

- 1) Explain PAM and BLOSUM scoring matrices.
 - a) What kind of biological information they are built upon?
 - b) Explain the difference between PAM250 and PAM500 and the difference between BLOSUM62 and BLOSUM95.
- 2) You will see 5 sequences. Use blastn to answer the following questions. Add screenshots to your assignment.
 - a) Align sequence_1 to sequence_DB, comment on the scores and the dotplot.
 - b) Align sequence_2 to sequence_DB, comment on the scores and the dotplot.
 - c) Align sequence_3 to sequence_DB, comment on the scores and the dotplot.
 - d) Align sequence_4 to sequence_DB, comment on the scores and the dotplot.
- 3) Use “unknown.fasta” and search for the source using NCBI BLAST, UCSC BLAT, and Ensembl BLAST/BLAT.
 - a) Share the list of the results. Write down the name and the type (gene, transcript, etc.) of the source.
 - b) Select the top scoring hit (both in terms of E-Value and score). Click on the link that will direct you to the genome browser on each database. Share a screenshot from each genome browser.

- 4) Use “protein.fasta” and run a search using BLAST and PSI-BLAST.
 - a) How many hits there are in both results?
 - b) From the results list, select the last five hits (uncheck all checkboxes and go to the bottom of the list and select the last five). After that, go to the “alignments” tab. From the “Alignment View” drop-down menu, select “Flat query-anchored with dots for identities”. Do this for both BLAST and PSI-BLAST. Compare the results and comment on the differences.

PAM= Percent Accepted Mutations (replacement of single amino acids): Based on global alignments of the sequences, these alignments have high similarity (at least 85 % identity) comparing to the BLOSUM , in these matrices mutations are very significant, and higher numbers show greater distance in the evolutionary pathway. In each row & column, 20 standard amino acids are represented.

BLOSUM= Blocks Substitution Matrix: Based on the local alignments of the sequences, it represent highly-conserved regions, high numbers represent smaller evolutionary distance. It is a substitution matrix that is for sequence alignments of proteins.

In PAM matrices, each 1 PAM represents a 1% change in amino acids (observed mutation frequencies). PAM 250 represents nearly 250 mutation for per 100 amino acid can be occur. Therefore, each time the PAM matrix increases in number, its evolutionary similarity decreases (PAM250>PAM 500 in terms of identity), PAM 500=500 mutations per 100 residues. Greater numbers==bigger evolutionary distance.

BLOSUM 62 is a matrix designed for BLAST. It is designed to detect approximately 25% identity. The logic of BLOSUM matrices is inverse of PAM, so as the number of BLOSUM matrix increases, identity increases, ie BLOSUM95>BLOSUM62, in terms of identity. Because the numbers in BLOSUM represent percent of sequence identity. In other words, there is 95 percent identity similarity in BLOSUM 95.

2.

[BOOKMARK](#)

Enter Query Sequence

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

Query subrange [?](#)

From

To

Or, upload file

sequence_1.fasta [?](#)

Job Title

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

Align two or more sequences [?](#)

Enter Subject Sequence

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

[Clear](#) Subject subrange [?](#)

From

To

Or, upload file

sequence_DB.fasta [?](#)

Program Selection

Optimize for

- Highly similar sequences (megablast)
- More dissimilar sequences (discontiguous megablast)
- Somewhat similar sequences (blastn)

Choose a BLAST algorithm [?](#)

New columns added to the Description Table

Click 'Select Columns' or 'Manage Columns'.



Format Request

Job Title: sequence_1

Request ID	U4MSRSSV114
Status	Searching
Time since submission	00:00:00

This page will be automatically updated in 1 seconds until search is done



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Job Title	sequence_1	Filter Results			
RID	U4MSRSSV114 <small>Search expires on 11-28 22:47 pm</small> Download All ▾	Percent Identity	<input type="text"/> to <input type="text"/>	E value	<input type="text"/> to <input type="text"/>
Program	Blast 2 sequences Citation ▾	Query Coverage	<input type="text"/> to <input type="text"/>	Filter	Reset
Query ID	Icl Query_5523 (dna)				
Query Descr	sequence_1				
Query Length	281340				
Subject ID	Icl Query_5525 (dna)				
Subject Descr	Database				
Subject Length	411120				
Other reports	MSA viewer ?				

max score: highest alignment score btw query && db sequence

total score: sum up the alignments btw query && db sequence- overall segments
high total score: extensive alignment
Dot Plot

lower E (Expect) value (closer to zero)== significant match

Screenshots illustrating the results of a sequence search:

Top navigation bar: Descriptions, Graphic Summary, Alignments, Dot Plot.

Section: Sequences producing significant alignments.

Filter: select all 1 sequences selected.

Table headers: Description, Scientific Name, Max Score, Total Score, Query Cover, E value, Per. Ident, Acc. Len, Accession.

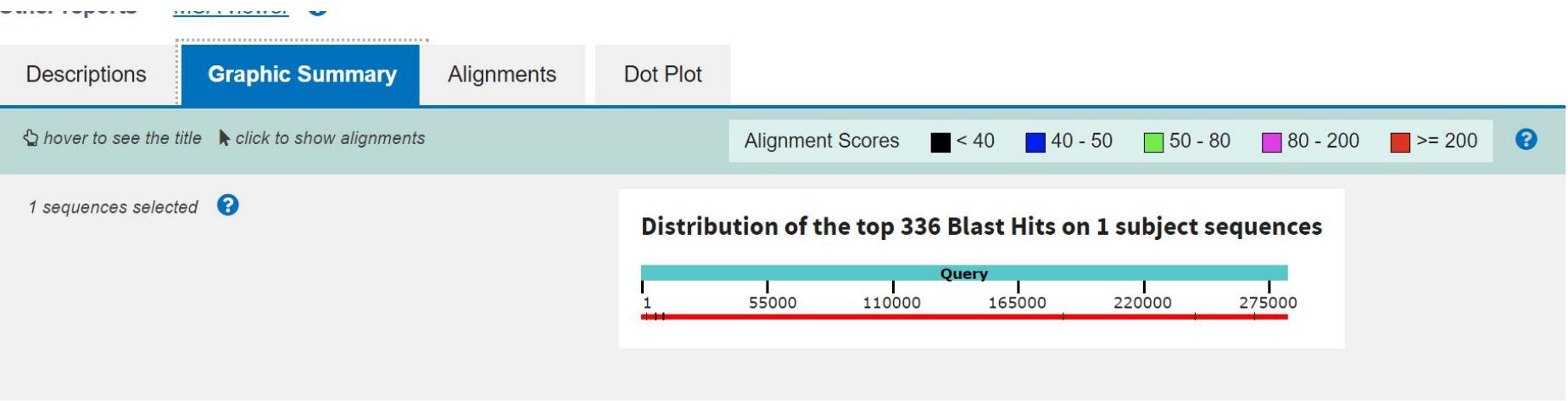
Row data: Database, 3.203e+05, 5.997e+05, 100%, 0.0, 100.00%, 411120, Query_5525.

Annotations:

- A red box highlights the "E value" column header.
- A red arrow points from the "E value" column header to the "E value" cell in the table row.
- A red box highlights the "Per. Ident" column header.
- A red arrow points from the "Per. Ident" column header to the "Per. Ident" cell in the table row.



identity percent btw sequences



1 sequences selected

[Download](#) ▾[Graphics](#)

Sort by:

E value



▼ Next ▲ Previous



Database

Sequence ID: Query_5525 Length: 411120 Number of Matches: 336

Range 1: 15821 to 189280 [Graphics](#)[▼ Next Match](#) [▲ Previous Match](#)

	Score 3.203e+05 bits(173460)	Expect 0.0	Identities 173460/173460(100%)	Gaps 0/173460(0%)	Strand Plus/Plus	
Query	9731	TACAGTAGCCAAAACAGCATGGTATTGGTACATAGACATATAGACCAATGGAACAGAATA			9790	
Sbjct	15821	TACAGTAGCCAAAACAGCATGGTATTGGTACATAGACATATAGACCAATGGAACAGAATA			15880	
Query	9791	GAGAACTCAGAAATAAGCCACACACCTACAGCCATCTGATCATCAATAAAATCAACAAA			9850	
Sbjct	15881	GAGAACTCAGAAATAAGCCACACACCTACAGCCATCTGATCATCAATAAAATCAACAAA			15940	
Query	9851	AATATGCCATGGGAAAAGACTTCATATTCAATAATGGCACAGGGATACTGGCTCCCCA			9910	
Sbjct	15941	AATATGCCATGGGAAAAGACTTCATATTCAATAATGGCACAGGGATACTGGCTCCCCA			16000	
Query	9911	TATGCAGAGGAATGAAGTCAGACTCCTATCTATCACCATAACAAAAATTAAAGACAGAT			9970	
Sbjct	16001	TATGCAGAGGAATGAAGTCAGACTCCTATCTATCACCATAACAAAAATTAAAGACAGAT			16060	
Query	9971	TAGACGTGGCCAGGCACAGTGGCTCATGCCTGTAATCCTAGCACTTGGGAGGCCAAGGT			10030	
Sbjct	16061	TAGACGTGGCCAGGCACAGTGGCTCATGCCTGTAATCCTAGCACTTGGGAGGCCAAGGT			16120	
Query	10021	CCCTCCATCATCCCCCTCAGCACTTTACACCACTTCCCCAACCTCTCAACCCCCATCT			10080	

deletions (exists in db sequence but not exist in query seq) (db seq== y axis, query seq==x axis)

Descriptions

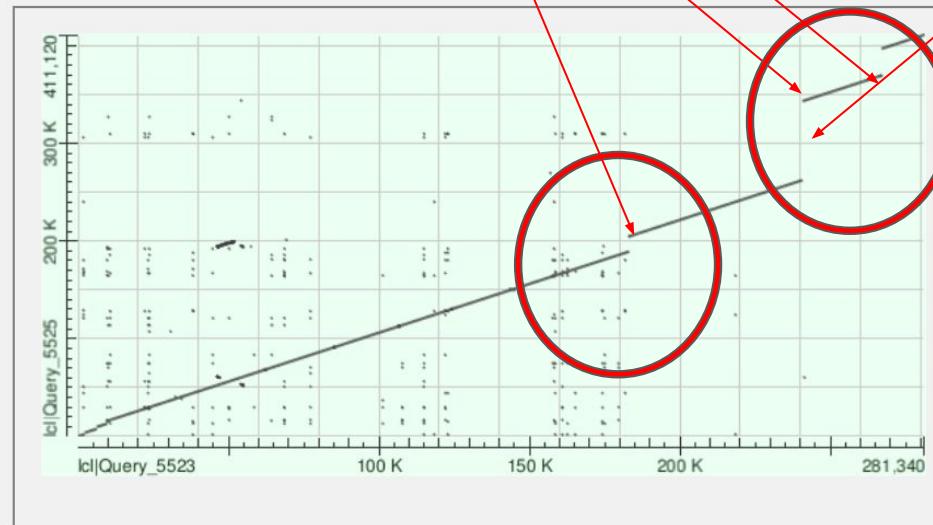
Graphic Summary

Alignments

Dot Plot

deletion size is bigger in this comparing to the other two

Plot of lcl|Query_5523 vs lcl|Query_5525 ?



[blastn](#)[blastp](#)[blastx](#)[tblastn](#)[tblastx](#)

Align Sequences Nucleotide BLAST

BLASTN programs search nucleotide subjects using a nucleotide 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

Dosya Seç sequence_2.fasta [?](#)

Job Title

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

Align two or more sequences [?](#)

New columns added to the Description Table

Click 'Select Columns' or 'Manage Columns'.



Enter Subject Sequence

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

Subject subrange [?](#)

From

To

Or, upload file

Dosya Seç sequence_DB.fasta [?](#)

Program Selection

Optimize for

- Highly similar sequences (megablast)
 More dissimilar sequences (discontiguous megablast)

Format Request**Job Title:** sequence_2

Request ID

U543G3S8114

Status

Searching

Time since submission

00:00:00

This page will be automatically updated in **1** seconds until search is done[Blog](#)[Support Center](#)

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Job Title	sequence_2
RID	U543G3S8114 Search expires on 11-29 03:09 am Download All ▾
Program	Blast 2 sequences Citation ▾
Query ID	Icl Query_40969 (dna)
Query Descr	sequence_2
Query Length	655420
Subject ID	Icl Query_40971 (dna)
Subject Descr	Database
Subject	411120
Length	
Other reports	MSA viewer ?

Filter Results

Percent Identity

 to

E value

 to

Query Coverage

 to [Filter](#)[Reset](#)[Descriptions](#)[Graphic Summary](#)[Alignments](#)[Dot Plot](#)

max score: highest alignment score btw query && db sequence

total score: sum up the alignments btw query && db sequence- overall segments
high total score: extensive alignment

lower E (Expect) value (closer to zero)== significant match

Other reports [MSA viewer](#) ?

Descriptions	Graphic Summary	Alignments	Dot Plot	Download	Select columns	Show 100	?
Sequences producing significant alignments							
<input checked="" type="checkbox"/> select all 1 sequences selected	Description	Scientific Name	Max Score	Total Score	E value	Per. Ident	Graphics MSA Viewer
<input checked="" type="checkbox"/> Database			6.081e+05	1.409e+06	100%	0.0	100.00% 411120 Query_40971

identity percent btw sequences

Length

Other reports [MSA viewer](#) [?](#)

Descriptions

Graphic Summary

Alignments

Dot Plot

hover to see the title click to show alignments

Alignment Scores < 40 40 - 50 50 - 80 80 - 200 >= 200

?

1 sequences selected [?](#)

Distribution of the top 822 Blast Hits on 1 subject sequences



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Alignment view

Pairwise



CDS feature

[Restore defaults](#)[Download](#) ▾

1 sequences selected

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Sort by:

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Database

Sequence ID: **Query_40971** Length: **411120** Number of Matches: **822**Range 1: 1 to 329280 [Graphics](#)[▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Identities	Gaps	Strand
6.081e+05 bits(329280)	0.0	329280/329280(100%)	0/329280(0%)	Plus/Plus
Query 1	TGCAGCCATGAAAAAGAATAAAACCATGTCATCTGCAGCAACATGGGTCCAGCTGGACAC	60		
Sbjct 1	TGCAGCCATGAAAAAGAATAAAACCATGTCATCTGCAGCAACATGGGTCCAGCTGGACAC	60		
Query 61	CATTATCCTAACGAAATTAACTGAGGAACCGGAAAACCAAATACCACATGTTCTCACTTAT	120		
Sbjct 61	CATTATCCTAACGAAATTAACTGAGGAACCGGAAAACCAAATACCACATGTTCTCACTTAT	120		
Query 121	AAGTGGGAAAGTGGGAACTAAATGATGGGTGCTCATAGACATAGAGGGACAACAATAGAC	180		
Sbjct 121	AAGTGGGAAAGTGGGAACTAAATGATGGGTGCTCATAGACATAGAGGGACAACAATAGAC	180		
Query 181	ACTGGGGACTGGTAGATGGTGGGGGAGCAAGCGTTGAAAACATTGGCTACCATTGTCA	240		
Sbjct 181	ACTGGGGACTGGTAGATGGTGGGGGAGCAAGCGTTGAAAACATTGGCTACCATTGTCA	240		
Query 241	CTATCTGGGTGATGGGATCATCCATACCCCCAACCTCAGCATCACGCAATATAACCTATGT	300		

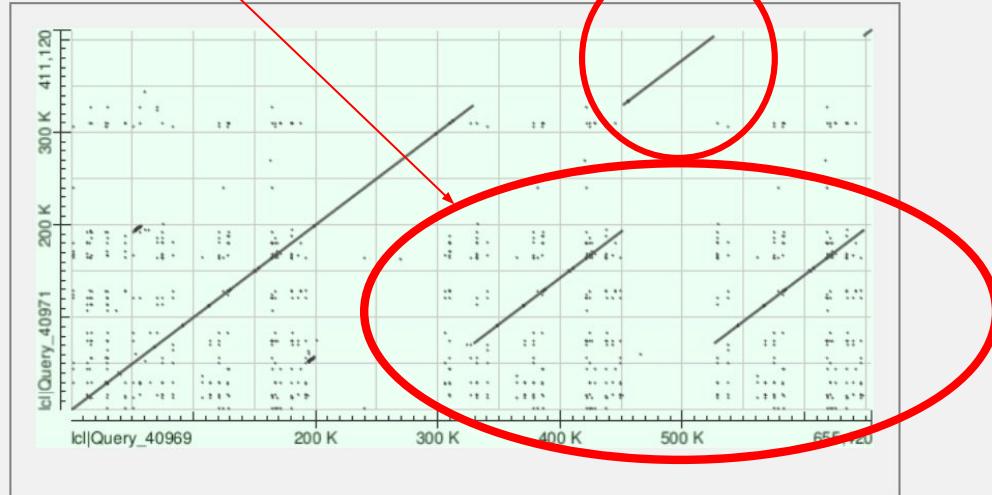


duplications: the second (right) duplication occurs after the insertion event, includes insertion part also

insertion

Descriptions Graphic Summary Alignments Dot Plot

Plot of lcl|Query_40969 vs lcl|Query_40971 ?



blastn

blastp

blastx

tblastn

tblastx

Align Sequences Nucleotide BLAST

BLASTN programs search nucleotide subjects using a nucleotide query. [more...](#)[Reset page](#)

E

Enter Query Sequence

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

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Dosya Seç sequence_3.fasta [?](#)

Job Title

Enter a descriptive title for your BLAST search [?](#) Align two or more sequences [?](#)**New columns added to the Description Table**

Click 'Select Columns' or 'Manage Columns'.

