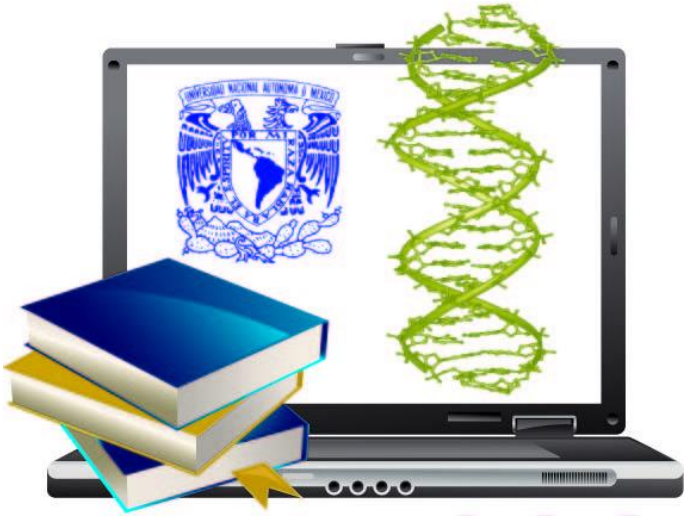
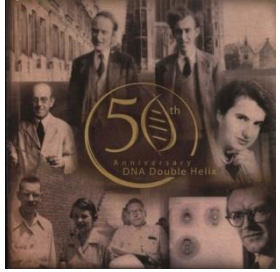
BANCO DE DADOS BIOLÓGICOS

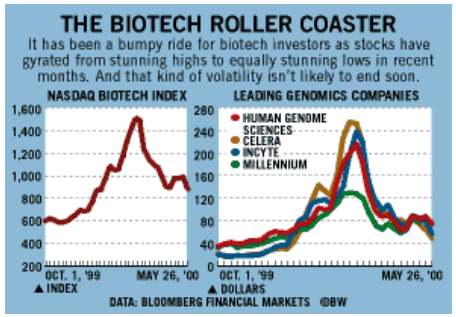
Aula 11

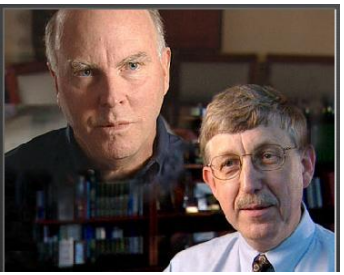
LGN232 – Genética Molecular



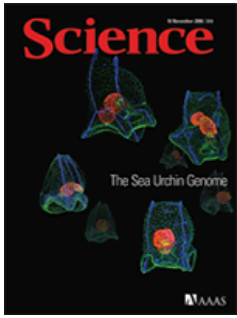
Maria Carolina Quecine
Departamento de Genética
mquecine@usp.br

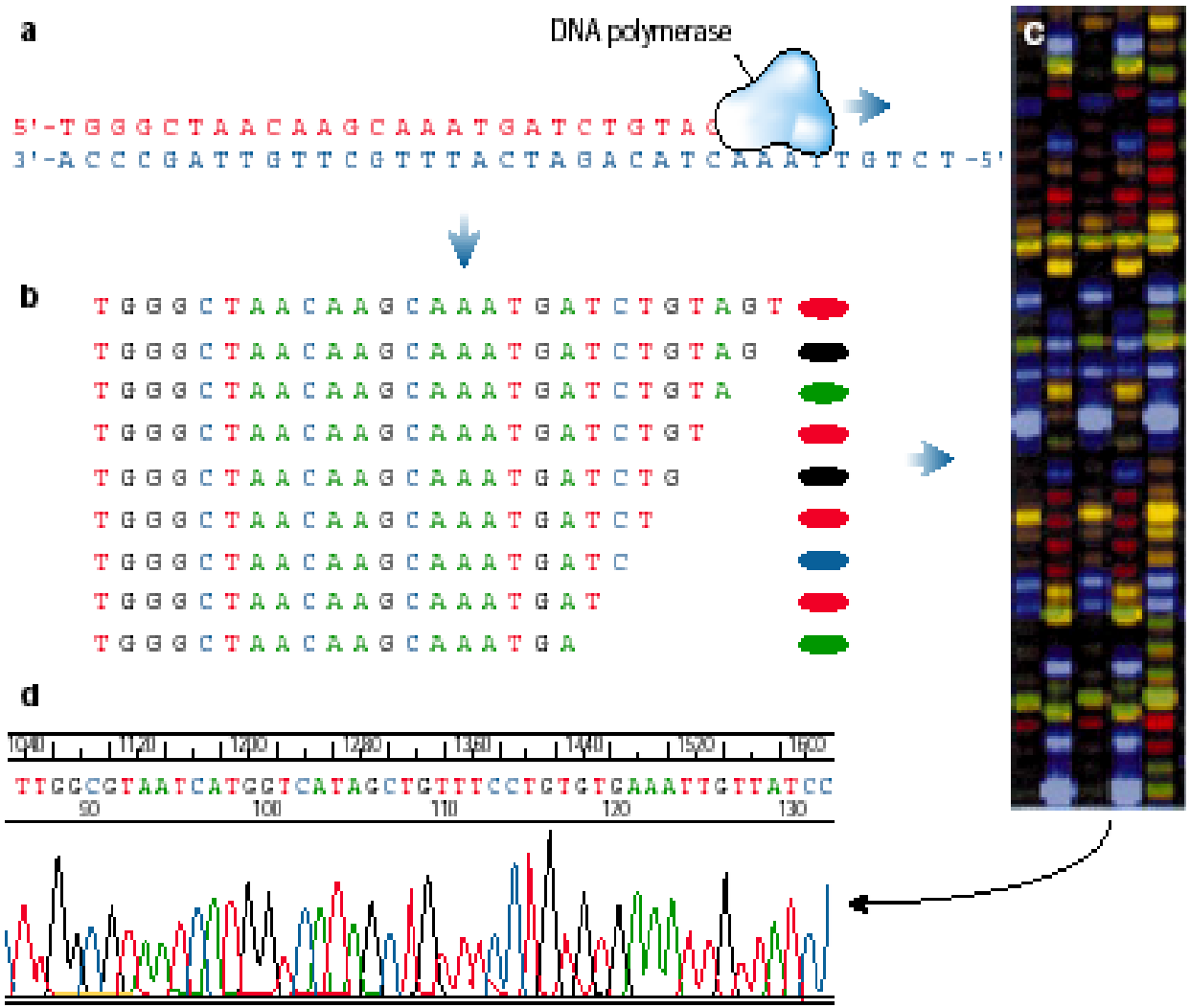






1866	Experimentos de Mendel
1871	Descoberta dos ácidos nucléicos
1930	**Introdução da palavra genoma**
1944	DNA material genético em todos os seres vivos
1951	Primeira proteína (insulina) sequenciada (**Fred Sanger**)
1953	Dupla hélice do DNA (**Watson** & Crick)
1960s	Elucidação do código genético
1977	**Sequenciamento do DNA (Fred Sanger)**
1986	Sequenciamento do DNA automatizado
1995	Primeiro genoma de bactéria sequenciado (*Haemophilus influenza*)
1998	Google
1999	Primeiro cromossomo humano sequenciado (cromossomo 22)
2000	Genomas *Drosophia* / *Arabidopsis* / ***Xylella***
2001	Genomas humano e camundongo
2003	99% genoma humano
2004	Metagenômica (*Environmental genomics*)
2005	Sequenciar um genoma de procarioto por US$1 000.
2007	**DNA de James Watson sequenciado**
2009	Sequenciar seu próprio genoma por US$ 50 000.



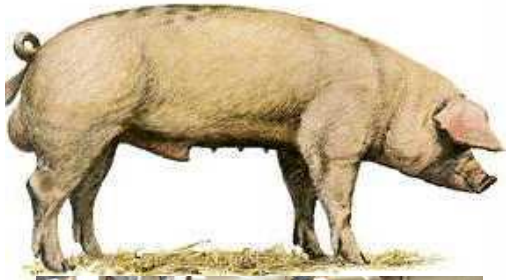


MAS PORQUE EU FAÇO SEQUENCIAMENTO?

Arroz

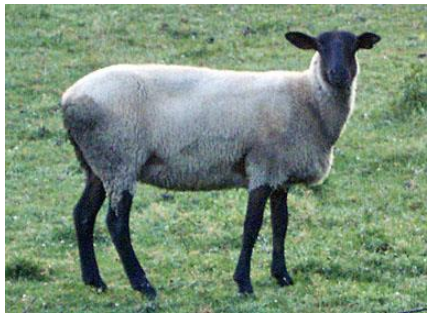
Soja

Arabdopsis



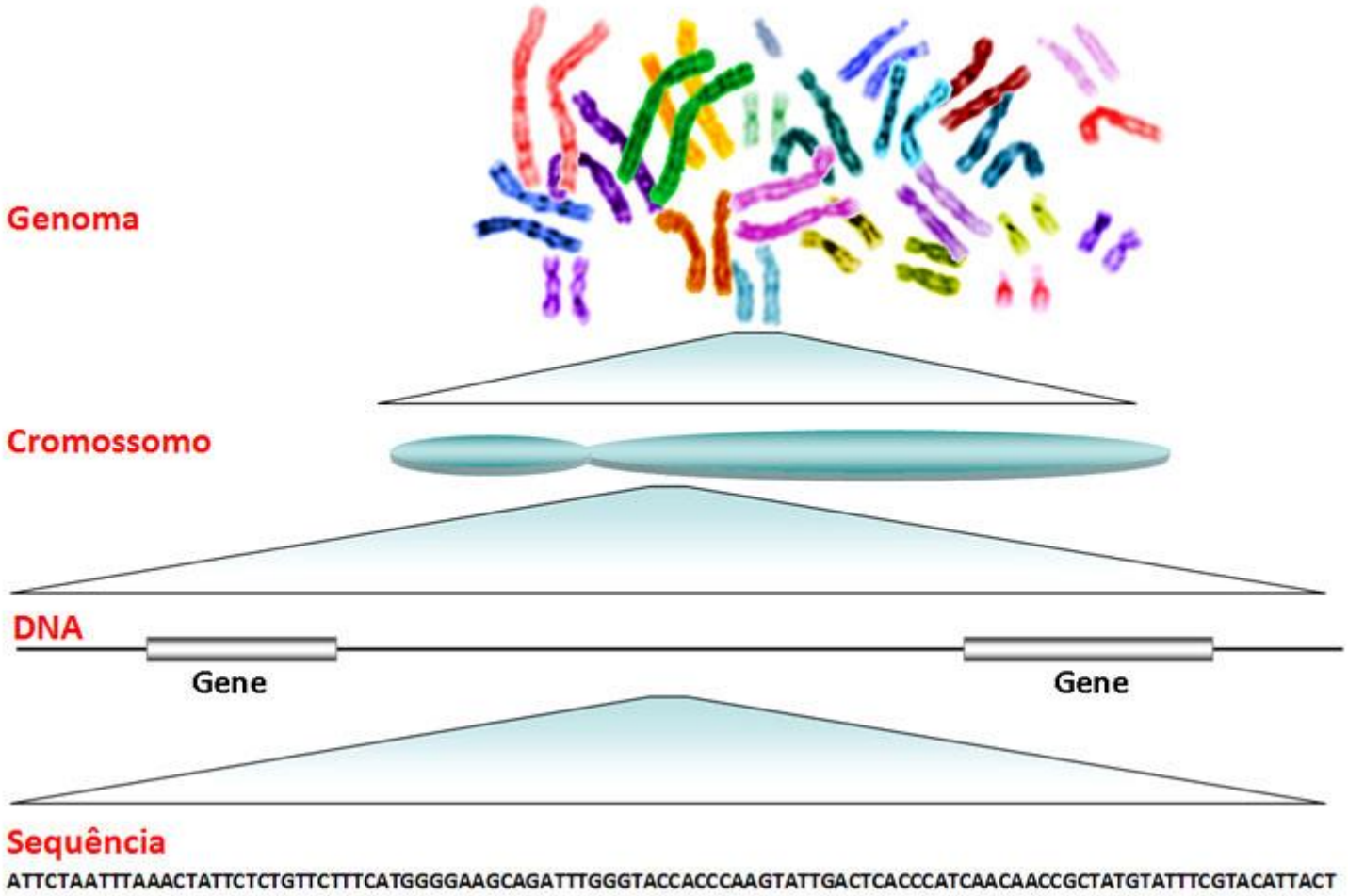
Milho

Tomate



Poplar Genome Sequenced and Published; Model Crop for Biofuels

GENE X GENOMA



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CATAAAACGTAATGCGGCAAGTAAACCCAACTTATAAAGTAATGTATCTTCGTTCGGA
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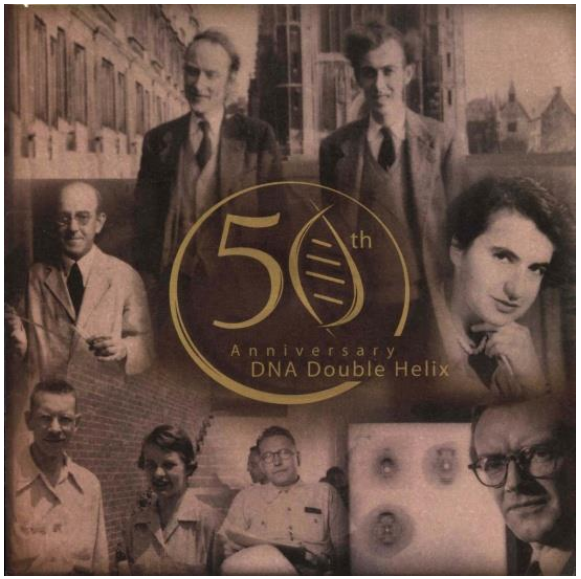
O que fazer com a informação:

