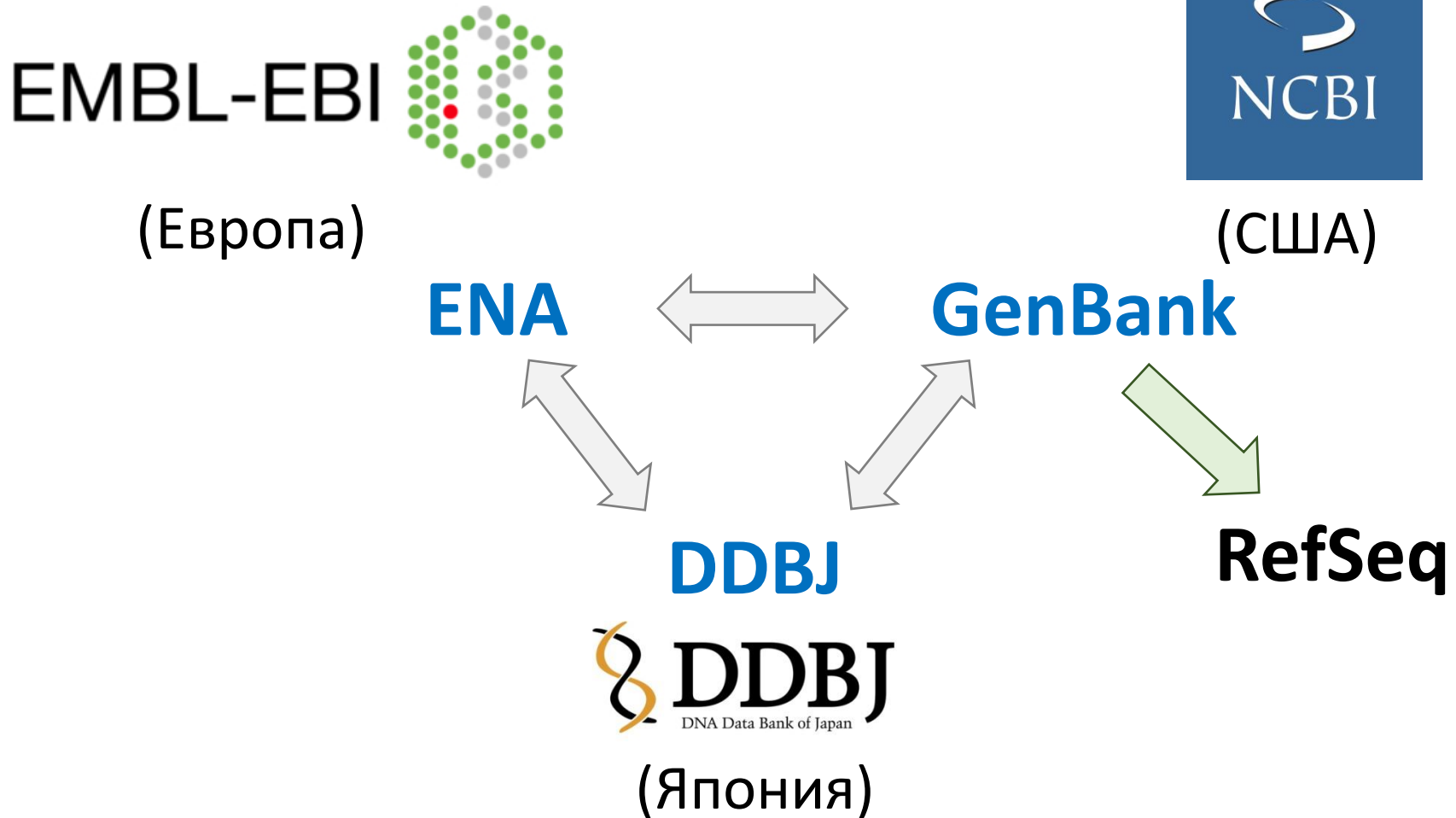


Поиск в нуклеотидных БД

С.А.Спирин, 8 ноября 2022

International Nucleotide Sequence Database Collaboration





Log in

Nucleotide

Nucleotide

Search

[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](#)



Nucleotide Advanced Search Builder

Use the builder below to create your search

[Edit](#)

Builder

All Fields ▾



[Show index list](#)

AND ▾

All Fields ▾



[Show index list](#)

Search

or [Add to history](#)



Library of Medicine

for Biotechnology Information

Log in

- 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

Nucleo

Nucleo

Use the

[Edit](#)

Builder

h Builder

our search

All Fields ▾



[Show index list](#)

AND ▾

All Fields ▾



[Show index list](#)

Search

or [Add to history](#)

Запись банка RefSeq (формат общий с GenBank)

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, 6
Minas Gerais 31270-901, Brazil

Казалось бы, поле Definition важное.
Но на сайте NCBI поиска по нему нет...

