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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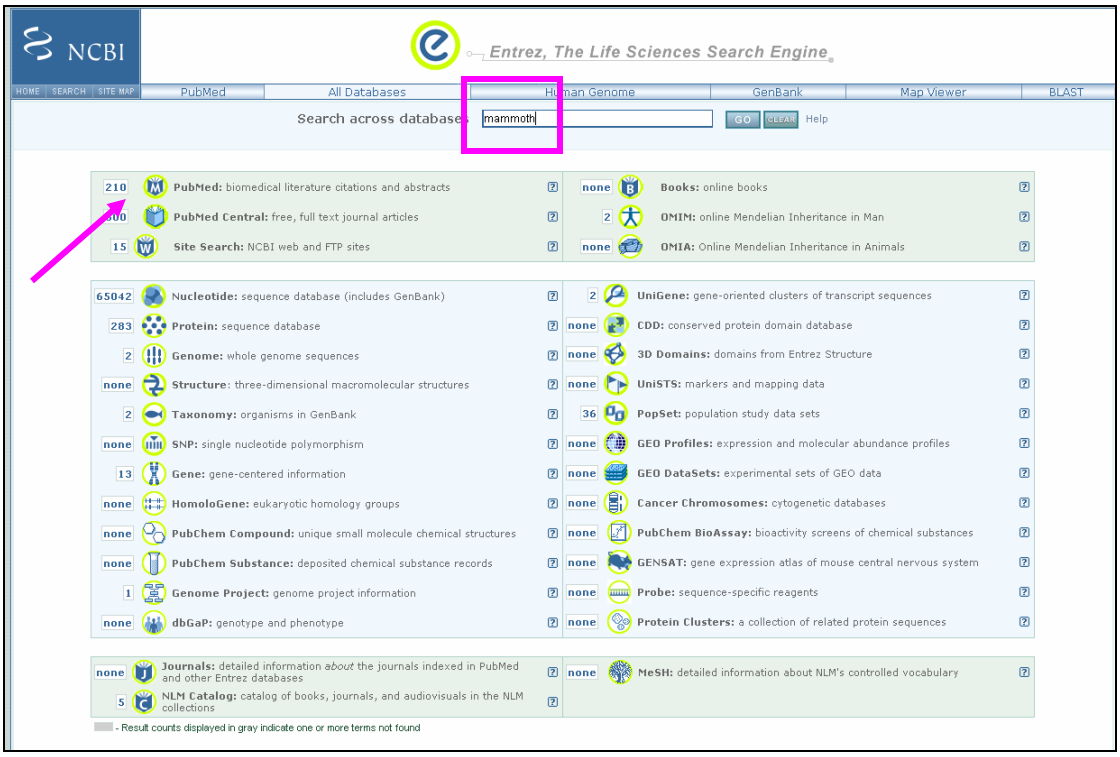
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13 Gene: gene-centered information
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1 Genome Project: genome project information
none dbGaP: genotype and phenotype
2 UniGene: gene-oriented clusters of transcript sequences
none CDD: conserved protein 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
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none GENSAT: gene expression atlas of mouse central nervous system
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Complete mitochondrial genome and phylogeny of Pleistocene Mammoth Mammuthus primigenius.

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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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DBAli tools: mining the protein structure space.
Nucleic Acids Res. 2007 Jul 1;35(Web Server issue):W393-7. Epub 2007 May 3.
PMID: 17478513 [PubMed - in process]

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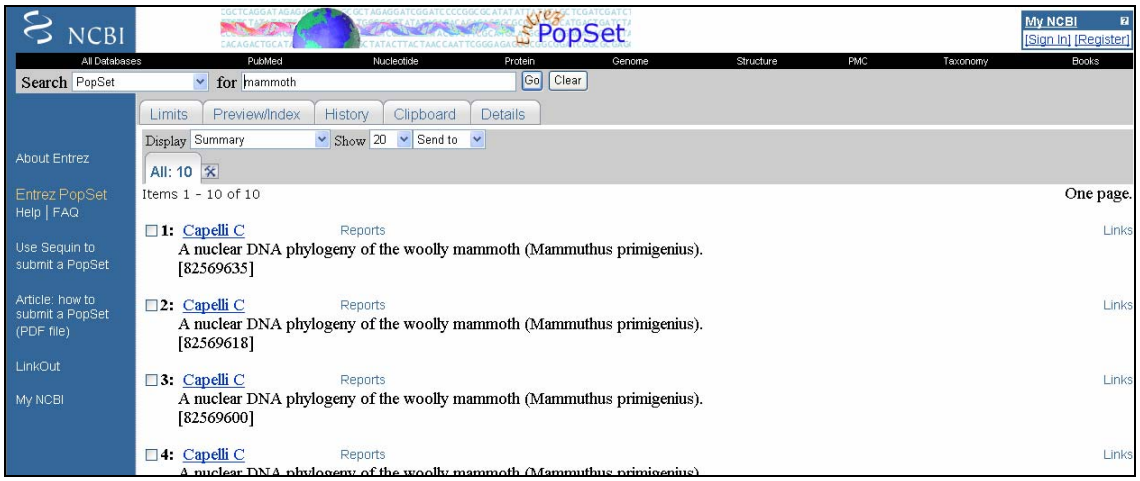
[Schizophrenia and culture: reality and perspectives based on the Tunisian experience]
Encephale. 2007 Jan-Feb;33(1):21-9. French.
PMID: 17457291 [PubMed - indexed for MEDLINE]

7: Orlando L, Pages M, Calvignac S, Hughes S, Hanni C. Related Articles, Links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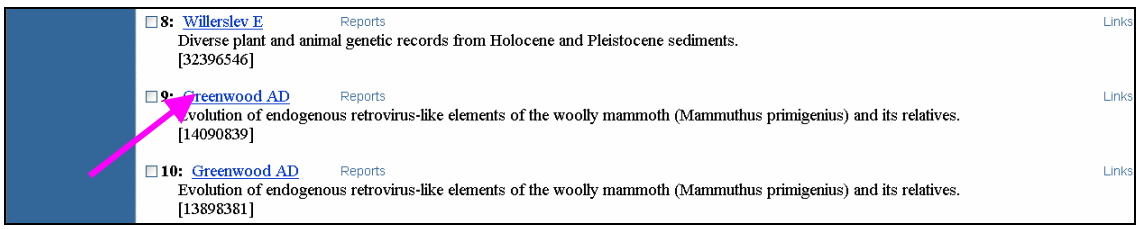
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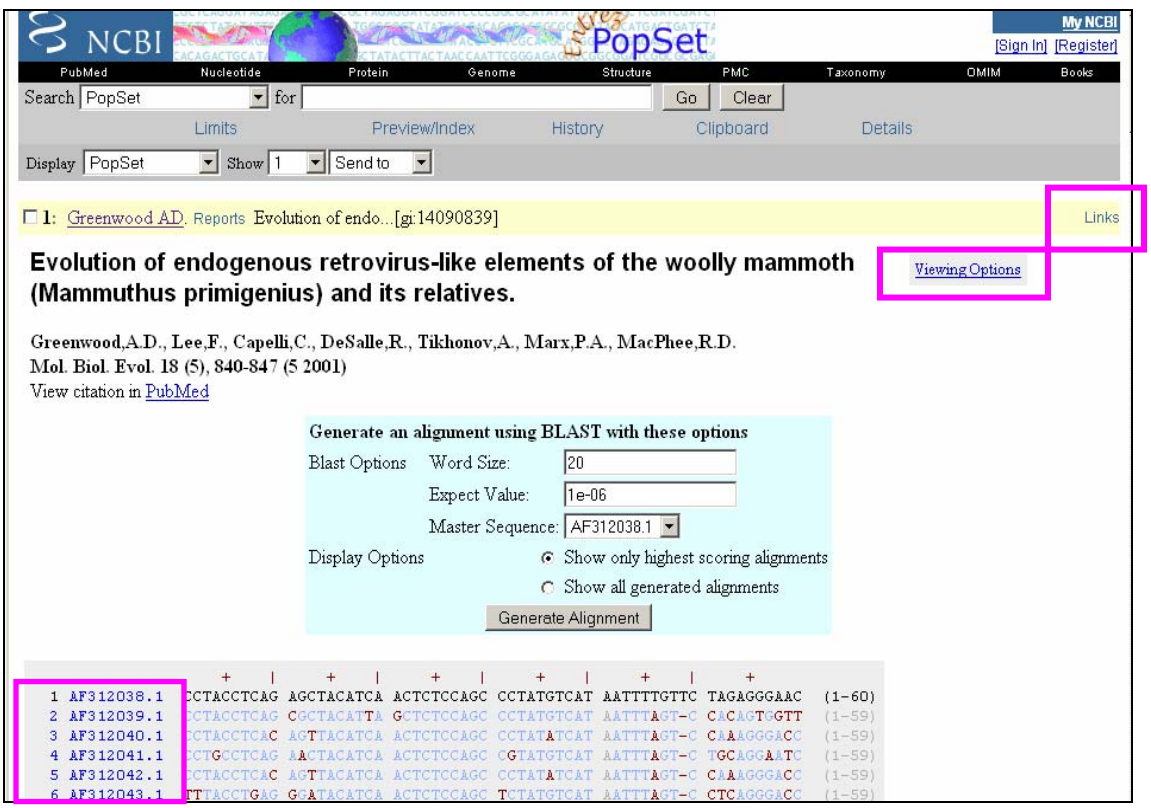
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Viewing Options
Greenwood,A.D., Lee,F., Capelli,C., DeSalle,R., Tikhonov,A., Marx,P.A., MacPhee,R.D.
