

NCBI/ IGBLAST: Formatting Results: Job id = ipRmCxcJriWdA5k1wC66U8Env0Le

Database: imgt.Homo_sapiens.V.f.orf.p; imgt.Homo_sapiens.D.f.orf;
imgt.Homo_sapiens.J.f.orf
556 sequences; 145,506 total letters

Query=
Length=756

Sequences producing significant alignments: (Bits)		Score	E Value
IGLV8-61*01	germline gene	26.8	0.82
IGLV8-61*02	germline gene	26.8	0.82
IGLV8-61*03	germline gene	26.8	0.82

Domain classification requested: imgt
V-(D)-J rearrangement summary for query sequence (multiple equivalent top matches having the same score and percent identity, if present, are separated by a comma):

Top V gene match	Top J gene match	Chain type	stop codon	V-J frame	Productive	Strand
IGLV8-61*01.IGLV8-61*02.IGLV8-61*03	N/A	VL	No			+

V-(D)-J junction details based on top germline gene matches:

V region end	V-J junction*	J region start
CGCAG		

*: Overlapping nucleotides may exist at V-D-J junction (i.e., nucleotides that could be assigned to either rearranging gene). Such nucleotides are indicated inside a parenthesis (i.e., (TACAT)) but are not included under the V, D or J gene itself.

Alignment summary between query and top germline V gene hit:

	from	to	length	matches	mismatches	gaps	identitv(%)
FR3-IMGT	20	39	20	18	2	0	90
Total			20	18	2	0	90

Alignments

				<-----FR3-IMGT----->							
				T	I	T	G	P	Q		
V	90.0%	(18/20)	Query_1	20	TCACCATCACGGGGCCGCAG					39	
			IGLV8-61*01	224	G.C...					243	
					T	I	T	G	A	Q	
V	90.0%	(18/20)	IGLV8-61*02	224	G.C...					243	
V	90.0%	(18/20)	IGLV8-61*03	216	G.C...					235	