Enter Subject Sequence

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

Or, upload file

Dosya Seç sequence_DB.fasta [?](#)

Format Request

Job Title: sequence_3

Request ID	U54P604M11N
Status	Searching
Time since submission	00:00:00

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Query ID Icl|Query_243553 (dna)

Query Descr sequence_3

Query Length 411120

Subject ID Icl|Query_243555 (dna)

Subject Descr Database

Subject 411120

Length

Other reports [MSA viewer](#) [?](#)**Filter Results**

Percent Identity

 to

E value

 to

Query Coverage

 to **Filter****Reset****Descriptions**[Graphic Summary](#)[Alignments](#)[Dot Plot](#)**Sequences producing significant alignments**[Download](#) ▾[New Select columns](#) ▾[Show](#)

100 ▾

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max score: highest alignment score btw query && db sequence

total score: sum up the alignments btw query && db sequence- overall segments
high total score: extensive alignment

lower E (Expect) value (closer to zero)== significant match

The screenshot shows a web-based search results page for protein sequences. At the top, there are tabs for 'Descriptions', 'Graphic Summary', 'Alignments', and 'Dot Plot'. Below the tabs, a green header bar displays the title 'Sequences producing significant alignments', download and select column options, and a 'Show 100' dropdown. A red arrow points from the 'max score' text to the 'Max Score' column in the table. Another red arrow points from the 'total score' text to the 'Total Score' column. A red circle highlights the 'E value' column, with a red arrow pointing from the 'lower E (Expect) value' text to it. A red arrow also points from the 'identity percent' text to the 'Per. Ident' column.

Sequences producing significant alignments								
<input checked="" type="checkbox"/> select all 1 sequences selected		Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident
<input checked="" type="checkbox"/>	Database			3.758e+05	8.628e+05	100%	0.0	100.00%

identity percent btw sequences

Other reports [MSA viewer](#) [?](#)

Descriptions

Graphic Summary

Alignments

Dot Plot

ⓘ hover to see the title ⚡ click to show alignments

Alignment Scores █ < 40 █ 40 - 50 █ 50 - 80 █ 80 - 200 █ >= 200

?

1 sequences selected [?](#)

Distribution of the top 409 Blast Hits on 1 subject sequences



Alignment view [Pairwise](#) CDS feature [Restore defaults](#)[Download](#)

1 sequences selected

[Download](#) [Graphics](#) [Sort by:](#) E value [▼ Next](#) [▲ Previous](#) [◀ Descriptions](#)

Database

Sequence ID: **Query_243555** Length: **411120** Number of Matches: **409**Range 1: 123551 to 327040 [Graphics](#)[▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Identities	Gaps	Strand	
3.758e+05 bits(203490)	0.0	203490/203490(100%)	0/203490(0%)	Plus/Plus	
Query 1		CTGATTTCCCCTGGTTGAGGTTGAGGGTCCAGGGTCTGTCTGCCATAATGACAAGATT		60	
Sbjct 123551		CTGATTTCCCCTGGTTGAGGTTGAGGGTCCAGGGTCTGTCTGCCATAATGACAAGATT		123610	
Query 61		CAGTACCAATAGCGAACGCCGTCACTGGCAGTGACTGTGCCTTAGGGTGTCCCGTTGGCAT		120	
Sbjct 123611		CAGTACCAATAGCGAACGCCGTCACTGGCAGTGACTGTGCCTTAGGGTGTCCCGTTGGCAT		123670	
Query 121		CCAGGGCCCCCGTGAAGGATGGCACCGAGCACCAATTCAACATAAGTCTTCAGCGTTC		180	
Sbjct 123671		CCAGGGCCCCCGTGAAGGATGGCACCGAGCACCAATTCAACATAAGTCTTCAGCGTTC		123730	
Query 181		CGATGAAACAAGATTAGGGGAATTTACAGCTTGCTGTGTTTCCACCCAGGGCCCTT		240	



translocation: changed the position, beginning moved to the end

insertion

Other reports MSA viewer

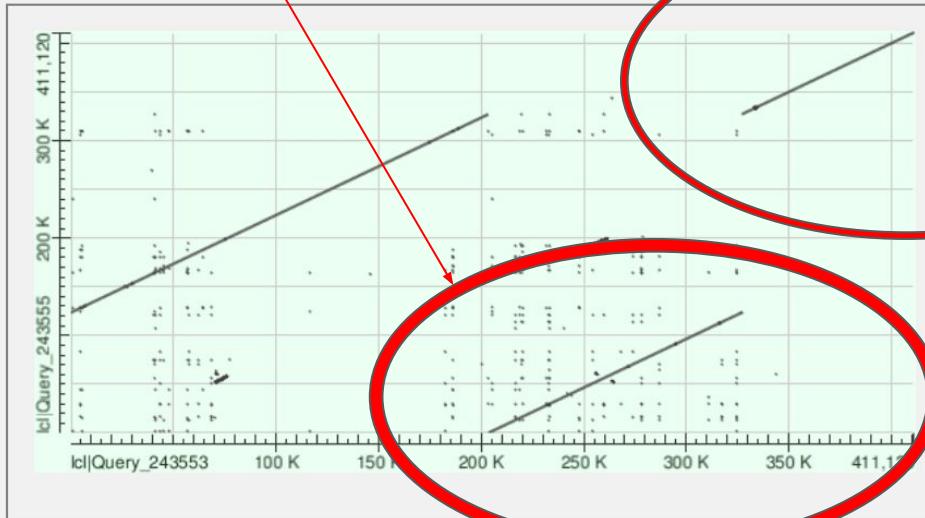
Descriptions

Graphic Summary

Alignments

Dot Plot

Plot of lcl|Query_243553 vs lcl|Query_243555 ?



Align Sequences Nucleotide BLAST

[blastn](#)[blastp](#)[blastx](#)[tblastn](#)[tblastx](#)

BLASTN programs search nucleotide subjects using a nucleotide 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

Dosya Seç sequence_4.fasta [?](#)

Job Title

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

Align two or more sequences [?](#)

New columns added to the Description Table

Click 'Select Columns' or 'Manage Columns'.

Enter Subject Sequence

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

Subject subrange [?](#)

From

To

Or, upload file

Dosya Seç sequence_DB.fasta [?](#)

Program Selection

Optimize for

- Highly similar sequences (megablast)
- More dissimilar sequences (discontiguous megablast)
- Somewhat similar sequences (blastn)

**Format Request****Job Title:** sequence_4

Request ID	U54T8X5D11N
Status	Searching
Time since submission	00:00:00

This page will be automatically updated in **1** seconds until search is done

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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 **sequence_4**RID **U54T8X5D11N** Search expires on 11-29 03:20 am [Download All](#) ▾Program Blast 2 sequences [Citation](#) ▾

Query ID Icl|Query_247737 (dna)

Query Descr sequence_4

Query Length 424490

Subject ID Icl|Query_247739 (dna)

Subject Descr Database

Subject 411120

Length

Other reports [MSA viewer](#) **Filter Results**

Percent Identity

to

E value

to

Query Coverage

to

Filter**Reset****Descriptions**

Graphic Summary

Alignments

Dot Plot

Sequences producing significant alignments[Download](#) ▾[New Select columns](#) ▾[Show](#)

100 ▾

[Feedback](#)

max score: highest alignment score btw query && db sequence

total score: sum up the alignments btw query && db sequence- overall segments
high total score: extensive alignment

lower E (Expect) value (closer to zero)== significant match

Other reports [MSA viewer](#)

Descriptions Graphic Summary Alignments Dot Plot

Sequences producing significant alignments Download New Select columns Show 100 ?

select all 1 sequences selected

Database

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
			2.129e+05	1.126e+05	100%	0.0	100.00%	411120	Query_247739

identity percent btw sequences

Other reports [MSA viewer](#) [?](#)

Descriptions

Graphic Summary

Alignments

Dot Plot

ⓘ hover to see the title ⚡ click to show alignments

Alignment Scores < 40 40 - 50 50 - 80 80 - 200 >= 200 [?](#)

1 sequences selected [?](#)

Distribution of the top 519 Blast Hits on 1 subject sequences



[Descriptions](#)[Graphic Summary](#)[Alignments](#)[Dot Plot](#)

Alignment view

Pairwise



CDS feature

[Restore defaults](#)[Download](#)

1 sequences selected

 [Download](#) ▾[Graphics](#)

Sort by: E value

[▼ Next](#)[▲ Previous](#)[◀ Descriptions](#)

Database

Sequence ID: **Query_247739** Length: **411120** Number of Matches: **519**Range 1: 170451 to 285743 [Graphics](#)[▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Identities	Gaps	Strand
2.129e+05 bits(115293)	0.0	115293/115293(100%)	0/115293(0%)	Plus/Plus

Query 255151 TTTGATCCACtttttggttttATGGATTGAGTTACCAACTGGTGGTATTCCTTACT 255210

Sbjct 170451 TTTGATCCACTTTTGGTTTTATGGATTGAGTTACCAACTGGTGGTATTCCTTACT 170510

Query 255211 CTAGAACAGCTTGCTCTATTTACCTCCTTGCTCTTGCTTTGGATATATGTGAAC TT 255270

Sbjct 170511 CTAGAACAGCTTGCTCTATTTACCTCCTTGCTCTTGCTTTGGATATATGTGAAC TT 170570

Query 255271 CCTGGGAGCACTTCCTTTGCCTGAAGAACTTCCTCTAGTAGTTCTTACAAAAGTGGTC 255330

Sbjct 170571 CCTGGGAGCACTTCCTTTGCCTGAAGAACTTCCTCTAGTAGTTCTTACAAAAGTGGTC 170630

Query 255331 TGCTAACAGGAATTCTGTTTTGTTATCTGGGAATGCTTTATTTGCCCTTTTG 255390



Other reports MSA viewer ?

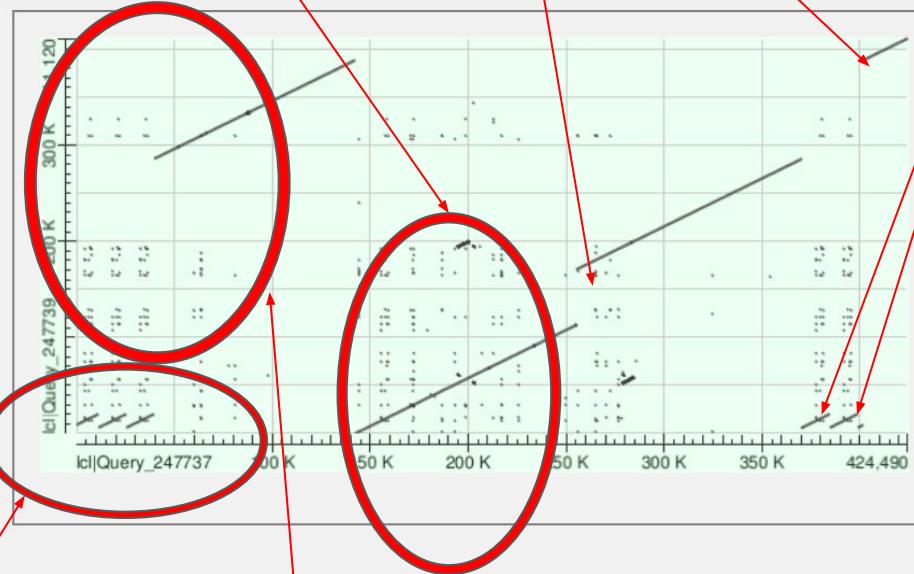
Descriptions

Graphic Summary

Alignments

Dot Plot

Plot of lcl|Query_247737 vs lcl|Query_247739 ?



3.

Assignment #4_Lem... PSI-BLAST Tutorial X BLAST: Basic Local X YouTube X Hu

genome.ucsc.edu/cgi-bin/hgBlat

MPN navigator yön... Makale draft leman... GeoGebra - 100 ... Middle East Technic... Probabilistic Graphi... Nizamettin Aydin

All Results (no minimum matches) Submit

Paste in a query sequence to find its location in the genome. Multiple sequences may be searched if separated by lines by the sequence.

File upload: Rather than pasting a sequence, you can choose to upload a text file containing the sequence.

Upload sequence: unknown.fasta

Only DNA sequences of 25,000 or fewer bases and protein or translated sequence of 10000 or fewer letters will be processed can be submitted at the same time. The total limit for multiple sequence submissions is 50,000 bases or 25,000 letters. A valid example is GTCCCTGGAACCGAGCCTCGGCCTGGCCTAGCG (human SOD1).

The **Search all** checkbox allows you to search all genomes at the same time. Search all is only available for default assemblies with dedicated BLAT servers. The new dynamic BLAT servers are not supported, and they are noted as skipped in the output. [FAQ for more information.](#)

The **All Results** checkbox disables minimum matches filtering so all results are seen. For example, with a human dna search matches required, based on the genome size, to filter out lower-quality results. This checkbox can be useful with short queries genomes of microorganisms.

For locating PCR primers, use [In-Silico PCR](#) for best results instead of BLAT.

List: genomes with chromosomes

← → C ⌂ genome.ucsc.edu/cgi-bin/hgBlat ⌂

MPN navigator yön... Makale draft leman... GeoGebra - 100 mil... Middle East Technic... Probabilistic Graphi... Nizamettin Aydin » Diğer yer işaretleri Okuma listesi

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All Genomes BLAT Results

The single best alignment found for each assembly is shown below. The approximate results below are sorted by number of matching 'tiles', perfectly matching subsequences of length 11 (DNA) or 4 (protein). Using only tile hits, this speedy method can not see mismatches. Click the 'assembly' link to trigger a full BLAT alignment for that genome. The entire alignment, including mismatches and gaps, must score 20 or higher in order to appear in the Blat output. For more details see the [BLAT FAQ](#).

