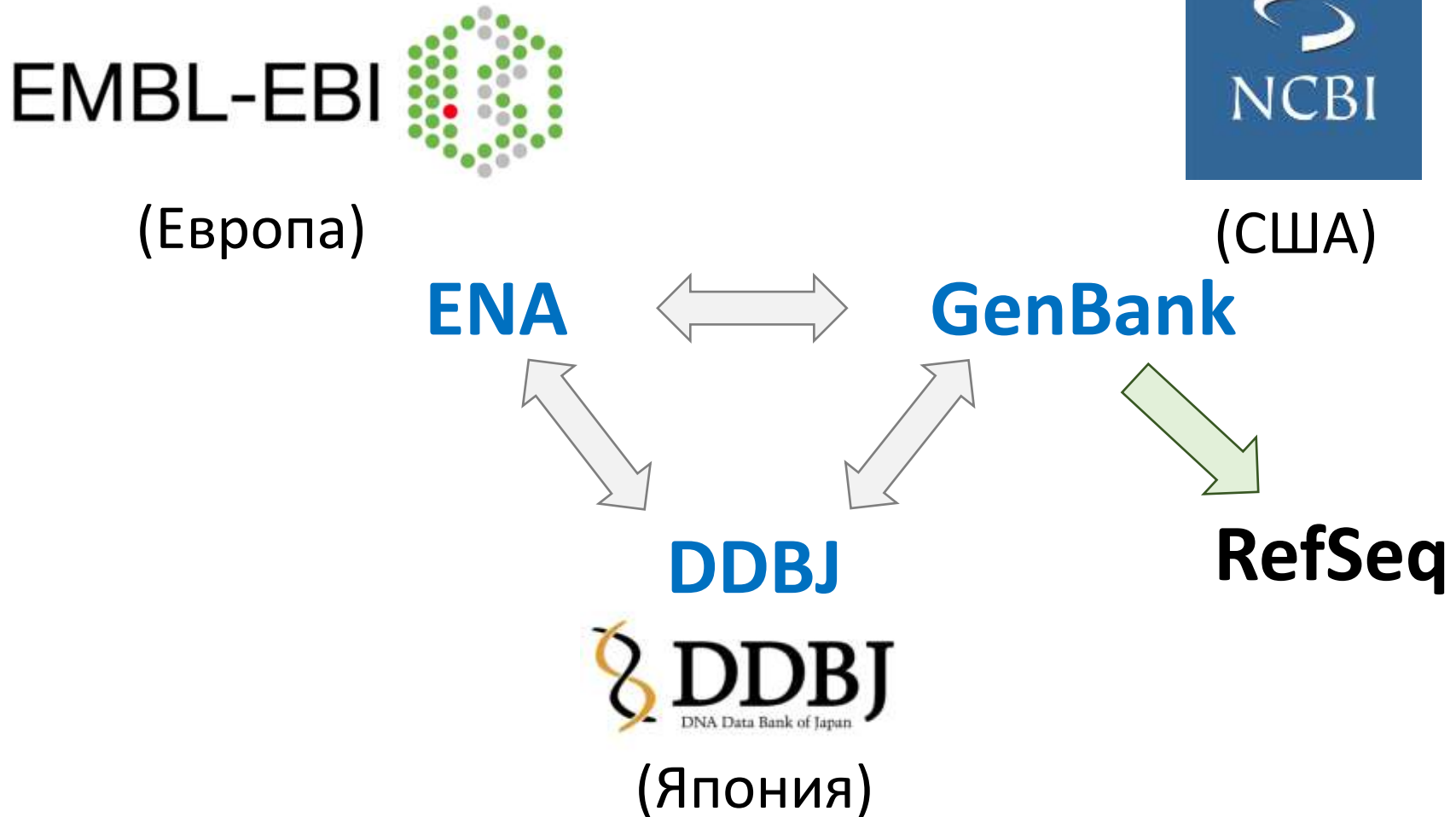


Поиск в нуклеотидных БД

С.А.Спирин, 7 ноября 2023

International Nucleotide Sequence Database Collaboration



Заглавная страница NCBI

National Center for Biotechnology Information

ncbi.nlm.nih.gov

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

NIH National Library of Medicine
National Center for Biotechnology Information

Log in

All Databases Search

NCBI Home

Resource List (A-Z)

- All Resources
- Chemicals & Bioassays
- Data & Software
- DNA & RNA
- Domains & Structures
- Genes & Expression
- Genetics & Medicine
- Genomes & Maps
- Homology
- Literature
- Proteins
- Sequence Analysis
- Taxonomy
- Training & Tutorials

Welcome to NCBI

The National Center for Biotechnology Information advances science and health by providing access to biomedical and genomic information.

