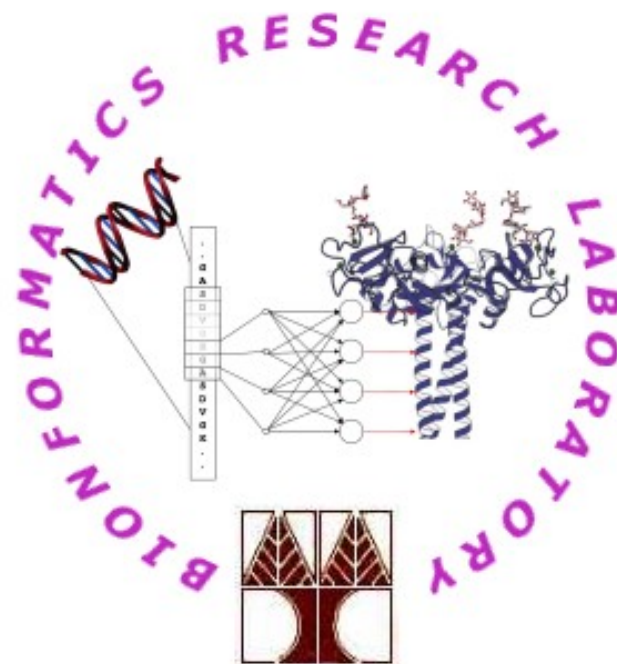


Γονιδιωματικές βάσεις δεδομένων



Vasilis Promponas

Bioinformatics Research Laboratory

Department of Biological Sciences

University of Cyprus

BIO003

Εισαγωγή στη Βιοπληροφορική

ΣΥΝΟΨΗ

- Σύντομη ιστορία των γονιδιωμάτων
- Περιήγηση σε διαδικτυακές πηγές
 - GOLD
 - Sorcerer II
 - UCSC
 - NCBI
 - ENSEMBL
- Συζήτηση ..

Η ιστορία της γονιδιωματικής ...

- 1953 – Διπλή έλικα DNA
- 1972 – Τεχνολογία Ανασυνδυασμένου DNA
- 1975-77 – Βελτιωμένες μεθοδολογίες προσδιορισμού νουκλεοτιδικών αλληλουχιών
 - 1980 – Νόμπελ χημείας (¼ Walter Gilbert, ¼ Fred Sanger)
- 1977 – Το πρώτο γονιδίωμα (βακτηριοφάγος φX174, 5386 βάσεις, 11 γονίδια, Sanger *et al.*, Nature)
- 1985 – αυτοματοποίηση PCR (Kary Mullis, ½ Νόμπελ Χημείας 1993)

... η ιστορία της γονιδιωματικής ...

- 1986 – Αυτοματοποιημένη αλληλούχιση (L.Hood-CIT)
- 1989/1990 – Έναρξη Human Genome Project (DOE)
 - 3×10^9 \$, 15 χρόνια, διεθνής συνεργασία
 - “περιφερειακά” genome projects
- 1995 – *Haemophilus influenzae* (Venter, Fraser and Smith, μέγεθος ~1.8Mb)
- 1996 – *Saccharomyces cerevisiae* (Goffeau, et al., ~12Mb)
- 1997 – *Escherichia coli* K-12 (Blattner, Plunkett et al., μέγεθος ~5Mb)
- 1999/2000 – *Drosophila melanogaster* (Celera ++, ~180Mb)
- 2001 – *Homo sapiens* (2 publications, ~3Gb)

και συνεχίζουμε ..