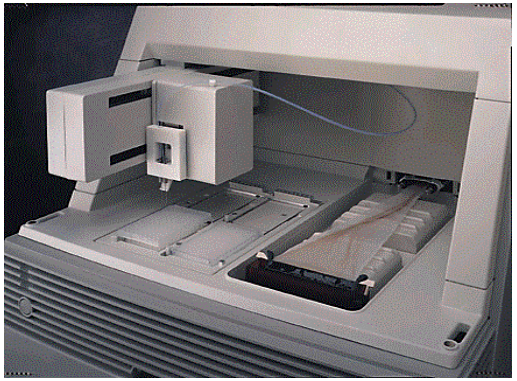


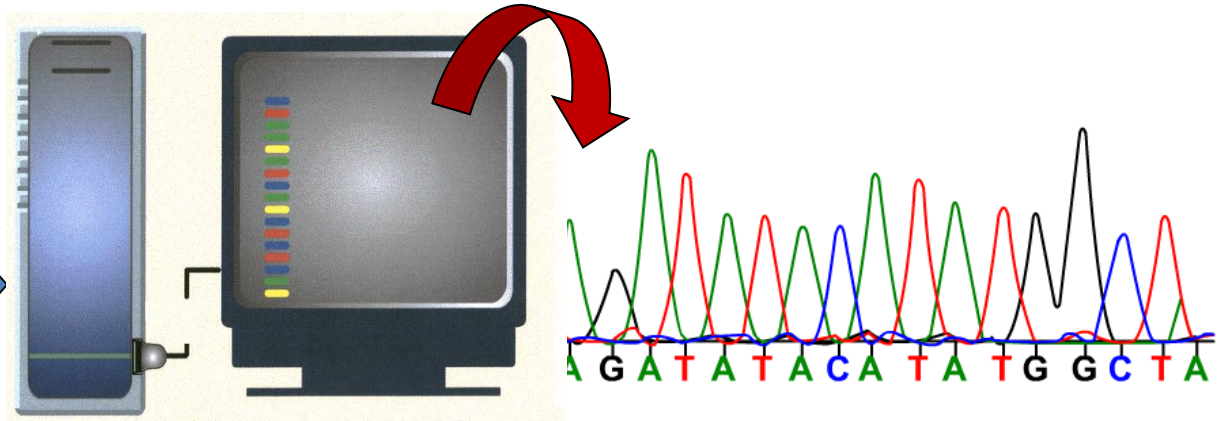
1953-2003

- Produção de Informações

↓

- Sequenciamento de DNA





ABI 3700 Applied Biosystems

BIOINFORMÁTICA

*A bioinformática consiste no desenvolvimento de métodos computacionais, matemáticos e estatísticos para **organizar** e **analisar** informações biológicas em grande escala e de maneira integrada.*

Organização e Armazenamento → **- Bancos de Dados Biológicos**

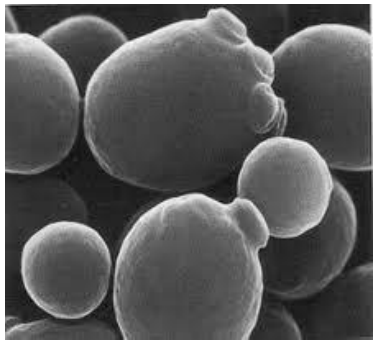
Visualização e Análise → **- Ferramentas computacionais**
- Compreensão do significado biológico

BANCO DE DADOS BIOLÓGICOS

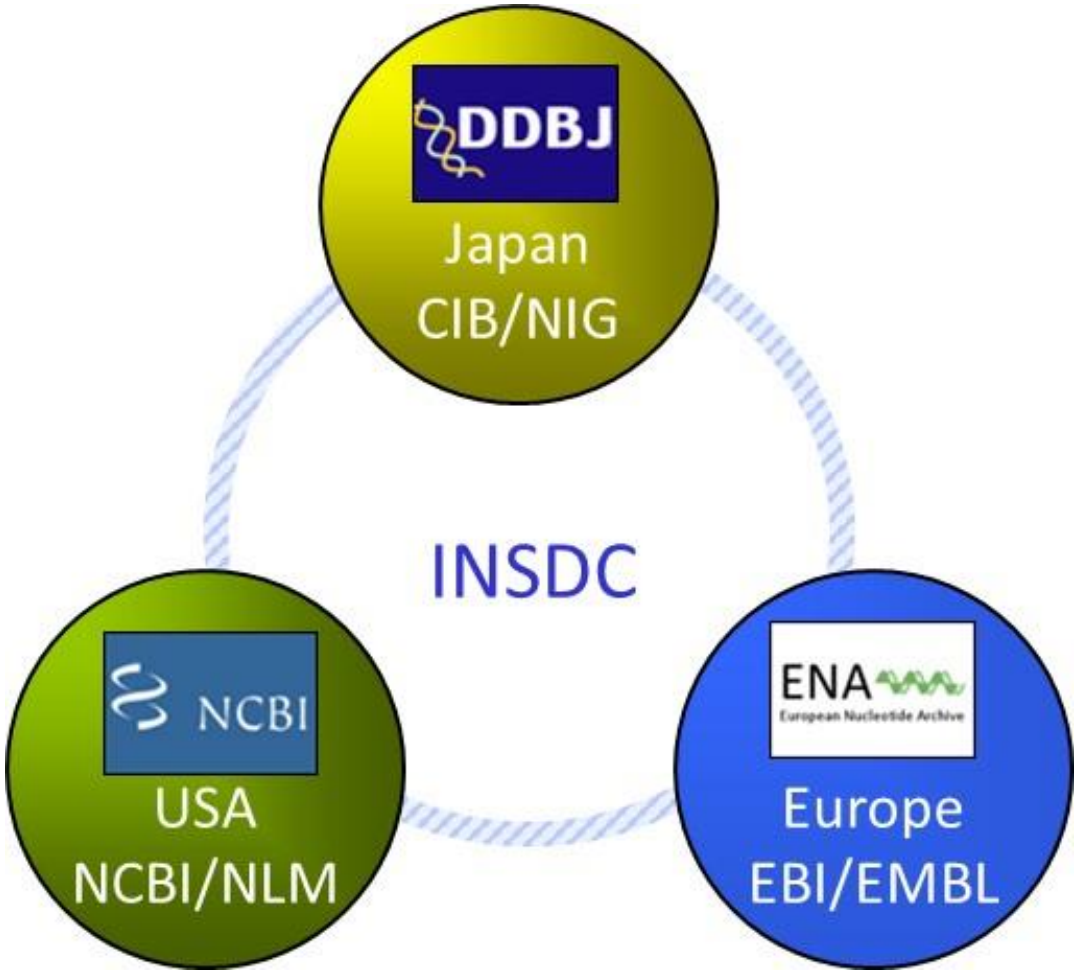
Nucleotídeos :

- International Collaboration
  - NCBI(EUA), EMBL(Europa), DDBJ (Japão)

- Organismo-específico
  - http://flybase.org/
  - http://poultry.mph.msu.edu/
  - http://www.maizegdb.org/
  - http://rice.plantbiology.msu.edu/
  - http://www.yeastgenome.org/
  - http://soybeangenome.siu.edu/
  - http://www.ornl.gov/sci/techresources/Human_Genome/home.shtml



BANCOS DE DADOS MUNDIAIS



Sequências de > 300,000 espécies
genoma completo de > 1,500 organismos.

BANCOS DE DADOS MUNDIAIS

Genbank http://www.ncbi.nlm.nih.gov/
Banco de dados americano de seqüências de DNA e proteínas.
EBI http://www.ebi.ac.uk/
Banco de dados europeu de seqüências de DNA.
DDBJ http://www.ddbj.nig.ac.jp/
Banco de dados japonês de seqüências de DNA.

Atualizações diárias

Troca de informações

National Center for Biotechnology Information (NCBI)

http://www.ncbi.nlm.nih.gov/

National Center for Biotechnology In...

NCBI Resources How To

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National Center for Biotechnology Information

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Search Clear

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- Domains & Structures
- Genes & Expression
- Genetics & Medicine
- Genomes & Maps
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- Literature
- Proteins
- Sequence Analysis
- Small Molecules
- Taxonomy
- Training & Tutorials
- Variation

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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Genome

1000 prokaryotic genomes are now completed and available in the Genome database.

1 2 3 4

How To...

- Determine conserved synteny between the genomes of two organisms
- Find a homolog for a gene in another organism
- Obtain the full text of an article
- Design PCR primers and check them for specificity

See all ...

Popular Resources

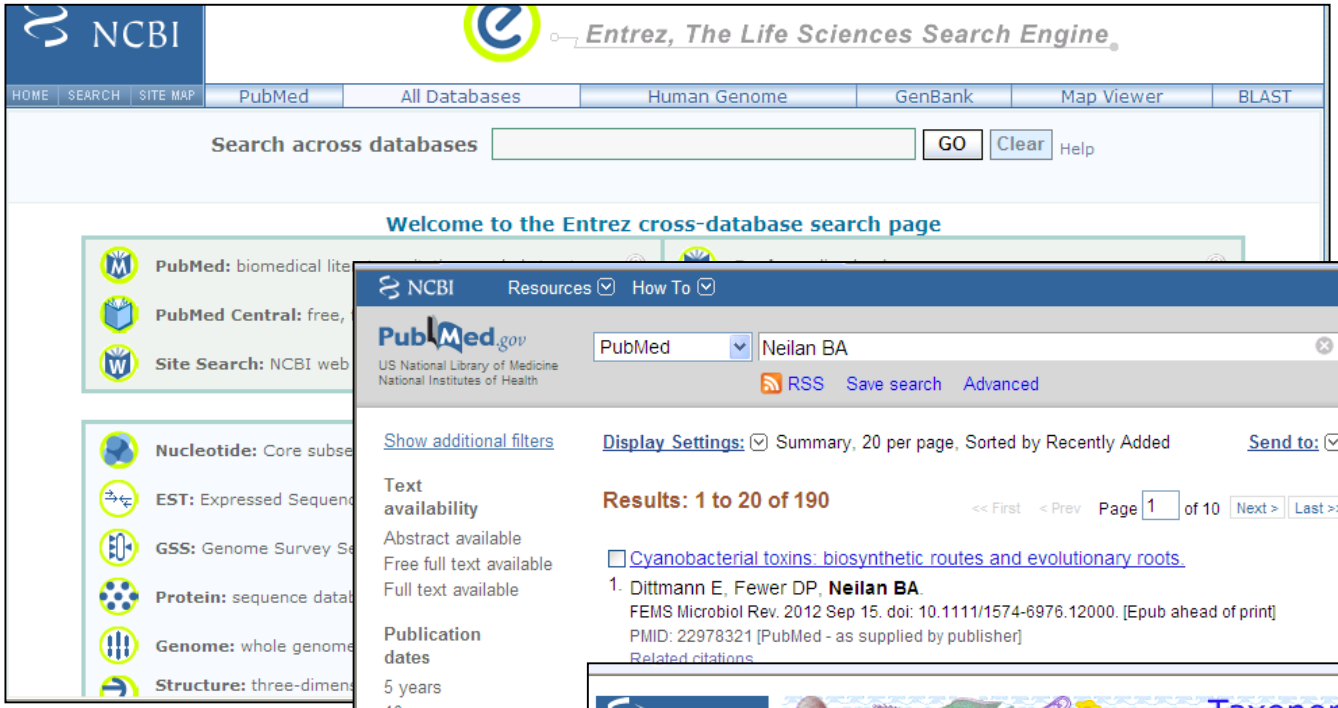
- BLAST
- Bookshelf
- Gene
- Genome
- Nucleotide
- OMIM
- Protein
- PubChem
- PubMed
- PubMed Central
- SNP