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Deposit data or manuscripts into NCBI databases

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Find help documents, attend a class or watch a tutorial

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Explore NCBI research

Popular Resources

- PubMed
- Bookshelf
- PubMed Central
- BLAST
- Nucleotide**
- Genome
- SNP
- Gene
- Protein
- PubChem

NCBI News & Blog

New Annotations in RefSeq 24 Oct 2023

In July, August, and September, the NCBI Eukaryotic Genome Annotation



Log in

Nucleotide [Advanced](#) [Help](#)

Вам сюда



Nucleotide

The Nucleotide database is a collection of sequences from several sources, including GenBank, RefSeq, TPA and PDB. Genome, gene and transcript sequence data provide the foundation for biomedical research and discovery.

- ### Using Nucleotide
- [Quick Start Guide](#)
 - [FAQ](#)
 - [Help](#)
 - [GenBank FTP](#)
 - [RefSeq FTP](#)

- ### Nucleotide Tools
- [Submit to GenBank](#)
 - [LinkOut](#)
 - [E-Utilities](#)
 - [BLAST](#)
 - [Batch Entrez](#)

- ### Other Resources
- [GenBank Home](#)
 - [RefSeq Home](#)
 - [Gene Home](#)
 - [SRA Home](#)
 - [INSDC](#)

Advanced search на NCBI

The screenshot shows the NCBI Nucleotide Advanced Search Builder interface. At the top, there is a navigation bar with the NIH logo and the text "National Library of Medicine National Center for Biotechnology Information". A "Log in" button is located in the top right corner. Below the navigation bar, there are two tabs: "Nucleotide Home" and "Help". The main heading is "Nucleotide Advanced Search Builder". Below this, there is a message: "Filters activated: RefSeq. [Clear all](#)". A large text box contains the instruction: "Use the builder below to create your search". Below the text box, there are two links: "Edit" and "Clear". The "Builder" section contains two rows of search criteria. The first row has a dropdown menu set to "All Fields", an empty text input field, a minus sign, and a link "Show index list". The second row has a dropdown menu set to "AND", another dropdown menu set to "All Fields", an empty text input field, a minus sign, a plus sign, and a link "Show index list". Below the builder section, there is a "Search" button and a link "or Add to history". At the bottom, there is a "History" section with a table. The table has columns for "Search", "Add to builder", "Query", "Items found", and "Time". There are also links "Download history" and "Clear history" to the right of the table.

Advanced search - Nucleotide - 1 x +

ncbi.nlm.nih.gov/nuccore/advanced

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NIH National Library of Medicine
National Center for Biotechnology Information

Log in

Nucleotide Home Help

Nucleotide Advanced Search Builder

i Filters activated: RefSeq. [Clear all](#)

Use the builder below to create your search

[Edit](#) [Clear](#)

Builder

All Fields - [Show index list](#)

AND All Fields - + [Show index list](#)

Search or [Add to history](#)

History

[Download history](#) [Clear history](#)

Search	Add to builder	Query	Items found	Time
--------	----------------	-------	-------------	------

Advanced search на NCBI

The screenshot shows the NCBI Advanced Search page. The browser address bar displays `ncbi.nlm.nih.gov/nuccore/advanced`. The page header includes the NIH logo and the text "National Center for Human Genome Research". A "Log in" button is visible in the top right corner. A dropdown menu is open, listing various search fields such as "Accession", "All Fields", "Assembly", "Author", "BioProject", "BioSample", "Breed", "Component Accession", "Cultivar", "Division", "EC/RN Number", "Feature key", "Filter", "Gene Name", "Isolate", "Issue", "Journal", "Keyword", "Modification Date", "Organism", and "All Fields". The "All Fields" option is currently selected. Below the dropdown, there are search input fields, a "Search" button, and a "History" section with a table of previous searches.

Advanced search - Nucleotide - [+](#)

[ncbi.nlm.nih.gov/nuccore/advanced](#)

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

NIH National Center for Human Genome Research **Medicine** [Log in](#)

Nucleotide Home [Help](#)

Nucleotide Advanced Search

Filters activated: RefSeq

Use the [Clear](#)

[Edit](#)

Builder

[-](#) [Show index list](#)

[-](#) [+](#) [Show index list](#)

[Search](#) or [Add to history](#)

History [Download history](#) [Clear history](#)

Search	Add to builder	Query	Items found	Time
--------	----------------	-------	-------------	------