Name	Genome	Assembly	Tiles	Chrom
unknown	S. cerevisiae	sacCer3	7999	chr11
unknown	Human	hg38	7295	chr11
unknown	Chimp	panTro6	5509	chr11
unknown	Gorilla	gorGor6	5446	chr11
unknown	Gibbon	nomLeu3	3891	chr4
unknown	Bonobo	panPan3	3469	chr11
unknown	Orangutan	ponAbe3	2689	chr11
unknown	Marmoset	calJac4	1303	chr11
unknown	SARS-CoV-2	wuhCor1	1087	NC_045512v2
unknown	Bushbaby	otoGar3	551	GL873653
unknown	White rhinoceros	cerSim1	480	JH767824
unknown	Green monkey	chlSab2	465	chr11
unknown	Golden snub-nosed monkey	rhiRox1	448	KN294226v1
unknown	Baboon	papAnu4	447	chr4

unknown Proboscis monkey	<u>nasLar1</u>	437 chr3
unknown Crab-eating macaque	<u>macFas5</u>	432 chr11
unknown Rhesus	<u>rheMac10</u>	416 chr11
unknown Guinea pig	<u>cavPor3</u>	400 scaffold_42
unknown Dolphin	<u>turTru2</u>	359 JH472593
unknown Cow	<u>bosTau9</u>	326 chr29
unknown Sheep	<u>oviAri4</u>	276 chr21
unknown Hawaiian monk seal	<u>neoSch1</u>	246 NW_018734298v1
unknown Chinese pangolin	<u>manPen1</u>	228 KN006209
unknown Minke whale	<u>balAcu1</u>	227 KI537401
unknown Squirrel monkey	<u>saiBol1</u>	224 JH378106
unknown Alpaca	<u>vicPac2</u>	199 KB632549
unknown Cat	<u>felCat9</u>	182 chrD1
unknown Horse	<u>equCab3</u>	172 chr12
unknown Ferret	<u>musFur1</u>	156 GL896969
unknown Rat	<u>rn6</u>	155 chrUn_KL568304v1
unknown C. brenneri	<u>caePb2</u>	110 chrUn
unknown Southern sea otter	<u>enhLutNer1</u>	98 QQQE01000404v1
unknown Turkey	<u>melGal5</u>	61 chrUn_NW_011146834v1
unknown Ebola virus	<u>eboVir3</u>	58 KM034562v1

unknown.fasta



protein.fasta



Tümünü göster



unknown	Ebola virus	<u>eboVir3</u>	58	KM034562v1
unknown	Pika	<u>ochPri3</u>	57	JH802207
unknown	Bison	<u>bisBis1</u>	53	JPYT01299747v1
unknown	P. pacificus	<u>priPac1</u>	52	chrUn
unknown	A. mellifera	<u>apiMel2</u>	41	Group11
unknown	Mouse lemur	<u>micMur2</u>	40	KQ058448v1
unknown	Platypus	<u>ornAna2</u>	37	chrUn_AAPN01098469v1
unknown	Hedgehog	<u>eriEur2</u>	36	JH836149
unknown	Rabbit	<u>oryCun2</u>	34	chr1
unknown	Malayan flying lemur	<u>galVar1</u>	33	NW_007727268v1
unknown	C. remanei	<u>caeRem3</u>	28	chrUn
unknown	C. elegans	<u>ce11</u>	27	chrIV
unknown	Dog	<u>canFam4</u>	26	chr13
unknown	Panda	<u>ailMel1</u>	23	GL193079.1
unknown	C. briggsae	<u>cb3</u>	23	chrI_random
unknown	Megabat	<u>pteVam1</u>	23	scaffold_7937
unknown	Pig	<u>susScr11</u>	23	chr13
unknown	Tarsier	<u>tarSyr2</u>	22	KE936497v1
unknown	Sloth	<u>choHof1</u>	21	scaffold_215705
unknown	Naked mole-rat	<u>hetGla2</u>	21	JH602196
unknown	Little brown bat	<u>myoLuc2</u>	21	GL429771

unknown Little brown bat	<u>myoLuc2</u>	21 GL429771
unknown C. intestinalis	<u>ci3</u>	20 chr9
unknown Lamprey	<u>petMar2</u>	20 GL476540
unknown Squirrel	<u>speTri2</u>	20 JH393459
unknown Elephant shark	<u>calMil1</u>	19 KI635882
unknown Rock hyrax	<u>proCap1</u>	17 scaffold_84322
unknown Kangaroo rat	<u>dipOrd1</u>	16 scaffold_1658
unknown Chinese hamster	<u>criGriChoV2</u>	15 LT883694v1
unknown Tenrec	<u>echTel2</u>	14 JH980369
unknown Tree shrew	<u>tupBel1</u>	14 scaffold_99955.1-25599
unknown Armadillo	<u>dasNov3</u>	13 JH564900
unknown Shrew	<u>sorAra2</u>	13 JH798178
unknown Tetraodon	<u>tetNig2</u>	12 chrUn_random
unknown Manatee	<u>triMan1</u>	12 JH594694
unknown D. melanogaster	<u>dm6</u>	11 chr2L
unknown Golden eagle	<u>aquChr2</u>	10 KN265652v1
unknown Painted turtle	<u>chrPic1</u>	10 JH584775
unknown Elephant	<u>loxAfr3</u>	10 scaffold_32
unknown Mouse	<u>mm10</u>	10 chr10
unknown C. japonica	<u>caeJap1</u>	9 chrUn
unknown Finch	<u>fr2</u>	8 chr1

unknown.fasta ^

protein.fasta ^

Tümünü göster

Unknown genome	Assembly	Chromosome
unknown D. pseudoobscura	dp3	8 chr2
unknown D. ananassae	droAna2	8 scaffold_13248
unknown D. simulans	droSim1	8 chr2L
unknown D. virilis	droVir2	8 scaffold_12875
unknown D. yakuba	droYak2	8 chrU
unknown Atlantic cod	gadMor1	8 CAEA01266033
unknown Chicken	galGal6	8 chr1
unknown Wallaby	macEug2	8 ABQO010278808
unknown Opossum	monDom5	8 chr2
unknown Sea hare	aplCal1	7 scaffold_40
unknown D. grimshawi	droGri1	7 scaffold_25029
unknown D. mojavensis	droMoj2	7 scaffold_6496
unknown D. sechellia	droSec1	7 super_0
unknown Tibetan frog	nanPar1	7 KN909592v1
unknown Zebra finch	taeGut2	7 chr1
unknown Lizard	anoCar2	6 chr1
unknown Brown kiwi	aptMan1	6 NW_013987741v1
unknown Lancelet	braFlo1	6 chrUn
unknown Zebrafish	danRer11	6 chr10
unknown D. erecta	droEre1	6 scaffold_4690

unknown D. sechellia	<u>droSec1</u>	7 super_0
unknown Tibetan frog	<u>nanPar1</u>	7 KN909592v1
unknown Zebra finch	<u>taeGut2</u>	7 chr1
unknown Lizard	<u>anoCar2</u>	6 chr1
unknown Brown kiwi	<u>aptMan1</u>	6 NW_013987741v1
unknown Lancelet	<u>braFlo1</u>	6 chrUn
unknown Zebrafish	<u>danRer11</u>	6 chr10
unknown D. erecta	<u>droEre1</u>	6 scaffold_4690
unknown D. persimilis	<u>droPer1</u>	6 super_1
unknown Stickleback	<u>gasAcu1</u>	6 chr1
unknown Medium ground finch	<u>geoFor1</u>	6 JH739887
unknown Coelacanth	<u>latCha1</u>	6 JH126563
unknown Budgerigar	<u>melUnd1</u>	6 JH556236
unknown Nile tilapia	<u>oreNil2</u>	6 chrLG1
unknown Medaka	<u>oryLat2</u>	6 ultracontig269
unknown S. purpuratus	<u>strPur2</u>	6 Scaffold23793
unknown African clawed frog	<u>xenLae2</u>	6 chr1L
unknown X. tropicalis	<u>xenTro10</u>	6 chr1
unknown American alligator	<u>allMis1</u>	5 AKHW01015036

Top scoring:

The single best alignment found for each assembly is shown below. The approximate results below are sorted by number of matching 'tiles', perfectly matching subsequences of length 11 (DNA) or 4 (protein). Using only tile hits, this speedy method can not see mismatches. Click the 'assembly' link to trigger a full BLAT alignment for that genome. The entire alignment, including mismatches and gaps, must score 20 or higher in order to appear in the Blat output. For more details see the [BLAT FAQ](#).

Name	Genome	Assembly	Tiles	Chrom
unknown	S. cerevisiae	sacCer3	7999	chr11
unknown	Human	hg38	7295	chr11
unknown	Chimp	panTro6	5509	chr11
unknown	Gorilla	gorGor6	5446	chr11
unknown	Gibbon	nomLeu3	3891	chr4
unknown	Bonobo	panPan3	3469	chr11
unknown	Orangutan	ponAbe3	2689	chr11
unknown	Marmoset	calJac4	1303	chr11
unknown	SARS-CoV-2	wuhCor1	1087	NC_045512v2
unknown	Bushbaby	otoGar3	551	GL873653
unknown	White rhinoceros	cerSim1	480	JH767824
unknown	Green monkey	chlSab2	465	chr11
unknown	Golden snub-nosed monkey	rhiRox1	448	KN294226v1
unknown	Baboon	papAnu4	447	chr4



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S. cerevisiae BLAT Search

BLAT Search Genome

Genome: Search all

Assembly:

Query type:

Sort output:

Output type:

 All Results (no minimum matches)

Paste in a query sequence to find its location in the genome. Multiple sequences may be searched if separated by lines starting with '>' followed by the sequence name.

File Upload: Rather than pasting a sequence, you can choose to upload a text file containing the sequence.

BLAST/BLAT search ?

New job

Clear form

Sequence data:

>unknown
TCCATTTCCTTGTGAATTCTTTACCCATTGATTATTAAGAATGTAGTGGTTTAA
TTCAGCATGTGATGTTCCATTCTTGTACTGAGTTCTACTTTATTCTATT
ATTCAAGAAAAGATACTTGTATTATTCATCCTTTAAATTATGCAGGTTGTTCG
TGACTTAGCATATGGTCCTTGGAGAATGTCATGTGCACTTGAAACTGTATAT
TCAATTGTTGGTTGGGCAAGTGCTCTATAATTACCTTTGAGTCTAGTGGTTTATG
GTGTTGCTCATATCTCTGTTCCATTGATCTTCTTCTGTTACTACACATTGAA
AGTGGAGTGTGAAGTCTCAAACACTATTGTTGAATTGGTATTCTCTGTTCACT
GTCAGTTTGTCTTATGTTTACTTCTATTGTTAGGTGAATATATGTTATATAC
ATTGTTATCTCTCATGAATGCAATTATCATTAGGATATTATGTTAACTTCAGT
AACATTCTTAAATTAAACCTCTTGTACTTATAGACCTTCAGGTTACTATGGT
GCTGCTTACATGATATATCTTCCATCCTTACTTCTAGTTGGCATTTATCATCTAA
AGTGTGCCCCATATAGATGGAATACAGATGGATCTGTTTCAAACTGGTCTGATAAT
TCTCGCCCTTGTAGTATGTTTAACTCATTCATTAAATTATATTGATTAATAATT
GATTATTATCACACATTTTCTTGTCTTCTATGTAATTCTGTTCTCTTATT
TCTCTTGTCTTCTTCCATCTAGTGACTIONTCTAATATAATTCTATTCT
TTTATGATTCTCATATTCTATTGTTAGTGTGCTCTAGGCCACCTTATGTA
TCGTCTCAAATTACTCATATTATTAATCCTGGAGATACAGAAGTTATTCTG
TATGAGTTTACTGCTTACACTTTTGTGTTATGTTACATATTACATCTTATT
ATGCGCTATTATAATGATCATACTATATAATGATATATCTTAAAGAAGCTGAAAGGAGA
GCAAGTATATTCTGTTCTGTTTAACTCCCTTATCATATATTGATCACC
TTTGTGTTTATGATGTTGAGTACCAACTGGTGTATTCTCTACTTAGAACAG
TTGCTCTTACCTCTGCTCTTGTGTTGATATTGTAACCTCTGGAGACA
CTTCCCTTGTCTGAAGAACTTCTCTAGTGTCTTACAAAACGGTCTGTAACAAAG
GAATCTGTTTGTGTTATCTGGGAATGCTTATTTGCTCTTGTGAAAGAAACTT
CTGCGAGCAGTACTCTCTGCTCTTGTGTTGATATTGTAACCTCTGGAGACA

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nucleotide (gene)

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Analysis	Jobs	Submitted at		
BLASTN	 unknown	Done: 24 hits found	View results	27/11/2021, 20:44 (GMT)    

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gene(genomic)

Job details

Job name unknown



Species Japanese quail (*Coturnix japonica*)

Assembly *Coturnix_japonica_2.0*

Search type BLASTN (NCBI Blast)

 Download results file

New job

Results table

Show	All	entries	Show/hide columns (2 hidden)						Filter		
Genomic Location	Overlapping Gene(s)		Orientation	Query start	Query end	Length	Score	E-val	%ID		
2:94307067-94307092 [Sequence]			Forward	62398	62423	26 [Sequence]	51.9	0.016	100.00	[Alignment]	
2:127957422-127957444 [Sequence]	TG, SLA		Forward	61930	61952	23 [Sequence]	46.0	1.00	100.00	[Alignment]	
7:8421070-8421098 [Sequence]			Forward	63262	63292	31 [Sequence]	46.0	1.00	93.55	[Alignment]	
6:8100538-8100560 [Sequence]	CTNNA3		Forward	74179	74201	23 [Sequence]	46.0	1.00	100.00	[Alignment]	
3:69257700-69257722 [Sequence]			Reverse	42683	42705	23 [Sequence]	46.0	1.00	100.00	[Alignment]	
3:95248130-95248152 [Sequence]			Forward	62631	62653	23 [Sequence]	46.0	1.00	100.00	[Alignment]	
2:10869013-10869034 [Sequence]	ENSCJPG00005003321		Forward	55630	55651	22 [Sequence]	44.0	3.9	100.00	[Alignment]	
2:17290770-17290794 [Sequence]	MLLRP1		Forward	46921	46942	22 [Sequence]	44.0	3.9	100.00	[Alignment]	

Genomic Location	Overlapping Gene(s)	Orientation	Query start	Query end	Length	Score	E-val	%ID
2:94307067-94307092 [Sequence]		Forward	62398	62423	26 [Sequence]	51.9	0.016	100.00 [Alignment]
2:127957422-127957444 [Sequence]	TG, SLA	Forward	61930	61952	23 [Sequence]	46.0	1.00	100.00 [Alignment]
7:8421070-8421098 [Sequence]		Forward	63262	63292	31 [Sequence]	46.0	1.00	93.55 [Alignment]
6:8100538-8100560 [Sequence]	CTNNA3	Forward	74179	74201	23 [Sequence]	46.0	1.00	100.00 [Alignment]
3:69257700-69257722 [Sequence]		Reverse	42683	42705	23 [Sequence]	46.0	1.00	100.00 [Alignment]
3:95248130-95248152 [Sequence]		Forward	62631	62653	23 [Sequence]	46.0	1.00	100.00 [Alignment]
2:10869013-10869034 [Sequence]	ENSCJPG00005003321	Forward	55630	55651	22 [Sequence]	44.0	3.9	100.00 [Alignment]
2:17223773-17223794 [Sequence]	MALRD1	Forward	46921	46942	22 [Sequence]	44.0	3.9	100.00 [Alignment]
2:55776003-55776024 [Sequence]	CDH18	Reverse	45991	46012	22 [Sequence]	44.0	3.9	100.00 [Alignment]
2:68828364-68828385 [Sequence]		Forward	54776	54797	22 [Sequence]	44.0	3.9	100.00 [Alignment]
6:20478657-20478678 [Sequence]		Reverse	62500	62521	22 [Sequence]	44.0	3.9	100.00 [Alignment]
KQ966699:55775-55801 [Sequence]	BICRA	Forward	54713	54738	27 [Sequence]	44.0	3.9	96.30 [Alignment]
Z:27015995-27016020 [Sequence]		Forward	51041	51066	26 [Sequence]	44.0	3.9	96.15 [Alignment]
Z:51441827-51441848 [Sequence]	MCTP1	Forward	61930	61951	22 [Sequence]	44.0	3.9	100.00 [Alignment]
26:4381374-4381395 [Sequence]		Forward	43621	43642	22 [Sequence]	44.0	3.9	100.00 [Alignment]
23:793827-793848 [Sequence]	HIVEP3	Reverse	65803	65824	22 [Sequence]	44.0	3.9	100.00 [Alignment]
23:3923310-3923331 [Sequence]	DLGAP3	Reverse	42688	42709	22 [Sequence]	44.0	3.9	100.00 [Alignment]
22:2567722-2567743 [Sequence]	ENSCJPG00005015129	Forward	44921	44942	22 [Sequence]	44.0	3.9	100.00 [Alignment]
20:10426189-10426214 [Sequence]		Reverse	55879	55904	26 [Sequence]	44.0	3.9	96.15 [Alignment]
18:3101174-3101195 [Sequence]		Reverse	51043	51064	22 [Sequence]	44.0	3.9	100.00 [Alignment]
11:13597129-13597154 [Sequence]		Reverse	46907	46933	27 [Sequence]	44.0	3.9	96.30 [Alignment]
4:2897830-289791 [Sequence]	LRBA	Forward	53759	53080	22 [Sequence]	44.0	3.9	100.00 [Alignment]

