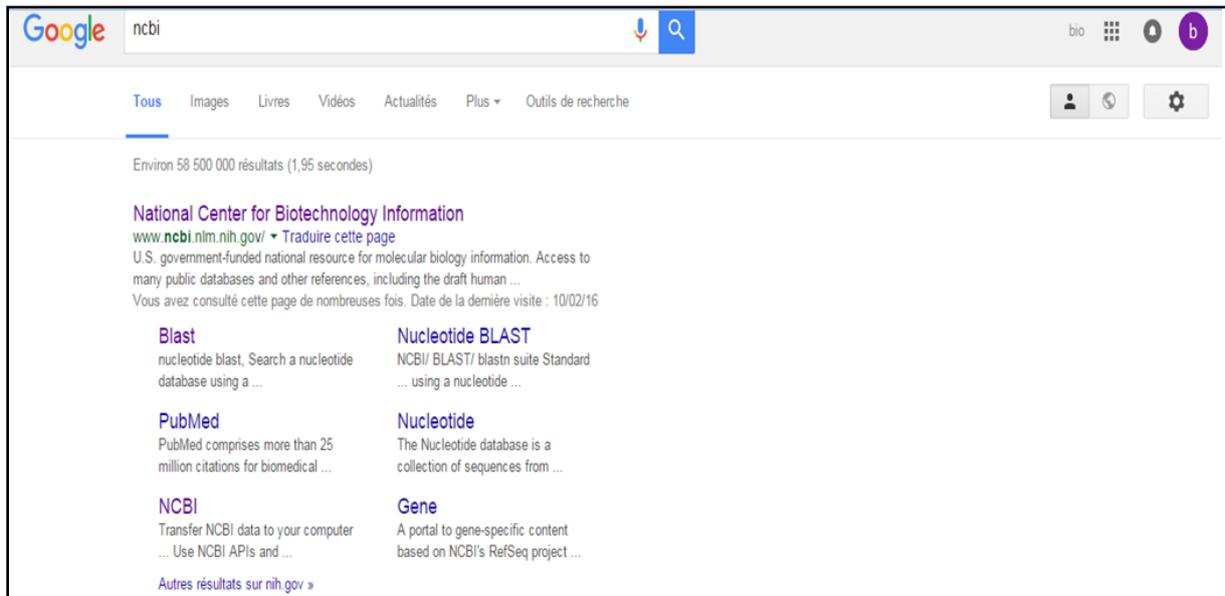


Recherche d'Alignement des séquences du gène ARNr16S sur NCBI

Etapes du travail

1. Ouverture du lien NCBI sur internet par l'utilisation du moteur de recherche Google
2. Choix du programme BLAST
3. Choix de l'outil nucleotide BLASTn
4. Insertion de la séquence ADN ou le Numéro d'Accès sur Gene Bank et activation de l'outil BLAST
5. Lecture de la liste des résultats de l'Alignement
6. Lecture du détail des résultats de l'Alignement
7. Récolte des informations sur l'individu par le numéro d'accès sur Gene Bank : Auteur, affiliation, publication, séquence, etc.

1. Ouverture du lien NCBI sur internet par l'utilisation du moteur de recherche Google



2. Choix du programme BLAST

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National Center for Biotechnology Information

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- Data & Software
- DNA & RNA
- Domains & Structures
- Genes & Expression
- Genetics & Medicine
- Genomes & Maps
- Homology
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- Proteins
- Sequence Analysis

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- BLAST**
- Nucleotide
- Genome
- SNP
- Gene
- Protein
- PubChem

NCBI Announcements

3. Choix de l'outil nucléotide BLASTn

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](#)

NEWS Magic-BLAST 1.2.0 released
A new version of the BLAST RNA-seq mapping tool is now available.
Mon, 27 Feb 2017 14:00:00 EST [More BLAST news...](#)

Web BLAST

Nucleotide BLAST
nucleotide ► nucleotide

blastx
translated nucleotide ► protein

tblastn
protein ► translated nucleotide

Protein BLAST
protein ► protein

4. Insertion de la séquence ADN ou le Numéro d'Accès sur Gene Bank et activation de l'outil BLAST

BLAST® Basic Local Alignment Search Tool

Home Recent Results Saved Strategies Help My NCBI Sign In (Registered)

NCBI BLAST/blastn suite Standard Nucleotide BLAST

blastn blasto blastx tblastn tblastx

Enter Query Sequence

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

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

MGATAGSITTCCTCGGTATCCGATTAATACACACATAATCCACCGCTT999CGGCCCCCGTCAATTCCTTTGAGTTLGGGTTGCTACTCCCCAGGTGGCTAACTTATCACTTCCCTAGTCTGAGCTACGCCCCAAAAGAGTATGATCGTTTACGCGCTG6ACTACCA699TATCTAATCTGTTCGCTCCCA6CCTTTCCTCATAGSITTCAGTGTTCCTTAGTAACCTGCTTCCGATTCGCAATTTGTTCTAAGTAATATCTATGCAATTCACCGCTACACTTATTCAGCTACTTCAACCAACTCAAGACTCGAGTATCAATGGCAG

Clear Query subrange

From To

Or, upload file

Choisissez un fichier Aucun fichier choisi

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)

