGKGLEWLAHIWWD...DVKRYNPALK.SRLTISK
I2V-T11G-L12I-V13L-K14Q-T16S-T20S-T24S-S35Y-V37M-P46S-A49G-L55H-Y57W-D64V-G68N-S70A-T79S-K84G-N85S-V88F-T90K-M91I-T92A-N93S-M94V-P

IGHV2-5*05 (collier_perles_allele.cgi?alleleid=2858&type=V&dom=1)
Homo sapiens

VH_mouse (Collier-de-Perles.cgi?
type=V&insertions1=&sequence1=EVTLKESGP.GILQPSQTLSLTCSFSGFSLS..TYGMGVGWIRQPSGKGLEWLAHIWWD...DVKRYNPALK.SRLTISK
I2V-T11G-L12I-V13L-K14Q-T16S-T20S-T24S-S35Y-V37M-P46S-A49G-L55H-Y57W-D64V-G68N-S70A-T79S-K84G-N85S-V88F-T90K-M91I-T92A-N93S-M94V-P

IGHV2-5*06 (collier_perles_allele.cgi?alleleid=2859&type=V&dom=1)
Homo sapiens

VH_mouse (Collier-de-Perles.cgi?
type=V&insertions1=&sequence1=EVTLKESGP.GILQPSQTLSLTCSFSGFSLS..TYGMGVGWIRQPSGKGLEWLAHIWWD...DVKRYNPALK.SRLTISK
A11G-L12I-V13L-K14Q-T16S-T20S-T24S-S35Y-R38G-S40G-P46S-A49G-L55H-Y57W-D64V-S68N-S70A-T79S-K84G-N85S-V88F-T90K-M91I-T92A-N93S-M94V

IGHV2-5*08 (collier_perles_allele.cgi?alleleid=2861&type=V&dom=1)
Homo sapiens

| Sequence name: VL_mouse |

ⓘ Move your mouse over the amino acids below the alignment for the characterization of AA changes

🔵 **Closest reference gene and allele(s) from the IMGT V domain directory:** *Homo sapiens* (human)

Species	Gene and allele	Domain	Domain label	Smith-Waterman score	% identity	Overlap	Show alignment
Homo sapiens	**IGKV4-1*01 (/genedb/individualEntry?name=IGKV4-1&species=Homo sapiens)**	1	V-KAPPA	587	83.2	101	🔵
Homo sapiens	**IGKV4-1*02 (/genedb/individualEntry?name=IGKV4-1&species=Homo sapiens)**	1	V-KAPPA	587	83.2	101	○
Homo sapiens	**IGKV4-1*03 (/genedb/individualEntry?name=IGKV4-1&species=Homo sapiens)**	1	V-KAPPA	587	83.2	101	○
Homo sapiens	**IGKV2-28*01 (/genedb/individualEntry?name=IGKV2-28&species=Homo sapiens)**	1	V-KAPPA	450	67.3	101	○
Homo sapiens	**IGKV2D-28*01 (/genedb/individualEntry?name=IGKV2D-28&species=Homo sapiens)**	1	V-KAPPA	450	67.3	101	○

Species	Gene and allele	Domain	Domain label	Smith-Waterman score	% identity	Overlap
Homo sapiens	**IGKJ2*02 (/genedb/individualEntry?name=IGKJ2&species=Homo sapiens)**	1		62	90.9	11

These matches correspond to the first candidate in the previous table.

Alignment with the closest gene and allele from the IMGT V domain directory: *Homo sapiens* **(human)**

VL_mouse (Collier-de-Perles.cgi?
type=V&insertions1=&sequence1=DIVMSQSPSSLAVSVGEKVTMSCKSSQSLLYNNNQKNYLAWYQQKPGQSPKLLIYWA.......STRESGVP.DRFTGSG
D9S-L15V-R18K-A19V-I21M-N22S-V29L-S32N-S33N-N35Q-P49S-S77T-L94V-Q95K-V99L-T114Y-&CDR3=9)

IGKV4-1*01 (collier_perles_allele.cgi?alleleid=3101&type=V&dom=1)
Homo sapiens

Region(s) and domain(s) identified in your sequence (by comparison with the closest genes and alleles *Homo sapiens* **IGKV4-1*01 and IGKJ2*02)**

```
DIVMSQSPSSLAVSVGEKVTMSCKSSQSLLYNNNQKNYLAWYQQKPGQSP
KLLIYWASTRESGVPDRFTGSGSGTDFTLTISSVKAEDLAVYYCQQYYSY
PFTFGSGTKLEIK
```

