Mini Courses NCBI Resources one course at a time

Entrez Quick Start

NCBI's Entrez is an integrated, text-based search and retrieval system for more than 30 biologically-oriented databases. Entrez provides links to related records within the same database and between other databases in Entrez. This course will demonstrate how to:

- Obtain information about various database entries
- Search databases effectively using features such as Limits, Preview/Index and History
- Filter search results
- Highlight search terms
- Access, download and save records in various formats
- Access related entries in the database and other databases
- Save search strategies and results
- Retrieve large amounts of data as a batch
- Select an option to automatically update and e-mail search results

These are some of the examples of searches you will be able to perform after participating in this class:

- an organism and obtain its available data from the Entrez databases such as the genome sequence, proteins and their homologs, expressed sequences, Single Nucleotide Polymorphisms, etc.
- genes expressed in a particular tissue
- homologs among the annotated genes of several completely sequenced eukaryotic genomes
- aligned sequences from a population, phylogenetic, or mutation study
- SNPs on a certain chromosome that change amino acid sequence and have links to OMIM and structure databases
- articles that have free full text access

This course will cover databases such as PubMed, PubMed Central (PMC), Taxonomy, PopSet, OMIM, Homologene, Unigene, and the Single Nucleotide Polymorphism database (dbSNP). Some of the other databases are covered in mini-courses such as GenBank QuickStart and Entrez Gene QuickStart.

The following handout includes the screen shots of the exercises demonstrated in the class. The web page for the course is at http://www.ncbi.nlm.nih.gov/Class/minicourses/entrez.html

Example 1:

I. PubMed, PMC, Taxonomy and PopSet

Perform a search for mammoth across all of the Entrez databases. Which databases contain records associated with the term mammoth? Link to the mammoth literature citations in the PubMed database. Identify the articles available free in PMC. Access the article "The year of the mammoth". What are the cited articles in this publication? Download the abstracts of these articles. How many of them are available free in PMC? Access publications of some of the authors of these articles.
Go back to the mammoth search in Pubmed. Display the PopSet links. Access the record by Greenwood with PopSet ID 14090839. View the alignment in various formats. Link from the record to the Nucleotide database. The sequence alignment of which gene is studied in this PopSet? Display the Taxonomy Links for the PopSet and list the organisms covered.
Access the Taxonomy record for *Mammuthus primigenius*. What is the origin of the mammoth's specimens for some of the sequences reported in the Entrez databases? What is the lineage for mammoth? Which are the three major divisions of cellular organisms? Which of these has the highest number of entries in the "Structure" database?

II. OMIM, UniGene and Homologene

Perform an unlimited search for cytochrome c oxidase in the OMIM database. Repeat the query for "cytochrome c oxidase" as a term. Which search is more restrictive? Limit the retrieved entries only to those with gene location on chromosomes 4, 6 and 19. How many records have you retrieved? What is the chromosomal location of gene COX7A1 (OMIM record 123995)? Note the information about muscle and liver isoforms. Are there any known disease phenotypes (allelic variants) associated with the COX7A1 gene? Access the UniGene links from this record. Examine the expression profiles of the two genes. What do you conclude from the expression profiles? Access the Preview/Index page. Search for the UniGene records that have expression evidence of at least 100 ESTs? How many of these UniGene records are from mammals? Sort the records by organism.
Access the HomoloGene database and perform a search for records relating to COX genes (Preview/Index—gene name and use cox* as a query). How many records do you retrieve? Are COX7A1 and COX7A2 members of the same HomoloGene group?
Are all COX genes equally conserved in evolution? What are their common ancestors? Are there any COX genes that are conserved throughout the superkingdom of Eukaryota (Use the Preview/Index page—ancestor-- (*Taxonomy ID:* 2759)? Display the taxonomy tree for organisms included in the HomoloGene COX1 record.

III. dbSNP

Access the SNP database and select its Limits page. Check the appropriate boxes to allow selection for human nonsynonymous SNPs in the coding regions of chromosome 22. Add two more requirements that the SNP has an OMIM link and is associated with a structure. Retrieve and download the UI List for these records. Use the saved file to retrieve the records with the UI List in Batch Entrez.

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Established in 1988 as a national resource for molecular biology information, NCBI creates public databases, conducts research in computational biology, develops software tools for analyzing genome data, and disseminates biomedical information - all for the better understanding of molecular processes affecting human health and disease. More...
New Protein Clusters
Entrez Protein Clusters database
The new Entrez Protein Clusters database is a collection of Reference Sequence (RefSeq) proteins, from the complete genomes of prokaryotes, plasmids, and organelles, that have been grouped and annotated based on sequence similarity and protein function. Click here to find out more about the Protein Clusters database.
New dbGaP
NCBI's dbGaP Genome Wide Association Database
NCBI's dbGaP (database of Genotype and Phenotype) provides data from Genome Wide Association (GWA) studies. The resource is intended to help elucidate the link between genes and disease. For each study, users have access to detailed information about the phenotypic variables measured and pre-computed associations between subjects' phenotypes and genotypes. Click here to read the press release. To read more about GWA projects, see NCBI's GWA resource page
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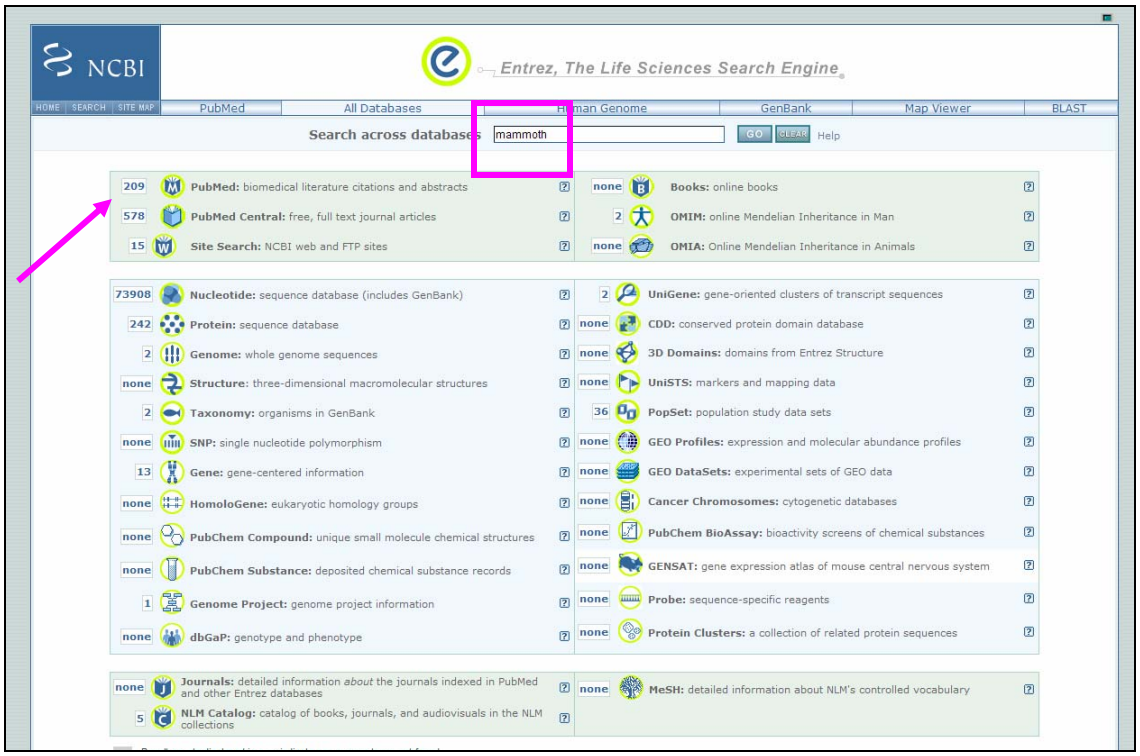
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578 PubMed Central: free, full text journal articles
15 Site Search: NCBI web and FTP sites
none Books: online books
2 OMIM: online Mendelian Inheritance in Man
none OMIA: Online Mendelian Inheritance in Animals
73908 Nucleotide: sequence database (includes GenBank)
242 Protein: sequence database
2 Genome: whole genome sequences
none Structure: three-dimensional macromolecular structures
2 Taxonomy: organisms in GenBank
none SNP: single nucleotide polymorphism
13 Gene: gene-centered information
none HomoloGene: eukaryotic homology groups
none PubChem Compound: unique small molecule chemical structures
none PubChem Substance: deposited chemical substance records
1 Genome Project: genome project information
none dbGaP: genotype and phenotype
2 UniGene: gene-oriented clusters of transcript sequences
none CDD: conserved protein domain database
none 3D Domains: domains from Entrez Structure
none UniSTS: markers and mapping data
36 PopSet: population study data sets
none GEO Profiles: expression and molecular abundance profiles
none GEO DataSets: experimental sets of GEO data
none Cancer Chromosomes: cytogenetic databases
none PubChem BioAssay: bioactivity screens of chemical substances
none GENSAT: gene expression atlas of mouse central nervous system
none Probe: sequence-specific reagents
none Protein Clusters: a collection of related protein sequences
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none MeSH: detailed information about NLM's controlled vocabulary

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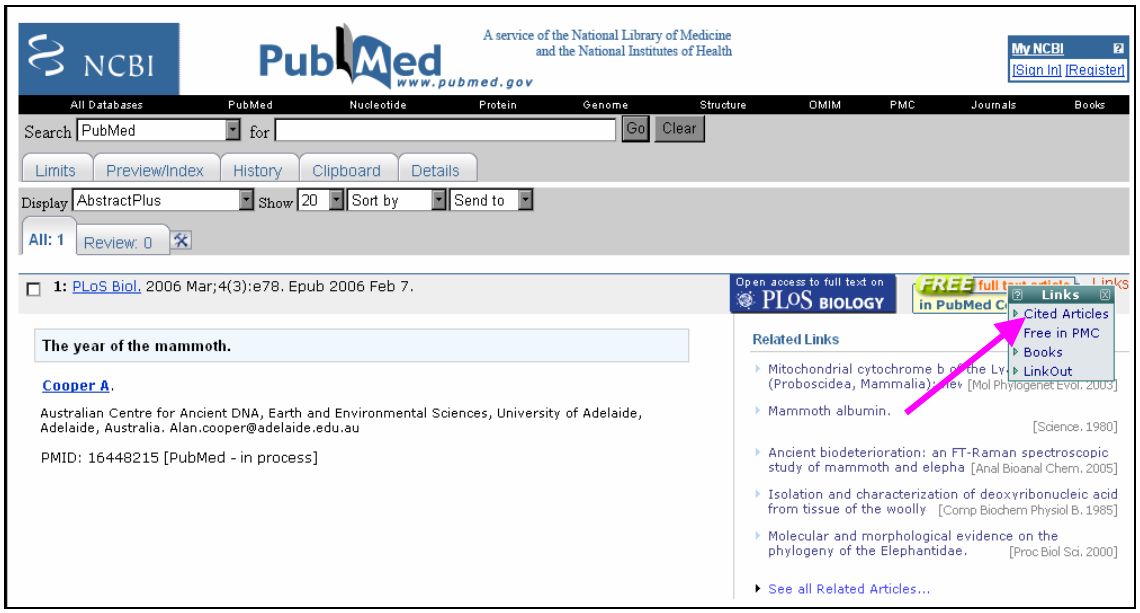
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Complete mitochondrial genome and phylogeny of Pleistocene Mammoth Mammuthus primigenius.

Rogaev EI, Moliaka YK, Malyarchuk BA, Kondrashov FA, Derenko MV, Chumakov I, Grigorenko AP.

Brudnick Neuropsychiatric Research Institute, Department of Psychiatry, University of Massachusetts Medical School, Worcester, Massachus
Evgeny.Rogaev@umassmed.edu

Phylogenetic relationships between the extinct woolly mammoth (Mammuthus primigenius), and the Asian (Elephas maximus) and African savanna (Loxodonta africana) elephants remain unresolved. Here, we report the sequence of the complete mitochondrial genome (16,842 base pairs) of a woolly mammoth extracted from permafrost-preserved remains from the Pleistocene epoch--the oldest mitochondrial genome sequence determined to date. We demonstrate that well-preserved mitochondrial genome fragments, as long as approximately 1,600-1700 base pairs, can be retrieved from pre-Holocene remains of an extinct species. Phylogenetic reconstruction of the Elephantinae clade suggests that M. primigenius and E. maximus are sister species that diverged soon after their common ancestor split from the L. africana lineage. Low nucleotide diversity found between independently determined mitochondrial genomic sequences of woolly mammoths separated geographically and in time suggests that north-eastern Siberia was occupied by a relatively homogeneous population of M. primigenius throughout the late Pleistocene.

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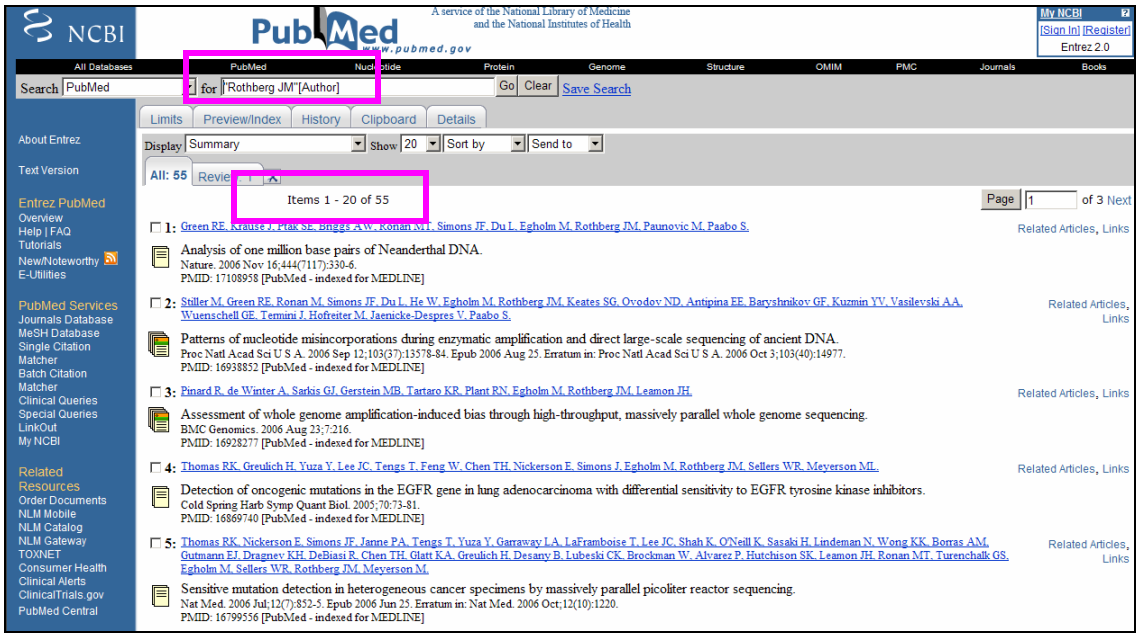
454 Life Sciences Corp., 20 Commercial Street, Branford, Connecticut 06405, USA.

