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

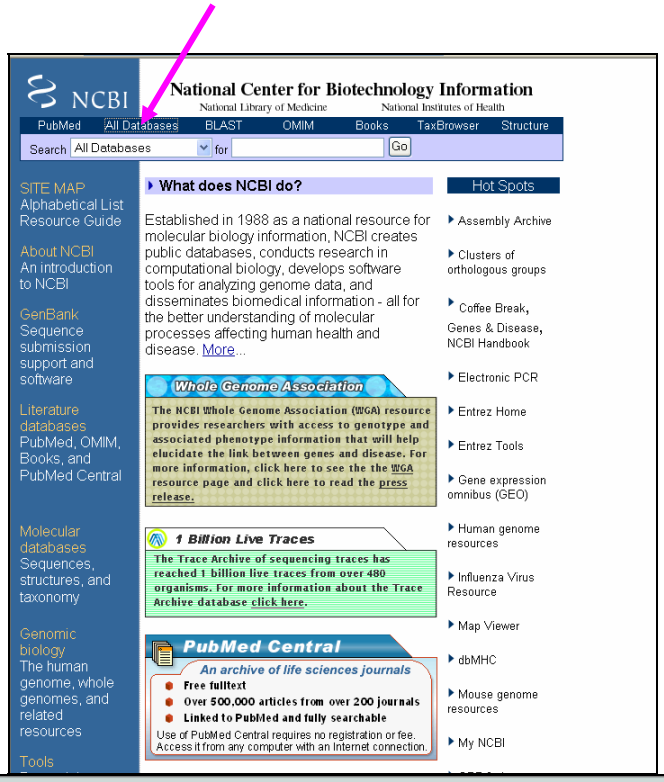
Perform a search for mammoth across all of the Entrez databases. Which databases contain records associated with the term mammoth? Link to the mammoth literature citations in the PubMed database. Identify the articles available free in PMC. Access the article "The year of the mammoth". What are the cited 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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Whole Genome Association
The NCBI Whole Genome Association (WGA) resource provides researchers with access to genotype and associated phenotype information that will help elucidate the link between genes and disease. For more information, click here to see the the WGA resource page and click here to read the press release.
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73907 Nucleotide: sequence database (includes GenBank)
240 Protein: sequence database
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none Structure: three-dimensional macromolecular structures
2 Taxonomy: organisms in GenBank
none SNP: single nucleotide polymorphism
13 Gene: gene-centered information
1 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
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
35 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
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Complete mitochondrial genome and phylogeny of Pleistocene Mammoth Mammuthus primigenius.
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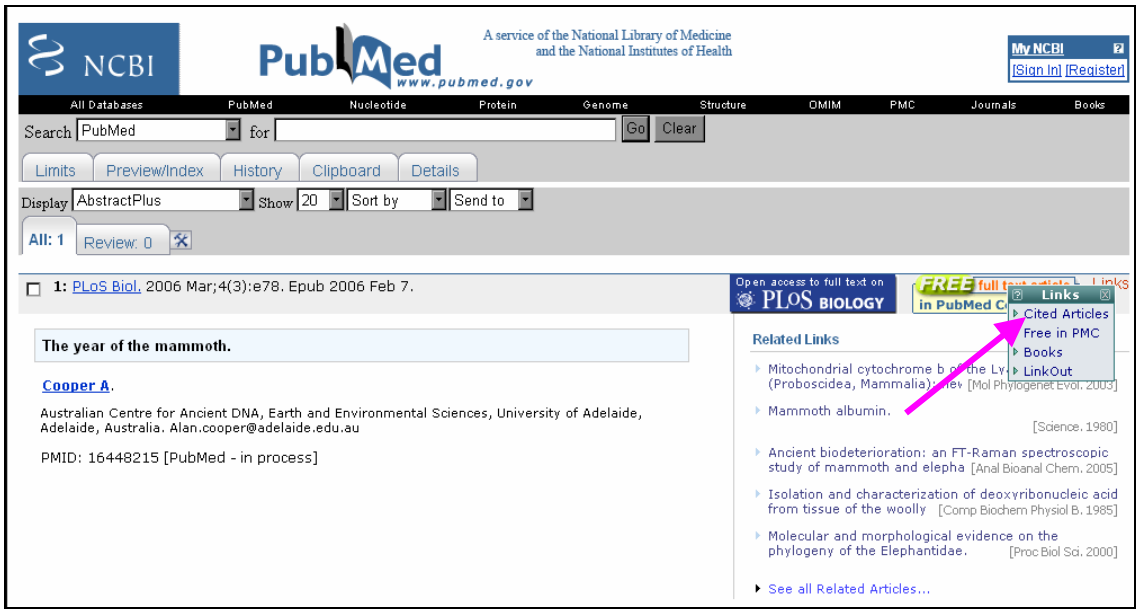
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Isolation and characterization of deoxyribonucleic acid from tissue of the woolly [Comp Biochem Physiol B. 1985]
Molecular and morphological evidence on the phylogeny of the Elephantidae. [Proc Biol Sci. 2000]
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2: Margulies M, Egholm M, Altman WE, Attiya S, Bader JS, Bemben LA, Berka J, Braverman MS, Chen YJ, Chen Z, Dewell SB, Du L, Fierro JM, Gomes XV, Godwin BC, He W, Helgesen S, Ho CH, Irzyk GP, Jando SC, Alenquer ML, Jarvie TP, Jirage KB, Kim JB, Knight JR, Lanza JR, Leamon JH, Lefkowitz SM, Lei M, Li J, Lohman KL, Lu H, Makhijani VB, McDade KE, McKenna MP, Myers EW, Nickerson E, Nobile JR, Plant R, Puc BP, Ronan MT, Roth GT, Sarkis GJ, Simons JF, Simpson JW, Srinivasan M, Tartaro KR, Tomasz A, Vogt KA, Volkmer GA, Wang SH, Wang Y, Weiner MP, Yu P, Begley RF, Rothberg JM. Related Articles, Links
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Nature. 2005 Sep 15;437(7057):376-80. Epub 2005 Jul 31.
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Science. 2005 Jul 22;309(5734):597-9. Epub 2005 Jun 2.

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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, Massachusetts, USA. 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.

PMID: 16448217 [PubMed - in process]

2: Nature. 2005 Sep 15;437(7057):376-80. Epub 2005 Jul 31. Related Articles, Links

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Erratum in:
- Nature. 2006 May 4;441(7089):120. Ho, Chun He [corrected to Ho, Chun Heen].

Comment in:
- Nature. 2005 Sep 15;437(7057):326-7.

Genome sequencing in microfabricated high-density picolitre reactors.

Margulies M, Egholm M, Altman WE, Attiya S, Bader JS, Bemben LA, Berka J, Braverman MS, Chen YJ, Chen Z, Dewell SB, Du L, Fierro JM, Gomes XV, Godwin BC, He W, Helgesen S, Ho CH, Irzyk GP, Jando SC, Alenquer ML, Jarvie TP, Jirage KB, Kim JB, Knight JR, Lanza JR, Leamon JH, Lefkowitz SM, Lei M, Li J, Lohman KL, Lu H, Makhijani VB, McDade KE, McKenna MP, Myers EW, Nickerson E, Nobile JR, Plant R, Puc BP, Ronan MT, Roth GT, Sarkis GJ, Simons JF, Simpson JW, Srinivasan M, Tartaro KR, Tomasz A, Vogt KA, Volkmer GA, Wang SH, Wang Y, Weiner MP, Yu P, Begley RF, Rothberg JM.

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 accuracy, in one four-hour run. To achieve an approximately 100-fold increase in throughput over current Sanger sequencing technology, we have developed an emulsion method for DNA amplification and an instrument for sequencing by synthesis using a pyrosequencing protocol optimized for solid support and picolitre-scale volumes. Here we show the utility, throughput, accuracy and robustness of this system by shotgun sequencing and de novo assembly of the Mycoplasma genitalium genome with 96% coverage at 99.96% accuracy in one run of the machine.

