

Find a Gene Project Report

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[Q1]

Name: FoxP3 (fork-head box P3)

Accession: ABQ15210

Species: Homo Sapiens

[Q2]

Method: TBLASTN

Database: Expressed Sequence Tags (est)

Organism: nematodes (taxid:6231)

BLAST® » tblastn

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blastn blastp blastx **tblastn** tblastx

Translated BLAST: tblastn

TBLASTN search translated nucleotide databases using a protein query. more...

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Enter Query Sequence

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

Query subrange [?](#)

From

To

Or, upload file No file chosen [?](#)

Job Title

Enter a descriptive title for your BLAST search [?](#)

☐ Align two or more sequences [?](#)

Choose Search Set

Database [?](#)

Organism ☐ exclude

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

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

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

☒ Show results in a new window

Note: Parameter values that differ from the default are highlighted in yellow and marked with a sign icon

+ Algorithm parameters

Feedback

Chosen match: Accession **BE029116.1**, a 450 base pair clone from *strongyloides stercoralis*. See below for alignment details.

Job Title	ABQ15210.1 FOXP3 [Homo sapiens]		
GRID	KXY9D7MA013	Search expires on 10-31 08:30 am	Download All ▼
Program	TBLASTN ?	Citation ▼	
Database	est	See details ▼	
Query ID	lcl Query_102747		
Description	ABQ15210.1 FOXP3 [Homo sapiens]		
Molecule type	amino acid		
Query Length	431		
Other reports	?		

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**

Sequences producing significant alignments Download ▾ Select columns ▾ Show 100 ▾ ?

[GenBank](#) [Graphics](#)

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
✓	kp25a10.y1.TBN95TM-SSFH Strongyloides stercoralis cDNA 5' similar to TR:O60827.O60827.JM2 PROTEIN.C...	Strongyloides ste...	140	140	23%	1e-38	63.37%	450	BE029116.1
✓	Ps_Lib14_4DE02_PSC02382 Unstressed mixed stage Panagrolaimus superbus nematodes Panagrolaimus supe...	Panagrolaimus s...	140	140	22%	8e-38	63.92%	654	GW409327.1
✓	Pd_3pr_70O06.Panagrolaimus davidi 4 degree Panagrolaimus davidi cDNA_mRNA sequence	Panagrolaimus d...	139	139	22%	1e-36	63.92%	868	JZ619881.1
✓	Aa_aamk2_25A09_T7 Aphelenchus avenae mixed-stage library Aphelenchus avenae cDNA clone Aa_aamk2_25...	Aphelenchus ave...	134	134	21%	8e-36	61.60%	633	GQ479605.1
✓	HY539018 full-length enriched (oligo-capping) cDNA library: dev_stage: mixed Diploscapter coronatus cDNA clon...	Diploscapter cor...	129	129	21%	6e-34	60.64%	634	HY539018.1
✓	P19_r_PDT_11_066 Panagrolaimus davidi 20 degree Panagrolaimus davidi cDNA_mRNA sequence	Panagrolaimus d...	131	131	20%	8e-34	66.67%	859	JZ680731.1
✓	P19_r_PDT_11_066 Panagrolaimus davidi 20 degree Panagrolaimus davidi cDNA_mRNA sequence	Panagrolaimus d...	122	122	19%	1e-30	61.63%	802	JZ680698.1
✓	Pd_3pr_42N18.Panagrolaimus davidi 4 degree Panagrolaimus davidi cDNA_mRNA sequence	Panagrolaimus d...	122	122	19%	3e-30	64.29%	855	JZ609980.1
✓	Pd_3pr_47M16.Panagrolaimus davidi 4 degree Panagrolaimus davidi cDNA_mRNA sequence	Panagrolaimus d...	122	122	20%	3e-30	54.95%	866	JZ611701.1

[Download](#) [GenBank](#) [Graphics](#) [Next](#) [Previous](#) [Descriptions](#)