The proliferation of large-scale DNA-sequencing projects in recent years has driven a search for alternative methods to reduce time and cost. Here we describe a scalable, highly parallel sequencing system with raw throughput significantly greater than that of state-of-the-art capillary electrophoresis instruments. The apparatus uses a novel fibre-optic slide of individual wells and is able to sequence 25 million bases, at 99% or better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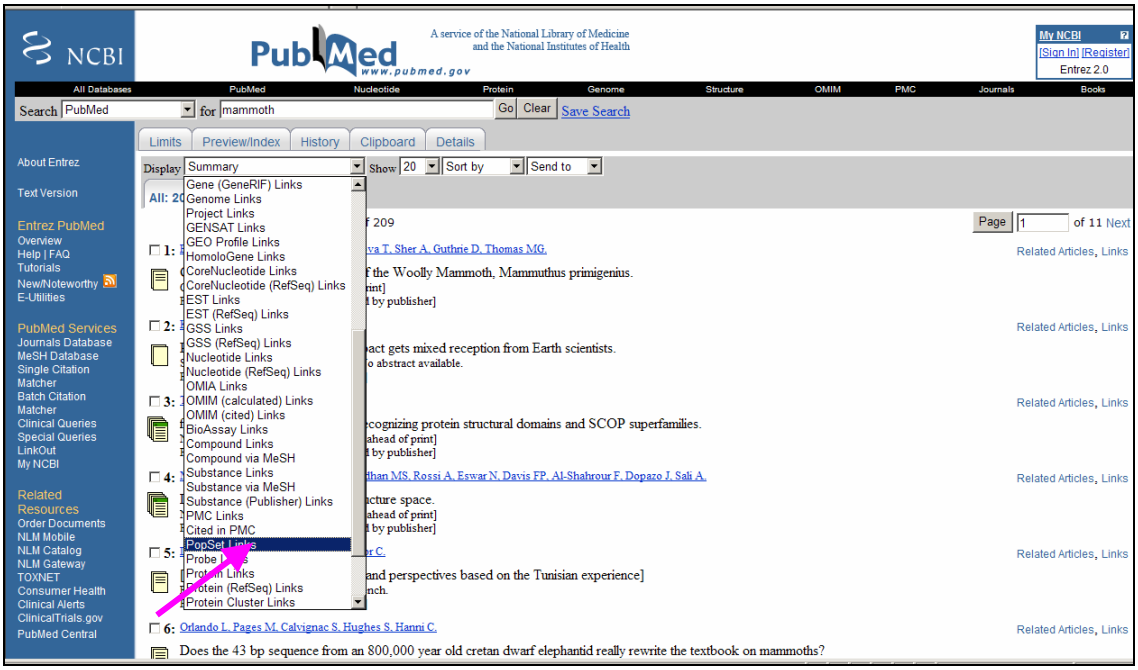
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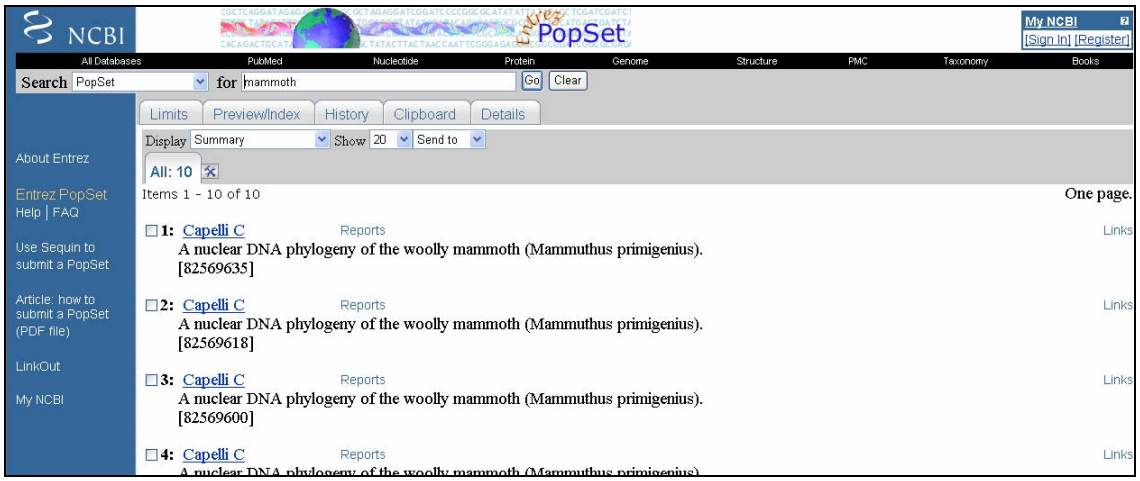
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One page.
1: Capelli C Reports Links
A nuclear DNA phylogeny of the woolly mammoth (Mammuthus primigenius).
[82569635]
2: Capelli C Reports Links
A nuclear DNA phylogeny of the woolly mammoth (Mammuthus primigenius).
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3: Capelli C Reports Links
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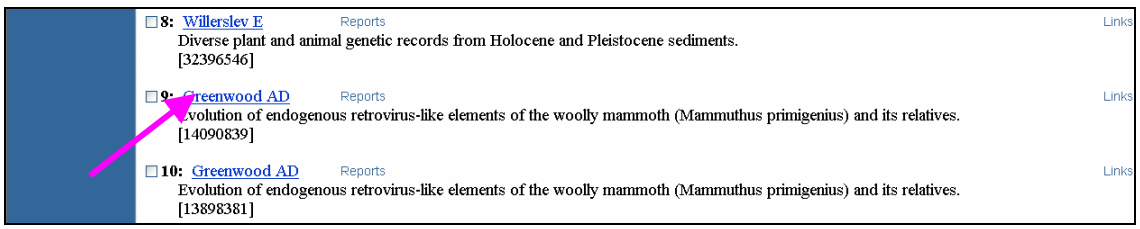
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Diverse plant and animal genetic records from Holocene and Pleistocene sediments.
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9: Greenwood AD Reports Links
Evolution of endogenous retrovirus-like elements of the woolly mammoth (Mammuthus primigenius) and its relatives.
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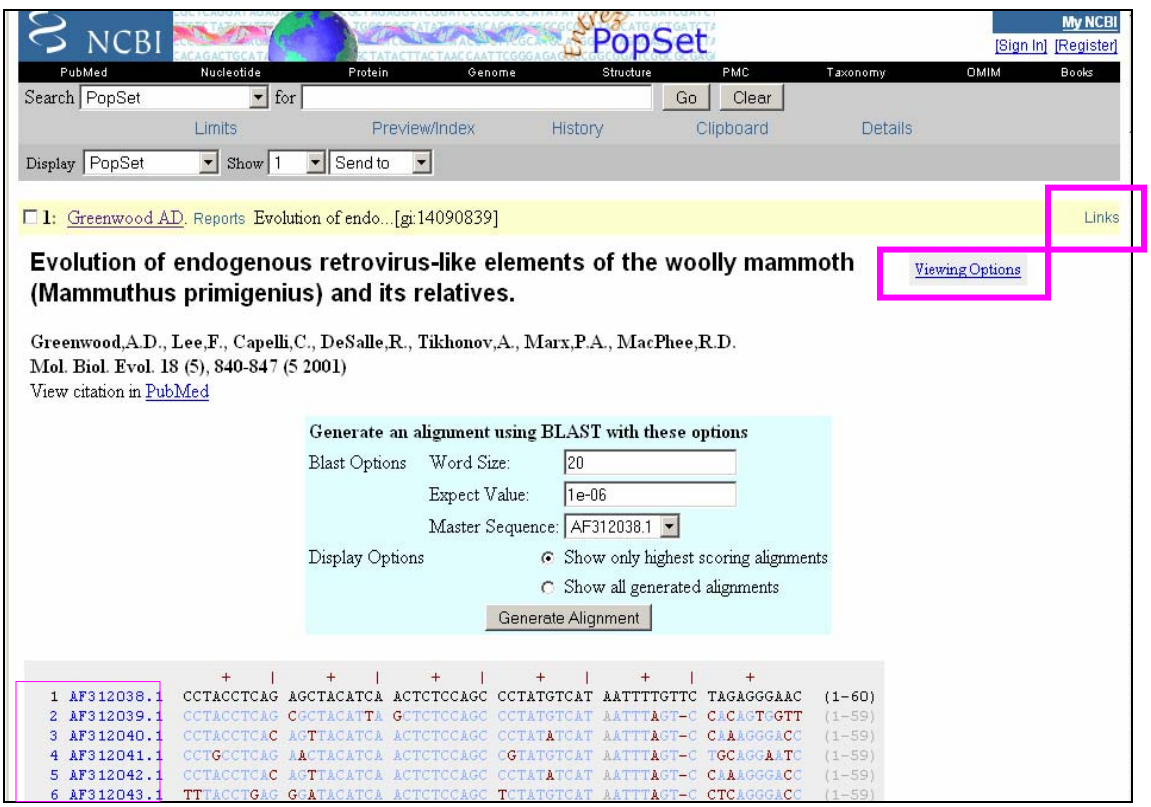
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1: Greenwood AD. Reports Evolution of endo...[gi:14090839]
Links
Evolution of endogenous retrovirus-like elements of the woolly mammoth (Mammuthus primigenius) and its relatives.
Viewing Options
Greenwood,A.D., Lee,F., Capelli,C., DeSalle,R., Tikhonov,A., Marx,P.A., MacPhee,R.D.
Mol. Biol. Evol. 18 (5), 840-847 (5 2001)
View citation in PubMed
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Expect Value: 1e-06
Master Sequence: AF312038.1
Display Options Show only highest scoring alignments
Show all generated alignments
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5 AF312042.1 CCTACCTCAC AGTTACATCA ACTCTCCAGC CCTATATCAT AATTTAGT-C CAAAGGGACC (1-59)
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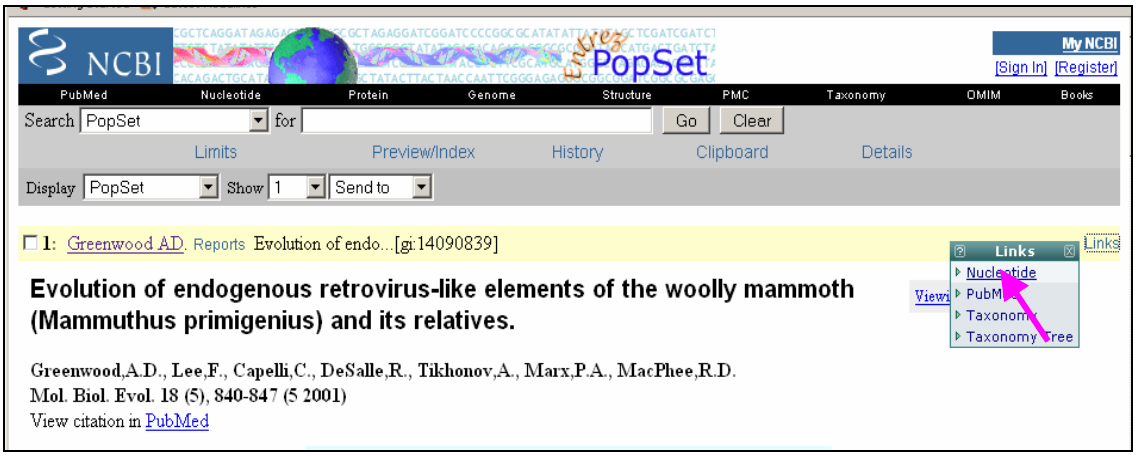
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1: Greenwood AD. Reports Evolution of endo...[gi:14090839]
Links
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Evolution of endogenous retrovirus-like elements of the woolly mammoth (Mammuthus primigenius) and its relatives.
Greenwood,A.D., Lee,F., Capelli,C., DeSalle,R., Tikhonov,A., Marx,P.A., MacPhee,R.D.
Mol. Biol. Evol. 18 (5), 840-847 (5 2001)
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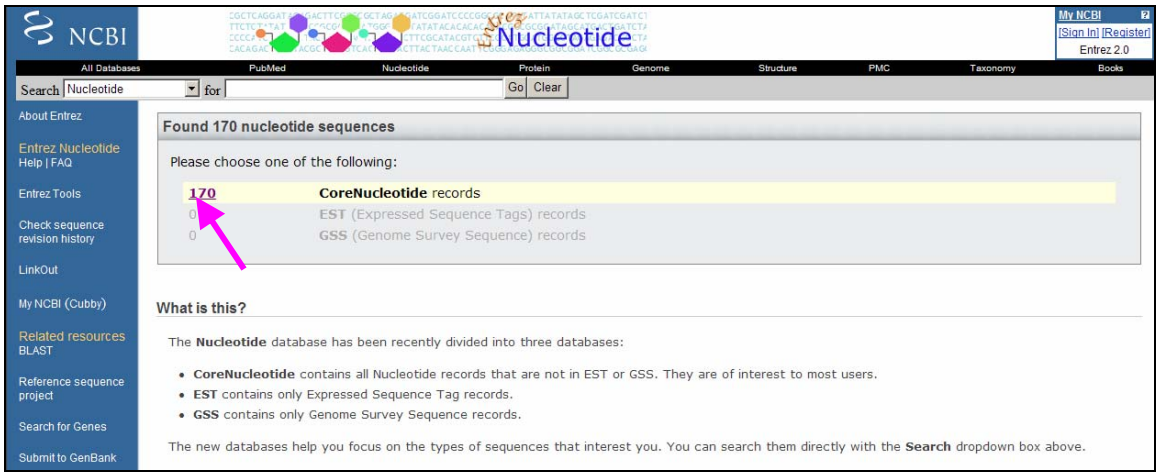
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Search for Genes
Submit to GenBank
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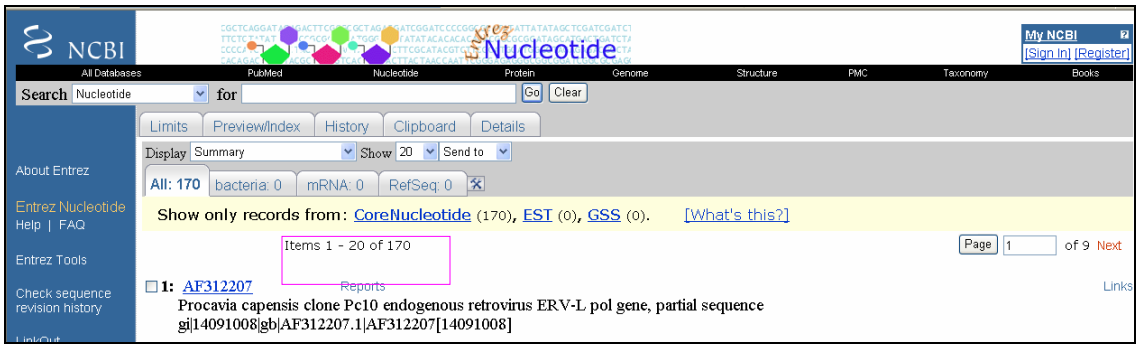
Please choose one of the following:
170 CoreNucleotide records
0 EST (Expressed Sequence Tags) records
0 GSS (Genome Survey Sequence) records
What is this?
The Nucleotide database has been recently divided into three databases:
CoreNucleotide contains all Nucleotide records that are not in EST or GSS. They are of interest to most users.
EST contains only Expressed Sequence Tag records.
GSS contains only Genome Survey Sequence records.
The new databases help you focus on the types of sequences that interest you. You can search them directly with the Search dropdown box above.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All: 170 bacteria: 0 mRNA: 0 RefSeq: 0
Show only records from: CoreNucleotide (170), EST (0), GSS (0). [What's this?]
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Procavia capensis clone Pc10 endogenous retrovirus ERV-L pol gene, partial sequence
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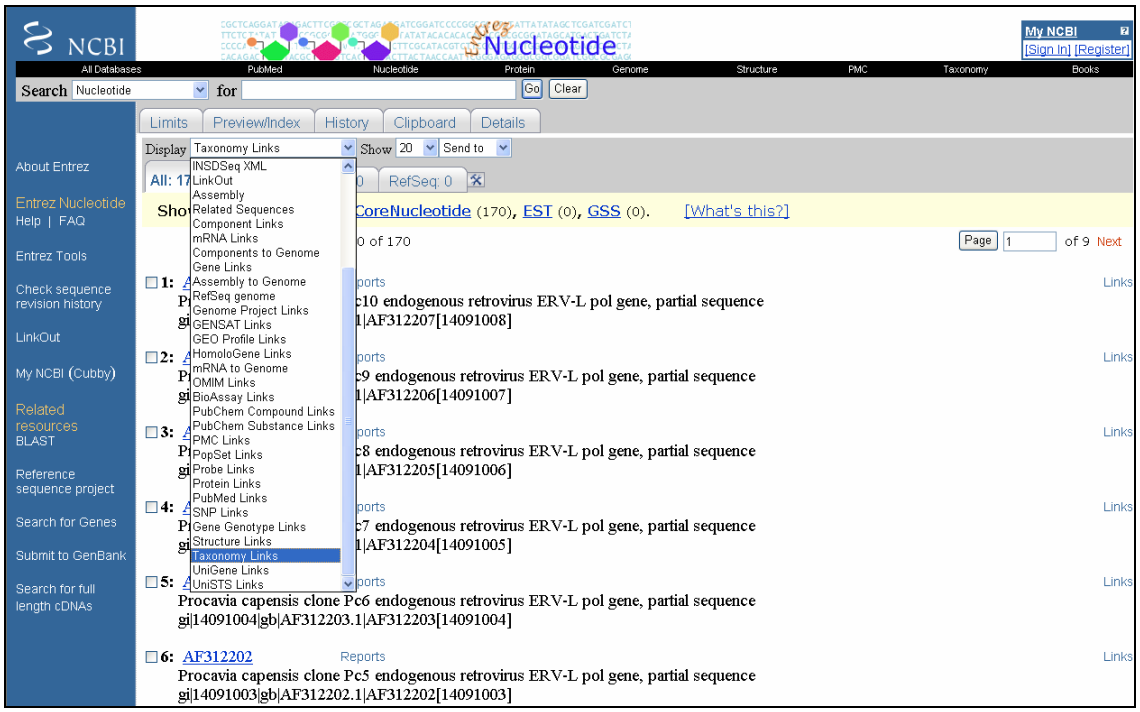
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Component Links
mRNA Links
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Gene Links
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Search for full length cDNAs
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CoreNucleotide (170), EST (0), GSS (0). [What's this?]
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Links
Procavia capensis clone Pc6 endogenous retrovirus ERV-L pol gene, partial sequence
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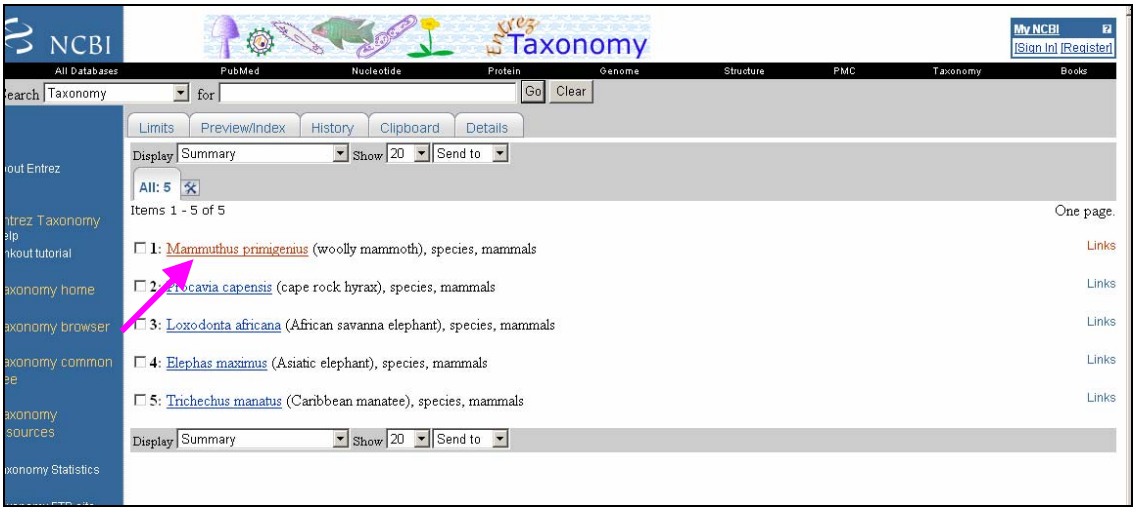
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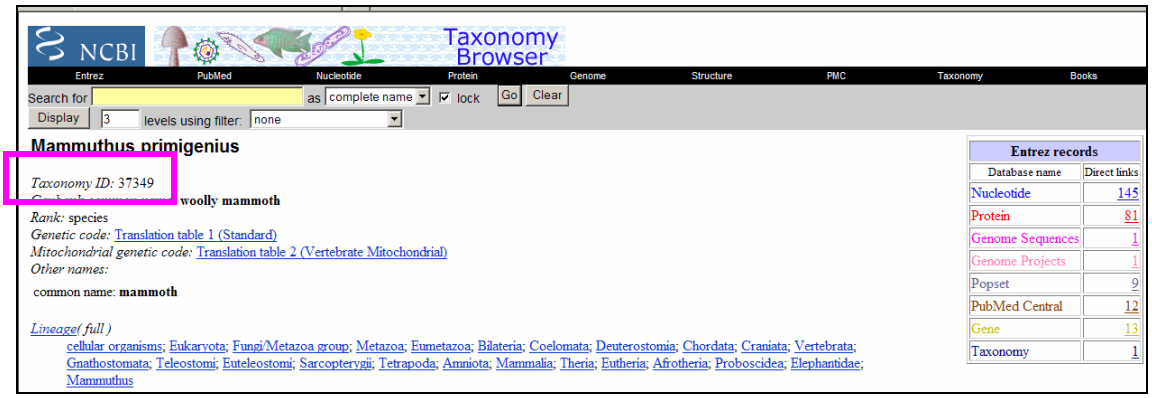
All: 5
Items 1 - 5 of 5
One page.
1: Mammuthus primigenius (woolly mammoth), species, mammals
2: Procavia capensis (cape rock hyrax), species, mammals
3: Loxodonta africana (African savanna elephant), species, mammals
4: Elephas maximus (Asiatic elephant), species, mammals
5: Trichechus manatus (Caribbean manatee), species, mammals
Links
Taxonomy home
Taxonomy browser
Taxonomy Statistics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Search for as complete name lock Go Clear
Display 3 levels using filter: none
Mammuthus primigenius
Taxonomy ID: 37349
woolly mammoth
Rank: species
Genetic code: Translation table 1 (Standard)
Mitochondrial genetic code: Translation table 2 (Vertebrate Mitochondrial)
Other names:
common name: mammoth
Lineage(full)
cellular organisms; Eukaryota; Fungi/Metazoa group; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Afrotheria; Proboscidea; Elephantidae; Mammuthus
Entrez records
Database name Direct links
Nucleotide 145
Protein 81
Genome Sequences 1
Genome Projects 1
Popset 9
PubMed Central 12
Gene 13
Taxonomy 1

Comments and References:

extinct
This taxon is extinct.

