

BLAST двух последовательностей

С.А.Спирин, 21 октября 2025

BLAST: Basic Local Alignment Search Tool

https://blast.ncbi.nlm.nih.gov/Blast.cgi

An official website of the United States government [Here's how you know](#)

NIH National Library of Medicine
National Center for Biotechnology Information

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Basic Local Alignment Search Tool

BLAST finds regions of similarity between biological sequences. The program compares nucleotide or protein sequences to sequence databases and calculates the statistical significance. [Learn more](#)

BLAST+ 2.13.0 is here!

Starting with this release, we are including the blastn_vdb and tblastn_vdb executables in the BLAST+ distribution.

Thu, 17 March 2022 [More BLAST news...](#)

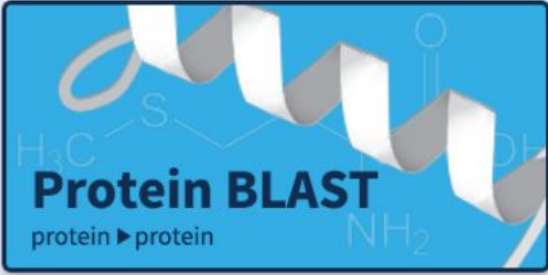
Web BLAST



Nucleotide BLAST
nucleotide ► nucleotide

blastx
translated nucleotide ► protein

tblastn
protein ► translated nucleotide



Protein BLAST
protein ► protein

Nucleotide BLAST: Search nucleot...
https://blast.ncbi.nlm.nih.gov/Blast.cgi?PROGRAM=blastn&PAGE_TYPE=BlastSearch&LINK_LOC=blasthome

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BLAST® » blastn suite Home Recent Results Saved Strategies Help

Standard Nucleotide BLAST

blastn blastp blastx tblastn tblastx

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

Enter Query Sequence

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

Query subrange [?](#)

From

To

Or, upload file Не выбран ... один файл [?](#)

Job Title

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

☐ Align two or more sequences [?](#)

Choose Search Set

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

Nucleotide collection (nr/nt) [?](#)

Organism Optional ☐ exclude [Add organism](#)

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

Exclude ☐ Models (XM/XP) ☐ Uncultured/environmental sample sequences

Align Sequences Nucleotide BLAST

blastn

blastp

blastx

tblastn

tblastx

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

Reset page

Bookmark

Enter Query Sequence

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

AE010300

Query subrange ?

From

To

Or, upload file

Выбор файла Не выбран ... один файл ?

Job Title

AE010300:Leptospira interrogans serovar Lai...

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

AE016823

Subject subrange ?

From

To

[Edit Search](#)

[Save Search](#)

[Search Summary](#) ▼

[How to read this report?](#)

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Job Title	AE010300:Leptospira interrogans serovar Lai...
RID	PKXMGDCT114 Search expires on 11-09 13:26 pm Download All ▼
Program	Blast 2 sequences Citation ▼
Query ID	AE010300.2 (nucleic acid)
Query Descr	Leptospira interrogans serovar Lai str. 56601 chromosom ...
Query Length	4338762
Subject ID	AE016823.1 (nucleic acid)
Subject Descr	Leptospira interrogans serovar Copenhageni str. Fiocruz ...
Subject Length	4277185
Other reports	MSA viewer ?

Filter Results

Percent Identity

 to

E value

 to

Query Coverage

 to

[Filter](#)

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Descriptions

[Graphic Summary](#)

[Alignments](#)

[Dot Plot](#)

Sequences producing significant alignments

[Download](#) ▼

[Select columns](#) ▼

[Show](#)

100 ▼

?

☒ select all 1 sequences selected

[GenBank](#)

[Graphics](#)

[MSA Viewer](#)

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☒	Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130, chromosome I, complete sequ...	Leptospira interrogans	2.038e+05	1.560e+07	97%	0.0	99.42%	4277185	AE016823.1

Карта локального сходства

Query ID [CP002549.1](#) (nucleic acid)
Query Descr Chlamydia psittaci 6BC, complete genome
Query Length 1171660
Subject ID [CP002744.1](#) (nucleic acid)
Subject Descr Chlamydia psittaci Mat116 chromosome, complete genome
Subject Length 1163362
Other reports [MSA viewer](#) ?