Mol. Biol. Evol. 18 (5), 840-847 (5 2001)
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Expect Value: 1e-06
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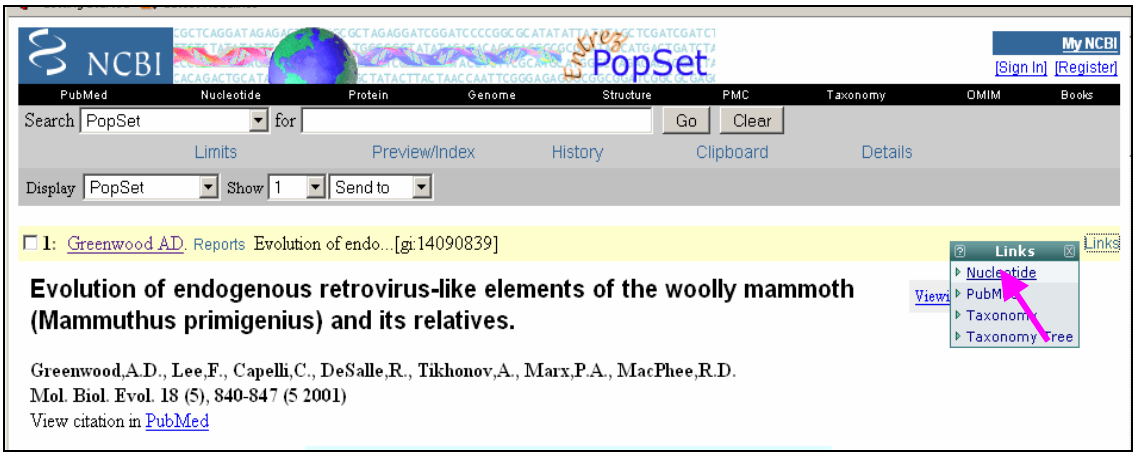
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1: Greenwood AD. Reports Evolution of endo...[gi:14090839]
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Evolution of endogenous retrovirus-like elements of the woolly mammoth (Mammuthus primigenius) and its relatives.
Greenwood,A.D., Lee,F., Capelli,C., DeSalle,R., Tikhonov,A., Marx,P.A., MacPhee,R.D.
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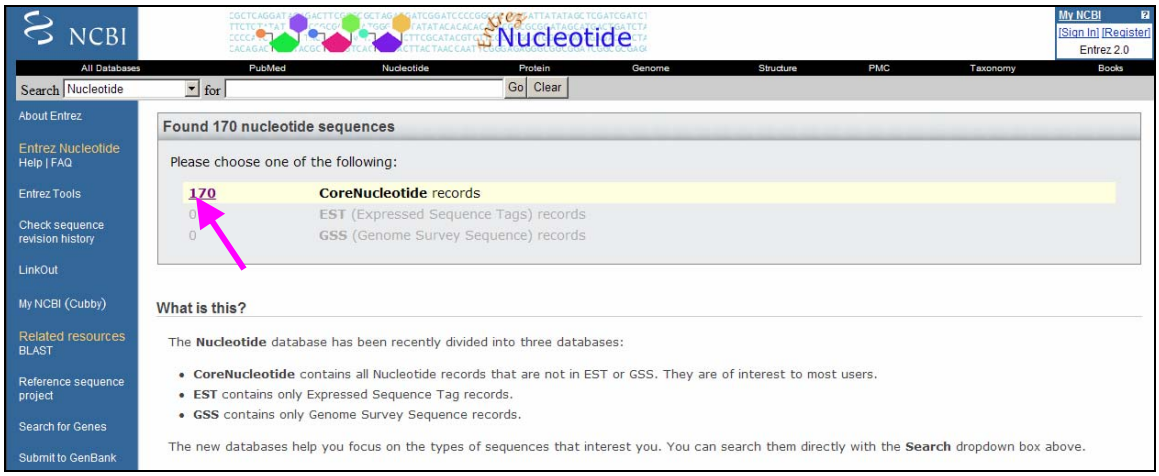
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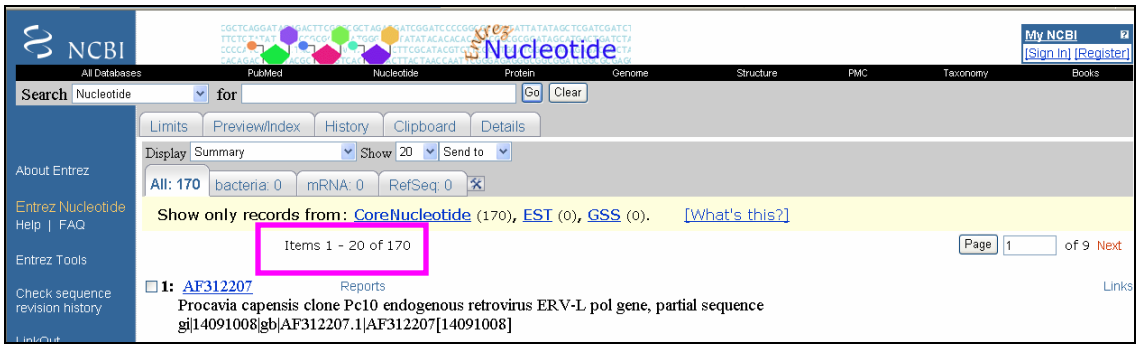
CoreNucleotide contains all Nucleotide records that are not in EST or GSS. They are of interest to most users.
EST contains only Expressed Sequence Tag records.
GSS contains only Genome Survey Sequence records.
The new databases help you focus on the types of sequences that interest you. You can search them directly with the Search dropdown box above.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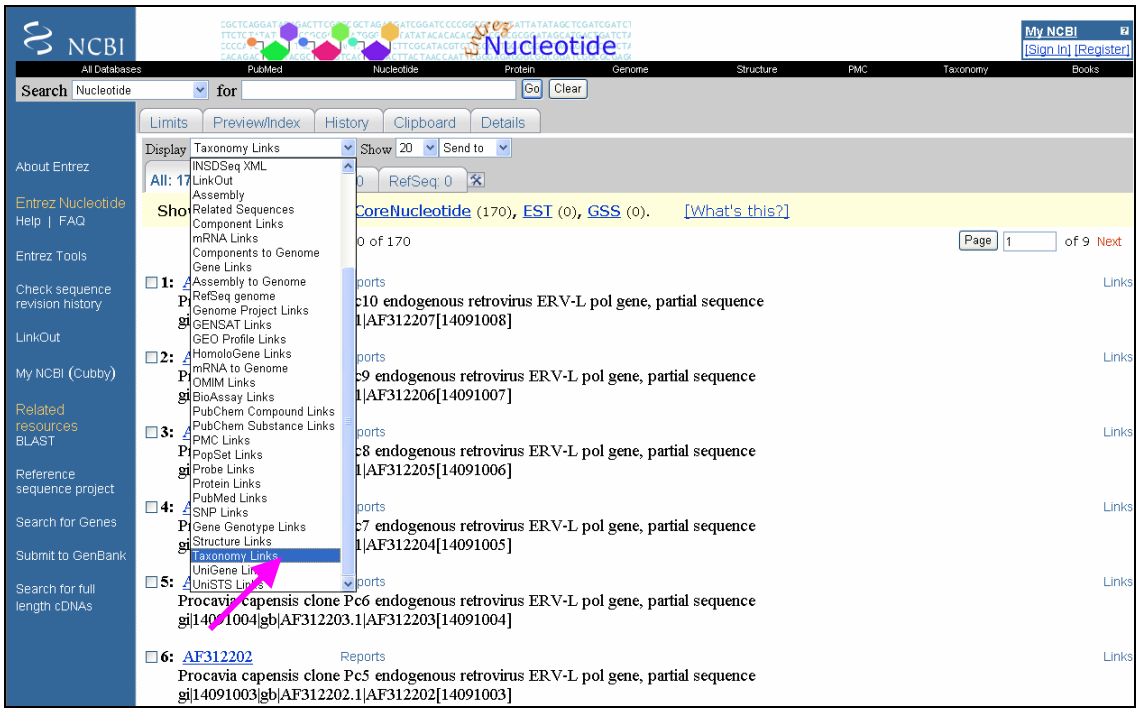
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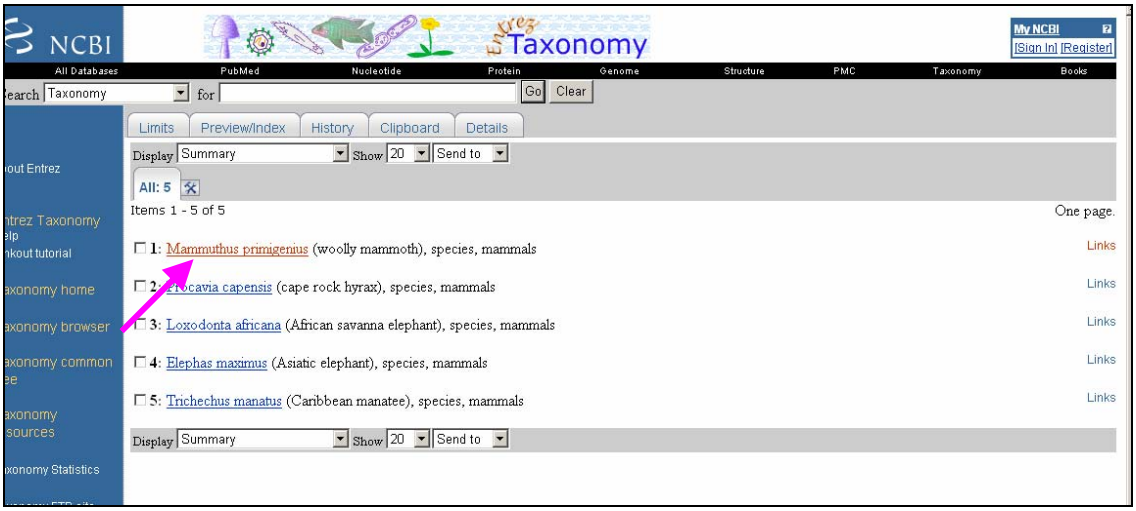
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1: Mammuthus primigenius (woolly mammoth), species, mammals Links
2: Procavia capensis (cape rock hyrax), species, mammals Links
3: Loxodonta africana (African savanna elephant), species, mammals Links
4: Elephas maximus (Asiatic elephant), species, mammals Links
5: Trichechus manatus (Caribbean manatee), species, mammals Links
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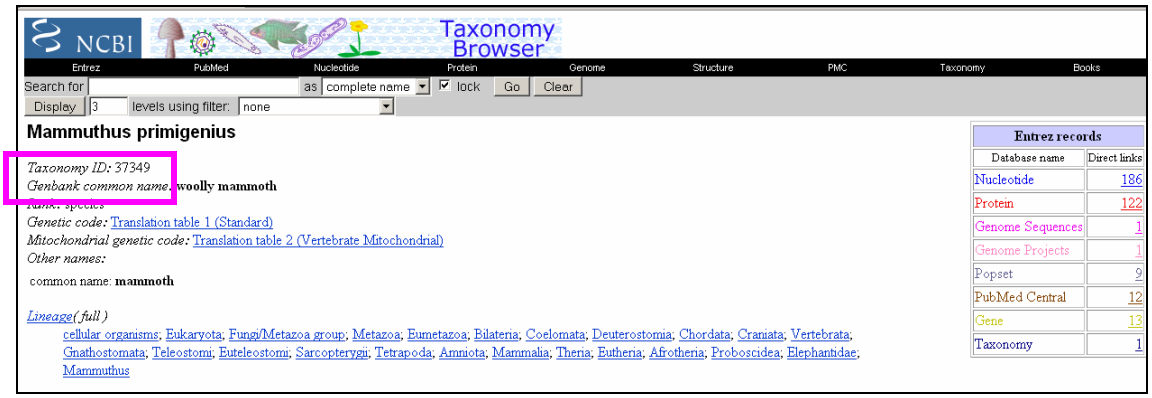
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Taxonomy Browser
Entrez PubMed Nucleotide Protein Genome Structure PMC Taxonomy Books
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Mammuthus primigenius
Taxonomy ID: 37349