NCBI News

Discovery Workshop
09 Aug 2010
A two-day NCBI learning workshop will be held on the NIH

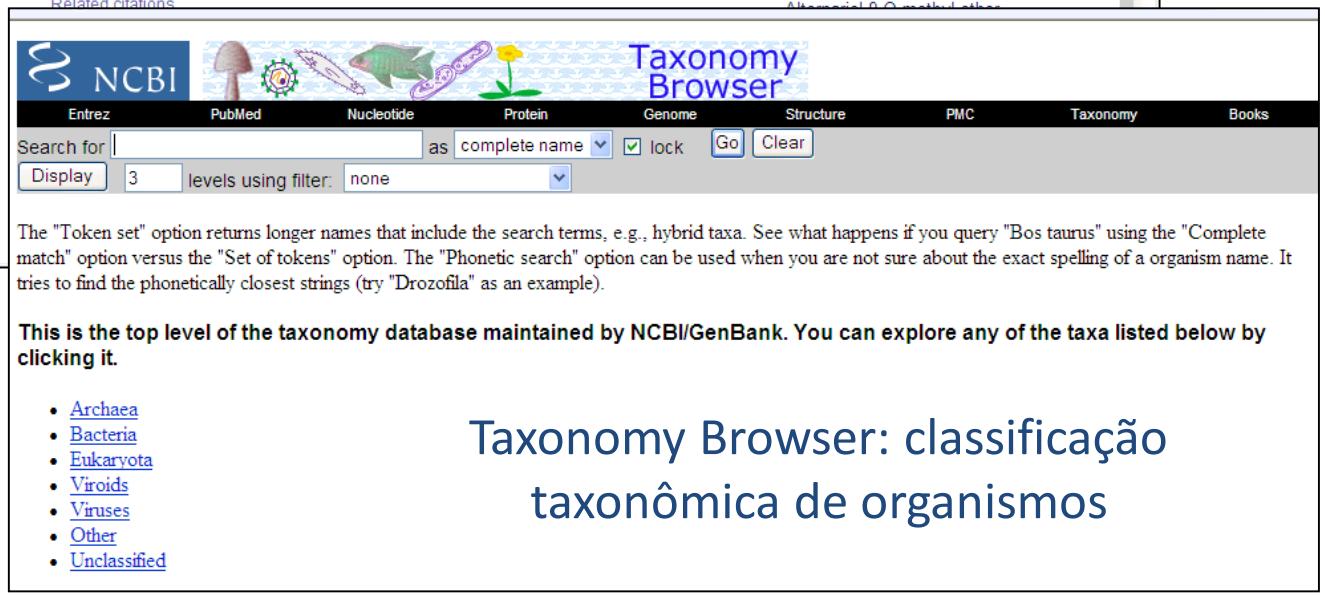
Selected Structures, Taxonomy on Wikipedia
23 Jul 2010
The June NCBI News is available on the Bookshelf

FERRAMENTAS



ENTREZ: ferramenta de busca do banco de dados do NCBI

PubMed: artigos científicos



Taxonomy Browser: classificação taxonômica de organismos

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The New York Times

Dining & Wine

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FASHION & STYLE | DINING & WINE | HOME & GARDEN | WEDDINGS

Creamy, Healthier Ice Cream? What's the Catch?

By JULIA MOSKIN
Published: July 26, 2006

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SINGLE PAGE
REPRINTS

IN its quest to create ice cream as voluptuous as butter and as virtuous as broccoli, the ice cream industry has probed the depths of the Arctic Ocean, studied the intimate structures of algae and foisted numerous failures on the American public.

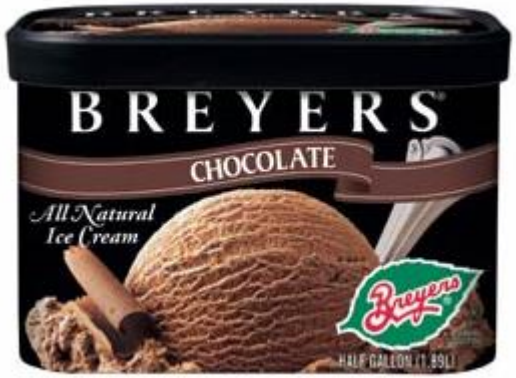
Tony Cenicola/The New York Times

SCOOP OF SCIENCE Companies are using new methods to make ice cream a guiltless pleasure.

"I have tried them all as they came down the pike: dairy-free, fat-free, sugar-free; with tofu, yogurt, rice, whatever," said Linda Calhoun, a teacher who lives near Flagstaff, Ariz., cataloguing the disappointments she has tasted over the years. "They always make me sad."

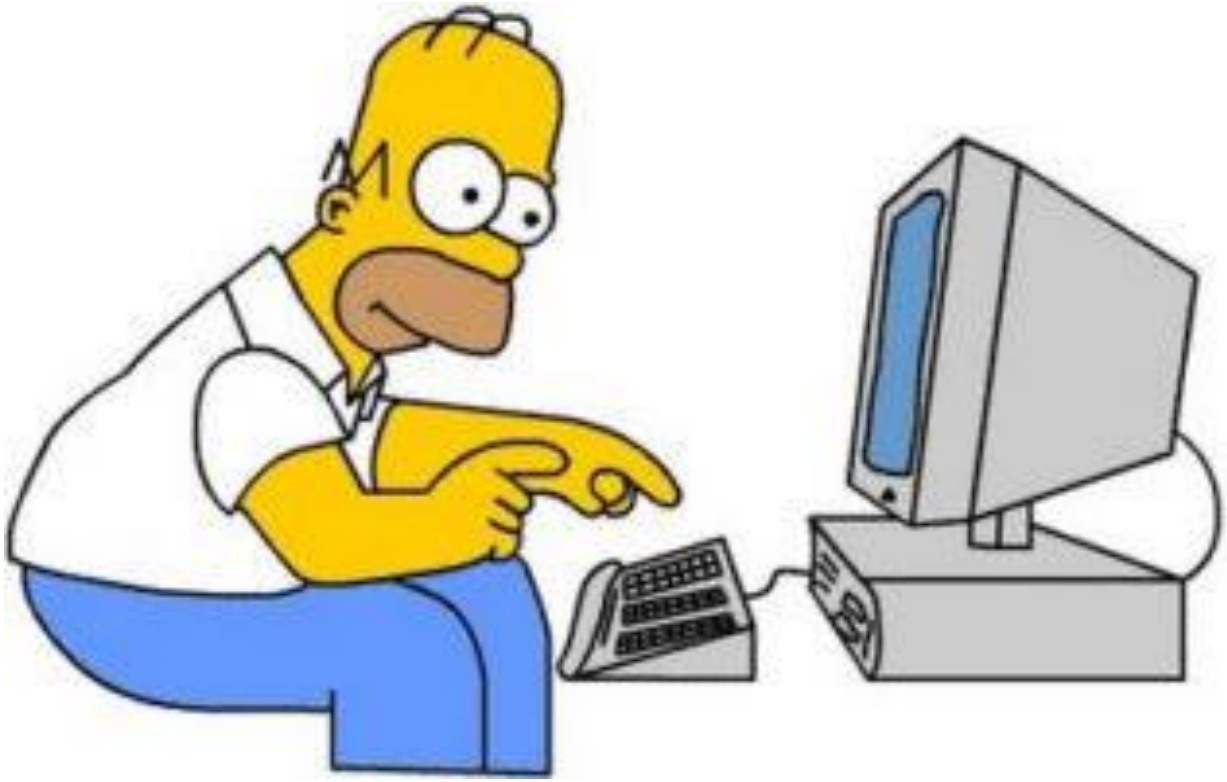
For Americans who spend each summer wrestling with temptation, there is fresh hope in the freezer case. New industrial processes, including one that involves a protein

Ocean pout vive em regiões polares



http://www.unilever.com/innovation/productinnovations/coolicecreaminnovations/

http://academicsreview.org/reviewed-content/genetic-roulette/section-7/part-7-3/



http://www.ncbi.nlm.nih.gov/nuccore/X07506?

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DEFINITION  Winter flounder antifreeze protein gene (AFP).
ACCESSION   X07506
VERSION     X07506.1  GI:64211
KEYWORDS    antifreeze protein.
SOURCE      Pseudopleuronectes americanus (winter flounder)
  ORGANISM  Pseudopleuronectes americanus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
            Pleuronectoidei; Pleuronectidae; Pleuronectinae;
            Pseudopleuronectes.
```

```
REFERENCE   1  (bases 1 to 1095)
  AUTHORS   Scott,G.K., Davies,P.L., Kao,M.H. and Fletcher,G.L.
  TITLE     Differential amplification of antifreeze protein genes in the
            pleuronectinae
  JOURNAL   J. Mol. Evol. 27 (1), 29-35 (1988)
   PUBMED   3133486
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polyA signal 969..974