Genome Information

Trace records (raw single-pass reads of DNA sequence)		
Center name	Record counts per type	
	454	ALL
CCGB - Center for Comparative Genomics and Bioinformatics, PennState University, USA	303,789	303,789
Total	303,789	**303,789**

External Information Resources (NCBI LinkOut)

LinkOut	Subject	LinkOut Provider
Mammuthus primigenius taxonomy	taxonomy/phylogenetic	Arctos Specimen Database
Mammuthus primigenius	taxonomy/phylogenetic	Global Biodiversity Information Facility
Mammuthus primigenius taxonomy	herbarium/museum collections	Museum of Vertebrate Zoology

Notes:
Groups interested in participating in the LinkOut program should visit the LinkOut home page.
A list of our current non-bibliographic LinkOut providers can be found here.
To see LinkOut links in this lineage click here

Information from sequence entries

Show organism modifiers

Organism modifiers

To hide organism modifiers click here

isolate			
33,000 year-old woolly mammoth [1 1]	Chekurovka [1 1]	Eng.Creek.A [2 2 1]	Eng.Creek.A3 [1 1]
Eng.Creek.A5 [1 1]	Eng.Creek.B [2 2 1]	Eng.Creek.B3 [1 1]	Eng.Creek.B5 [1 1]
Engineer Creek [1 1]	The Khatanga mammoth (>50000 years bp, Siberia) [1]	The Yuribei mammoth (9700 yrs bp, Siberia) [1]	Wrangel Island 1 [1 1]
Wrangel Island 2 [1 1]	alaska8460 [2]	chekurovkam [1]	

NCBI Taxonomy Browser

Entrez PubMed Nucleotide Protein Genome Structure PMC Taxonomy Books

Search for as complete name lock Go Clear

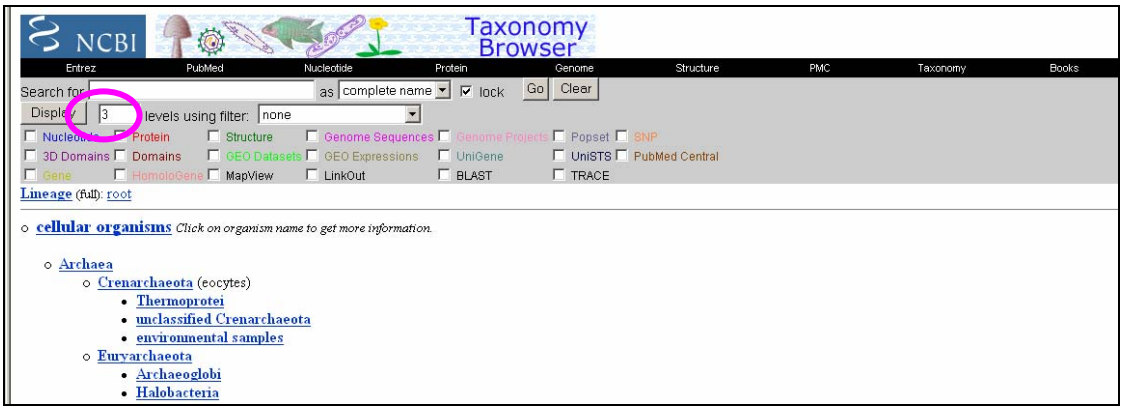
Display 3 levels using filter: none

Mammuthus primigenius

Taxonomy ID: 37349
Genbank common name: **woolly mammoth**
Rank: species
Genetic code: Translation table 1 (Standard)
Mitochondrial genetic code: Translation table 2 (Vertebrate Mitochondrial)
Other names:
common name: **mammoth**

Lineage(full)
cellular organisms; Eukaryota; Fungi/Metazoa group; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Afrotheria; Proboscidea; Elephantidae; Mammuthus

Entrez records	
Database name	Direct links
Nucleotide	145
Protein	81
Genome Sequences	1
Genome Projects	1
Popset	9
PubMed Central	12
Gene	13
Taxonomy	1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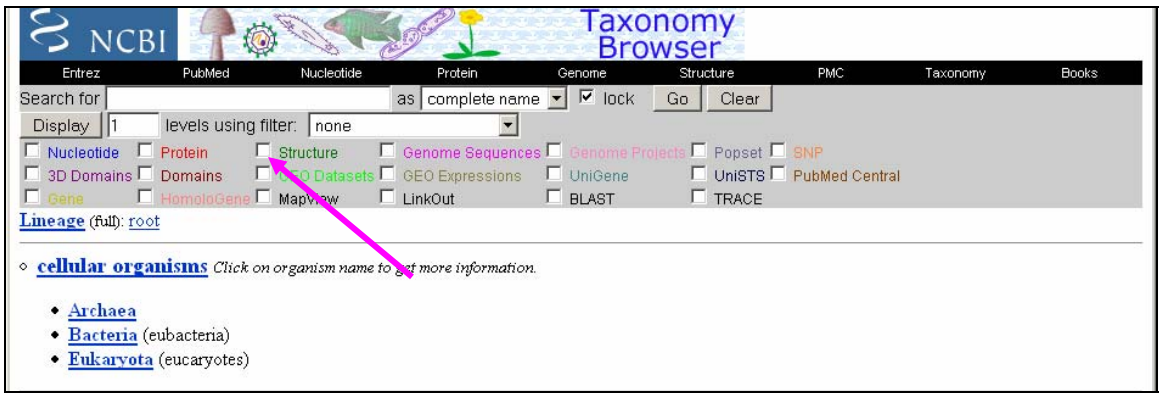
Nucleotide Protein Structure Genome Sequences Genome Projects Popset SNP
3D Domains Domains GEO Datasets GEO Expressions UniGene UniSTS PubMed Central
Gene HomoloGene MapView LinkOut BLAST TRACE
Lineage (full): root
cellular organisms Click on organism name to get more information.
Archaea
Crenarchaeota (eocytes)
Thermoprotei
unclassified Crenarchaeota
environmental samples
Euryarchaeota
Archaeoglobi
Halobacteria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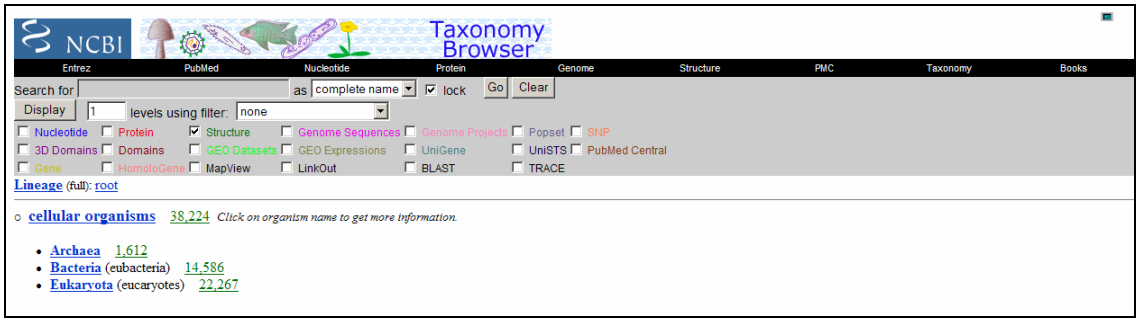
Gene HomoloGene MapView LinkOut BLAST TRACE
Lineage (full): root
cellular organisms Click on organism name to get more information.
Archaea
Bacteria (eubacteria)
Eukaryota (eucaryotes)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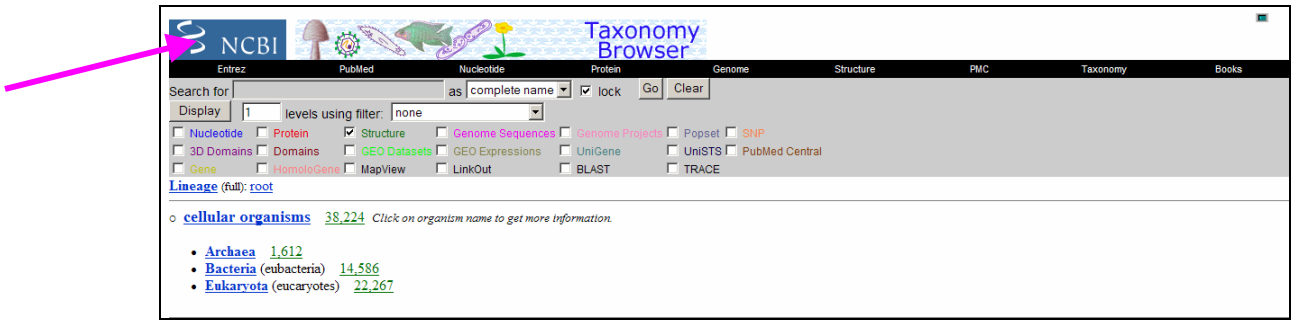
Nucleotide Protein Structure Genome Sequences Genome Projects Popset SNP
3D Domains Domains GEO Datasets GEO Expressions UniGene UniSTS PubMed Central
Gene HomoloGene MapView LinkOut BLAST TRACE
Lineage (full): root
cellular organisms 38,224 Click on organism name to get more information.
Archaea 1,612
Bacteria (eubacteria) 14,586
Eukaryota (eucaryotes) 22,267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Nucleotide Protein Structure Genome Sequences Genome Projects Popset SNP
3D Domains Domains GEO Datasets GEO Expressions UniGene UniSTS PubMed Central
Gene HomoloGene MapView LinkOut BLAST TRACE
Lineage (full): root
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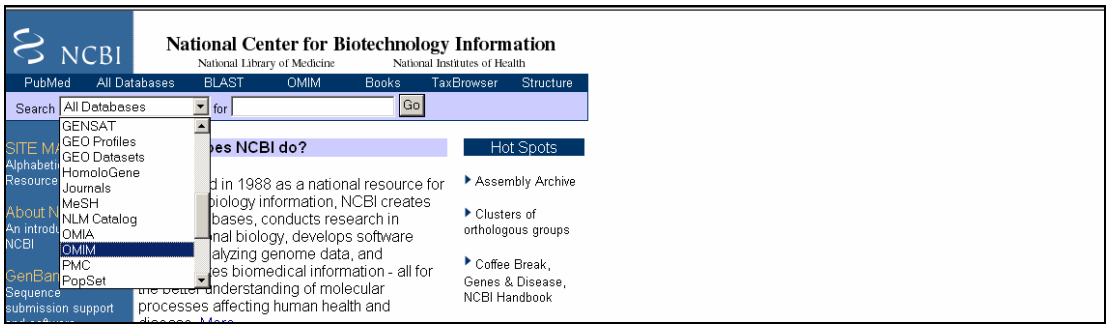
Archaea 1,612
Bacteria (eubacteria) 14,586
Eukaryota (eucaryotes) 22,267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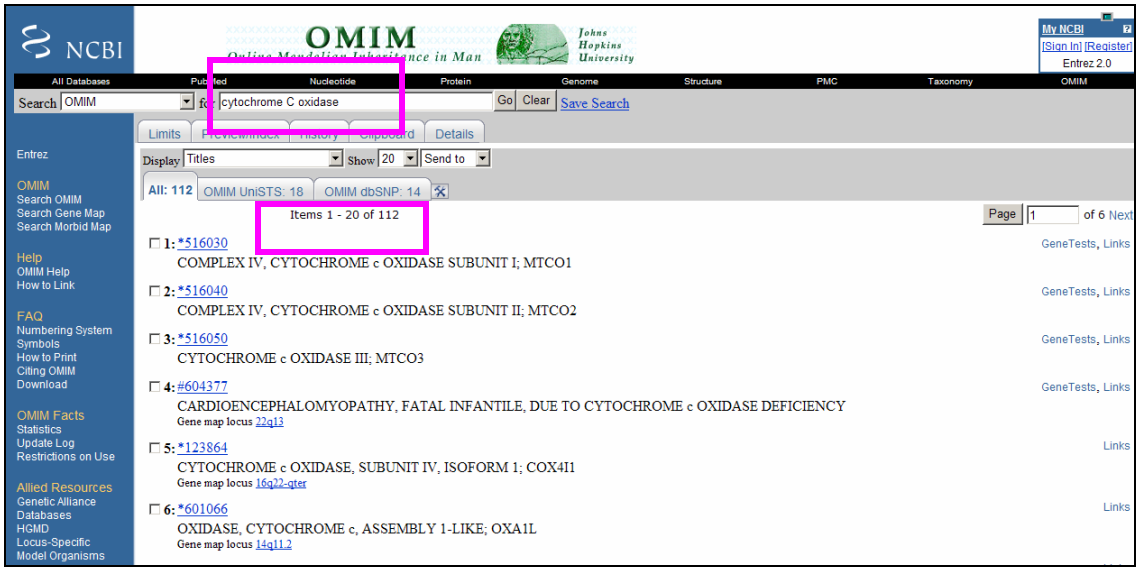
Clusters of orthologous groups
Coffee Break, Genes & Disease, NCBI Handbook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COMPLEX IV, CYTOCHROME c OXIDASE SUBUNIT I; MTCO1
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COMPLEX IV, CYTOCHROME c OXIDASE SUBUNIT II; MTCO2
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CYTOCHROME c OXIDASE III; MTCO3
GeneTests, Links
4: #604377
CARDIOENCEPHALOMYOPATHY, FATAL INFANTILE, DUE TO CYTOCHROME c OXIDASE DEFICIENCY
Gene map locus 22q13
GeneTests, Links
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Gene map locus 14q11.2
Links
Entrez
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Search OMIM
Search Gene Map
Search Morbid Map
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FAQ
Numbering System
Symbols
How to Print
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Databases
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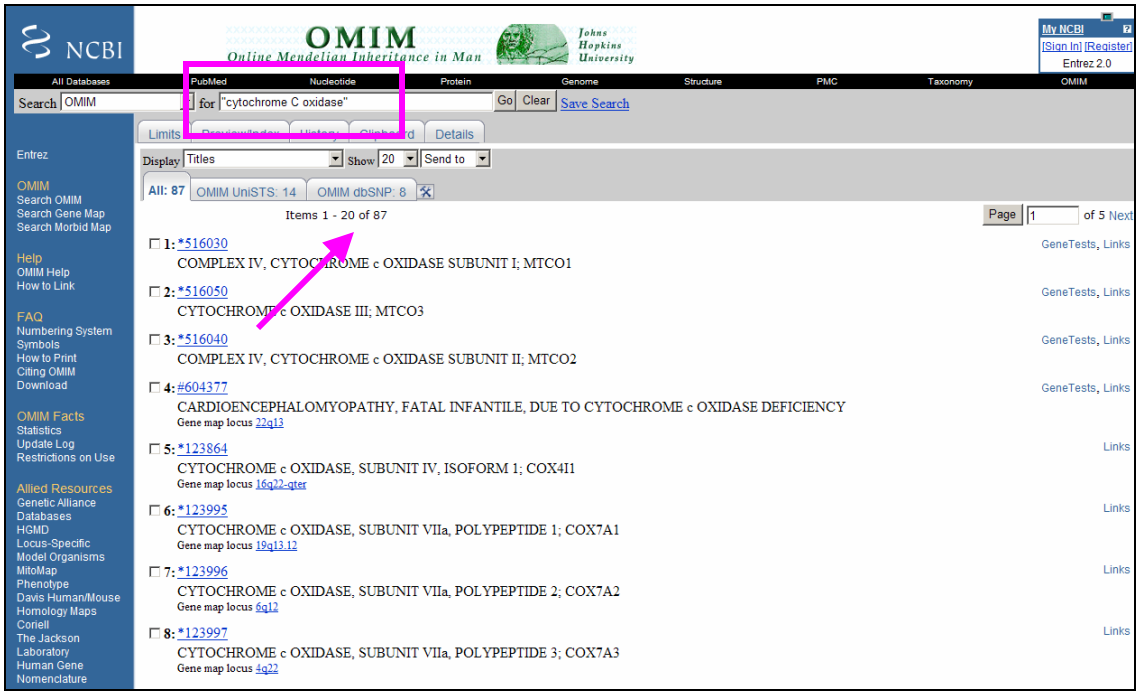
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CYTOCHROME c OXIDASE III; MTCO3
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CARDIOENCEPHALOMYOPATHY, FATAL INFANTILE, DUE TO CYTOCHROME c OXIDASE DEFICIENCY
Gene map locus 22q13
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Search Gene Map
Search Morbid Map
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FAQ
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How to Print
Citing OMIM
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Statistics
Update Log
Restrictions on Use
Allied Resources
Genetic Alliance
Databases
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Locus-Specific
Model Organisms
MitoMap
Phenotype
Davis Human/Mouse
Homology Maps
Coriell
The Jackson Laboratory
Human Gene Nomenclature

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*516030 GeneTests, Links

COMPLEX IV, CYTOCHROME c OXIDASE SUBUNIT I; MTCO1

Alternative titles; symbols

CYTOCHROME c OXIDASE I; COI

TEXT

DESCRIPTION

Cytochrome c oxidase subunit I (COI or MTCO1) is 1 of 3 mitochondrial DNA (mtDNA) encoded subunits (MTCO1, MTCO2, MTCO3) of respiratory Complex IV. Complex IV is located within the mitochondrial inner membrane and is the third and final enzyme of the electron transport chain of mitochondrial oxidative phosphorylation. It collects electrons from reduced cytochrome c and transfers them to oxygen to give water. The energy released is used to transport protons across the mitochondrial inner membrane. Complex IV is composed of 13 polypeptides. Subunits I, II, and III (MTCO1, MTCO2, MTCO3) are encoded by mtDNA while subunits IV, Va, Vb, VIa, VIb, VIc, VIIa, VIIb, VIIc, and VIII are nuclear encoded (Kadenbach et al., 1983; Shoffner and Wallace, 1995). While the mammalian Complex IV has a complex structure, several prokaryotic enzyme systems have the same catalytic functions, but are much simpler.