Sequence without gaps (SeqFasta.cgi?
domtype=V&seq=DIVMSQSPSSLAVSVGEKVTMSCKSSQSLLYNNNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTISSVKAEDLAVYYCQ
*1*01&score=83.2&species=Homo sapiens&gaps=no&alleleJ=IGKJ2*02&scoreJ=90.9)* 🔖 *(SeqFasta.cgi?*
domtype=V&seq=DIVMSQSPSSLAVSVGEKVTMSCKSSQSLLYNNNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTISSVKAEDLAVYYCQ
*1*01&score=83.2&species=Homo sapiens&gaps=no&alleleJ=IGKJ2*02&scoreJ=90.9&download)* *Sequence with gaps (SeqFasta.cgi?*
domtype=V&seq=DIVMSQSPSSLAVSVGEKVTMSCKSSQSLLYNNNQKNYLAWYQQKPGQSPKLLIYWA.......STRESGVP.DRFTGSG..SGTDFTLTISSVKAEDLAV
*1*01&score=83.2&species=Homo sapiens&gaps=yes&alleleJ=IGKJ2*02&scoreJ=90.9)* 🔖 *(SeqFasta.cgi?*
domtype=V&seq=DIVMSQSPSSLAVSVGEKVTMSCKSSQSLLYNNNQKNYLAWYQQKPGQSPKLLIYWA.......STRESGVP.DRFTGSG..SGTDFTLTISSVKAEDLAV
*1*01&score=83.2&species=Homo sapiens&gaps=yes&alleleJ=IGKJ2*02&scoreJ=90.9&download)*

Results summary (by comparison with the closest genes and alleles *Homo sapiens* **IGKV4-1*01 and IGKJ2*02)**

Sequence name	V-REGION identity percentage	CDR-IMGT lengths	Number of different AA in CDR1- and CDR2-IMGT	FR-IMGT lengths	Number of different AA in FR-IMGT	Total number of AA changes in V-DOMAIN
VL_mouse	83.2%	[12.3.9]	4	[26.17.36.10] = 89 AA	12	16

▶ AA changes in strands and loops

Strands	Number of different AA	AA changes
A (1-15)	3	T5>S (+ - +) similar D9>S (- - -) very dissimilar L15>V (+ - +) similar
B (16-26)	4	R18>K (+ + +) very similar A19>V (+ - +) similar I21>M (+ + -) similar N22>S (- - -) very dissimilar
C (39-46)	0	-
C' (47-55)	1	P49>S (+ - -) dissimilar
C'' (66-74)	0	-
D (75-84)	1	S77>T (+ - +) similar
E (85-96)	2	L94>V (+ - +) similar Q95>K (+ - -) dissimilar
F (97-104)	1	V99>L (+ - +) similar
G (118-128)	0	-

Loops	Number of different AA	AA changes
BC (27-38)	4	V29>L (+ - +) similar S32>N (- - -) very dissimilar S33>N (- - -) very dissimilar N35>Q (+ - +) similar
C'C" (56-65)	0	-
FG (105-117)	1	T114>Y (+ - -) dissimilar

▶ AA changes in FR-IMGT and CDR-IMGT

FR-IMGT	Number of different AA	AA changes
FR1-IMGT (1-26)	7	T5>S (+ - +) similar D9>S (- - -) very dissimilar L15>V (+ - +) similar R18>K (+ + +) very similar A19>V (+ - +) similar I21>M (+ + -) similar N22>S (- - -) very dissimilar
FR2-IMGT (39-55)	1	P49>S (+ - -) dissimilar
FR3-IMGT (66-104)	4	S77>T (+ - +) similar L94>V (+ - +) similar Q95>K (+ - -) dissimilar V99>L (+ - +) similar
FR4-IMGT (118-129)	0	-

CDR-IMGT	Number of different AA	AA changes
CDR1-IMGT (27-38)	4	V29>L (+ - +) similar S32>N (- - -) very dissimilar S33>N (- - -) very dissimilar N35>Q (+ - +) similar
CDR2-IMGT (56-65)	0	-
CDR3-IMGT (105-117)	1	T114>Y (+ - -) dissimilar

Alignment with other(s) gene(s) and allele(s) from the IMGT V domain directory: *Homo sapiens* (human)

VL_mouse (Collier-de-Perles.cgi?
type=V&insertions1=&sequence1=DIVMSQSPSSLAVSVGEKVTMSCKSSQSLLYNNNQKNYLAWYQQKPGQSPKLLIYWA.......STRESGVP.DRFTGS(
D9S-L15V-R18K-A19V-I21M-N22S-V29L-S32N-S33N-N35Q-P49S-S77T-L94V-Q95K-V99L-T114Y-&CDR3=9)

