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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	IGH
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. [1](#)

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

Sequence: 1 1

Analysed sequence length: 365.

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)

```
>1
agggtgcagctgggtggagtctgggggaaacttgaacagcctggggggtcccttagactct
cctgtacagcctctggattcaccttttagcagatctgcatgaactgggtccgcccgggctc
caggggaaggggctggagtgggtctcaggaattagtggtagtggtggtcgaacatactacg
cagactccgtgaagggccggttcaccatctccagagacaattccaagaatacgctatatc
tgcaaatgaacagcctgagcgccgaggacacggccgcatattactgtgcgaaagattcgt
atactaccagttggtacggagggtatggacgtctggggccacgggaccacggtcaccgtct
cctca
```

Result summary: 1	Productive IGH rearranged sequence (no stop codon and in-frame junction)		
V-GENE and allele	Homsap IGHV3-23*04 F	score = 1282	identity = 94.08% (270/287 nt)
J-GENE and allele	Homsap IGHJ6*02 F	score = 202	identity = 80.65% (50/62 nt)
D-GENE and allele by IMGT/JunctionAnalysis	Homsap IGHD6-13*01 F	D-REGION is in reading frame 1	
FR-IMGT lengths, CDR-IMGT lengths and AA JUNCTION	[24.17.38.11]	[8.8.15]	CAKDSYTTSWYGGMDVW
JUNCTION length (in nt) and decryption	51 nt = (11)+1{2}-2(19)+1{2}-17(15)	(3'V)3'(N1)5'(D)3'(N2)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)

		Score	Identity
AC245166	Homsap IGHV3-23*04 F	1282	94.08% (270/287 nt)
M99660	Homsap IGHV3-23*01 F	1273	93.73% (269/287 nt)
AC244492	Homsap IGHV3-23D*01 F	1273	93.73% (269/287 nt)
M35415	Homsap IGHV3-23*02 F	1255	93.03% (267/287 nt)
AY757302	Homsap IGHV3-23*05 F	1219	91.64% (263/287 nt)
AM940223	Homsap IGHV3-23*03 F	1201	90.94% (261/287 nt)
M99675	Homsap IGHV3-48*01 F	1129	88.15% (253/287 nt)
AB019438	Homsap IGHV3-48*02 F	1120	87.80% (252/287 nt)
U03893	Homsap IGHV3-48*03 F	1120	87.80% (252/287 nt)
HM855336	Homsap IGHV3-48*04 F	1120	87.80% (252/287 nt)

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

1	<----- FR1-IMGT ----->
AC245166 Homsap IGHV3-23*04 F	.agggtgcagctggtggagtctggggga...aacttggaacagcctggggggtcccttaga
M99660 Homsap IGHV3-23*01 F	g-----t-----g---
AC244492 Homsap IGHV3-23D*01 F	g-----t-----g---
M35415 Homsap IGHV3-23*02 F	g-----t-----g---
AY757302 Homsap IGHV3-23*05 F	g-----t-----g---
AM940223 Homsap IGHV3-23*03 F	g-----t-----g---
M99675 Homsap IGHV3-48*01 F	g-----t-----g---
AB019438 Homsap IGHV3-48*02 F	g-----t-----g---
U03893 Homsap IGHV3-48*03 F	g-----t-----a-----g---
HM855336 Homsap IGHV3-48*04 F	g-----t-----g---
1	----->_____ CDR1-IMGT _____<-----
AC245166 Homsap IGHV3-23*04 F	ctctcctgtacagcctctggattcaccttt.....agcagatctgccatgaac
M99660 Homsap IGHV3-23*01 F	-----g-----c-a-----g-
AC244492 Homsap IGHV3-23D*01 F	-----g-----c-a-----g-
M35415 Homsap IGHV3-23*02 F	-----g-----c-a-----g-
AY757302 Homsap IGHV3-23*05 F	-----g-----c-a-----g-
AM940223 Homsap IGHV3-23*03 F	-----g-----c-a-----g-
M99675 Homsap IGHV3-48*01 F	-----g-----c-----t--c-a-ag-----
AB019438 Homsap IGHV3-48*02 F	-----g-----c-----t--c-a-ag-----
U03893 Homsap IGHV3-48*03 F	-----g-----c-----t--t-a--aa-----
HM855336 Homsap IGHV3-48*04 F	-----g-----c-----t--c-a-ag-----
	----- FR2-IMGT ----->_____ CDR