ORIGIN

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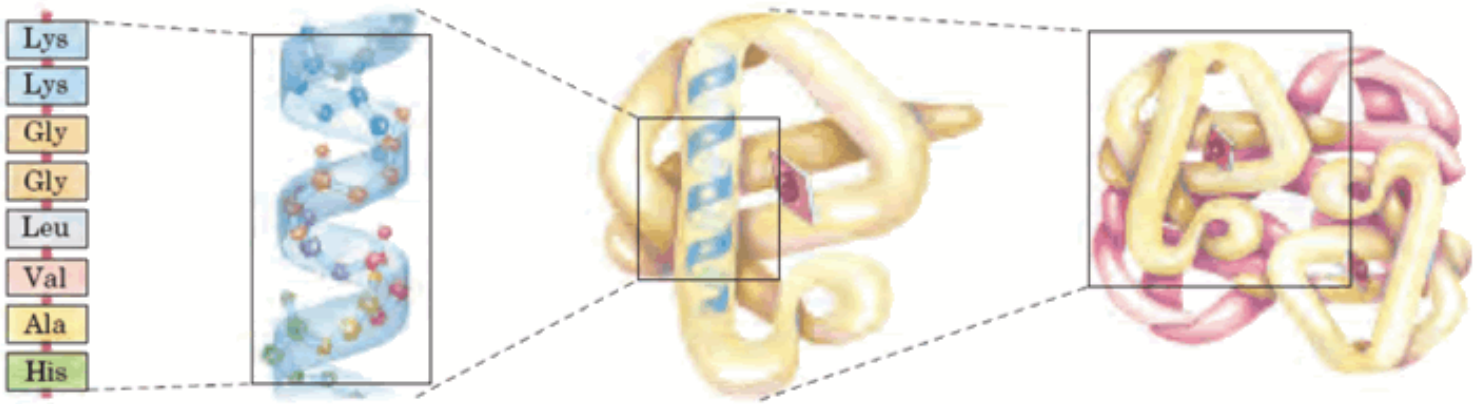
1081 ctgttgaacc tgcag
```

//

PROTÉINAS

- NCBI: Protein database (http://www.ncbi.nlm.nih.gov/genbank/)

- UniPRot/Swiss-Prot: (http://www.uniprot.org/)



UniProt Protein knowledgebase

http://www.uniprot.org/

UniProt

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Search in: Protein Knowledgebase (UniProtKB)

Query: Search Clear Fields »

WELCOME

The mission of UniProt is to provide the scientific community with a comprehensive, high-quality and freely accessible resource of protein sequence and functional information.

What we provide

UniProtKB	Protein knowledgebase, consists of two sections: Swiss-Prot, which is manually annotated and reviewed. TrEMBL, which is automatically annotated and is **not** reviewed. Includes Complete Proteome Sets.
UniRef	Sequence clusters, used to speed up sequence similarity searches.
UniParc	Sequence archive, used to keep track of sequences and their identifiers.
Supporting data	Literature citations, taxonomy, keywords and more.

Getting started

NEWS

UniProt release 2010_09 - Aug 10, 2010

'De-merge' of multi-gene entries derived from a single species in UniProtKB/Swiss-Prot

› Statistics for UniProtKB: Swiss-Prot · TrEMBL
› Forthcoming changes
› News archives

SITE TOUR

Learn how to make best use of the tools and data on this site.

http://www.uniprot.org/uniprot/P04002

www.uniprot.org/uniprot/P04002

UniProt

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Basket

P04002 - ANPA_PSEAM

Protein	**Ice-structuring protein A**
Gene	*N/A*
Organism	*Pseudopleuronectes americanus (Winter flounder) (Pleuronectes americanus)*
Status	Reviewed - - Experimental evidence at protein level

Display None

- FUNCTION
- NAMES & TAXONOMY
- SUBCELLULAR LOCATION
- PATHOLOGY & BIOTECH
- PTM / PROCESSING
- EXPRESSION
- INTERACTION
- STRUCTURE
- FAMILY & DOMAINS
- SEQUENCE

BLAST Align Format Add to basket History

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Function

Contributes to protect fish blood from freezing at subzero sea water temperatures. Lowers the blood freezing point. Binds to nascent ice crystals and prevents further growth. 2 Publications

GO - Molecular function

- ice binding Source: UniProtKB

GO - Biological process

- homoiothermy Source: UniProtKB
- response to freezing Source: UniProtKB

Complete GO annotation...

Keywords - Molecular function

Antifreeze protein

Names & Taxonomy

Protein names *Recommended name:*

BUSCA EM BLAST

BLAST: Basic Local Alignment Search Tool

- Por sequência de nucleotídeos ou de aminoácidos (proteínas);
- Comparação de sequências a fim de identificar similaridade de DNA ou proteína para inferir origem, função, filogênia;
- Realiza comparações entre pares de sequências, buscando regiões com similaridade local;
- Alinhamento local (segmentos) é a base da busca por BLAST;
- Usa algoritmos para gerar alinhamento de sequências;

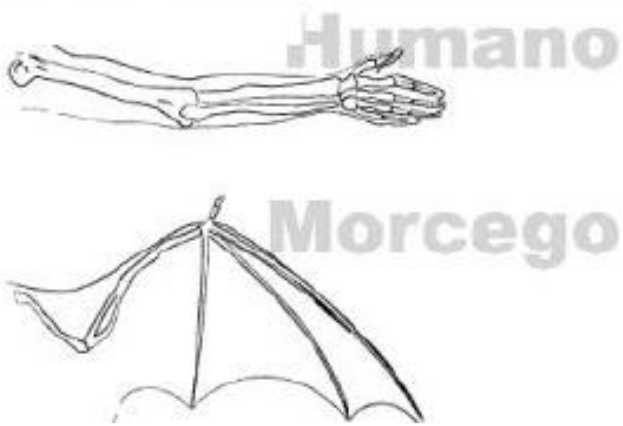
BUSCA EM BLAST

Algoritmos em Blast:

- Não avaliam homologia

A análise de sequências objetiva encontrar similaridades importantes que permitam inferir sobre homologia

- Medem similaridade e identidade de seqüências



Exemplos:

Órgãos homólogos – asas de morcego e mãos de humanos (mesma origem)

Órgãos similares – asas de morcego e asas de borboleta (mesma função)

BUSCA EM BLAST

Identidade x Similaridade x Homologia

- **Identidade** = ocorrência do mesmo nucleotídeo ou aminoácido na mesma posição nas seqüências alinhadas

- **Similaridade** = considera combinações próximas e avaliada por medidas de diferença/igualdade

- **Homologia** = dividem mesma ancestralidade, com significado evolutivo

Homologia => conceito central de Evolução

BUSCA EM BLAST

National Center for Biotechnology Information - Windows Internet Explorer

http://www.ncbi.nlm.nih.gov/

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Genome

1000 prokaryotic genomes are now completed and available in the Genome database.

1 2 3 4

How To...

- Determine conserved synteny between the genomes of two organisms
- Find a homolog for a gene in another organism
- Obtain the full text of an article
- Design PCR primers and check them for specificity

See all ...

Popular Resources

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

NCBI News

Education resource information in the May NCBI News
07 Jun 2010
May NCBI News is available.

OMIM's new look, Epigenomics in April NCBI News
10 May 2010
The April NCBI News issue is now available.

NIH Roadmap Epigenomics Project data in GEO database
22 Apr 2010
GEO's Roadmap Epigenomics Project Data Listings page allows

More...

BUSCA EM BLAST

BLAST — Basic Local Alignment Search Tool

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NCBI/ BLAST Home

BLAST finds regions of similarity between biological sequences. more...

Learn more about how to use the new BLAST design

BLAST Assembled 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, discontiguous megablast
protein blast	Search **protein** database using a **protein** query *Algorithms:* blastp, psi-blast, phi-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

News

BLAST 2.2.18 now available
The binaries for BLAST 2.2.18 are now available at our FTP site
2008-04-01 07:50:00

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 intetesting to examine the intro-exon structure even across species. Often, the only data available is the mRNA sequence from a cDNA or a curated database such as refseq. Is it possible, however, to see how the mRNA aligns to genomic sequence using BLAST and thus arrive at an idea of its possible intron exon structure.

More tips...

BUSCA EM BLAST

Formato FASTA: formato universalmente aceito para se processado

Identificador

```
>gi|226347322|gb|FJ830553.1| Anabaena planctonica CENA210 ribulose-1,5-
bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds
CCGGCGAAATTAAAGGTCACTACCTCAACGTTACCGCTCCTACCTGCGAAGAAATGTTGAAACGGGCTGA
GTACGCTAAAGAACTCAAAATGCCCATCATCATGCACGACTACCTAACCGCAGGTTTCACCGCTAACACC
ACATTGGCTCGTTGGTGTCGTGATAACGGTATTTTATTGCACATTCACCGTGCTATGCACGCTGTAATTG
ACCGTCAAAAAAATCACGGTATCCACTTCCGCGTATTAGCTAAAGCCCTCCGCTTGTCCGGTGGTGATCA
CATCCACACTGGTACAGTTGTTGGTAAGTTAGAAGGTGAACGCGGTATTACCATGGGCTTCGTTGACTTA
TTACGTGAAAACTACGTTGAGCAAGACAAGTCTCGCGGTATTTACTTTACCCAAGATTGGGCGTCTCTAC
CTGGTGTAATGGCCGTTGCTTCTGGTGGTATCCACGTATGGCATATGCCCGCGTTGGTTGAGATCTTCGG
TGATGACTCCGTATTACAATTCGGTGGTGGTACACTCGGACATCCTTGGGGTAACGCTCCTGGTGCTACA
GCTAACCGCGTAGCTCTAAAAGCAGTTGTTCAAGCTCGTAACGAAGGCCGTAACTTAGCTCGTGAAGGTA
ACGATATTATCCGCGAAGCTGCTAAGTGGTCTCCTGAGTTGGCTGTTGCTTGCGAACTG
```