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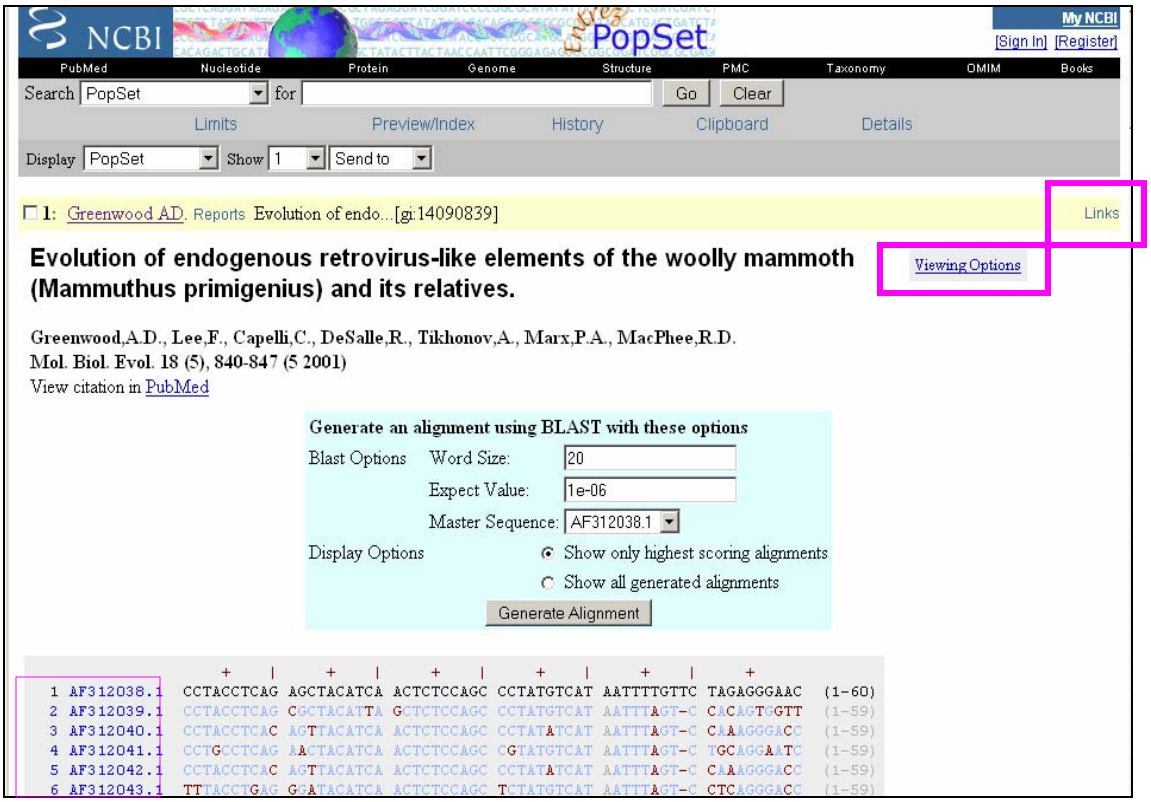
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3 AF312040.1 CCTACCTCAC AGTTACATCA ACTCTCCAGC CCTATATCAT AATTTAGT-C CAAAGGGACC (1-59)
4 AF312041.1 CCTGCCTCAG AACTACATCA ACTCTCCAGC CGTATGTCAT AATTTAGT-C TGCAGGAATC (1-59)
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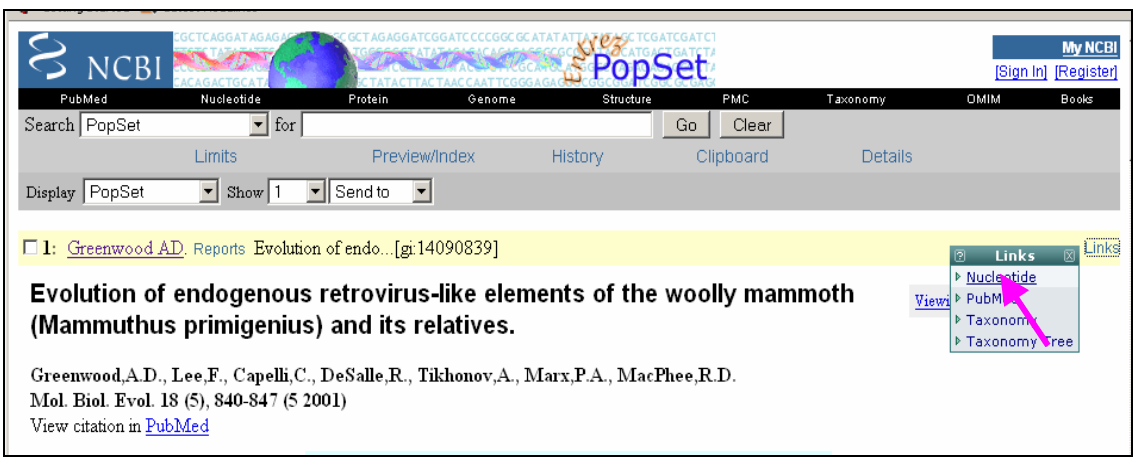
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Links
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Taxonomy Tree
Evolution of endogenous retrovirus-like elements of the woolly mammoth (Mammuthus primigenius) and its relatives.
Greenwood,A.D., Lee,F., Capelli,C., DeSalle,R., Tikhonov,A., Marx,P.A., MacPhee,R.D.
Mol. Biol. Evol. 18 (5), 840-847 (5 2001)
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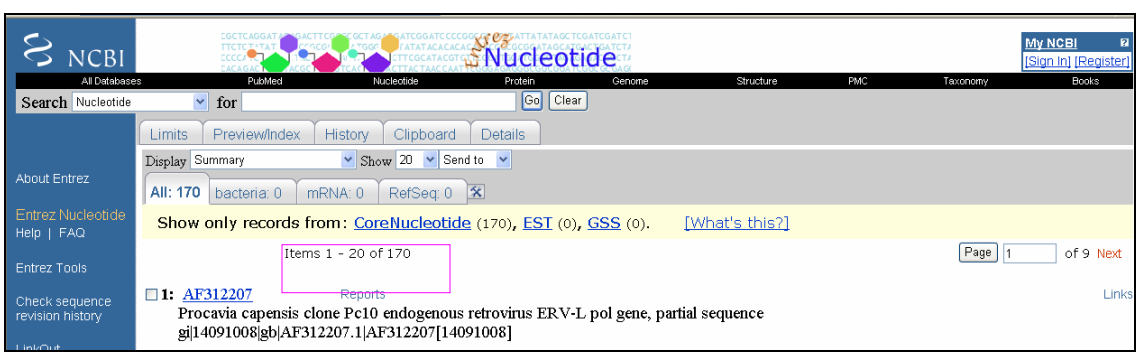
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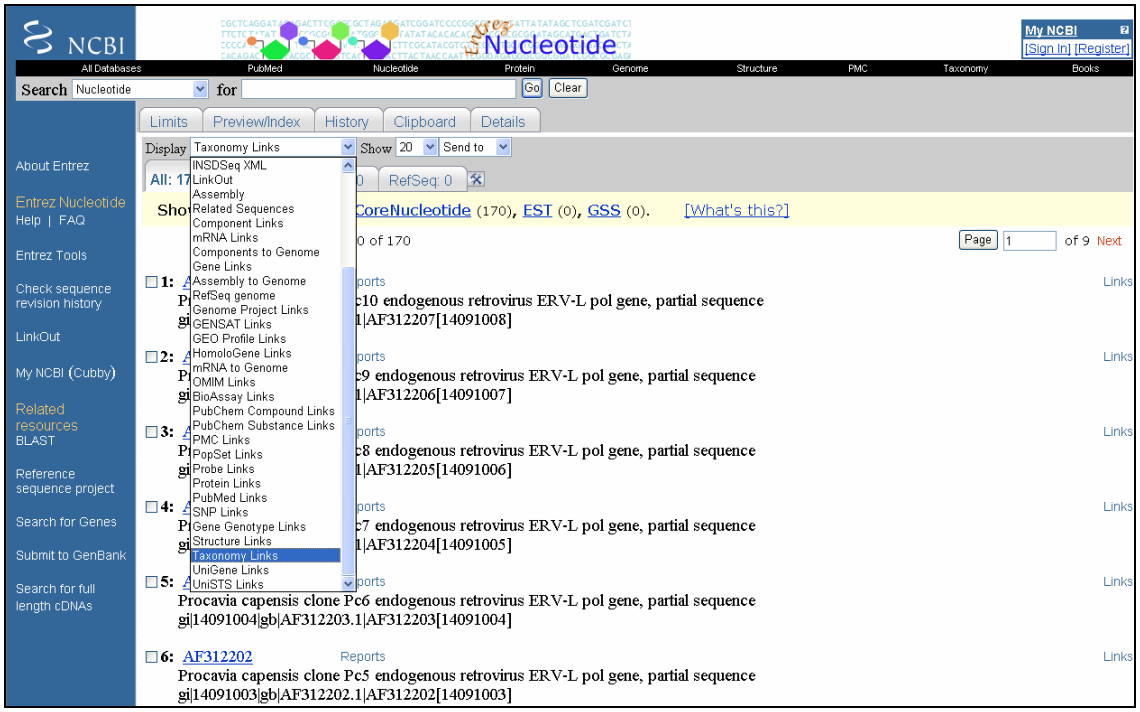
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mRNA to Genome
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BioAssay Links
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PMC Links
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Probe Links
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Procavia capensis clone Pc6 endogenous retrovirus ERV-L pol gene, partial sequence
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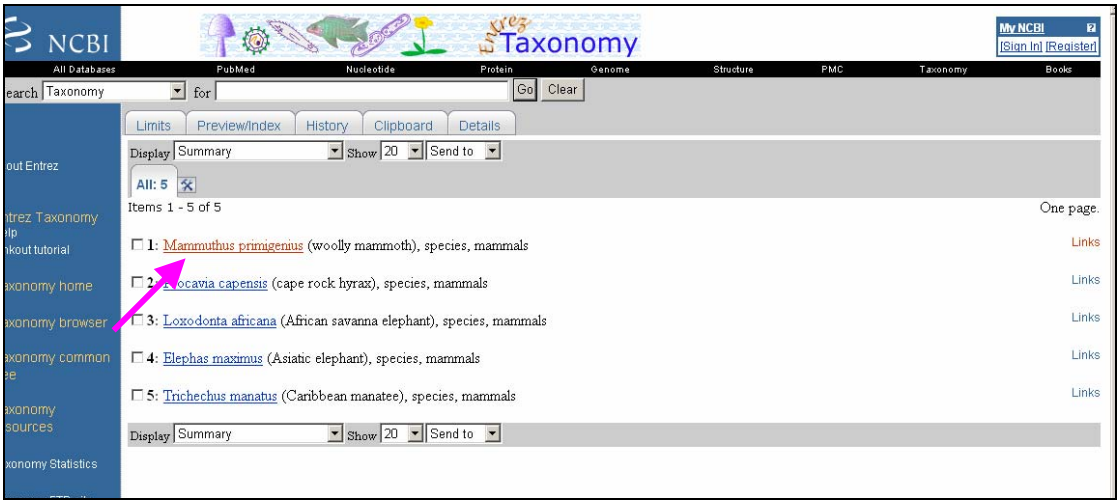
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Items 1 - 5 of 5
One page.
1: Mammuthus primigenius (woolly mammoth), species, mammals Links
2: Procavia capensis (cape rock hyrax), species, mammals Links
3: Loxodonta africana (African savanna elephant), species, mammals Links
4: Elephas maximus (Asiatic elephant), species, mammals Links
5: Trichechus manatus (Caribbean manatee), species, mammals Links
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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	131
Protein	76
Genome Sequences	1
Genome Projects	1
Popset	5
PubMed Central	8
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	302,692	302,692
Total	302,692	**302,692**

External Information Resources (NCBI LinkOut)

LinkOut	Subject	LinkOut Provider
Mammuthus primigenius	taxonomy/phylogenetic	Global Biodiversity Information Facility
Mammuthus primigenius taxonomy	taxonomy/phylogenetic	University of Alaska Museum

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]	

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Display 3 levels using filter: none
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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
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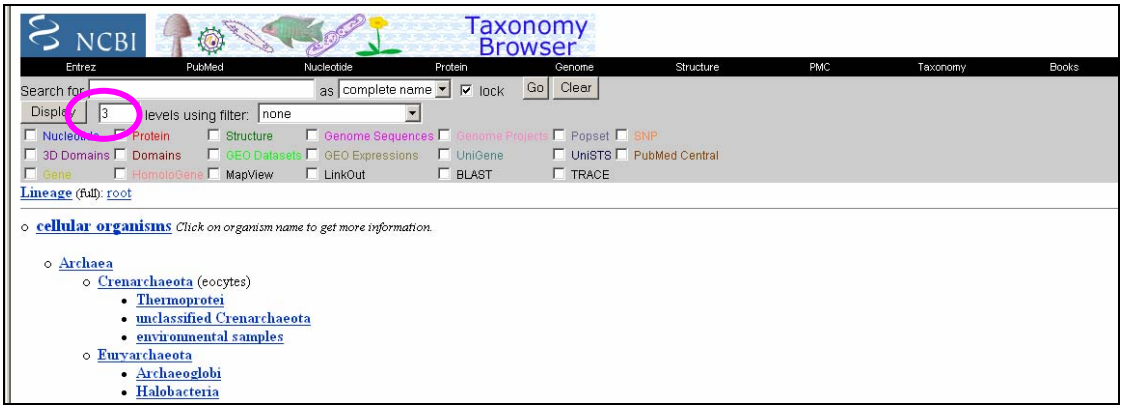
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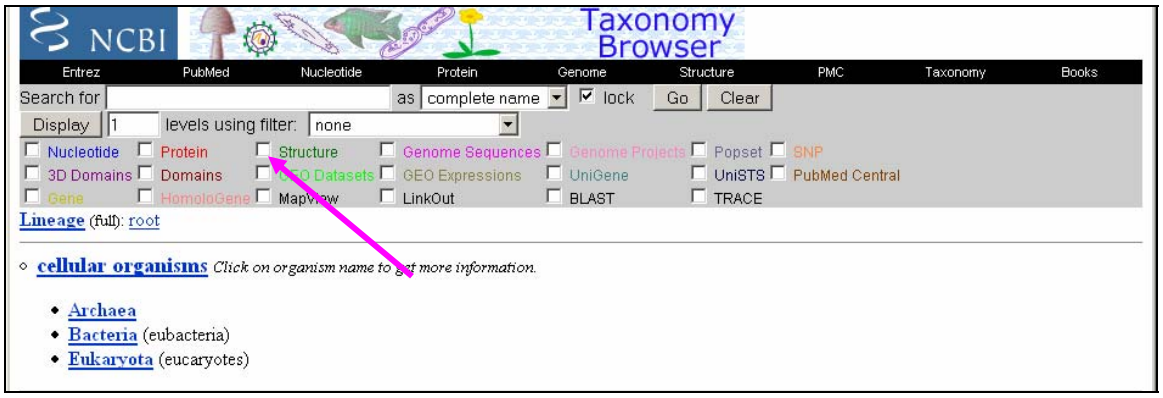
Lineage (full): root
cellular organisms Click on organism name to get more information.
Archaea
Crenarchaeota (eocytes)
Thermoprotei
unclassified Crenarchaeota
environmental samples
Euryarchaeota
Archaeoglobi
Halobacteria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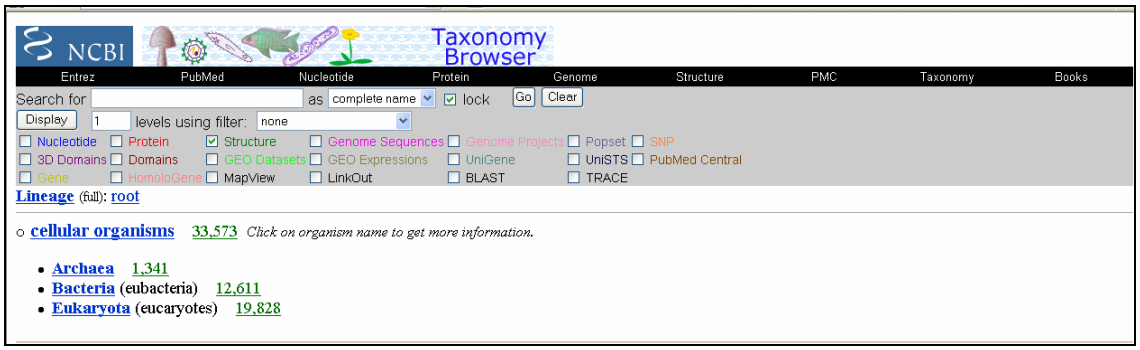
3D Domains Domains GEO Datasets GEO Expressions UniGene UniSTS PubMed Central
Gene HomoloGene MapView LinkOut BLAST TRACE
Lineage (full): root
cellular organisms Click on organism name to get more information.
Archaea
Bacteria (eubacteria)
Eukaryota (eucaryotes)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Lineage (full): root
cellular organisms 33,573 Click on organism name to get more information.
Archaea 1,341
Bacteria (eubacteria) 12,611
Eukaryota (eucaryotes) 19,828