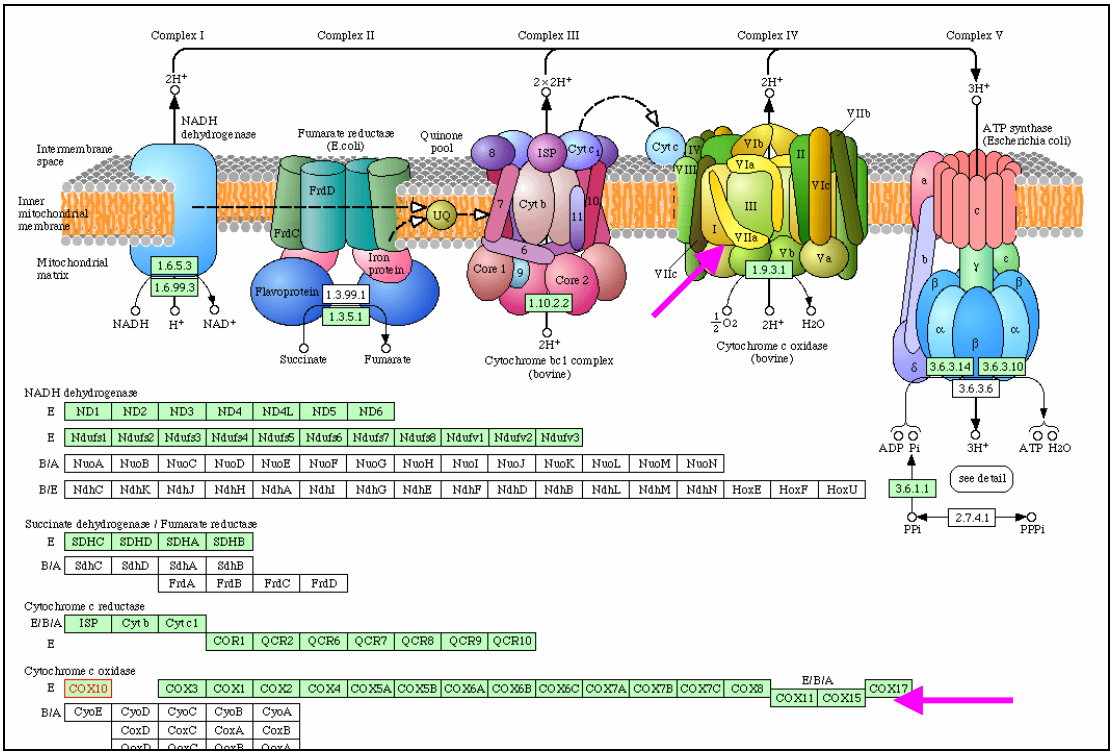
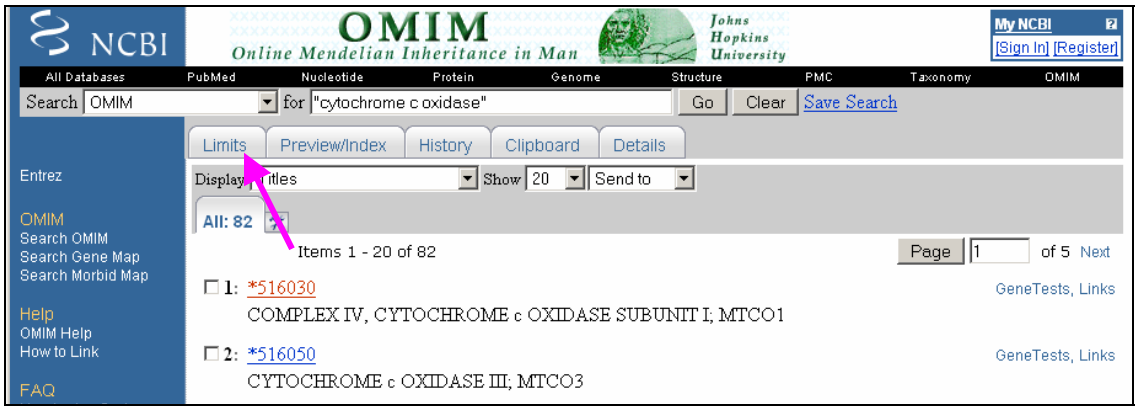


Figure from KEGG **Oxidative phosphorylation - Reference pathway (KO)**
http://www.genome.jp/dbget- in/show_pathway?ko00190+ko:K02270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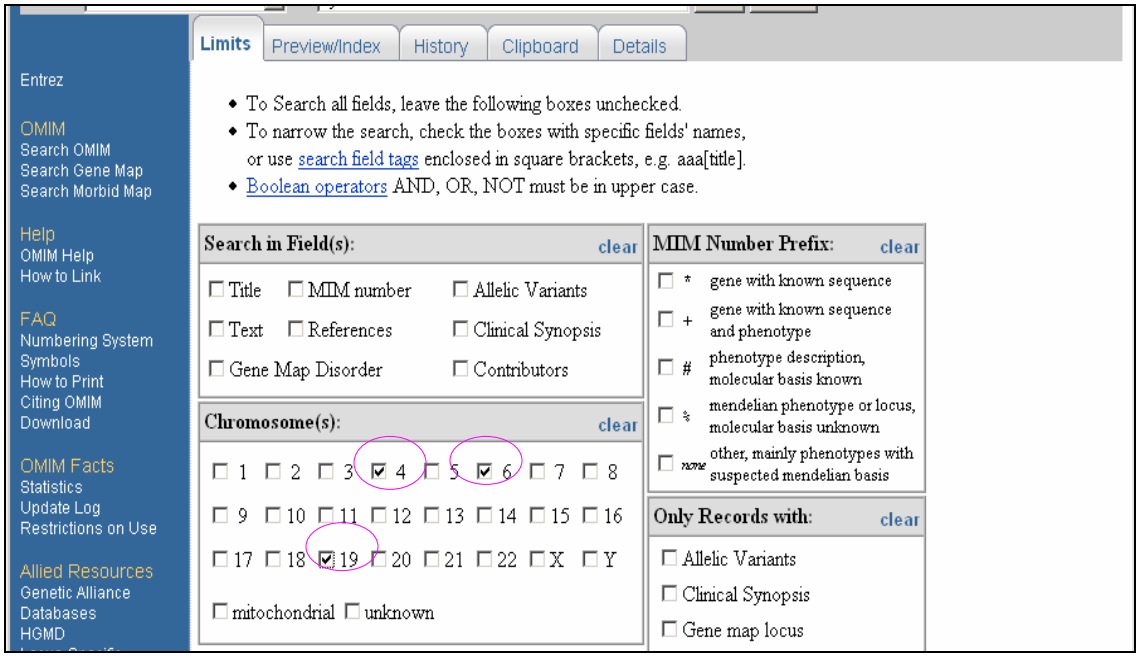
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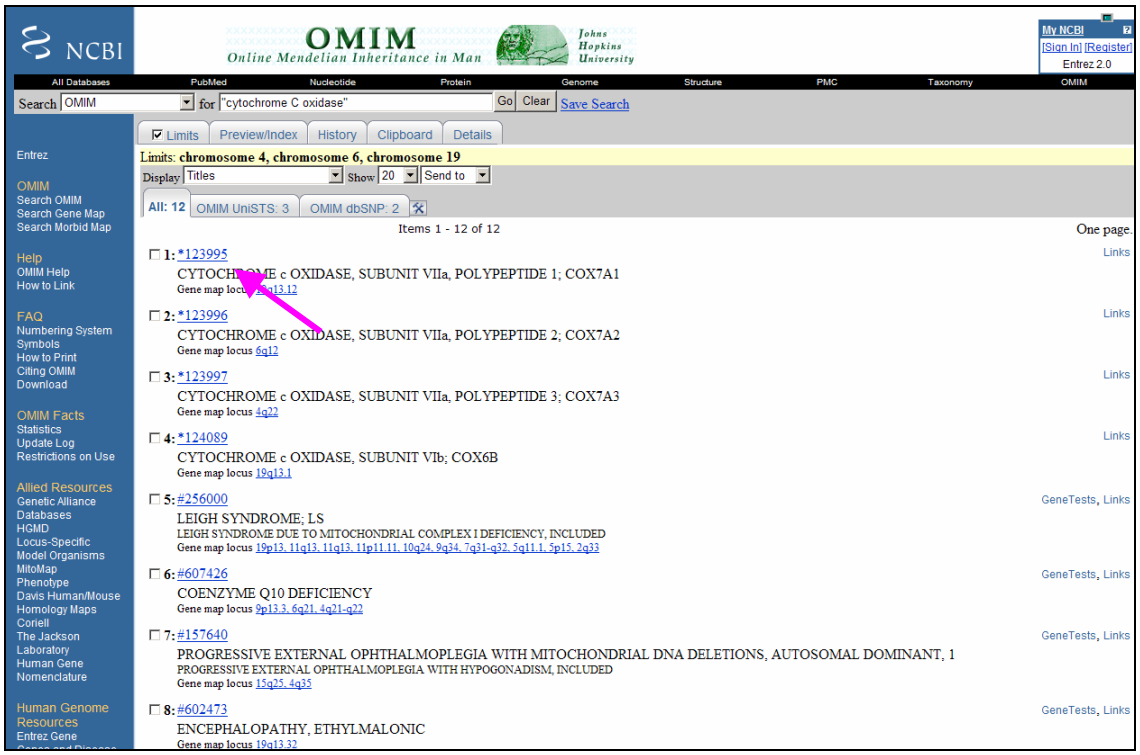
Boolean operators AND, OR, NOT must be in upper case.
Search in Field(s): clear
Title MIM number Allelic Variants
Text References Clinical Synopsis
Gene Map Disorder Contributors
Chromosome(s): clear
1 2 3 4 5 6 7 8
9 10 11 12 13 14 15 16
17 18 19 20 21 22 X Y
mitochondrial unknown
MIM Number Prefix: clear
* gene with known sequence
+ gene with known sequence and phenotype
# phenotype description, molecular basis known
% mendelian phenotype or locus, molecular basis unknown
none other, mainly phenotypes with suspected mendelian basis
Only Records with: clear
Allelic Variants
Clinical Synopsis
Gene map locus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Search OMIM for "cytochrome C oxidase" Go Clear Save Search
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Limits: chromosome 4, chromosome 6, chromosome 19
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All: 12 OMIM UniSTS: 3 OMIM dbSNP: 2
Items 1 - 12 of 12
One page.
1: *123995
CYTOCHROME c OXIDASE, SUBUNIT VIIa, POLYPEPTIDE 1; COX7A1
2: *123996
CYTOCHROME c OXIDASE, SUBUNIT VIIa, POLYPEPTIDE 2; COX7A2
Gene map locus 6q12
3: *123997
CYTOCHROME c OXIDASE, SUBUNIT VIIa, POLYPEPTIDE 3; COX7A3
Gene map locus 4q22
4: *124089
CYTOCHROME c OXIDASE, SUBUNIT VIb; COX6B
Gene map locus 19q13.1
5: #256000
LEIGH SYNDROME; LS
LEIGH SYNDROME DUE TO MITOCHONDRIAL COMPLEX I DEFICIENCY, INCLUDED
6: #607426
COENZYME Q10 DEFICIENCY
Gene map locus 9p13.3, 6q21, 4q21-q22
7: #157640
PROGRESSIVE EXTERNAL OPHTHALMOPLEGIA WITH MITOCHONDRIAL DNA DELETIONS, AUTOSOMAL DOMINANT, 1
PROGRESSIVE EXTERNAL OPHTHALMOPLEGIA WITH HYPOGONADISM, INCLUDED
Gene map locus 15q25, 4q35
8: #602473
ENCEPHALOPATHY, ETHYLMALONIC
Links
GeneTests, Links
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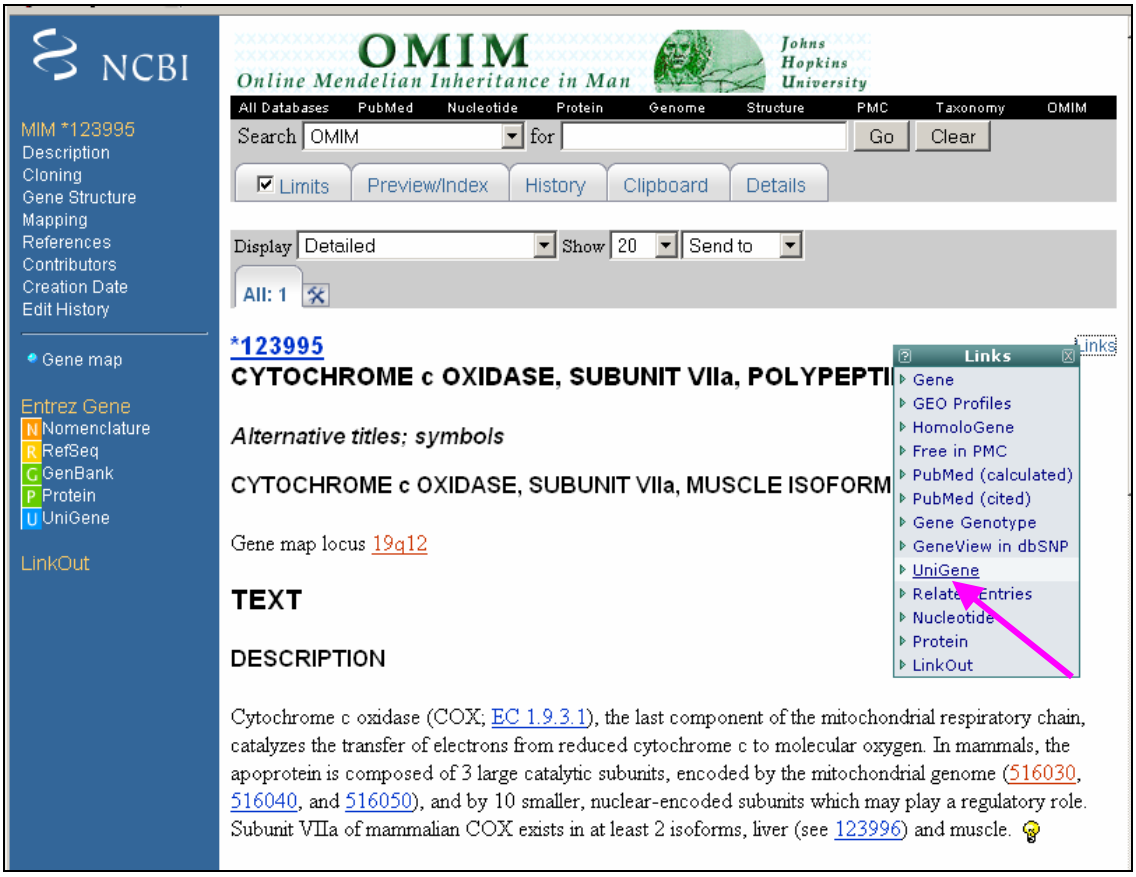
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MIM *123995
Description
Cloning
Gene Structure
Mapping
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Contributors
Creation Date
Edit History
Gene map
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Nomenclature
RefSeq
GenBank
Protein
UniGene
LinkOut
*123995
CYTOCHROME c OXIDASE, SUBUNIT VIIa, POLYPEPTI
Links
Alternative titles; symbols
CYTOCHROME c OXIDASE, SUBUNIT VIIa, MUSCLE ISOFORM
Gene map locus 19q12
TEXT
DESCRIPTION
Cytochrome c oxidase (COX; EC 1.9.3.1), the last component of the mitochondrial respiratory chain, catalyzes the transfer of electrons from reduced cytochrome c to molecular oxygen. In mammals, the apoprotein is composed of 3 large catalytic subunits, encoded by the mitochondrial genome (516030, 516040, and 516050), and by 10 smaller, nuclear-encoded subunits which may play a regulatory role. Subunit VIIa of mammalian COX exists in at least 2 isoforms, liver (see 123996) and muscle.
Links
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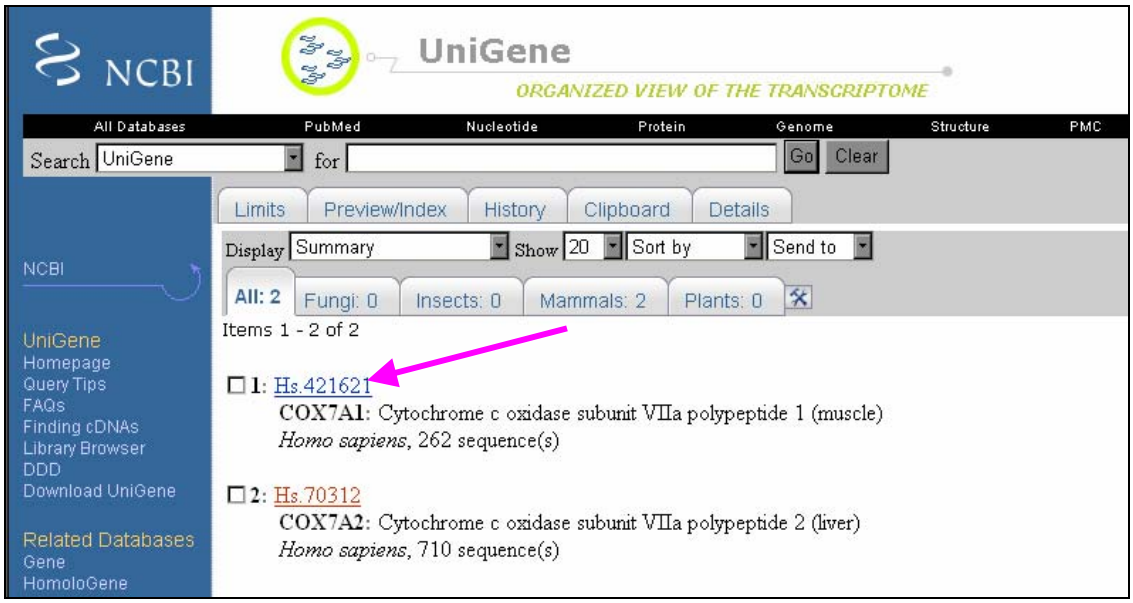
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Insects: 0
Mammals: 2
Plants: 0
Items 1 - 2 of 2
1: Hs.421621
COX7A1: Cytochrome c oxidase subunit VIIa polypeptide 1 (muscle)
Homo sapiens, 262 sequence(s)
2: Hs.70312
COX7A2: Cytochrome c oxidase subunit VIIa polypeptide 2 (liver)
Homo sapiens, 710 sequence(s)
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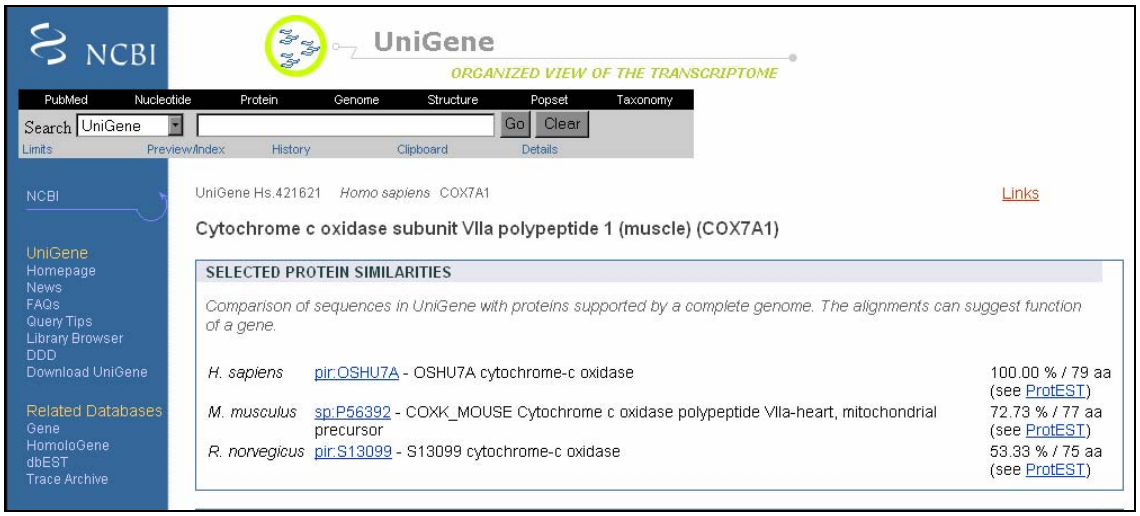
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UniGene Hs.421621 Homo sapiens COX7A1
Links
Cytochrome c oxidase subunit VIIa polypeptide 1 (muscle) (COX7A1)
SELECTED PROTEIN SIMILARITIES
Comparison of sequences in UniGene with proteins supported by a complete genome. The alignments can suggest function of a gene.
H. sapiens pir:OSHU7A - OSHU7A cytochrome-c oxidase 100.00 % / 79 aa (see ProtEST)
M. musculus sp:P56392 - COXK_MOUSE Cytochrome c oxidase polypeptide VIIa-heart, mitochondrial precursor 72.73 % / 77 aa (see ProtEST)
R. norvegicus pir:S13099 - S13099 cytochrome-c oxidase 53.33 % / 75 aa (see ProtEST)
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GENE EXPRESSION

Tissues and development stages from this gene's sequences survey gene expression. Links to other NCBI expression resources.

