

Задание 3.

Последовательность длины 10.

Standard Nucleotide BLAST

blastnblastpblastxtblastntblastx

BLASTN programs search nucleotide databases using a

Enter Query Sequence

Enter accession number(s), gi(s), or FASTA sequence(s)

AATAACAACCTCTGTTGACCGACTCGGCATGGTATGAAGCCCCAGGTAGAAGCTTCGCCTGCCTTATCACTCGGCACGGTGATGCAATCTCGAGCGAG

Clear

Query subrange

From

To

Or, upload file

Browse...

No file selected.

Job Title

Enter a descriptive title for your BLAST search

Align two or more sequences

Choose Search Set

Database

Human genomic + transcript

Mouse genomic + transcript

Others (nr etc.):

Nucleotide collection (nr/nt)

Organism

Optional

Enter organism name or id--completions will be suggested

Exclude

Optional

Limit to

Optional

Entrez Query

Optional

Enter an Entrez query to limit search

Exclude

Optional

Limit to

Optional

Entrez Query

Optional

Enter an Entrez query to limit search

Program Selection

Optimize for

Highly similar sequences (megablast)

More dissimilar sequences (discontiguous megablast)

Somewhat similar sequences (blastn)

Choose a BLAST algorithm

BLAST

Search database Nucleotide collection (nr/nt) using Blastn (Optimize for somewhat similar sequences)

DescriptionsGraphic SummaryAlignmentsTaxonomy

Alignment viewPairwiseCDS featureDownload

1 sequences selected

DownloadGenBank Graphics

NextPreviousDescriptions

PREDICTED: Mizuhopecten yessoensis E3 ubiquitin-protein ligase HECTD1-like (LOC110454650), mRNA

Sequence ID: XM_021504285.1Length: 10841Number of Matches: 1

Range 1: 7794 to 7815GenBankGraphics

Next MatchPrevious Match

Score	Expect	Identities	Gaps	Strand
41.0 bits(44)	7.7	22/22(100%)	0/22(0%)	Plus/Plus

Query25GCCATGGTATGAAGCCCCAGG46

Sbjct7794GCCATGGTATGAAGCCCCAGG7815

Related Information

Gene-associated gene details

Genome Data Viewer-aligned genomic context

Последовательность длины 1000.

blastnblasttblastntblastx

Enter Query Sequence

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Clear

Query subrange

From

To

Or, upload file

Browse...

seq1000.txt

Job Title

Enter a descriptive title for your BLAST search

Align two or more sequences

Choose Search Set

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Human genomic + transcript

Mouse genomic + transcript

Others (nr etc.):

Nucleotide collection (nr/nt)

Organism

Optional

Enter organism name or id--completions will be suggested

Exclude

+

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

Exclude

Optional

Models (XM/XP)

Uncultured/environmental sample sequences

Limit to

Optional

Sequences from type material

Entrez Query

Optional

Enter an Entrez query to limit search

YouTube

Create custom database

Program Selection

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Highly similar sequences (megablast)

More dissimilar sequences (discontiguous megablast)

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BLAST

Search database Nucleotide collection (nr/nt) using Blastn (Optimize for somewhat similar sequences)

Show results in a new window

Query Length 1000

Other reports [Distance tree of results](#) [MSA viewer](#)