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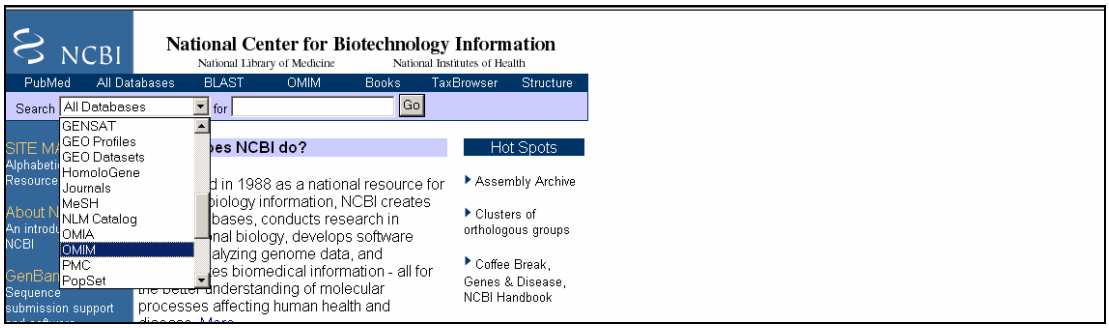
Archaea 1,341
Bacteria (eubacteria) 12,611
Eukaryota (eucaryotes) 19,828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Assembly Archive
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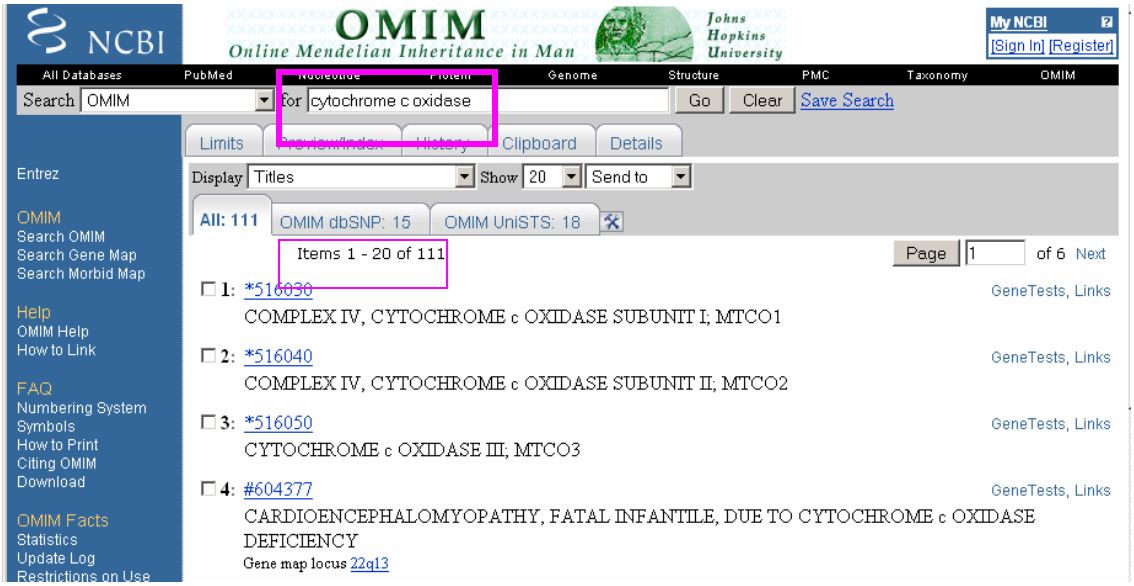
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CYTOCHROME c OXIDASE III; MTCO3
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CARDIOENCEPHALOMYOPATHY, FATAL INFANTILE, DUE TO CYTOCHROME c OXIDASE DEFICIENCY
Gene map locus 22q13

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COMPLEX IV, CYTOCHROME c OXIDASE SUBUNIT I; MTCO1

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CYTOCHROME c OXIDASE III; MTCO3

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COMPLEX IV, CYTOCHROME c OXIDASE SUBUNIT II; MTCO2

4: #604377 GeneTests, Links
CARDIOENCEPHALOMYOPATHY, FATAL INFANTILE, DUE TO CYTOCHROME c OXIDASE DEFICIENCY
Gene map locus 22q13

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Clinical Synopsis

Entrez Gene
Nomenclature
RefSeq
GenBank
Protein

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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.

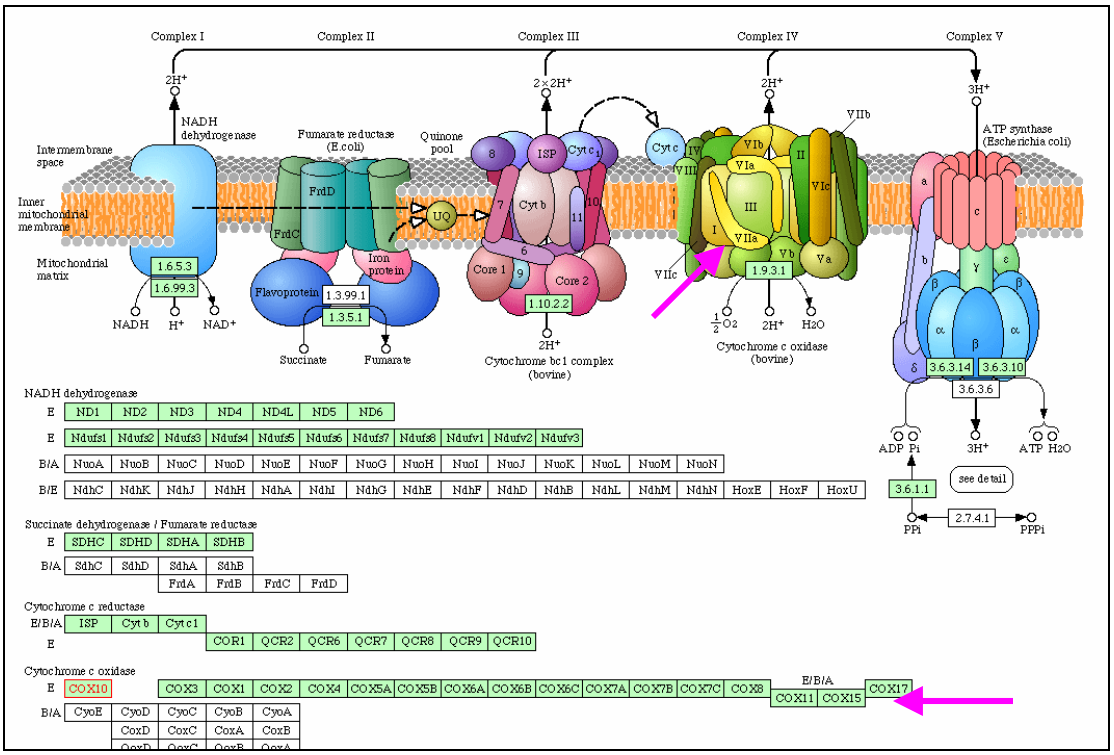

Figure from KEGG **Oxidative phosphorylation - Reference pathway (KO)**
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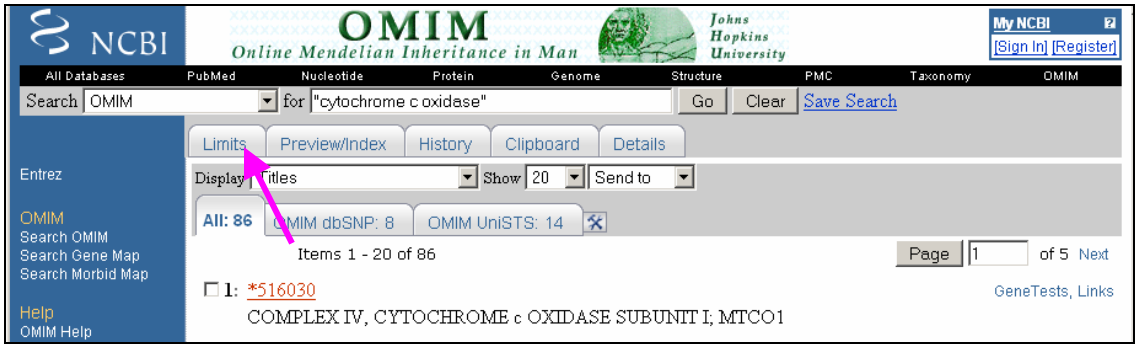

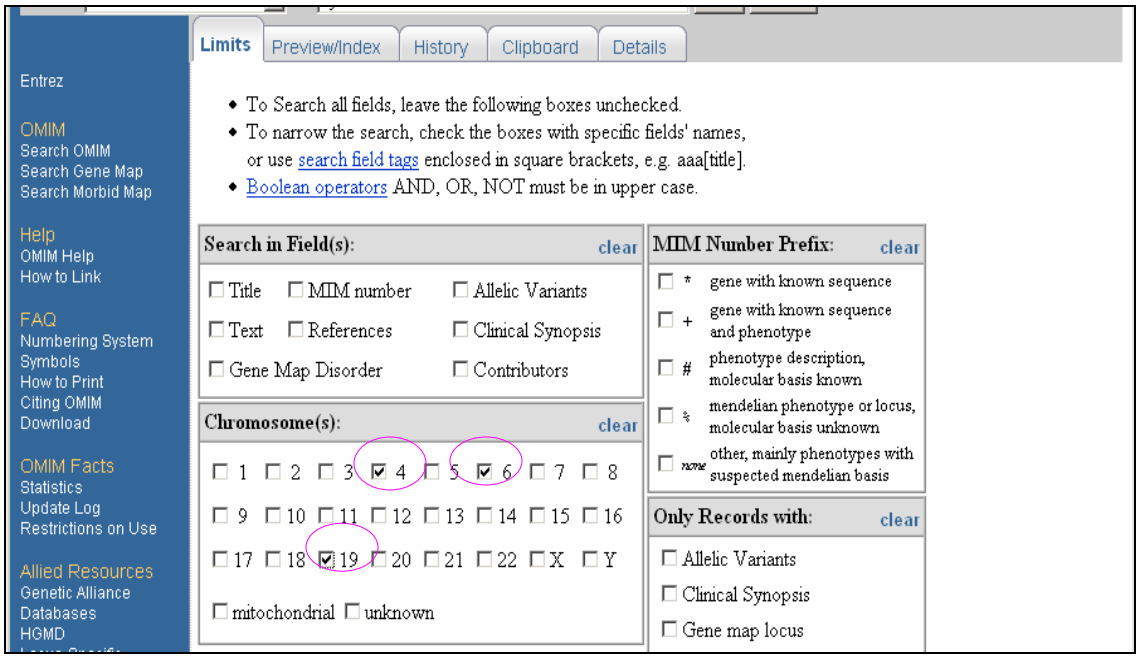
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+ gene with known sequence and phenotype
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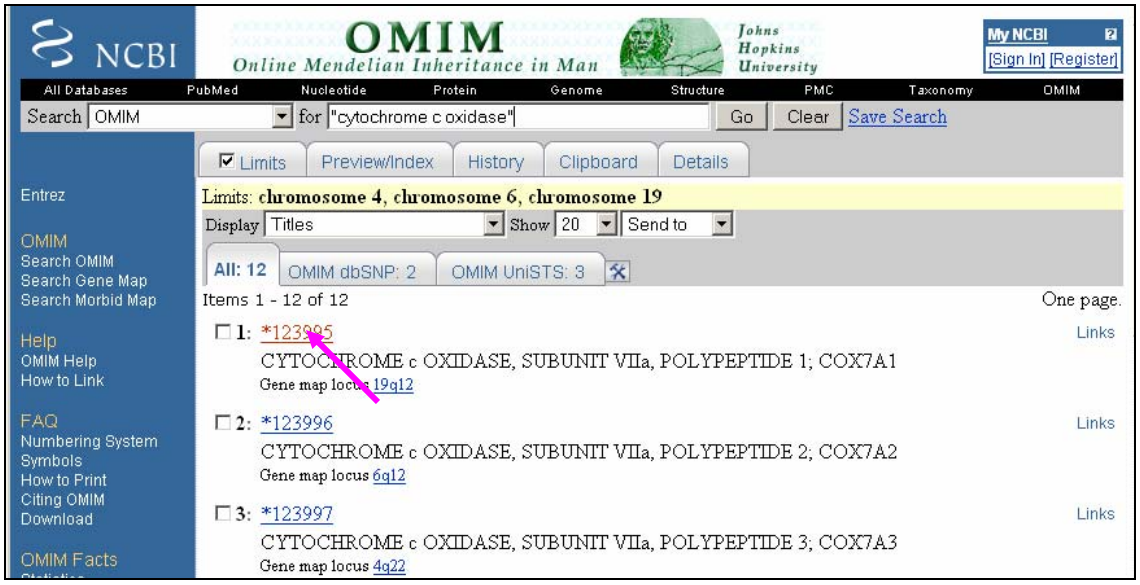
Allelic Variants
Clinical Synopsis
Gene map locus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Gene map locus 19q12
2: *123996
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CYTOCHROME c OXIDASE, SUBUNIT VIIa, POLYPEPTIDE 2; COX7A2
Gene map locus 6q12
3: *123997
Links
CYTOCHROME c OXIDASE, SUBUNIT VIIa, POLYPEPTIDE 3; COX7A3
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Limits: chromosome 4, chromosome 6, chromosome 19