Запись банка RefSeq

LOCUS NZ_CP012604 355432 bp DNA circular CON 30-OCT-2022
DEFINITION *Leptospira interrogans* serovar Hardjo str. Norma voucher *Leptospira interrogans* isolate Cattle chromosome II, complete sequence.
ACCESSION NZ_CP012604
VERSION NZ_CP012604.1
DBLINK BioProject: PRJNA224116
BioSample: SAMN03853357
Assembly: GCF_001293065.1
KEYWORDS RefSeq.
SOURCE *Leptospira interrogans* serovar Hardjo str. Norma
ORGANISM *Leptospira interrogans* serovar Hardjo str. Norma
Bacteria; Spirochaetes; Leptospirales; Leptospiraceae; *Leptospira*.
REFERENCE 1 (bases 1 to 355432)
AUTHORS Cosate,M.R., Soares,S.C., Mendes,T.A., Raittz,R.T., Moreira,E.C.,
Leite,R., Fernandes,G.R., Haddad,J.P. and Ortega,J.M.
TITLE Whole-Genome Sequence of *Leptospira interrogans* Serovar Hardjo
Subtype Hardjoprajitno Strain Norma, Isolated from Cattle in a
Leptospirosis Outbreak in Brazil
JOURNAL Genome Announc 3 (6), e01302-15 (2015)
PUBMED 26543126
REMARK Publication Status: Online-Only
REFERENCE 2 (bases 1 to 355432)
AUTHORS Cosate,M.R.V., Soares,S.C., Mendes,T.A., Fernandes,G., Raitzz,R.T.,
Leite,R.C., Haddad,J.P.A., Moreira,E.C. and Ortega,J.M.
TITLE Direct Submission
JOURNAL Submitted (02-SEP-2015) Preventive Veterinary Medicine, Federal
University of Minas Gerais, Av Antonio Carlos, Belo Horizonte, 7
Minas Gerais 31270-901, Brazil

В форме поиска NCBI поле DEFINITION
называется Title

Search builder

The screenshot shows a web browser window with the URL `ncbi.nlm.nih.gov/nuccore/advanced`. The page header includes the NIH logo and the text "National Library of Medicine National Center for Biotechnology Information". A "Log in" button is visible in the top right. Below the header, there are navigation links for "Nucleotide Home" and "Help". The main content area is titled "Nucleotide Advanced Search Builder". A search query box contains the text "(chromosome[Title]) AND Leptospira[Organism]". Below the query box are links for "Edit" and "Clear". The "Builder" section contains three rows of search criteria: "Title" with the value "chromosome", "AND" with "Organism" and the value "Leptospira", and "AND" with "All Fields". Each row has a "Show index list" link. At the bottom of the builder section, there is a "Search" button and a link to "Add to history". The "History" section at the bottom shows a table with columns for "Search", "Add to builder", "Query", "Items found", and "Time".

Advanced search - Nucleotide - x +

ncbi.nlm.nih.gov/nuccore/advanced

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

NIH National Library of Medicine
National Center for Biotechnology Information

Log in

Nucleotide Home Help

Nucleotide Advanced Search Builder

(chromosome[Title]) AND Leptospira[Organism]

[Edit](#) [Clear](#)

Builder

Title	▼	chromosome	⊖	Show index list		
AND	▼	Organism	▼	Leptospira	⊖	Show index list
AND	▼	All Fields	▼		⊖ ⊕	Show index list

[Search](#) or [Add to history](#)

History

[Download history](#) [Clear history](#)

Search	Add to builder	Query	Items found	Time

Результат поиска

(chromosome[Title] AND leptosp: x +

ncbi.nlm.nih.gov/nuccore?term=(chromosome%5BTitle%5D)%20AND%20leptospira%5BOrganism%5D

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NIH National Library of Medicine
National Center for Biotechnology Information Log in

Nucleotide (chromosome[Title] AND leptospira[Organism]

Create alert Advanced Help

Species Summary ▾ 20 per page ▾ Sort by Default order ▾ **Запрос** Send to: ▾ **Filters:** [Manage Filters](#)

Bacteria (509)
Customize ...

Molecule types
genomic DNA/RNA (509)
Customize ...

Source databases **БД**
INSDC (GenBank) (264)
RefSeq (245)
Customize ...

Sequence Type
Nucleotide (509)

Sequence length
Custom range...

Release date
Custom range...

Revision date

Items: 1 to 20 of 509

<< First < Prev Page of 26 Next > Last >>

[Leptospira interrogans strain CUDO8 chromosome I map unlocalized](#)
1. [B_tig00000952_np1212, whole genome shotgun sequence](#)
50,270 bp linear DNA
Accession: NZ_NKYG02000004.1 GI: 2592316042
[Assembly](#) [BioProject](#) [BioSample](#) [Protein](#) [Taxonomy](#)
[GenBank](#) [FASTA](#) [Graphics](#)

[Leptospira interrogans strain CUDO8 chromosome II, whole genome shotgun](#)
2. [sequence](#)
357,163 bp circular DNA
Accession: NZ_NKYG02000002.1 GI: 2592316016
[Assembly](#) [BioProject](#) [BioSample](#) [Protein](#) [Taxonomy](#)
[GenBank](#) [FASTA](#) [Graphics](#)

Results by taxon

Top Organisms [Tree]
Leptospira interrogans (214)
Leptospira borgpetersenii (156)
Leptospira noguchii (38)
Leptospira santarosai (20)
Leptospira kirschneri (16)
All other taxa (65)
More...