Filter

Reset

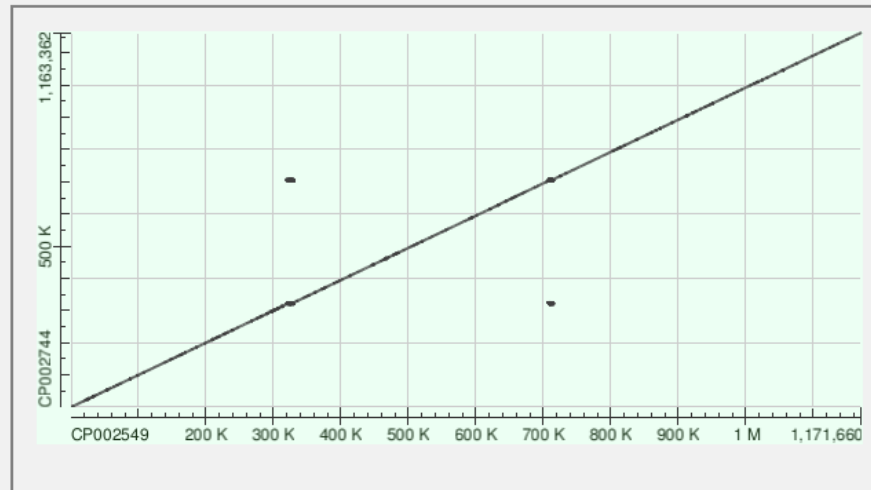
Descriptions

Graphic Summary

Alignments

Dot Plot

Plot of CP002549.1 vs CP002744.1 ?



Query Length 1171660
Subject ID [CP006571.1](#) (nucleic acid)
Subject Descr Chlamydia avium 10DC88 chromosome, complete genome
Subject Length 1041170
Other reports [MSA viewer](#) ?

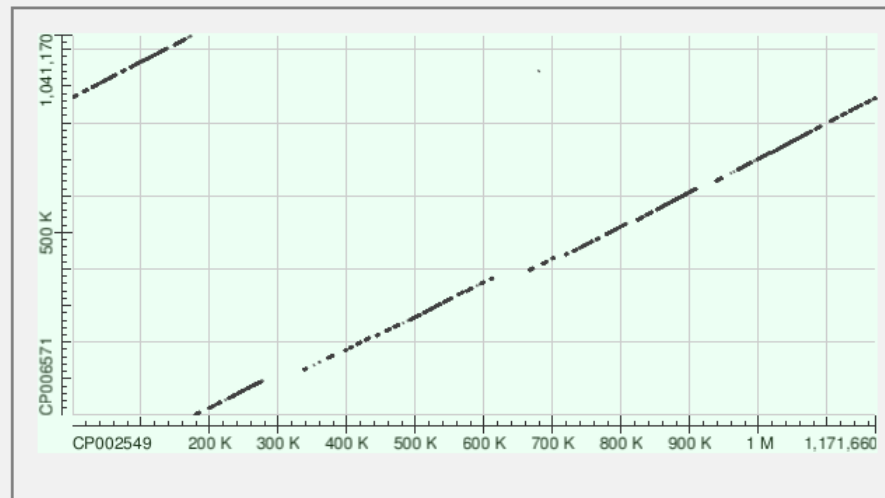
Descriptions

Graphic Summary

Alignments

Dot Plot

Plot of CP002549.1 vs CP006571.1 ?



RID [PKY2THTT114](#) Search expires on 11-09 13:34 pm [Download All](#) ▾

Program Blast 2 sequences [Citation](#) ▾

Query ID [CP002549.1](#) (nucleic acid)

Query Descr Chlamydia psittaci 6BC, complete genome

Query Length 1171660

Subject ID [CP017730.1](#) (nucleic acid)

Subject Descr Chlamydia trachomatis strain SQ32 chromosome, comple ...

Subject Length 1047716

Other reports [MSA viewer](#) ?

Percent Identity to

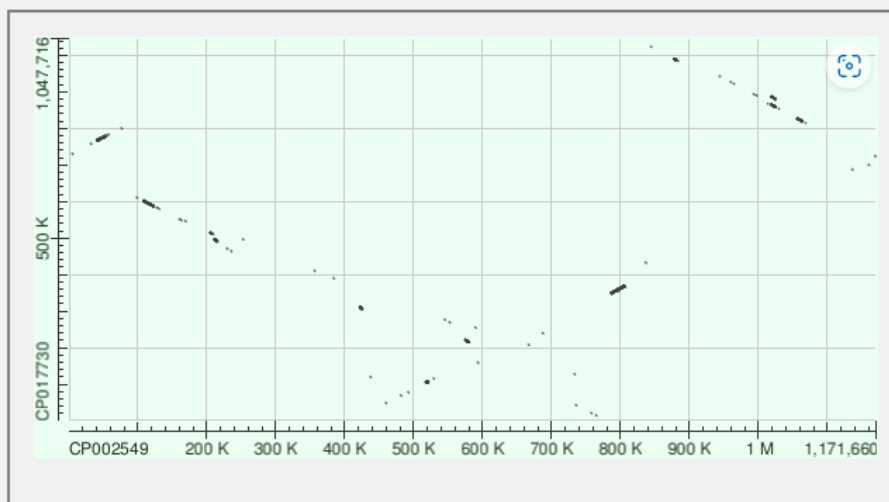
E value to

Query Coverage to

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

Descriptions Graphic Summary Alignments **Dot Plot**

Plot of CP002549.1 vs CP017730.1 ?



