

THANK YOU for using IMGT/V-QUEST



IMGT®, the international ImMunoGeneTics information system®

<http://www.imgt.org>

Citing IMGT/V-QUEST:

Brochet, X. et al., Nucl. Acids Res. 36, W503-508 (2008). [PMID: 18503082](#). [PDF](#)

Giudicelli, V., Brochet, X., Lefranc, M.-P., Cold Spring Harb Protoc. 2011 Jun 1;2011(6). pii: pdb.prot5633. doi: 10.1101/pdb.prot5633.

[PMID: 21632778](#) [Abstract](#) also in *IMGT booklet with generous provision from Cold Spring Harbor (CSH) Protocols* [PDF](#) (high res). [PDF](#) (lower res)

IMGT/V-QUEST program version: [3.5.24](#) (9 March 2021) - IMGT/V-QUEST reference directory release: [202113-2](#) (30 March 2021)

Species	Homo sapiens (human)
Receptor type or locus	IGK
IMGT directory reference set	F+ORF+ in-frame P
Search for insertions and deletions	no

A. Detailed results for the IMGT/V-QUEST analysed sequences

Number of analysed sequences: **1**

1. [9](#)

Hyphens (-) show nucleotide identity, dots (.) represent gaps

Sequence: 1 9

Analysed sequence length: 323.

Sequence analysis category: 1 (no indel search).

Sequence compared with the [Homo sapiens \(human\) IG set](#) from the [IMGT reference directory](#) (set: F+ORF+ in-frame P)

>9

```
acatccagatgacccagtctccatcttccgtgtctgcatctgtaggagacagagtcacca  
tacttgtcggcgagtcagggtattttcagctggttagcctggtatcagcagaaaccag  
gaaaagcccctaagctcctgatctatgctgcttccagtttacaagtggggtcccatcaa  
gattcagcggcagtggtatctgggacagatttcactctcaccatcagcagcctgcagcctg  
aggattttgcaatttactattgtcaacaggctaacagtggtcccgatcaccttcggccaag  
ggacacgactggagattaaacga
```

Result summary: 9

Productive IGK rearranged sequence (no stop codon and in-frame junction)

Result summary: 9		Productive IGK rearranged sequence (no stop codon and in-frame junction)	
V-GENE and allele	Homsap IGKV1-12*01 F , or Homsap IGKV1-12*02 F or Homsap IGKV1D-12*02 F	score = 1318	identity = 97.12% (270/278 nt)
J-GENE and allele	Homsap IGKJ5*01 F	score = 190	identity = 100.00% (38/38 nt)
FR-IMGT lengths, CDR-IMGT lengths and AA JUNCTION	[25.17.36.10]	[6.3.9]	CQQANSVPITF
JUNCTION length (in nt) and decryption	33 nt = (23)-3{0}0(10)	(3'V)3'(N)5'(5'J)	

V-REGION partial 5' missing nt nb: 1

1. Alignment for V-GENE and allele identification

Closest V-REGIONS (evaluated from the V-REGION first nucleotide to the 2nd-CYS codon plus 15 nt of the CDR3-IMGT)

		Score	Identity
V01577	Homsap IGKV1-12*01 F	1318	97.12% (270/278 nt)
V01576	Homsap IGKV1-12*02 F	1318	97.12% (270/278 nt)
V01576	Homsap IGKV1D-12*02 F	1318	97.12% (270/278 nt)
X17263	Homsap IGKV1D-12*01 F	1300	96.40% (268/278 nt)
K01323	Homsap IGKV1D-16*01 F	1210	92.81% (258/278 nt)
V00558	Homsap IGKV1D-16*02 F	1201	92.45% (257/278 nt)
J00248	Homsap IGKV1-16*01 F	1165	91.01% (253/278 nt)
FM164406	Homsap IGKV1-16*02 [F]	1156	90.65% (252/278 nt)
KM455566	Homsap IGKV1-17*03 F	1156	90.65% (252/278 nt)
X59315	Homsap IGKV1-39*01 F	1156	90.65% (252/278 nt)