- GOLD <http://www.genomesonline.org/>
- Μεταγονιδιώματα ...
 - 1985 – οι πρώτες προσπάθειες
 - 2000+ Μεγάλη κλίμακα
 - Breitbart *et al.*, PNAS 2002 [uncultured marine viruses]
 - Venter *et al.*, Science 2004 [Sorcerer II expeditions]
 - <http://www.sorcerer2expedition.org/version1/HTML/main.htm>
 - <http://collections.plos.org/plosbiology/gos-2007.php>
- Φυλογονιδιωματική ...
- Διπλοειδές γονιδίωμα ανθρώπου

Περιήγηση σε διαδικτυακές πηγές

- Γονίδιο στόχος:
 - *ACHE* (ακετυλχολινεστεράση)
 - <http://en.wikipedia.org/wiki/Acetylcholinesterase>

The UCSC Genome Browser

<http://genome.ucsc.edu>

- Αναπτύσσεται από το University of California (Santa Cruz Genome Bioinformatics Group)
 - Karolchik D, *et al.*, *Nucleic Acids Res.* 2007 Dec 17; [Epub ahead of print].
- Δεδομένα κυρίως για Ευκαρυωτικά γονιδιώματα (+)
- Δέχεται σχολιασμό και από “εξωτερικές” πηγές
- Πρόσβαση σε υπολογιστικά εργαλεία (π.χ. BLAT)
- Διασύνδεση με άλλες διαδικτυακές πηγές

Human Genome Browser Gateway - Mozilla

Back Forward Reload Stop <http://genome.ucsc.edu/cgi-bin/hgGateway> Search Print

Home Genome Browser Blast Table Browser FAQ Help

Human Genome Browser Gateway

The UCSC Genome Browser was created by the [Genome Bioinformatics Group of UC Santa Cruz](#).
Software Copyright (c) The Regents of the University of California. All rights reserved.

genome assembly position image width
 Human July 2003 ACHE 680 Submit

[Click here to reset the browser user interface settings to their defaults.](#)
 Add Your Own Custom Tracks

About the *Homo sapiens* assembly

The July 2003 human reference sequence (UCSC version hg16) is based on NCBI Build 34 and was produced by the International Human Genome Sequencing Consortium. The sequence covers about 99 percent of the gene-containing regions in the genome, and has been sequenced to an accuracy of 99.99 percent. Of note in this release is the addition of the pseudoautosomal regions of the Y chromosome. This sequence was taken from the corresponding regions in the X chromosome and is an exact duplication of that sequence.

There are 2,843,433,602 finished sequenced bases in the ordered and oriented portion of the assembly, which is an increase of 0.4 percent, or approximately 11 Mb, over the Build 33 assembly. The reference sequence is considered to be "finished", a technical term indicating that the sequence is highly accurate (with fewer than one error per 10,000 bases) and highly contiguous (with the only remaining gaps corresponding to regions whose sequence cannot be reliably resolved with current technology). Future work on the reference sequence will focus on improving accuracy and reducing gaps in the sequence.

Some sequence joins between adjacent clones in this assembly could not be computationally validated because the clones originated from different haplotypes and contained polymorphisms in the overlapping sequence, or the overlap was too small to be reliable. In these instances, the sequencing center responsible for the particular chromosome has provided data to support the join in the form of an electronic certificate. These certificates may be reviewed through the link below.

Bulk downloads of the sequence and annotation data are available via the Genome Browser [FTP server](#) or the [Downloads](#) page. The hg16 annotation tracks were generated by UCSC and collaborators worldwide. See the [Credits](#) page for a detailed list of the organizations and individuals who contributed to the success of this release.

Statistical information

- [Non-Standard Join Certificates](#)
- [Summary Statistics](#)

Sample position queries

A genome position can be specified by the accession number of a sequenced genomic clone, an mRNA or EST or STS marker, or a cytological band, a chromosomal coordinate range, or keywords from the GenBank description of an mRNA. The following list shows examples of valid position queries for the human genome. See the [User's Guide](#) for more information.

| Request | Genome Browser Response: |
|-----------------|--|
| chr7 | Displays all of chromosome 7 |
| 20p13 | Displays region for band p13 on chr 20 |
| chr3:1-1000000 | Displays first million bases of chr 3, counting from p arm telomere |
| scaf: 1-1000000 | Displays first million bases of scaffold 1 of an unmapped genome assembly |
| D16S3046 | Displays region around STS marker D16S3046 from the Genethon/Marshfield maps. Includes 100,000 bases on each side as well. |