```
>gi|226347323|gb|ACO50079.1| ribulose-1,5-bisphosphate
carboxylase/oxygenase large subunit [Anabaena planctonica CENA210]
GEIKGHYLNVTAPTCEEMLKRAEYAKELKMPIIMHDYLTAGFTANTTLARWCRDNGILLHIHRAMHAVID
RQKNHGIHFRVLAKALRLSGGDHIHTGTVVGKLEGERGITMGFVDLLRENYVEQDKSRGIYFTQDWASLP
GVMAVASGGIHVWHMPALVEIFGDDSVLQFGGGTLGHPWGNAPGATANRVALKAVVQARNEGRNLAREGN
DIIREAAKWSPELAVACEL
```

BUSCA EM BLAST

BLAST — Basic Local Alignment Search Tool

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NCBI/ BLAST Home

BLAST finds regions of similarity between biological sequences. more...

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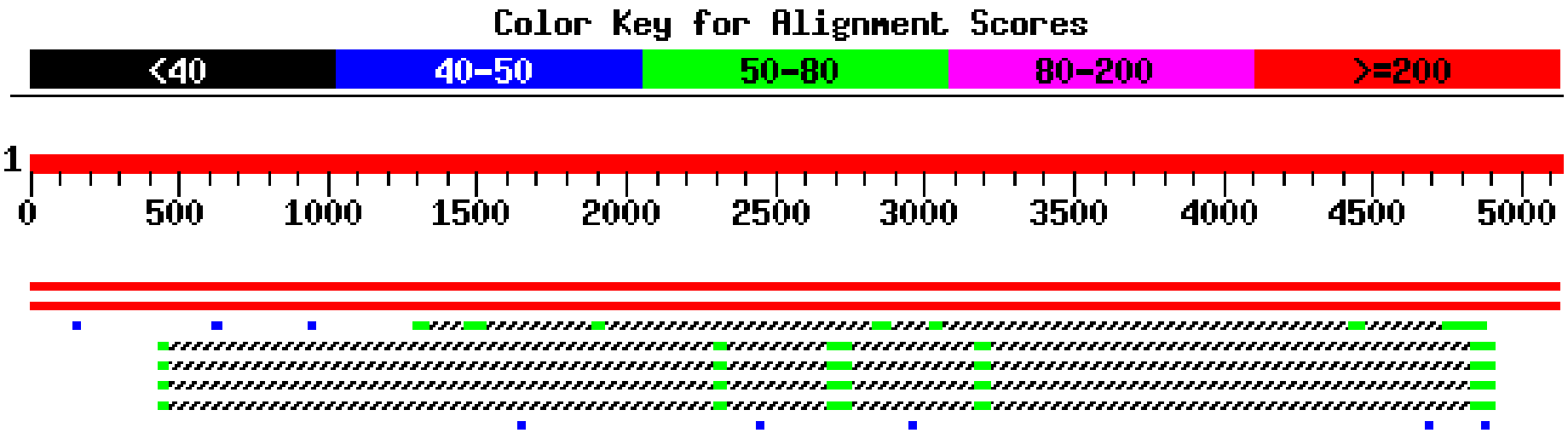
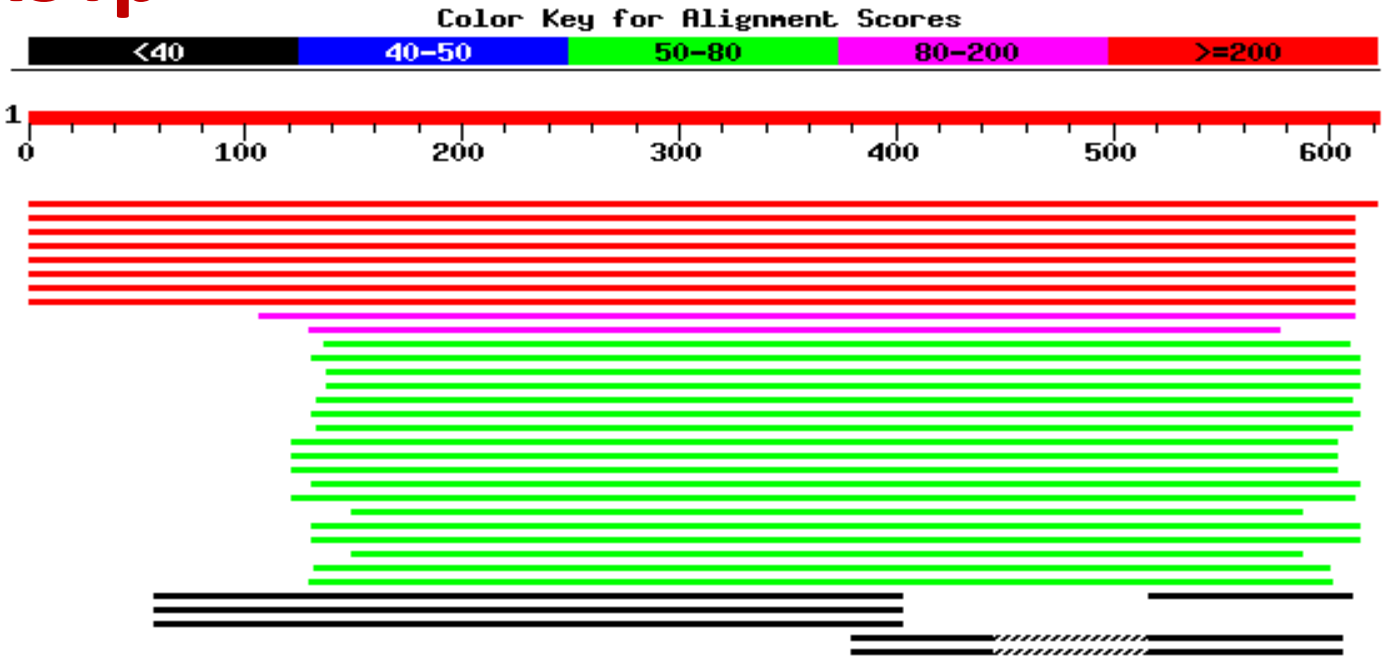
More tips...

BLASTn



Sequences producing significant alignments:		Score (bits)	E Value
gi|15149239|gb|AF367362.1|AF367362	Heliothis virescens cadh...	1.013e+04	0.0
gi|15149241|gb|AF367363.1|AF367363	Heliothis virescens trun...	5749	0.0
gi|11545673|gb|AF319973.1|AF319973	Manduca sexta cadherin-r...	80	2e-11
gi|9049398|dbj|AB041510.1|AB041510	Bombyx mori btrl75c mRNA...	58	7e-05
gi|9049396|dbj|AB041509.1|AB041509	Bombyx mori btrl75b mRNA...	58	7e-05
gi|9049394|dbj|AB041508.1|AB041508	Bombyx mori btrl75a mRNA...	58	7e-05
gi|4666281|dbj|AB026260.1|AB026260	Bombyx mori btrl75 mRNA ...	58	7e-05
gi|285645|dbj|D13613.1|BOVRP3A	Bovine mRNA for rabphilin-3A...	46	0.25
gi|13877227|gb|AC079832.16|AC079832	Mus musculus clone rp23...	44	1.0
gi|3355667|emb|AL031124.1|SC1C2	Streptomyces coelicolor cos...	44	1.0
gi|6598432|gb|AC004680.2|AC004680	Arabidopsis thaliana chro...	42	4.0
gi|7417993|gb|L19596.3|RCAPPSA	Rhodobacter sphaeroides RS62...	42	4.0
gi|15074266|emb|AL591787.1|SME591787	Sinorhizobium meliloti...	42	4.0
gi|10799539|emb|AL158050.8|AL158050	Human DNA sequence from...	42	4.0
gi|6598827|gb|AC005768.17|AC005768	Homo sapiens chromosome ...	42	4.0

BLASTp



Sequences producing significant alignments:		Score (bits)	E Value
gi|15149240|gb|AAK85198.1|AF367362_1	(AF367362) cadherin-li...	1175	0.0
gi|15149242|gb|AAK85199.1|AF367363_1	(AF367363) truncated c...	1213	0.0
gi|7475983|pir||JE0128	Bombyx mori receptor precursor - Bac...	752	0.0
gi|9049395|dbj|BAA99404.1|	(AB041508) cadherin-like membran...	751	0.0
gi|9049399|dbj|BAA99406.1|	(AB041510) cadherin-like membran...	751	0.0
gi|9049397|dbj|BAA99405.1|	(AB041509) cadherin-like membran...	751	0.0
gi|11545674|gb|AAG37912.1|AF319973_2	(AF319973) cadherin-re...	693	0.0
gi|913012|gb|AAB33758.1|	insecticidal toxin receptor, BT-R1...	671	0.0
gi|7299907|gb|AAF55082.1|	(AE003705) CG3389 gene product [D...	109	7e-23
gi|10726475|gb|AAF54717.2|	(AE003693) CG6977 gene product [...	93	8e-18
gi|7293994|gb|AAF49351.1|	(AE003524) CG6445 gene product [D...	79	9e-14
gi|13876330|gb|AAK26085.1|	(AY013796) protocadherin gamma A...	77	4e-13
gi|11056063|ref|NP_061743.1|	protocadherin gamma subfamily ...	74	3e-12
gi|14196477|ref|NP_114476.1|	protocadherin gamma subfamily ...	74	3e-12
gi|13876332|gb|AAK26086.1|	(AY013797) protocadherin gamma A...	74	6e-12
gi|13876344|gb|AAK26092.1|	(AY013803) protocadherin gamma A...	72	1e-11
gi|6753408|ref|NP_034016.1|	cadherin EGF LAG seven-pass G-t...	71	3e-11
gi|10727655|gb|AAF58763.2|	(AE003828) stan gene product [Dr...	70	7e-11
gi|5832705|dbj|BAA84069.1|	(AB028498) Flamingo [Drosophila ...	70	7e-11
gi|6049492|gb|AAF02618.1|AF172329_1	(AF172329) starry night...	69	8e-11
gi|13876336|gb|AAK26088.1|	(AY013799) protocadherin gamma A...	69	1e-10
gi|11995466|ref|NP_059088.1|	cadherin EGF LAG seven-pass G-...	69	1e-10
gi|13876296|gb|AAK26068.1|	(AY013779) protocadherin beta 18...	69	2e-10

BUSCA EM BLAST

- Nossa sequência – *query* (consulta),

- O resultado da busca em BLAST pode ser um ou mais *hits* em sequências-sujeito (*subject*), ou seja, sequências pertecentes o banco,

```
Query: 181 catcaactacaactccaaagacacccttacacccactaggatatcaacaaacctacccac 240
           |||||||| |||| |||||| ||||| | |||||||||||||||||||||||||||||||
Sbjct: 189 catcaactgcaaccccaaagccacccct-cacccactaggatatcaacaaacctacccac 247
```

- Os melhores resultados de escores são relatados,
- usar valor *E*
  - valor *E* <0.01

Quanto menor o *e-value*, mais significativo o alinhamento!!!

NUCLEOTÍDEOS

FORMATO FASTA

>gi|47933333|gb|AY262820.1| Pinus radiata cellulose synthase (CesA10) mRNA, complete cds
GCACGAGGATTTAATCGAACTCGGTAATTGTTATCATCGTGGTGAGGACTAGTGCTT
GATATTTTAGTTTTATTCTCGAAATTTCATAATAGCTTGGGCTTTCTAAAAAGGGGAAT
GGTGGAATGGGTGTGAGAGTGAAGAGGAATGGTATCGAACCACTAAGAAAAGTAG
TCGTGCAAGTATTAGATGGTTGGCTGTGATAGTTGGAAA...

>LINHA DO NOME

MÁXIMA DE 80 CARACTERES POR LINHA

NCBI Entrez Nucleotide

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PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

Search CoreNucleotide for Go Clear

Limits Preview/Index History Clipboard Details

Display GenBank Show 5 Send to Hide: sequence all but gene, CDS and mRNA features

Range: from begin to end Reverse complemented strand Features: + Refresh

1: AY262820. Reports Pinus radiata cel...[gi:47933333] Links

Features Sequence

```
LOCUS       AY262820                4428 bp    mRNA    linear   PLN 23-MAY-2005
DEFINITION  Pinus radiata cellulose synthase (CesA10) mRNA, complete cds.
ACCESSION   AY262820
VERSION     AY262820.1  GI:47933333
KEYWORDS    .
SOURCE      Pinus radiata (Monterey pine)
  ORGANISM  Pinus radiata
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
REFERENCE   1  (bases 1 to 4428)
  AUTHORS   Krauskopf,E., Harris,P.J. and Putterill,J.
  TITLE     The cellulose synthase gene PrCESA10 is involved in cellulose
            biosynthesis in developing tracheids of the gymnosperm Pinus
            radiata
  JOURNAL   Gene 350 (2), 107-116 (2005)
   PUBMED   15823508
REFERENCE   2  (bases 1 to 4428)
  AUTHORS   Krauskopf,E.H., Harris,P.J. and Putterill,J.J.
  TITLE     Direct Submission
```

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Limits Preview/Index History Clipboard Details

Display FASTA Show 5 Send to

Range: from begin to end Reverse complemented strand Refresh

1: AY262820. Reports Pinus radiata cel...[gi:47933333] Links

```
>gi|47933333|gb|AY262820.1| Pinus radiata cellulose synthase (CesA10) mRNA, complete cds
GCACGAGGATTTAATCGAACTCGGTAATTGTTATCATCGTGGTGAGGACTAGTGCTTGATATTTTAGTTT
TATTCTCGAAATTTCATAATAGCTTGGGCTTTCTAAAAAGGGGAATGGTGGAATGGGTGTGAGAGTGAAG
AGGAATGGTATCGAACCACTAAGAAAAGTAGTCGTGCAAGTATTAGATGGTTGGCTGTGATAGTTGGAAA
AGGAATAGTAGAAATGGGACAGAAGTTTCATTCTGTAAGCTTTTTCATGGACTGTTAGTCTTCTCTTTGC
TTTCAGCTTAAGCAGCTTTAGTGCTGGCATTTTGATGCTCAGTAATCACAAGTTGGAGCTTTGGTCTGGA
TTAGAAGGATTTGAGCCTGTTTTAGTGCATTACAGACCGTTTTAAGGTTGCTTTTTGCAGTTTTGATAAG
GCTGGGATTGAAGTGGGGAGTTTAATGATGGCTAGGATGAAGGAGAGGCTGAGATACTGGGCATTTTGAT
GTGGGTTAAGCTGGATTTCAGCTGATTTCAATACCTTTTTGTTCTGGGGAGCAGAAATCAGTGAACGGGA
CTTTAGCAGGAAGAACCCATTTTGACGTGGAGCTAAGTGTTGTTAGGATTCAAAGGTGATCAATTAGTGC
GCGGGAGGTTCAGTGGCAATGGAGGCTAGAACAAACACAGCAGCAGGTTCTAACAAAAGGAATGTGCGTG
TTTCGGTTCGAGATGATGGAGAACTTGGGCCTAAGCCTCCACAACACATAAATAGCCACATTTGCCAGAT
ATGTGGAGAAGATGTTGGCTTAGCAGCAGATGGGGAGTTCTTTGTAGCTTGCAATGAGTGTGCATTTCCA
GTATGCAGGCCTTGCTATGAATATGAGTGGAAGGATGGAAATCAATCTTGTCCACAATGCAAGACTAGAT
ACAAGTGGCATAAAGGTAGCCCTCAAGTGGATGGTGACAAGGAAGATGAATGTGCAGATGATTTGGATCA
TGACTTCAACTCCACTCAGGGTAACAGGAATGAAAAACAGCAGATTGCAGAGGCCATGTTGCATTGGCAA
ATGGCCTATGGACGAGGGGAGGATGTTGGTCCATCACGCTCAGAAAGTCAGGAGCTTCCTCAGCTTCAAG
TTCCCCTTATTACCAATGGACAAGCTATTTCCGGTGAGTTGCCAGCAGGATCCTCAGAGTATCGTAGGAT
TGCTGCTCCACCCACTGGTGGTGGTAGTGGGAAGCGTGTTCATCCACTTCCTTTTCCTGATTCGACTCAA
ACAGGTCAAGTGAGAGCTGAGGACCCTGCCAAAGATTTCAATTCCTATGGATTTGGAAATGTTGCCTGGA
AGGAGAGAGTAGAAAGCTGGAAGAATAAACAGGACAAAAATACATTGCAAGTGACTAGTGATACTTACTA
```

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BLAST — Basic Local Alignment Search Tool

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BLAST fruit fly

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protein blast	Search **protein** database using a **protein** query *Algorithms:* blastp, psi-blast, phi-blast
blastx	Search **protein** database using a **translated nucleotide** query

News

Old BLAST Web Pages to be deleted June 11th 2007

As previously announced access to the old pages will be removed on June 11, 2007.

2007-06-01 12:15:00

More BLAST news...

Tip of the Day

Using Tree View to Examine Relationships Between Sequences.

The new Tree View option on the NCBI Web BLAST service presents a dendrogram

http://www.ncbi.nlm.nih.gov/genome/seq/BlastGen/BlastGen.cgi?taxid=7227 Internet 100%

Enter accession number, gi, or FASTA sequence

Clear

Colar a sequência que deseja analisar

Query subrange

From

To

Or, upload file

Procurar...

Job Title

Enter a descriptive title for your BLAST search

Choose Search Set

Database

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

Human genomic plus transcript

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 Test/gpipe/9606/allcontig_and_rna using Megablast (Optimize for highly simi sequences)

Show results in a new window

Concluído Internet 100%

To

Or, upload file

Procurar...

Job Title

Enter a descriptive title for your BLAST search

Choose Search Set

Database

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

Nucleotide collection (nr/nt)

Organism
Optional

op taxa will be shown.

Entrez Query
Optional

- ***Genomic plus Transcript***
  - Human genomic plus transcript
  - Mouse genomic plus transcript
- ***Other Databases***
  - Nucleotide collection (nr/nt)
  - Reference mRNA sequences (refseq_rna)
  - Reference genomic sequences (refseq_genomic)
  - Expressed sequence tags (est)
  - Non-human, non-mouse ESTs (est_others)
  - Genomic survey sequences (gss)
  - High throughput genomic sequences (HTGS)
  - Patent sequences(pat)
  - Protein Data Bank (pdb)
  - Human ALU repeat elements (alu_repeats)
  - Sequence tagged sites (dbsts)
  - Whole-genome shotgun reads (wgs)
  - Environmental samples (env_nt)

Program Select

Optimize for

BLAST

Search database nr using Blastn (Optimize for somewhat similar sequences)

Show results in a new window

Internet 100%

Enter accession number, gi, or FASTA sequence

Clear

Query subrange

From

To