Nucleotide BLAST: Align two or more sequences

https://blast.ncbi.nlm.nih.gov/Blast.cgi

Bookmark

Enter Query Sequence

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

gb|CP002549

Query subrange ?

From

To

Or, upload file

Выбор файла

Не выбран ни один файл ?

Job Title

CP002549:Chlamydia psittaci 6BC chromosome,....

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

gb|CP017730

Subject subrange ?

From

To

Or, upload file

Выбор файла

Не выбран ни один файл ?

Program Selection

Optimize for

☒ Highly similar sequences (megablast)

☐ More dissimilar sequences (discontiguous megablast)

☐ Somewhat similar sequences (blastn)

Choose a BLAST algorithm ?

BLAST

Search nucleotide sequence using Megablast (Optimize for highly similar sequences)

☐ Show results in a new window

+ Algorithm parameters

FOLLOW NCBI

Megablast и BLASTN

Megablast предназначен для очень быстрого поиска той же самой последовательности (возможно, с небольшими ошибками или немногими мутациями)

- Длина слова 28
- Линейные (не афинные) штрафы за гэпы
- Слова в запросе для поиска в индексах берутся с шагом 4

BLASTN предназначен для поиска (достаточно близких, но всё же) гомологов

- Длина слова по умолчанию 11 (в веб-интерфейсе можно уменьшить до 7, в standalone варианте — до 4)
- Афинные штрафы за гэпы
- Берутся все слова запроса

Те же последовательности, но BLASTN вместо Megablast

NCBI Blast:CP002549:Chlamydia

https://blast.ncbi.nlm.nih.gov/Blast.cgi

Job Title CP002549:Chlamydia psittaci 6BC chromosome,...

RID PKY61277114 Search expires on 11-09 13:35 pm [Download All](#) ▼

Program Blast 2 sequences [Citation](#) ▼

Query ID CP002549.1 (nucleic acid)

Query Descr Chlamydia psittaci 6BC, complete genome

Query Length 1171660

Subject ID CP017730.1 (nucleic acid)

Subject Descr Chlamydia trachomatis strain SQ32 chromosome, comple ...

Subject Length 1047716

Other reports [MSA viewer](#) ?

Filter Results

Percent Identity to

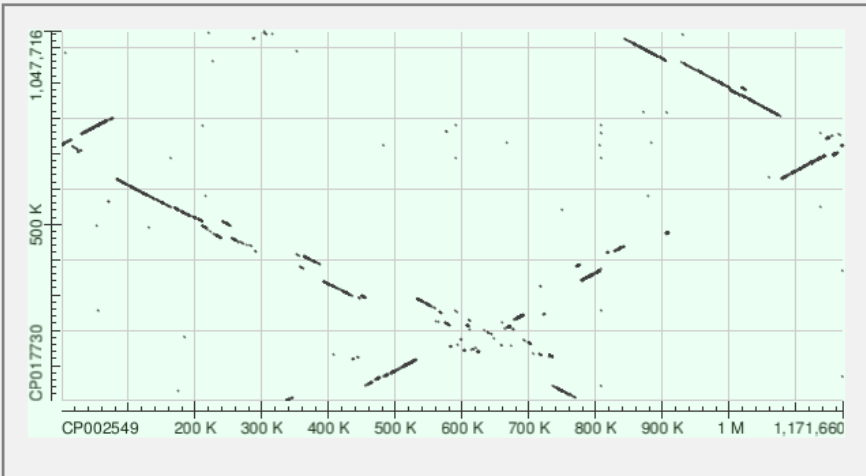
E value to

Query Coverage to

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

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

Plot of CP002549.1 vs CP017730.1 ?



CP017730

CP002549

200 K 300 K 400 K 500 K 600 K 700 K 800 K 900 K 1 M 1,171,660

500 K 1,047,716

[Feedback](#)

TBLASTX — транслируется и запрос, и база!

tbblastx: Align translated DNA wi x +

blast.ncbi.nlm.nih.gov/Blast.cgi?PAGE=Translations&PROGRAM=tbblastx&BLAST_PROGRAMS=tbblastx&PAGE_TYPE=BlastSearch&BLAST_SPEC...