Nucleotide Advanced Search Builder

Leptospira[Organism] [Edit](#) [Clear](#)

Builder

Organism [Show index list](#)
AND [Show index list](#)

or [Add to history](#)

History

There is no recent history

Nucleotide

Nucleotide

leptospira[Organism]

Search

Create alert Advanced

Help

Species

Bacteria (263,475)
Customize ...

Molecule types

genomic
DNA/RNA (263,263)
mRNA (17)
rRNA (48)
Customize ...

Source databases

INSDC (GenBank) (131,603)
RefSeq (131,579)
Customize ...

Sequence Type

Nucleotide (263,432)
GSS (43)

Genetic compartments

Plasmid (257)

Sequence length

Custom range...

Release date

Summary 20 per page Sort by Default order

Запрос

Send to: Filters: [Manage Filters](#)

Items: 1 to 20 of 263475

<< First < Prev Page 1 of 13174 Next > Last >>

- [Leptospira interrogans strain SN4 16S ribosomal RNA gene, partial sequence](#)
1. 494 bp linear DNA
Accession: OP740800.1 GI: 2323118029
[GenBank](#) [FASTA](#) [Graphics](#)
- [Leptospira sp. strain QN2 16S ribosomal RNA gene, partial sequence](#)
2. 641 bp linear DNA
Accession: OP740799.1 GI: 2323118028
[GenBank](#) [FASTA](#) [Graphics](#)
- [Uncultured Leptospira sp. clone PO20_2 16S ribosomal RNA gene, partial sequence](#)
3. 303 bp linear DNA
Accession: OM406205.1 GI: 2183996333
[PubMed](#) [Taxonomy](#)
[GenBank](#) [FASTA](#) [Graphics](#)
- [Uncultured Leptospira sp. clone PT116 16S ribosomal RNA gene, partial sequence](#)
4. 303 bp linear DNA
Accession: OM406204.1 GI: 2183996331

БД

Results by taxon

Top Organisms [\[Tree\]](#)

[Leptospira interrogans \(166250\)](#)
[Leptospira borgpetersenii \(25475\)](#)
[Leptospira kirschneri \(12110\)](#)
[Leptospira noguchii \(10263\)](#)
[Leptospira santarosai \(9824\)](#)
All other taxa (39553)
More...

Find related data

Database:

Find items

Search details

"Leptospira"[Organism]

Nucleotide
Create alert Advanced Help

- Species**
Bacteria (131,579)
Customize ...
- Molecule types**
genomic
DNA/RNA (131,540)
rRNA (39)
Customize ...
- Source databases**
INSDC (GenBank) (0)
 RefSeq (131,579)
Customize ...
- Sequence Type**
Nucleotide (131,579)

Summary ▾ 20 per page ▾ Sort by Default order ▾ Send to: ▾

Filters: [Manage Filters](#)

TAXONOMY Was this helpful?

[Leptospira](#)

Leptospira is a genus of bacteria in the family *Leptospiraceae*.

Taxonomy ID: [171](#)

[Taxonomy browser](#) [Genomes](#)

- Results by taxon**
- Top Organisms [\[Tree\]](#)
- Leptospira interrogans (79537)
 - Leptospira borgpetersenii (18733)
 - Leptospira kirschneri (5948)
 - Leptospira noguchii (5028)
 - Leptospira santarosai (4591)
 - All other taxa (17742)
- [More...](#)

Find related data

Database:

Items: 1 to 20 of 131579

<< First < Prev Page of 6579 Next > Last >>

- Filters activated:** RefSeq. [Clear all](#)
- [Leptospira interrogans serovar Hardjo str. Norma voucher Leptospira interrogans isolate Cattle chromosome II, complete sequence](#)
355,432 bp circular DNA
Accession: NZ_CP012604.1 GI: 983533025
[Assembly](#) [BioProject](#) [BioSample](#) [Protein](#) [PubMed](#) [Taxonomy](#)
[GenBank](#) [FASTA](#) [Graphics](#)
 - [Leptospira interrogans serovar Hardjo str. Norma voucher Leptospira interrogans](#)

Search details

"Leptospira"[Organism] AND refseq[filter]

[See more...](#)

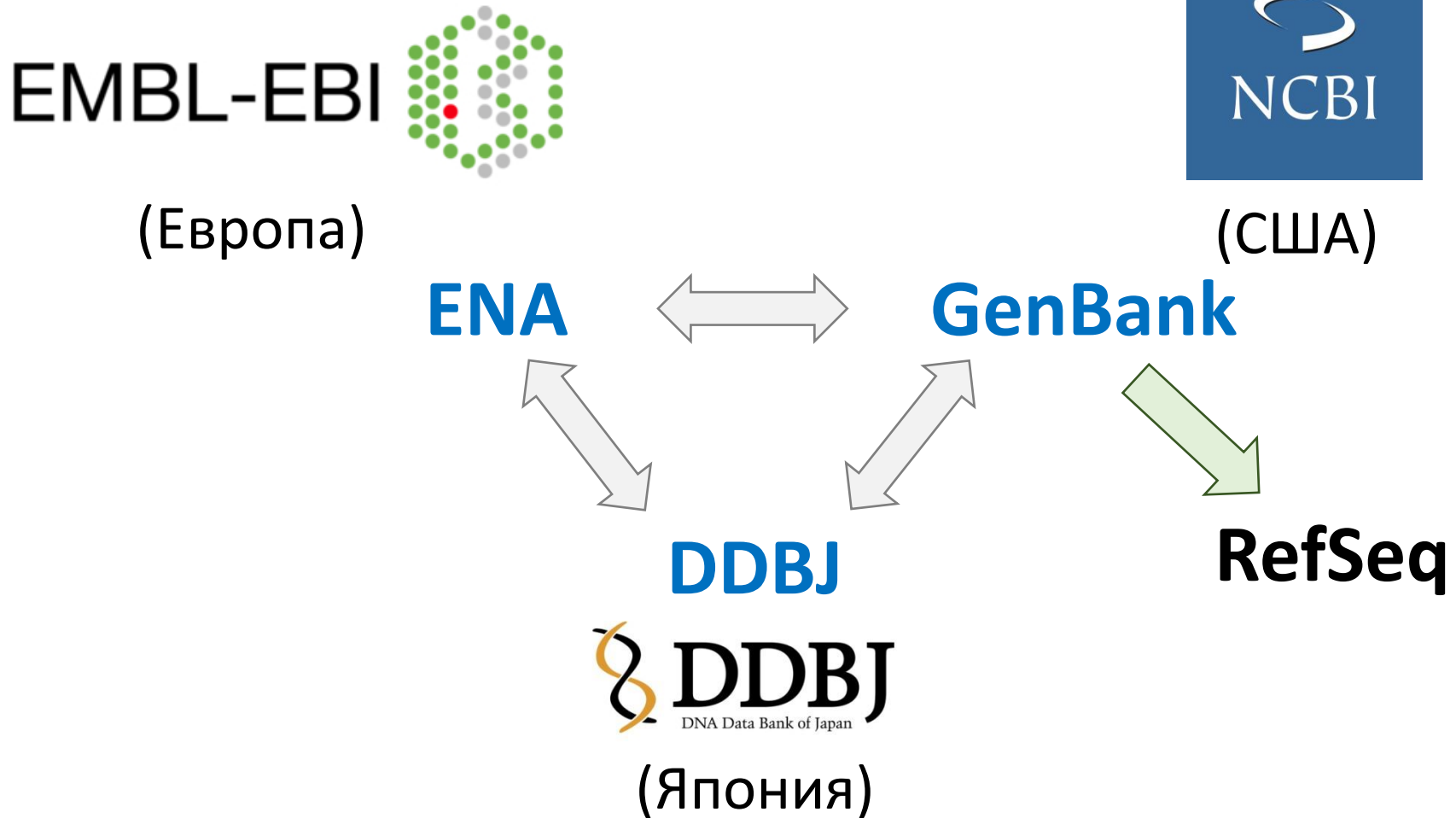
- Genetic compartments**
Plasmid (125)
- Sequence length**
Custom range...
- Release date**
Custom range...
- Revision date**
Custom range...
- [Clear all](#)
- [Show additional filters](#)