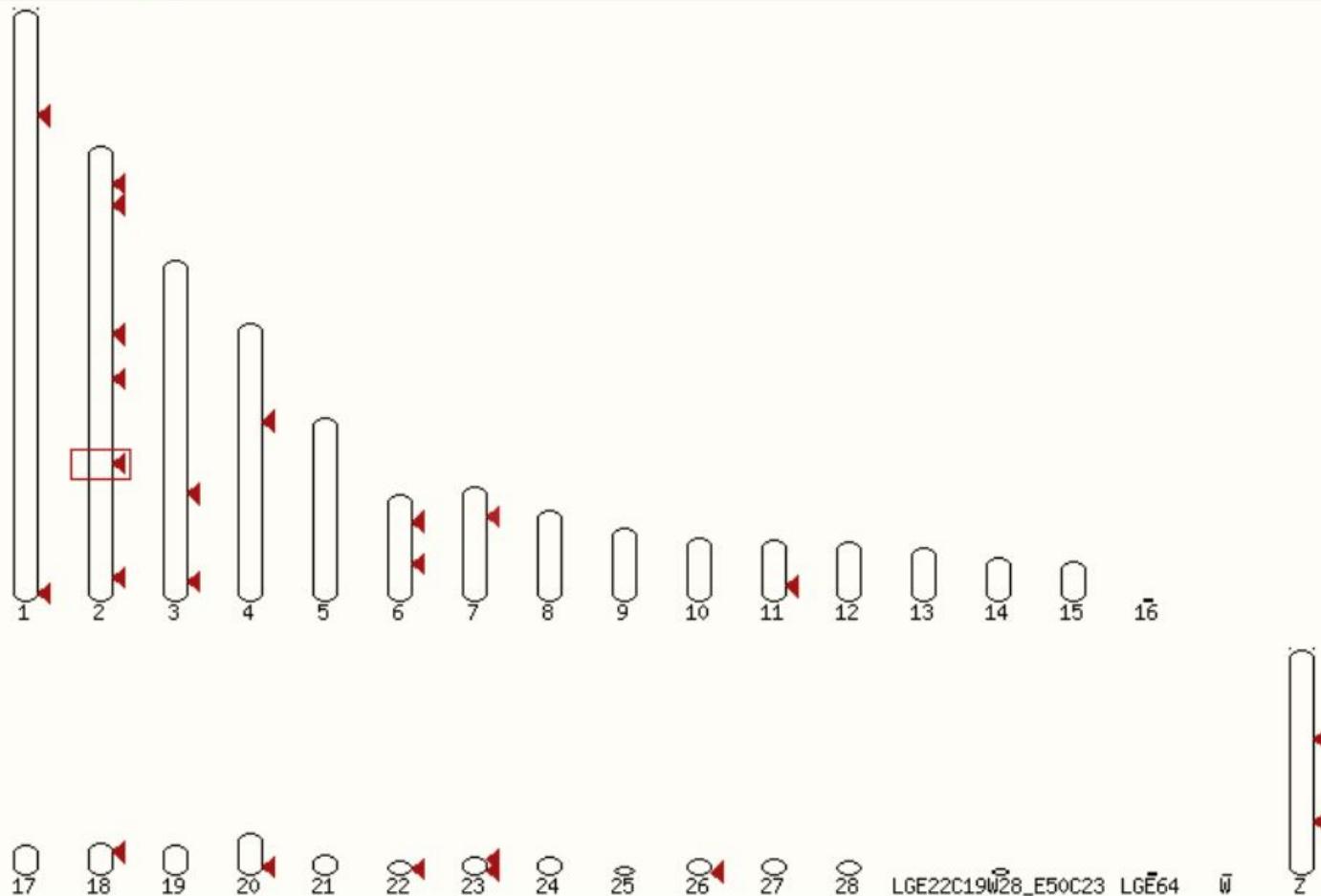
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U_204 / U051 / -204 / U070 [Sequence]		Reverse	U2000	U2021	22 [Sequence]	44.0	3.9	100.00 [Alignment]
KQ966699:55775-55801 [Sequence]	BICRA	Forward	54713	54738	27 [Sequence]	44.0	3.9	96.30 [Alignment]
Z:27015995-27016020 [Sequence]		Forward	51041	51066	26 [Sequence]	44.0	3.9	96.15 [Alignment]
Z:51441827-51441848 [Sequence]	MCTP1	Forward	61930	61951	22 [Sequence]	44.0	3.9	100.00 [Alignment]
26:4381374-4381395 [Sequence]		Forward	43621	43642	22 [Sequence]	44.0	3.9	100.00 [Alignment]
23:793827-793848 [Sequence]	HIVEP3	Reverse	65803	65824	22 [Sequence]	44.0	3.9	100.00 [Alignment]
23:3923310-3923331 [Sequence]	DLGAP3	Reverse	42688	42709	22 [Sequence]	44.0	3.9	100.00 [Alignment]
22:2567722-2567743 [Sequence]	ENSCJPG00005015129	Forward	44921	44942	22 [Sequence]	44.0	3.9	100.00 [Alignment]
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18:3101174-3101195 [Sequence]		Reverse	51043	51064	22 [Sequence]	44.0	3.9	100.00 [Alignment]
11:13597129-13597154 [Sequence]		Reverse	46907	46933	27 [Sequence]	44.0	3.9	96.30 [Alignment]
4:28978890-28978911 [Sequence]	LRBA	Forward	53059	53080	22 [Sequence]	44.0	3.9	100.00 [Alignment]
1:31549595-31549616 [Sequence]		Forward	51041	51062	22 [Sequence]	44.0	3.9	100.00 [Alignment]
1:173430035-173430056 [Sequence]		Reverse	51046	51067	22 [Sequence]	44.0	3.9	100.00 [Alignment]

HSP distribution on genome ▾





Click on the image above to jump to a chromosome, or click and drag to select a region

clicking

Job details 

Job name

unknown



Species



Japanese quail (*Coturnix japonica*)

Assembly

Coturnix_japonica_2.0

Search type

BLASTN (NCBI Blast)

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Results table 

Show	All	entries	Show/hide columns (2 hidden)						Filter		
Genomic Location	Overlapping Gene(s)		Orientation	Query start	Query end	Length	Score	E-val	%ID		
2:94307067-94307092 [Sequence]			Forward	62398	62423	26	51.9	0.016	100.00	[Alignment]	
2:127957422-127957444 [Sequence]	TG, SLA		Forward	61930	61952	23	46.0	1.00	100.00	[Alignment]	
7:8421070-8421098 [Sequence]			Forward	63262	63292	31	46.0	1.00	93.55	[Alignment]	
6:8100538-8100560 [Sequence]	CTNNA3		Forward	74179	74201	23	46.0	1.00	100.00	[Alignment]	
3:69257700-69257722 [Sequence]			Reverse	42683	42705	23	46.0	1.00	100.00	[Alignment]	
3:95248130-95248152 [Sequence]			Forward	62631	62653	23	46.0	1.00	100.00	[Alignment]	
2:10869013-10869034 [Sequence]	ENSCJPG00005003321		Forward	55630	55651	22	44.0	3.9	100.00	[Alignment]	
2:17290770-17290794 [Sequence]	MLXBP1		Forward	46921	46943	22	44.0	3.9	100.00	[Alignment]	

Japanese quail (*Coturnix japonica* 2.0) ▾

Location: 2:94,307,065-94,307,093

BLAST/BLAT results ▾

location-based displays

Whole genome

Chromosome summary

Region overview

Region in detail

Comparative Genomics

Synteny

Alignments (image)

Alignments (text)

Region Comparison

Genetic Variation

Variant table

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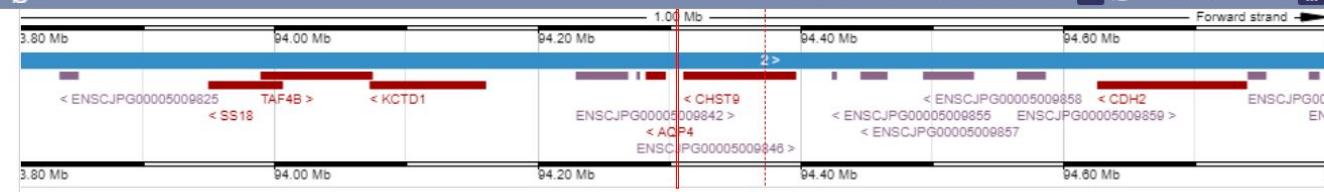
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Primary_assembly 2: 94,307,065-94,307,093



Region in detail ?

Scroll:   Track height:    Drag/Select:   Forward strand Contigs
Genes (Ensembl)

Gene Legend

Ensembl protein coding
RNA gene

Location: 2:94307065-94307093

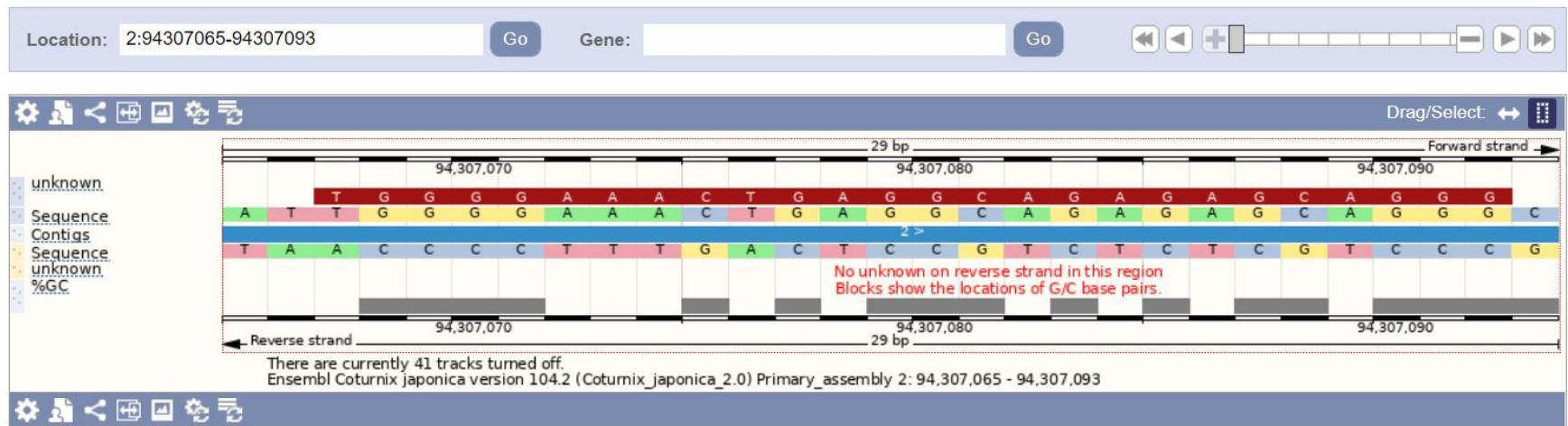
Go

Gene:

Go



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Web Tools

BLAST/BLAT

Ticket

unknown

- Alignment
- Query Sequence

Genomic Sequence

- Variant Effect Predictor
- Linkage Disequilibrium Calculator
- Variant Recoder
- File Chameleon
- Assembly Converter
- ID History Converter
- VCF to PED Converter
- Data Slicer
- Post-GWAS

BLAST/BLAT Genomic Sequence

BLAST/BLAT type

BLASTN

Query location

unknown 62398 to 62423 (+)

Database location

2 94307067 to 94307092 (+)

Genomic location

2 94307067 to 94307092 (+)