Alignment with [FR-IMGT](#) and [CDR-IMGT](#) delimitations

	<-----FR1-IMGT----->
9	.acatccagatgacccagtcctccatcttccgtgtctgcatctgtaggagacagagtcacc
V01577 Homsap IGKV1-12*01 F	g-----
V01576 Homsap IGKV1-12*02 F	g-----
V01576 Homsap IGKV1D-12*02 F	g-----
X17263 Homsap IGKV1D-12*01 F	g-----t-----
K01323 Homsap IGKV1D-16*01 F	g-----c--ac-----
V00558 Homsap IGKV1D-16*02 F	g-----c--ac-----
J00248 Homsap IGKV1-16*01 F	g-----c--ac-----
FM164406 Homsap IGKV1-16*02 [F]	g-----c--ac-----
KM455566 Homsap IGKV1-17*03 F	g-----g--a-----
X59315 Homsap IGKV1-39*01 F	g-----c--c-----
	----->-----CDR1-IMGT-----<-----
9	atcacttgctcgggcgagtcagggtatt.....ttcagctgggttagcc
V01577 Homsap IGKV1-12*01 F	-----ag-----
V01576 Homsap IGKV1-12*02 F	-----ag-----
V01576 Homsap IGKV1D-12*02 F	-----ag-----
X17263 Homsap IGKV1D-12*01 F	-----ag-----
K01323 Homsap IGKV1D-16*01 F	-----ag-----
V00558 Homsap IGKV1D-16*02 F	-----g-----ag-----
J00248 Homsap IGKV1-16*01 F	-----c-----ag--at-at----
FM164406 Homsap IGKV1-16*02 [F]	-----c-----ag--at-at----
KM455566 Homsap IGKV1-17*03 F	-----c-----ag--at-at----
X59315 Homsap IGKV1-39*01 F	-----c-----a-----a-c-----ag----at---aat
	-----FR2-IMGT----->-----CDR
9	tggtatcagcagaaccaggaaaagcccctaagctcctgatctatgctgct.....
V01577 Homsap IGKV1-12*01 F	-----g-----a-----
V01576 Homsap IGKV1-12*02 F	-----g-----a-----

V01576 Homsap	IGKV1D-12*02	F	-----g-----a.....
X17263 Homsap	IGKV1D-12*01	F	-----g-----a.....
K01323 Homsap	IGKV1D-16*01	F	-----ag-----tc-----a.....
V00558 Homsap	IGKV1D-16*02	F	-----ag-----tc-----a.....
J00248 Homsap	IGKV1-16*01	F	---t-----g-----tc-----a.....
FM164406 Homsap	IGKV1-16*02	[F]	---t-----g-----tc-----a.....
KM455566 Homsap	IGKV1-17*03	F	---t-----g---t-----g-----a.....
X59315 Homsap	IGKV1-39*01	F	-----g-----a.....

9	2-IMGT	_____<-----	
V01577 Homsap	IGKV1-12*01	F	tccagtttacaaagtggggtccca...tcaagattcagcggcagtgga
V01576 Homsap	IGKV1-12*02	F	-g-----g-----
V01576 Homsap	IGKV1D-12*02	F	-g-----g-----
X17263 Homsap	IGKV1D-12*01	F	-g-----g-----
K01323 Homsap	IGKV1D-16*01	F	-g-----g-----
V00558 Homsap	IGKV1D-16*02	F	-g-----g-----
J00248 Homsap	IGKV1-16*01	F	-g-----g-----
FM164406 Homsap	IGKV1-16*02	[F]	-g-----ag-----
KM455566 Homsap	IGKV1-17*03	F	-g-----g-----
X59315 Homsap	IGKV1-39*01	F	-g-----g---t-----

9	FR3-IMGT	-----	
V01577 Homsap	IGKV1-12*01	F	tctgggacagatttcactctcaccatcagcagcctgcagcctgaggattttgca
V01576 Homsap	IGKV1-12*02	F	-----a-----
V01576 Homsap	IGKV1D-12*02	F	-----a-----
X17263 Homsap	IGKV1D-12*01	F	-----t-----a-----
K01323 Homsap	IGKV1D-16*01	F	-----a-----
V00558 Homsap	IGKV1D-16*02	F	-----a-----
J00248 Homsap	IGKV1-16*01	F	-----a-----
FM164406 Homsap	IGKV1-16*02	[F]	-----a-----
KM455566 Homsap	IGKV1-17*03	F	-a-----a-----a-----
X59315 Homsap	IGKV1-39*01	F	-----t---a---a-----

9	----->_____	CDR3-IMGT	_____
V01577 Homsap	IGKV1-12*01	F	atttactattgtcaacaggctaacagtgtcccgatcaccttcggccaaggacacgactg
V01576 Homsap	IGKV1-12*02	F	-c-----t---tcc
V01576 Homsap	IGKV1D-12*02	F	-c-----t---ttc
X17263 Homsap	IGKV1D-12*01	F	-c-----t---tcc
K01323 Homsap	IGKV1D-16*01	F	-c---t-c-c-----ta---t---ta---tcc
V00558 Homsap	IGKV1D-16*02	F	-c---t-c-c-----ta---t---ta---tcc
J00248 Homsap	IGKV1-16*01	F	-c---t-c-c-----ta---t---ta---tcc
FM164406 Homsap	IGKV1-16*02	[F]	-c---t-c-c-----ta---t---ta---tcc
KM455566 Homsap	IGKV1-17*03	F	-c---t-c---t---ca---t---ta---tcc
X59315 Homsap	IGKV1-39*01	F	-c-----c-----ag-t---ac---tcc

9	gagattaaacga	
V01577 Homsap	IGKV1-12*01	F
V01576 Homsap	IGKV1-12*02	F
V01576 Homsap	IGKV1D-12*02	F
X17263 Homsap	IGKV1D-12*01	F
K01323 Homsap	IGKV1D-16*01	F
V00558 Homsap	IGKV1D-16*02	F
J00248 Homsap	IGKV1-16*01	F
FM164406 Homsap	IGKV1-16*02	[F]
KM455566 Homsap	IGKV1-17*03	F
X59315 Homsap	IGKV1-39*01	F