Recent activity

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)
- Нет поиска по полю “Definition”
- В запросах нельзя использовать маски

International Nucleotide Sequence Database Collaboration



ENA Browser x +

https://www.ebi.ac.uk/ena/browser/home

EMBL-EBI Services Research Training About us

ENA European Nucleotide Archive

Enter text search terms Search

Examples: histone, BN000065

Enter accession View

Examples: Taxon:9606, BN000065, PRJEB402

Home Submit Search Rulespace About Support

We recommend that you subscribe to the ENA-announce mailing list for updates on services.

For SARS-CoV-2 data submissions, users should contact us in advance of submission at virus-dataflow@ebi.ac.uk for specific advice on options and to access the highest levels of support. We have also launched a [Drag-and-Drop Data Submission Service](#) (currently in Beta) suitable for certain SARS-Cov-2 submissions. We are inviting submitters to try this out. Please contact us at the email above for details.

European Nucleotide Archive

The European Nucleotide Archive (ENA) provides a comprehensive record of the world's nucleotide sequencing information, covering raw sequencing data, sequence assembly information and functional annotation. [More about ENA.](#)

Access to ENA data is provided through the browser, through search tools, through large scale file download and through the API.

Submit Search Rulespace Support

[Tweets by ENA](#)

Search & discover ENA data

Latest ENA news

[ENA: Improving spatio-temporal annotations](#) Dec 1, 2021, 3:00:00 AM

The European Nucleotide Archive, along with its partners in the International Nucleotide Sequen

[Read more >](#)

[ENA: Improving spatio-temporal annotations](#) browser on 5th August 2020 Jul 16, 2020, 3:00:00 AM

https://www.ebi.ac.uk/ena/browser/search



Enter text search terms Search

Examples: histone, BN000065

Enter accession View

Examples: Taxon:9606, BN000065, PRJEB402

- Home
- Submit
- Search
- Rulespace
- About
- Support

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](#)

EMBL-EBI [Intranet for staff](#)



Enter text search terms Search

Examples: histone, BN000065

Enter accession View

Examples: Taxon:9606, BN000065, PRJEB402

- Home
- Submit
- Search
- Rulespace
- About
- Support

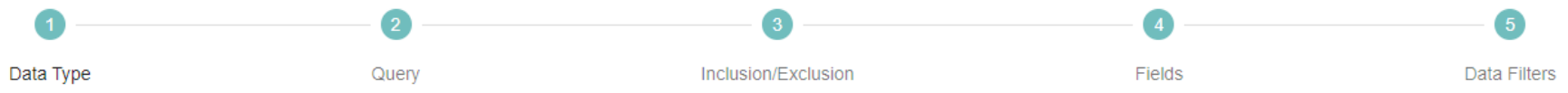
Advanced Search

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

Не так просто, зато...

ENA Browser

https://www.ebi.ac.uk/ena/browser/advanced-search

EMBL-EBI Services Research Training About us

EMBL-EBI

Enter text search terms Search

Examples: histone, BN000065

Enter accession View

Examples: Taxon:9606, BN000065, PRJEB402

Home Submit Search Rulespace About Support

Advanced Search

Customise your own search query and retrieve a set of ENA records tailored to your search criteria. [Documentation](#)

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1 Data Type 2 Query 3 Inclusion/Exclusion 4 Fields 5 Data Filters

Query: [Build Query ?](#) [Reset](#)

Type to filter query params

Taxonomy and related

Geographical location

Geography

Collection event

15

Back Copy Curl Request Next Search

... можно искать по Description и использовать маску (звёздочку *)

The screenshot shows the ENA Browser advanced search interface. At the top, the browser address bar displays `https://www.ebi.ac.uk/ena/browser/advanced-search`. The current query is `tax_tree(171)`. Below the query input, there is a "Build Query" button with a help icon. A search filter input field contains the text "Type to filter query params". On the left side, a vertical list of filter categories is shown, with "Titles, aliases and descriptions" highlighted in dark teal. A dropdown menu is open over the "Build Query" area, showing "Select filter" options, with "Description" selected. The dropdown also includes "AND" and "OR" operators, "Add rule", "Add group", and "Delete" buttons. On the right side, there are "Reset" and "Update query" buttons. At the bottom right, there are navigation buttons: "Back", "Copy Curl Request", "Next", and "Search". The page number "16" is visible in the bottom right corner.