<http://genome.ucsc.edu>

BIO003

Εισαγωγή στη Βιοπληροφορική

Human ACHE - UCSC Genome Browser v59 - Mozilla

Back Forward Reload Stop <http://genome.ucsc.edu/cgi-bin/hgTracks?org=Human&db=hg16&position=ACHE> Search Print

Known Genes

[ACHE at chr7:100099014-100104904](#) - (AF394270) Apoptosis-related acetylcholinesterase [BC 3.1.1.7].
[ACHE at chr7:100103168-100105936](#) - (AY389977) N-terminal extended acetylcholinesterase [Fragment].
[ACHE at chr7:100099014-100103408](#) - (M5940) acetylcholinesterase (XT blood group)

RefSeq Genes

[ACHE at chr7:100099014-100104892](#) - (NM_006665) acetylcholinesterase hydrophilic form precursor
[ACHE at chr7:100099014-100104893](#) - (NM_015883) acetylcholinesterase PI-linked form precursor
[MATA at chr4:1272542-1272721](#) - (NM_005882) macrophage erythroblast attachor
[FLJ11196 at chr15:68859597-68862316](#) - (NM_018357) acheron isoform 1
[MATS1 at chr3:17270487-17272879](#) - (NM_006317) brain abundant, membrane attached signal protein
[FLJ11196 at chr15:68859597-68862316](#) - (NM_197958) acheron isoform 2

