

## Find a Gene Assignment – BGGN213

Jason Hsiao (A15871650)

### 1) Protein: Human IL-4 Isoform 3 Precursor

Accession Number: **NP\_001341919.1**

Species: **Human**

### 2) BLAST Method Used: tblastn 2.14.1+

Database: Expressed sequence tags (est)

Job Title	NP_001341919:interleukin-4 isoform 3 precursor...		
RID	<a href="#">KJV3BYJR013</a>	Search expires on 10-27 03:28 am	<a href="#">Download All</a> ▼
Program	TBLASTN	<a href="#">?</a>	<a href="#">Citation</a> ▼
Database	est	<a href="#">See details</a> ▼	
Query ID	<a href="#">NP_001341919.1</a>		
Description	interleukin-4 isoform 3 precursor [Homo sapiens]		
Molecule type	amino acid		
Query Length	136		
Other reports	<a href="#">?</a>		

✓	<a href="#">AGENCOURT_14496778 NIH_MGC_195 Homo sapiens cDNA clone IMAGE:6971779 5', mRNA sequence</a>	<a href="#">Homo sapiens</a>	106	177	72%	3e-36	85.25%	537	<a href="#">CD559679.2</a>
✓	<a href="#">EST365300 MAGE resequences_MAGB Homo sapiens cDNA, mRNA sequence</a>	<a href="#">Homo sapiens</a>	106	177	72%	4e-36	83.87%	602	<a href="#">AW953230.1</a>
✓	<a href="#">AGENCOURT_14532625 NIH_MGC_191 Homo sapiens cDNA clone IMAGE:30415895 5', mRNA sequence</a>	<a href="#">Homo sapiens</a>	105	177	72%	4e-36	85.25%	648	<a href="#">CD640452.1</a>
✓	<a href="#">AGENCOURT_14496806 NIH_MGC_195 Homo sapiens cDNA clone IMAGE:6971780 5', mRNA sequence</a>	<a href="#">Homo sapiens</a>	105	177	72%	4e-36	85.25%	556	<a href="#">CD559525.2</a>
✓	<a href="#">AGENCOURT_14496680 NIH_MGC_195 Homo sapiens cDNA clone IMAGE:6971778 5', mRNA sequence</a>	<a href="#">Homo sapiens</a>	105	177	72%	4e-36	85.25%	526	<a href="#">CD559527.2</a>
✓	<a href="#">14573 Full Length cDNA from the Mammalian Gene Collection Homo sapiens cDNA 5' similar to BC067514, mRNA...</a>	<a href="#">Homo sapiens</a>	105	177	72%	4e-36	85.25%	625	<a href="#">EL736798.1</a>
✓	<a href="#">AGENCOURT_14496716 NIH_MGC_195 Homo sapiens cDNA clone IMAGE:6971778 5', mRNA sequence</a>	<a href="#">Homo sapiens</a>	105	177	72%	5e-36	85.25%	541	<a href="#">CD559680.2</a>
✓	<a href="#">AGENCOURT_14496840 NIH_MGC_195 Homo sapiens cDNA clone IMAGE:6971780 5', mRNA sequence</a>	<a href="#">Homo sapiens</a>	105	177	72%	5e-36	85.25%	539	<a href="#">CD559678.2</a>
✓	<a href="#">AGENCOURT_14496742 NIH_MGC_195 Homo sapiens cDNA clone IMAGE:6971779 5', mRNA sequence</a>	<a href="#">Homo sapiens</a>	105	177	72%	5e-36	85.25%	559	<a href="#">CD559526.2</a>
✓	<a href="#">AGENCOURT_14497059 NIH_MGC_195 Homo sapiens cDNA clone IMAGE:6971784 5', mRNA sequence</a>	<a href="#">Homo sapiens</a>	104	176	72%	9e-36	83.61%	664	<a href="#">CK130262.1</a>