Поля не разбиваются на слова (в отличие от Uniprot и NCBI)!
Поэтому для выделения отдельного слова используйте маску.

The screenshot shows the ENA Browser's Advanced Search page. At the top, there is a navigation bar with the ENA logo and a search bar. Below the navigation bar, the page title is "Advanced Search". The main content area contains a description of the search process and a progress indicator with six steps: Data Type, Query, Inclusion/Exclusion, Fields, Data Filters, and Results. The "Query" step is currently active, showing a search query: `tax_tree(171) AND description=*** chromosome**`. Below the query input, there is a "Build Query" button with a question mark icon. To the left of the query input, there is a "Type to filter query params" input field. Below the query input, there is a "Rule Builder" section with a sidebar on the left containing categories: "Taxonomy and related", "Geographical location", "Geography", and "Collection event information". The "Rule Builder" section has a dropdown menu for "AND OR", a "Description" dropdown, an "=" operator dropdown, and a text input field containing `* chromosome*`. There are also "Add rule", "Add group", and "Delete" buttons. At the bottom right, there is an "Update query" button. The page number "17" is visible in the bottom right corner.

ENA Browser

https://www.ebi.ac.uk/ena/browser/advanced-search

Enter text search terms Search

Examples: histone, BN000065

Enter accession View

Examples: Taxon:9608, BN000065, PRJEB402

Home Submit Search Rulespace About Support

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](#).

Data Type Query Inclusion/Exclusion Fields Data Filters Results

Query: `tax_tree(171) AND description=*** chromosome**` Reset

Build Query ?

Type to filter query params

Taxonomy and related

Geographical location

Geography

Collection event information

AND OR

+ Add rule + Add group

Description = * chromosome* Delete

brief sequence description

Update query

17

Back Copy Curl Request Next Search

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

```
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; Leptospirales; 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 Zhong Y., Zheng H.-J., Wang S.-Y., Guo X.-K., Zhao G.-P.;
RT "Complete genome sequence of Leptospira interrogans serovar Lai strain
RT 56601";
RL Unpublished.
```

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...](#)

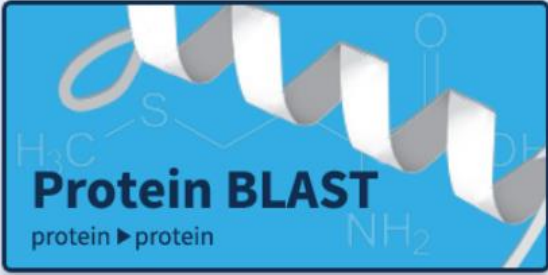
Web BLAST



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

Or, upload file

[< 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 to
E value to
Query Coverage to

[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](#)

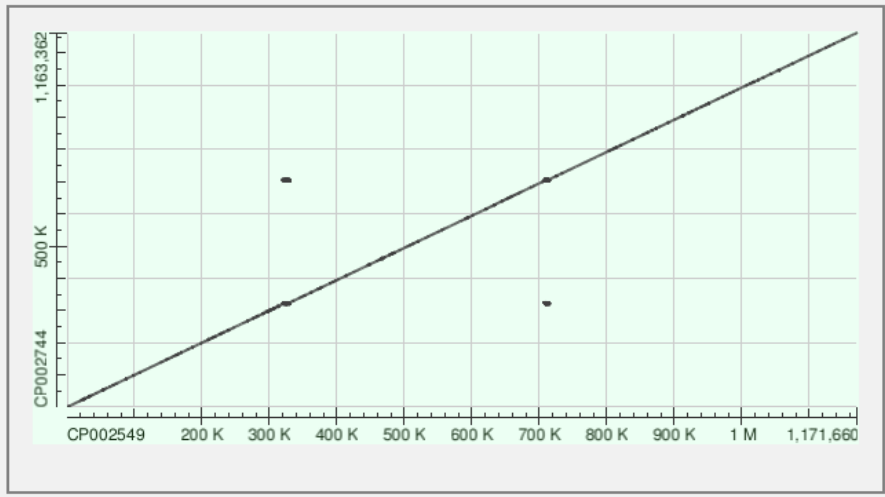
	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130, chromosome I, complete sequ...	Leptospira interrog...	2.038e+05	1.560e+07	97%	0.0	99.42%	4277185	AE016823.1