Genbank common name: woolly mammoth
Genetic code: Translation table 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 186
Protein 122
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]	AM 4136 [1 1]	AM 493 [1 1]	AM 8744 [1 1]
BL-O13 [1 1]	BL-O179 [1 1]	BL-O208 [1 1]	BL-O219 [1 1]
BL-O240 [1 1]	BL-O250 [1 1]	BL-O308 [1 1]	BL-O309 [1 1]
BL-O310 [1 1]	BL-O443 [1 1]	BL-O503 [1 1]	BL-O585 [1 1]
BL-O59 [1 1]	BL-O723 [1 1]	BL-O865 [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]	ILC.01(10915) [1 1]
ILC.04(11028) [1 1]	ILC.06(1138a) [1 1]	ILC.08(10643) [1 1]	MKh-O326 [1 1]
MKh-O381 [1 1]	MKh-O422 [1 1]	MKh-O428 [1 1]	MKh-O429 [1 1]
MKh-O430 [1 1]	MKh-O435 [1 1]	MKh-O437 [1 1]	MKh-O438 [1 1]
MKh-O447 [1 1]	MKh-O533 [1 1]	MKh-O621 [1 1]	Mkh-O433 [1 1]
Nag-99-O203 [1 1]	PIN 3751-161 [1 1]	PIN 3751-162 [1 1]	The Khatanga mammoth (>50000 years bp, Siberia) [1]
The Yuribei mammoth (9700 yrs bp, Siberia) [1]	WS.02 [1 1]	WS.04 [1 1]	Wrangel Island 1 [1 1]
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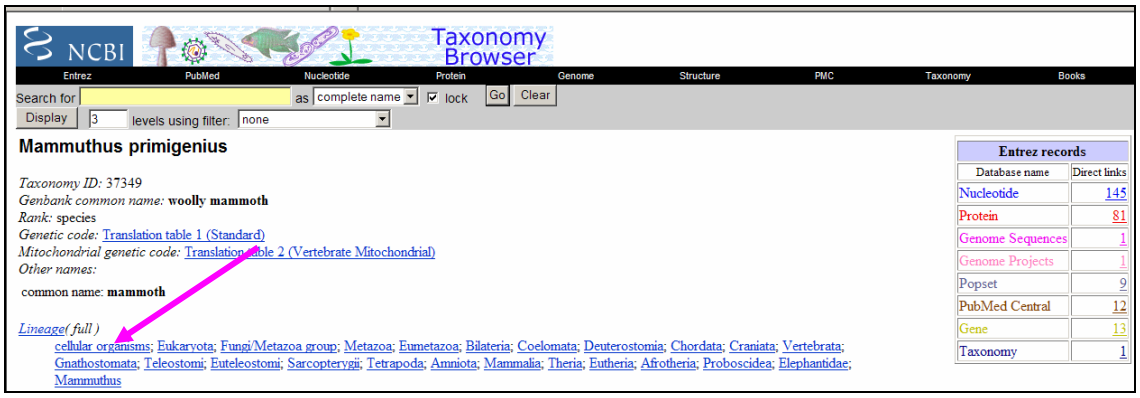
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Display 3 levels using filter: none
Mammuthus primigenius
Taxonomy ID: 37349
Genbank common name: woolly mammoth
Rank: species
Genetic code: Translation table 1 (Standard)
Mitochondrial genetic code: Translation table 2 (Vertebrate Mitochondrial)
Other 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
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Database name Direct links
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Protein 81
Genome Sequences 1
Genome Projects 1
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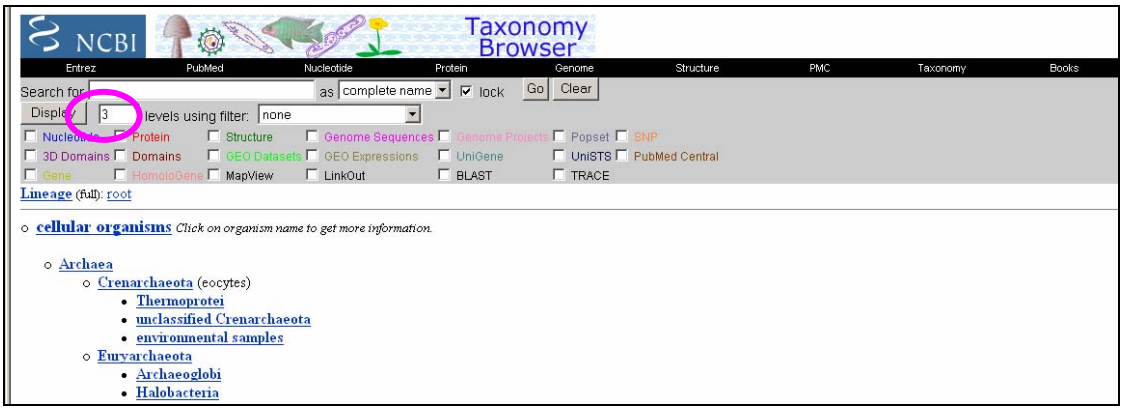
PubMed Central 12
Gene 13
Taxonomy 1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3D Domains Domains GEO Datasets GEO Expressions UniGene UniSTS PubMed Central
Gene HomoloGene MapView LinkOut BLAST TRACE
Lineage (full): root
cellular organisms Click on organism name to get more information.
