

BioInf Institute Algo. HW3

Sequence length 100

Parameters

blastnblastpblasttblastntblastx

Enter Query Sequence

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

Clear

Query subrange

From

To

Or, upload file random_g...e_100.txt

Job Title

Enter a descriptive title for your BLAST search

☐ Align two or more sequences

Choose Search Set

Database ☒ Standard databases (nr etc.): ☐ rRNA/ITS databases ☐ Genomic + transcript databases ☐ Betacoronavirus

Nucleotide collection (nr/nt)

Organism Optional ☐ 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 [Create custom database](#)

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 Megablast (Optimize for highly similar sequences)

☐ Show results in a new window

Algorithm parameters

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

General Parameters

Max target sequences

Select the maximum number of aligned sequences to display

Short queries ☒ Automatically adjust parameters for short input sequences

Expect threshold

Word size

Max matches in a query range

Scoring Parameters

Match/Mismatch Scores

Gap Costs

Filters and Masking

Filter ☒ Low complexity regions

☐ Species-specific repeats for:

Mask ☒ Mask for lookup table only

☐ Mask lower case letters

BLAST

Search database Nucleotide collection (nr/nt) using Megablast (Optimize for highly similar sequences)

☐ Show results in a new window

Results

BLAST® » blastn suite » results for RID-T2TYM6SB014

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< Edit Search

Save Search

Search Summary

How to read this report?

BLAST Help Videos

Back to Traditional Results Page

Job Title

Nucleotide Sequence

RID

T2TYM6SB014

Search expires on 10-23 19:07 pm

Download All

Program

BLASTN

Citation

Database

nt

See details

Query ID

lcl|Query_12595

Description

None

Molecule type

dna

Query Length

100

Other reports

Distance tree of results

MSA viewer

Filter Results

Organism

only top 20 will appear

☐ exclude

Type common name, binomial, taxid or group name

+ Add organism

Percent Identity

E value

Query Coverage

to

to

to

Filter

Reset

Descriptions

Graphic Summary

Alignments

Taxonomy

Sequences producing significant alignments

Download

Manage columns

Show

100

☒ select all

14 sequences selected

GenBank

Graphics

Distance tree of results

	Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
<input checked="" type="checkbox"/>	PREDICTED: Salmo trutta protodcadherin-18-like (LOC115187355) .transcript variant X2 .mRNA	43.7	43.7	33%	2.8	90.91%	XM_029746420.1
<input checked="" type="checkbox"/>	PREDICTED: Salmo trutta protodcadherin-18-like (LOC115187355) .transcript variant X1 .mRNA	43.7	43.7	33%	2.8	90.91%	XM_029746419.1
<input checked="" type="checkbox"/>	PREDICTED: Salmo salar protodcadherin-18-like (LOC106602138) .transcript variant X2 .mRNA	43.7	43.7	33%	2.8	90.91%	XM_014194607.1
<input checked="" type="checkbox"/>	PREDICTED: Salmo salar protodcadherin-18-like (LOC106602138) .transcript variant X1 .mRNA	43.7	43.7	33%	2.8	90.91%	XM_014194606.1
<input checked="" type="checkbox"/>	Caenorhabditis remanei hypothetical protein (CRE_11310) mRNA .complete cds	43.7	43.7	50%	2.8	79.63%	XM_003098056.1
<input checked="" type="checkbox"/>	PREDICTED: Phoenix dactylifera uncharacterized LOC103720610 (LOC103720610) .transcript variant X4 .mRNA	42.8	42.8	41%	2.8	84.09%	XM_008810402.2
<input checked="" type="checkbox"/>	PREDICTED: Phoenix dactylifera uncharacterized LOC103720610 (LOC103720610) .transcript variant X3 .mRNA	42.8	42.8	41%	2.8	84.09%	XM_008810401.2
<input checked="" type="checkbox"/>	PREDICTED: Phoenix dactylifera uncharacterized LOC103720610 (LOC103720610) .transcript variant X1 .mRNA	42.8	42.8	41%	2.8	84.09%	XM_026809816.1
<input checked="" type="checkbox"/>	Setaria viridis cultivar ME034v chromosome 7	41.9	41.9	25%	9.8	96.00%	CP050801.1
<input checked="" type="checkbox"/>	Pseudochaenichthys georgianus genome assembly .chromosome_12	41.0	41.0	33%	9.8	88.24%	LR792557.1
<input checked="" type="checkbox"/>	Pseudochaenichthys georgianus genome assembly .chromosome_5	41.0	41.0	33%	9.8	88.24%	LR792550.1
<input checked="" type="checkbox"/>	PREDICTED: Anolis carolinensis hdc homolog .cell cycle regulator (heca) .mRNA	41.0	41.0	32%	9.8	87.50%	XM_003223277.3
<input checked="" type="checkbox"/>	Desulfovibrio plezophilus C-1TLV30 complete genome	41.0	41.0	36%	9.8	82.50%	FO203427.1
<input checked="" type="checkbox"/>	Anas platyrhynchos genome assembly .chromosome_9	41.0	41.0	22%	9.8	100.00%	LS423619.1

