

Utiliser BLAST: logiciel d'identification de séquences

Démarche d'analyse de séquence:

- Dans le dossier 'Données Brutes', le fichier 'ex1.txt' contient une séquence d'ADN de 18S inconnue.

1/ Ce site: <http://blast.ncbi.nlm.nih.gov/Blast.cgi> permet de comparer notre séquence inconnue à une immense base de donnée; il faut choisir le programme 'Nucleotide blast'

NCBI BLAST Home

BLAST finds regions of similarity between biological sequences. [more...](#)

New DELTA-BLAST, a more sensitive protein-protein search [Go](#)

BLAST Assembled RefSeq Genomes

Choose a species genome to search, or [list all genomic BLAST databases](#).

- Human
- Mouse
- Rat
- Arabidopsis thaliana*
- Oryza sativa*
- Bos taurus*
- Danio rerio*
- Drosophila melanogaster*
- Gallus gallus*
- Pan troglodytes*
- Microbes
- Apis mellifera*

Basic BLAST

Choose a BLAST program to run.

- nucleotide blast** Search a nucleotide database using a nucleotide query
Algorithms: blastn, megablast, discontinuous megablast
- protein blast Search protein database using a protein query
Algorithms: blastp, psi-blast, phi-blast, delta-blast
- blastx Search protein database using a translated nucleotide query
- tblastn Search translated nucleotide database using a protein query
- tblastx Search translated nucleotide database using a translated nucleotide query

Specialized BLAST

Your Recent Results [New](#)

[All Recent results...](#)

News

[Update to organism BLAST databases](#)

The organism BLAST pages are being updated to use top-level (chromosome + unplaced and unlocalized scaffolds) RefSeq genomic records instead of scaffold records.
Thu, 17 Oct 2013 14:00:00 EST

[More BLAST news...](#)

Tip of the Day

[Use Genomic BLAST to see the genomic context](#)

If you are interested in the evolution of a particular gene or gene family it is often interesting to examine the intro-exon structure even across species.

[More tips...](#)

2/-coller la séquence dans la case prévue à cet effet:

-choisir l'option "séquence à peu près similaire"

-appuyer sur BLAST (lance la recherche)

blast.ncbi.nlm.nih.gov/Blast.cgi?PROGRAM=blastn&PAGE_TYPE=BlastSearch&LINK_LOC=blasthome

BLAST® Basic Local Alignment Search Tool

NCBI BLAST/ blastn suite Standard Nucleotide BLAST

Enter Query Sequence

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

Clear Query subrange

From To

Or, upload file

Choose File No file chosen

Job Title

Enter a descriptive title for your BLAST search

Align two or more sequences

Choose Search Set

Database

Human genomic + transcript Mouse genomic + transcript Others (nr etc.)

Nucleotide collection (nr/nt)

Organism

Optional

Enter organism name or id - completions will be sug

Exclude

Optional

Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown

Exclude

Optional

Models (X/M/X/P) Uncultured/environmental sample sequences

Entrez Query

Optional

Enter an Entrez query to limit search

Program Selection

Optimize for

Highly similar sequences (megablast)

More dissimilar sequences (discontiguous megablast)

Somewhat similar sequences (blastn)

Choose a BLAST algorithm

BLAST

Search database Nucleotide collection (nr/nt) using Blastn (Optimize for somewhat similar sequences)

show results in a new window

Algorithm parameters

3/ analyse des résultats:

- les resultats sont le noms des séquences trouvées dans le base de donnée, qui ressemblent à notre séquence inconnue
- les résultats sont classés par du pus grand au plus petit pourcentage d'identité entre nos séquences inconnues et les séquences ressemblantes.
- si on a 100% d'identité, on peut confirmer l'identité de la séquence inconnue. En dessous de 85%, on ne peut rien dire.

blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1418672

BLAST® Basic Local Alignment Search Tool

NCBI BLAST/ blastn suite/ Formatting Results - BV8ZSKRC015

Edit and Resubmit Save Search Strategies Formatting options Download

YouTube How to read this page Blast report description

Nucleotide Sequence (1798 letters)

RID BV8ZSKRC015 (Expires on 12-28 22:59 pm)

Query ID lc124071

Description None

Molecule type nucleic acid

Query Length 1798

Database Name nr

Description Nucleotide collection (nt)

Program BLASTN 2.2.29+ Citation

Other reports: Search Summary Taxonomy reports Distance tree of results

Graphic Summary

Descriptions

Sequences producing significant alignments:

Select: All None Selected: 0

Alignments @Download -> GenBank Graphics Distance tree of results

Description	Max score	Total score	Query cover	E value	Ident	Accession
C. rostratus 18S rRNA gene	3232	3232	100%	0.0	100%	U85381.1
Chaetoceros sp. p442 18S rRNA gene, clone p442	2994	2994	100%	0.0	97%	AJ535197.1
Chaetoceros pervianus strain ECT3821-Chaetoceros 18S small subunit ribosomal RNA gene, partial sequence	2892	2892	91%	0.0	99%	HQ912950.1
Uncultured eukaryote gene for SSU rRNA, partial sequence, clone DSGM-34	2715	2715	93%	0.0	96%	AB275034.1
Hemialus sinensis strain CCH-2 18S small subunit ribosomal RNA gene, partial sequence	2553	2553	91%	0.0	94%	HQ912924.1
Brookmannella brookmanni strain CCMP151 18S small subunit ribosomal RNA gene, partial sequence	2545	2545	99%	0.0	92%	HQ912955.1
Chaetoceros muelleri strain CCAP 1010/3 18S ribosomal RNA gene, partial sequence	2545	2545	99%	0.0	92%	AY525895.1
Chaetoceros californicus strain Jfrermer-Argenton 18S ribosomal RNA gene, partial sequence	2536	2536	99%	0.0	92%	DQ687755.1
Chaetoceros gracilis strain UTEX LB 2375 18S ribosomal RNA gene, partial sequence	2536	2536	99%	0.0	92%	AY525895.1
Biddulphia troides isolate ECT39028r 18S ribosomal RNA gene, partial sequence	2529	2529	98%	0.0	92%	JX401228.1
Attheya longicornis strain CCMP214 18S ribosomal RNA gene, partial sequence	2522	2522	99%	0.0	91%	AY485450.1
Attheya longicornis strain CCMP 214 18S ribosomal RNA gene, partial sequence	2518	2518	99%	0.0	91%	JX401230.1
Minutocellus polymorphus strain CCMP497 18S small subunit ribosomal RNA gene, partial sequence	2518	2518	99%	0.0	92%	HQ912955.1
Chaetoceros muelleri strain CCMP1319 18S ribosomal RNA gene, partial sequence	2516	2516	98%	0.0	92%	AY485453.1
Biddulphia alternans isolate ECT3885Balt 18S ribosomal RNA gene, partial sequence	2511	2511	97%	0.0	92%	JX401229.1

http://ssu-rna.org/downloads_eukaryotic_Download_taxonomy_browser.html

ce lien permet de télécharger des séquences de références et d'aller les chercher dans blast pour s'entraîner!