Archaea
Crenarchaeota (eocytes)
Thermoprotei
unclassified Crenarchaeota
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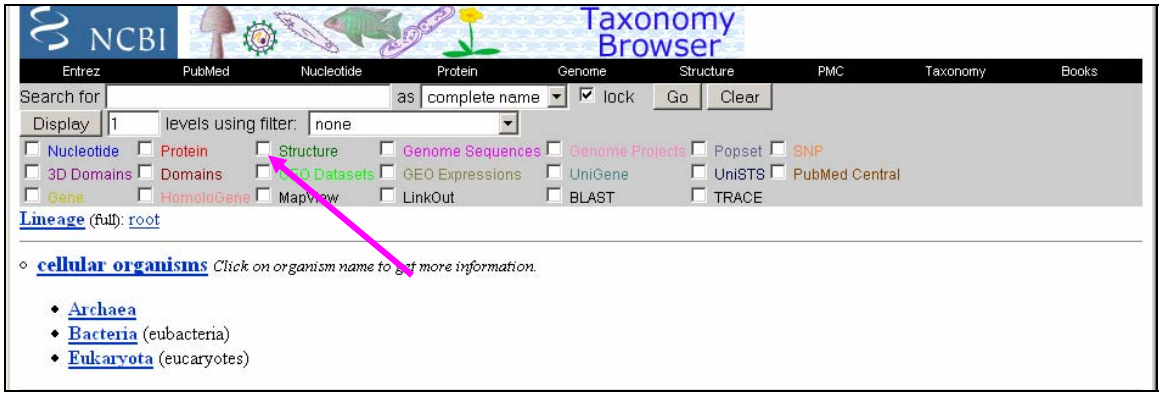
Euryarchaeota
Archaeoglobi
Halobacteria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Gene HomoloGene MapView LinkOut BLAST TRACE
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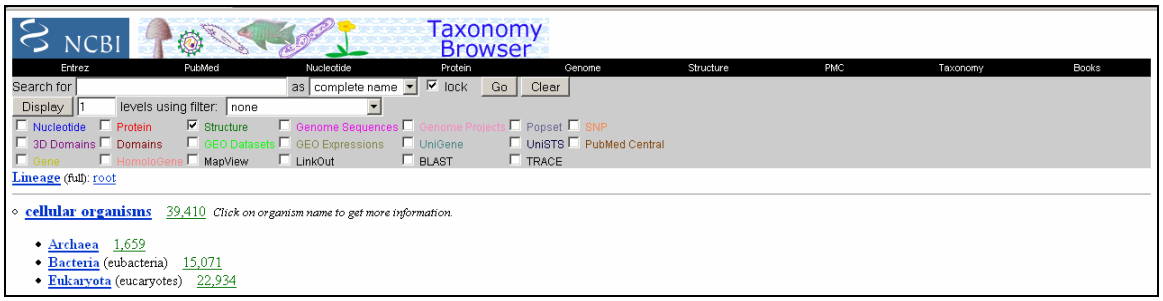
Archaea
Bacteria (eubacteria)
Eukaryota (eucaryotes)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3D Domains Domains GEO Datasets GEO Expressions UniGene UniSTS PubMed Central
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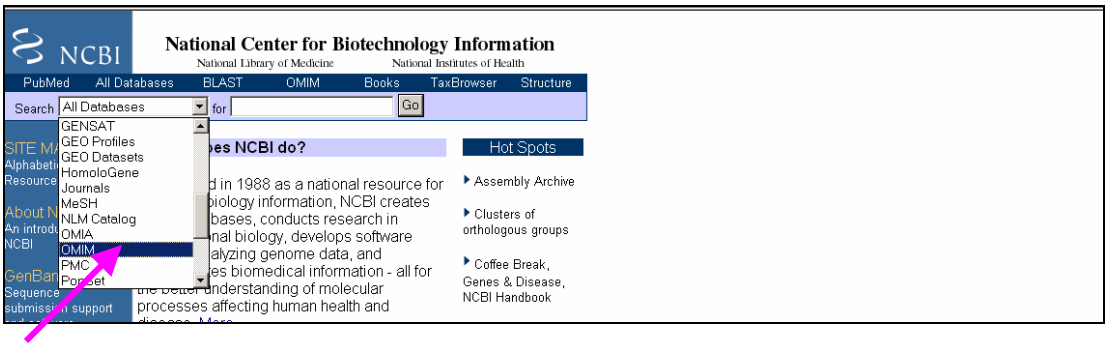
Bacteria (eubacteria) 15,071
Eukaryota (eucaryotes) 22,934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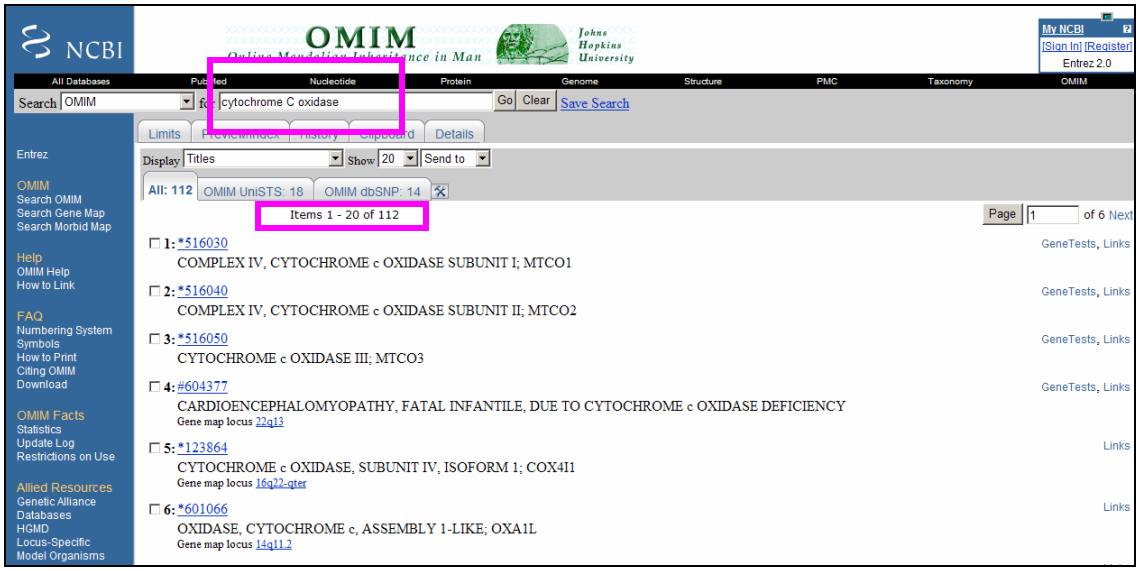
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GeneTests, Links
2: *516040
COMPLEX IV, CYTOCHROME c OXIDASE SUBUNIT II; MTCO2
GeneTests, Links
3: *516050
CYTOCHROME c OXIDASE III; MTCO3
GeneTests, Links
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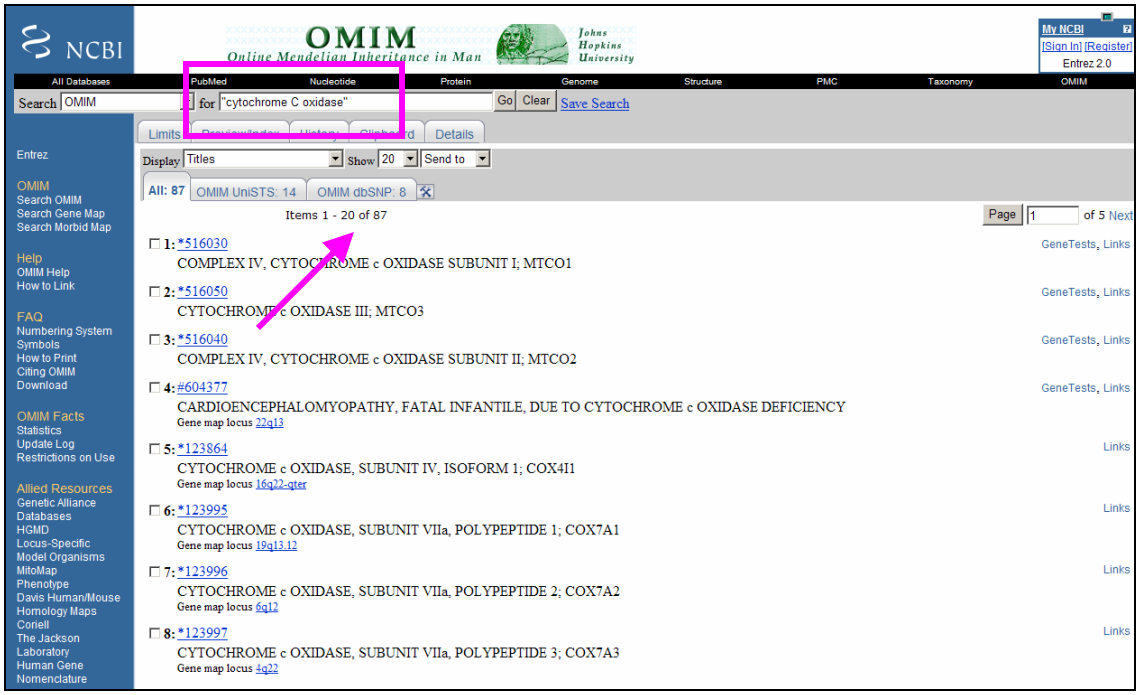
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COMPLEX IV, CYTOCHROME c OXIDASE SUBUNIT I; MTCO1

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.