```
TCACCAAATAAGATCCACTGAAAAGACGCTGGTAACTGATGGCATTGTGATATTGAAGACAGTTGTTTGT
GTACTGTGCCGAGTTCTGCCGAACATGGCACAATTGCAAGCTATAGTTAAGAAATTTTGACTGTAGTGTG
ATTCCGTATCTGAAGATAATCTGACCTCCTGTGACAACGCCCAAGAGGGTTTGTGTAATATATTCATCAT
AAAAAAAAAAAAAAAAAA
```

Or, upload file

Procurar...

Job Title

gi|47933333|gb|AY262820.1| Pinus radiata cellulose...

Enter a descriptive title for your BLAST search

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 suggested

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

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

Internet

100%

Or, upload file

Procurar...

Job Title

gi|47933333|gb|AY262820.1| Pinus radiata cellulose...

Enter a descriptive title for your BLAST search

Choose Search Set

Database

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

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Optional

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Choose a BLAST algorithm

BLAST

Search database nr using Blastn (Optimize for somewhat similar sequences)

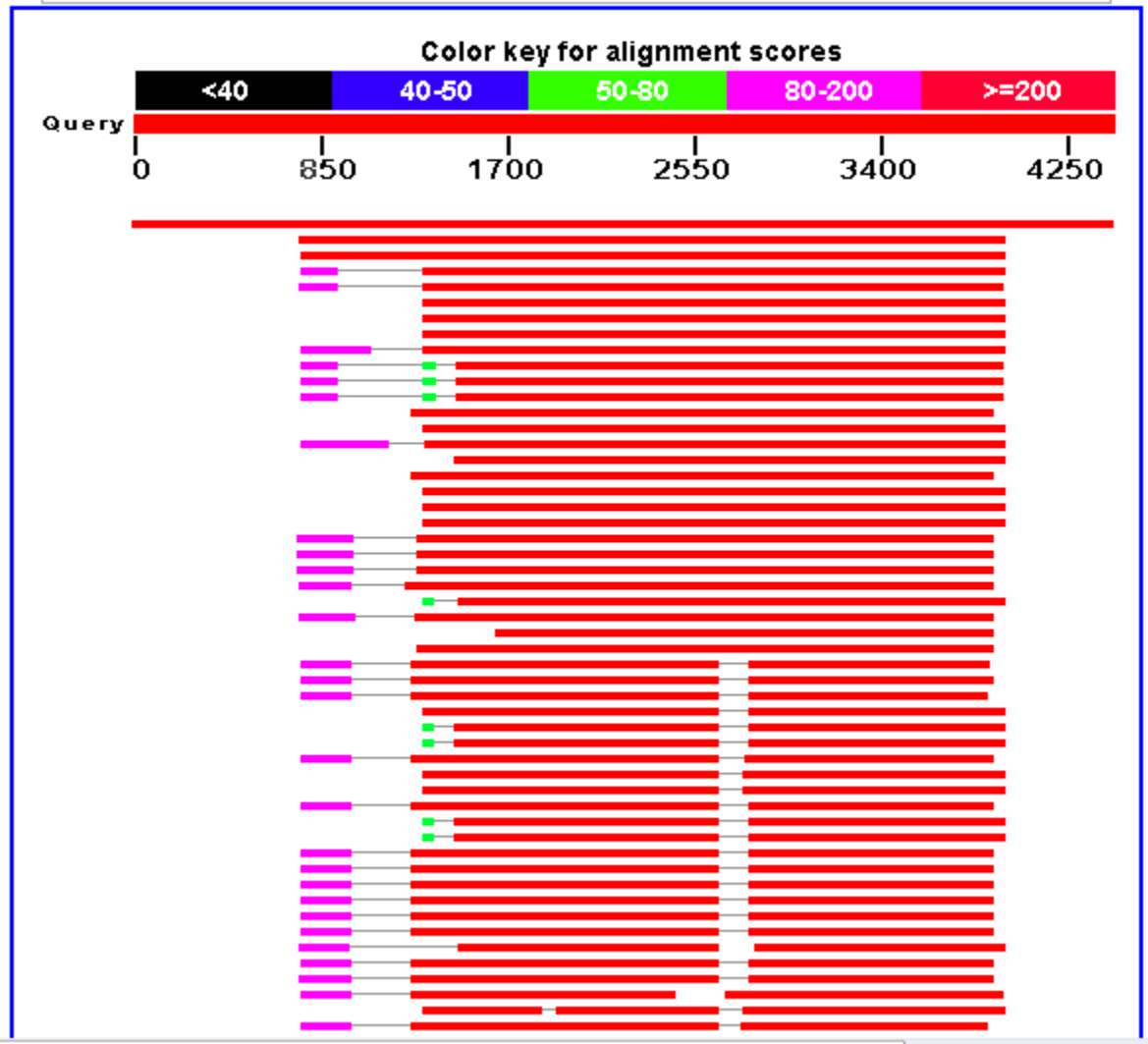
Show results in a new window

Algorithm parameters

Note: Parameter values that differ from the default are highlight

Concluído Internet 100%

Mouse-over to show defline and scores, click to show alignments



Internet 100%

RID=1123597061-15515-159087652210.BLASTQ3, gi|47933333|gb|AY262820.1| Pinus radiata cellulose s - Microsoft Internet ...

Arquivo Editar Exibir Favoritos Ferramentas Ajuda

Endereço http://www.ncbi.nlm.nih.gov/BLAST/Blast.cgi#47933333 Ir Links Norton AntiVirus

```
> gi|47933333|gb|AY262820.1|  Pinus radiata cellulose synthase (CesA10) mRNA, complete cds
          Length=4428

 Score = 7374 bits (3720),  Expect = 0.0
 Identities = 3741/3741 (100%), Gaps = 0/3741 (0%)
 Strand=Plus/Plus

Query  1     GCACGAGGATTTAATCGAACTCGGTAATTGTTATCATCGTGGTGAGGACTAGTGCTTGAT  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     GCACGAGGATTTAATCGAACTCGGTAATTGTTATCATCGTGGTGAGGACTAGTGCTTGAT  60

Query  61    ATTTTAGTTTTATTCTCGAAATTTCATAATAGCTTGGGCTTTCTAAAAAGGGGAATGGTG  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    ATTTTAGTTTTATTCTCGAAATTTCATAATAGCTTGGGCTTTCTAAAAAGGGGAATGGTG  120

Query  121   GAATGGGTGTGAGAGTGAAGAGGAATGGTATCGAACCACTAAGAAAAGTAGTCGTGCAAG  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   GAATGGGTGTGAGAGTGAAGAGGAATGGTATCGAACCACTAAGAAAAGTAGTCGTGCAAG  180

Query  181   TATTAGATGGTTGGCTGTGATAGTTGGAAAAGGAATAGTAGAAATGGGACAGAAGTTTCA  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   TATTAGATGGTTGGCTGTGATAGTTGGAAAAGGAATAGTAGAAATGGGACAGAAGTTTCA  240

Query  241   TTCTGTAAGCTTTTTCATGGACTGTTAGTCTTCTCTTTGCTTTCAGCTTAAGCAGCTTTA  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   TTCTGTAAGCTTTTTCATGGACTGTTAGTCTTCTCTTTGCTTTCAGCTTAAGCAGCTTTA  300
```

Barra = Identidade

Internet

RID=1163438066-7525-53995425163.BLASTQ2, gi|47933333|gb|AY262820.1| Pinus radiata cellulose syn - Microsoft Internet ...

Arquivo Editar Exibir Favoritos Ferramentas Ajuda

Endereço http://www.ncbi.nlm.nih.gov/BLAST/Blast.cgi#47933335

```
> gi|47933335|gb|AY262821.1|  Pinus radiata cellulose synthase (CesA2) mRNA, partial cds
Length=3603

 Score =  866 bits (437),  Expect = 0.0
 Identities = 977/1157 (84%), Gaps = 0/1157 (0%)
 Strand=Plus/Plus

Query  1450  GAAGACCTTCAAATGAGTGATGAAGCACGCCAGCCCCTATCAAGAAAGGTTCCTATTGCT  1509
             |||||||| ||||||| ||||||||| || || || || || ||||||||  | ||| ||
Sbjct  697   GAAGACCTGCAAATGAATGATGAAGCTCGTCAACCTCTCTCTAGAAAGGTGTCCATTCCT  756

Query  1510  TCTTCCAAGATCAATCCGTACAGGATGGTGATTGTTCTACGGCTTGTGATCTTGTGTTTT  1569
             |||||||||||||||||| || || |||||||| ||| | |||||| |  |||||||| ||
Sbjct  757   TCTTCCAAGATCAATCCATATAGAATGGTGATCGTTATCCGGCTTTTTGTCTTGTGTGTT  816

Query  1570  TTCTTCCGCTACCGAATATTGAATCCTGTTCGCAATGCTTATGGACTTTGGTTTACTTCA  1629
             ||||||||||| || ||| || ||||||||  |||||| |||||||| |||||||| ||
Sbjct  817   TTCTTCCGCTATCGGATAATGCATCCTGTTAACAATGCATATGGACTATGGTTTACCTCT  876

Query  1630  GTAATATGTGAGATTTGGTTTGCCATATCCTGGATTCTTGATCAGTTTCCTAAATGGCTT  1689
             || ||||||||| ||||||||||||| || ||||| || ||||||||||| ||||||||
Sbjct  877   GTGATATGTGAGGTTTGGTTTGCCATTTCATGGATCCTGGATCAGTTTCCGAAATGGCTA  936