✓	<a href="#">AGENCOURT_14496930 NIH_MGC_195 Homo sapiens cDNA clone IMAGE:6971782 5', mRNA sequence</a>	<a href="#">Homo sapiens</a>	105	175	72%	2e-35	85.25%	536	<a href="#">CD559523.2</a>
✓	<a href="#">AGENCOURT_14496966 NIH_MGC_195 Homo sapiens cDNA clone IMAGE:6971782 3', mRNA sequence</a>	<a href="#">Homo sapiens</a>	105	175	72%	2e-35	85.25%	528	<a href="#">CD559676.1</a>
✓	<a href="#">AGENCOURT_14496867 NIH_MGC_195 Homo sapiens cDNA clone IMAGE:6971781 5', mRNA sequence</a>	<a href="#">Homo sapiens</a>	104	175	72%	2e-35	83.61%	561	<a href="#">CD559524.2</a>
✓	<a href="#">AGENCOURT_14496902 NIH_MGC_195 Homo sapiens cDNA clone IMAGE:6971781 3', mRNA sequence</a>	<a href="#">Homo sapiens</a>	104	175	72%	2e-35	83.61%	528	<a href="#">CD559677.1</a>
✓	<a href="#">AGENCOURT_14354235 NIH_MGC_191 Homo sapiens cDNA clone IMAGE:30409212 5', mRNA sequence</a>	<a href="#">Homo sapiens</a>	95.5	167	61%	3e-33	95.74%	851	<a href="#">CD521402.1</a>
✓	<a href="#">EST71622 Human White blood cells Homo sapiens cDNA 5' end similar to interleukin 4 (HT716), mRNA sequence</a>	<a href="#">Homo sapiens</a>	81.3	120	60%	5e-19	80.65%	290	<a href="#">T29166.1</a>
✓	<a href="#">020829OSI1024037HT OSI Ovis aries cDNA, mRNA sequence</a>	<a href="#">Ovis aries</a>	76.6	112	62%	7e-17	59.68%	546	<a href="#">EE850889.1</a>
✓	<a href="#">est_t_truncatus2245 HML_TuTr_IL-2_PBL Tursiops truncatus cDNA, mRNA sequence</a>	<a href="#">Tursiops truncatus</a>	73.2	73.2	31%	1e-14	74.42%	303	<a href="#">DV799593.1</a>
✓	<a href="#">DC391247 SPLEN2 Homo sapiens cDNA clone SPLEN2031387 5', mRNA sequence</a>	<a href="#">Homo sapiens</a>	56.2	56.2	20%	2e-07	100.00%	560	<a href="#">DC391247.1</a>
✓	<a href="#">HL01018B2H10 Equine lymphocyte cDNA Library Equus caballus cDNA clone HL01018B2H10, mRNA sequence</a>	<a href="#">Equus caballus</a>	55.1	55.1	47%	4e-07	48.48%	527	<a href="#">DN506696.1</a>
✓	<a href="#">EST00005 Cattle PBMC library Bos taurus x Bos indicus cDNA clone PDFMD-Beas/Bovine IL-4 clone similar to B...</a>	<a href="#">Bos indicus x Bo...</a>	40.4	40.4	29%	0.037	55.00%	289	<a href="#">HS091871.1</a>

3)

## 020829OSI1024037HT OSI Ovis aries cDNA, mRNA sequence

Sequence ID: [EE850889.1](#) Length: 546 Number of Matches: 2

Range 1: 47 to 232 [GenBank](#) [Graphics](#)

[▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
76.6 bits(187)	7e-17	Compositional matrix adjust.	42/62(68%)	47/62(75%)	0/62(0%)	+2
Query 1		MGLTSQ11pplffllACAGNFVHGHKCDITLQEIIKTLNSLTEQKTLCTELTVTDIFAAS				60
		MGLTSQ1+P L LL C +FVHGHKCDITL+EIIKTLN LT +K C EL V D+FAA				
Sbjct 47		MGLTSQ1PALVCLLVCTSHFVHGHKCDITLEEIIKTLNILTSRKNSCMELPVADVFAAP				226
Query 61	KQ 62					
	K					
Sbjct 227	KN 232					