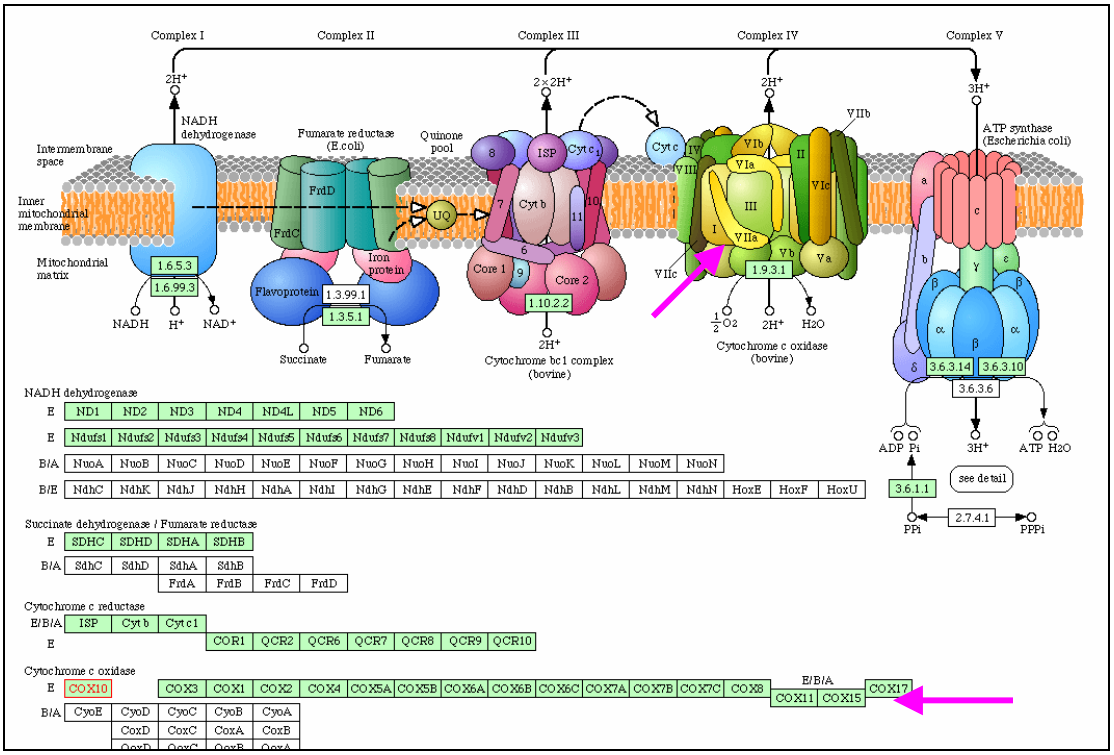
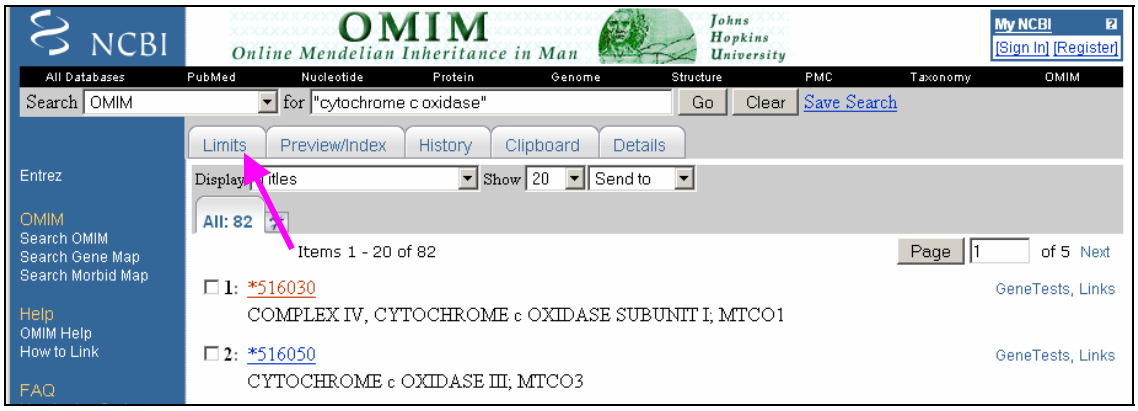


Figure from KEGG **Oxidative phosphorylation - Reference pathway (KO)**
http://www.genome.jp/dbget- in/show_pathway?ko00190+ko:K02270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All: 82
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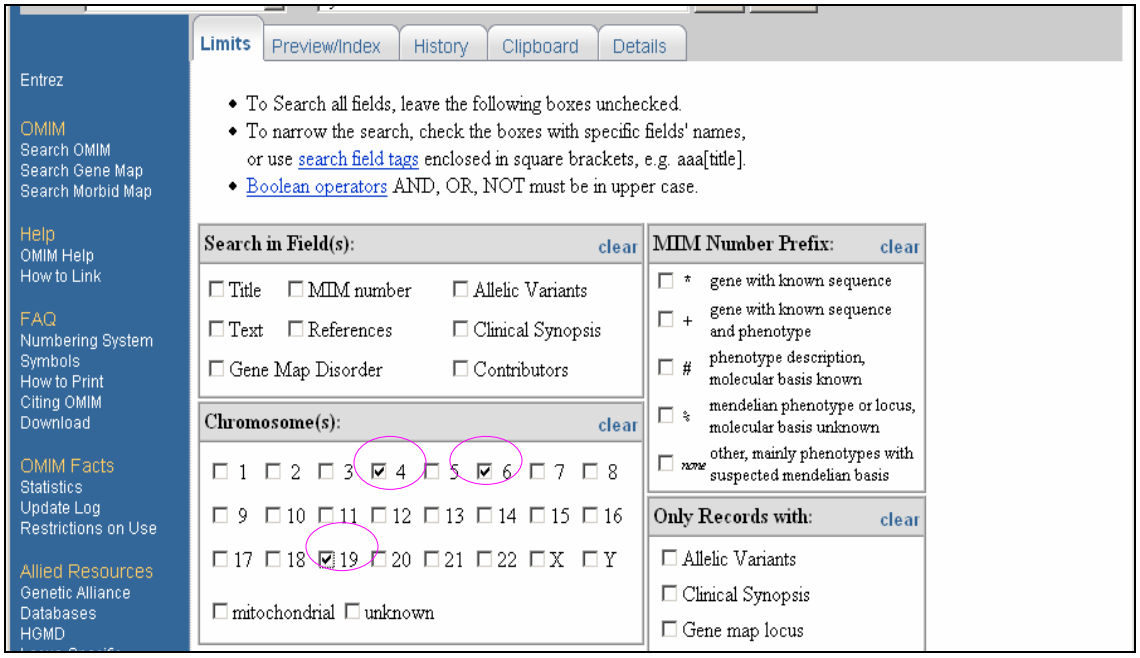
1: *516030
GeneTests, Links
COMPLEX IV, CYTOCHROME c OXIDASE SUBUNIT I; MTCO1
2: *516050
GeneTests, Links
CYTOCHROME c OXIDASE III; MTCO3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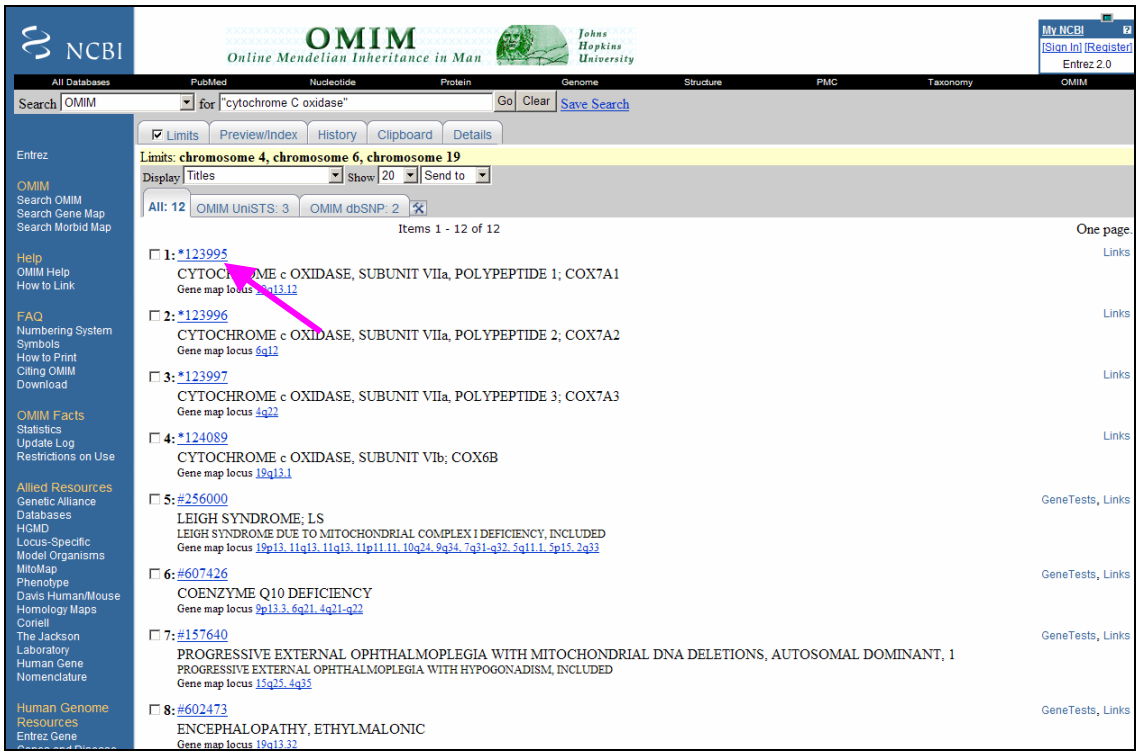
9 10 11 12 13 14 15 16
17 18 19 20 21 22 X Y
mitochondrial unknown
MIM Number Prefix: clear
* gene with known sequence
+ gene with known sequence and phenotype
# phenotype description, molecular basis known
% mendelian phenotype or locus, molecular basis unknown
none other, mainly phenotypes with suspected mendelian basis
Only Records with: clear
Allelic Variants
Clinical Synopsis
Gene map locus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One page.
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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
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Gene map locus 19q13.32
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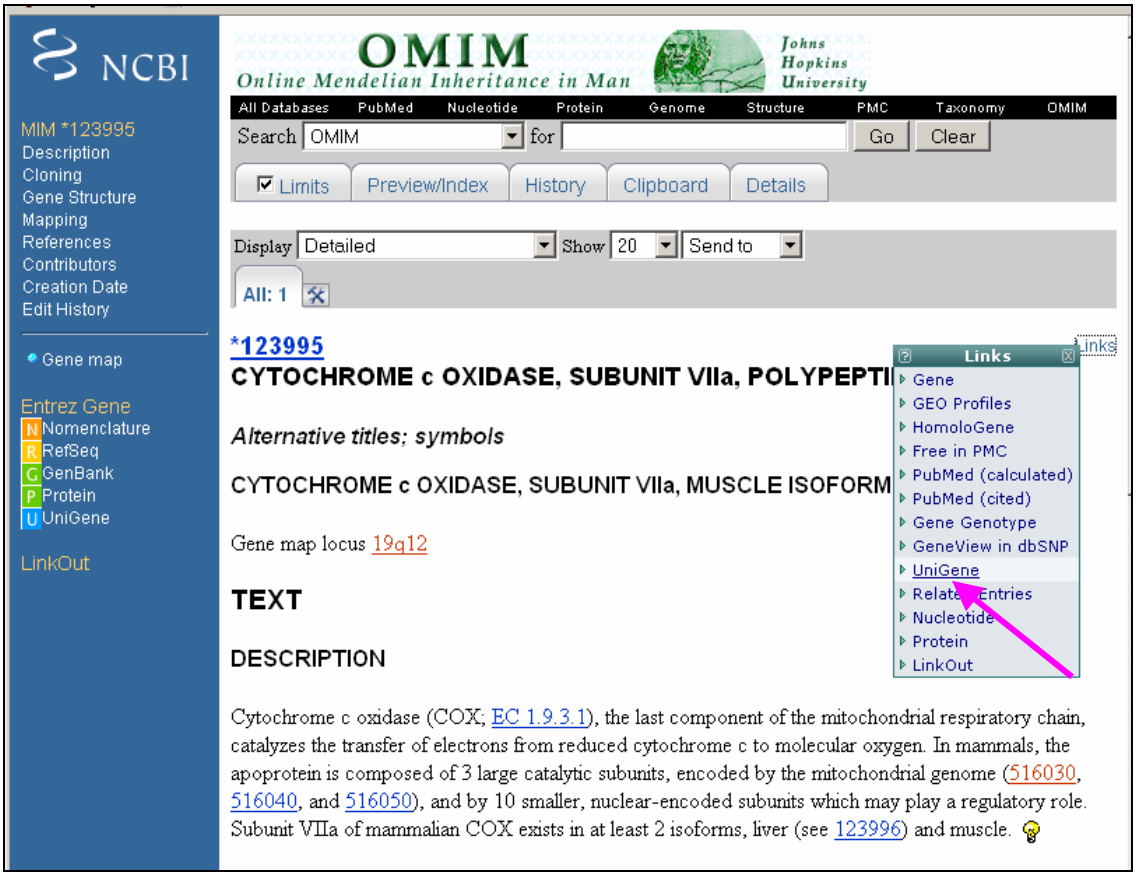
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Nomenclature
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CYTOCHROME c OXIDASE, SUBUNIT VIIa, POLYPEPTI
Links
Alternative titles; symbols
CYTOCHROME c OXIDASE, SUBUNIT VIIa, MUSCLE ISOFORM
Gene map locus 19q12
TEXT
DESCRIPTION
Cytochrome c 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.