Alignment score

51.9

E-value

0.016

Alignment length

26

Percentage identity

100.00

HSP Location of selected alignment

Markup loaded

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>primary_assembly:Coturnix_japonica_2.0:2:94306767:94307392:1
94306767 AATGCCCTGGCAGGGCTTGACAGATGCACAGTGTGTTGAAACAGAGCTTGATTCTTAAGG 94306826
94306827 CTGCCAACTGCACAAACAGAACAGAACTGAATGGAGCAGTTCTTGCTGGAAACAAAAGCTGGAA 94306886
94306887 GTCCTGGCTCTCTCATTCATTCAATTGGAAAAAAATATCAAGAAAAGGCATGAACATCCTA 94306946
94306947 TGAGATAAGTCCATACTAAGACCTTACTTCAAAACACAGCTATTATGTGAGAGTACA 94307006
94307007 AAGCCCTTAGCAGAAAGCATGTGGTATAATTATCATCCATTACAGTCCAATTGGCCAT 94307066
94307067 TGGGAAACTGAGGCAGAGAGCAGGGCATGTTGCTCAACAAGCATGTGAAGTTACCAAGC 94307126
94307127 ATAGAGGAGATCCAGCTGCTGAAGTCACATCTGCTACTGCAGATAAAGCAGAGCTA 94307186
94307187 CACCTCAGCTATCTATGGAACCTCCCTGCAATTAGCTATAGACCAAAGAGCTTAGCCATT 94307246
94307247 TCTCTCAATCAGATAACGCTTATGACCTAATTCTACTGAAAGCATTCTCAATAAACT 94307306
94307307 AAATAAGATCATATGCTCATAGAACTATTAAAGGTGGAAAAGACCTCTAAAGATCATCTAG 94307366
94307367 TCCAACCACCAACCCATTCCCACCAT 94307392
```

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Nucleotide collection (nr/nt)

Organism Enter organism name or id—completions will be suggested exclude

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Tümünü göster

blastn:nucleotide molecule
type:dna/gene

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Makale draft leman...

GeoGebra - 100 mil...

Middle East Technic...

Probabilistic Graphi...

Nizamettin Aydin



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Current time	Sat Nov 27 15:45:40 2021
Time since submission	00:00:35

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Database	nt	See details ▾	
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Description	unknown		
Molecule type	dna		
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Percent Identity to **E value** to **Query Coverage** to

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Distance tree of results

MSA Viewer

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	Homo sapiens KCNQ1 opposite strand/antisense transcript 1 (KCNQ1OT1), RefSeqGene (LRG_1...	Homo sapiens	1.375e+05	1.389e+05	100%	0.0	100.00%	98671	NG_016178.2
<input checked="" type="checkbox"/>	Homo sapiens KCNQ1 opposite strand/antisense transcript 1 (KCNQ1OT1), long non-coding RNA	Homo sapiens	1.375e+05	1.384e+05	100%	0.0	100.00%	91671	NR_002728.3
<input checked="" type="checkbox"/>	Homo sapiens potassium voltage-gated channel subfamily Q member 1 (KCNQ1), RefSeqGene (L...	Homo sapiens	1.375e+05	1.573e+05	100%	0.0	100.00%	411120	NG_008935.1
<input checked="" type="checkbox"/>	Homo sapiens chromosome 11, clone RP4-608B4, complete sequence	Homo sapiens	1.372e+05	1.411e+05	100%	0.0	99.92%	133815	AC124055.6
<input checked="" type="checkbox"/>	Human Chromosome 11p15.5 pac pDJ608b4, complete sequence	Homo sapiens	1.371e+05	1.399e+05	100%	0.0	99.89%	132960	AC002403.1
<input checked="" type="checkbox"/>	Homo sapiens KVLQT1 gene	Homo sapiens	1.370e+05	1.549e+05	100%	0.0	99.87%	404123	AJ006345.1
<input checked="" type="checkbox"/>	TPA: Homo sapiens Long non-coding sense-intronic RNA Kcnq1ot1 (Kncq1 gene)	Homo sapiens	79763	79763	57%	0.0	100.00%	59461	HG975405.1
<input checked="" type="checkbox"/>	Homo sapiens chromosome 11, clone RP11-38L8, complete sequence	Homo sapiens	68088	68858	50%	0.0	100.00%	181025	AC021424.6
<input checked="" type="checkbox"/>	Human Chromosome 11p15.5 pac pDJ74k15, complete sequence	Homo sapiens	66894	67665	49%	0.0	99.76%	120229	U90095.1
<input checked="" type="checkbox"/>	Pongo abelii BAC clone CH276-288L22 from chromosome unknown, complete sequence	Pongo abelii	59056	63099	50%	0.0	97.30%	196430	AC199098.4
<input checked="" type="checkbox"/>	Pongo abelii BAC clone CH276-6K23 from chromosome unknown, complete sequence	Pongo abelii	26506	77732	49%	0.0	96.89%	203223	AC217537.3
<input checked="" type="checkbox"/>	Homo sapiens genomic DNA, chromosome 11 clone RP11-847E17, complete sequence	Homo sapiens	9912	27515	17%	0.0	99.81%	165857	AP006463.2
<input checked="" type="checkbox"/>	Eukaryotic synthetic construct chromosome 13	Eukaryotic synth.	9124	3.780e+06	8%	0.0	01.20%	000000078	CPD24516.1

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Alignment Scores

< 40

40 - 50

50 - 80

80 - 200

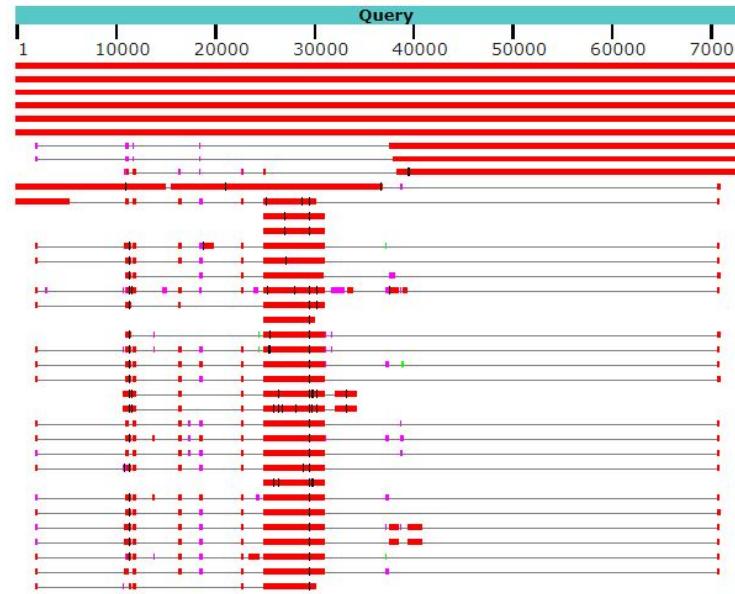
≥ 200



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Distribution of the top 17286 Blast Hits on 100 subject sequences



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Homo sapiens KCNQ1 opposite strand/antisense transcript 1 (KCNQ1OT1), RefSeqGene (LRG_1052) on chromosome 11

Sequence ID: [NG_016178.2](#) Length: 98671 Number of Matches: 10

Range 1: 21269 to 95748 [GenBank](#) [Graphics](#)

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Score	Expect	Identities	Gaps	Strand
1.375e+05 bits(74480)	0.0	74480/74480(100%)	0/74480(0%)	Plus/Minus
Query 1	TCCATTTCCCTTGTGAATTCTTCACCCATTGATTATTAAGAACATGTAGTGTTGTTAAAT	60		
Sbjct 95748	TCCATTTCCCTTGTGAATTCTTCACCCATTGATTATTAAGAACATGTAGTGTTGTTAAAT	95689		
Query 61	TTCCACATGTGTATGTTCCCTAATTCCTTGTACTGAGTTCTACTTTTATTCATTAT	120		
Sbjct 95688	TTCCACATGTGTATGTTCCCTAATTCCTTGTACTGAGTTCTACTTTTATTCATTAT	95629		
Query 121	ATTCAAGAAAAAGATAACCTTGATTATTCAACTCCTTTAAATTATGCAGGTTGTTTCG	180		
Sbjct 95628	ATTCAAGAAAAAGATAACCTTGATTATTCAACTCCTTTAAATTATGCAGGTTGTTTCG	95569		
Query 181	TGACTTAGCATATGGCTTCTTGGAGAATGTCTCATGTGCACTTGAAAATACTGTATAT	240		
Sbjct 95568	TGACTTAGCATATGGCTTCTTGGAGAATGTCTCATGTGCACTTGAAAATACTGTATAT	95509		
Query 241	TCAATGTTGGTTGGCGAAGTGTCTATAATTACCTTTGAGTCTAGTTGGTTTATG	300		
Sbjct 95508	TCAATGTTGGTTGGCGAAGTGTCTATAATTACCTTTGAGTCTAGTTGGTTTATG	95449		
Query 301	GTGTTGCTCATATCTCTGTTCCATTGATCTTCTGTACTACACATTATTGAA	360		
Sbjct 95448	GTGTTGCTCATATCTCTGTTCCATTGATCTTCTGTACTACACATTATTGAA	95389		

F

Descriptions	Graphic Summary	Alignments	Taxonomy	
Reports	Lineage	Organism	Taxonomy	
100 sequences selected ?				
Organism	Blast Name	Score	Number of Hits	Description
root			102	
. Eukaryota	eukaryotes		96	
. . Hominidae	primates		95	
. . . Homininae	primates		91	
. . . . Homo sapiens	primates	1.375e+05	80	Homo sapiens hits
. . . . Pan troglodytes	primates	6986	10	Pan troglodytes hits
. . . . Gorilla gorilla gorilla	primates	6977	1	Gorilla gorilla gorilla hits
. . . . Pongo abelii	primates	59056	4	Pongo abelii hits
. . Naegleria fowleri	eukaryotes	7210	1	Naegleria fowleri hits
. eukaryotic synthetic construct	other sequences	8431	6	eukaryotic synthetic construct hits

clicking:

Other reports Distance tree of results

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Distance tree of results

New MSA Viewer

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	Homo sapiens KCNQ1 opposite strand/antisense transcript 1 (KCNQ1OT1), RefSeqGene (LRG_1...	Homo sapiens	1.375e+05	1.389e+05	100%	0.0	100.00%	98671	NG_016178.2
<input checked="" type="checkbox"/>	Homo sapiens KCNQ1 opposite strand/antisense transcript 1 (KCNQ1OT1), long non-coding RNA	Homo sapiens	1.375e+05	1.384e+05	100%	0.0	100.00%	91671	NR_002728.3
<input checked="" type="checkbox"/>	Homo sapiens potassium voltage-gated channel subfamily Q member 1 (KCNQ1), RefSeqGene (L...	Homo sapiens	1.375e+05	1.573e+05	100%	0.0	100.00%	411120	NG_008935.1
<input checked="" type="checkbox"/>	Homo sapiens chromosome 11, clone RP4-608B4, complete sequence	Homo sapiens	1.372e+05	1.411e+05	100%	0.0	99.92%	133815	AC124055.6
<input checked="" type="checkbox"/>	Human Chromosome 11p15.5 pac pDJ608b4, complete sequence	Homo sapiens	1.371e+05	1.399e+05	100%	0.0	99.89%	132960	AC002403.1
<input checked="" type="checkbox"/>	Homo sapiens KVLQT1 gene	Homo sapiens	1.370e+05	1.549e+05	100%	0.0	99.87%	404123	AJ006345.1
<input checked="" type="checkbox"/>	TPA: Homo sapiens Long non-coding sense-intronic RNA Kcnq1ot1 (Kncq1 gene)	Homo sapiens	79763	79763	57%	0.0	100.00%	59461	HG975405.1
<input checked="" type="checkbox"/>	Homo sapiens chromosome 11, clone RP11-38L8, complete sequence	Homo sapiens	68088	68858	50%	0.0	100.00%	181025	AC021424.6
<input checked="" type="checkbox"/>	Human Chromosome 11p15.5 pac pDJ74k15, complete sequence	Homo sapiens	66894	67665	49%	0.0	99.76%	120229	U90095.1
<input checked="" type="checkbox"/>	Pongo abelii BAC clone CH276-288L22 from chromosome unknown, complete sequence	Pongo abelii	59056	63099	50%	0.0	97.30%	196430	AC199098.4
<input checked="" type="checkbox"/>	Pongo abelii BAC clone CH276-6K23 from chromosome unknown, complete sequence	Pongo abelii	26506	77732	49%	0.0	96.89%	203223	AC217537.3
<input checked="" type="checkbox"/>	Homo sapiens genomic DNA, chromosome 11 clone RP11-847E17, complete sequence	Homo sapiens	9912	27515	17%	0.0	99.81%	165857	AP006463.2
<input checked="" type="checkbox"/>	Eukaryotic synthetic construct chromosome 13	eukaryotic synth.	9124	3.780e+06	8%	0.0	01.30%	00080078	CD024516.1

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Homo sapiens KCNQ1 opposite strand/antisense transcript 1 (KCNQ1OT1), RefSeqGene (LRG_1052) on chromosome 11

Sequence ID: [NG_016178.2](#) Length: 98671 Number of Matches: 10

Range 1: 21269 to 95748 [GenBank](#) [Graphics](#)

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Score	Expect	Identities	Gaps	Strand
1.375e+05 bits(74480)	0.0	74480/74480(100%)	0/74480(0%)	Plus/Minus

Query 1	TCCATTCCCTTGTGAATTCTTCACCCATTGATTATTAAGAATGAGTGTGTTAAAT	60
Sbjct 95748	TCCATTCCCTTGTGAATTCTTCACCCATTGATTATTAAGAATGAGTGTGTTAAAT	95689
Query 61	TTCCACATGTGTATGTTCCCTAATTCTTGCTACTGAGTCTACTTTATTCATTAT	120
Sbjct 95688	TTCCACATGTGTATGTTCCCTAATTCTTGCTACTGAGTCTACTTTATTCATTAT	95629
Query 121	ATTCAAGAAAAAGATACTTGATTATTCAATCCTTAAATTATGCAGGTTGTTTCG	180
Sbjct 95628	ATTCAAGAAAAAGATACTTGATTATTCAATCCTTAAATTATGCAGGTTGTTTCG	95569
Query 181	TGACTTAGCATATGGCCTTCTTGAGAATGCTCATGTGCACTTGAAAATACTGTATAT	240
Sbjct 95568	TGACTTAGCATATGGCCTTCTTGAGAATGCTCATGTGCACTTGAAAATACTGTATAT	95509
Query 241	TCAATGTTGGTTGTTGGCGAAGTGCCTATAATTACCTTTGAGTCAGTTGGTTATG	300
Sbjct 95508	TCAATGTTGGTTGTTGGCGAAGTGCCTATAATTACCTTTGAGTCAGTTGGTTATG	95449
Query 301	GTGTTGCTCATATCTCTGTTCCATTGATCTCTTCTTGACTACACATTATTGAA	360
Sbjct 95448	GTGTTGCTCATATCTCTGTTCCATTGATCTCTTCTTGACTACACATTATTGAA	95389
Query 361	AGTGGAGTGTGAAGTCTCCAACACTATTGTTGAATTGGCTATTCTGTTCAAGTTCT	420
Sbjct 95388	AGTGGAGTGTGAAGTCTCCAACACTATTGTTGAATTGGCTATTCTGTTCAAGTTCT	95329
Query 421	GTCAGTTTGCTTCTATGTTAGTTCTATTGTTAGGTGAATATATGTTATAATC	480
Sbjct 95328	GTCAGTTTGCTTCTATGTTAGTTCTATTGTTAGGTGAATATATGTTATAATC	95269



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Homo sapiens KCNQ1 opposite strand/antisense transcript 1 (KCNQ1OT1), RefSeqGene (LRG_1052) on chromosome 11

NCBI Reference Sequence: NG_016178.2

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LOCUS NG_016178 98671 bp DNA linear PRI 08-FEB-2021
DEFINITION Homo sapiens KCNQ1 opposite strand/antisense transcript 1 (KCNQ1OT1), RefSeqGene (LRG_1052) on chromosome 11.
ACCESSION NG_016178
VERSION NG_016178.2
KEYWORDS RefSeq; RefSeqGene.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 98671)
AUTHORS Mohammad F, Mondal T and Kanduri C.

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Articles about the KCNQ1OT1 gene

A general mechanism of KCNE1 modulation of KCNQ1 channels involving i [Commun Biol. 2021]

Association Analysis of Candidate Gene Polymorphisms and Tinnitus [Otol Neurotol. 2021]

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4.

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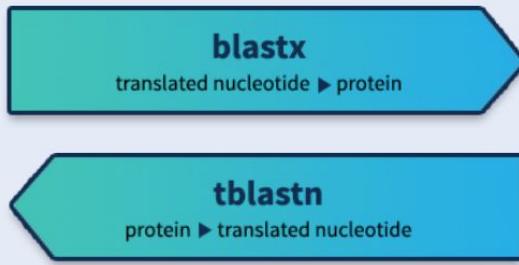
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Align two or more sequences [?](#)