Find related data

Database:

Search details 9

Результат поиска, ограниченный на RefSeq

The screenshot shows a web browser window displaying the NCBI Nucleotide search results page. The search query is "(chromosome[Title]) AND leptospira[Organism]". The results are filtered to show only RefSeq entries. The first result is "Leptospira interrogans strain CUDO8 chromosome I map unlocalized" with a whole genome shotgun sequence of 50,270 bp linear DNA. The second result is "Leptospira interrogans strain CUDO8 chromosome II, whole genome shotgun sequence" with a whole genome shotgun sequence of 357,163 bp circular DNA. The page includes navigation controls, filters, and a list of top organisms.

Search results for: (chromosome[Title]) AND leptospira[Organism]

Species: Bacteria (245)

Molecule types: genomic DNA/RNA (245)

Source databases: INSDC (GenBank) (0), RefSeq (245)

Sequence Type: Nucleotide (245)

Sequence length: Custom range...

Release date: Custom range...

Revision date: GenBank FASTA Graphics

Items: 1 to 20 of 245

Filters activated: RefSeq. Clear all

1. [Leptospira interrogans strain CUDO8 chromosome I map unlocalized](#)
[B_tig00000952_np1212, whole genome shotgun sequence](#)
50,270 bp linear DNA
Accession: NZ_NKYG02000004.1 GI: 2592316042
[Assembly](#) [BioProject](#) [BioSample](#) [Protein](#) [Taxonomy](#)
[GenBank](#) [FASTA](#) [Graphics](#)

2. [Leptospira interrogans strain CUDO8 chromosome II, whole genome shotgun sequence](#)
357,163 bp circular DNA
Accession: NZ_NKYG02000002.1 GI: 2592316016
[Assembly](#) [BioProject](#) [BioSample](#) [Protein](#) [Taxonomy](#)
[GenBank](#) [FASTA](#) [Graphics](#)

Results by taxon

Top Organisms [Tree]

- Leptospira interrogans (103)
- Leptospira borgpetersenii (76)
- Leptospira noguchii (18)
- Leptospira weilii (8)
- Leptospira kirschneri (8)
- All other taxa (32)