IGKV4-1*02 (collier_perles_allele.cgi?alleleid=23641&type=V&dom=1)
Homo sapiens

VL_mouse (Collier-de-Perles.cgi?
type=V&insertions1=&sequence1=DIVMSQSPSSLAVSVGEKVTMSCKSSQSLLYNNNQKNYLAWYQQKPGQSPKLLIYWA.......STRESGVP.DRFTGS(
D9S-L15V-R18K-A19V-I21M-N22S-V29L-S32N-S33N-N35Q-P49S-S77T-L94V-Q95K-V99L-T114Y-&CDR3=9)

IGKV4-1*03 (collier_perles_allele.cgi?alleleid=24249&type=V&dom=1)
Homo sapiens

VL_mouse (Collier-de-Perles.cgi?
type=V&insertions1=&sequence1=DIVMSQSPSSLAVSVGEKVTMSCKSSQSLLYNNNQKNYLAWYQQKPGQSPKLLIYWA.......STRESGVP.DRFTGSO
L9S-P12A-T14S-P15V-P18K-A19V-S20T-I21M-R24K-H31Y-S32N-G35Q-Y36K-D40A-L43Q-Q51K-L56W-G57A-N66T-A68E-S77T-K90T-R93S-E95K-V99L-G100A

IGKV2-28*01 (collier_perles_allele.cgi?alleleid=3078&type=V&dom=1)
Homo sapiens

VL_mouse (Collier-de-Perles.cgi?
type=V&insertions1=&sequence1=DIVMSQSPSSLAVSVGEKVTMSCKSSQSLLYNNNQKNYLAWYQQKPGQSPKLLIYWA.......STRESGVP.DRFTGSO
L9S-P12A-T14S-P15V-P18K-A19V-S20T-I21M-R24K-H31Y-S32N-G35Q-Y36K-D40A-L43Q-Q51K-L56W-G57A-N66T-A68E-S77T-K90T-R93S-E95K-V99L-G100A

IGKV2D-28*01 (collier_perles_allele.cgi?alleleid=3079&type=V&dom=1)
Homo sapiens

Color menu for regions and domains

V-REGION	[0, 238, 0]	[#00EE00]	J-REGION	[255, 51, 0]	[#FFCC00]
C-REGION	[193, 217, 249]	[#C1D9F9]	V-LIKE-DOMAIN	[161, 238, 161]	[#A1EEA1]
CH1 DOMAIN	[193, 217, 249]	[#C1D9F9]	CH2 DOMAIN	[193, 217, 249]	[#E0F2F5]
CH3 DOMAIN	[193, 217, 249]	[#C1D9F9]	CH4 DOMAIN	[193, 217, 249]	[#E0F2F5]
(N-D)-REGION	[255, 51, 0]	[#FF3300]	HINGE-REGION	[0, 117, 255]	[#0075FF]
C-LIKE-DOMAIN	[190, 228, 234]	[#BEE4EA]	GROOVE-DOMAIN	[254, 234, 200]	[#FEEAC8]

Color menu for CDR-IMGT

CDR1-IMGT (Heavy)	[200, 0, 0]	[#C80000]	CDR2-IMGT (Heavy)	[255, 169, 0]	[#FFA900]	CDR3-IMGT (Heavy)	[156, 65, 215]	[#9C41D7]
CDR1-IMGT (Light)	[200, 0, 0]	[#0000E4]	CDR2-IMGT (Light)	[70, 213, 0]	[#46D500]	CDR3-IMGT (Light)	[0, 122, 0]	[#007A00]

IMGT mutation and AA change description (see **IMGT amino acid classes (/IMGTeducation/Aide-memoire/_UK/aminoacids/IMGTclasses.html)**)

AA changes

AA changes are qualified as:

very similar: (+ + +)

similar: (+ + -) or (+ - +)

dissimilar: (+ - -) or (- + -) or (- - +)

very dissimilar: (- - -)

IMGT Home page (/) | **IMGT Repertoire (IG and TR) (/IMGTrepertoire/)** | **IMGT Repertoire (MH) (/IMGTrepertoireMH/)** | **IMGT Repertoire (RPI) (/IMGTrepertoireRPI/)** | **IMGT Index (/IMGTindex/)** | **IMGT Scientific chart (/IMGTScientificChart/)** | **IMGT Education (/IMGTeducation/)** | **IMGT Latest news (/rss/)**

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