Restricted Expression: muscle [Show more like this]

Expression Profile:	View expression levels using UniGene's EST ProfileViewer [Show more entries with profiles like this]
Note:	Highly represented (1.4 pct) in cDNA library dbEST:14148, HM3/RH2.
Note:	Highly represented (1.2 pct) in cDNA library dbEST:384, HM1.
GEO profiles:	Gene expression profiles in the NCBI Gene Expression Omnibus database
cDNA sources:	muscle ; heart ; prostate ; mixed ; brain ; other ; uterus ; uncharacterized tissue ; kidney ; pituitary gland ; pancreas ; embryonic tissue ; parathyroid ; vascular ; spleen ; eye ; colon ; tongue ; lung ; thyroid ; umbilical cord ; skin ; parathyroid gland ; bone

MAPPING POSITION

Genomic location specified by transcript mapping, radiation hybrid mapping, genetic mapping or cytogenetic mapping.

Chromosome:	19		
CytoGenetic map:	19q13.1		
UniSTS entry:	Chr 19	RH93348	[MapView]

Expression profile suggested by analysis of EST counts.
Hs.421621- COX7A1: Cytochrome c oxidase subunit VIIa polypeptide 1 (muscle)

See Legend
Note: Please mouseover the Tissue criterion to view complete details

Breakdown by Tissue

	Hs.421621	
adipose tissue	0	0 / 12641
adrenal gland	0	0 / 32737
ascites	0	0 / 39840
bladder	0	0 / 29029
blood	0	0 / 118824
bone	14	1 / 71212
bone marrow	0	0 / 47557
brain	9	9 / 929741
cervix	0	0 / 47067
cochlea	0	0 / 15805
colon	11	2 / 176351
connective tissue	0	0 / 147722
cranial nerve	55	1 / 18050
embryonic tissue	10	2 / 194498
esophagus	0	0 / 19661
eye	25	5 / 197979
heart	217	19 / 87179
kidney	28	6 / 208158
larynx	0	0 / 22490
liver	0	0 / 203135
lung	3	1 / 330072
lymph	0	0 / 44051
lymph node	0	0 / 89251
mammary gland	0	0 / 146592
mouth	60	4 / 65837
muscle	1459	154 / 105522
nerve	0	0 / 15513
ovary	0	0 / 99399
pancreas	14	3 / 211690
parathyroid	148	3 / 20153
pharynx	0	0 / 40462
pituitary gland	185	3 / 16191
placenta	0	0 / 274038
prostate	54	10 / 182408
salivary gland	0	0 / 19977
skin	5	1 / 194123
small intestine	0	0 / 44587
spleen	18	1 / 53176
stomach	0	0 / 94175

NCBI ? UniGene ? EST Profile Viewer

Pubmed Nucleotide Protein Genome Structure Popset Taxonomy

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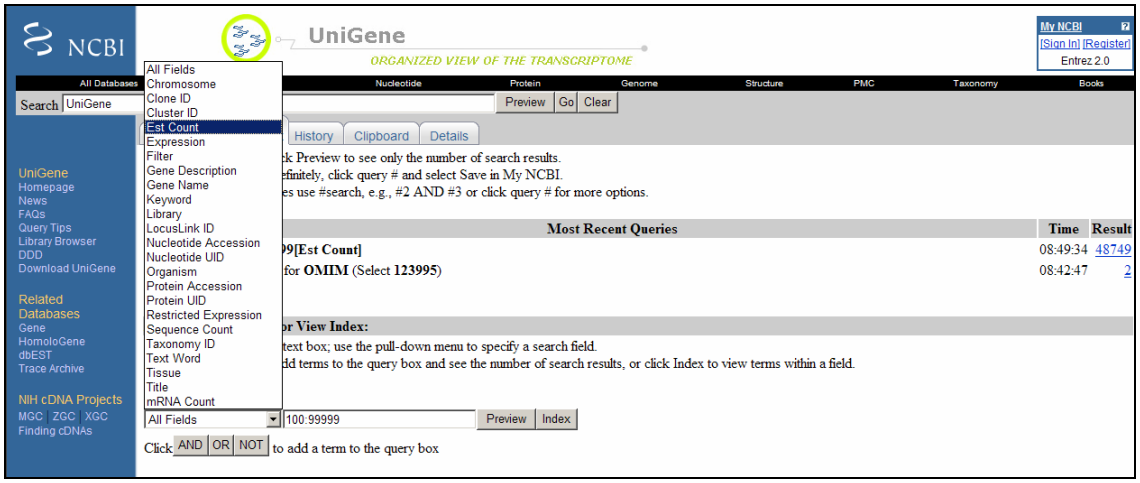
Limits Index History Details

Expression profile suggested by analysis of EST counts.
Hs.421621- COX7A1: Cytochrome c oxidase subunit VIIa polypeptide 1 (muscle)

See Legend
Note: Please mouseover the Tissue criterion to view complete details

Breakdown by Tissue

	Hs.421621	
blood	0	0 / 111420
bone	13	1 / 72260
bone marrow	0	0 / 48827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Cluster ID
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Nucleotide UID
Organism
Protein Accession
Protein UID
Restricted Expression
Sequence Count
Taxonomy ID
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Tissue
Title
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Time
Result
08:49:34 48749
08:42:47 2
100:99999
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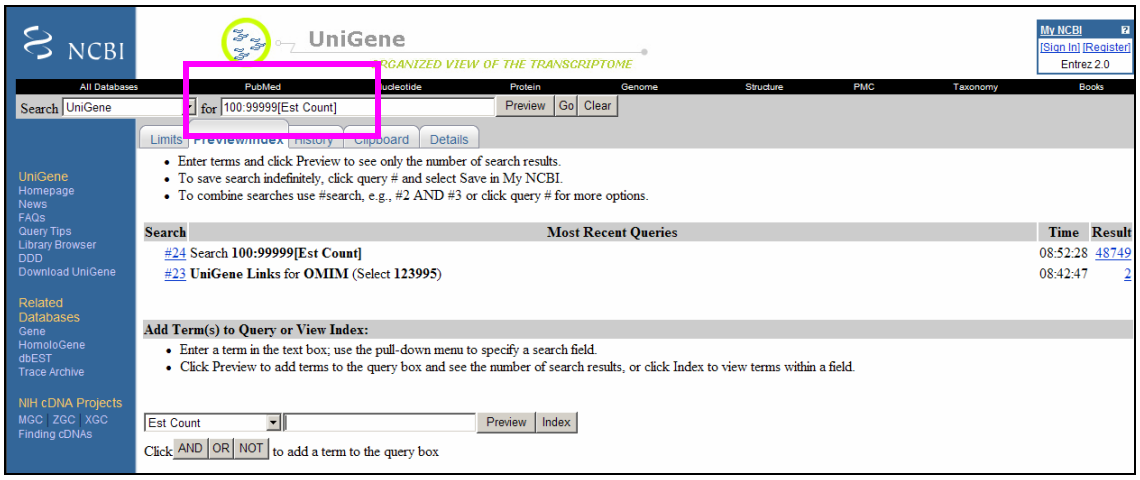
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Time
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#24 Search 100:99999[Est Count]
08:52:28 48749
#23 UniGene Links for OMIM (Select 123995)
08:42:47 2
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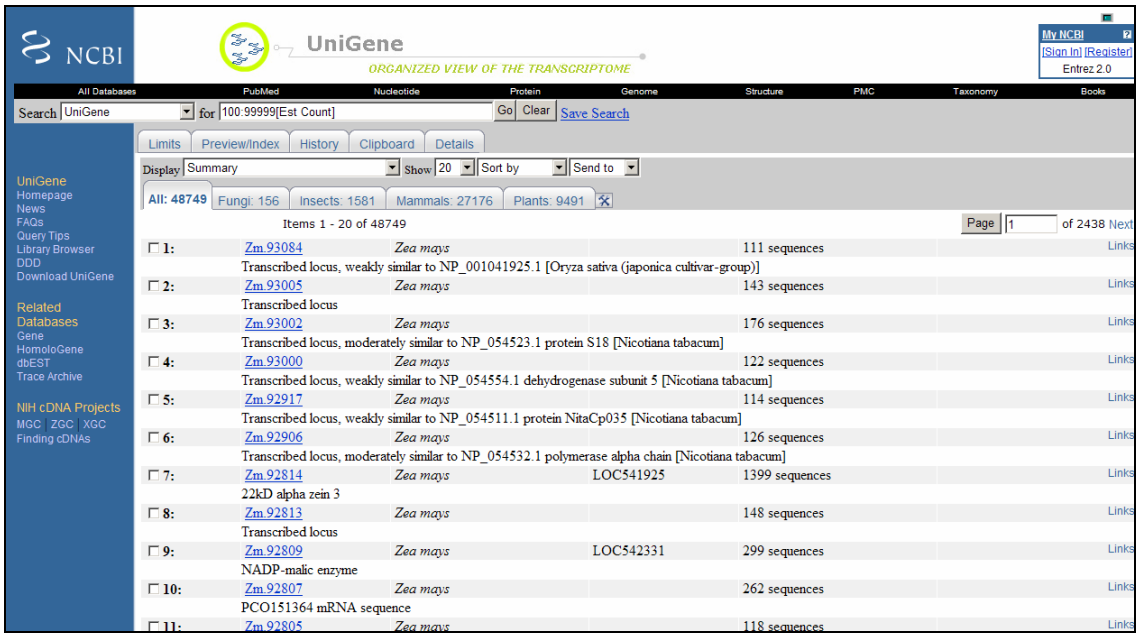
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All: 48749
Fungi: 156
Insects: 1581
Mammals: 27176
Plants: 9491
Items 1 - 20 of 48749
Page 1 of 2438 Next
1: Zm.93084 Zea mays 111 sequences Links
Transcribed locus, weakly similar to NP_001041925.1 [Oryza sativa (japonica cultivar-group)]
2: Zm.93005 Zea mays 143 sequences Links
Transcribed locus
3: Zm.93002 Zea mays 176 sequences Links
Transcribed locus, moderately similar to NP_054523.1 protein S18 [Nicotiana tabacum]
4: Zm.93000 Zea mays 122 sequences Links
Transcribed locus, weakly similar to NP_054554.1 dehydrogenase subunit 5 [Nicotiana tabacum]
5: Zm.92917 Zea mays 114 sequences Links
Transcribed locus, weakly similar to NP_054511.1 protein NitaCp035 [Nicotiana tabacum]
6: Zm.92906 Zea mays 126 sequences Links
Transcribed locus, moderately similar to NP_054532.1 polymerase alpha chain [Nicotiana tabacum]
7: Zm.92814 Zea mays LOC541925 1399 sequences Links
22kD alpha zein 3
8: Zm.92813 Zea mays 148 sequences Links
Transcribed locus
9: Zm.92809 Zea mays LOC542331 299 sequences Links
NADP-malic enzyme
10: Zm.92807 Zea mays 262 sequences Links
PCO151364 mRNA sequence
11: Zm.92805 Zea mays 118 sequences Links
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All: 48749 | Fungi: 156 | Insects: 1581 | Mammals: 27176 | Plants: 9491

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1:	Zm.93084	*Zea mays*		111 sequences	Links
	Transcribed locus, weakly similar to NP_001041925.1 [Oryza sativa (japonica cultivar-group)]				
2:	Zm.93005	*Zea mays*		143 sequences	Links
	Transcribed locus				
3:	Zm.93002	*Zea mays*		176 sequences	Links
	Transcribed locus, moderately similar to NP_054523.1 protein S18 [Nicotiana tabacum]				
4:	Zm.93000	*Zea mays*		122 sequences	Links
	Transcribed locus, weakly similar to NP_054554.1 dehydrogenase subunit 5 [Nicotiana tabacum]				
5:	Zm.92917	*Zea mays*		114 sequences	Links
	Transcribed locus, weakly similar to NP_054511.1 protein NitaCp035 [Nicotiana tabacum]				
6:	Zm.92906	*Zea mays*		126 sequences	Links
	Transcribed locus, moderately similar to NP_054532.1 polymerase alpha chain [Nicotiana tabacum]				
7:	Zm.92814	*Zea mays*	LOC541925	1399 sequences	Links
	22kD alpha zein 3				
8:	Zm.92813	*Zea mays*		148 sequences	Links
	Transcribed locus				

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	Zm.93084	*Zea mays*		111 sequences	Links
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	Zm.93005	*Zea mays*		143 sequences	Links
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	Transcribed locus, weakly similar to NP_054511.1 protein NitaCp035 [Nicotiana tabacum]				
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	Zm.92814	*Zea mays*	LOC541925	1399 sequences	Links
	22kD alpha zein 3				
	Zm.92813	*Zea mays*		148 sequences	Links
	Transcribed locus				
	Zm.92809	*Zea mays*	LOC542331	299 sequences	Links

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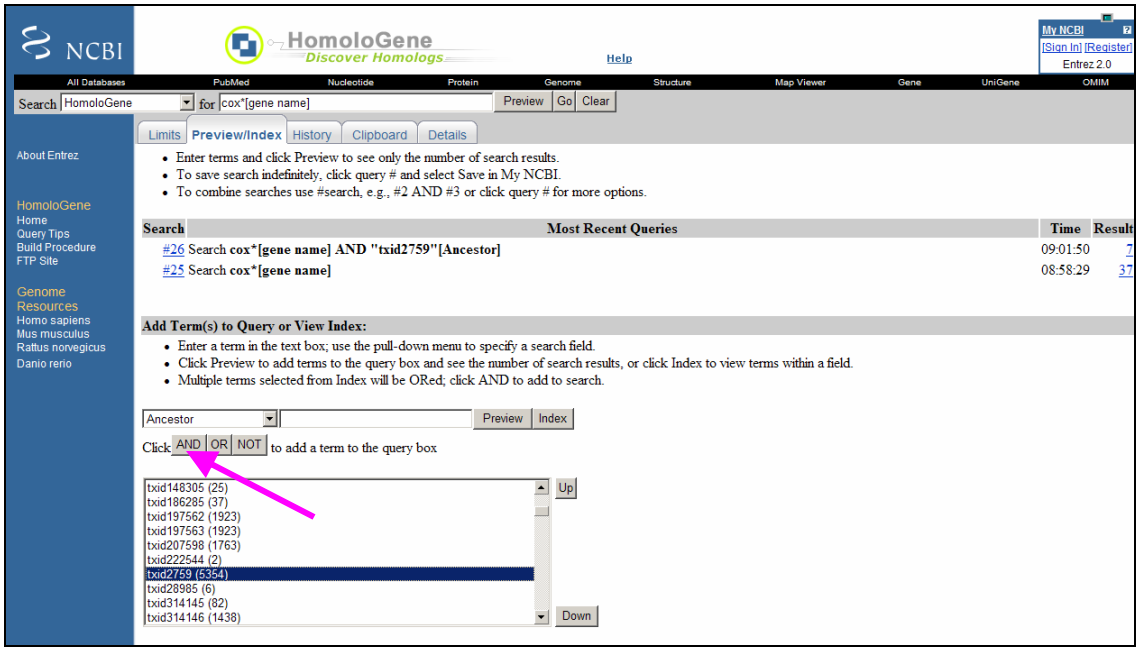
Mus musculus
Rattus norvegicus
Danio rerio

1: HomoloGene:5016. Gene conserved in Eukaryota Links

H.sapiens	COX1	cytochrome c oxidase subunit I
P.troglodytes	COX1	cytochrome c oxidase subunit I
C.lupus	COX1	cytochrome c oxidase subunit I
M.musculus	COX1	cytochrome c oxidase subunit I
R.norvegicus	COX1	cytochrome c oxidase subunit I
G.gallus	COX1	cytochrome c oxidase subunit I
D.melanogaster	COX1	cytochrome c oxidase subunit I
A.gambiae	COX1	cytochrome c oxidase subunit I
C.elegans	COX1	cytochrome c oxidase subunit I
S.pombe	cox1	cytochrome c oxidase 1
S.cerevisiae	COX1	Cox1p
K.lactis	COX1	cytochrome c oxidase subunit 1
E.gossypii	AMI002W	AMI002Wp
A.thaliana	cox1	cytochrome c oxidase subunit 1
O.sativa	cox1	cytochrome c oxidase subunit 1