Range 2: 222 to 290 [GenBank](#) [Graphics](#)

[▼ Next Match](#) [▲ Previous Match](#) [▲ First Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
35.8 bits(81)	7e-17	Compositional matrix adjust.	17/23(74%)	18/23(78%)	0/23(0%)	+3
Query 93		PERTQLRRKPSAGLRLCSGSSTA	115			
		P+RTQLRRKPSAGL L G ST				
Sbjct 222		PQRTQLRRKPSAGLELSLGVSTG	290			

>EE850889.1 020829OSI1024037HT OSI Ovis aries cDNA, mRNA sequence

GTAAACTAATTGTCTCACACTGTCAAGTCAAATAGAGATACTATTAATGGGTCTCACCTCCCAGCTGATCCCA  
GCGCTGGTCTGCTTACTGGTATGTACCAGCCACTTCGTCCATGGACACAAGTGTGATATTACCTTAGAAGAG  
ATCATCAAAACGCTGAACATCCTCACATCGAGAAAGAATTCATGCATGGAGCTGCCTGTAGCAGACGTCTT  
TGCTGCCCCAAAGAACGCAACTGAGAAGGAAACCTTCTGCAGGGCTGGAATTGAGCTTAGGCGTATCTAC  
AGGAGCCACATGTGCTTGAACAAATTCCTGGGCGGACTTGACAGGAATCTCAGCAGCCTGGCAAGCAAG  
ACCTGTTCTGTGAATGAAGCCAAGACGAGTACAAGTACGCTGAGAGACCTCTTGGAAGGCTAAAGACTA  
TTATGAAGGAGAAATACTCAAAGTGTGAAGCTGAATATTTAATTTATGACTTTTTAATAGCCTTATTTAA  
ACATATTTATATTTATACTCATCGTAAATAAAGTATATGTAGAA

### Translated Protein Sequence via Emboss Transeq

>EMBOSS\_001\_1

VN\*LSHTV\$ANRDTINGSHLPADPSAGLLTGMYPQLRPWTQV\*YYLRRDHQNAEHPHIEK  
EFMHGAAC\$RRLCCPKERN\*EGNLLQGWN\*A\*AYLQEPHVLEQIPGRT\*QESQQPGKQDL  
FCE\*\$QDEYKYAERPLGKAKDYEGEILKVLKLNILYDFLIALF\*TYLYIYNSS\*NKVY  
VE

4)

Job Title

Protein Sequence

RID

[KJXK9ANX01N](#)
Search expires on 10-27 04:11 am
[Download All](#)

Program

BLASTP [Citation](#)

Database

nr [See details](#)

Query ID

lcl|Query\_681803

Description

unnamed protein product

Molecule type

amino acid

Query Length

182

Other reports

[Distance tree of results](#)
[Multiple alignment](#)
[MSA viewer](#)

Filter Results

Organism

only top 20 will appear

☐ exclude

Type common name, binomial, taxid or group name

[+ Add organism](#)

Percent Identity

to

E value

to

Query Coverage

to

Filter

Reset

Compare these results against the new Clustered nr database

BLAST

Descriptions

Graphic Summary

Alignments

Taxonomy

Sequences producing significant alignments

Download

Select columns

Show 100

☒ select all 1 sequences selected

[GenPept](#)
[Graphics](#)
[Distance tree of results](#)
[Multiple alignment](#)
[MSA Viewer](#)

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	hypothetical protein QTO34_016060 [Eptesicus nilssonii]	<a href="#">Eptesicus nilssonii</a>	53.1	53.1	25%	8e-05	63.04%	174	<a href="#">KAK1343282.1</a>