Filter

Reset

Descriptions	Graphic Summary	Alignments	Taxonomy				
Sequences producing significant alignments							
Download Manage Columns Show 100							
select all 38 sequences selected							
GenBank Graphics Distance tree of results							
Description		Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
Cohnella sp. 18JY8-7 chromosome, complete genome		45.5	45.5	3%	9.3	90.62%	CP033433.1
PREDICTED: Leptonychotes weddellii sodium voltage-gated channel alpha subunit 10 (SCN10A), transcript variant X3, mRNA		44.6	44.6	2%	9.3	100.00%	XM_031028264.1
PREDICTED: Leptonychotes weddellii sodium voltage-gated channel alpha subunit 10 (SCN10A), transcript variant X2, mRNA		44.6	44.6	2%	9.3	100.00%	XM_031028263.1
Denticipes clupeioides genome assembly, chromosome: 2		44.6	44.6	4%	9.3	85.37%	LR535814.1
PREDICTED: Ursus arctos horribilis sodium voltage-gated channel alpha subunit 10 (SCN10A), transcript variant X3, mRNA		44.6	44.6	2%	9.3	100.00%	XM_026496749.1
PREDICTED: Ursus arctos horribilis sodium voltage-gated channel alpha subunit 10 (SCN10A), transcript variant X2, mRNA		44.6	44.6	2%	9.3	100.00%	XM_026496748.1
PREDICTED: Ursus arctos horribilis sodium voltage-gated channel alpha subunit 10 (SCN10A), transcript variant X1, mRNA		44.6	44.6	2%	9.3	100.00%	XM_026496747.1
PREDICTED: Eumetopias jubatus sodium voltage-gated channel alpha subunit 10 (SCN10A), transcript variant X3, mRNA		44.6	44.6	2%	9.3	100.00%	XM_028107096.1
PREDICTED: Eumetopias jubatus sodium voltage-gated channel alpha subunit 10 (SCN10A), transcript variant X2, mRNA		44.6	44.6	2%	9.3	100.00%	XM_028107095.1
PREDICTED: Eumetopias jubatus sodium voltage-gated channel alpha subunit 10 (SCN10A), transcript variant X1, mRNA		44.6	44.6	2%	9.3	100.00%	XM_028107093.1
PREDICTED: Zalophus californianus sodium voltage-gated channel alpha subunit 10 (SCN10A), transcript variant X3, mRNA		44.6	44.6	2%	9.3	100.00%	XM_027584952.1
PREDICTED: Zalophus californianus sodium voltage-gated channel alpha subunit 10 (SCN10A), transcript variant X2, mRNA		44.6	44.6	2%	9.3	100.00%	XM_027584951.1
PREDICTED: Zalophus californianus sodium voltage-gated channel alpha subunit 10 (SCN10A), transcript variant X1, mRNA		44.6	44.6	2%	9.3	100.00%	XM_027584950.1
PREDICTED: Puma concolor sodium voltage-gated channel alpha subunit 10 (SCN10A), transcript variant X3, mRNA		44.6	44.6	2%	9.3	100.00%	XM_025913005.1
PREDICTED: Puma concolor sodium voltage-gated channel alpha subunit 10 (SCN10A), transcript variant X2, mRNA		44.6	44.6	2%	9.3	100.00%	XM_025913004.1
PREDICTED: Puma concolor sodium voltage-gated channel alpha subunit 10 (SCN10A), transcript variant X1, mRNA		44.6	44.6	2%	9.3	100.00%	XM_025913003.1
PREDICTED: Callorhinus ursinus sodium voltage-gated channel alpha subunit 10 (SCN10A), transcript variant X3, mRNA		44.6	44.6	2%	9.3	100.00%	XM_025870906.1
PREDICTED: Callorhinus ursinus sodium voltage-gated channel alpha subunit 10 (SCN10A), transcript variant X2, mRNA		44.6	44.6	2%	9.3	100.00%	XM_025870897.1
PREDICTED: Callorhinus ursinus sodium voltage-gated channel alpha subunit 10 (SCN10A), transcript variant X1, mRNA		44.6	44.6	2%	9.3	100.00%	XM_025870888.1
PREDICTED: Felis catus sodium voltage-gated channel alpha subunit 10 (SCN10A), mRNA		44.6	44.6	2%	9.3	100.00%	XM_023260720.1
Thauera sp. K11 chromosome, complete genome		44.6	44.6	2%	9.3	100.00%	CP023439.1

Последовательность длины 100000.

Enter Query Sequence

BLASTN programs search nucleoti

Enter accession number(s), gi(s), or FASTA sequence(s)

Clear

Query subrange

From

To

Or, upload file

Browse...

seq10000.txt

Job Title

Nucleotide Sequence

Enter a descriptive title for your BLAST search

☐ Align two or more sequences

Choose Search Set

Database

☐ Human genomic + transcript

☐ Mouse genomic + transcript

☒ Others (nr etc.):

Nucleotide collection (nr/nt)

Organism

Optional

Enter organism name or id--completions will be suggested

☐ exclude

+

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

Exclude

Optional

☐ Models (XM/XP)

☐ Uncultured/environmental sample sequences

Limit to

Optional

☐ Sequences from type material

Entrez Query

Optional

Enter an Entrez query to limit search

YouTube

Create custom database

Program Selection

Optimize for

☐ Highly similar sequences (megablast)

☐ More dissimilar sequences (discontiguous megablast)

☒ Somewhat similar sequences (blastn)

Choose a BLAST algorithm

BLAST

Search database Nucleotide collection (nr/nt) using Blastn (Optimize for somewhat similar sequences)

☐ Show results in a new window

Query Length 100000

Other reports [Distance tree of results](#) [MSA viewer](#)

Filter

Reset

Descriptions

Graphic Summary

Alignments

Taxonomy

Sequences producing significant alignments

Download

Manage Columns

Show

100

☒ select all 9 sequences selected

[GenBank](#)

[Graphics](#)

[Distance tree of results](#)

	Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
<input checked="" type="checkbox"/>	Sphaeramia orbicularis genome assembly, chromosome: 14	53.6	53.6	0%	1.9	86.96%	LR597471.1
<input checked="" type="checkbox"/>	Sphaeramia orbicularis genome assembly, chromosome: 9	53.6	53.6	0%	1.9	86.96%	LR597466.1
<input checked="" type="checkbox"/>	Sphaeramia orbicularis genome assembly, chromosome: 7	53.6	160	0%	1.9	86.96%	LR597464.1
<input checked="" type="checkbox"/>	Sphaeramia orbicularis genome assembly, chromosome: 10	52.7	158	0%	6.5	85.42%	LR597467.1
<input checked="" type="checkbox"/>	Pan troglodytes BAC clone CH251-459G7 from chromosome 2, complete sequence	52.7	52.7	0%	6.5	87.80%	AC193898.3
<input checked="" type="checkbox"/>	Homo sapiens BAC clone RP11-549D18 from 2, complete sequence	52.7	52.7	0%	6.5	87.80%	AC010745.4
<input checked="" type="checkbox"/>	Protopolystoma xenopodis genome assembly, scaffold: PXEA_scaffold0005244	51.8	51.8	0%	6.5	93.94%	LM683862.1
<input checked="" type="checkbox"/>	Sphaeramia orbicularis genome assembly, chromosome: 20	51.8	51.8	0%	6.5	86.67%	LR597477.1
<input checked="" type="checkbox"/>	Thermotoga profunda AZM34c06 DNA, complete genome	51.8	51.8	0%	6.5	83.33%	AP014510.1