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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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UGID:224558 UniGene Hs.421621 *Homo sapiens* COX7A1 — Order cDNA clone, 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 % / 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)

GENE EXPRESSION

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

Expression Profile:	View expression levels using UniGene's EST ProfileViewer
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; uncharacterized tissue; other; vascular; whole body; kidney; pituitary gland; uterus; pancreas; parathyroid; embryonic tissue; spleen; eye; colon; cranial nerve; mouth; lung; thyroid; umbilical cord; skin; bone

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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

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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	
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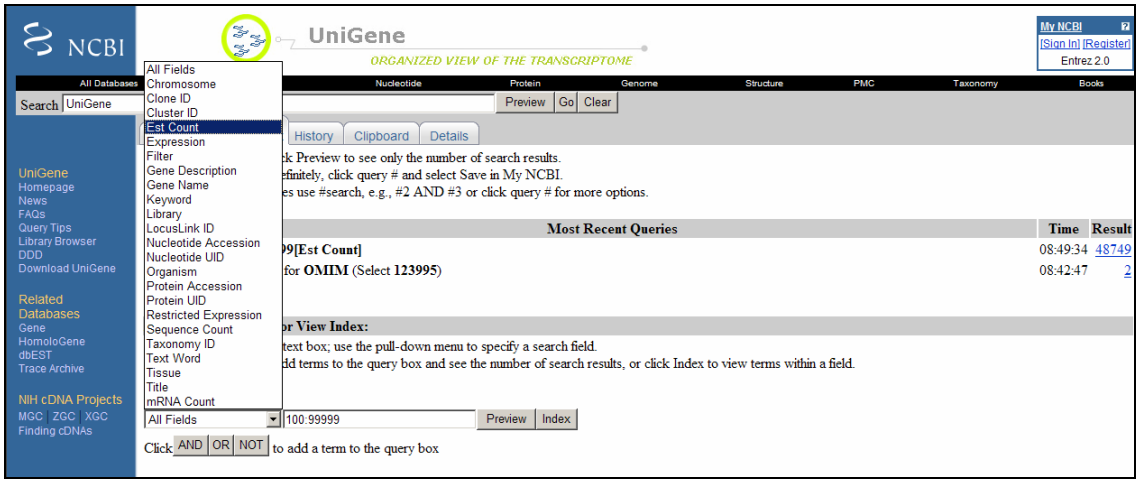
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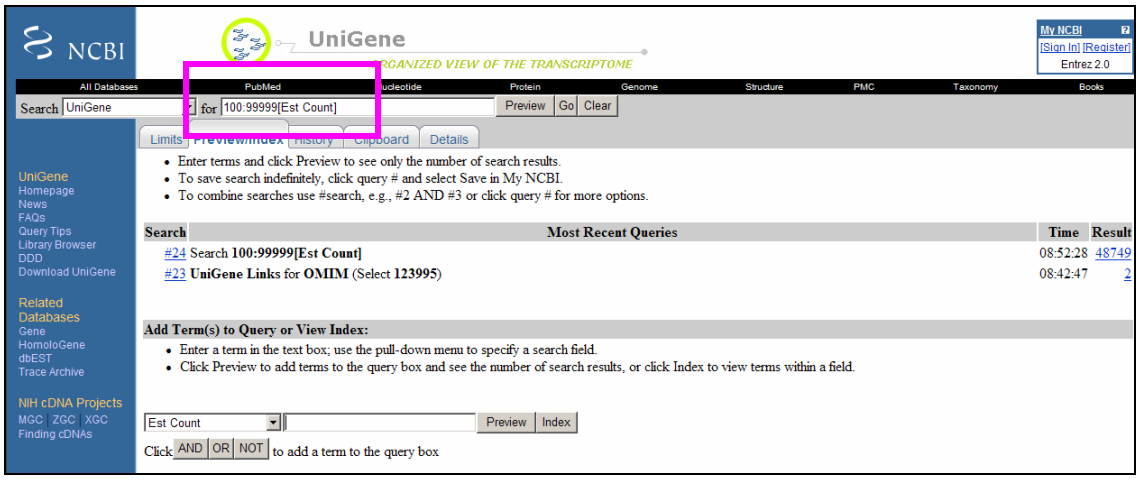
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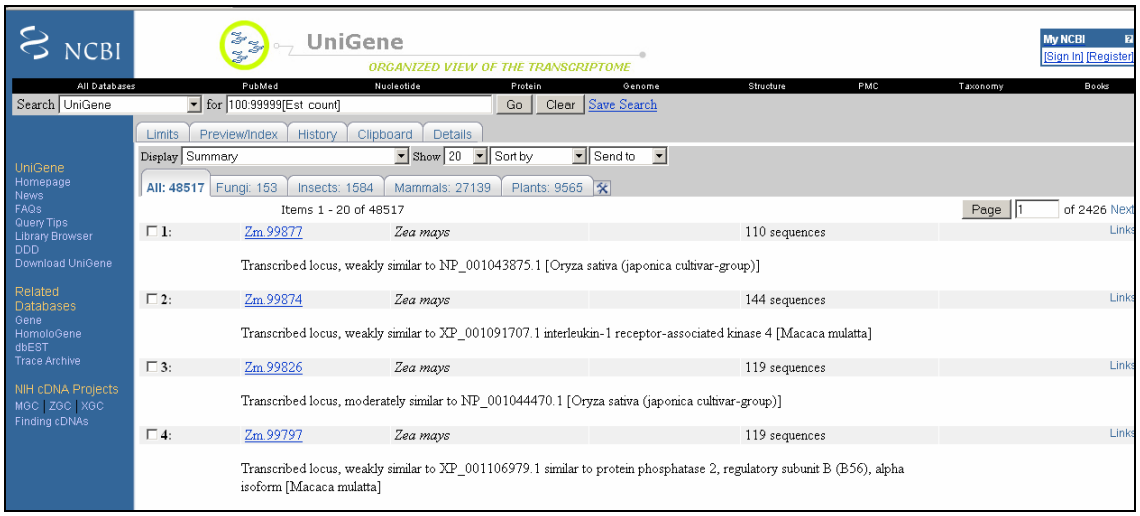
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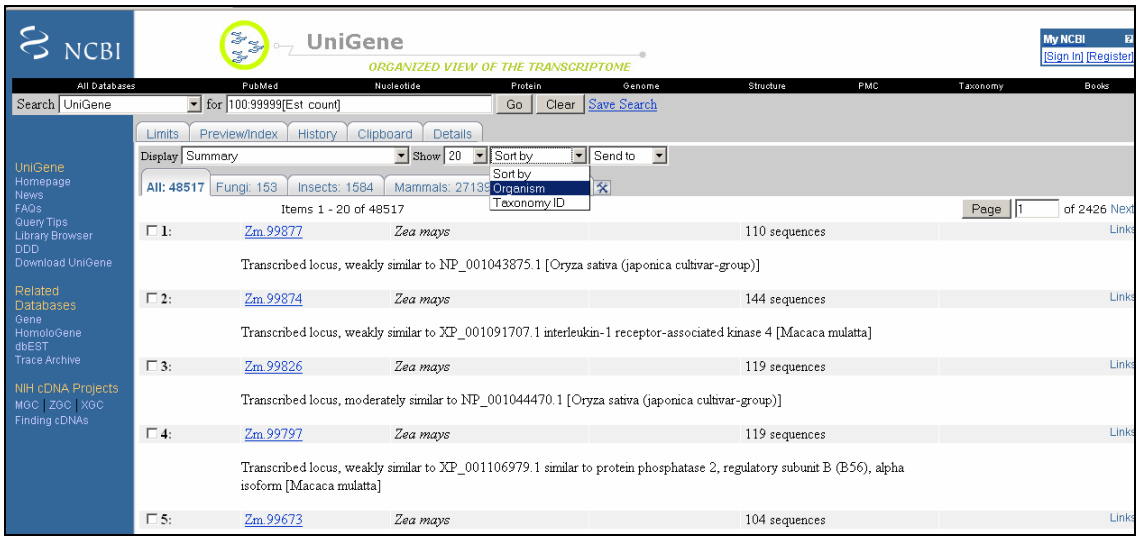
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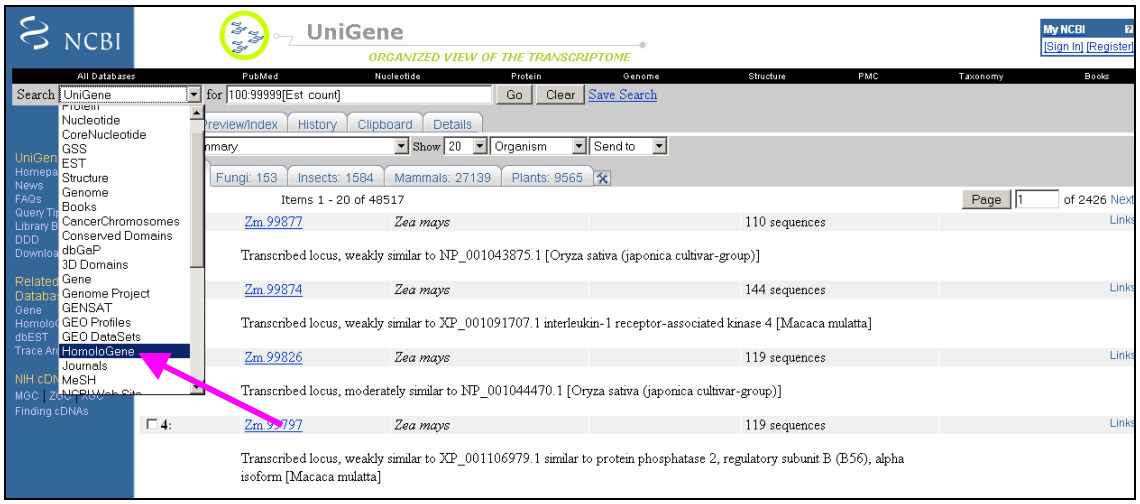
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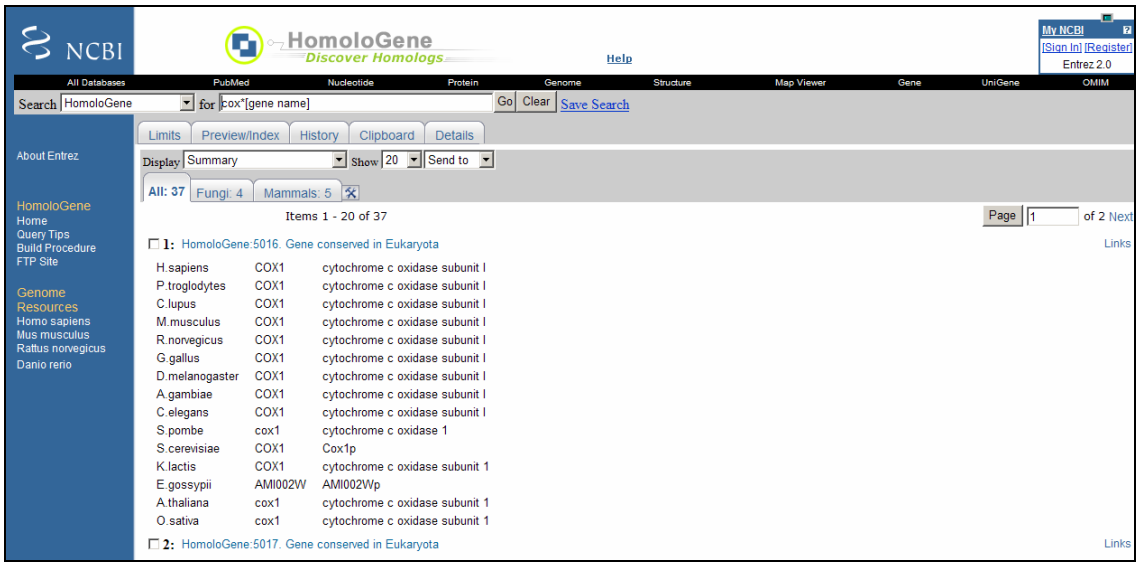
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M.musculus COX1 cytochrome c oxidase subunit I
R.norvegicus COX1 cytochrome c oxidase subunit I
G.gallus COX1 cytochrome c oxidase subunit I
D.melanogaster COX1 cytochrome c oxidase subunit I
A.gambiae COX1 cytochrome c oxidase subunit I
C.elegans COX1 cytochrome c oxidase subunit I
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S.cerevisiae COX1 Cox1p
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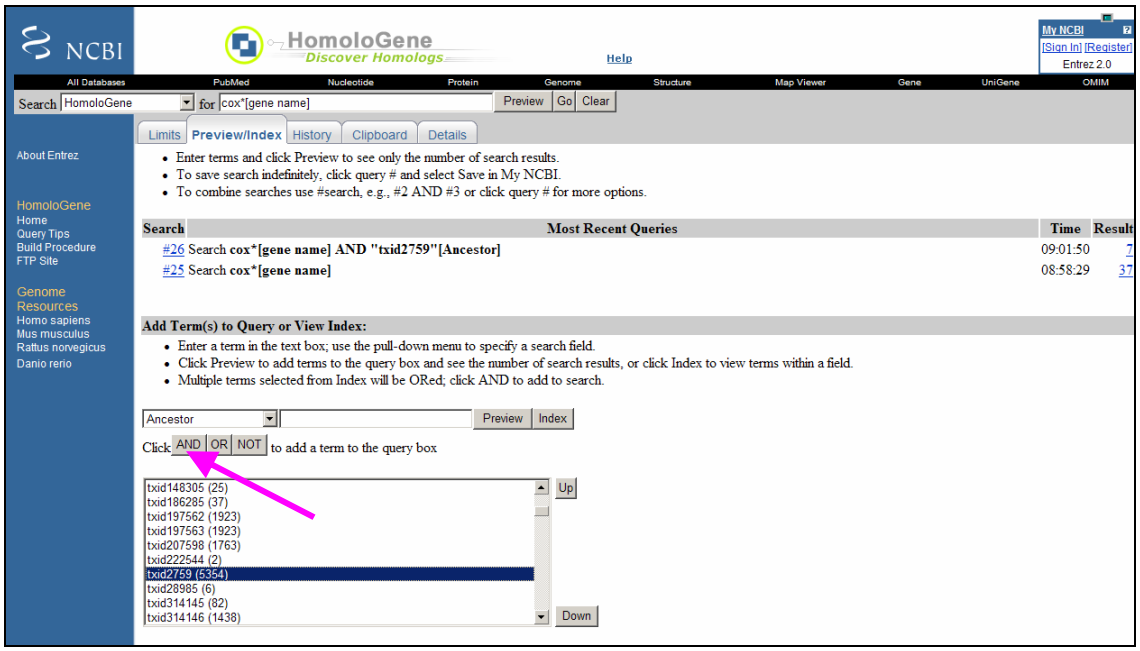