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**

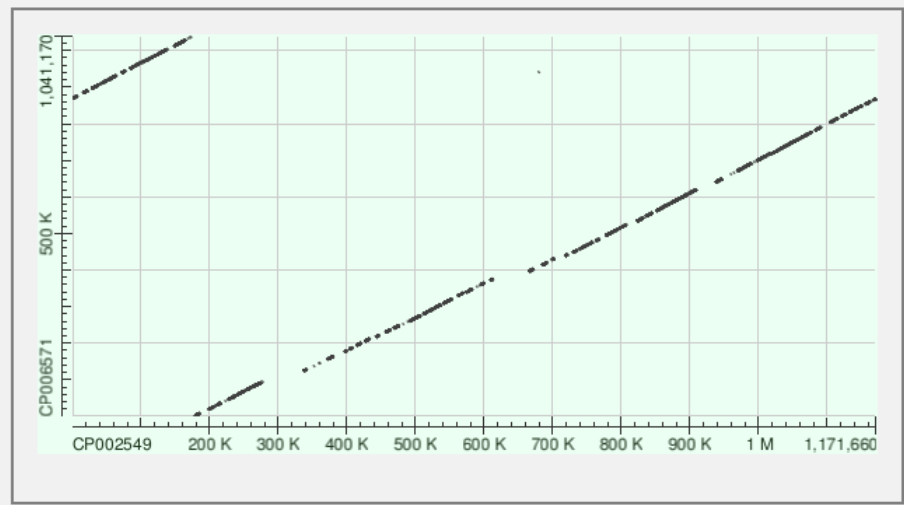
Plot of CP002549.1 vs CP002744.1 ?



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 [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

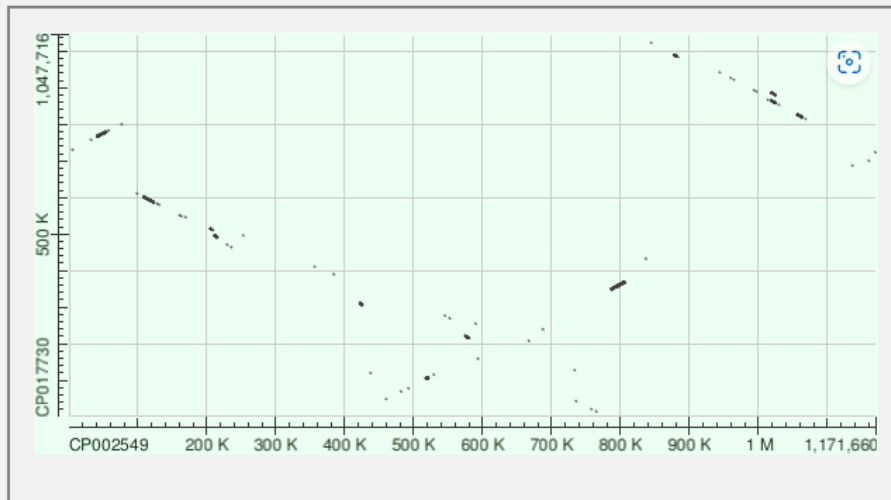
E value to

Query Coverage to

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

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

Plot of CP002549.1 vs CP017730.1 ?



Bookmark

Enter Query Sequence

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

Query subrange [?](#)

From

To

Or, upload file

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

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

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](#) ▾

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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

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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

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Query ID [AE010300.2](#) (nucleic acid)
Query Descr Leptospira interrogans serovar Lai str. 56601 chromosom ...
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Subject ID [AE016823.1](#) (nucleic acid)
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Plot of AE010300.2 vs AE016823.1 ?