1	tgggtccgccgggctccaggggaaggggctggagtgggtctcaggaattagtggtagt...
AC245166 Homsap IGHV3-23*04 F	-----a-----ct-----...
M99660 Homsap IGHV3-23*01 F	-----a-----ct-----...
AC244492 Homsap IGHV3-23D*01 F	-----a-----ct-----...
M35415 Homsap IGHV3-23*02 F	-----a-----ct-----...
AY757302 Homsap IGHV3-23*05 F	-----a-----ct---ta-a-c---...
AM940223 Homsap IGHV3-23*03 F	-----a-----tt---ta-a-cg---...
M99675 Homsap IGHV3-48*01 F	-----a-----t---tac-----a-----...
AB019438 Homsap IGHV3-48*02 F	-----a-----t---tac-----a-----...
U03893 Homsap IGHV3-48*03 F	-----a-----t---tac-----a-----...
HM855336 Homsap IGHV3-48*04 F	-----a-----t---tac-----a-----...

1	2-IMGT _____<-----
AC245166 Homsap IGHV3-23*04 F	...ggtgggtcgaacatactacgcagactccgtgaag...ggccgggttcaccatctccaga
M99660 Homsap IGHV3-23*01 F	...-----a-c-----...-----
AC244492 Homsap IGHV3-23D*01 F	...-----a-c-----...-----
M35415 Homsap IGHV3-23*02 F	...-----a-c-----g-----a---
AY757302 Homsap IGHV3-23*05 F	...--a-a-c-----t-----...-----
AM940223 Homsap IGHV3-23*03 F	...--a-a-c-----t-----...-----
M99675 Homsap IGHV3-48*01 F	...a-a-acc-t-----t-----...-----a-----
AB019438 Homsap IGHV3-48*02 F	...a-a-acc-t-----t-----...-----a-----
U03893 Homsap IGHV3-48*03 F	...--a-a-acc-t-----t-----...-----a-----
HM855336 Homsap IGHV3-48*04 F	...a-a-a-acc-t-----t-----...-----a-----

1	FR3-IMGT -----
AC245166 Homsap IGHV3-23*04 F	gacaattccaagaatacgtctatatctgcaaatgaacagcctgagcgccgaggacacggcc
M99660 Homsap IGHV3-23*01 F	-----c-----g-----a-----
AC244492 Homsap IGHV3-23D*01 F	-----c-----g-----a-----
M35415 Homsap IGHV3-23*02 F	-----c-----g-----a-----
AY757302 Homsap IGHV3-23*05 F	-----c-----g-----a-----
AM940223 Homsap IGHV3-23*03 F	--t-----c-----g-----a-----
M99675 Homsap IGHV3-48*01 F	-----g-----ct-a-g-----a-----t
AB019438 Homsap IGHV3-48*02 F	-----g-----ct-a-g-----a-a-----t
U03893 Homsap IGHV3-48*03 F	----cg-----ct-a-g-----a-----t
HM855336 Homsap IGHV3-48*04 F	----cg-----ct-a-g-----a-----t

1	----->_____ CDR3-IMGT _____
AC245166 Homsap IGHV3-23*04 F	gcatattactgtgcgaaagattcgtatactaccagttggtacggaggtatggacgtctgg
M99660 Homsap IGHV3-23*01 F	-t-----
AC244492 Homsap IGHV3-23D*01 F	-t-----
M35415 Homsap IGHV3-23*02 F	-t-----
AY757302 Homsap IGHV3-23*05 F	-t-----
AM940223 Homsap IGHV3-23*03 F	-t-----
M99675 Homsap IGHV3-48*01 F	-tg-----g---
AB019438 Homsap IGHV3-48*02 F	-tg-----g---
U03893 Homsap IGHV3-48*03 F	-tt-----g---
HM855336 Homsap IGHV3-48*04 F	-tg-----g---

1	ggccacgggaccacgggtcaccgtctcctca
AC245166 Homsap IGHV3-23*04 F	
M99660 Homsap IGHV3-23*01 F	
AC244492 Homsap IGHV3-23D*01 F	
M35415 Homsap IGHV3-23*02 F	
AY757302 Homsap IGHV3-23*05 F	
AM940223 Homsap IGHV3-23*03 F	
M99675 Homsap IGHV3-48*01 F	
AB019438 Homsap IGHV3-48*02 F	
U03893 Homsap IGHV3-48*03 F	
HM855336 Homsap IGHV3-48*04 F	