Find related data

Database: Select

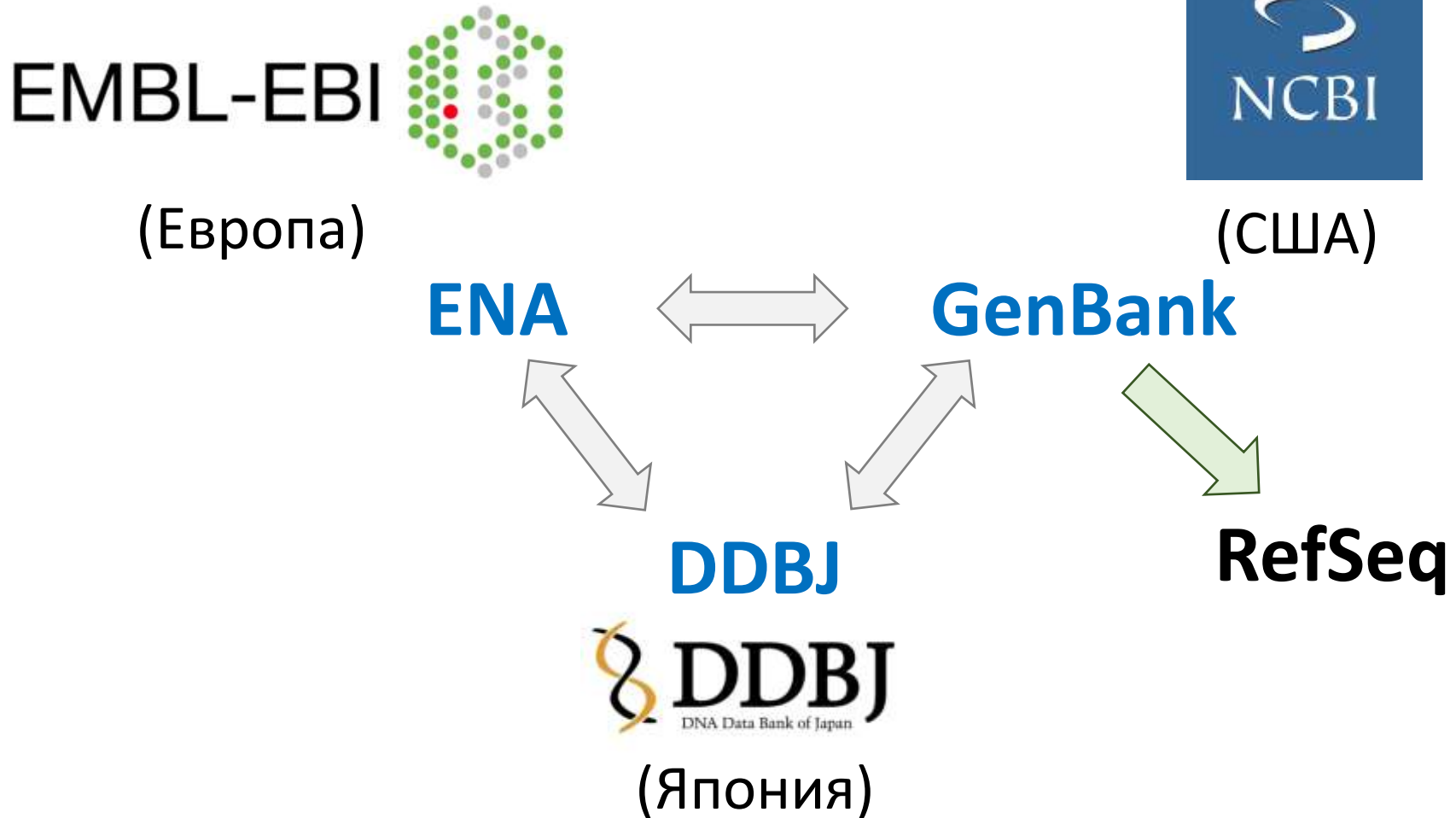
Find items

Search details

Поиск в нуклеотидных БД на сайте NCBI

- Два банка: GenBank и RefSeq
 - GenBank — архивная БД. Много лишнего
 - RefSeq — частично автоматическая, частично курируемая.
Геномы можно искать там (но лучше через NCBI genomes)
- Чтобы искать по полю “Definition”, нужно выбрать “Title”
- В запросах нельзя использовать маски (т.е. *)

International Nucleotide Sequence Database Collaboration





Enter text search terms Search

Examples: histone, BN000065

Enter accession View

Examples: Taxon:9606, BN000065, PRJEB402

Searching ENA

Вам сюда

ENA data can be searched and retrieved interactively and programmatically and visualized using the ENA Browser. Please refer to the following sections for more information about the ENA data access functionality with links to more detailed documentation.

Search term: Search

Uses [EBI Search](#) to perform a free text search across ENA data.

- Free Text Search
- Advanced Search
- Cross References
- Sequence Similarity Search
- Sequence Version Archive



The European Nucleotide Archive (ENA) is part of the ELIXIR infrastructure
The ENA is an ELIXIR Core Data Resource. [Learn more](#)



Enter text search terms Search

Examples: histone, BN000065

Enter accession View

Examples: Taxon:9606, BN000065, PRJEB402

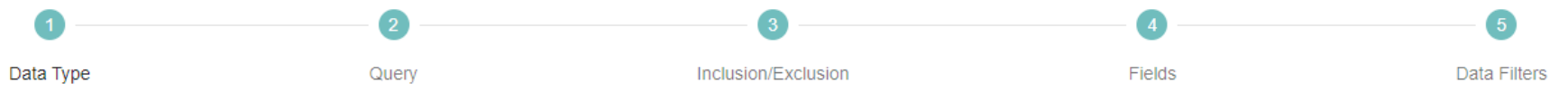
Advanced Search

Customise your own search query and retrieve a set of ENA records tailored to your search criteria.

[Documentation](#)

All searches are performed against a subset of the archive specified by the *Data type* you choose to search against. You can then build your search query to specify what data you are looking for and select what fields you want to retrieve from your search. There are additional options to include/exclude specific datasets as well as filter the number of results you wish to return.

If you intend to repeat the same search at a later date, you can save this as a Rule using [Rulespace](#). If you want to access the same data programmatically, you can copy the produced curl request and run this yourself against the [ENA Portal API](#).



Select datatype to build a new search

Data type:

- Studies used for nucleotide sequence analyses from reads
- Nucleotide sequence analyses from reads
- Genome assemblies
- Coding sequences
- Genome assembly contig sets (WGS)
- Transcriptome assembly contig sets (TSA)
- Targeted locus study contig sets (TLS)
- Environmental samples
- Non-coding sequences
- Studies used for raw reads
- Experiments used for raw reads
- Raw reads
- Samples
- Nucleotide sequences
- Studies

Use a previously defined Rulespace search

Rule ID/Name:

Reset

Next

Advanced Search

Customise your own search query and retrieve a set of ENA records tailored to your search criteria.

