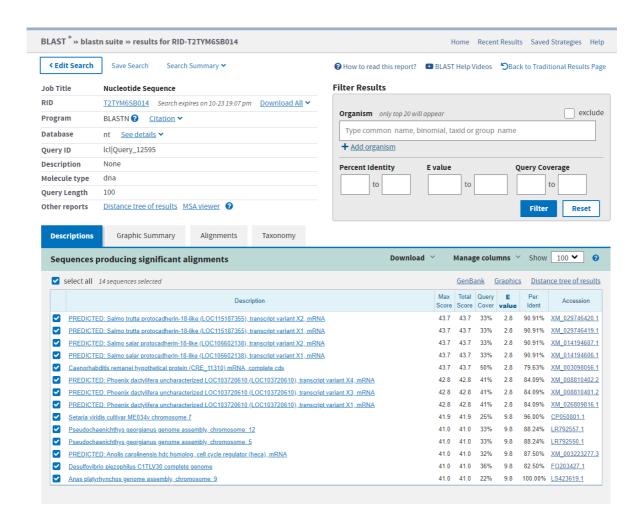
BioInf Institute Algo. HW3

Sequence length 100

Parameters

blastn blastp blastx	tblastn tblastx
Busin Busin	Windows Windows
Enter Query Sec	quence
Enter accession nun	nber(s), gi(s), or FASTA sequence(s) Query subrange
	From
	То
Or, upload file	Выберите файл random_ge_100.txt 😣
Job Title	Dalvephrie wanti Talluolii ge_100.0xt
	Enter a descriptive title for your BLAST search 😡
☐ Align two or more	sequences 9
Choose Search	Set
Database	Standard databases (nr etc.): OrRNA/ITS databases OGenomic + transcript databases OBetacoronavirus OGENOMIC + transcript databases OBetacoronavirus
	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	☐ Sequences from type material
Optional Entrez Query	You Tube Create custom database
Optional	Enter an Entrez query to limit search 🚇
Program Selection	on
Optimize for	O Highly similar sequences (megablast)
	O More dissimilar sequences (discontiguous megablast)
	Somewhat similar sequences (blastn) Choose a BLAST algorithm
	One of a DEAT ago in in the
BLAST	Search database Nucleotide collection (nr/nt) using Megablast (Optimize for highly similar sequences) Show results in a new window
Algorithm paramete	Note: Parameter values that differ from the default are highlighted in yellow and marked with * sign
General Parar	
Max target sequences	Select the maximum number of aligned sequences to display 🚇
Short queries	☑ Automatically adjust parameters for short input sequences ⊌
	Automatically adjust parameters for short input sequences
Expect threshold	+ 10
Word size	♦ ▼ 9
Max matches in a	
query range	0
Scoring Paran	neters
Match/Mismatch	
Scores	◆ [2,-3 ♥]
Gap Costs	Linear ▼ ⊌
Filters and Ma	sking
Filter	
Tittel	✓ Low complexity regions □ Species-specific repeats for: Homo sapiens (Human) ✓ ⊌
Mask	✓ Mask for lookup table only ⊌
	Mask lower case letters
DIACT	Search database Nucleotide collection (nr/nt) using Megablast (Optimize for highly similar sequences)
BLAST	Show results in a new window

Results

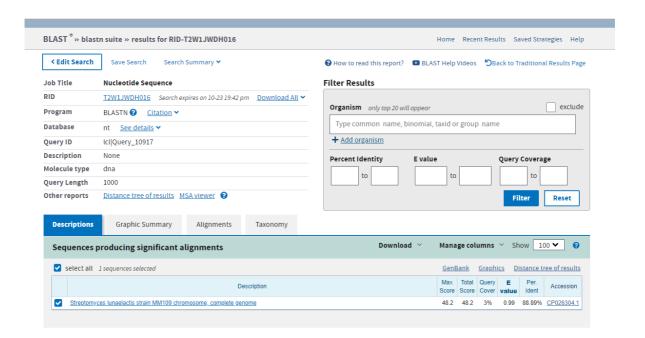


Sequence length 1000

Parameters

blastn blastp blastx	tblastn tblastx
Enter Query Seq	
Enter accession num	nber(s), gi(s), or FASTA sequence(s) Clear Query subrange From
	To
Or, upload file	Выберите файл random_g1000.txt 🕑
Job Title	
	Enter a descriptive title for your BLAST search 🚇
☐ Align two or more	sequences 🚇
Choose Search S	Set
Database	●Standard databases (nr etc.): OrRNA/ITS databases OGenomic + transcript databases OBetacoronavirus
	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	□ Sequences from type material
Optional Entrez Query	You Tobs Create custom database
Optional	Enter an Entrez query to limit search 😡
Program Selection	n
Optimize for	O Highly similar sequences (megablast)
	O More dissimilar sequences (discontiguous megablast)
	Somewhat similar sequences (blastn) Change 30 ACT startistics
	Choose a BLAST algorithm (a)
BLAST	Search database Nucleotide collection (nr/nt) using Blastn (Optimize for somewhat similar sequences) Show results in a new window
Algorithm parameter	Note: Parameter values that differ from the default are highlighted in yellow and marked with + sign
General Paran	netere
Max target	100 V
sequences	Select the maximum number of aligned sequences to display 📵
Short queries	☑ Automatically adjust parameters for short input sequences
Expect threshold	
Expect till colloid	♦ <u>10</u>
Word size	11 🗸 🚇
Max matches in a query range	0
Scoring Param	neters
Match/Mismatch	
Scores	2,3 ♥ ₩
Gap Costs	Existence: 5 Extension: 2 ✓ 🥹
Filters and Ma	Sking
Filter	
Titol	☑ Low complexity regions ⊎ ☐ Species-specific repeats for: Homo sapiens (Human) ✓ ⊌
Mask	☑ Mask for lookup table only ⊌
	☐ Mask lower case letters
DIACT	Search database Nucleotide collection (nr/nt) using Blastn (Optimize for somewhat similar sequences)
BLAST	Search database Nucleotide collection (nr/nt) using Blastn (Optimize for somewhat similar sequences) Show results in a new window

Results



Sequence length 10000

Parameters

hlastn hlastn hlasty	thlastn thlastv	
blastn blastp blastx tblastx tblastx		
Enter Query Seq	uence	
Enter accession nun	nber(s), gi(s), or FASTA sequence(s) 🚇 Clear Query subrange 🚇	
	From	
	То	
Or, upload file	Выберите файл random_g00000.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 OGenomic + transcript databases OBetacoronavirus	
	Nucleotide collection (nr/nt)	
Organism		
Optional	Enter organism name or id—completions will be suggested ————————————————————————————————————	
	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	You Tibbs Create custom database Enter an Entrez query to limit search	
Program Selection	on	
Optimize for	O Highly similar sequences (megablast)	
	O 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 parameter	Note: Parameter values that differ from the default are highlighted in yellow and marked with * sign	
0 10		
General Paran	neters	
Max target sequences	Select the maximum number of aligned sequences to display 🚇	
Short queries	☑ Automatically adjust parameters for short input sequences ⊌	
Expect threshold	♦ 100 3	
Word size	11 V (i)	
Max matches in a		
query range		
Scoring Param	neters	
Match/Mismatch	2,3 ▼ 🚇	
Scores Gap Costs	Existence: 5 Extension: 2 🗸 🥹	
Sup costs	Existence, 3 Extension, 2 ♥	
Filters and Ma	sking	
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