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Gene map locus 19q12

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Gene map locus 19q13.1

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MIM *123995
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Cloning
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Mapping
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Contributors
Creation Date
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Gene map

Entrez Gene
N Nomenclature
R RefSeq
G GenBank
P Protein
U UniGene

LinkOut

*123995
CYTOCHROME c OXIDASE, SUBUNIT VIIa, POLYPEPTI

Links
Gene
GEO Profiles
HomoloGene
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PubMed (calculated)
PubMed (cited)
Gene Genotype
GeneView in dbSNP
UniGene
Related Entries
Nucleotide
Protein
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Alternative titles; symbols

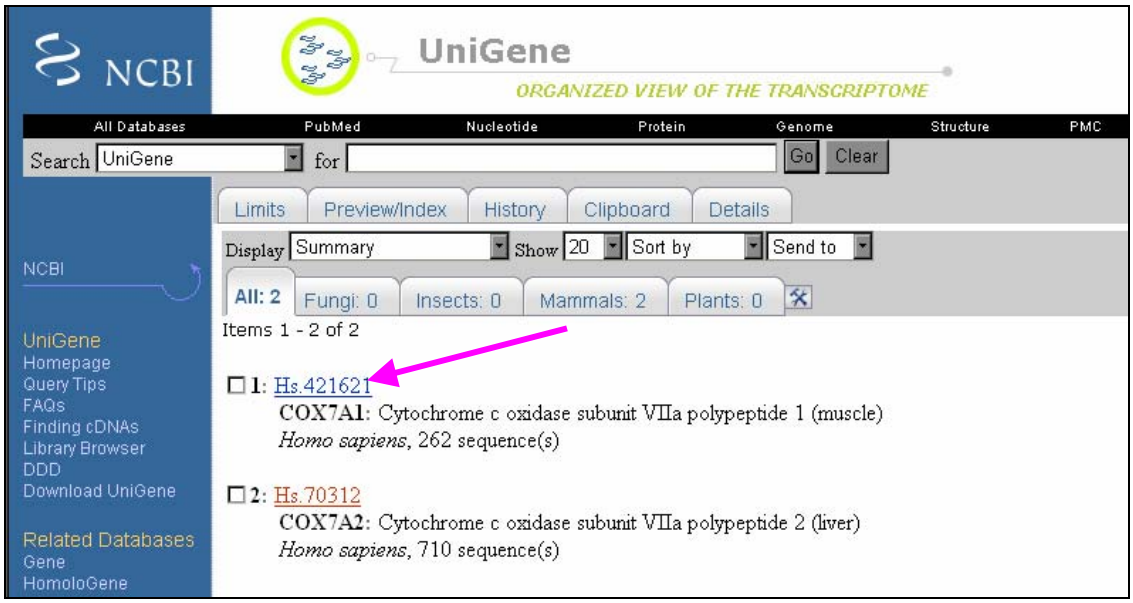
CYTOCHROME c OXIDASE, SUBUNIT VIIa, MUSCLE ISOFORM

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.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Mammals: 2
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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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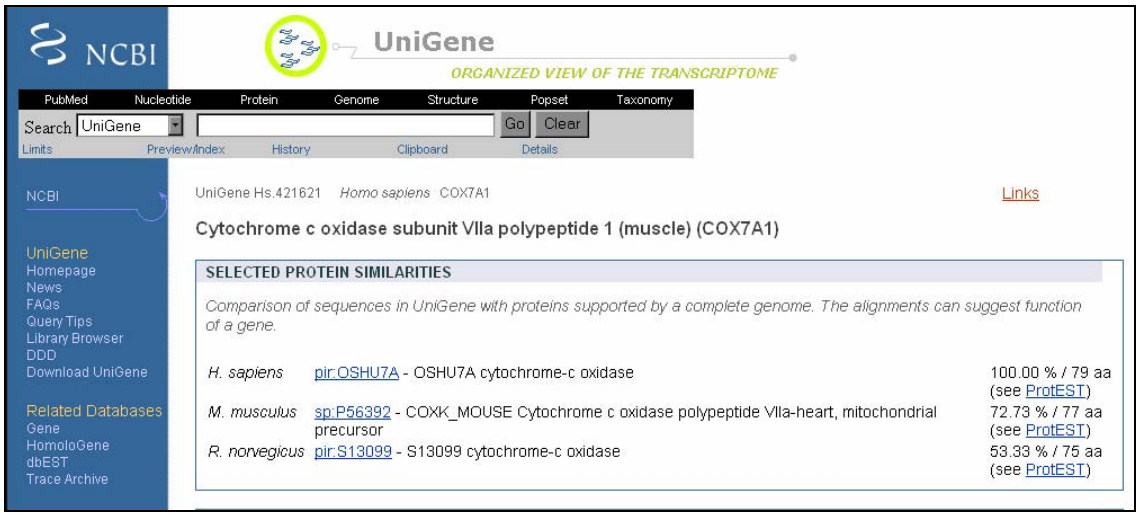
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UniGene Hs.421621 Homo sapiens COX7A1
Links
Cytochrome c oxidase subunit VIIa polypeptide 1 (muscle) (COX7A1)
SELECTED PROTEIN SIMILARITIES
Comparison of sequences in UniGene with proteins supported by a complete genome. The alignments can suggest 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]

Breakdown by Tissue

	Hs.421621	
blood	0	0 / 111420
bone	13	1 / 72260
bone marrow	0	0 / 48827
brain	9	9 / 933463
connective tissue	0	0 / 107437
adipose tissue	0	0 / 13879
ear	0	0 / 16691
liver	0	0 / 209741
pancreas	13	3 / 219173
adrenal gland	0	0 / 31066
parathyroid	143	3 / 20837
thyroid	18	1 / 54920
pituitary gland	171	3 / 17477
placenta	0	0 / 296769
eye	24	5 / 207123
embryonic tissue	10	2 / 199222
abdominal cavity	0	0 / 40397
cervix	0	0 / 48034
ovary	0	0 / 106265
uterus	8	2 / 238763
prostate	71	11 / 154822
testis	0	0 / 348176
bladder	0	0 / 30298
kidney	28	6 / 212609
tongue	60	4 / 66626
larynx	0	0 / 30370
pharynx	0	0 / 14868
salivary gland	0	0 / 20411
heart	212	19 / 89584
lymph node	0	0 / 95317
lymph	0	0 / 44599
tonsil	0	0 / 17168
spleen	18	1 / 52804
thymus	0	0 / 73960
mammary gland	0	0 / 170913
muscle	1342	154 / 114677
lung	2	1 / 347374

NCBI ? UniGene ? EST Profile Viewer

Pubmed Nucleotide Protein Genome Structure Popset Taxonomy

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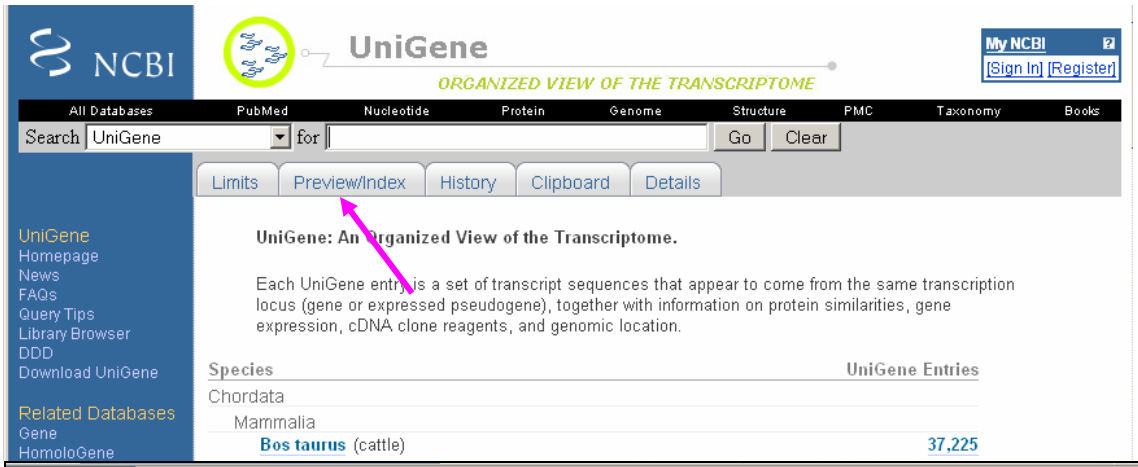
Limits Index History Details