Limit by

Organism BioProjectID WGS Project

5. Lecture de la liste des résultats de l'Alignement

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
<input type="checkbox"/> Chryseobacterium indologenes partial 16S rRNA gene, isolate 6	1328	1328	100%	0.0	100%	HF678414.1
<input type="checkbox"/> Chryseobacterium indologenes partial 16S rRNA gene, isolate 12	1323	1323	100%	0.0	99%	HF678418.1
<input type="checkbox"/> Chryseobacterium indologenes partial 16S rRNA gene, isolate 3	1323	1323	100%	0.0	99%	HF678415.1
<input type="checkbox"/> Bacterium 14S134 16S ribosomal RNA gene, partial sequence	1317	1317	100%	0.0	99%	KC734365.1
<input type="checkbox"/> Bacterium 14S132 16S ribosomal RNA gene, partial sequence	1317	1317	100%	0.0	99%	KC734363.1
<input type="checkbox"/> Chryseobacterium enrichment culture clone RA-M137 16S ribosomal RNA gene, partial sequence	1317	1317	100%	0.0	99%	JQ083171.1

6. Lecture du détail des résultats de l'Alignement

[Download](#) [GenBank](#) [Graphics](#) [Next](#) [Previous](#) [Descriptions](#)

Chryseobacterium indologenes partial 16S rRNA gene, isolate 6
Sequence ID: [em|HF678414.1](#) Length: 719 Number of Matches: 1

Range 1: 1 to 719 [GenBank](#) [Graphics](#) [Next Match](#) [Previous Match](#)

Score	Expect	Identities	Gaps	Strand
1328 bits(719)	0.0	719/719(100%)	0/719(0%)	Plus/Minus

```

Query 1  TGCGGATTACTAGCGATTCCAGCTTCATAGAGTCGAGTTGCAGACTCCAATCCGAACTG 60
Sbjct 719 TGCGGATTACTAGCGATTCCAGCTTCATAGAGTCGAGTTGCAGACTCCAATCCGAACTG 60

Query 61  AGACCGGCTTTGAGATTGTCATCACATCGCTGTGTAGCTGCCCTGTGTACCGGCCATTG 120
Sbjct 659  AGACCGGCTTTGAGATTGTCATCACATCGCTGTGTAGCTGCCCTGTGTACCGGCCATTG 600

Query 121 TATTACGTGTGTGGCCAAAGCGTAAGGGCCGTGATGATTGACGTCAATCCCACTTCC 180
Sbjct 599  TATTACGTGTGTGGCCAAAGCGTAAGGGCCGTGATGATTGACGTCAATCCCACTTCC 540

Query 181  TCTCTACTGGCTAGGCACTCTCACTAGAGTCCCAACTTAATGATGGCACTAGTGACA 240
Sbjct 539  TCTCTACTGGCTAGGCACTCTCACTAGAGTCCCAACTTAATGATGGCACTAGTGACA 480

Query 241  GGGGTGGCTCTGTTGCAGACTTAACCTAACACTCACGGCAGAGCTGACGACAACCA 300
Sbjct 479  GGGGTGGCTCTGTTGCAGACTTAACCTAACACTCACGGCAGAGCTGACGACAACCA 420

Query 301  TGCAGCACCTTGAAAAATGCCGAAGAAAAGTCTATTTCTAAACTGTCAATTTCCCATTT 360
Sbjct 419  TGCAGCACCTTGAAAAATGCCGAAGAAAAGTCTATTTCTAAACTGTCAATTTCCCATTT 360
  
```

Related Information

7. Récolte des informations sur l'individu par le numéro d'accès sur Gene Bank : Auteur, affiliation, publication, séquence, etc.

Chryseobacterium indologenes partial 16S rRNA gene, isolate 6

GenBank: [HF678414.1](#)

[FASTA](#) [Graphics](#)

[Go to:](#)

LOCUS HF678414 719 bp DNA linear BCT 21-FEB-2013
DEFINITION Chryseobacterium indologenes partial 16S rRNA gene, isolate 6.
ACCESSION HF678414
VERSION HF678414.1 GI:452084714
KEYWORDS .
SOURCE Chryseobacterium indologenes
ORGANISM [Chryseobacterium indologenes](#)
Bacteria; Bacteroidetes; Flavobacteriia; Flavobacteriales;
Flavobacteriaceae; Chryseobacterium.
REFERENCE 1
AUTHORS Boubendir,A.
TITLE Analyse et prevalence du risque infectieux de Listeria monocytogenes dans les laits crus recoltes dans deux regions a climat different (Zone semi-aride et le Nord-Est algeriens) : Modelisation spatiale de la diversite floristique
JOURNAL Thesis (2012) Constantine 1 University, Algeria
REFERENCE 2 (bases 1 to 719)
AUTHORS Hamidechi,A.
TITLE Direct Submission
JOURNAL Submitted (11-FEB-2013) Constantine University, Constantine, Route de Ain El-Bey, 25000, ALGERIA
FEATURES
source
1..719
/organism="Chryseobacterium indologenes"
/mol_type="genomic DNA"
/isolate="6"
/isolation_source="raw milk"
/db_xref="taxon:253"

Customize view

Analyze this sequence

Run BLAST

Pick Primers

Highlight Sequence Features

Find in this Sequence

Related information

Taxonomy

LinkOut to external resources

Ribosomal Database Project II

[Ribosomal Database Project II]

SILVA SSU Database

[SILVA]

Recent activity

Turn Off

Clear

Chryseobacterium indologenes partial 16S

rRNA gene, isolate 6

Nucleotide

Nucleotide Sequence (719 letters)

BLAST