2: HomoloGene:5017. Gene conserved in Eukaryota Links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To combine searches use #search, e.g., #2 AND #3 or click query # for more options.
Search Most Recent Queries Time Result
#26 Search cox*[gene name] AND "txid2759"[Ancestor] 09:01:50 7
#25 Search cox*[gene name] 08:58:29 37
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Click AND OR NOT to add a term to the query box
txid148305 (25)
txid186285 (37)
txid197562 (1923)
txid197563 (1923)
txid207598 (1763)
txid222544 (2)
txid2759 (5354)
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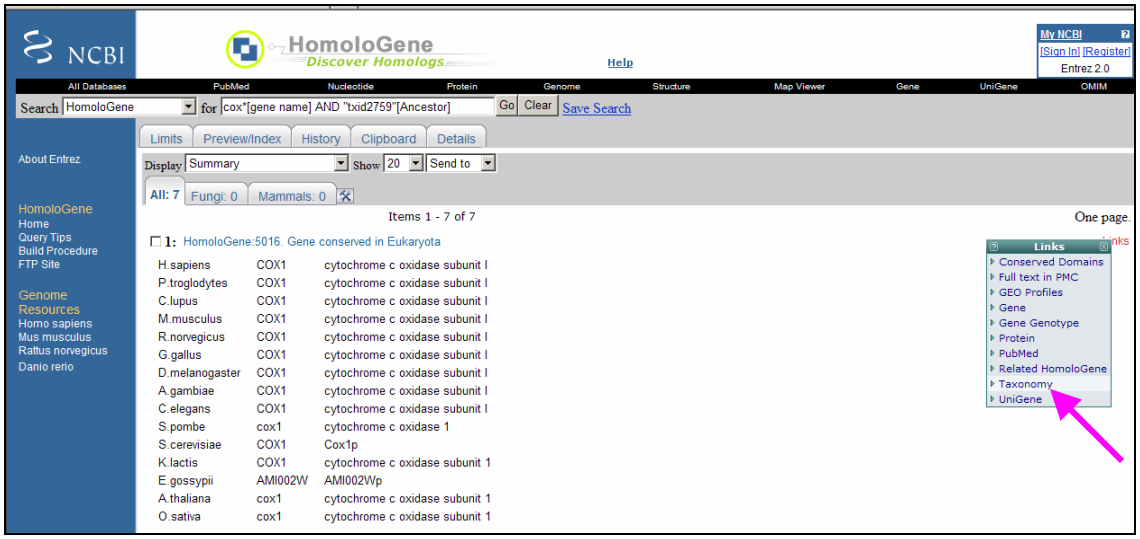
txid314146 (1438)
Up
Down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One page.
1: HomoloGene:5016. Gene conserved in Eukaryota
H.sapiens COX1 cytochrome c oxidase subunit I
P.troglodytes COX1 cytochrome c oxidase subunit I
C.lupus COX1 cytochrome c oxidase subunit I
M.musculus COX1 cytochrome c oxidase subunit I
R.norvegicus COX1 cytochrome c oxidase subunit I
G.gallus COX1 cytochrome c oxidase subunit I
D.melanogaster COX1 cytochrome c oxidase subunit I
A.gambiae COX1 cytochrome c oxidase subunit I
C.elegans COX1 cytochrome c oxidase subunit I
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S.cerevisiae COX1 Cox1p
K.lactis COX1 cytochrome c oxidase subunit 1
E.gossypii AMI002W AMI002Wp
A.thaliana cox1 cytochrome c oxidase subunit 1
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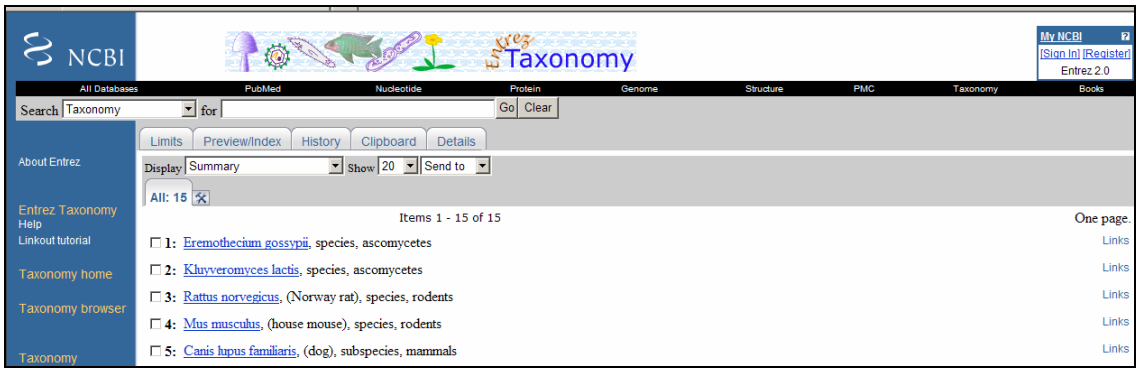
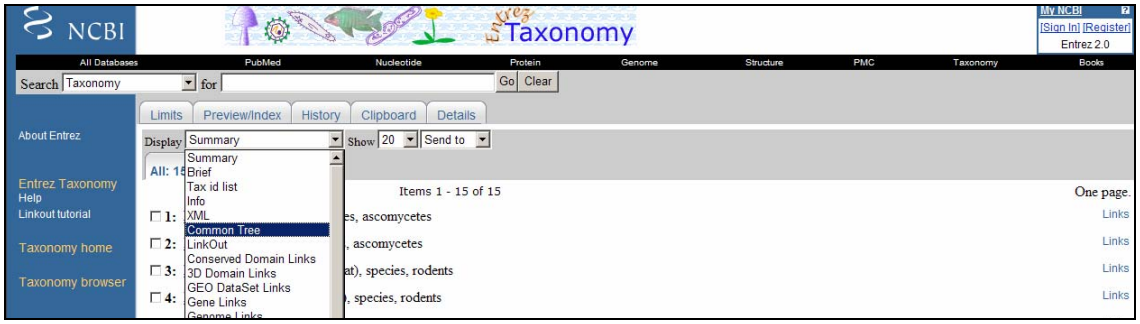
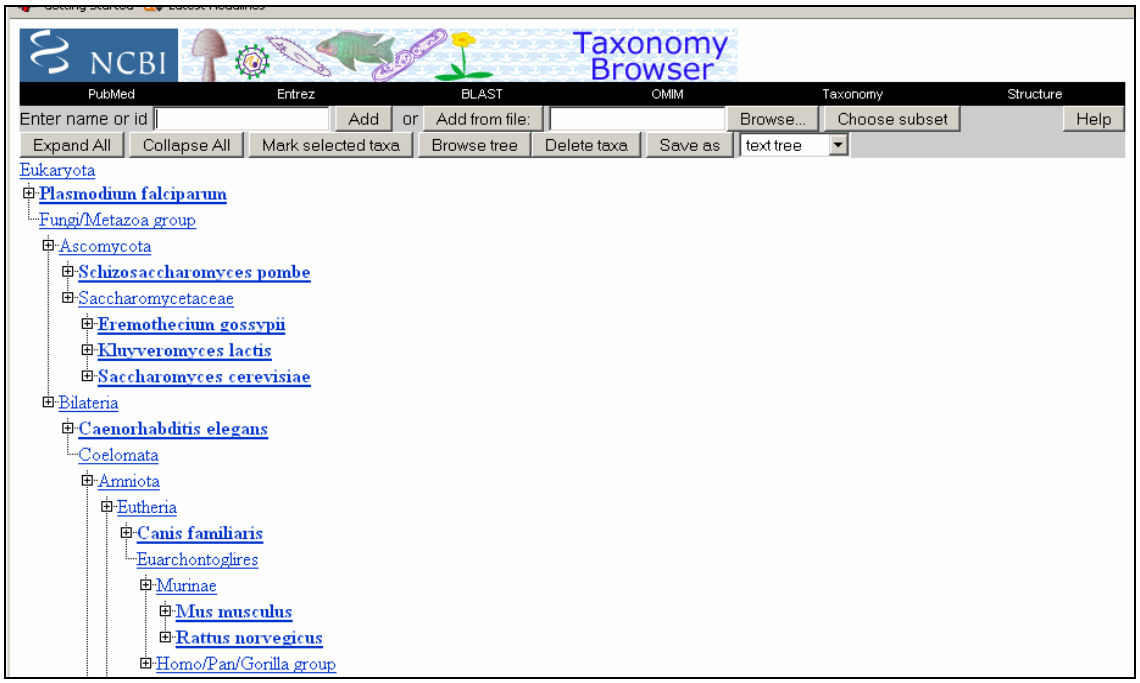
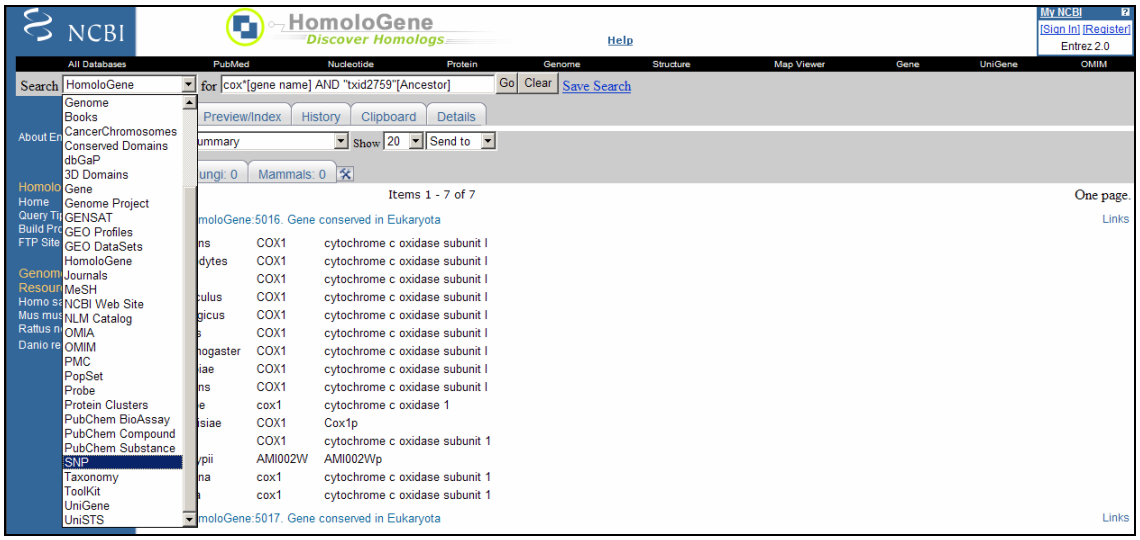
Taxonomy
UniGene


NCBI
Entrez Taxonomy
My NCBI
[Sign In] [Register]
Entrez 2.0
All Databases PubMed Nucleotide Protein Genome Structure PMC Taxonomy Books
Search Taxonomy for Go Clear
Limits Preview/Index History Clipboard Details
About Entrez
Display Summary Show 20 Send to
All: 15
Entrez Taxonomy
Help
Linkout tutorial
Taxonomy home
Taxonomy browser
Taxonomy
Items 1 - 15 of 15
One page.
1: Eremothecium gossypii, species, ascomycetes
2: Kluyveromyces lactis, species, ascomycetes
3: Rattus norvegicus, (Norway rat), species, rodents
4: Mus musculus, (house mouse), species, rodents
5: Canis lupus familiaris, (dog), subspecies, mammals
Links


NCBI
Entrez Taxonomy
My NCBI
[Sign In] [Register]
Entrez 2.0
All Databases PubMed Nucleotide Protein Genome Structure PMC Taxonomy Books
Search Taxonomy for Go Clear
Limits Preview/Index History Clipboard Details
About Entrez
Display Summary Show 20 Send to
Summary
Brief
Tax id list
Info
XML
Common Tree
LinkOut
Conserved Domain Links
3D Domain Links
GEO DataSet Links
Gene Links
Genome Links
Entrez Taxonomy
Help
Linkout tutorial
Taxonomy home
Taxonomy browser
Items 1 - 15 of 15
One page.
Links


NCBI
Taxonomy Browser
PubMed Entrez BLAST OMIM Taxonomy Structure
Enter name or id Add or Add from file: Browse... Choose subset Help
Expand All Collapse All Mark selected taxa Browse tree Delete taxa Save as text tree
Eukaryota
Plasmodium falciparum
Fungi/Metazoa group
Ascomycota
Schizosaccharomyces pombe
Saccharomycetaceae
Eremothecium gossypii
Kluyveromyces lactis
Saccharomyces cerevisiae
Bilateria
Caenorhabditis elegans
Coelomata
Amniota
Eutheria
Canis familiaris
Euarchontoglires
Murinae
Mus musculus
Rattus norvegicus
Homo/Pan/Gorilla group


NCBI
HomoloGene
Discover Homologs
Help
My NCBI
[Sign In] [Register]
Entrez 2.0
All Databases
PubMed
Nucleotide
Protein
Genome
Structure
Map Viewer
Gene
UniGene
OMIM
Search HomoloGene for cox*[gene name] AND "txid2759"[Ancestor]
Go
Clear
Save Search
Preview/Index
History
Clipboard
Details
Show 20
Send to
Mammals: 0
Items 1 - 7 of 7
One page.
Links
Genome
Books
CancerChromosomes
Conserved Domains
dbGaP
3D Domains
Gene
Genome Project
GENSAT
GEO Profiles
GEO DataSets
HomoloGene
Journals
MeSH
NCBI Web Site
NLM Catalog
OMIA
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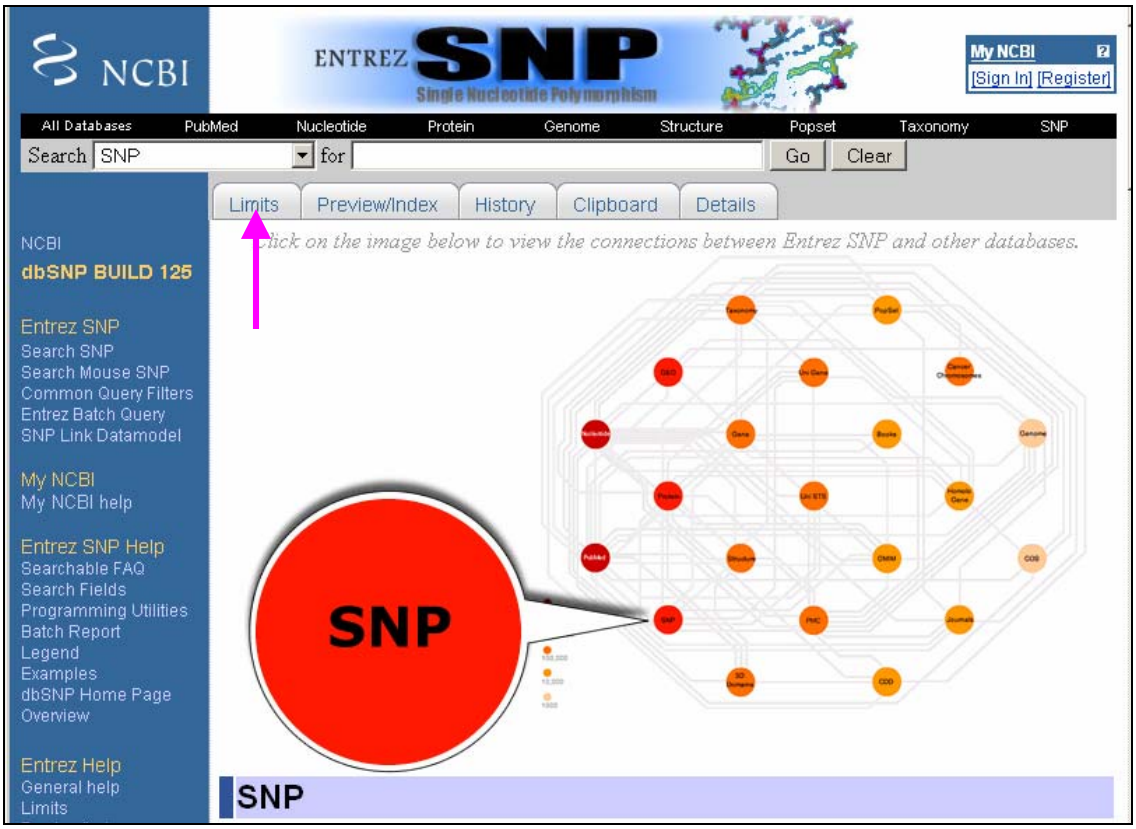
Taxonomy
ToolKit
UniGene
UniSTS


NCBI
ENTREZ SNP
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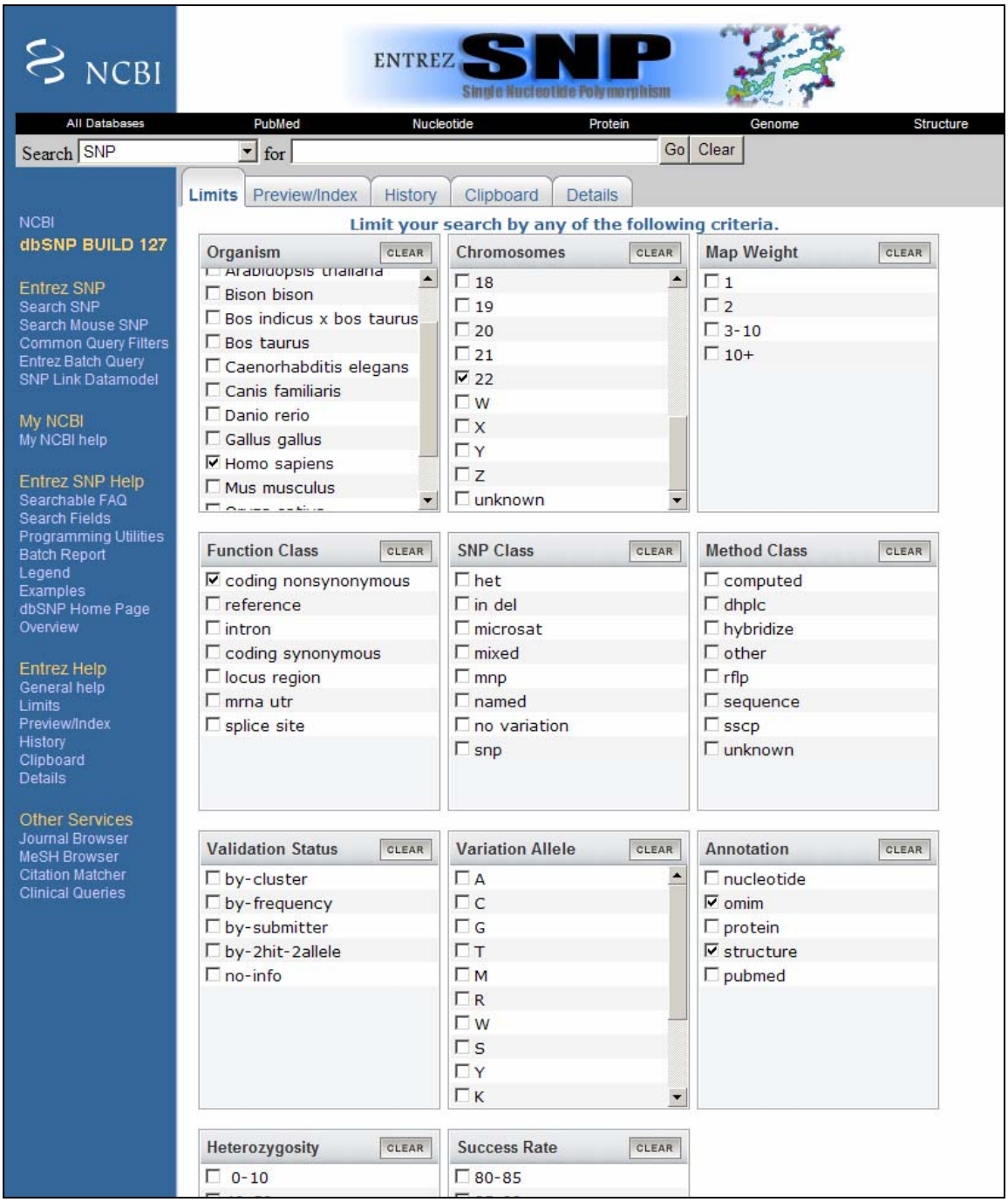
My NCBI
[Sign In] [Register]
All Databases
PubMed
Nucleotide
Protein
Genome
Structure
Popset
Taxonomy
SNP
Search SNP for
Go
Clear
Limits
Preview/Index
History
Clipboard
Details
Click on the image below to view the connections between Entrez SNP and other databases.
NCBI
dbSNP BUILD 125
Entrez SNP
Search SNP
Search Mouse SNP
Common Query Filters
Entrez Batch Query
SNP Link Datamodel
My NCBI
My NCBI help
Entrez SNP Help
Searchable FAQ
Search Fields
Programming Utilities
Batch Report
Legend
Examples
dbSNP Home Page
Overview
Entrez Help
General help
Limits
SNP
SNP