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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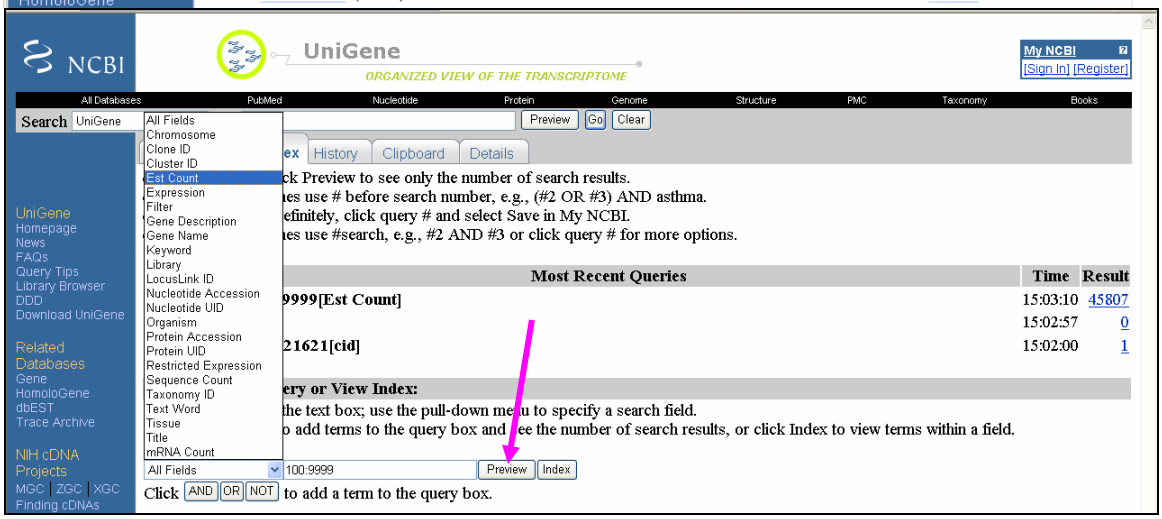
Each UniGene entry is a set of transcript sequences that appear to come from the same transcription locus (gene or expressed pseudogene), together with information on protein similarities, gene expression, cDNA clone reagents, and genomic location.
Species
UniGene Entries
Chordata
Mammalia
Bos taurus (cattle)
37,225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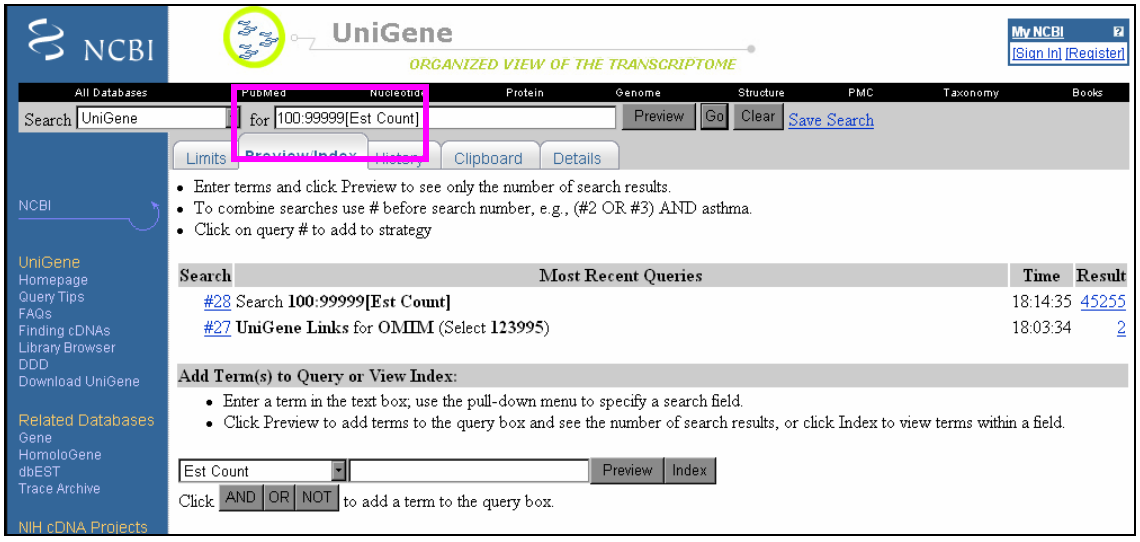
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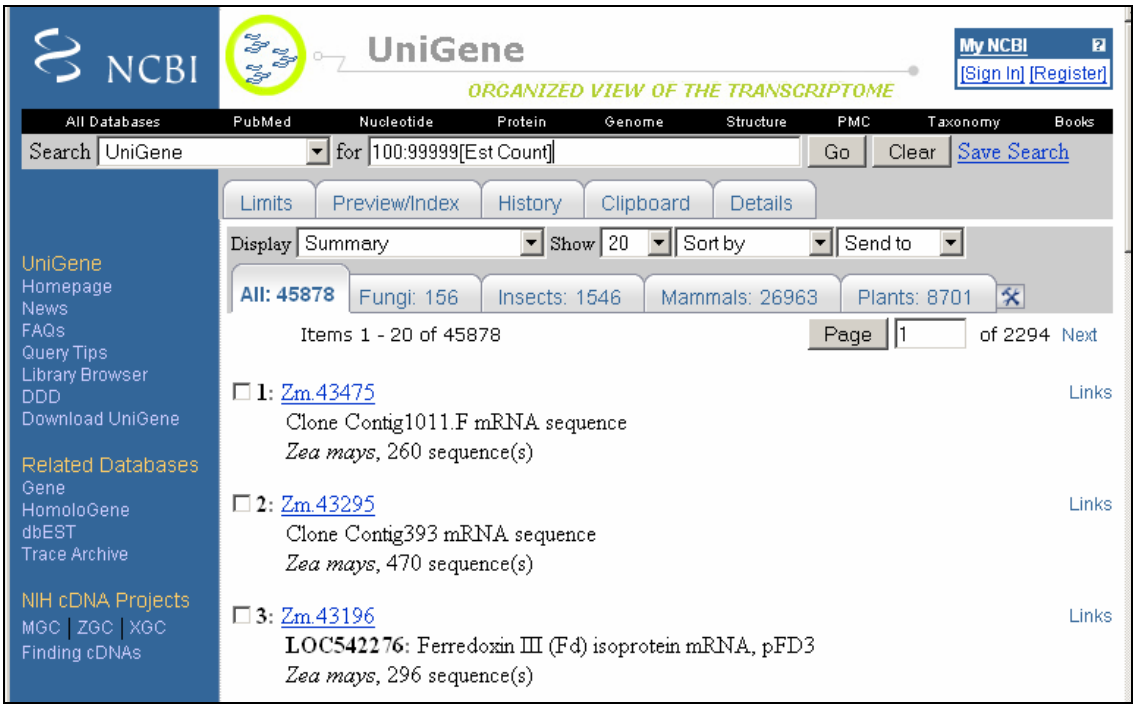
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Clone Contig393 mRNA sequence
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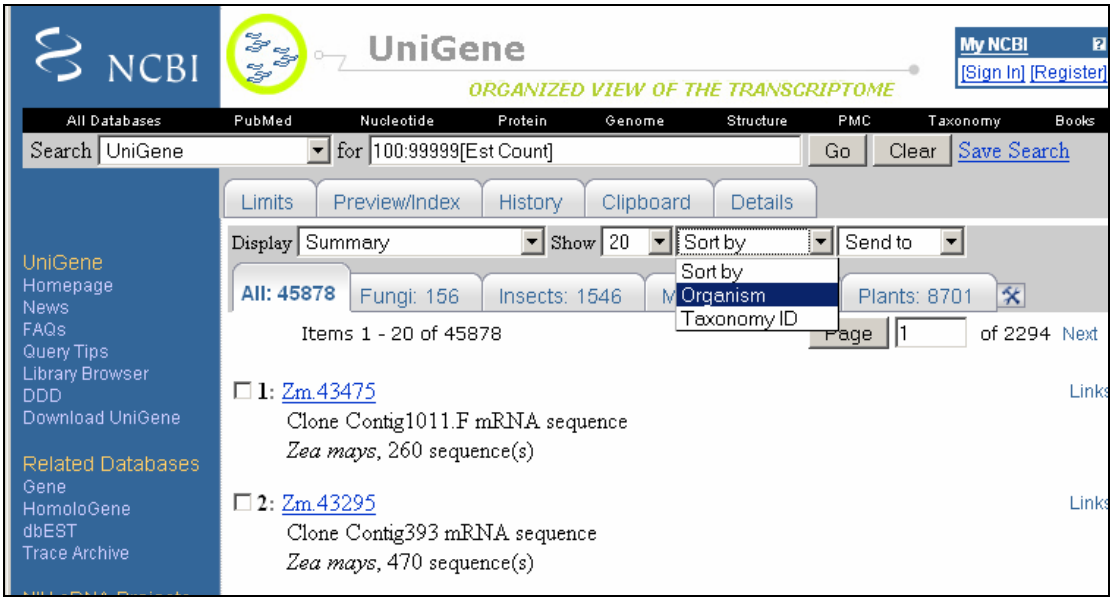
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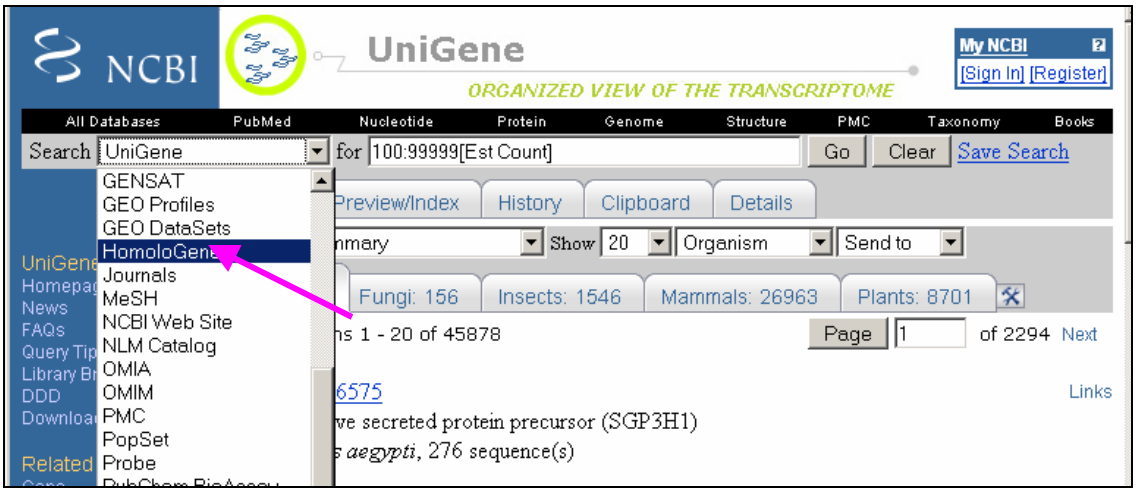
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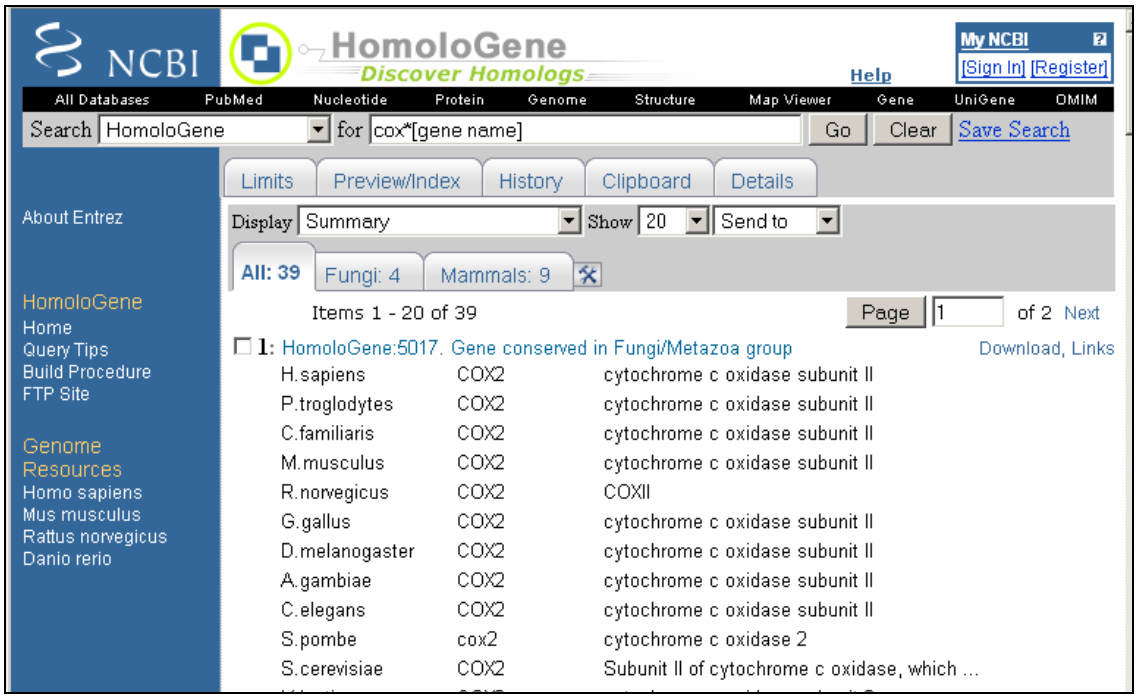
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G.gallus COX2 cytochrome c oxidase subunit II