Sequence ID: [BE029116.1](#) Length: 450 Number of Matches: 1

Range 1: 86 to 388 [GenBank](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities		Positives	Gaps	Frame
140 bits(353)	1e-38	Compositional matrix adjust.	64/101(63%)	79/101(78%)	1/101(0%)	+2	
Query	326	HHMDYFKFHNMRPPTYATLIRXAEPEKQRTLNEIYWFTRMFAGFRNHPATKNAI					385
		L R ++K ++RPP+TYA+LIR AILE+ E Q TLNEIY WFT FAFR FHTKNAI					
Sbjct	86	RNRFFYKNDNRPPPTYASLIRQAILESGQLTLNEIYQWFTTFAFFRNAAHTKNAI					265
Query	386	RHNLSLHKCFVRVSE -KGAVMTVDELEFRKRSQRSPRCS					425
		RHNLSLHKCF R+E KGAVMTVD+ EF K+R QR +S					
Sbjct	266	RHNLSLHKCFTRTEONCVKGAVMTVDYDQEFYKRRPTGVS					388

kp25a10.y1 TBN95TM-SSFH Strongyloides stercoralis cDNA 5' similar to R:O60827
O60827 JM2 PROTEIN, COMPLETE CDS, mRNA sequence
Sequence ID: BE029116.1Length: 450Number of Matches: 1
Range 1: 86 to 388 GenBankGraphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps	Frame
140 bits (353)	1e-38	Compositional matrix adjust.	64/101 (63%)	79/101 (78%)	1/101 (0%)	+2

```

Query   326  HNMDYFKFHNMRPPFTYATLIRWAILEAPEKQRTLNEIYHWFTRMFAFFRNHPATWKNAI  385
        N +++K +++RPP+TYA+LIR AILE+ E Q TLNEIY WFT  FAFFR + ATWKNA+
Sbjct   86  RNREFYKNNDVRPPYTYASLIRQAILESKEGQLTLNEIYQWFTETFAFFRRNAATWKNAV  265

Query   386  RHNLSLHKCFVRVESE-KGAVWTVDELEFRKKRSQRPSRCS  425
        RHNLSLHKCF R+E   KGAVWTVDD+ EF K+R QR +   S
Sbjct   266  RHNLSLHKCFTRIEQNVKGAVWTVDDQEFYKRRPQRTNGVS  388

```

[Q3]

>Strongyloides stercoralis protein (sequence translated from BLAST result)

IKEESRQTSTPRKRVS DK SILPMQADIDRNREFYKNNDVRPPYTYASLIRQAILESKEGQLTLNEIY
 QWFTETFAFFRRNAATWKNAV RHNLSLHKCFTRIEQNVKGAVWTVDDQEFYKRRPQRTNGVST
 SSVIKSKPSTPKPENSVTGS

Name: Fork-head box protein like protein

Species: Strongyloides stercoralis

Eukaryota; Metazoa; Ecdysozoa; Nematoda; Chromadorea; Rhabditida; Tylenchina; anagrolaimomorpha;
 Strongyloidoidea; Strongyloididae; Strongyloides.

[Q4]

Standard Protein BLAST

blastn **blastp** blastx tblastn tblastx

BLASTP programs search protein databases using a protein query. more...

Reset page Bookmark

Enter Query Sequence

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

>Strongyloides stercoralis protein (sequence translated from BLAST result)
 IKEESRQTSTPRKRVS DK SILPMQADIDRNREFYKNNDVRPPYTYASLIRQAILESKEGQLTLNEIY QWFTETFAFFRRNAATWKNAV RHNLSLHKCFTRIEQNVKGAVWTVDDQEFYKRRPQRTNGVST SSVIKSKPSTPKPENSVTGS

Query subrange

From

To

Or, upload file No file chosen

Job Title

Enter a descriptive title for your BLAST search

☐ Align two or more sequences

Choose Search Set

Databases ☒ Standard databases (nr etc.) [New](#) ☐ Experimental databases

Compare ☐ Select to compare standard and experimental database

Standard

Database

Organism

Optional ☐ exclude [Add organism](#)

Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown

Exclude ☐ Models (XM/XP) ☐ Non-redundant RefSeq proteins (WP) ☐ Uncultured/environmental sample sequences

Program Selection

Algorithm ☐ Quick BLASTP (Accelerated protein-protein BLAST)

☒ blastp (protein-protein BLAST)

☐ PSI-BLAST (Position-Specific Iterated BLAST)

☐ PHI-BLAST (Pattern Hit Initiated BLAST)

☐ DELTA-BLAST (Domain Enhanced Lookup Time Accelerated BLAST)

Choose a BLAST algorithm

[Feedback](#)

[BLAST](#) Search database nr using Blastp (protein-protein BLAST)

☐ Show results in a new window

+ Algorithm parameters

Job Title	Strongyloides stercoralis protein (sequence...		
RID	KY0R22KW016	Search expires on 10-31 09:12 am	Download All ▾
Program	BLASTP ?	Citation ▾	
Database	nr	See details ▾	
Query ID	cd Query_130286		
Description	Strongyloides stercoralis protein (sequence translated from ...		
Molecule type	amino acid		
Query Length	150		
Other reports	Distance tree of results	Multiple alignment	MSA viewer ?