NCBI
ENTREZ SNP
Single Nucleotide Polymorphism
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Nucleotide
Protein
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NCBI
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Search SNP
Search Mouse SNP
Common Query Filters
Entrez Batch Query
SNP Link Datamodel
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My NCBI help
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Searchable FAQ
Search Fields
Programming Utilities
Batch Report
Legend
Examples
dbSNP Home Page
Overview
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General help
Limits
Preview/Index
History
Clipboard
Details
Other Services
Journal Browser
MeSH Browser
Citation Matcher
Clinical Queries
Limit your search by any of the following criteria.
Organism CLEAR
Bison bison
Bos indicus x bos taurus
Bos taurus
Caenorhabditis elegans
Canis familiaris
Danio rerio
Gallus gallus
Homo sapiens
Mus musculus
Chromosomes CLEAR
18
19
20
21
22
W
X
Y
Z
unknown
Map Weight CLEAR
1
2
3-10
10+
Function Class CLEAR
coding nonsynonymous
reference
intron
coding synonymous
locus region
mrna utr
splice site
SNP Class CLEAR
het
in del
microsat
mixed
mnp
named
no variation
snp
Method Class CLEAR
computed
dhplc
hybridize
other
rflp
sequence
sscp
unknown
Validation Status CLEAR
by-cluster
by-frequency
by-submitter
by-2hit-2allele
no-info
Variation Allele CLEAR
A
C
G
T
M
R
W
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Y
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omim
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structure
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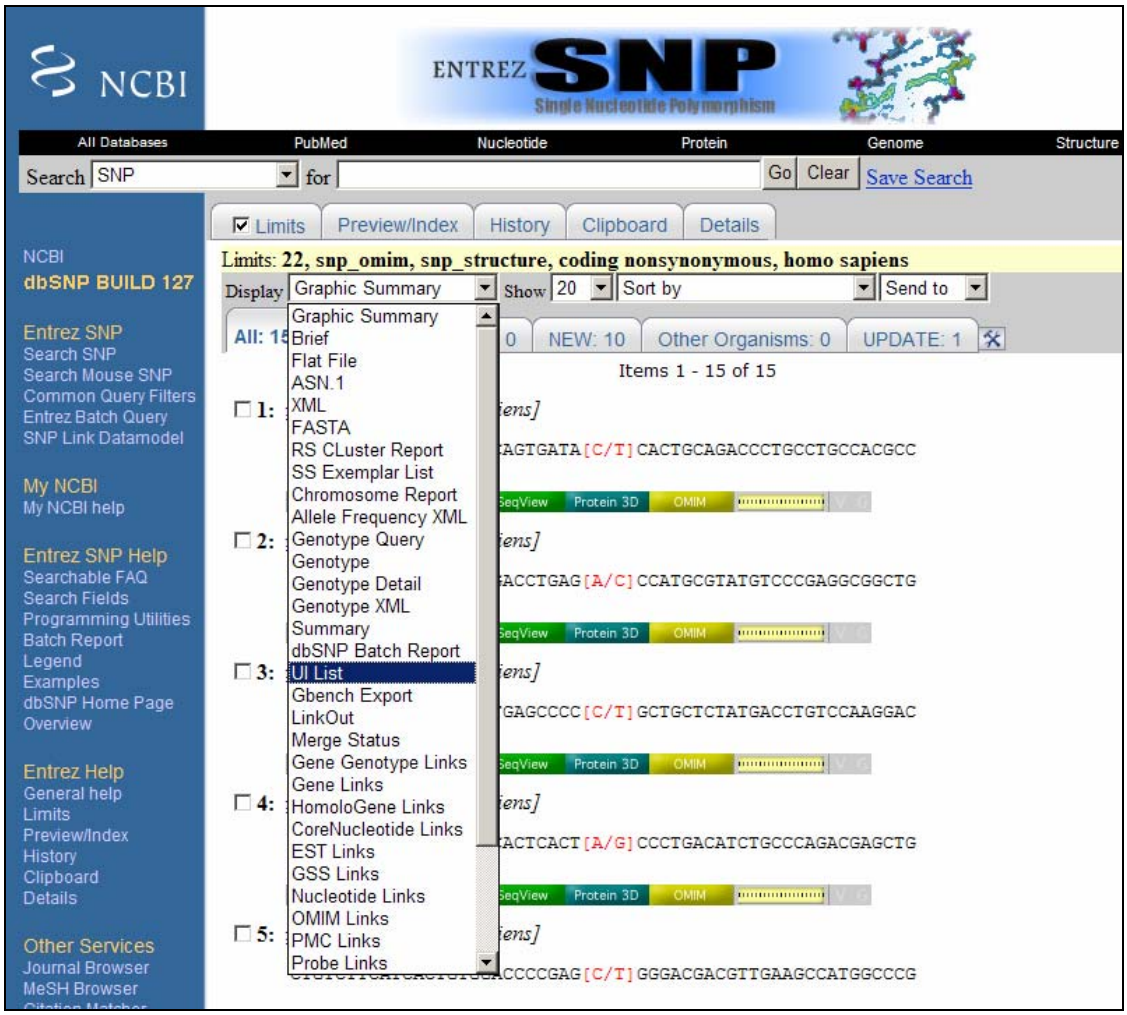
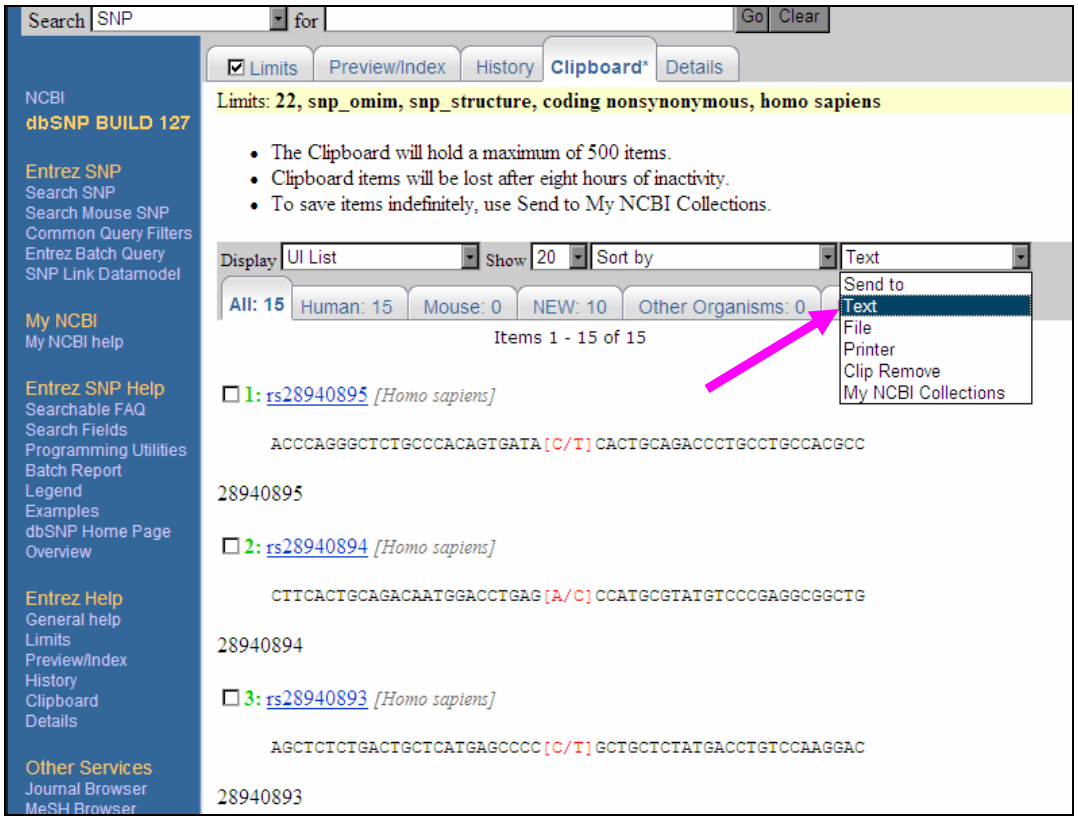
Heterozygosity CLEAR
0-10
Success Rate CLEAR
80-85


NCBI
ENTREZ SNP
Single Nucleotide Polymorphism
All Databases
PubMed
Nucleotide
Protein
Genome
Structure
Search SNP for Go Clear Save Search
Limits
Preview/Index
History
Clipboard
Details
NCBI
dbSNP BUILD 127
Entrez SNP
Search SNP
Search Mouse SNP
Common Query Filters
Entrez Batch Query
SNP Link Datamodel
My NCBI
My NCBI help
Entrez SNP Help
Searchable FAQ
Search Fields
Programming Utilities
Batch Report
Legend
Examples
dbSNP Home Page
Overview
Entrez Help
General help
Limits
Preview/Index
History
Clipboard
Details
Other Services
Journal Browser
MeSH Browser
Limits: 22, snp_omim, snp_structure, coding nonsynonymous, homo sapiens
Display Graphic Summary
Show 20
Sort by
Send to
Graphic Summary
Brief
Flat File
ASN.1
XML
FASTA
RS CLuster Report
SS Exemplar List
Chromosome Report
Allele Frequency XML
Genotype Query
Genotype
Genotype Detail
Genotype XML
Summary
dbSNP Batch Report
UI List
Gbench Export
LinkOut
Merge Status
Gene Genotype Links
Gene Links
HomoloGene Links
CoreNucleotide Links
EST Links
GSS Links
Nucleotide Links
OMIM Links
PMC Links
Probe Links
NEW: 10
Other Organisms: 0
UPDATE: 1
Items 1 - 15 of 15
1:
2:
3:
4:
5:
SeqView
Protein 3D
OMIM


Search SNP for Go Clear
Limits Preview/Index History Clipboard* Details
NCBI
dbSNP BUILD 127
Entrez SNP
Search SNP
Search Mouse SNP
Common Query Filters
Entrez Batch Query
SNP Link Datamodel
My NCBI
My NCBI help
Entrez SNP Help
Searchable FAQ
Search Fields
Programming Utilities
Batch Report
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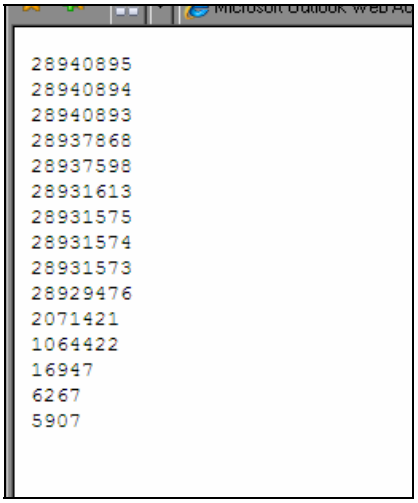
Preview/Index
History
Clipboard
Details
Other Services
Journal Browser
MeSH Browser
Limits: 22, snp_omim, snp_structure, coding nonsynonymous, homo sapiens
The Clipboard will hold a maximum of 500 items.
Clipboard items will be lost after eight hours of inactivity.
To save items indefinitely, use Send to My NCBI Collections.
Display UI List Show 20 Sort by Text
Send to
Text
File
Printer
Clip Remove
My NCBI Collections
All: 15 Human: 15 Mouse: 0 NEW: 10 Other Organisms: 0
Items 1 - 15 of 15
1: rs28940895 [Homo sapiens]
ACCCAGGGCTCTGCCCACAGTGATA[C/T]CACTGCAGACCCTGCCTGCCACGCC
28940895
2: rs28940894 [Homo sapiens]
CTTCACTGCAGACAATGGACCTGAG[A/C]CCATGCGTATGTCCCGAGGCGGCTG
28940894
3: rs28940893 [Homo sapiens]
AGCTCTCTGACTGCTCATGAGCCCC[C/T]GCTGCTCTATGACCTGTCCAAGGAC
28940893