D.melanogaster COX2 cytochrome c oxidase subunit II
A.gambiae COX2 cytochrome c oxidase subunit II
C.elegans COX2 cytochrome c oxidase subunit II
S.pombe cox2 cytochrome c oxidase 2
S.cerevisiae COX2 Subunit II of cytochrome c oxidase, which ...
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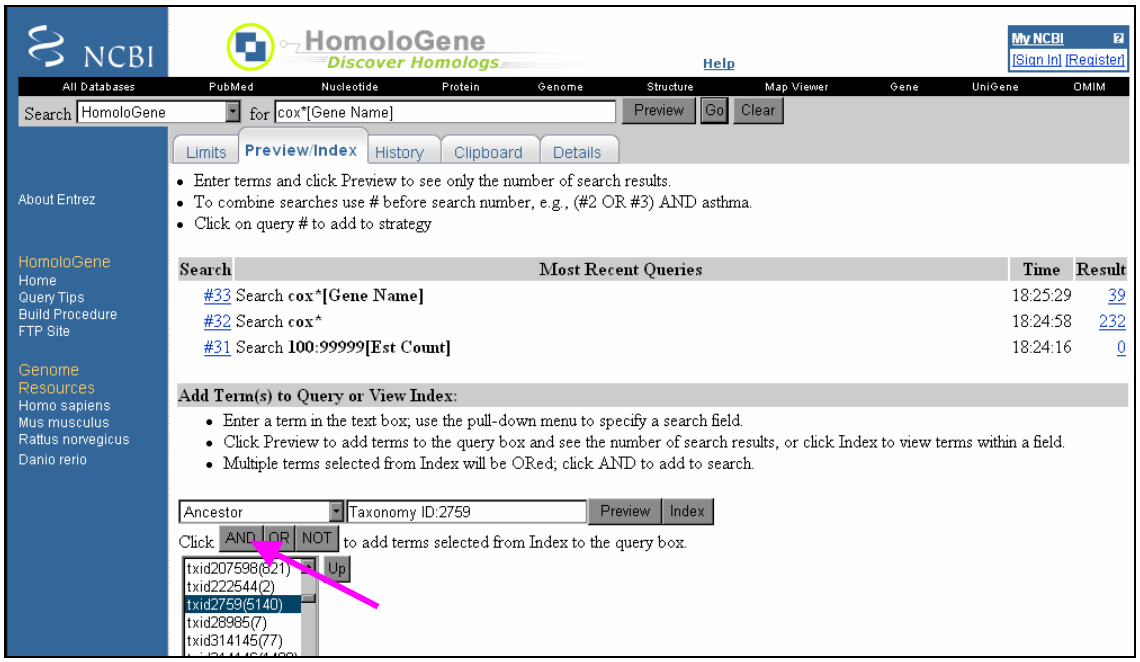
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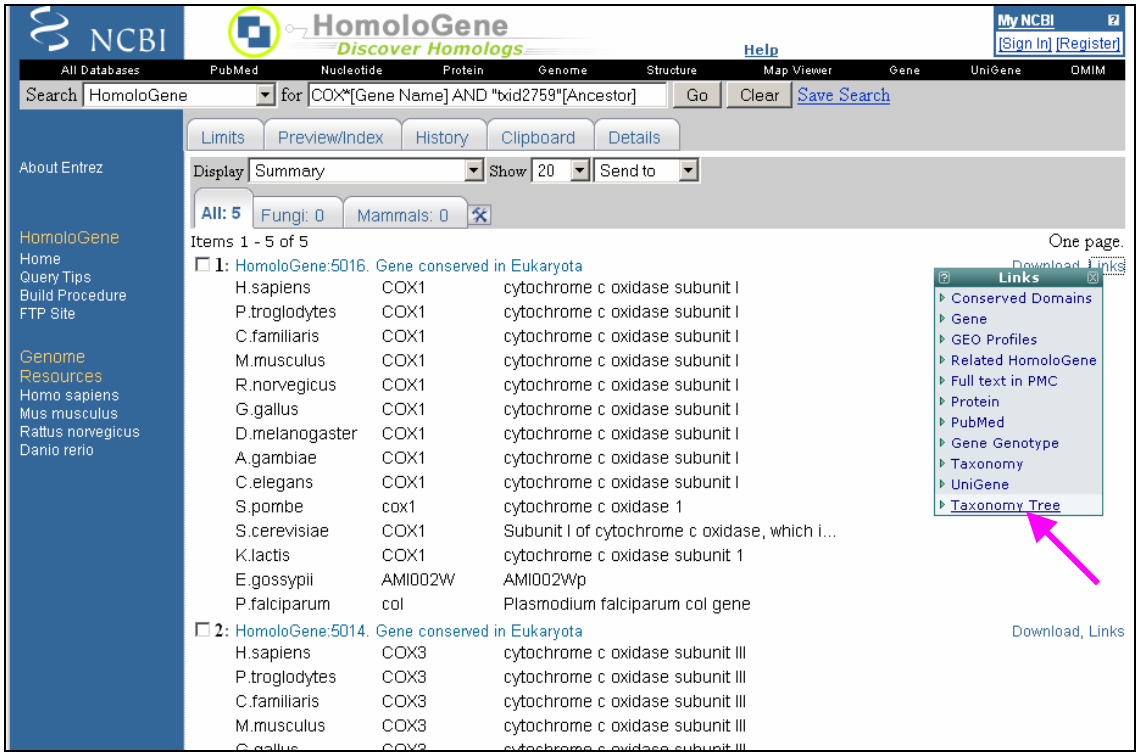
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H.sapiens COX1 cytochrome c oxidase subunit I
P.troglodytes COX1 cytochrome c oxidase subunit I
C.familiaris COX1 cytochrome c oxidase subunit I
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D.melanogaster COX1 cytochrome c oxidase subunit I
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 Subunit I of cytochrome c oxidase, which i...
K.lactis COX1 cytochrome c oxidase subunit 1
E.gossypii AMI002W AMI002Wp
P.falciparum cox1 Plasmodium falciparum cox1 gene
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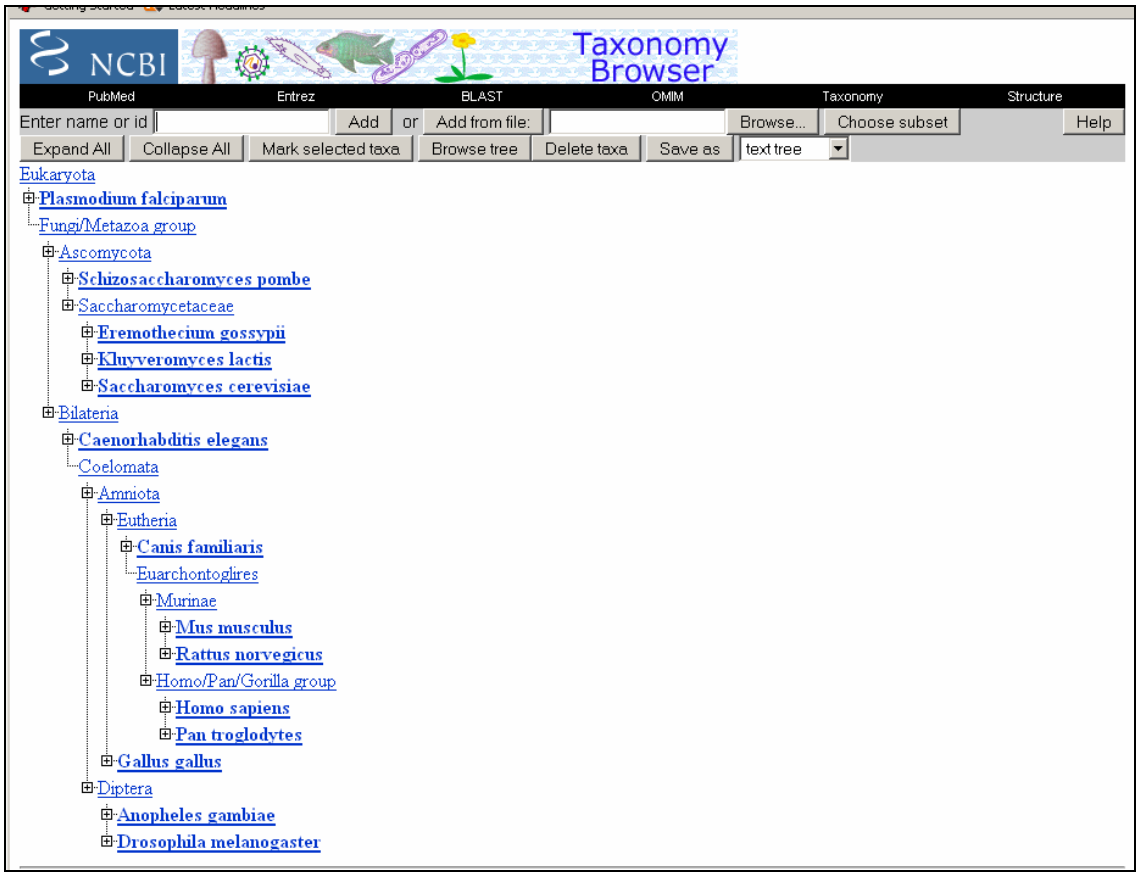
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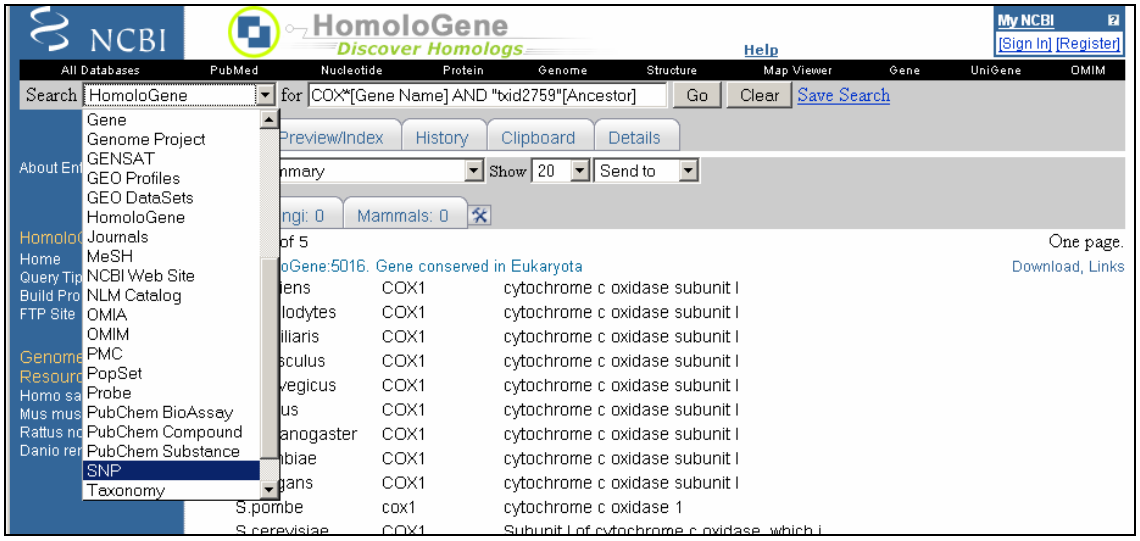
