

Jessica Diaz-Vigil

Find a Gene Project

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1. Name of a protein you are interested in including the species and the accession number:

- Name: Amyloid Beta Precursor Protein
- P05067.3
- Species: Homo Sapiens

Translated BLAST: tblastn

blastn blastp blastx **tblastn** tblastx

TBLASTN search translated nucleotide databases using a protein query. more... [Reset page](#) [Bookmark](#)

Enter Query Sequence

Enter accession number(s), gi(s), or FASTA sequence(s) [Clear](#) [Query subrange](#)

sp|P05067.3

From To

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Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown [?](#)

Exclude ☐ Models (XM/XP) ☐ Uncultured/environmental sample sequences

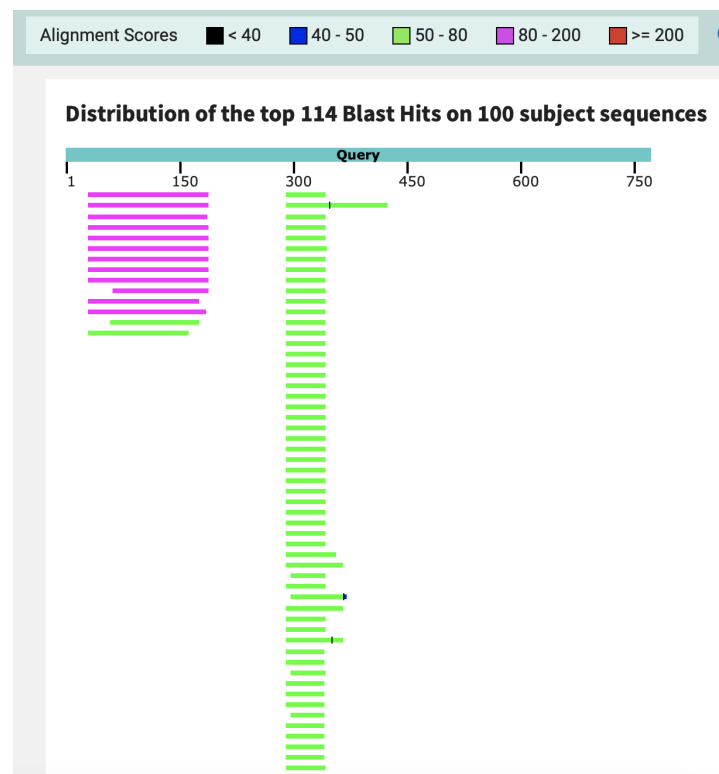
Limit to ☐ Sequences from type material

Entrez Query [YouTube](#) [Create custom database](#)

Enter an Entrez query to limit search [?](#)

BLAST Search database est using Tblastn (search translated nucleotide databases using a protein query)

☐ Show results in a new window



2. Perform a BLAST search against a DNA database, such as a database consisting of genomic DNA or ESTs. The BLAST server can be at NCBI or elsewhere. Include details of the BLAST method used, database searched and any limits applied (e.g. Organism).

- Method: BLASTn search against platyhelminthes ESTs
- Database: Expressed sequence tags (est)
- Organism: Platyhelminthes (taxid: 6157)
- Chosen Match: Accession BP186991.1, a 500 base pair mRNA Sequence

	Score	Expect	Method	Identities	Positives	Gaps	Frame
	97.4 bits (241)	3e-2 2	Composition-based stats.	54/166 (33%)	82/166 (49%)	13/166 (7%)	+2
Query	31	EPQIAMFCGR LNMHMNVQNGKWDSDPSGTKTCIDTKEGILQYCQEVYPQLQITNVVEANQ					90
		EPQ+A CG+ + +N +W D + CI + ++++CQ+ +P L+I A					
Sbjct	8	EPQVAFLCGKPSKVF--KNNQWILDFQ--QGCIKNEVKVVKFCQKSFPSLKILTAEPAIT					175
Query	91	PVTIQNWCKRGRKQCKTHPHFVIPYRCLVGEFVSDALLVPDKCKFLHQERMDVCETHLHW					150
		NWC + C+ + + P++CL F SDAL++P C+F H C + W					
Sbjct	176	KAKFTNWCDFNQNCENVNE-IRPFKCLDKNFQSDALILPRNCQFGHLFNESECLIYKDW					352
Query	151	HTVAKETCSEKST-NLHDYGM L L P C G I D K-----FRGVEFVCCP					188
		A C +K + YGML PCG + F+GVEFVCCP					
Sbjct	353	VKRATNQCLQKQDWIIKSYGMLFPCGNHRKEIKPMFFKGVFVCCP					490