Human Aligned mRNA Search Results

BC006082 - Homo sapiens acheron, transcript variant 1, mRNA (cDNA clone MGC:12583 IMAGE:2961597), complete cds.
 BC009446 - Homo sapiens acheron, transcript variant 1, mRNA (cDNA clone MGC:15884 IMAGE:3529516), complete cds.
 BC014018 - Homo sapiens acheron, transcript variant 1, mRNA (cDNA clone MGC:20301 IMAGE:4127153), complete cds.
 BC008518 - Homo sapiens brain abundant, membrane attached signal protein 1, mRNA (cDNA clone MGC:8555 IMAGE:2822874), complete cds.
 U0006927 - Homo sapiens macrophage erythroblast attachor mRNA, complete cds.
 AY136975 - Homo sapiens ribosome attached membrane protein 4 mRNA, complete cds.
 AF442828 - Homo sapiens acheron mRNA, complete cds.
 AF443829 - Homo sapiens acheron mRNA, complete cds.
 AF334270 - Homo sapiens apoptosis-related acetylcholinesterase (ARACHE) mRNA, complete cds, alternatively spliced.
 M5940 - Human acetylcholinesterase [ACHE] mRNA, complete cds.
 AY288977 - Homo sapiens N-terminal extended acetylcholinesterase (ACHE) mRNA, exon 1id and partial cds.
 AY539962 - Homo sapiens clone EX1A-1 MDD1 mRNA, partial sequence.
 AY539963 - Homo sapiens clone EX1A-2 MDD1 mRNA, partial sequence.
 AY539964 - Homo sapiens clone EX1A-3 MDD1 mRNA, partial sequence.
 AY539965 - Homo sapiens clone EX1A-4 MDD1 mRNA, partial sequence.
 AY539966 - Homo sapiens clone EX1A-5 MDD1 mRNA, partial sequence.
 AY539967 - Homo sapiens clone EX1A-6 MDD1 mRNA, partial sequence.
 AY539968 - Homo sapiens clone EX1A-7 MDD1 mRNA, partial sequence.
 AY539969 - Homo sapiens clone EX1A-8 MDD1 mRNA, partial sequence.
 AY539970 - Homo sapiens clone EX1A-9 MDD1 mRNA, partial sequence.
 AY539971 - Homo sapiens clone EX1A-10 MDD1 mRNA, partial sequence.
 AY539972 - Homo sapiens clone EX1A-11 MDD1 mRNA, partial sequence.
 AY539973 - Homo sapiens clone EX1A-12 MDD1 mRNA, partial sequence.
 AY539974 - Homo sapiens clone EX1A-13 MDD1 mRNA, partial sequence.
 AY539975 - Homo sapiens clone EX1A-14 MDD1 mRNA, partial sequence.
 AY539976 - Homo sapiens clone EX1C-1 MDD1 mRNA, partial sequence.
 AY539977 - Homo sapiens clone EX1C-2 MDD1 mRNA, partial sequence.
 AY539978 - Homo sapiens clone EX1C-3 MDD1 mRNA, partial sequence.
 AY539979 - Homo sapiens clone EX2C-1 MDD1 mRNA, partial sequence.
 AY539980 - Homo sapiens clone EX2C-2 MDD1 mRNA, partial sequence.
 AY539981 - Homo sapiens clone EX2C-3 MDD1 mRNA, partial sequence.
 AY539982 - Homo sapiens clone EX2D-1 MDD1 mRNA, partial sequence.
 AY539983 - Homo sapiens clone EX2D-2 MDD1 mRNA, partial sequence.
 AY539984 - Homo sapiens clone EX2D-3 MDD1 mRNA, partial sequence.
 AY539985 - Homo sapiens clone EX2D-4 MDD1 mRNA, partial sequence.
 AY539986 - Homo sapiens clone EX2D-5 MDD1 mRNA, partial sequence.
 AY539987 - Homo sapiens clone EX2D-6 MDD1 mRNA, partial sequence.
 AY539988 - Homo sapiens clone EX2D-7 MDD1 mRNA, partial sequence.
 AY539989 - Homo sapiens clone EX2D-8 MDD1 mRNA, partial sequence.
 AY539990 - Homo sapiens clone EX2D-9 MDD1 mRNA, partial sequence.
 AY539991 - Homo sapiens clone EX2D-10 MDD1 mRNA, partial sequence.
 AY539992 - Homo sapiens clone EX2D-11 MDD1 mRNA, partial sequence.
 AY539993 - Homo sapiens clone EX2E-1 MDD1 mRNA, partial sequence.
 AY539994 - Homo sapiens clone EX2F-1 MDD1 mRNA, partial sequence.
 AY539995 - Homo sapiens clone EX2F-2 MDD1 mRNA, partial sequence.
 AY539996 - Homo sapiens clone EX2F-3 MDD1 mRNA, partial sequence.
 AY539997 - Homo sapiens clone EX2F-4 MDD1 mRNA, partial sequence.
 AY539998 - Homo sapiens clone EX2F-5 MDD1 mRNA, partial sequence.
 AY539999 - Homo sapiens clone EX2F-6 MDD1 mRNA, partial sequence.
 AY540000 - Homo sapiens clone EX2F-7 MDD1 mRNA, partial sequence.
 AY540001 - Homo sapiens clone EX2F-8 MDD1 mRNA, partial sequence.
 AY540002 - Homo sapiens clone EX2F-9 MDD1 mRNA, partial sequence.
 AY540003 - Homo sapiens clone EX2G-1 MDD1 mRNA, partial sequence.

http://genome.ucsc.edu/cgi-bin/hgTracks?...597-68862316&hgid=30900095&refGene=pack

BIO003

Εισαγωγή στη Βιοπληροφορική

Από: Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins, 3rd Edition

UCSC Genome Browser on Human July 2003 Freeze

position chr7:100,099,014-100,104,893 size 5,880 bp. image width: 800

Click on a feature for details. Click on base position to zoom in around cursor. Click on left mini-buttons for track-specific options

Use drop down controls below and press refresh to alter tracks displayed. Tracks with lots of items will automatically be displayed in more compact modes.

