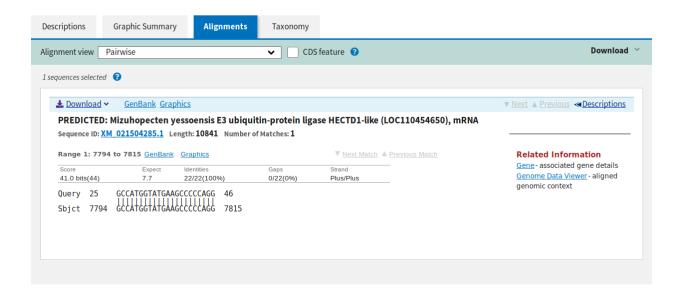
## Задание 3.

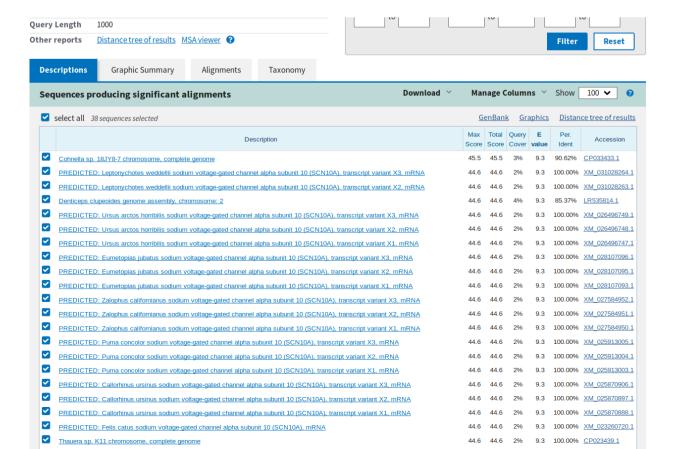
## Последовательность длины 10.

Enter Query Sequence  Enter accession number(s), gl(s), or FASTA sequence(s)   ATMACHICITY (CONTINUE CONTINUE C		Standard Nucleotide BLAS
Enter accession number(s), gl(s), or FASTA sequence(s)    ATAMAMACTICISTIGNCCACCOCCACGATAGAAGCCCCCAGGATAGAAGCCCCCCAGGATAGAAGCCCCCCAGGATAGAAGCCCCCCAGGATAGAAGCCCCCCGCCTCTAGCAGCCCCCCCC	blastn blastp bl	astx tblastn tblastx tblastx
Enter accession number(s), gi(s), or FASTA sequence(s)	Enter Ouery S	BLASTN programs search nucleotide databases using a
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 common name, binomial, or tax id. Only 20 top taxa will be shown  Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown  Sequences from type material  Ditting  Exclude Optional Enter Optional Enter organism common tax id. Only 20 top taxa will be shown  Exclude Optional Enter organism common tax id. Only 20 top taxa will be shown  Exclude Optional Enter organism common tax id. Only 20 top taxa will be shown  Exclude Optional Enter Optional Enter Optional Enter Optional Enter Optional Enter Align two or more sequences (megablast)  More dissimilar sequences (megablast)  More dissimilar sequences (discontiguous megablast)		
Or, upload file Browse No file selected.  Job Title Enter a descriptive title for your BLAST search  Choose Search Set Choose Search Set Nucleotide collection (nr/nt)   Organism Optional Enter organism name or idcompletions will be suggested Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown  Exclude Optional Chinit to Optional Sequences from type material Sequences from type material Entrez Query Optional Enter an Entrez query to limit search  To  To  To  To  To  To  Others (nr etc.):  Nucleotide collection (nr/nt)  We exclude optional exclude exclu	AATAACAACTCTGTTGACC	ASTATTS2ST239AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
Or, upload file  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 idcompletions will be suggested Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown   Exclude Optional Limit to Optional Entrez Query Optional Enter an Entrez query to limit search   Program Selection  Optimize for  Highly similar sequences (discontiguous megablast)  More dissimilar sequences (discontiguous megablast)	CTGCGGCACGGTGATGCAA	ATCTCGAGCGACG From
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 idcompletions will be suggested Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown   Exclude Optional  Limit to Optional  Limit to Optional  Limit to Optional  Entrez Query Optional  Entrez Query Optional  Entrez Query Optional  Highly similar sequences (megablast)  More dissimilar sequences (discontiguous megablast)		То
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Align two or more sequences	Or, upload file	Browse No file selected
Enter a descriptive title for your BLAST search   Align two or more sequences   Choose Search Set  Database	Job Title	No line selected.
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More dissimilar sequences (discontiguous megablast)		
	Opanii Ze ioi	
Somewhat similal sequences (blastif)		
Choose a BLAST algorithm (a)		
Choose a bench algorium w		Citoose a DEAGT algorithm &
DI ACT Coreh database Musicotide collection (nr/nt) using Blasta (Ontimize for computat similar seguences)	DIACT	Coarch database Muslootide collection (print) using Blacta (Ontimize for computed similar cognitions)



## Последовательность длины 1000.

blastn blastp bl	astx tblastn tblastx	
Enter Query Sequence BLASTN programs search nucleotide		
	umber(s), gi(s), or FASTA sequence(s)   Clear Query subrange   From To	
Or, upload file  Job Title  Align two or mo	Browse seq1000.txt   Enter a descriptive title for your BLAST search   ore sequences	
Choose Search Set		
Organism Optional	O Human genomic + transcript O Mouse genomic + transcript O Others (nr etc.):  Nucleotide collection (nr/nt) ✓   Enter organism name or idcompletions will be suggested   exclude   exclude	
Exclude Optional Limit to	Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown   Models (XM/XP) Uncultured/environmental sample sequences  Sequences from type material	
Optional Entrez Query Optional	You Tube Create custom database  Enter an Entrez query to limit search	
Program Selec	ction	
Optimize for	<ul> <li>Highly similar sequences (megablast)</li> <li>More dissimilar sequences (discontiguous megablast)</li> <li>Somewhat similar sequences (blastn)</li> <li>Choose a BLAST algorithm </li> </ul>	
BLAST	Search database Nucleotide collection (nr/nt) using Blastn (Optimize for somewhat similar sequences)  Show results in a new window	



## Последовательность длины 100000.