Sequence length 1000

Parameters

blastn
blastp
blastx
tblastn
tblastx

Enter Query Sequence

Enter accession number(s), gi(s), or FASTA sequence(s)
Clear
Query subrange
From
To

Or, upload file
Выберите файл
random_g..._1000.txt

Job Title
Enter a descriptive title for your BLAST search

☐ Align two or more sequences

Choose Search Set

Database
Standard databases (nr etc.):
OrRNA/ITS databases
Genomic + transcript databases
Betacoronavirus
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

Algorithm parameters

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

General Parameters

Max target sequences
100
Select the maximum number of aligned sequences to display

Short queries
☒ Automatically adjust parameters for short input sequences

Expect threshold
♦ 10

Word size
11

Max matches in a query range
0

Scoring Parameters

Match/Mismatch Scores
2,-3

Gap Costs
Existence: 5 Extension: 2

Filters and Masking

Filter
☒ Low complexity regions
☐ Species-specific repeats for: Homo sapiens (Human)

Mask
☒ Mask for lookup table only
☐ Mask lower case letters

BLAST

Search database Nucleotide collection (nr/nt) using Blastn (Optimize for somewhat similar sequences)
☐ Show results in a new window

Results

BLAST® » blastn suite » results for RID-T2W1JWDH016

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← Edit Search

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Search Summary ▾

Job Title

Nucleotide Sequence

RID

T2W1JWDH016

Search expires on 10-23 19:42 pm

Download All ▾

Program

BLASTN ⓘ

Citation ▾

Database

nt

See details ▾

Query ID

lcl|Query_10917

Description

None

Molecule type

dna

Query Length

1000

Other reports

Distance tree of results

MSA viewer ⓘ

How to read this report? ⓘ

BLAST Help Videos ⓘ

Back to Traditional Results Page ⓘ

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

Descriptions

Graphic Summary

Alignments

Taxonomy

Sequences producing significant alignments

Download ▾

Manage columns ▾

Show

100 ▾

 ⓘ

☒ select all

1 sequences selected

GenBank

Graphics

Distance tree of results

	Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
<input checked="" type="checkbox"/>	Streptomyces lunaealactis strain MM109 chromosome, complete genome	48.2	48.2	3%	0.99	88.89%	CP026304.1

Sequence length 10000

Parameters

blastn
blastp
blastx
tblastn
tblastx

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Выберите файл
random_g...00000.txt

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☐ Uncultured/environmental sample sequences

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Optional
☐ Sequences from type material

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YouTube
Create custom database

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☒ Somewhat similar sequences (blastn)
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Search database Nucleotide collection (nr/nt) using Blastn (Optimize for somewhat similar sequences)
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Algorithm parameters
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General Parameters

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100
Select the maximum number of aligned sequences to display

Short queries
☒ Automatically adjust parameters for short input sequences

Expect threshold
♦ 100

Word size
11

Max matches in a query range
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Scoring Parameters

Match/Mismatch Scores
2,-3

Gap Costs
Existence: 5 Extension: 2

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BLAST
Search database Nucleotide collection (nr/nt) using Blastn (Optimize for somewhat similar sequences)
☐ Show results in a new window

Results

[< Edit Search](#) [Save Search](#) [Search Summary](#) [?](#)