NIH National Library of Medicine
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BLAST® » tbblastx

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Important update
The core nucleotide database (*core_nt*) is now the default nucleotide BLAST database. [Learn more about core_nt.](#)

blastn blastp blastx **tbblastx**

Align Sequences Translated BLAST: tbblastx

TBLASTX search translated nucleotide subjects using a translated nucleotide query. more...

Reset page Bookmark

Enter Query Sequence

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

CP002549

Query subrange [?](#)

From

To

Or, upload file

Выберите файл Файл не выбран [?](#)

Genetic code

Standard (1) v

Job Title

CP002549:Chlamydia psittaci 6BC chromosome,...

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

CP017730

Subject subrange [?](#)

From

To

Or, upload file

Выберите файл Файл не выбран [?](#)

BLAST

Search nucleotide sequence using Tblastx (Search translated nucleotide subjects using a translated nucleotide query)

☐ Show results in a new window

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

TBLASTX — транслируется и запрос, и база!

NCBI Blast:CP002549:Chlamydia × +

blast.ncbi.nlm.nih.gov/Blast.cgi

BLAST® » tblastx-2sequences » results for RID-J90FKJX3114

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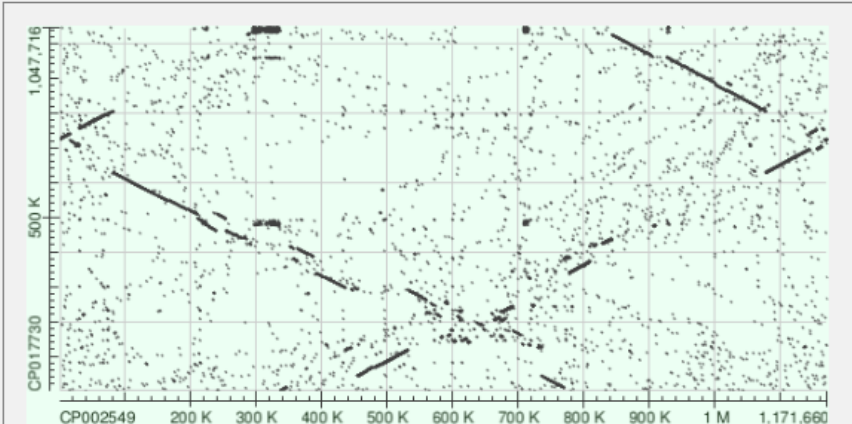
Job Title	CP002549:Chlamydia psittaci 6BC chromosome,...
RID	J90FKJX3114 Search expires on 11-02 15:23 pm Download All ▾
Program	Blast 2 sequences Citation ▾
Query ID	CP002549.1 (nucleic acid)
Query Descr	Chlamydia psittaci 6BC, complete genome
Query Length	1171660
Subject ID	CP017730.1 (nucleic acid)
Subject Descr	Chlamydia trachomatis strain SQ32 chromosome, comple...
Subject Length	1047716
Other reports	?

Filter Results

Percent Identity	E value	Query Coverage
to	to	to
Filter		Reset

Descriptions Graphic Summary Alignments **Dot Plot**

Plot of CP002549.1 vs CP017730.1 ?



CP017730 1,047,716 500 K

CP002549 200 K 300 K 400 K 500 K 600 K 700 K 800 K 900 K 1 M 1,171,660

Feedback

13

Повторы в геномах двух штаммов одного вида

NCBI Blast:AE010300:Leptospira

blast.ncbi.nlm.nih.gov/Blast.cgi

BLAST® » blastn suite-2sequences » results for RID-J91B1MKP114

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Important update

The core nucleotide database (**core_nt**) is now the default nucleotide BLAST database. [Learn more about core_nt.](#)

← Edit Search

Save Search

Search Summary ▾

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Job Title

AE010300:Leptospira interrogans serovar Lai...

RID

[J91B1MKP114](#) Search expires on 11-02 15:38 pm [Download All](#) ▾

Program

Blast 2 sequences [Citation](#) ▾

Query ID

[AE010300.2](#) (nucleic acid)

Query Descr

Leptospira interrogans serovar Lai str. 56601 chromosome ...

Query Length

4338762

Subject ID

[AE016823.1](#) (nucleic acid)

Subject Descr

Leptospira interrogans serovar Copenhageni str. Fiocruz L ...

Subject Length

4277185

Other reports

[MSA viewer](#) ?

Filter Results

Percent Identity

to

E value

to

Query Coverage

to

Filter

Reset

Descriptions

Graphic Summary

Alignments

Dot Plot

Plot of AE010300.2 vs AE016823.1 ?