28940895
28940894
28940893
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28931573
28929476
2071421
1064422
16947
6267
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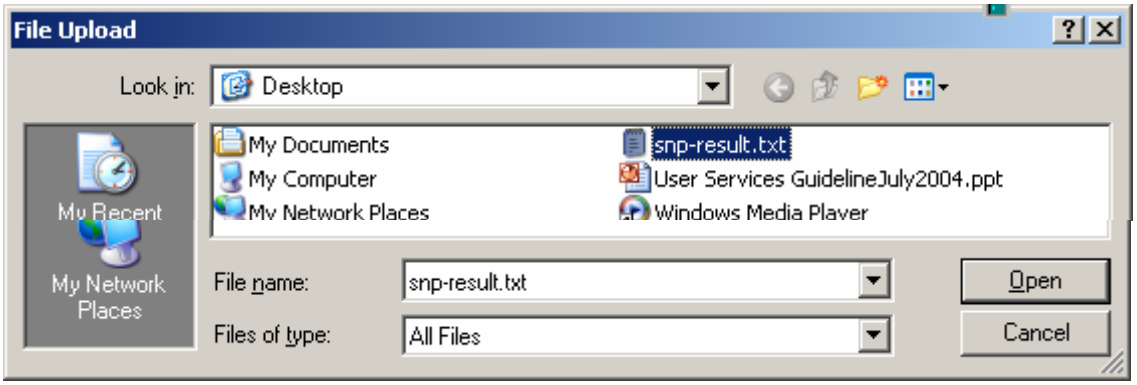
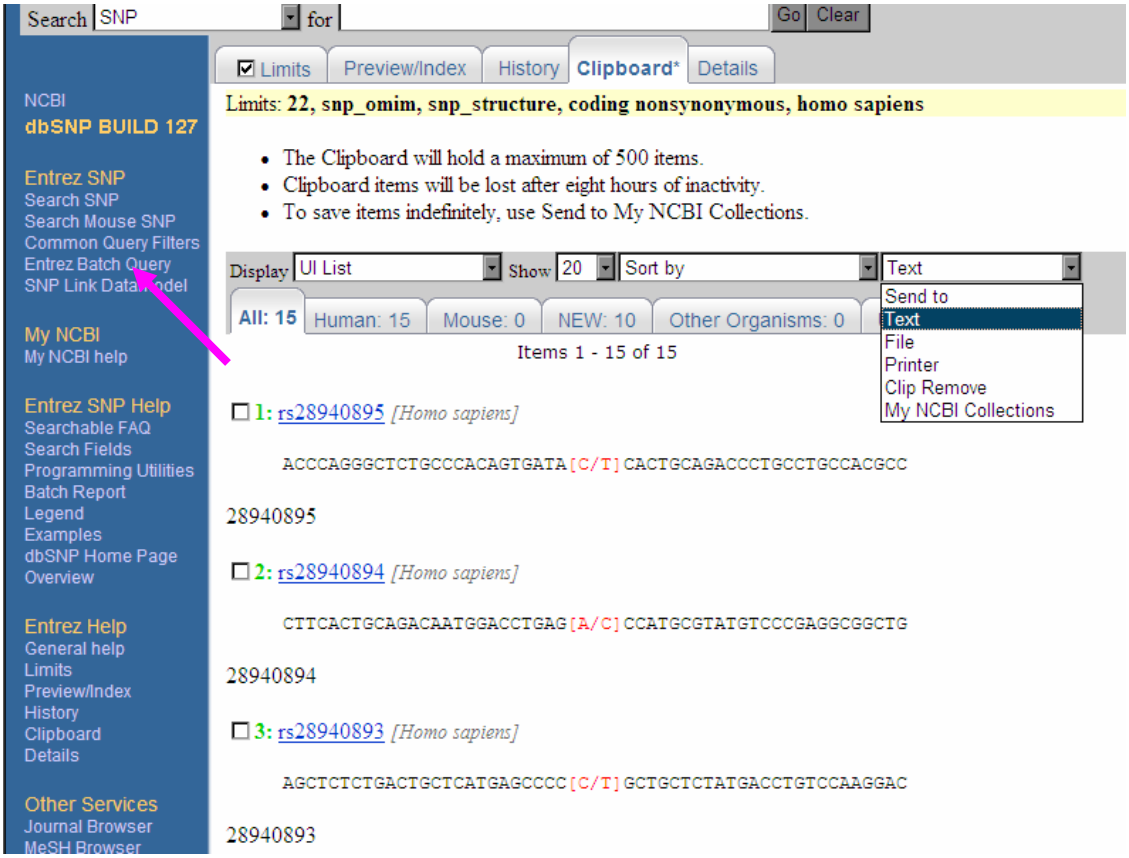
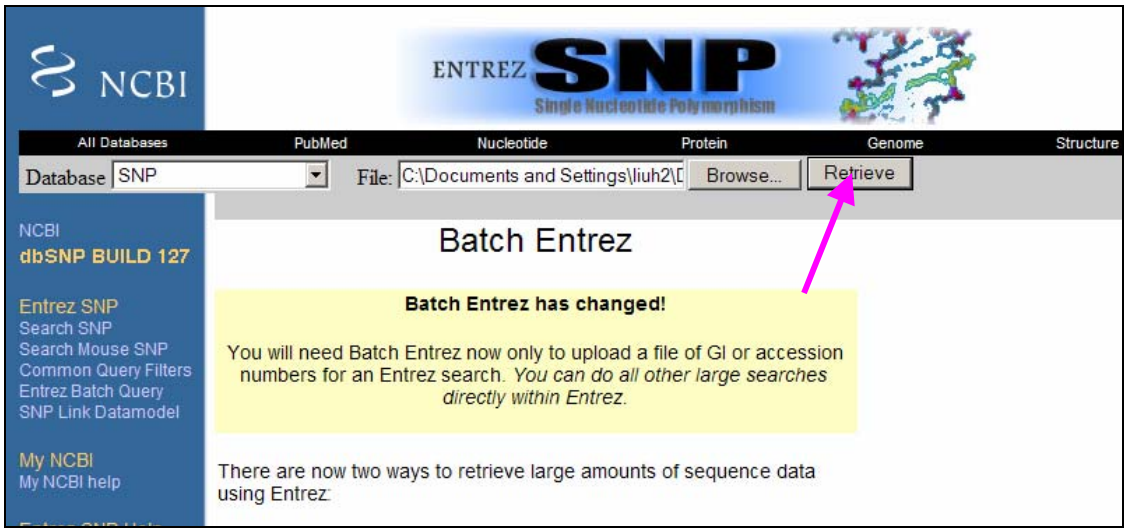
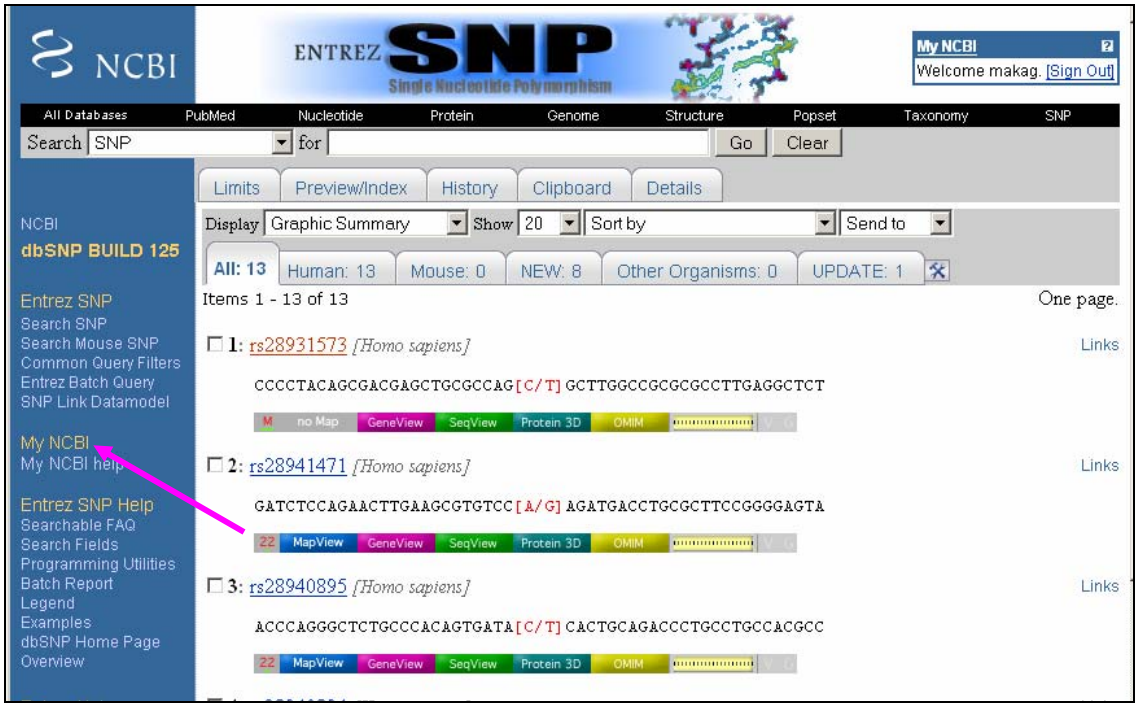
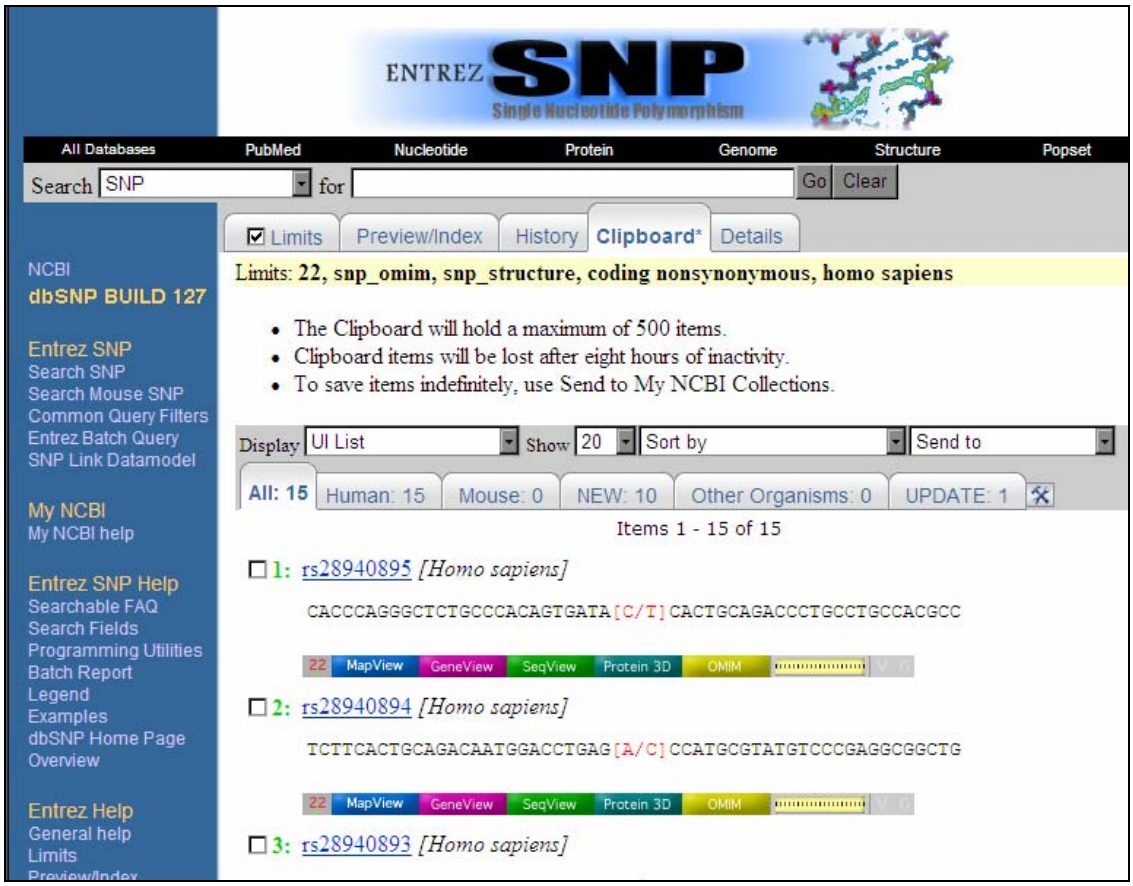

File Upload
Look in:
Desktop
My Documents
My Computer
My Network Places
snp-result.txt
User Services GuidelineJuly2004.ppt
Windows Media Player
My Recent
My Network Places
File name:
snp-result.txt
Files of type:
All Files
Open
Cancel


Search SNP for
Go Clear
Limits
Preview/Index
History
Clipboard*
Details
NCBI
dbSNP BUILD 127
Entrez SNP
Search SNP
Search Mouse SNP
Common Query Filters
Entrez Batch Query
SNP Link Data Model
My NCBI
My NCBI help
Entrez SNP Help
Searchable FAQ
Search Fields
Programming Utilities
Batch Report
Legend
Examples
dbSNP Home Page
Overview
Entrez Help
General help
Limits
Preview/Index
History
Clipboard
Details
Other Services
Journal Browser
MeSH Browser
Limits: 22, snp_omim, snp_structure, coding nonsynonymous, homo sapiens
The Clipboard will hold a maximum of 500 items.
Clipboard items will be lost after eight hours of inactivity.
To save items indefinitely, use Send to My NCBI Collections.
Display UI List
Show 20
Sort by
Text
Send to
Text
File
Printer
Clip Remove
My NCBI Collections
All: 15
Human: 15
Mouse: 0
NEW: 10
Other Organisms: 0
Items 1 - 15 of 15
1: rs28940895 [Homo sapiens]
ACCCAGGGCTCTGCCCACAGTGATA[C/T]CACTGCAGACCCTGCCTGCCACGCC
28940895
2: rs28940894 [Homo sapiens]
CTTCACTGCAGACAATGGACCTGAG[A/C]CCATGCGTATGTCCCGAGGCGGCTG
28940894
3: rs28940893 [Homo sapiens]
AGCTCTCTGACTGCTCATGAGCCCC[C/T]GCTGCTCTATGACCTGTCCAAGGAC
28940893


NCBI
ENTREZ SNP
Single Nucleotide Polymorphism
All Databases
PubMed
Nucleotide
Protein
Genome
Structure
Database SNP
File: C:\Documents and Settings\liuh2\
Browse...
Retrieve
NCBI
dbSNP BUILD 127
Entrez SNP
Search SNP
Search Mouse SNP
Common Query Filters
Entrez Batch Query
SNP Link Datamodel
My NCBI
My NCBI help
Batch Entrez
Batch Entrez has changed!
You will need Batch Entrez now only to upload a file of GI or accession numbers for an Entrez search. You can do all other large searches directly within Entrez.
There are now two ways to retrieve large amounts of sequence data using Entrez:


NCBI
ENTREZ SNP
Single Nucleotide Polymorphism
My NCBI
Welcome makag. [Sign Out]
All Databases
PubMed
Nucleotide
Protein
Genome
Structure
Popset
Taxonomy
SNP
Search SNP for
Go
Clear
Limits
Preview/Index
History
Clipboard
Details
Display Graphic Summary
Show 20
Sort by
Send to
All: 13
Human: 13
Mouse: 0
NEW: 8
Other Organisms: 0
UPDATE: 1
Items 1 - 13 of 13
One page.
NCBI
dbSNP BUILD 125
Entrez SNP
Search SNP
Search Mouse SNP
Common Query Filters
Entrez Batch Query
SNP Link Datamodel
My NCBI
My NCBI help
Entrez SNP Help
Searchable FAQ
Search Fields
Programming Utilities
Batch Report
Legend
Examples
dbSNP Home Page
Overview
1: rs28931573 [Homo sapiens]
Links
CCCCTACAGCGACGAGCTGCGCCAG[C/T]GCTTGGCCGCGCGCCTTGAGGCTCT
M no Map GeneView SeqView Protein 3D OMIM
2: rs28941471 [Homo sapiens]
Links
GATCTCCAGAACTTGAAGCGTGTCC[A/G]AGATGACCTGCGCTTCCGGGGAGTA
22 MapView GeneView SeqView Protein 3D OMIM
3: rs28940895 [Homo sapiens]
Links
ACCCAGGGCTCTGCCCACAGTGATA[C/T]CACTGCAGACCCTGCCTGCCACGCC
22 MapView GeneView SeqView Protein 3D OMIM


ENTREZ SNP
Single Nucleotide Polymorphism
All Databases PubMed Nucleotide Protein Genome Structure Popset
Search SNP for Go Clear
Limits Preview/Index History Clipboard* Details
NCBI
dbSNP BUILD 127
Entrez SNP
Search SNP
Search Mouse SNP
Common Query Filters
Entrez Batch Query
SNP Link Datamodel
My NCBI
My NCBI help
Entrez SNP Help
Searchable FAQ
Search Fields
Programming Utilities
Batch Report
Legend
Examples
dbSNP Home Page
Overview
Entrez Help
General help
Limits
Limits: 22, snp_omim, snp_structure, coding nonsynonymous, homo sapiens
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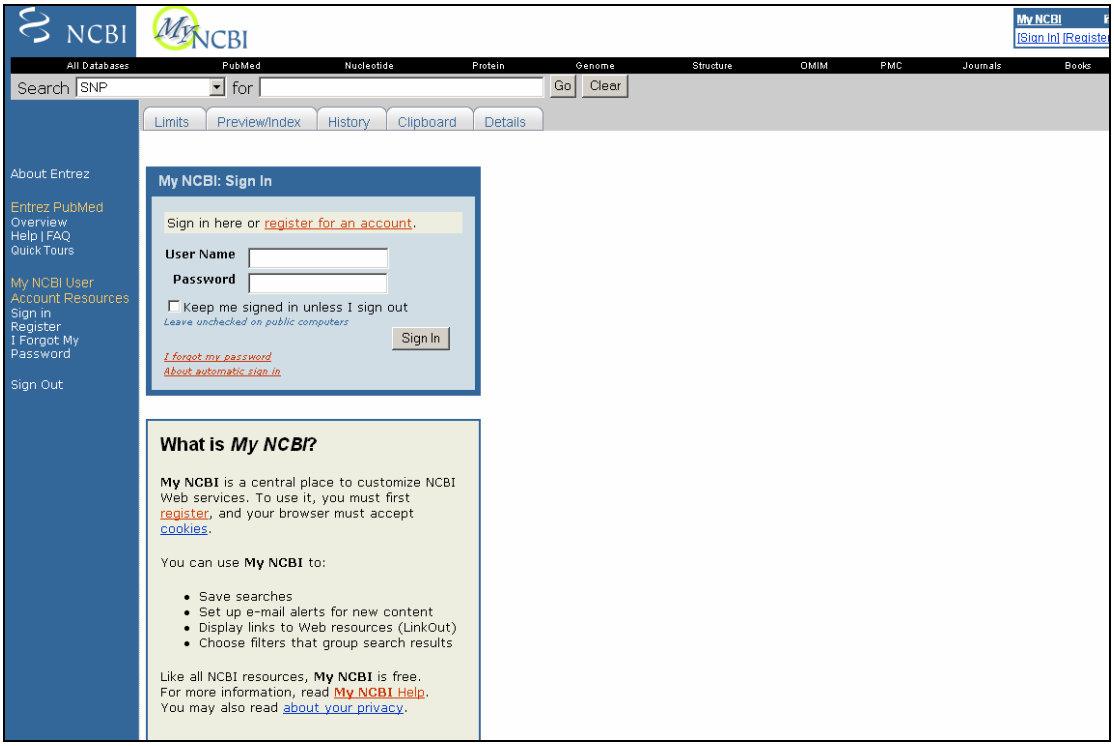
Display UI List Show 20 Sort by Send to
All: 15 Human: 15 Mouse: 0 NEW: 10 Other Organisms: 0 UPDATE: 1
Items 1 - 15 of 15
1: rs28940895 [Homo sapiens]
CACCCAGGGCTCTGCCCACAGTGATA[C/T]CACTGCAGACCCTGCCTGCCACGCC
22 MapView GeneView SeqView Protein 3D OMIM
2: rs28940894 [Homo sapiens]
TCTTCACTGCAGACAATGGACCTGAG[A/C]CCATGCGTATGTCCCGAGGCGGCTG
22 MapView GeneView SeqView Protein 3D OMIM
3: rs28940893 [Homo sapiens]


NCBI
MyNCBI
My NCBI
[Sign In] [Registe
All Databases PubMed Nucleotide Protein Genome Structure OMIM PMC Journals Books
Search SNP for Go Clear
Limits Preview/Index History Clipboard Details
About Entrez
Entrez PubMed
Overview
Help | FAQ
Quick Tours
My NCBI User Account Resources
Sign in
Register
I Forgot My Password
Sign Out
My NCBI: Sign In
Sign in here or register for an account.
User Name
Password
Keep me signed in unless I sign out
Leave unchecked on public computers
Sign In
I forgot my password
About automatic sign in
What is My NCBI?
My NCBI is a central place to customize NCBI Web services. To use it, you must first register, and your browser must accept cookies.
You can use My NCBI to:
Save searches
Set up e-mail alerts for new content
Display links to Web resources (LinkOut)
Choose filters that group search results
Like all NCBI resources, My NCBI is free.
For more information, read My NCBI Help.
You may also read about your privacy.

Example 2:

I. PubMed, PMC, Taxonomy and PopSet

Besides mammoth, how many other extinct organisms have data available in the Entrez databases? Go to the Preview/Index of the Taxonomy database, select the "Properties" field and from its index "Extinct". These records can be combined with the "Filter" that limits the search to those taxonomy records that have links to PubMed Central (PMC). The resulting search phrase:
"extinct"[Properties] AND "taxonomy pmc"[Filter]
Select the *Emeus crassus* entry. What is the origin of eastern moa's specimens that have their sequences reported in the Entrez databases? What is the lineage for this organism? Link to the PMC database and access the publication on giant moas. Link to full text of the article published by Baker et al., and from there to the figures and tables of the article, if you are interested in the appearance of these extinct birds.
Return to Taxonomy and from there link to the PopSet database. In the record submitted by Lambert DM, several ancient organisms were compared. Which gene was used in the sequence comparison? From the PopSet record link to the Nucleotide database. List all the organisms studied in this PopSet. Select the *Emeus crassus* and *Dinornis robustus* nucleotide records and temporarily save them on the Clipboard.

II. OMIM, UniGene and Homologene
Perform an unlimited search for records relating to cholesterol transport in the OMIM database. Repeat the query for "cholesterol transport" as a term. Which search is more

restrictive? Limit the retrieved entries only to those with gene location on chromosome 22. How many records have you retrieved? What is the chromosomal location of the gene APOL1 (OMIM record 603743)? How many APOL genes are clustered on chromosome 22? From the APOL1 OMIM record link to the UniGene database. Compare the expression profiles of the APOL1 and APOL2 genes focusing on the developmental stage. What do you conclude from the expression profiles?
Perform a search for those UniGene records with the expression restricted to "adult 17 years old". Combine the result of the search with the six records that you have obtained through the OMIM link. Which three members of the APOL gene family have expression restricted to adults? Is the evidence strong for all of them?
Search the HomoloGene database for records relating to APO genes (Preview/Index—Gene Name). How many records have you retrieved? Are all apolipoprotein genes equally conserved in evolution? What are their common ancestors? Which of these genes are conserved in placental mammals (Eutheria, Taxonomy ID 9347).
Display the taxonomy tree for organisms included in the record containing human APOL6 homologs.

III. dbSNP

Access the SNP database and select its Limits page. Check the appropriate boxes to allow selection for SNPs at the splice site of human chromosome 22. Sort the list by organism. Retrieve and download the UI List for these records. Use the saved file to retrieve the records with the UI List in Batch Entrez.

Course developed by:

Majda Valjavec-Gratian (gratianm@ncbi.nlm.nih.gov) and
Medha Bhagwat (bhagwat@ncbi.nlm.nih.gov)