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Job Title	Nucleotide Sequence		
RID	T2WCE6A4014	Search expires on 10-23 19:48 pm	Download All ▼
Program	BLASTN	?	Citation ▼
Database	nt	See details ▼	
Query ID	Ic Query_21049		
Description	None		
Molecule type	dna		
Query Length	100000		
Other reports	Distance tree of results		

Filter Results

Organism only top 20 will appear ☐ exclude

[+ Add organism](#)

Percent Identity
 to

E value
 to

Query Coverage
 to

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

Descriptions [Graphic Summary](#) [Alignments](#) [Taxonomy](#)

Sequences producing significant alignments		Download ▼		Manage columns ▼		Show	100 ▼	?
<input checked="" type="checkbox"/> select all	67 sequences selected	GenBank		Graphics		Distance tree of results		
	Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession	
<input checked="" type="checkbox"/>	Stenotrophomonas sp. YAU14A_MKIM14_1 chromosome	59.0	59.0	0%	0.057	86.00%	CP025998.1	
<input checked="" type="checkbox"/>	Stenotrophomonas sp. ZAC14D2_NAIM14_7 chromosome	59.0	59.0	0%	0.057	86.00%	CP025995.1	
<input checked="" type="checkbox"/>	Stirosoma radiotolerans strain DG5A_complete genome	57.2	57.2	0%	0.20	90.24%	CP010429.1	
<input checked="" type="checkbox"/>	Erineophilus fuscoopulatus DNA_LG7_complete sequence	55.4	55.4	0%	0.69	84.91%	AP022681.1	
<input checked="" type="checkbox"/>	Lateolabrax maculatus linkage group_12 sequence	54.5	54.5	0%	2.4	90.00%	CP032586.1	
<input checked="" type="checkbox"/>	Lateolabrax maculatus chromosome_Lm5	54.5	108	0%	2.4	90.00%	CP027266.1	
<input checked="" type="checkbox"/>	Stenotrophomonas sp. SAU14A_NAIM14_8 chromosome	54.5	54.5	0%	2.4	84.00%	CP025999.1	
<input checked="" type="checkbox"/>	Stenotrophomonas sp. YAU14D1_LEIMI4_1 chromosome	54.5	54.5	0%	2.4	84.00%	CP025997.1	
<input checked="" type="checkbox"/>	Aspergillus tanneri uncharacterized protein (ATNH1004_003184)_partial mRNA	53.6	53.6	0%	2.4	94.12%	XM_033567863.1	
<input checked="" type="checkbox"/>	Stenotrophomonas sp. NA06056_chromosome_complete genome	51.8	51.8	0%	8.4	78.69%	CP054931.1	
<input checked="" type="checkbox"/>	Canis lupus familiaris breed Labrador retriever chromosome 24a	50.9	50.9	0%	29	82.00%	CP050588.1	
<input checked="" type="checkbox"/>	Canis lupus familiaris breed Labrador retriever chromosome 24b	50.9	50.9	0%	29	82.00%	CP050543.1	
<input checked="" type="checkbox"/>	PREDICTED: Anopheles gambiae epidermal growth factor receptor substrate 15-like 1 (LOC108904746)_mRNA	50.9	50.9	0%	29	96.67%	XM_018707416.2	
<input checked="" type="checkbox"/>	Corynebacterium striatum strain 216 chromosome_complete genome	50.9	50.9	0%	29	88.10%	CP024932.1	
<input checked="" type="checkbox"/>	Corynebacterium striatum strain 215 chromosome_complete genome	50.9	50.9	0%	29	88.10%	CP024931.1	
<input checked="" type="checkbox"/>	PREDICTED: Canis lupus familiaris DSN1 homolog_MIS12 kinetochore complex component (DSN1)_transcript variant X7_mRNA	50.9	50.9	0%	29	82.00%	XM_022409280.1	
<input checked="" type="checkbox"/>	PREDICTED: Canis lupus familiaris DSN1 homolog_MIS12 kinetochore complex component (DSN1)_transcript variant X3_mRNA	50.9	50.9	0%	29	82.00%	XM_022409279.1	
<input checked="" type="checkbox"/>	Corynebacterium striatum strain KC-Na-01_complete genome	50.9	50.9	0%	29	88.10%	CP021252.1	