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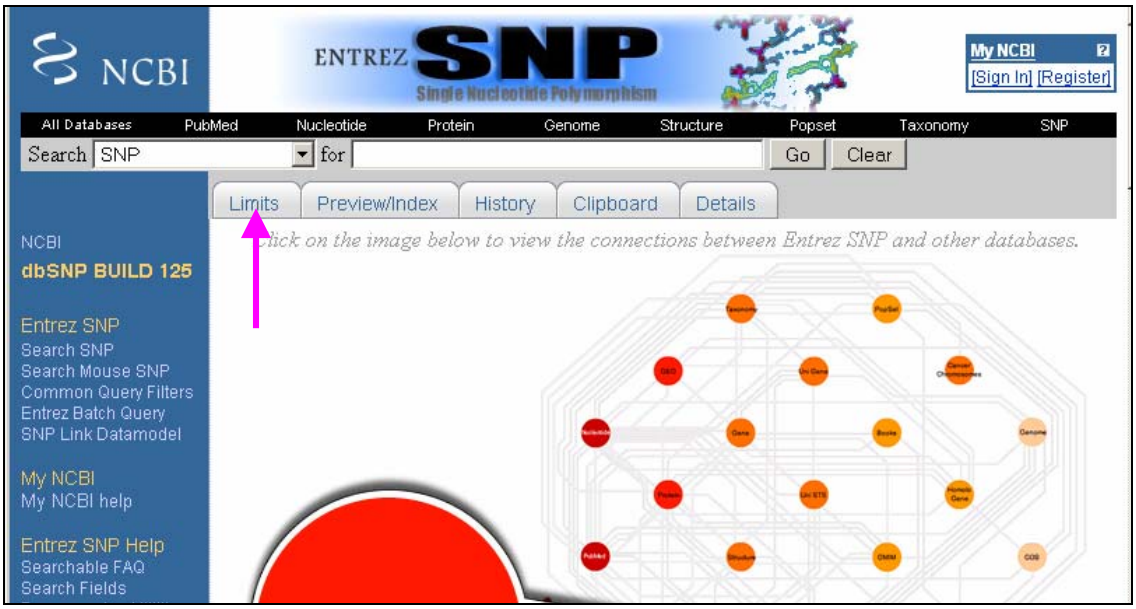
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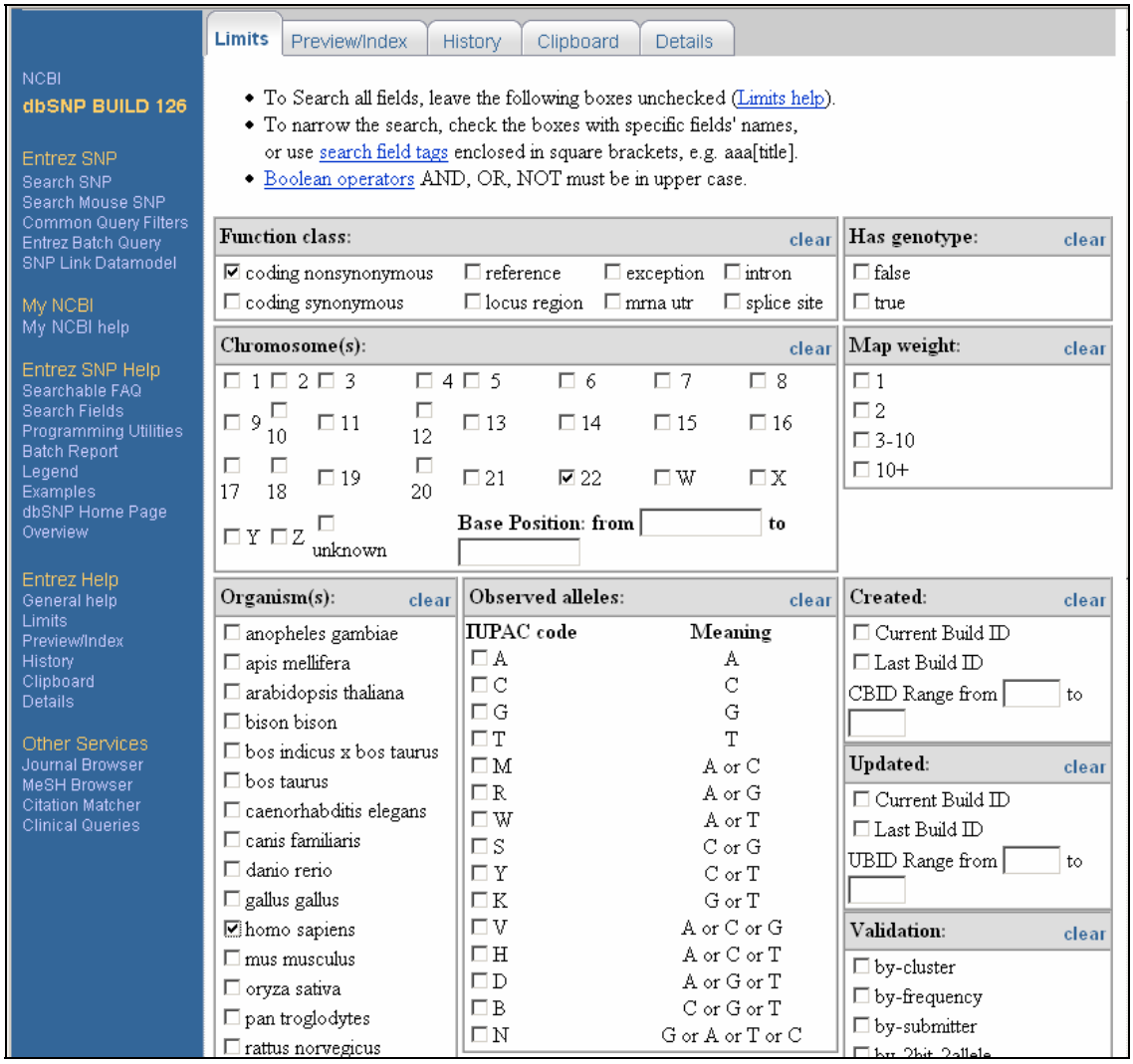
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coding nonsynonymous
coding synonymous
reference
locus region
exception
mrna utr
intron
splice site
Has genotype: clear
false
true
Chromosome(s): clear
1 2 3 4 5 6 7 8
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bison bison
bos indicus x bos taurus
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W A or T
S C or G
Y C or T
K G or T
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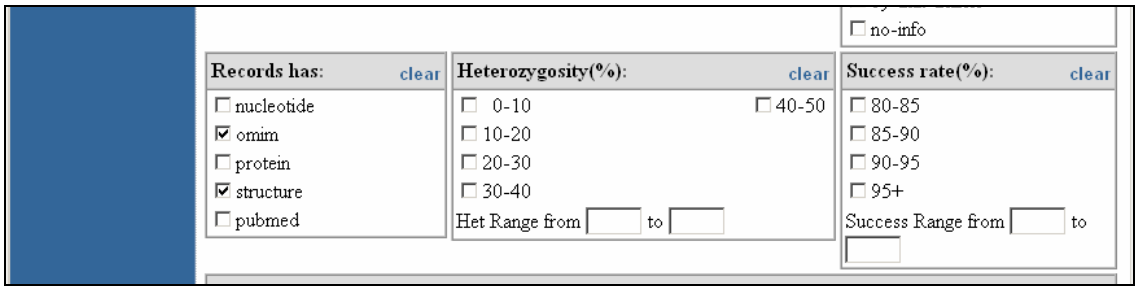
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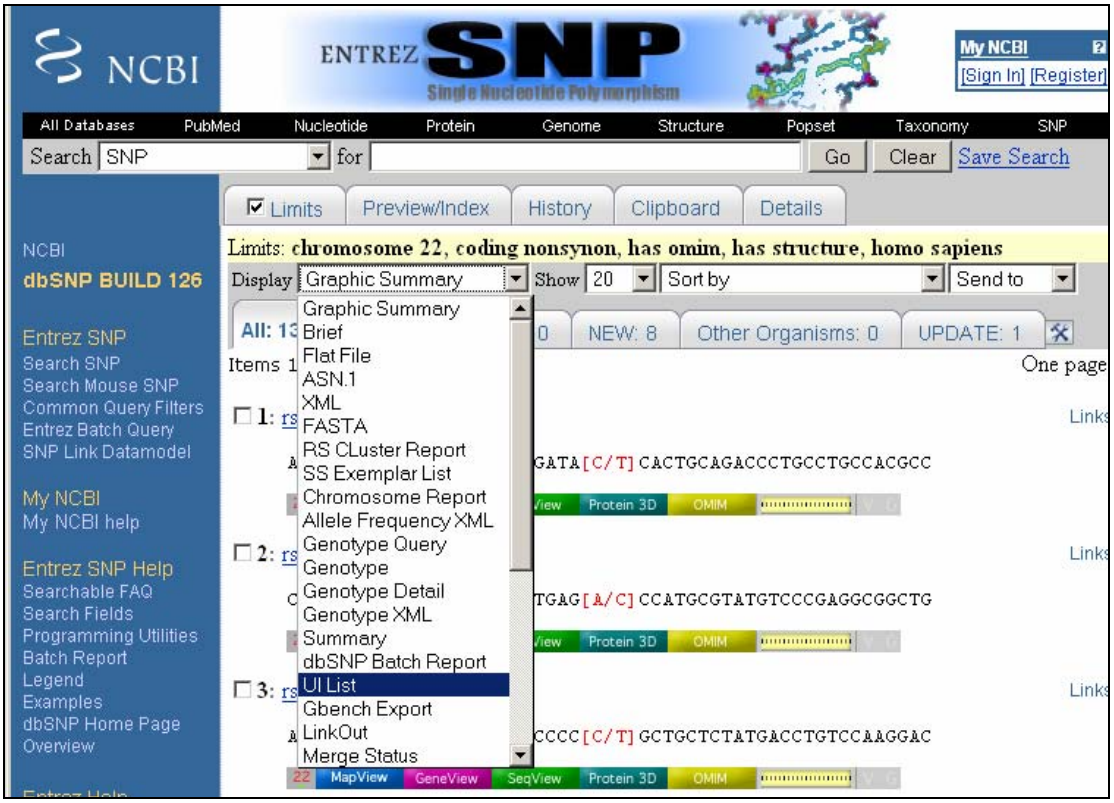
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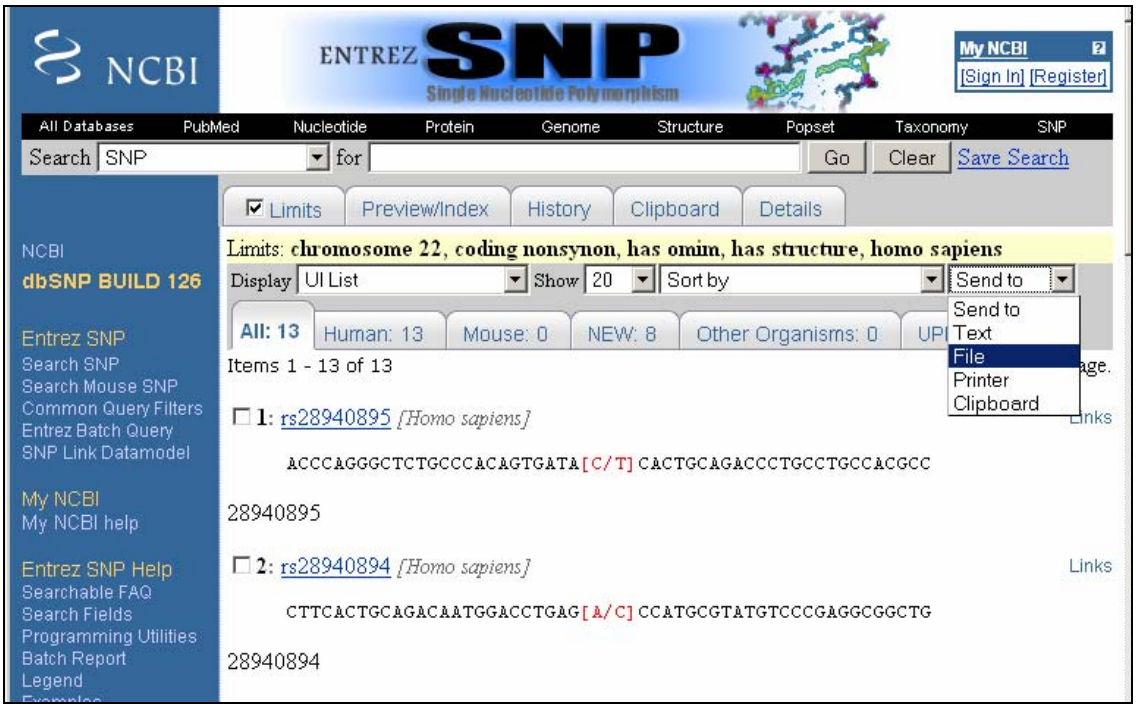
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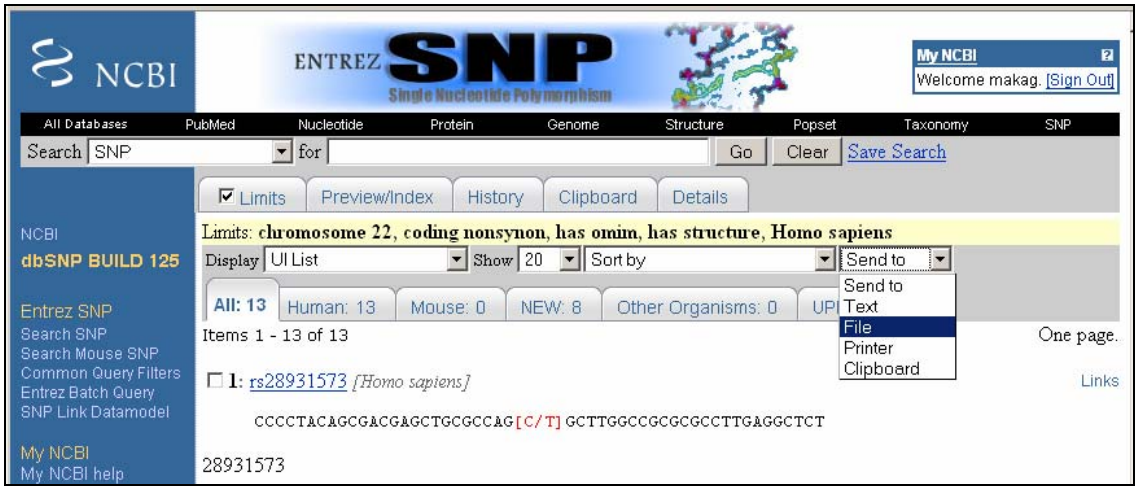
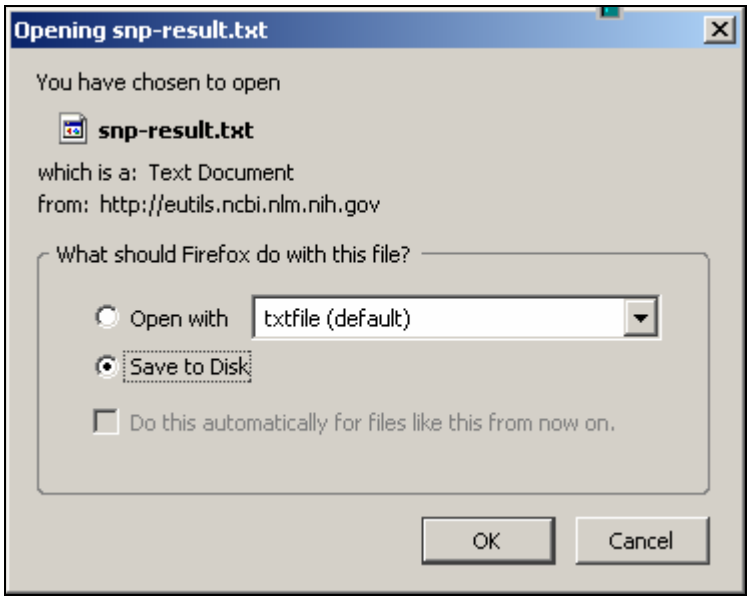
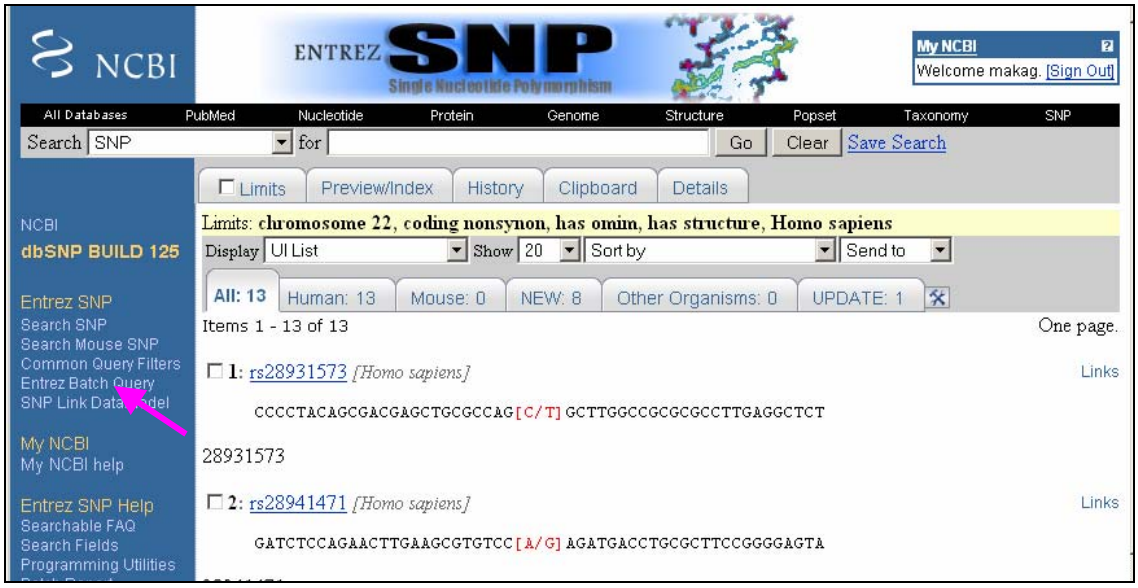
Batch Report
Legend