[Documentation](#)

All searches are performed against a subset of the archive specified by the *Data type* you choose to search against. You can then build your search query to specify what data you are looking for and select what fields you want to retrieve from your search. There are additional options to include/exclude specific datasets as well as filter the number of results you wish to return.

If you intend to repeat the same search at a later date, you can save this as a Rule using [Rulespace](#). If you want to access the same data programmatically, you can copy the produced curl request and run this yourself against the [ENA Portal API](#).



Query:

Reset

Build Query ?

Type to filter query params

- Taxonomy and related
- Geographical location
- Geography
- Collection event information
- Sampling information
- Sample state and conditions

AND OR + Add rule + Add group

NCBI Taxonomy = Leptospi ✕ Delete

Include subordinate taxa

NCBI taxonomic classification

Update query

Обязательно отметить!

Автодополнение названий таксонов

- Leptospira 171
- Leptospira abararensis 2810036
- Leptospira adleri 2023188
- Leptospira ainazelensis 2810034
- Leptospira ainlahdjerensis 2810033

Query:

tax_tree(171) AND description="chromosome"

Reset

Build Query ?

Type to filter query params

Taxonomy and related

Geographical location

Geography

Collection event information

Sampling information

Sample state and conditions

Host information

Sequencing information

Database record

Accessions

Titles, aliases and descriptions

AND OR

+ Add rule + Add group

Description

=

chromosome

Delete

brief sequence description

Update query

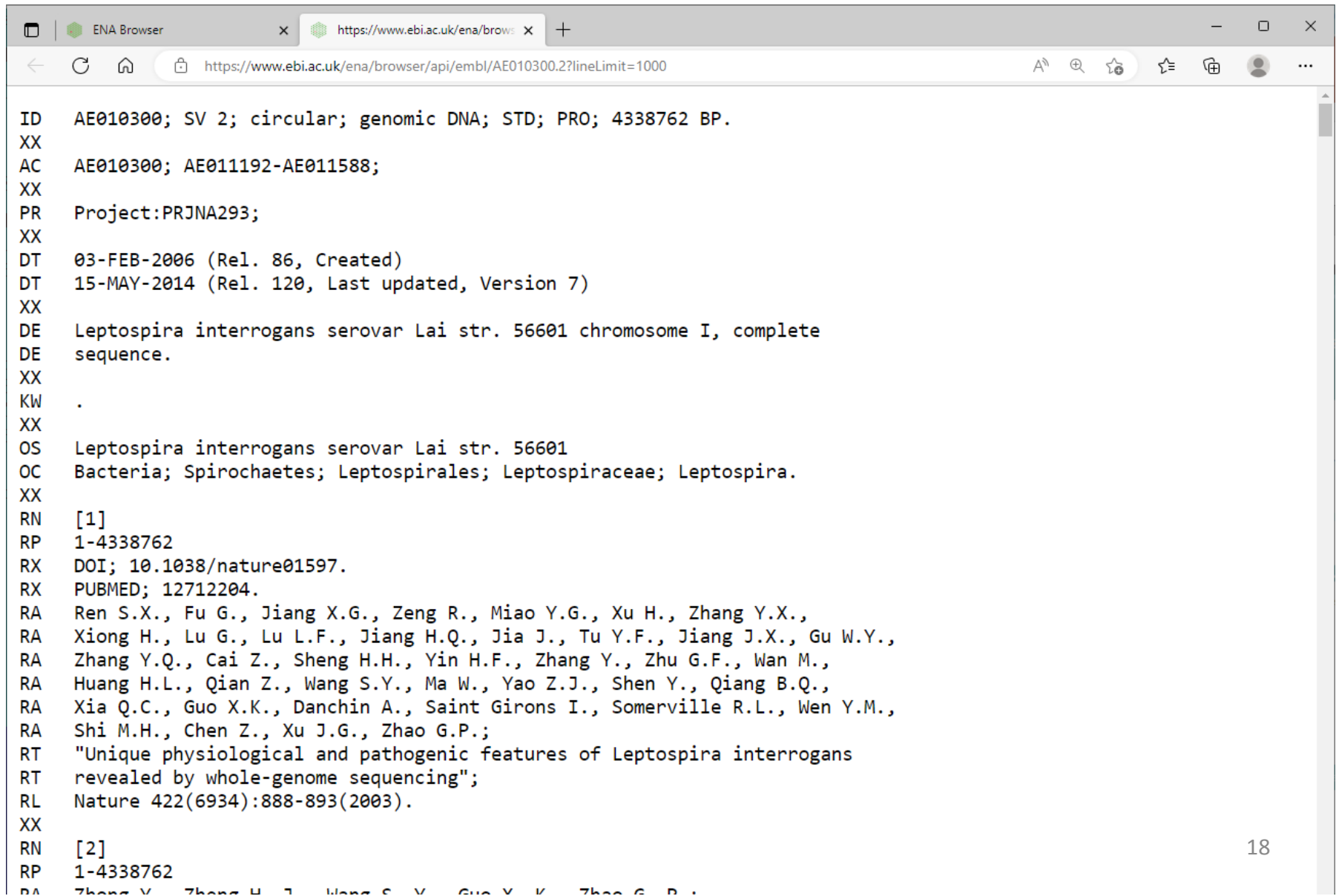
Back

Copy Curl Request

Next

Search

Запись банка EMBL (ENA), содержание общее с GenBank, формат другой



ENA Browser x https://www.ebi.ac.uk/ena/brow... x +
https://www.ebi.ac.uk/ena/browser/api/embl/AE010300.2?lineLimit=1000

ID AE010300; SV 2; circular; genomic DNA; STD; PRO; 4338762 BP.
XX
AC AE010300; AE011192-AE011588;
XX
PR Project:PRJNA293;
XX
DT 03-FEB-2006 (Rel. 86, Created)
DT 15-MAY-2014 (Rel. 120, Last updated, Version 7)
XX
DE Leptospira interrogans serovar Lai str. 56601 chromosome I, complete
DE sequence.
XX
KW .
XX