Query  1690  CCCATCAATAGGGAAACTTATCTTGACAGGCTTTGTTTGAGATACGATAGAGAAGGAGAG  1749
```

Internet

Iniciar Yes Real... Micr... 3 I... Pape... 15:15

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

removed on June 11, 2007.
2007-06-01 12:15:00

More BLAST news...

Basic BLAST

Choose a BLAST program to run.

nucleotide blast	Search a **nucleotide** database using a **nucleotide** query *Algorithms:* blastn, megablast, discontiguous megablast
protein blast	Search **protein** database using a **protein** query *Algorithms:* blastp, psi-blast, phi-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** quer

Specialized BLAST

Choose a type of specialized search (or database name in parentheses.)

- Search trace archives
- Find conserved domains in your sequence (cds)
- Find sequences with similar conserved domain architecture (cdart)

Tip of the Day

How to Search Custom Databases in Web-Blast Using Entrez Queries

A powerful feature of the BLAST Web interface is the ability to limit BLAST searches to a subset of any database using a standard Entrez query. Skillful use of Entrez queries allows the equivalent of on-the-fly construction of databases of exact composition

More tips...

Concluído | Internet | 100%

Enter Query Sequence

Enter accession number, gi, or FASTA sequence Clear

Query subrange

From

To

Or, upload file Procurar...

Genetic code Standard (1) [?]

Job Title

Enter a descriptive title for your BLAST search

Choose Search Set

Database Non-redundant protein sequences (nr)

- Non-redundant protein sequences (nr)
- Reference proteins (refseq_protein)
- Swissprot protein sequences(swissprot)
- Patented protein sequences(pat)
- Protein Data Bank proteins(pdb)
- Environmental samples(env_nr)

Organism Optional

be suggested

id. Only 20 top taxa will be shown.

Entrez Query Optional

BLAST Search database nr using Blastx (search protein databases using a translated nucleotide quer

Show results in a new window

Algorithm parameters

Concluído Internet 100%

Enter Query Sequence

Enter accession number, gi, or FASTA sequence Clear

```
>gi|47933333|gb|AY262820.1| Pinus radiata cellulose synthase (CesA10)
mRNA, complete cds
GCACGAGGATTTAATCGAACTCGGTAATTGTTATCATCGTGGTGAGGACTAGTGCTTGATATTTTAGTTT
TATTCTCGAAATTTCATAATAGCTTGGGCTTTCTAAAAAGGGGAATGGTGGAATGGGTGTGAGAGTGAAG
AGGAATGGTATCGAACCACTAAGAAAAGTAGTCGTGCAAGTATTAGATGGTTGGCTGTGATAGTTGGAAA
```

Query subrange

From

To

Or, upload file Procurar...

Genetic code Standard (1) [?]

Job Title gi|47933333|gb|AY262820.1| Pinus radiata cellulose...

Enter a descriptive title for your BLAST search

Choose Search Set

Database Non-redundant protein sequences (nr)

Organism
Optional

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

Entrez Query
Optional

Enter an Entrez query to limit search

BLAST Search database nr using Blastx (search protein databases using a translated nucleotide quer

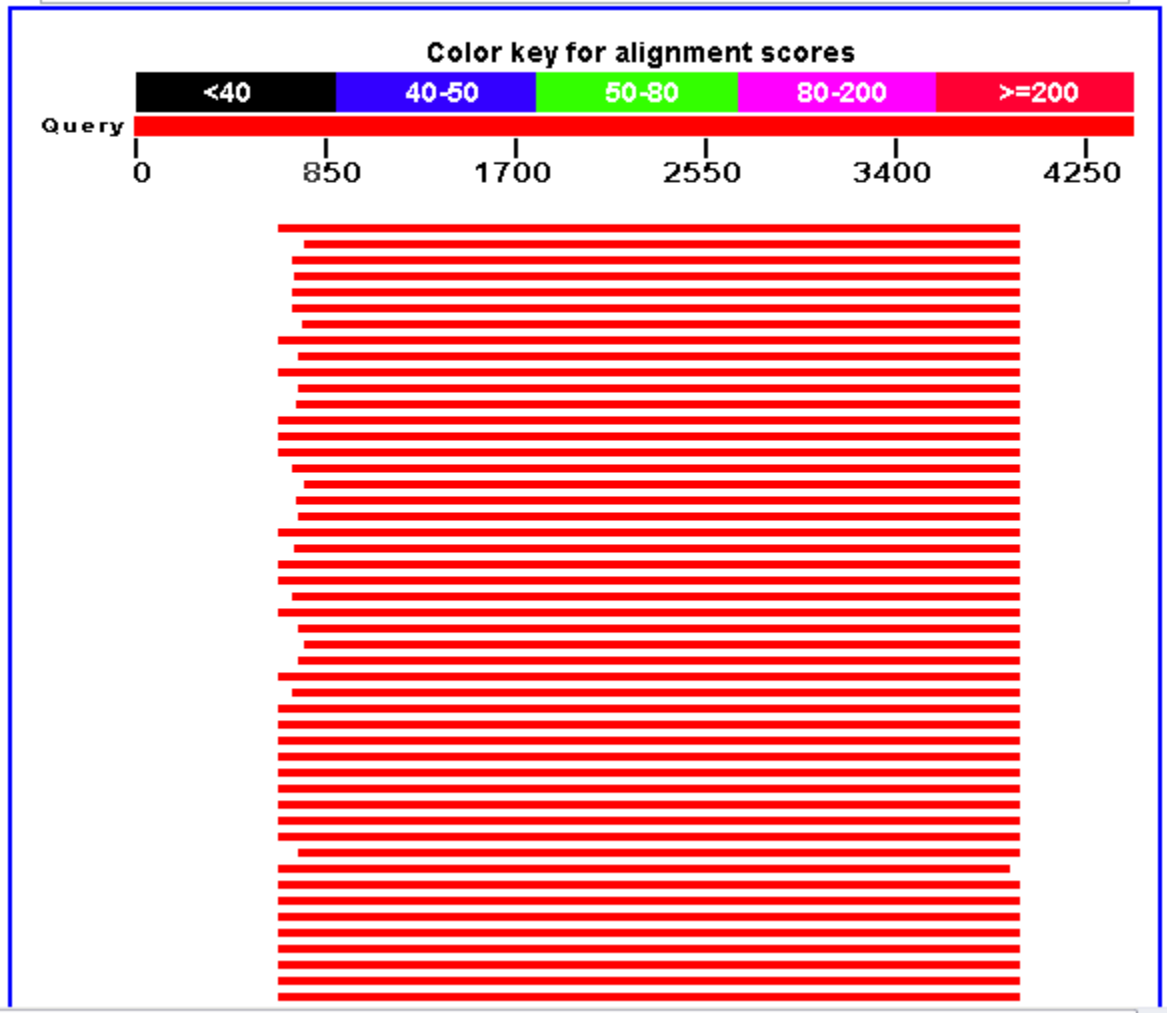
Show results in a new window

Algorithm parameters

Internet 100%

Distribution of 101 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments



Concluído

Internet

100%

RID=1123597122-19305-123349401779.BLASTQ3, gi|47933333|gb|AY262820.1| Pinus radiata cellulose s - Microsoft Internet ...

Arquivo Editar Exibir Favoritos Ferramentas Ajuda

Endereço http://www.ncbi.nlm.nih.gov/BLAST/Blast.cgi#47933334 Ir Links Norton AntiVirus

```
> gi|47933334|gb|AAQ63935.1|  cellulose synthase [Pinus radiata]
          Length=1096

 Score = 2221 bits (5754),  Expect = 0.0
 Identities = 1096/1096 (100%), Positives = 1096/1096 (100%), Gaps = 0/1096 (0%)
 Frame = +1

Query  649   MEARTNTAAGSNKRNVRVSVRDDGELGPKPPQHINSHICQICGEDVGLAADGEFFVACNE  828
             MEARTNTAAGSNKRNVRVSVRDDGELGPKPPQHINSHICQICGEDVGLAADGEFFVACNE
Sbjct  1     MEARTNTAAGSNKRNVRVSVRDDGELGPKPPQHINSHICQICGEDVGLAADGEFFVACNE  60

Query  829   CAFPVCRPCYEYEWKDGNQSCPQCKTRYKWHKGSPQVDGDKEDECADDLDHDFNSTQGNR  1008
             CAFPVCRPCYEYEWKDGNQSCPQCKTRYKWHKGSPQVDGDKEDECADDLDHDFNSTQGNR
Sbjct  61    CAFPVCRPCYEYEWKDGNQSCPQCKTRYKWHKGSPQVDGDKEDECADDLDHDFNSTQGNR  120

Query  1009  NEKQQIAEAMLHWQMAYGRGEDVGPSRSESQELPQLQVPLITNGQAISGELPAGSSEYRR  1188
             NEKQQIAEAMLHWQMAYGRGEDVGPSRSESQELPQLQVPLITNGQAISGELPAGSSEYRR
Sbjct  121   NEKQQIAEAMLHWQMAYGRGEDVGPSRSESQELPQLQVPLITNGQAISGELPAGSSEYRR  180

Query  1189  IAAPPTGGGSGKRVHPLPFPDSTQTGQVRAEDPAKDFNSYGFGNVAWKERVESWKNKQDK  1368
             IAAPPTGGGSGKRVHPLPFPDSTQTGQVRAEDPAKDFNSYGFGNVAWKERVESWKNKQDK
Sbjct  181   IAAPPTGGGSGKRVHPLPFPDSTQTGQVRAEDPAKDFNSYGFGNVAWKERVESWKNKQDK  240

Query  1369  NTLQVTSDTYYASEGKDGDIDGCVADEEDLQMSDEARQPLSRKVPIASSKINPYRMVIVL  1548
             NTLQVTSDTYYASEGKDGDIDGCVADEEDLQMSDEARQPLSRKVPIASSKINPYRMVIVL
Sbjct  241   NTLQVTSDTYYASEGKDGDIDGCVADEEDLQMSDEARQPLSRKVPIASSKINPYRMVIVL  300
```

Internet

RID=1163438291-19330-95885029726.BLASTQ2, gi|47933333|gb|AY262820.1| Pinus radiata cellulose sy - Microsoft Internet ...

Arquivo Editar Exibir Favoritos Ferramentas Ajuda

Endereço http://www.ncbi.nlm.nih.gov/BLAST/Blast.cgi#47933336

```
> gi|47933336|gb|AAQ63936.1|  cellulose synthase [Pinus radiata]
Length=1066

 Score = 1813 bits (4695),  Expect = 0.0
 Identities = 890/1066 (83%), Positives = 972/1066 (91%), Gaps = 9/1066 (0%)
 Frame = +1

Query  760   ICQICGEDVGLAADGEFFVACNECAFPVCRPCYEYEWKDGNQSCPQCKTRYKWHKGSPQV  939
             +CQICG+DVGL ADG+ FVACN CAFPVCRPCY+YE KDGNQSCPQCKTRYK HKGSP+V
Sbjct   3    VCQICGDDVGLTADGDLFVACNVCAFPVCRPCYDYERKDGNQSCPQCKTRYKMHKGSPRV  62

Query  940   DGDKEDECADDLDHDFN-STQGNRNEKQQIAEAMLHWQMAYGRGEDVGPSRSESQELPQL  1116
             +GD+ ++ ADD+ ++++    G+RNEKQ+IAEAML WQM+YGRGEDVG   S  QE+ +
Sbjct   63   EGDEGEDGADDVGNEYHYPPPGSRNEKQKIAEAMLRWQMSYGRGEDVGAPTSTRQEVSES  122

Query  1117  QVPLITNGQAISGELPAGSSEYRRIAAPPTGGGSGKRVHPLPFPDSTQTGQVRAEDPAKD  1296
             Q+P +TNGQ+ISGELPA S E+  + APP+ GG  KRVHPLP+ D+++  QVR  D ++D
Sbjct   123  QIPRLTNGQSISGELPALSPEHS-VGAPPSSGGGSKRVHPLPYTDASRPAQVRIVDHSRD  181

Query  1297  FNSYGFGNVAWKERVESWKNKQDKNTLQVTSDTYYASEGKDGDIDGCVADEEDLQMSDEA  1476
             FNSYGFGNVAWKERVESWKNKQ+KN LQVT+   YASEGK GD+D    + EDLQM+DEA
Sbjct   182  FNSYGFGNVAWKERVESWKNKQEKNMLQVTNSGDYASEGKGGDVDFGGGENEDLQMNDEA  241