Mapping and Sequencing Tracks

| | | | | |
|------------------|-----------------|-------------|-------------|---------------|
| Base Position | Chromosome Band | STS Markers | FISH Clones | Recomb Rate |
| on | dense | dense | wide | hide |
| Map Contigs | Assembly | Gap | Coverage | BAC End Pairs |
| hide | hide | dense | hide | hide |
| Fosmid End Pairs | GC Percent | | | |
| hide | hide | | | |

Genes and Gene Prediction Tracks

| | | | | |
|-----------------|---------------|---------------|------------|------------------|
| Known Genes | RefSeq Genes | MGC Genes | Vega Genes | Vega Pseudogenes |
| pack | pack | hide | hide | hide |
| Ensembl Genes | Acembly Genes | ECgene Genes | Twinscan | SGP Genes |
| dense | dense | hide | hide | hide |
| Fgenesh++ Genes | Geneid Genes | GenScan Genes | RNA Genes | Superfamily |
| hide | hide | dense | hide | hide |
| miRNA | | | | |
| hide | | | | |

mRNA and EST Tracks

Human Gene ACHE Description and Page Index - Mozilla

Human Gene ACHE Description and Page Index

Description: acetylcholinesterase (YT blood group)
Representative mRNA: [NM00440](#) **Protein:** [P22303](#)
RefSeq Summary: Acetylcholinesterase hydrolyzes the neurotransmitter, acetylcholine at neuromuscular junctions and brain cholinergic synapses, and thus terminates signal transmission. It is also found on the red blood cell membranes, where it constitutes the YT blood group antigen. Acetylcholinesterase exists in multiple molecular forms which possess similar catalytic properties, but differ in their oligomeric assembly and mode of cell attachment to the cell surface. It is encoded by the single ACHE gene, and the structural diversity in the gene products arises from alternative mRNA splicing, and post-translational associations of catalytic and structural subunits. The major form of acetylcholinesterase found in brain, muscle and other tissues is the hydrophilic species, which forms disulfide-linked oligomers with collagenous, or lipid-containing structural subunits. The other, alternatively spliced form, expressed primarily in the erythroid tissues, differs at the C-terminal end, and contains a cleavable hydrophobic peptide with a GPI-anchor site. It associates with the membranes through the phosphoinositide (PI) moieties added post-translationally.

| | | | | | |
|-------------------|---------------|--------------------|-------------------|------------|---------------|
| Page Index | Quick Links | SwissProt Comments | Sequence | Microarray | RNA Structure |
| Protein Structure | Other Species | GO Annotations | mRNA Descriptions | Pathways | |

Quick Links to Tools and Databases

| | | | | | |
|----------------|------------------|----------------|-----------|-----------------|---------|
| Genome Browser | Proteome Browser | Family Browser | SwissProt | LocusLink | PubMed |
| OMIM | GeneLink | GeneCards | CGAP | Stanford SOURCE | Ensembl |
| Jackson Labs | | | | | |

Human Gene ACHE Description and Page Index - Mozilla

Protein Domain and Structure Information

InterPro Domains: [Graphical view of domain structure](#)
[IPR002018](#) - Carboxylesterase, type B
[IPR000997](#) - Cholinesterase
[IPR000879](#) - Esterase/lipase/thioesterase

Pfam Domains:
[PF00136](#) - Carboxylesterase

Protein Data Bank (PDB) 3-D Structure

2C2L - 04-MAR-98

BIO003

Εισαγωγή στη Βιοπληροφορική

NCBI Map Viewer

<http://www.ncbi.nih.gov/mapview>

- Αναπτύσσεται από το NCBI
- Δεδομένα για ευκαρυωτικά γονιδιώματα
- Διασυνδεδεμένο με τις βάσεις δεδομένων του NCBI
- Ας ψάξουμε για 2 γενετικούς δείκτες (RH93969 και RH71410) που η βιβλιογραφία δείχνει να σχετίζονται με το γονίδιο *ACHE*

Reflect



Map Viewer Home

Help

The Map Viewer provides a wide variety of genome mapping and sequencing data. [More..](#)

Search

Search:

for:

Tools Legend

- Search or Browse the Genome
- BLAST
- Genome Resources page

News

Annotation update plans for Human Genome build 36 Oct 1, 2007

NCBI is planning to update its annotation of the human genom... [more](#)

[Show all](#)