OS Leptospira interrogans serovar Lai str. 56601
OC Bacteria; Spirochaetes; Leptosirales; Leptospiraceae; Leptospira.
XX
RN [1]
RP 1-4338762
RX DOI; 10.1038/nature01597.
RX PUBMED; 12712204.
RA Ren S.X., Fu G., Jiang X.G., Zeng R., Miao Y.G., Xu H., Zhang Y.X.,
RA Xiong H., Lu G., Lu L.F., Jiang H.Q., Jia J., Tu Y.F., Jiang J.X., Gu W.Y.,
RA Zhang Y.Q., Cai Z., Sheng H.H., Yin H.F., Zhang Y., Zhu G.F., Wan M.,
RA Huang H.L., Qian Z., Wang S.Y., Ma W., Yao Z.J., Shen Y., Qiang B.Q.,
RA Xia Q.C., Guo X.K., Danchin A., Saint Girons I., Somerville R.L., Wen Y.M.,
RA Shi M.H., Chen Z., Xu J.G., Zhao G.P.;
RT "Unique physiological and pathogenic features of Leptospira interrogans
RT revealed by whole-genome sequencing";
RL Nature 422(6934):888-893(2003).
XX
RN [2]
RP 1-4338762
RA Zhang Y., Zhang H., Wang S., Guo X., Zhao G. P. ;

Поиск на сайте ENA

- Нет RefSeq ☹️
- Содержание (почти) то же, что в GenBank. Но:
 - Есть поиск по полю “Description” (DE)
 - Можно использовать маски
(звёздочка * заменяет любое количество любых символов)

BLAST двух последовательностей

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

Log in

BLAST® Home Recent Results Saved Strategies Help

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!

**N
E
W
S** 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 nucleoc x +
https://blast.ncbi.nlm.nih.gov/Blast.cgi?PROGRAM=blastn&PAGE_TYPE=BlastSearch&LINK_LOC=blasthome

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

NIH National Library of Medicine
National Center for Biotechnology Information Log in

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
 ?

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?](#) [BLAST Help Videos](#) [Back to Traditional Results Page](#)

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 4277185
Length
Other reports [MSA viewer](#)

Filter Results

Percent Identity	E value	Query Coverage
<input type="text"/> to <input type="text"/>	<input type="text"/> to <input type="text"/>	<input type="text"/> to <input type="text"/>
		Filter Reset

Карта локального сходства

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

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

select all *1 sequences selected* [GenBank](#) [Graphics](#) [MSA Viewer](#)