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Database

[?](#)

Organism

Optional

Enter organism name or id--completions will be suggested 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

New columns added to the Description Table

Click 'Select Columns' or 'Manage Columns'.



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Align two or more sequences [?](#)

Choose Search Set

Database

Non-redundant protein sequences (nr) [?](#)

Organism
Optional

exclude [Add organism](#)

Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown. [?](#)

Exclude
Optional

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

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Optional

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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)

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BLAST

Select blastp (protein-protein BLAST)

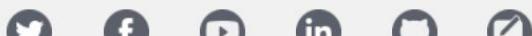
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Job Title: protein

Request ID	U54YJH9J016
Status	Searching
Submitted at	Sat Nov 27 15:23:46 2021
Current time	Sat Nov 27 15:23:49 2021
Time since submission	00:00:02

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Job Title	protein
RID	U54YJH9J016 Search expires on 11-29 03:23 am Download All ▾
Program	BLASTP ? Citation ▾
Database	nr See details ▾
Query ID	Icl Query_42362
Description	protein
Molecule type	amino acid
Query Length	525
Other reports	Distance tree of results Multiple alignment MSA viewer ?

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Percent Identity

 to

E value

 to

Query Coverage

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hits (found sequences) =100

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Sequences producing significant alignments Download New Select columns Show 100 ?

select all 100 sequences selected GenPept Graphics Distance tree of results Multiple alignment New MSA Viewer

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	potassium voltage-gated channel, KQT-like subfamily, member 1, isoform CRA_b [Homo sapiens]	Homo sapiens	1056	1056	100%	0.0	97.93%	586	EAX02518.1
<input checked="" type="checkbox"/>	potassium voltage-gated channel subfamily KQT member 1 isoform 2 precursor [Homo sapiens]	Homo sapiens	1056	1056	100%	0.0	97.93%	549	NP_861463.1
<input checked="" type="checkbox"/>	voltage_gated potassium channel [Homo sapiens]	Homo sapiens	1054	1054	100%	0.0	97.93%	581	AAC51781.1
<input checked="" type="checkbox"/>	potassium voltage-gated channel subfamily KQT member 1 isoform 1 [Homo sapiens]	Homo sapiens	1054	1054	100%	0.0	97.93%	676	NP_000209.2
<input checked="" type="checkbox"/>	KvLQT1 [Homo sapiens]	Homo sapiens	1053	1053	100%	0.0	97.74%	549	CAB44650.1
<input checked="" type="checkbox"/>	KvLQT1 [Homo sapiens]	Homo sapiens	1051	1051	100%	0.0	97.74%	676	CAB44649.1
<input checked="" type="checkbox"/>	potassium voltage-gated channel subfamily KQT member 1 isoform X2 [Pongo abelii]	Pongo abelii	1050	1050	100%	0.0	97.36%	549	XP_024111354.1
<input checked="" type="checkbox"/>	slow delayed rectifier channel subunit [Homo sapiens]	Homo sapiens	1050	1050	100%	0.0	97.74%	548	AAC05705.1
<input checked="" type="checkbox"/>	potassium voltage-gated channel subfamily KQT member 1 isoform X1 [Gorilla gorilla gorilla]	Gorilla gorilla go...	1049	1049	100%	0.0	97.36%	549	XP_004050494.1
<input checked="" type="checkbox"/>	potassium voltage-gated channel subfamily KQT member 1 isoform X1 [Pongo abelii]	Pongo abelii	1048	1048	100%	0.0	97.36%	676	XP_024111353.1
<input checked="" type="checkbox"/>	potassium voltage-gated channel subfamily KQT member 1 isoform X3 [Pan paniscus]	Pan paniscus	1048	1048	100%	0.0	97.36%	549	XP_034732610.1
<input checked="" type="checkbox"/>	potassium voltage-gated channel subfamily KQT member 1 isoform X4 [Pan troglodytes]	Pan troglodytes	1047	1047	100%	0.0	97.36%	549	XP_016732610.1

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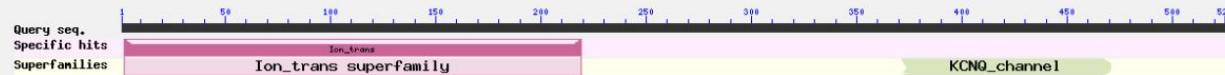
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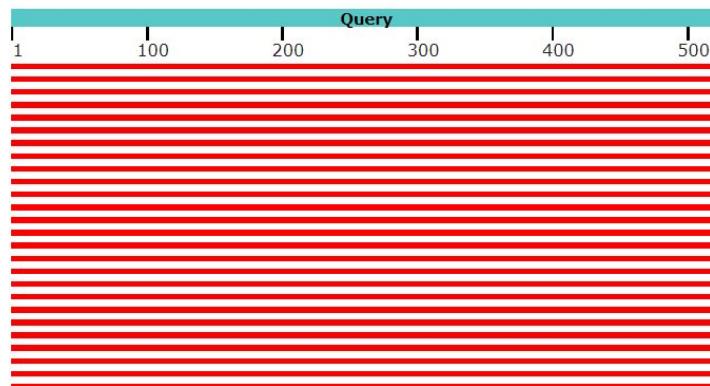
Alignment Scores

 < 40 40 - 50 50 - 80 80 - 200 >= 200

100 sequences selected

**Putative conserved domains have been detected, click on the image below for detailed results.**

Distribution of the top 100 Blast Hits on 100 subject sequences

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Alignment view

Pairwise

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100 sequences selected

[Download](#) ▾[GenPept](#) [Graphics](#)[▼ Next](#)[▲ Previous](#)[◀ Descriptions](#)**potassium voltage-gated channel, KQT-like subfamily, member 1, isoform CRA_b [Homo sapiens]**Sequence ID: [EAX02518.1](#) Length: 586 Number of Matches: 1Range 1: 51 to 581 [GenPept](#) [Graphics](#)[▼ Next Match](#) [▲ Previous Match](#)**Related Information**[Gene](#) - associated gene details

Score	Expect	Method	Identities	Positives	Gaps
1056 bits(2731)	0.0	Compositional matrix adjust.	520/531(98%)	520/531(97%)	6/531(1%)

Query 1 VLSTIEQYAA LATGTLFWMEIVLVVFFGTEYVVRLLWSAGCRSKYVGLWGRRLRFARKPISI 60

Sbjct 51 VLSTIEQYAA LATGTLFWMEIVLVVFFGTEYVVRLLWSAGCRSKYVGLWGRRLRFARKPISI

Query 61 IDLIVVVASMVVLCVGSKGQVFATSAIRWIRFLQILRMLHVDRQGGTWRLLSVVFIHRQ 120

Sbjct 111 IDLIVVVASMVVLCVGSKGQVFATSAIR IRLQILRMLHVDRQGGTWRLLSVVFIHRQ

Query 121 ELITTTLYIGFLGLIFSSYFVYLAEKDAVNESGRVEFGSYADALWWVVTVTTIGYGDKVP 180

Sbjct 171 ELITTTLYIGFLGLIFSSYFVYLAEKDAVNESGRVEFGSYADALWWGVVTTVTTIGYGDKVP

Query 181 QTWVGKTIASCFSVFAISFFALPAGILGSGFALKVQQKQRQKHFNROQIPAAASLIQTAWR 240

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potassium voltage-gated channel subfamily KQT member 1 isoform 2 precursor [Homo sapiens]

Sequence ID: [NP_861463.1](#) Length: 549 Number of Matches: 1

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Range 1: 14 to 544 [GenPept](#)

[▼ Next Match](#)



Next Match



Previous Match

Score	Expect	Method	Identities	Positives	Gaps
1056 bits(2730)	0.0	Compositional matrix adjust.	520/531(98%)	520/531(97%)	6/531(1%)
Query 1	VLSTIEQYAAALATGTLFWMEIVLVVFFGTEYVVRLWSAGCRSKYVGLWGRLRFARKPISI		60		
Sbjct 14	VLSTIEQYAAALATGTLFWMEIVLVVFFGTEYVVRLWSAGCRSKYVGLWGRLRFARKPISI				
Query 61	IDLIVVVASMVLCVGSKGQVFATSAIRWIRFLQIILRMLHVDRQGGTWRLLLGSVVFIIHQ		120		
Sbjct 74	IDLIVVVASMVLCVGSKGQVFATSAIR IRFLQIILRMLHVDRQGGTWRLLLGSVVFIIHQ				
Query 121	ELITTLTYIGFLGLIFSSYFVYLAEKDAVNESGRVEFGSYADALWWVVTVTTIGYGDKVP		180		
Sbjct 134	ELITTLTYIGFLGLIFSSYFVYLAEKDAVNESGRVEFGSYADALWWGVVTVTIGYGDKVP				
Query 181	QTWVGKTIASCFSVFAISFFPALPAGILGSGFALKVQQKQRQKHFNRFQIPAAASLIQTAWR		240		
Sbjct 194	QTWVGKTIASCFSVFAISFFPALPAGILGSGFALKVQQKQRQKHFNRFQIPAAASLIQTAWR				
Query 241	CYAAENPDSTS...KIYIRKAPRSHTLLSGSPKPKSVVVKKKKFKLDKDNGVTPGEKMLTV		300		
Sbjct 254	CYAAENPDSTS...KIYIRKAPRSHTLLSPSPKPKSVVVKKKKFKLDKDNGVTPGEKMLTV				

Related Information

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[Identical Proteins](#) - Identical proteins to NP_861463.1

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[Download](#) ▾ [GenPept](#) [Graphics](#)[▼ Next](#) [▲ Previous](#) [◀ Descriptions](#)**voltage gated potassium channel [Homo sapiens]**Sequence ID: [AAC51781.1](#) Length: 581 Number of Matches: 1Range 1: 46 to 576 [GenPept](#) [Graphics](#)[▼ Next Match](#) [▲ Previous Match](#)**Related Information**[Gene](#) - associated gene details

Score	Expect	Method	Identities	Positives	Gaps
1054 bits(2726)	0.0	Compositional matrix adjust.	520/531(98%)	520/531(97%)	6/531(1%)
Query 1	VLSTIEQYAALATGTLFWMEIVLVVFFGTEYVVRLWSAGCRSKYVGLWGRLRFARKPISI		60		
Sbjct 46	VLSTIEQYAALATGTLFWMEIVLVVFFGTEYVVRLWSAGCRSKYVGLWGRLRFARKPISI		105		
Query 61	IDLIVVVASMVVLCVGSKGQVFATSAIRWIRFLQILRMLHVDRQGGTWRLLGSVVFIHRQ		120		
Sbjct 106	IDLIVVVASMVVLCVGSKGQVFATSAIRWIRFLQILRMLHVDRQGGTWRLLGSVVFIHRQ		165		
Query 121	ELITTLYIGFLGLIFSSYFVYLAEKDAVNESGRVEFGSYADALWWVVTVTTIGYGDKVP		180		
Sbjct 166	ELITTLYIGFLGLIFSSYFVYLAEKDAVNESGRVEFGSYADALWWGVVTVTTIGYGDKVP		225		
Query 181	QTWVGKTIASCFSVFAISFFFALPAGILGSGFALKVQQKQRQKHFNQRQIPAAASLIQTAWR		240		
Sbjct 226	QTWVGKTIASCFSVFAISFFFALPAGILGSGFALKVQQKQRQKHFNQRQIPAAASLIQTAWR		285		
Query 241	CYAAENPDSSSTWKIYIRKAPRSHTLLSGSPPKKSVVVKKKKFKLDKDNGVTPGEKMLTV		300		
Sbjct 286	CYAAENPDSSSTWKIYIRKAPRSHTLLSPSPPKPKSVVVKKKKFKLDKDNGVTPGEKMLTV		345		
Query 301	PHITCDPPEERRLDHFSVDGYDSSVRKSPTLLEVSMPHFMRNTNSFAEDLDLEGETLLTPI		360		

Feedback

Descriptions

Graphic Summary

Alignments

Taxonomy

Reports

Lineage

Organism

Taxonomy

100 sequences selected



Organism	Blast Name	Score	Number of Hits	Description
root			136	
Boreoeutheria	placentals		130	
Euarchontoglires	placentals		91	
Primates	primates		75	
Simiiformes	primates		74	
Catarrhini	primates		69	
Hominoidea	primates		45	
Hominidae	primates		43	
Homininae	primates		39	
Homo sapiens	primates	1056	28	Homo sapiens hits
Gorilla gorilla gorilla	primates	1049	2	Gorilla_gorilla_gorilla hits
Pan paniscus	primates	1048	3	Pan_paniscus hits
Pan troglodytes	primates	1047	6	Pan_troglodytes hits
Pongo abelii	primates	1050	4	Pongo_abelii hits
Nomascus leucogenys	primates	1043	1	Nomascus_leucogenys hits

<input type="checkbox"/>	potassium voltage-gated channel subfamily KQT member 1 isoform X10 [Mustela putorius furo]
<input type="checkbox"/>	potassium voltage-gated channel subfamily KQT member 1 isoform X1 [Mustela putorius furo]
<input type="checkbox"/>	potassium voltage-gated channel subfamily KQT member 1 [Microtus ochrogaster]
<input type="checkbox"/>	potassium voltage-gated channel subfamily KQT member 1 [Orcinus orca]
<input type="checkbox"/>	potassium voltage-gated channel subfamily KQT member 1 isoform X2 [Jaculus jaculus]
<input type="checkbox"/>	potassium voltage-gated channel subfamily KQT member 1 isoform X6 [Halichoerus grypus]
<input checked="" type="checkbox"/>	potassium voltage-gated channel subfamily KQT member 1 isoform X2 [Manis javanica]
<input checked="" type="checkbox"/>	potassium voltage-gated channel subfamily KQT member 1 isoform X1 [Jaculus jaculus]
<input checked="" type="checkbox"/>	potassium voltage-gated channel subfamily KQT member 1 [Pteropus alecto]
<input checked="" type="checkbox"/>	potassium voltage-gated channel subfamily KQT member 1 isoform X1 [Otolemur garnettii]
<input checked="" type="checkbox"/>	potassium voltage-gated channel subfamily Q member 1 isoform CRA_c [Rattus norvegicus]

Mustela putorius...	921	921	100%	0.0	84.73%	572	XP_044922450.1
Microtus ochrog...	920	920	100%	0.0	88.14%	669	XP_005351635.1
Orcinus orca	919	919	100%	0.0	89.66%	673	XP_004278112.1
Jaculus jaculus	919	919	99%	0.0	89.25%	561	XP_045005992.1
Halichoerus gryp...	919	919	100%	0.0	88.91%	547	XP_035923692.1
Manis javanica	918	918	100%	0.0	89.47%	673	XP_036867365.1
Jaculus jaculus	918	918	99%	0.0	89.25%	664	XP_004654281.1
Pteropus alecto	917	917	100%	0.0	88.16%	728	XP_015444155.1
Otolemur garnettii	917	917	99%	0.0	89.25%	675	XP_003798416.1
Rattus norvegicus	916	916	100%	0.0	88.70%	546	EDM12192.1

Descriptions Graphic Summary Alignments Taxonomy

Alignment view Pairwise ▾

Pairwise
Pairwise with dots for identities
Query-anchored with dots for identities
Query-anchored with letters for identities
[Flat query-anchored with dots for identities](#)
Flat query-anchored with letters for identities

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5 sequences selected

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potassium

Member 1 isoform X2 [Manis javanica]

Sequence ID: [XP_036867365.1](#) Length: 673 Number of Matches: 1

Range 1: 139 to 668 [GenPept](#) [Graphics](#)

Score Expect Method Identities Positives Gaps