Query  1477  RQPLSRKVPIASSKINPYRMVIVLRLVILCFFFRYRILNPVRNAYGLWFTSVICEIWFAI  1656
```

Internet

Iniciar Yes Real... Micr... 3 I... Pape... 15:19

Basic BLAST

Choose a BLAST program to run.

nucleotide blast	Search a **nucleotide** database using a **nucleotide** query *Algorithms:* blastn, megablast, discontiguous megablast
protein blast	Search **protein** database using a **protein** query *Algorithms:* blastp, psi-blast, phi-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** quer

Specialized BLAST

Choose a type of specialized search (or database name in parentheses.)

- Search trace archives
- Find conserved domains in your sequence (cds)
- Find sequences with similar conserved domain architecture (cdart)
- Search sequences that have gene expression profiles (GEO)
- Search immunoglobulins (IgBLAST)
- Search for SNPs (snp)
- Screen sequence for vector contamination (vecscreen)
- Align two sequences using BLAST (bl2seq)

Tip of the Day

How to Search Custom Databases in Web-Blast Using Entrez Queries

A powerful feature of the BLAST Web interface is the ability to limit BLAST searches to a subset of any database using a standard Entrez query. Skillful use of Entrez queries allows the equivalent of on-the-fly construction of databases of exact composition

More tips...

NCBI/ BLAST/ blastp suite: BLASTP programs search protein databases using a protein query. more... Reset page Boo

Enter Query Sequence

Enter accession number, gi, or FASTA sequence Clear

```
>gi|47933334|gb|AAQ63935.1| cellulose synthase [Pinus radiata]
MEARTNTAAGSNKRNVRVSVRDDGELGPKPPQHINSHICQICGEDVGLAADGEFFVACNECAFPVCRPCY
EYEWKDGNQSCPQCKTRYKWHKGSPQVDGDKEDECADDLDHDFNSTQGNRNEKQQIAEAMLHWQMAYGRG
EDVGPSRSESQELPQLQVPLITNGQAISGELPAGSSEYRRIAAPPTGGGSGKRVHPLPFPDSTQTGQVRA
EDPAKDFNSYGFGNVAWKERVESWKNKQDKNTLQVTSDTYYASEGKDGDIDGCVADEEDLQMSDEARQPL
```

Query subrange

From

To

Or, upload file Procurar...

Job Title gi|47933334|gb|AAQ63935.1| cellulose synthase...

Enter a descriptive title for your BLAST search

Choose Search Set

Database Non-redundant protein sequences (nr)

- Non-redundant protein sequences (nr)
- Reference proteins (refseq_protein)
- Swissprot protein sequences(swissprot)
- Patented protein sequences(pat)
- Protein Data Bank proteins(pdb)
- Environmental samples(env_nr)

Organism Optional

be suggested

id. Only 20 top taxa will be shown.

Entrez Query Optional

Program Selection

Algorithm

- blastp (protein-protein BLAST)
- PSI-BLAST (Position-Specific Iterated BLAST)
- PHI-BLAST (Pattern Hit Initiated BLAST)

Choose a BLAST algorithm

Internet 100%

EDPAKDFNSYGFGNVAWKERVESWKNKQDKNTLQVTSDTYYASEGKDGDIDGCVADEEDLQMSDEARQPL

Or, upload file Procurar...

Job Title gi|47933334|gb|AAQ63935.1| cellulose synthase...

Enter a descriptive title for your BLAST search

Choose Search Set

Database Non-redundant protein sequences (nr)

Organism Optional

Enter organism name or id--completions will be suggested

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

Entrez Query Optional

Enter an Entrez query to limit search

Program Selection

Algorithm

- (•) blastp (protein-protein BLAST)
- ( ) PSI-BLAST (Position-Specific Iterated BLAST)
- ( ) PHI-BLAST (Pattern Hit Initiated BLAST)

Choose a BLAST algorithm

BLAST Search database nr using Blastp (protein-protein BLAST)

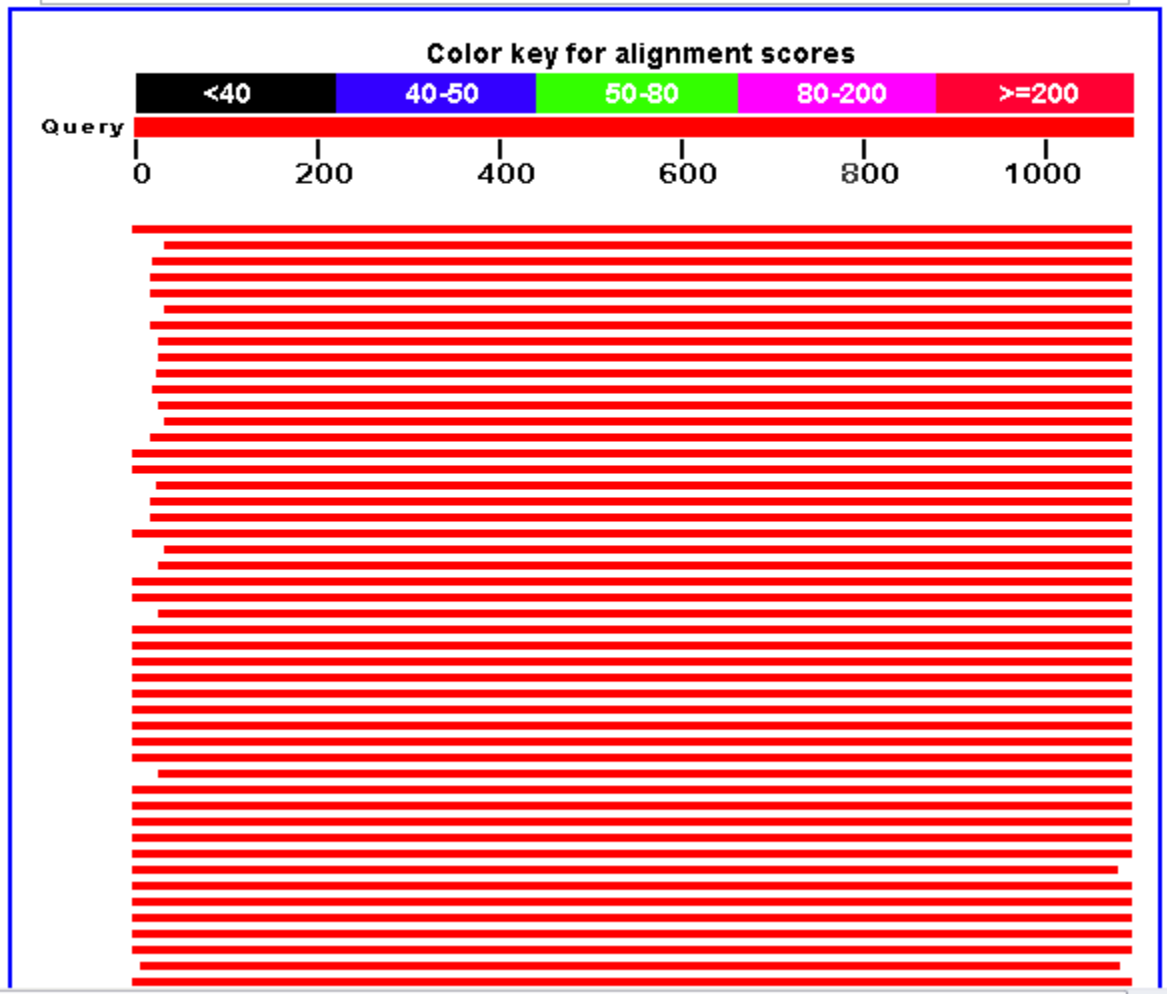
[x] Show results in a new window

▶ Algorithm parameters

Internet 100%

Distribution of 101 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments



Concluído

Internet

100%

RID=1123597492-5864-52185512549.BLASTQ3, gi|47933334|gb|AAQ63935.1| cellulose synthase [Pinus r - Microsoft Internet ...

Arquivo Editar Exibir Favoritos Ferramentas Ajuda

Endereço http://www.ncbi.nlm.nih.gov/BLAST/Blast.cgi#47933334 Ir Links Norton AntiVirus

```
> gi|47933334|gb|AAQ63935.1|  cellulose synthase [Pinus radiata]
          Length=1096

 Score = 2221 bits (5754),  Expect = 0.0
 Identities = 1096/1096 (100%), Positives = 1096/1096 (100%), Gaps = 0/1096 (0%)

Query  1     MEARTNTAAGSNKRNVRVSVRDDGELGPKPPQHINSHICQICGEDVGLAADGEFFVACNE  60
             MEARTNTAAGSNKRNVRVSVRDDGELGPKPPQHINSHICQICGEDVGLAADGEFFVACNE
Sbjct  1     MEARTNTAAGSNKRNVRVSVRDDGELGPKPPQHINSHICQICGEDVGLAADGEFFVACNE  60

Query  61    CAFPVCRPCYEYEWKDGNQSCPQCKTRYKWHKGSPQVDGDKEDECADDLDHDFNSTQGNR  120
             CAFPVCRPCYEYEWKDGNQSCPQCKTRYKWHKGSPQVDGDKEDECADDLDHDFNSTQGNR
Sbjct  61    CAFPVCRPCYEYEWKDGNQSCPQCKTRYKWHKGSPQVDGDKEDECADDLDHDFNSTQGNR  120

Query  121   NEKQQIAEAMLHWQMAYGRGEDVGPSRSESQELPQLQVPLITNGQAISGELPAGSSEYRR  180
             NEKQQIAEAMLHWQMAYGRGEDVGPSRSESQELPQLQVPLITNGQAISGELPAGSSEYRR
Sbjct  121   NEKQQIAEAMLHWQMAYGRGEDVGPSRSESQELPQLQVPLITNGQAISGELPAGSSEYRR  180

Query  181   IAAPPTGGGSGKRVHPLPFPDSTQTGQVRAEDPAKDFNSYGFGNVAWKERVESWKNKQDK  240
             IAAPPTGGGSGKRVHPLPFPDSTQTGQVRAEDPAKDFNSYGFGNVAWKERVESWKNKQDK
Sbjct  181   IAAPPTGGGSGKRVHPLPFPDSTQTGQVRAEDPAKDFNSYGFGNVAWKERVESWKNKQDK  240

Query  241   NTLQVTSDTYYASEGKDGDIDGCVADEEDLQMSDEARQPLSRKVPIASSKINPYRMVIVL  300
             NTLQVTSDTYYASEGKDGDIDGCVADEEDLQMSDEARQPLSRKVPIASSKINPYRMVIVL
Sbjct  241   NTLQVTSDTYYASEGKDGDIDGCVADEEDLQMSDEARQPLSRKVPIASSKINPYRMVIVL  300
```

Internet

VAMOS PRATICAR...

1. Utilizando o número selecionado para sua dupla :

a) Buscar a sequência no formato FASTA para cada um deles:

b) Realizar a análise BLAST e responder as seguintes questões:

Qual a ferramenta de comparação utilizada?
Qual o tipo de sequência foi utilizada como *query*?
Qual o tamanho da sequência *query*?
Qual o tamanho da sequência *subject*?
Qual a proteína codificada pela sequência *query* (produto do gene)?
A que organismo pertence a sequência *query*?
Qual a % de identidade encontrada entre a sequência *query* e *subject?*

2. Considere os dois alinhamentos possíveis. Qual o melhor deles?

Considere: **ACGGACT** e **ATCGGATCT**

```
A - C - G G - A C T
|   |   |       | |
A T C G G A T - C T
```

Alinhamento 1

```
A - C G G - A C T
|   | | |     | |
A T C G G A T C T
```

Alinhamento 2

Considere o seguinte esquema simples de score:

- + 2 para igualdade (match)
- - 1 para desigualdade (mismatch)
- - 2 para penalidade (gaps)

ESTUDO DIRIGIDO

1. Bancos de dados públicos e internacionais: NCBI, EMBL, DDBJ;
2. Definição de Bioinformática;
3. Análise da sequência no NCBI;
4. Busca de sequências por similaridade;
5. BLAST e Banco de dados de sequências.

Próxima semana – Inicio das apresentações sobre pareceres da CTNBio!
Vejam as normas no Stoa!!!!

BIBLIOGRAFIA RECOMENDADA

Documentos

224

O programa *BLAST*: guia prático de utilização

Embrapa

Manuscrito para capítulo do Biowork IV

Bioinformática aplicada à Genômica

Fabrício R. Santos[1] e José Miguel Ortega[2]

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