3. Gather information about this "novel" protein

>BP186991.1 BP186991 planarian head cDNA Dugesia japonica cDNA clone 00807_HH, mRNA sequence

```
CACTTACGAACCACAAGTTGCTTTTCTATGTGGAAAACCTTCTAAAGTGTTTAAGAACAATCAATGG
ATATTAGATTTTCAACAAGGCTGCATCAAAAATGAAGTGAAAGTTGTCAAGTTTTGTCAAAAATCAT
TTCCTTCATTGAAAATTCTTACTGCTGAACCAGCTATAACGAAAGCTAAATTTACAAATTGGTGTGA
TTTCAATAATCAAAAATTGTGAAGTTAATGTGGAAATTCGGCCTTTTAAATGCTTGGATAAAAACTTT
CAATCCGATGCTTTAATTCTTCTCGAAATTGTCAATTTGGCCATTTGTTTAAATGAAAGCGAATGTT
TAATATATAAAGATTGGGTGAAACGAGCTACTAATCAATGTCTTCAAAAACAAGACTGGATCATTA
ATCATAACGGAATGCTTTTCCCGTGTGGTAATCACAGAAAGGAAATAAAACCAATGTTTTTCAAAGGT
GTAGAATTTGTTTGTTCCTCGTTTTGAAC
```

- Name: BP186991 planarian head cDNA Dugesia japonica cDNA clone 00807_HH, mRNA sequence
- Species: [Dugesia japonica](#) Eukaryota; Metazoa; Spiralia; Lophotrochozoa; Platyhelminthes; Rhabditophora; Seriata; Tricladida; Continenticola; Geoplanioidea; Dugesidae; Dugesia.

4. Prove that this gene, and its corresponding protein, are novel.

- This gene is novel since the only gene found is only around 30% identical to the gene I found.

Descriptions	Graphic Summary	Alignments	Taxonomy						
Sequences producing significant alignments			Download ▾	Select columns ▾	Show	100 ▾	?		
<input checked="" type="checkbox"/> select all 57 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 BOX15_Mlig026873g1 [Macrostomum lignano]	Macrostomum lignano	94.7	94.7	77%	1e-21	34.07%	720	PAA91903.1
<input checked="" type="checkbox"/>	hypothetical protein BOX15_Mlig009810g3 [Macrostomum lignano]	Macrostomum lignano	94.7	94.7	77%	1e-21	34.07%	719	PAA91960.1
<input checked="" type="checkbox"/>	hypothetical protein BOX15_Mlig009810g2 [Macrostomum lignano]	Macrostomum lignano	94.4	94.4	77%	1e-21	34.07%	720	PAA58902.1
<input checked="" type="checkbox"/>	unnamed protein product [Trichobilharzia szidati]	Trichobilharzia szidati	88.6	88.6	97%	2e-19	33.33%	804	CAH8827068.1
<input checked="" type="checkbox"/>	unnamed protein product [Trichobilharzia regenti]	Trichobilharzia regenti	88.6	88.6	97%	2e-19	33.33%	803	CAH8824637.1
<input checked="" type="checkbox"/>	unnamed protein product [Schistosoma spindale]	Schistosoma spindale	85.9	85.9	97%	2e-18	32.14%	756	CAI2725499.1
<input checked="" type="checkbox"/>	hypothetical protein BOX15_Mlig001691g2 [Macrostomum lignano]	Macrostomum lignano	82.8	82.8	89%	4e-18	31.58%	270	PAA89607.1
<input checked="" type="checkbox"/>	unnamed protein product [Schistosoma mattheei]	Schistosoma mattheei	80.9	80.9	98%	5e-18	32.72%	199	VDO79771.1
<input checked="" type="checkbox"/>	unnamed protein product [Schistosoma rodhaini]	Schistosoma rodhaini	83.2	83.2	97%	1e-17	30.95%	727	CAH8436219.1
<input checked="" type="checkbox"/>	unnamed protein product [Schistosoma margrebowiei]	Schistosoma margrebowiei	80.1	80.1	98%	1e-17	32.10%	199	VDO93450.1
<input checked="" type="checkbox"/>	unnamed protein product [Schistosoma rodhaini]	Schistosoma rodhaini	83.2	83.2	97%	1e-17	30.95%	759	CAH8436185.1
<input checked="" type="checkbox"/>	unnamed protein product [Schistosoma rodhaini]	Schistosoma rodhaini	82.8	82.8	97%	2e-17	30.95%	743	CAH8436201.1
<input checked="" type="checkbox"/>	unnamed protein product [Schistosoma rodhaini]	Schistosoma rodhaini	81.3	81.3	97%	6e-17	31.55%	692	CAH8490270.1
<input checked="" type="checkbox"/>	alzheimer's disease beta-amyloid related [Schistosoma mansoni]	Schistosoma mansoni	81.3	81.3	98%	6e-17	31.36%	696	XP_018646151.1