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 Save Search
Limits Preview/Index History Clipboard Details
NCBI
dbSNP BUILD 125
Limits: chromosome 22, coding nonsynon, has omim, has structure, Homo sapiens
Display UI List Show 20 Sort by Send to
Send to
Text
File
Printer
Clipboard
All: 13 Human: 13 Mouse: 0 NEW: 8 Other Organisms: 0
Entrez SNP
Search SNP
Search Mouse SNP
Common Query Filters
Entrez Batch Query
SNP Link Datamodel
Items 1 - 13 of 13
One page.
1: rs28931573 [Homo sapiens]
Links
CCCCTACAGCGACGAGCTGCGCCAG[C/T]GCTTGGCCGCGCGCCTTGAGGCTCT
28931573
My NCBI
My NCBI help


Opening snp-result.txt
You have chosen to open
snp-result.txt
which is a: Text Document
from: http://eutils.ncbi.nlm.nih.gov
What should Firefox do with this file?
Open with
txtfile (default)
Save to Disk
Do this automatically for files like this from now on.
OK
Cancel

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


NCBI
ENTREZ SNP
Single Nucleotide Polymorphism
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Search SNP for Go Clear Save Search
Limits Preview/Index History Clipboard Details
Limits: chromosome 22, coding nonsynon, has omim, has structure, Homo sapiens
Display UI List 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.
1: rs28931573 [Homo sapiens]
Links
CCCCTACAGCGACGAGCTGCGCCAG[C/T]GCTTGGCCGCGCGCCTTGAGGCTCT
28931573
2: rs28941471 [Homo sapiens]
Links
GATCTCCAGAACTTGAAGCGTGTCC[A/G]AGATGACCTGCGCTTCCGGGGAGTA
NCBI
dbSNP BUILD 125
Entrez SNP
Search SNP
Search Mouse SNP
Common Query Filters
Entrez Batch Query
My NCBI
My NCBI help
Entrez SNP Help
Searchable FAQ
Search Fields
Programming Utilities

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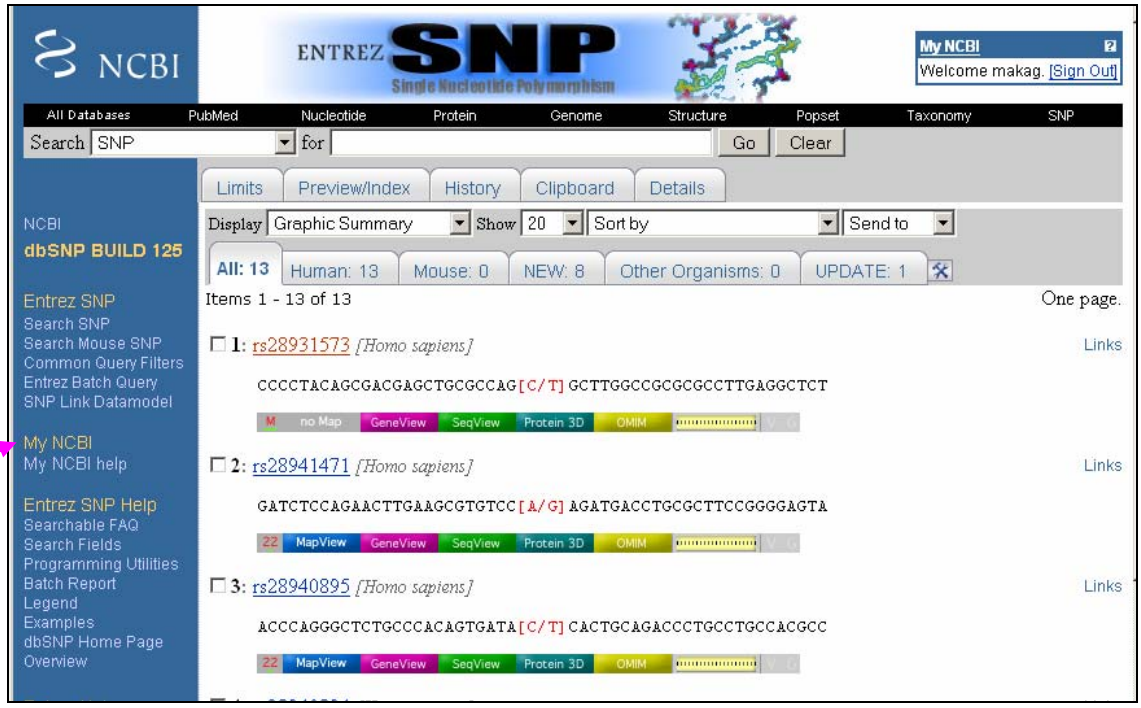
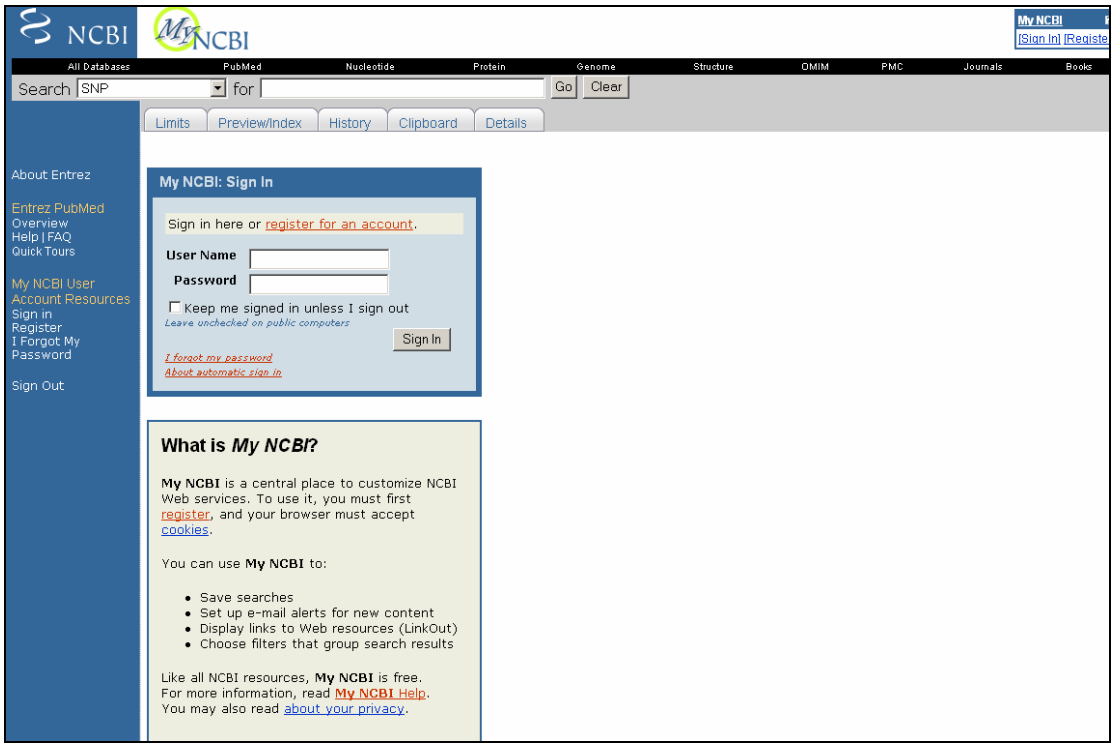
ENTREZ SNP
Single Nucleotide Polymorphism
My NCBI
[Sign In] [Register]
All Databases PubMed Nucleotide Protein Genome Structure Popset Taxonomy SNP
Database SNP
File: C:\Documents and Settings\gratia
Browse...
Retrieve
NCBI
dbSNP BUILD 125
Entrez SNP
Search SNP
Search Mouse SNP
Common Query Filters
Entrez Batch Query
SNP Link Datamodel
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.


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


NCBI
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All Databases PubMed Nucleotide Protein Genome Structure OMIM PMC Journals Books
Search SNP for Go Clear
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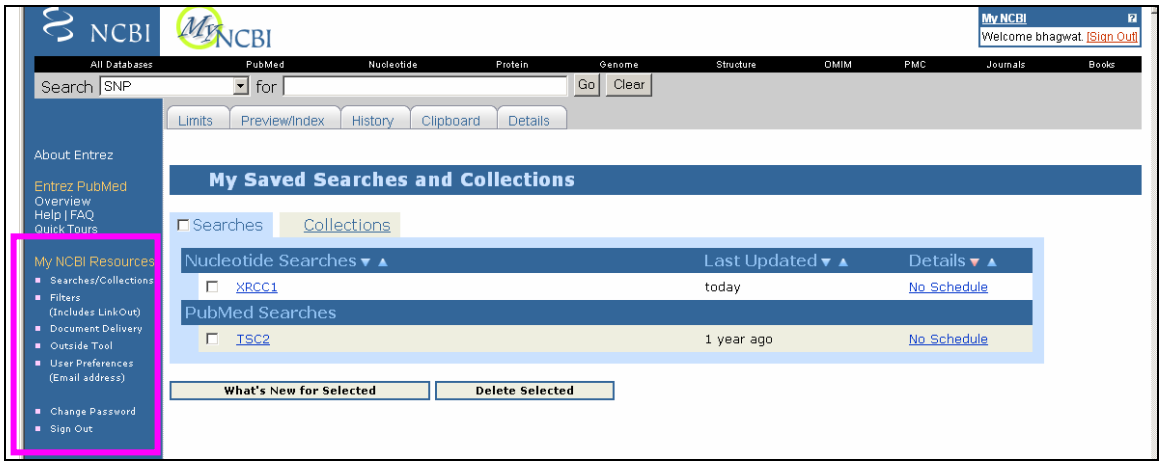
About Entrez
Entrez PubMed
Overview
Help | FAQ
Quick Tours
My NCBI User Account Resources
Sign in
Register
I Forgot My Password
Sign Out
My NCBI: Sign In
Sign in here or register for an account.
User Name
Password
Keep me signed in unless I sign out
Leave unchecked on public computers
Sign In
I forgot 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.


NCBI
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All Databases PubMed Nucleotide Protein Genome Structure OMIM PMC Journals Books
Search SNP for Go Clear
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About Entrez
Entrez PubMed
Overview
Help | FAQ
Quick Tours
My NCBI Resources
Searches/Collections
Filters (Includes LinkOut)
Document Delivery
Outside Tool
User Preferences (Email address)
Change Password
Sign Out
My Saved Searches and Collections
Searches
Collections
Nucleotide Searches
Last Updated
Details
XRCC1
today
No Schedule
PubMed Searches
TSC2
1 year ago
No Schedule
What's New for Selected
Delete Selected

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 using the Taxonomy link display. Go back and select the *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 APOL genes are clustered on chromosome 22? From the APOL1 (OMIM record 603743) link to the UniGene database. Examine the expression profile of the APOL1 gene focusing on the developmental stage.
Perform a search for those UniGene records with the expression restricted to "adult 17 years older". Combine the result of the search with the records that you have obtained through the OMIM link. Which 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 (use truncation and 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 homolog.

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. 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:
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Medha Bhagwat (bhagwat@ncbi.nlm.nih.gov)