Filter Results

Organism only top 20 will appear ☐ exclude

[+ Add organism](#)

Percent Identity

to

E value

to

Query Coverage

to

[Filter](#) [Reset](#)

Compare these results against the new Clustered nr database [?](#) [BLAST](#) [X](#)

- Descriptions
- Graphic Summary
- Alignments
- Taxonomy

Sequences producing significant alignments									
Download ▾ Select columns ▾ Show 100 ▾ ?									
<input checked="" type="checkbox"/> select all 100 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"/>	Forkhead box protein P3 [Strongyloides ratti]	Strongyloides ratti	315	315	100%	8e-103	98.00%	561	XP_024499265.1
<input checked="" type="checkbox"/>	unnamed protein product [Bursaphelenchus xylophilus]	Bursaphelenchus xylophilus	218	218	73%	4e-63	85.45%	872	CAD5224191.1
<input checked="" type="checkbox"/>	unnamed protein product [Bursaphelenchus okinawaensis]	Bursaphelenchus okinawaensis	225	225	76%	9e-67	85.22%	658	CAD5218261.1
<input checked="" type="checkbox"/>	FKH-7 protein [Aphelenchus avenae]	Aphelenchus avenae	217	217	74%	2e-63	84.68%	703	KAH7729625.1
<input checked="" type="checkbox"/>	forkhead domain-containing protein [Ditylenchus destructor]	Ditylenchus destructor	203	203	74%	1e-57	84.68%	830	KAI1713948.1
<input checked="" type="checkbox"/>	hypothetical protein WR25_14133 [Diploscapter pachys]	Diploscapter pachys	210	210	76%	4e-62	80.17%	539	PAV75835.1
<input checked="" type="checkbox"/>	hypothetical protein WR25_27304 [Diploscapter pachys]	Diploscapter pachys	209	209	76%	8e-62	80.17%	537	PAV69331.1
<input checked="" type="checkbox"/>	unnamed protein product [Mesorhabditis belari]	Mesorhabditis belari	211	211	82%	9e-63	78.23%	522	CAJ0931278.1
<input checked="" type="checkbox"/>	unnamed protein product [Mesorhabditis belari]	Mesorhabditis belari	211	211	82%	1e-62	78.23%	519	CAJ0931279.1

[Download](#) ▾ [GenPept](#) [Graphics](#) [Next](#) [Previous](#) [Descriptions](#)

Forkhead box protein P3 [Strongyloides ratti]
Sequence ID: [XP_024499265.1](#) Length: **561** Number of Matches: **1**
[See 1 more title\(s\)](#) ▾ [See all Identical Proteins\(IPG\)](#)

Range 1: 317 to 466 [GenPept](#) [Graphics](#) [Next Match](#) [Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps
315 bits(808)	8e-103	Compositional matrix adjust.	147/150(98%)	148/150(98%)	0/150(0%)
Query 1	IKEESRQTSTPRKRVSDKSILPMQADIDRNREFYKNNVDRPPYTYASLIHQAILLESKEGQ 60				
Sbjct 317	IKEESRQTSTPRKRVSDKSILPMQADIDRNREFYKNNVDRPPYTYASLIHQAILLESKEGQ 376				
Query 61	LTLNEIYQWFTETFAFFRRNAATWKNNAVRHNLHLKCFTRIEQNVKGAVWTVDDQEFYKR 120				
Sbjct 377	LTLNEIYQWFTETFAFFRRNAATWKNNAVRHNLHLKCFTRIEQNVKGAVWTVDDQEFYKR 436				
Query 121	RPORTNGVSTSSVIKSPSTPKPENSVTGS 150				
Sbjct 437	RPORTNGV + SVIKSPSTPKPENSVTGS 466				

Related Information
[Gene](#) - associated gene details
[AlphaFold Structure](#) - 3D structure displays
[Genome Data Viewer](#) - aligned genomic context
[Identical Proteins](#) - Identical proteins to XP_024499265.1

The top hit result yielded from BLASTP search against NR database is the Forkhead box protein P3 from Strongyloides ratti, with identity of 98%.