918 bits(2372) 0.0 Compositional matrix adjust. 476/532(89%) 491/532(92%) 9/532(1%)

Query	1	VLSTIEQYAALATGTLFWMEIVLVVFFGTTEYVVRLLWSAGCRSKYVGLWGRRLRFARKPISI VLSTIEQY ALATGTLFWMEIVLVVFFGTTEYVVRLLWSAGCRSKYVGLWGRRLRFARKPISI	60
Sbjct	139	VLSTIEQYVALATGTLFWMEIVLVVFFGTTEYVVRLLWSAGCRSKYVGIWGRRLRFARKPISI	198
Query	61	IDLIVVVASMVVLCVGSKGQVFATSAIRWIRFLQILRMLHVDRQGGTWRLLGSVVFIHQ IDLIVVVASMVVLCVGSKGQVFATSAIR IRFLQILRMLHVDRQGGTWRLLGSVVFIHQ	120
Sbjct	199	IDLIVVVASMVVLCVGSKGQVFATSAIRGIRFLQILRMLHVDRQGGTWRLLGSVVFIHQ	258
Query	121	ELITTLIGFLGLIFSSYFVYLAEKDAVNESGRVEFGSYADALWWVVTVTTIGYGDKVP ELITTLIGFLGLIFSSYFVYLAEKDAVNESGRVEFGSYADALWWVVTVTTIGYGDKVP	180
Sbjct	259	ELITTLIGFLGLIFSSYFVYLAEKDAVNESGRVEFGSYADALWWGVVTVTTIGYGDKVP	318
Query	181	QTWVGKTIASCFSVFAISFFALPAGILGSGFALKVQQKQRQKHFNQRQIPAAASLIQTAWR	240

Feedback

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

Alignment view

Flat query-anchored with dots for identities

Line length:

60



Restore defaults

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Query range 1: 1 to 60

Query	1	VLSTIEQYAALATGTLFWMEIVLVVFFGTEYVVRLWSAGCRSKYVGLWGRLLRFARKPISI	60
XP_036867365.1	139V.....	I..... 198
XP_004654281.1	138	V..... 197
XP_015444155.1	195V.....	I..... 254
XP_003798416.1	142I.....	I..... 201
EDM12192.1	18	I..... 77

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Query range 2: 61 to 120

Query	61	IDLIVVVASMVVLCVGSKGQVFATSAIRWIRFLQILRMLHVDRQGGTWRLLGSVVFIHQ	120
XP_036867365.1	199G.....	G..... 258
XP_004654281.1	198	G..... 257
XP_015444155.1	255G.....	G..... 314
XP_003798416.1	202G.....	G..... 261
EDM12192.1	78G.....	G..... 137

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Query range 3: 121 to 180

Query	121	ELITTLYIGFLGLIFSSYFVYLAEKDAVNESGRVEFGSYADALWWVVTVTTIGYGDKVP	180
XP_036867365.1	259G.....	318
XP_004654281.1	258I.....G.....	317
XP_015444155.1	315G.....	374
XP_003798416.1	262	..V.....G.....	321
EDM12192.1	138I.....G.....	197

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Query range 4: 181 to 240

Query	181	QTWVGKTIASCFSVFAISFFALPAGILGSGFALKVQQKQRQKHFNQRQIPAAASLIQTAWR	240
XP_036867365.1	319	378
XP_004654281.1	318	377
XP_015444155.1	375V.....	434
XP_003798416.1	322T.....	381
EDM12192.1	198	257

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Query range 5: 241 to 300

Query	241	CYAAENPDSSTWKIYIRKAPRSHTLLSGSPPKKSVVVKKKKFKLDKDNGVTPGEKMLTV	300
XP_036867365.1	379E.....V..PS...P...P.....AL.....G.....	438
XP_004654281.1	378V..PA...A...P.....M.....S.....	437
XP_015444155.1	435	...T....A....V..PS.G.S...P.....AMM.....R....S....T...	494
XP_003798416.1	382V..PS..PA...P.....M.....V.....S....K..I	441
EDM12192.1	258V..PA.....P.....M.....LS....IFN.	317

Feed

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Query	Start	Sequence	End
XP_036867365.1	301	PHITCDP-PEERRLDHFSVDGYDSSVRKSPTLLEVSMPHFMRTNSFAEDLDLEGETLLTP	359
XP_004654281.1	439E.VA.....P.....C....KR.M.....PA.....A.....	498
XP_015444155.1	438-.....P.....I.....T.....L.....D.....A.....	496
XP_003798416.1	495HV.D.Q.T.P....C....K..SM.....T.Q.V.....T.....A.....	554
EDM12192.1	442-.....Q.PG.....T.....T.....I.....A.....	500
EDM12192.1	318-.....D.P....I.....T.....L.....	376

[Download](#) ▾▼ [Next](#) ▲ [Previous](#) ▲ [First Range](#)**Query range 7: 361 to 420**

Query	Start	Sequence	End
XP_036867365.1	360	ITHISQLREHHRATIKVIRRMQYFVAKKKFQQARKGYDVRDVIEQYSQGHNLNMVRIKEL	419
XP_004654281.1	499	...V.....R.....P.....	558
XP_015444155.1	497	...V.....P.....	556
XP_003798416.1	555	...V.....V.....R.....P.....	614
EDM12192.1	501D.....P.....	560
EDM12192.1	377	...V....D.....P.....	436

[Download](#) ▾▼ [Next](#) ▲ [Previous](#) ▲ [First Range](#)**Query range 8: 421 to 480**

Query	Start	Sequence	End
XP_036867365.1	420	QRRLDQSIGKPSLFISVS----WSNTIGARLNRVEDKVTQLDQRALITDMLHQQLSL	473
XP_004654281.1	559A.EKSKDRGN.S.....V..E.....	618
XP_015444155.1	557LPI.EKGKDRG.....K.VV.....	616
XP_003798416.1	615EKS KDRG.....V.....	674
EDM12192.1	561P..EKSKDRGN.....V..L.....	620
EDM12192.1	437PI.EKSKDRG.....VI.....	496

[!\[\]\(20727a95b2fcc9d8fa24ad71abe03997_img.jpg\) Download](#) ▾

▼ [Next](#) ▲ [Previous](#) ▲ [First Range](#)

Query range 9: 481 to 532

Query	Start	Sequence	End
XP_036867365.1	474	HGGSTPGSGGPPREGGAHITQPCGSGGSVDPELFLPSNLTPLTYEQLTVPRRG	525
	619	.Q,GL...H..SGV..QVA.....S.IS.....SA.....	668
XP_004654281.1	617	YQ.GPAS.NR.QH..DSN-----IN.....A.....	658
XP_015444155.1	675	.Q.GP...RA.SGS..QLA....R..IN.....	723
XP_003798416.1	621	.R..P...SLG..RPLAV...V..STIN.....SP.....Q.	669
EDM12192.1	497	Q-----Q...TCNNRSQVV-ASDE...IN.....S.....QT.	541

Standard Protein BLAST

blastn **blastp** blastx tblastn tblastx

BLASTP programs search protein 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

Dosya Seç protein.fasta [?](#)

Job Title

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

Align two or more sequences [?](#)

New columns added to the Description Table

Click 'Select Columns' or 'Manage Columns'.



Choose Search Set

Database

Non-redundant protein sequences (nr) [?](#)

Organism

Optional

Enter organism name or id—completions will be suggested exclude [Add organism](#) [?](#)

Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown. [?](#)

Exclude

Optional

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

Program Selection

Algorithm

Quick BLASTP (Accelerated protein-protein BLAST)

Align two or more sequences [?](#)

Choose Search Set

Database

Non-redundant protein sequences (nr) [?](#)

Organism

Optional

Enter organism name or id—completions will be suggested

exclude

[Add organism](#)

Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown. [?](#)

Exclude

Optional

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 [?](#)

BLAST

Search database nr using PSI-BLAST (Position-Specific Iterated BLAST)

Show results in a new window

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

Algorithm parameters

Format Request**Job Title:** protein

Request ID	U55JKPNR01R
Status	Searching
Time since submission	00:00:00

This page will be automatically updated in **1** seconds until search is done[?](#) Support Center



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BLAST® » blastp suite » results for RID-U55JKPNR01R

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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 **protein**RID [U55JKPNR01R](#) Search expires on 11-29 03:34 am [Download All](#)Program PSI-BLAST Iteration 1 [Citation](#)Database nr [See details](#)

Query ID lcl|Query_126098

Description protein

Molecule type amino acid

Query Length 525

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

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

PSI-BLAST incl.

threshold

0.005

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

Run PSI-Blast iteration 2

[Feedback](#)

protein.fasta

[Tümünü göster](#)

number of hits: 100

Number of sequences 100 Run

Sequences producing significant alignments Download New Select columns Show 100 ?

100 sequences selected GenPept Graphics Distance tree of results Multiple alignment New MSA Viewer

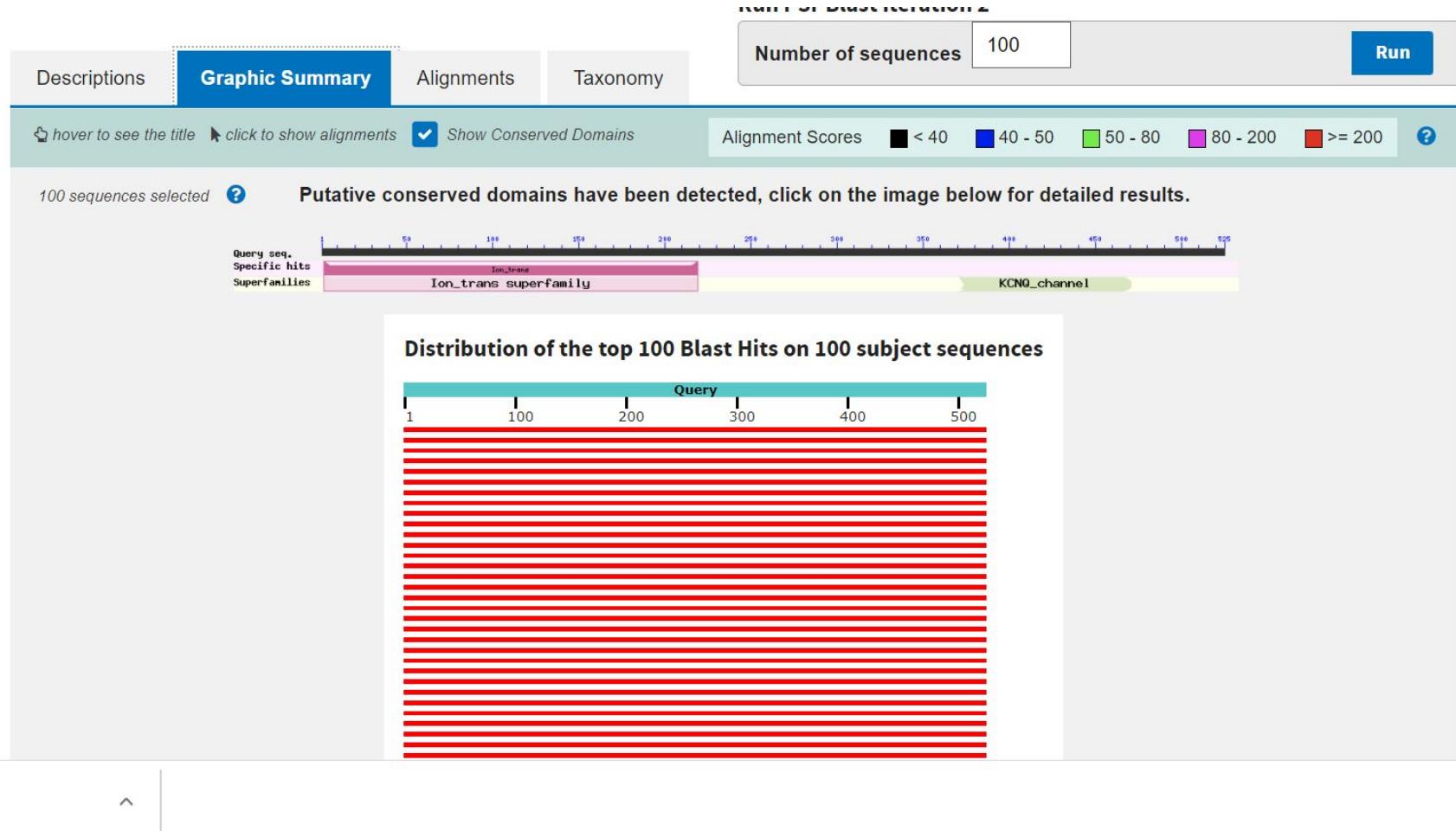
Sequences with E-value BETTER than threshold -

Select all 100 sequences selected PSI-BLAST iteration 1

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession	Select for PSI blast	Used to build PSSM	Newly added
<input checked="" type="checkbox"/>	potassium voltage-gated channel, KQT-like subfamily, member 1, isoform CRA_b [Homo sapiens]	Homo sapiens	1056	1056	100%	0.0	97.93%	586	EAX02518.1	<input checked="" type="checkbox"/>		
<input checked="" type="checkbox"/>	potassium voltage-gated channel subfamily KQT member 1 isoform 2 precursor [Homo sapiens]	Homo sapiens	1056	1056	100%	0.0	97.93%	549	NP_861463.1	<input checked="" type="checkbox"/>		
<input checked="" type="checkbox"/>	voltage gated potassium channel [Homo sapiens]	Homo sapiens	1054	1054	100%	0.0	97.93%	581	AAC51781.1	<input checked="" type="checkbox"/>		
<input checked="" type="checkbox"/>	potassium voltage-gated channel subfamily KQT member 1 isoform 1 [Homo sapiens]	Homo sapiens	1054	1054	100%	0.0	97.93%	676	NP_000209.2	<input checked="" type="checkbox"/>		
<input checked="" type="checkbox"/>	KvLQT1 [Homo sapiens]	Homo sapiens	1053	1053	100%	0.0	97.74%	549	CAB44650.1	<input checked="" type="checkbox"/>		
<input checked="" type="checkbox"/>	KvLQT1 [Homo sapiens]	Homo sapiens	1051	1051	100%	0.0	97.74%	676	CAB44649.1	<input checked="" type="checkbox"/>		
<input checked="" type="checkbox"/>	potassium voltage-gated channel subfamily KQT member 1 isoform X2 [Pongo abelii]	Pongo abelii	1050	1050	100%	0.0	97.36%	549	XP_024111354.1	<input checked="" type="checkbox"/>		
<input checked="" type="checkbox"/>	slow delayed rectifier channel subunit [Homo sapiens]	Homo sapiens	1050	1050	100%	0.0	97.74%	548	AAC05705.1	<input checked="" type="checkbox"/>		
<input checked="" type="checkbox"/>	potassium voltage-gated channel subfamily KQT member 1 isoform X1 [Gorilla gorilla gorilla] Gorilla gorilla...	Gorilla gorilla	1049	1049	100%	0.0	97.36%	549	XP_004050494.1	<input checked="" type="checkbox"/>		
<input checked="" type="checkbox"/>	potassium voltage-gated channel subfamily KQT member 1 isoform X1 [Pongo abelii]	Pongo abelii	1048	1048	100%	0.0	97.36%	676	XP_024111353.1	<input checked="" type="checkbox"/>		
<input checked="" type="checkbox"/>	potassium voltage-gated channel subfamily KQT member 1 isoform X2 [Pan paniscus]	Pan paniscus	1048	1048	100%	0.0	97.36%	549	XP_024178781.1	<input checked="" type="checkbox"/>		

Feedback

comparing the results: no difference btw graphic summaries



comparing the results: the first alignments are same

Descriptions Graphic Summary Alignments Taxonomy Number of sequences 100 Run

Alignment view Pairwise ? Restore defaults Download

100 sequences selected ?

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potassium voltage-gated channel, KQT-like subfamily, member 1, isoform CRA_b [Homo sapiens]

Sequence ID: [EAX02518.1](#) Length: 586 Number of Matches: 1

Range 1: 51 to 581 [GenPept](#) [Graphics](#) ▾ Next Match ▲ Previous Match

Score	Expect	Method	Identities	Positives	Gaps
1056 bits(2731)	0.0	Compositional matrix adjust.	520/531(98%)	520/531(97%)	6/531(1%)

Related Information
[Gene](#) - associated gene details

Query	51	VLSTIEQYAALATGTLFWMEIVLVVFFTEYVVRLLWSAGCRSKYVGLWGRRLFARKPISI	60
Query	61	IDLIVVVASMVVLCVGSKGQVFATSAIRWIRFLQILRMLHVDRQGGTWRLLLGSVVFIHRQ	120
Query	121	ELITTLTIGFLGLIFSSYFVYLAEKDAVNESGRVEFGSYADALWWVVTVTIIGYGDKVP	180
Query	181	QTWVGKTIASCFSVFAISFFALPAGILGSGFALKVQQKQRQKHNRQIPAAASLIQTAWR	240
Query	241	CYAAENPDSTSWKIYIRKAPRSHTLLSGSPKPKKS VVVKKKKFKLKDNGVTPGEKMLTV	300
Sbjct	51	VLSTIEQYAALATGTLFWMEIVLVVFFTEYVVRLLWSAGCRSKYVGLWGRRLFARKPISI	110
Sbjct	111	IDLIVVVASMVVLCVGSKGQVFATSAIRWIRFLQILRMLHVDRQGGTWRLLLGSVVFIHRQ	170
Sbjct	171	ELITTLTIGFLGLIFSSYFVYLAEKDAVNESGRVEFGSYADALWWVVTVTIIGYGDKVP	230
Sbjct	231	QTWVGKTIASCFSVFAISFFALPAGILGSGFALKVQQKQRQKHNRQIPAAASLIQTAWR	290

comparing the results: the second alignments are same

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potassium voltage-gated channel subfamily KQT member 1 isoform 2 precursor [Homo sapiens]

Sequence ID: [NP_861463.1](#) Length: 549 Number of Matches: 1

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Range 1: 14 to 544 [GenPept](#) [Graphics](#) ▼ Next Match ▲ Previous Match

Score	Expect	Method	Identities	Positives	Gaps
1056 bits(2730)	0.0	Compositional matrix adjust.	520/531(98%)	520/531(97%)	6/531(1%)

Query 1 VLSTIEQYAALATGTLFWMEIVLVVFFGTEYVVRWLWSAGCRSKYVGLWGRRLFARKPISI 60
Sbjct 14 VLSTIEQYAALATGTLFWMEIVLVVFFGTEYVVRWLWSAGCRSKYVGLWGRRLFARKPISI 73