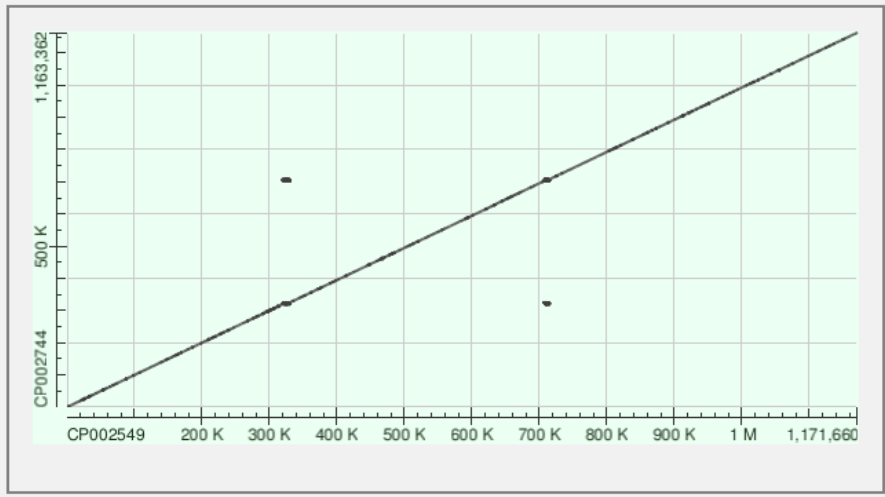
	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130, chromosome I, complete sequ...	Leptospira interrog...	2.038e+05	1.560e+07	97%	0.0	99.42%	4277185	AE016823.1

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](#)**

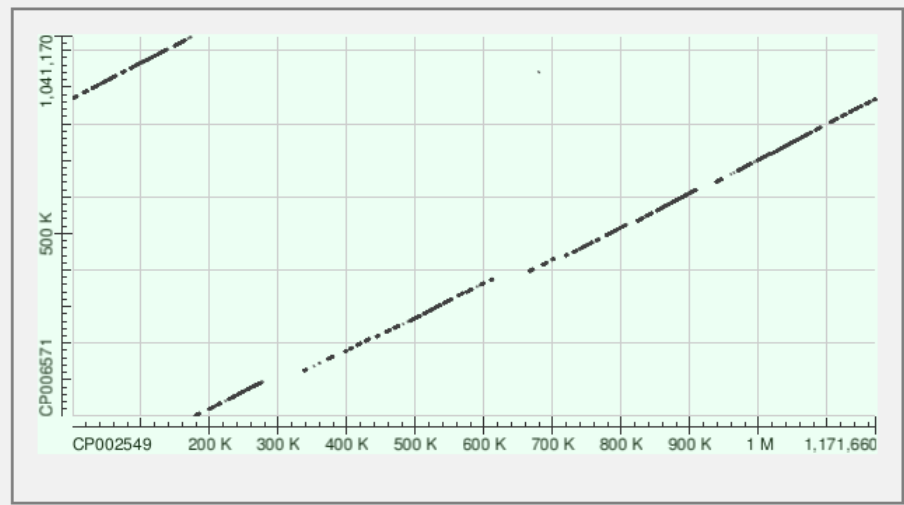
Plot of CP002549.1 vs CP002744.1 ?



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 [PKY2HTTT114](#) 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

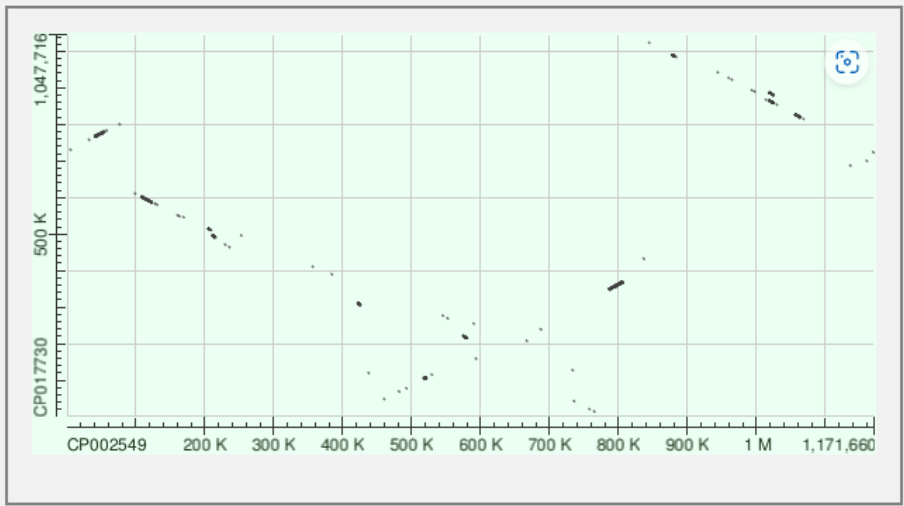
E value to

Query Coverage to

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

- Descriptions
- Graphic Summary
- Alignments
- Dot Plot**

Plot of CP002549.1 vs CP017730.1 ?



Bookmark

Enter Query Sequence

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

Query subrange [?](#)

From

To

Or, upload file

Выбор файла Не выбран ни один файл [?](#)

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

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

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 x +

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

1,047,716

500 K

[Feedback](#)

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 4277185
Length
Other reports [MSA viewer](#) ?

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

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

Plot of AE010300.2 vs AE016823.1 ?