Related Resources

- ◆ NCBI Home
- ◆ NCBI Web Search
- ◆ NCBI Site map
- ◆ Genome Biology
- ◆ Taxonomy
- ◆ Entrez (Global Query)
- ◆ BLAST
- ◆ Map Viewer FTP

Small Genomes

- ◆ Bacteria
- ◆ Organelles
- ◆ Viruses

| | | | |
|---------------------------------|--------------------|----------------------------|--------------|
| ▼ Vertebrates | (15) | | |
| ▼ Mammals | (13) | | |
| ▼ Primates | (3) | | |
| Scientific name | Common name | Build | Tools |
| <i>Homo sapiens</i> | human | Build 36.2 | |
| | | Build 35.1 | |
| <i>Macaca mulatta</i> | rhesus macaque | Build 1.1 | |
| <i>Pan troglodytes</i> | chimpanzee | Build 2.1 | |
| ▼ Rodents | (2) | | |
| Scientific name | Common name | Build | Tools |
| <i>Mus musculus</i> | laboratory mouse | Build 37.1 | |
| | | Build 36.1 | |
| <i>Rattus norvegicus</i> | rat | RGSC v3.4 | |
| ▶ Monotremes | (1) | | |
| ▶ Marsupials | (1) | | |
| ▶ Other Mammals | (6) | | |
| ▶ Other Vertebrates | (2) | | |
| ▶ Invertebrates | (8) | | |
| ▶ Protozoa | (7) | | |
| ▶ Plants | (42) | | |
| ▼ Fungi | (17) | | |
| Scientific name | Common name | Build | Tools |
| <i>Aspergillus clavatus</i> | | Build 1.1 | |
| <i>Aspergillus fumigatus</i> | | Build 2.1 | |
| <i>Aspergillus niger</i> | | Build 1.1 | |
| <i>Candida glabrata</i> | | Build 1.1 | |
| <i>Cryptococcus neoformans</i> | | Build 2.1 | |
| <i>Debaryomyces hansenii</i> | | Build 1.1 | |
| <i>Encephalitozoon cuniculi</i> | | Build 1.1 | |
| <i>Eremothecium gossypii</i> | | Build 3.1 | |
| <i>Gibberella zeae</i> | | Build 1.2 | |
| <i>Kluyveromyces lactis</i> | | Build 1.1 | |
| <i>Magnaporthe oryzae</i> | rice blast fungus | Build 3.1 | |
| <i>Neurospora crassa</i> | | Build 1.1 | |

Reflect



NCBI Map Viewer

Map Viewer Home

Help

Search

Search: Select Group or Organism
for:
Go

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News

Annotation update plans for Human Genome build 36
NCBI is planning to update its annotation of the human genom... more
Show all

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Entrez (Global Query)
BLAST
Map Viewer FTP

Small Genomes

- Bacteria
Organelles
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- Vertebrates
Mammals
Primates
Scientific name
Homo sapiens
Macaca mulatta
Pan troglodytes
Rodents
Scientific name
Mus musculus
Rattus norvegicus
Monotremes
Marsupials
Other Mammals
Other Vertebrates
Invertebrates
Protozoa
Plants
Fungi
Scientific name
Aspergillus clavatus
Aspergillus fumigatus
Aspergillus niger
Candida glabrata
Cryptococcus neoformans
Debaryomyces hansenii
Encephalitozoon cuniculi
Eremothecium gossypii
Gibberella zeae
Kluyveromyces lactis
Magnaporthe grisea
Neurospora crassa



Map Viewer Home

Search

Search: Homo sapiens
for: RH93969 OR RH7141
Go

Tools Legend

- Search or Browse the Genome
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Genome Resources page

News

The M

Tools

- Q B G
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Q B G

Tools

- Q B G
Q B
Q B G

Tools

- 1 Q B G
2.1 Q B G
1 Q B G
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2.1 Q B
1 Q B
1 Q B
Build 3.1 Q B
Build 1.2 Q B
Build 1.1 Q B
Build 3.1 Q B
Build 1.1 Q B

rice blast fungus

Reflect



NCBI Map Viewer

Map Viewer Home

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Search

Search: Select Group or Organism
for:
Go

Tools Legend

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Annotation update plans for Human Genome build 36
NCBI is planning to update its annotation of the human genom... more
Show all