Query 61 IDLIVVVASMVVLCVGSKGQVFATSAIRWIRFLQILRMLHVDRQGGTWRLLLGSVVFIHRQ 120
Sbjct 74 IDLIVVVASMVVLCVGSKGQVFATSAIRGIRFLQILRMLHVDRQGGTWRLLLGSVVFIHRQ 133

Query 121 ELITTLTYIGFLGLIFSSYFVYLAEKDAVNESGRVEFGSYADALWWVVTVTTIGYGDKVP 180
Sbjct 134 ELITTLTYIGFLGLIFSSYFVYLAEKDAVNESGRVEFGSYADALWW VVTVTITIGYGDKVP 193

Query 181 QTWVGKTIASCFSVFAISFFALPAGILGSGFALKVQQKQRQKHFNRRQIPAAASLIQTAWR 240
Sbjct 194 QTWVGKTIASCFSVFAISFFALPAGILGSGFALKVQQKQRQKHFNRRQIPAAASLIQTAWR 253

Query 241 CYAAENPDSTSSTWKIYIRKAPRSHTLLSGSPPKKSVVKKKKFKLDKDNGVTPEKMLTV 300
Sbjct 254 CYAAENPDSTSSTWKIYIRKAPRSHTLLSPSPKPKKSVVKKKKFKLDKDNGVTPEKMLTV 313

Query 301 PHITCDPPEERRLDHFSVDGYDSSVRKSPTLLEVSMPHFMRNTNSFAEDLDLEGETLLTPI 360
Sbjct 314 PHITCDPPEERRLDHFSVDGYDSSVRKSPTLLEVSMPHFMRNTNSFAEDLDLEGETLLTPI 373

Related Information

[Gene](#) - associated gene details
[Genome Data Viewer](#) - aligned genomic context
[Identical Proteins](#) - Identical proteins to NP_861463.1

[Feedback](#)

comparing the results: the third alignments are same

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voltage gated potassium channel [Homo sapiens]
Sequence ID: AAC51781.1 Length: 581 Number of Matches: 1

Range 1: 46 to 576 GenPept Graphics ▾ Next Match ▲ Previous Match

Score	Expect	Method	Identities	Positives	Gaps
1054 bits(2726)	0.0	Compositional matrix adjust.	520/531(98%)	520/531(97%)	6/531(1%)

Query 1 VLSTIEQYAALATGTLFWMEIVLVVFFGTEYVVRLWSAGCRSKYVGLWGRRLRFARKPISI 60
VLSTIEQYAALATGTLFWMEIVLVVFFGTEYVVRLWSAGCRSKYVGLWGRRLRFARKPISI
Sbjct 46 VLSTIEQYAALATGTLFWMEIVLVVFFGTEYVVRLWSAGCRSKYVGLWGRRLRFARKPISI 105

Query 61 IDLIVVVASMVLCVGSKQVFATSAIRWIRFLQILRMLHVDRQGGTWRLLGSVVFIIHQ 120
IDLIVVVASMVLCVGSKQVFATSAIR IRFLQILRMLHVDRQGGTWRLLGSVVFIIHQ
Sbjct 106 IDLIVVVASMVLCVGSKQVFATSAIRGIRFLQILRMLHVDRQGGTWRLLGSVVFIIHQ 165

Query 121 ELITTLYIGFLGLIFSSYFVYLAEKDAVNESGRVEFGSYADALWWVVTVTTIGYGDKVP 180
ELITTLYIGFLGLIFSSYFVYLAEKDAVNESGRVEFGSYADALWW VVTVTITIGYGDKVP
Sbjct 166 ELITTLYIGFLGLIFSSYFVYLAEKDAVNESGRVEFGSYADALWWGVVTVTITIGYGDKVP 225

Query 181 QTWVGKTIASCFSVFAISFFALPAGILGSGFALKVQQKQRQKHFNQRQIPAAASLIQTAWR 240
QTWVGKTIASCFSVFAISFFALPAGILGSGFALKVQQKQRQKHFNQRQIPAAASLIQTAWR
Sbjct 226 QTWVGKTIASCFSVFAISFFALPAGILGSGFALKVQQKQRQKHFNQRQIPAAASLIQTAWR 285

Query 241 CYAAENPDSTS WKIYIRKAPRSHTLLSGSPKPKKSVVVKKKFKLKDNGVTPGEKMLTV 300
CYAAENPDSTS WKIYIRKAPRSHTLLS SPKP KKSVVVKKKFKLKDNGVTPGEKMLTV
Sbjct 286 CYAAENPDSTS WKIYIRKAPRSHTLLSPSPKPKKSVVVKKKFKLKDNGVTPGEKMLTV 345

Query 301 PHITCDPPEERRLDHFSVDGYDSSVRKSPTLLEVSMPHFMRTNSFAEDLDLEGETLLTPI 360
PHITCDPPEERRLDHFSVDGYDSSVRKSPTLLEVSMPHFMRTNSFAEDLDLEGETLLTPI
Sbjct 346 PHITCDPPEERRLDHFSVDGYDSSVRKSPTLLEVSMPHFMRTNSFAEDLDLEGETLLTPI 405

Query 361 THISQLREHHHRATIKVIRRMRQYFVAKKKFQQARKGYDVRDVIEQYSQGHNLNMVRIKELO 420
THISQLREHHHRATIKVIRRMRQYFVAKKKFQQARK YDVRDVIEQYSQGHNLNMVRIKELO
Sbjct 406 THTSOLREHHHRATTKVTRRMOYEVAKKKFQQARKPVYDVRDVIEQYSOGHNI MVRTKELO 465

Related Information
[Gene](#) - associated gene details

comparing the results: taxonomic distributions are the same

Run PSI-Blast Iteration 2

Number of sequences 100

Descriptions Graphic Summary Alignments Taxonomy

Reports Lineage Organism Taxonomy

100 sequences selected ?

Organism	Blast Name	Score	Number of Hits	Description
root		136		
Boreoeutheria	placentals	130		
Euarchontoglires	placentals	91		
Primates	primates	75		
Simiiformes	primates	74		
Catarrhini	primates	69		
Hominoidea	primates	45		
Hominidae	primates	43		
Homininae	primates	39		
Homo sapiens	primates	1056	28	Homo sapiens hits
Gorilla gorilla gorilla	primates	1049	2	Gorilla gorilla gorilla hits
Pan paniscus	primates	1048	3	Pan paniscus hits
Pan troglodytes	primates	1047	6	Pan troglodytes hits
Pongo abelii	primates	1050	4	Pongo abelii hits
Nomascus leucogenys	primates	1043	1	Nomascus leucogenys hits
Hylobates moloch	primates	1043	1	Hylobates moloch hits

<input type="checkbox"/>	potassium voltage-gated channel subfamily KQT member 1 isoform X1 [Physeter catodon]	Physeter cato...	926	926	100%	0.0	89.85%	677	XP_023989081.1	<input checked="" type="checkbox"/>
<input type="checkbox"/>	potassium voltage-gated channel subfamily KQT member 1 [Marmota flaviventris]	Marmota flavi...	926	926	100%	0.0	88.89%	671	XP_027800317.1	<input checked="" type="checkbox"/>
<input type="checkbox"/>	potassium voltage-gated channel subfamily KQT member 1 [Enhydra lutris kenyoni]	Enhydra lutris...	923	923	100%	0.0	86.59%	667	XP_022362746.1	<input checked="" type="checkbox"/>
<input type="checkbox"/>	potassium voltage-gated channel subfamily KQT member 1 isoform X1 [Lontra canadensis]	Lontra canad...	922	922	100%	0.0	87.22%	670	XP_032735647.1	<input checked="" type="checkbox"/>
<input type="checkbox"/>	potassium voltage-gated channel subfamily KQT member 1 [Ictidomys tridecemlineatus]	Ictidomys trid...	922	922	100%	0.0	88.89%	590	XP_005340461.2	<input checked="" type="checkbox"/>
<input type="checkbox"/>	potassium voltage-gated channel subfamily Q member 1 [Ictidomys tridecemlineatus]	Ictidomys trid...	922	922	100%	0.0	88.89%	591	KAG3284425.1	<input checked="" type="checkbox"/>
<input type="checkbox"/>	potassium voltage-gated channel subfamily KQT member 1 isoform X10 [Mustela putorius]	Mustela putori...	921	921	100%	0.0	84.73%	572	XP_044922430.1	<input checked="" type="checkbox"/>
<input type="checkbox"/>	potassium voltage-gated channel subfamily KQT member 1 isoform X1 [Mustela putorius f.	Mustela putori...	920	920	100%	0.0	84.73%	688	XP_044922403.1	<input checked="" type="checkbox"/>
<input type="checkbox"/>	potassium voltage-gated channel subfamily KQT member 1 [Microtus ochrogaster]	Microtus ochr...	920	920	100%	0.0	88.14%	669	XP_005351635.1	<input checked="" type="checkbox"/>
<input type="checkbox"/>	potassium voltage-gated channel subfamily KQT member 1 [Orcinus orca]	Orcinus orca	919	919	100%	0.0	89.66%	673	XP_004278112.1	<input checked="" type="checkbox"/>
<input type="checkbox"/>	potassium voltage-gated channel subfamily KQT member 1 isoform X2 [Jaculus jaculus]	Jaculus jaculus	919	919	99%	0.0	89.25%	561	XP_045005992.1	<input checked="" type="checkbox"/>
<input type="checkbox"/>	potassium voltage-gated channel subfamily KQT member 1 isoform X6 [Halichoerus grypus]	Halichoerus g...	919	919	100%	0.0	88.91%	547	XP_035923692.1	<input checked="" type="checkbox"/>
<input checked="" type="checkbox"/>	potassium voltage-gated channel subfamily KQT member 1 isoform X2 [Manis javanica]	Manis javanica	918	918	100%	0.0	89.47%	673	XP_036867365.1	<input checked="" type="checkbox"/>
<input checked="" type="checkbox"/>	potassium voltage-gated channel subfamily KQT member 1 isoform X1 [Jaculus jaculus]	Jaculus jaculus	918	918	99%	0.0	89.25%	664	XP_004654281.1	<input checked="" type="checkbox"/>
<input checked="" type="checkbox"/>	potassium voltage-gated channel subfamily KQT member 1 [Pteropus alecto]	Pteropus alecto	917	917	100%	0.0	88.16%	728	XP_015444155.1	<input checked="" type="checkbox"/>
<input checked="" type="checkbox"/>	potassium voltage-gated channel subfamily KQT member 1 isoform X1 [Otolemur garnettii]	Otolemur gar...	917	917	99%	0.0	89.25%	675	XP_003798416.1	<input checked="" type="checkbox"/>
<input checked="" type="checkbox"/>	potassium voltage-gated channel subfamily Q member 1 isoform CRA_c [Rattus norvegicus]	Rattus norveg...	916	916	100%	0.0	88.70%	546	EDM12192.1	<input checked="" type="checkbox"/>

Run PSI-BLAST Iteration 2 with max number of sequences

100

Run

Feedback

Run PSI-Blast Iteration 2

Number of sequences 100 Run

Descriptions Graphic Summary Alignments Taxonomy

Alignment view Pairwise ▾

Pairwise
Pairwise with dots for identities
Query-anchored with dots for identities
Query-anchored with letters for identities
Flat query-anchored with dots for identities
Flat query-anchored with letters for identities

5 sequences selected

Loading align...

Restore defaults Download ▾



? Support Center

comparing results: same matches with BLAST and
PSI_BLAST

Number of sequences 100 **Run**

Descriptions Graphic Summary **Alignments** Taxonomy

Alignment view Flat querv-anchored with dots for identities Line length: 60 **Restore defaults** Download

Download ▾ **Query range 1: 1 to 60**

Query	Length	Sequence	Length
XP_036867365_1	139	VLSTIEQYAALATGTLFWMEIVLVFFGTEYVVRWLWSAGCRSKYVGLWGRRLFARKPISI	60
XP_004654281_1	138V.....	198
XP_015444155_1	195V.....	197
XP_003798416_1	142I.....	254
EDM12192_1	18I.....	201
	I.....	77

Download ▾ **Query range 2: 61 to 120**

Query	Length	Sequence	Length
XP_036867365_1	199	IDLIVVVASMVVLCVGSKGQVFATSAIRWIRFLQILRMLHVDRQGGTWRLLGSVVFIRHQ	120
XP_004654281_1	198G.....	258
XP_015444155_1	255G.....	257
XP_003798416_1	202G.....	314
EDM12192_1	78G.....	261
	G.....	137

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Query range 3: 121 to 180

Query	Start	Sequence	End
XP_036867365_1	121	ELITTLIGFLGLIFSSYFVYLAEKDAVNESGRVEFGSYADALWWVVTVTTIGYGDKV	180
XP_004654281_1	259G.....	318
XP_015444155_1	258	I.....G.....	317
XP_003798416_1	315G.....	374
EDM12192_1	262	..V.....G.....	321
EDM12192_1	138I.....G.....	197

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Query range 4: 181 to 240

Query	Start	Sequence	End
XP_036867365_1	181	QTWVGKTIASCFSVFAISFFALPAGILGSGFALKVQQKQRQKHFNQRQIPAAASLIQTAWR	240
XP_004654281_1	319	378
XP_015444155_1	318	377
XP_003798416_1	375V.....	434
EDM12192_1	322T.....	381
EDM12192_1	198	257

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Query range 5: 241 to 300

Query	Start	Sequence	End
XP_036867365_1	241	CYAAENPDSSTWKIYIRKAPRSHTLLGSPKPCKSVVKKKKFKLDKDNGVTPEKMLTV	300
XP_004654281_1	379E.....V..PS...P...P.....AL.....G.....	438
XP_015444155_1	378V..PA...A...P.....M.....S.....	437
XP_003798416_1	435	...T.....A.....V..PS.G.S...P.....AMM.....R.....S.....T...	494
EDM12192_1	382V..PS..PA...P.....M.....V.....S....K..I	441
EDM12192_1	258V..PA.....P.....M.....LS....IFN.	317

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Query range 6: 301 to 360

Query	Start	Sequence	End	Score
XP_036867365_1	301	PHITCDP-PEERRLDHFSVDGYDSSVRKSPTLLEVSMPHFMRTNSFAEDLDLEGETLLTP	359	
XP_004654281_1	439E.VA....P.....C....KR..M....PA.....A.	498	
XP_015444155_1	438-.....P.....I.....T..L.....D.....A.	496	
XP_003798416_1	495HV.D.Q.T.P....C....K..SM....T.Q.V....T.....A.	554	
EDM12192_1	442-.....Q.PG.....T.....T..I.....A.	500	
	318-.....D..P.....I.....T..L.....	376	

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Query range 7: 361 to 420

Query	Start	Sequence	End	Score
XP_036867365_1	360	I THISQLREHHHRATIKVIRRMQYFVAKKKFQQARKGYDVRDVIEQYSQGHLNL MVRIKEL	419	
XP_004654281_1	499	...V.....R.....P.....	558	
XP_015444155_1	497	...V.....P.....	556	
XP_003798416_1	555	...V.....V.....R.....P.....	614	
EDM12192_1	501D.....P.....	560	
	377	...V...D.....P.....	436	

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Query range 8: 421 to 480

Query	Start	Sequence	End	Score
XP_036867365_1	420	QRRLDQSIGKPSLFISVS-----WSNTIGARLN RVEDKVTQLDQRLALITDMLHQ LLSL	473	
XP_004654281_1	559A.EKS KDRGN.S.....V..E.....	618	
XP_015444155_1	557LPI.EKG KDRG.....K.VV.....	616	
XP_003798416_1	615EKS KDRG.....V.....	674	
EDM12192_1	561P..EKS KDRGN.....V..L.....	620	
	437PI.EKS KDRG.....VI.....	496	

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Query range 9: 481 to 532

Query	Start	Sequence	End
XP_036867365.1	474	HGGSTPGSGGPPREGGAHITQPCGSGGSVDPELFLPSNLTLPYEQLTVPRRG	525
XP_004654281.1	619	.Q.GL...H..SGV..QVA.....S.IS.....SA.....	668
XP_015444155.1	617	YQ.GPAS.NR.QH..DSN-----IN.....A.....	658
XP_003798416.1	675	.Q.GP...RA.SGS..QLA....R..IN.....	723
EDM12192.1	621	.R..P...SLG..RPLAV...V..STIN.....SP.....Q.	669
	497	Q-----Q...TCNNRSQVV-ASDE...IN.....S.....QT.	541

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