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Taxonomy
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Small Genomes

- Bacteria
Organelles
Viruses

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Mammals
Primates
Scientific name
Homo sapiens
Macaca mulatta
Pan troglodytes
Rodents
Scientific name
Mus musculus
Rattus norvegicus
Monotremes
Marsupials
Other Mammals
Other Vertebrates
Invertebrates
Protozoa
Plants
Fungi
Scientific name
Aspergillus clavatus
Aspergillus fumigatus
Aspergillus niger
Candida glabrata
Cryptococcus neoformans
Debaryomyces hansenii
Encephalitozoon cuniculi
Eremothecium gossypii
Gibberella zeae
Kluyveromyces lactis
Magnaporthe grisea
Neurospora crassa



Map Viewer Home

Search

Search: Homo sapiens
for: RH93969 OR RH7141
Go

Tools Legend

- Search or Browse the Genome
BLAST
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News

The M

Tools

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Tools

- Q B G
Q B
Q B G

Tools

- 1 Q B G
1.1 Q B G
1 Q B G
1 Q B
1.1 Q B
1.1 Q B
1 Q B
1 Q B
Build 3.1 Q B
Build 1.2 Q B
Build 1.1 Q B
Build 3.1 Q B
Build 1.1 Q B

rice blast fungus

Άσκηση για το σπίτι ...

- Συνεχίστε την προηγούμενη αναζήτηση στο assembly CRA_TCAGchr7v2
 - Σχετίζεται πράγματι το *ACHE* με τους παραπάνω δείκτες;
- Πραγματοποιήστε αναζήτηση στο Map Viewer με το όνομα του γονιδίου *ACHE*
- Συγκρίνετε τα αποτελέσματα

ENSEMBL

<http://www.ensembl.org/>

- Αναπτύσσεται από το EBI-EMBL και το Sanger Institute - Wellcome Trust
- Κυρίως ευκαρυωτικά γονιδιώματα

<http://www.ensembl.org/>

The screenshot shows the Ensembl Genome Browser homepage. At the top, there is a search bar with the text "Search all species for" and a dropdown menu set to "Anything". Below the search bar, there is a section titled "About Ensembl" which describes the project as a joint effort between EMBL, EBI, and the Sanger Institute. To the right of this section is a table titled "Species - Ensembl v20" listing various species and their corresponding Ensembl IDs and dates. Below the "About Ensembl" section, there is a "Help and documentation" section with links to "Take the Ensembl tour", "For help on this page", and "There is also an Ensembl help page". At the bottom right, there is a section titled "Have you tried...?" featuring a banner for *Caenorhabditis briggsae* with the Ensembl logo and a link to "Click for more information".

| Species | Ensembl ID | Date |
|-------------|--------------|-------------|
| Human | 34: NCBI:34 | 01-Apr-2004 |
| Chicken | 1: WASHUC1 | June 2004 |
| Chimp | 1: OROAO:1 | TBA |
| Mouse | 32: NCBI:m32 | 01-Apr-2004 |
| Rat | 32: RGD:3.1 | 09-Feb-2004 |
| Zebrafish | 32: VZS1Z:0 | 01-Apr-2004 |
| Flu | 32: EMBL:2.0 | 01-Apr-2004 |
| Mosquito | 32: M02:0 | 01-Apr-2004 |
| Fruitfly | 34: RSGF:3.1 | 02-Jul-2005 |
| C. elegans | 116: V03:116 | 01-Apr-2004 |
| C. briggsae | 22: v03:2008 | 02-Jul-2005 |

Συζήτηση ...

Διδακτικό υλικό:

Prof. Doug Brutlag's Lecture
on the Human Genome Project and Genomic Databases
<http://biochem218.stanford.edu/03Genome%20Databases.html>

<http://troodos.biol.ucy.ac.cy/BRL/courses/BIO003/index.html>