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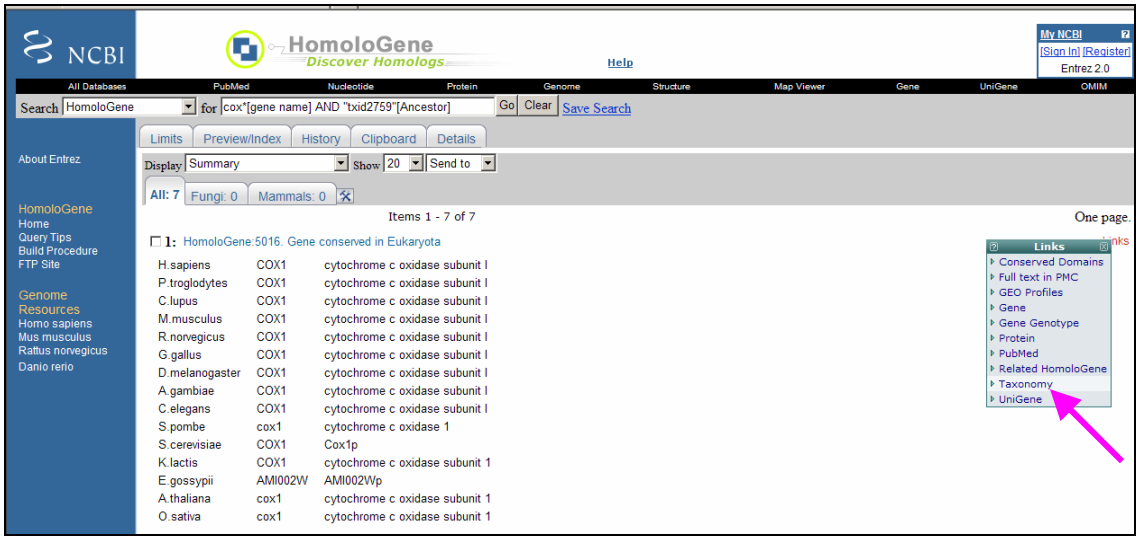
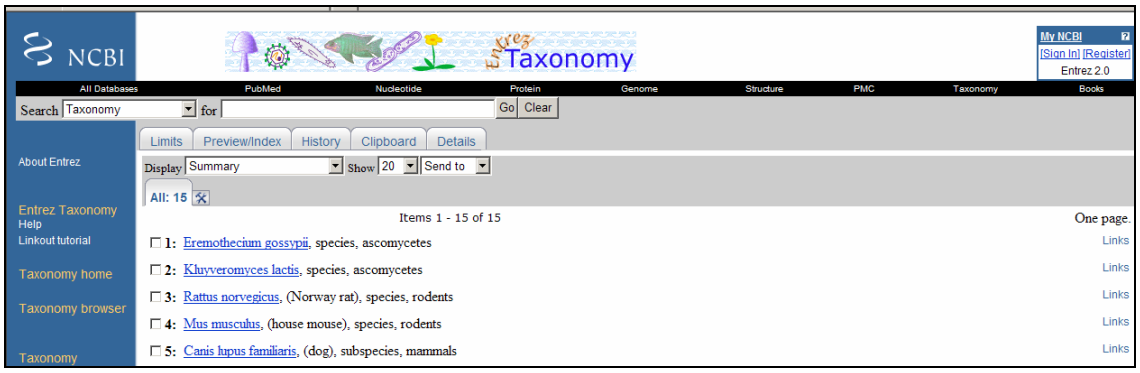
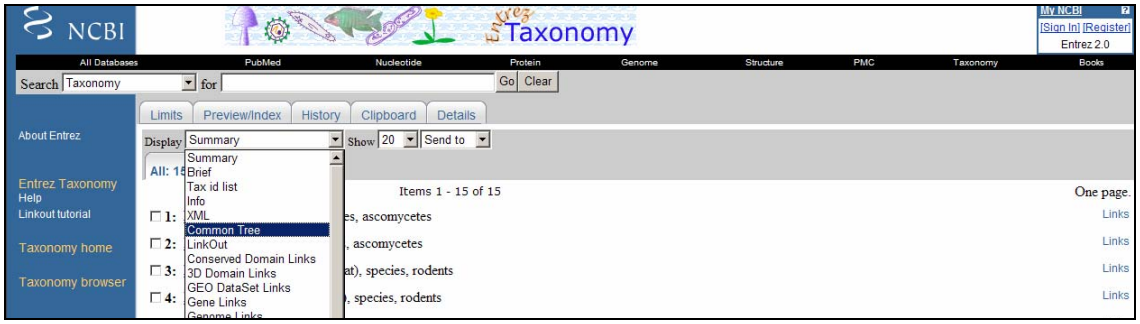
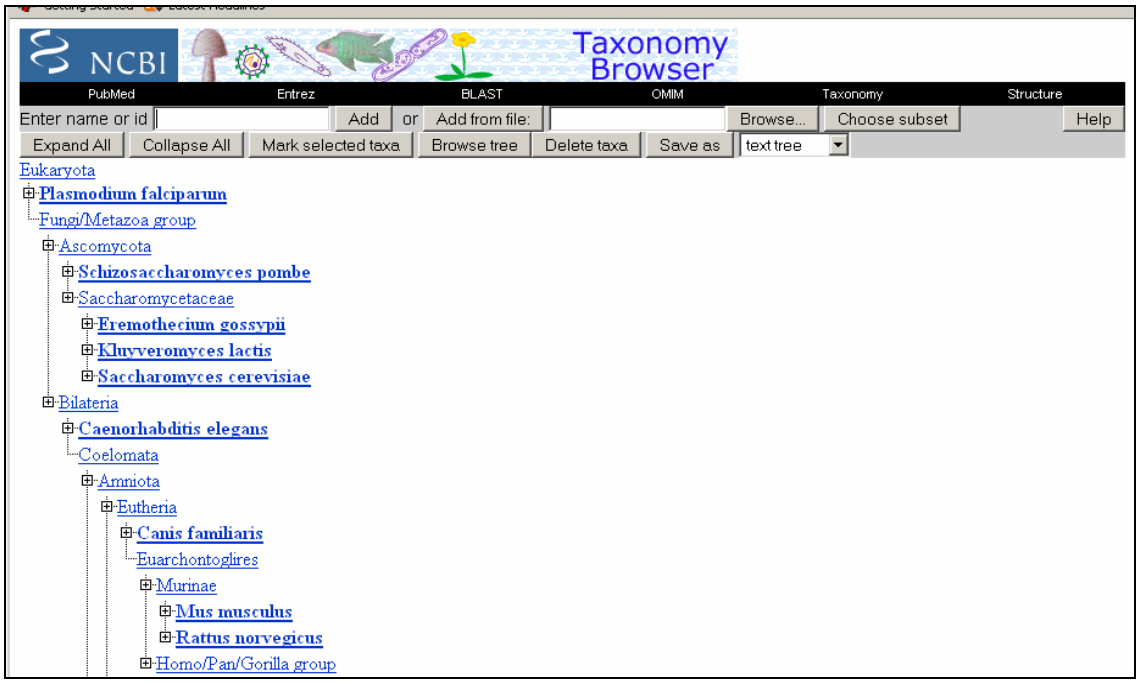
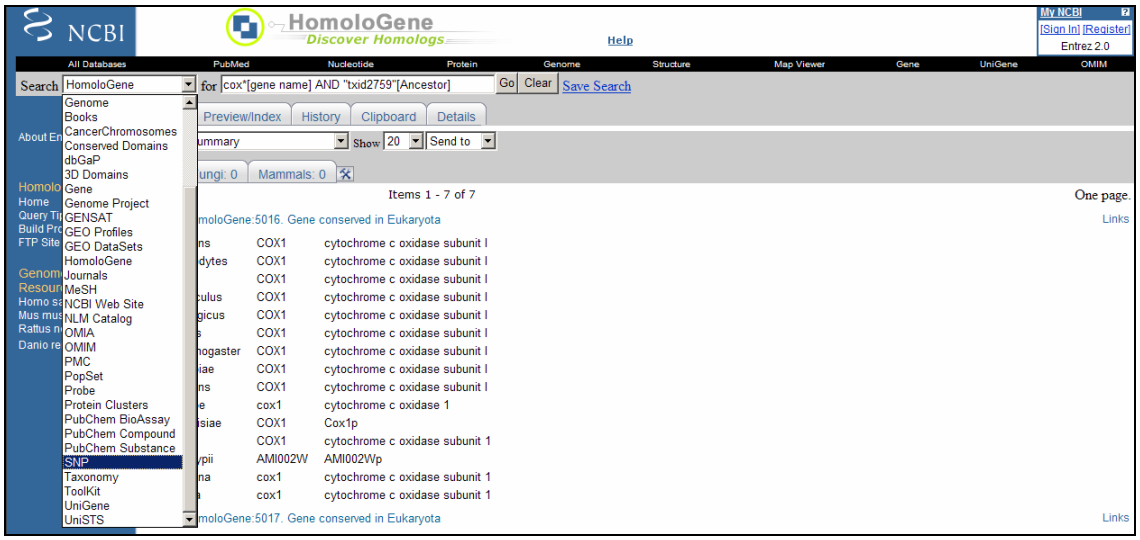
Up
Down


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
Limits Preview/Index History Clipboard Details
About Entrez
HomoloGene
Home
Query Tips
Build Procedure
FTP Site
Genome Resources
Homo sapiens
Mus musculus
Rattus norvegicus
Danio rerio
Display Summary Show 20 Send to
All: 7 Fungi: 0 Mammals: 0
Items 1 - 7 of 7
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
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
Links
Conserved Domains
Full text in PMC
GEO Profiles
Gene
Gene Genotype
Protein
PubMed
Related HomoloGene
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
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Help
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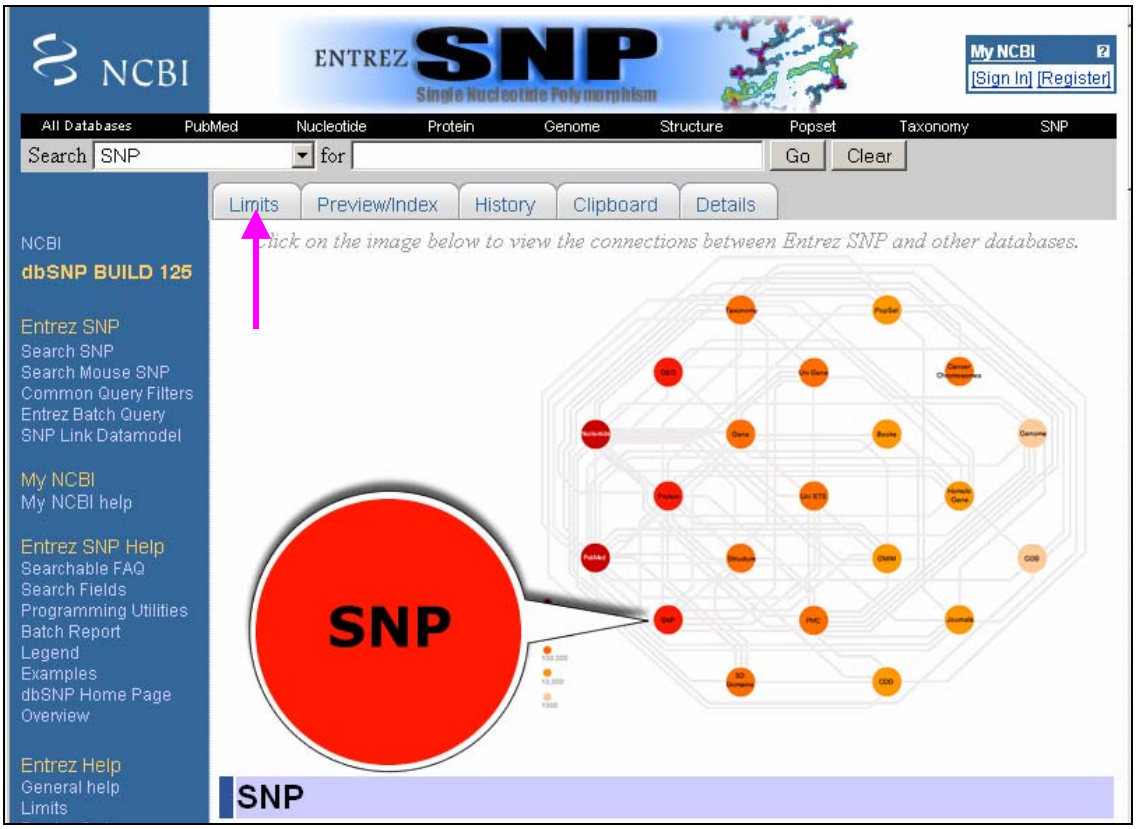
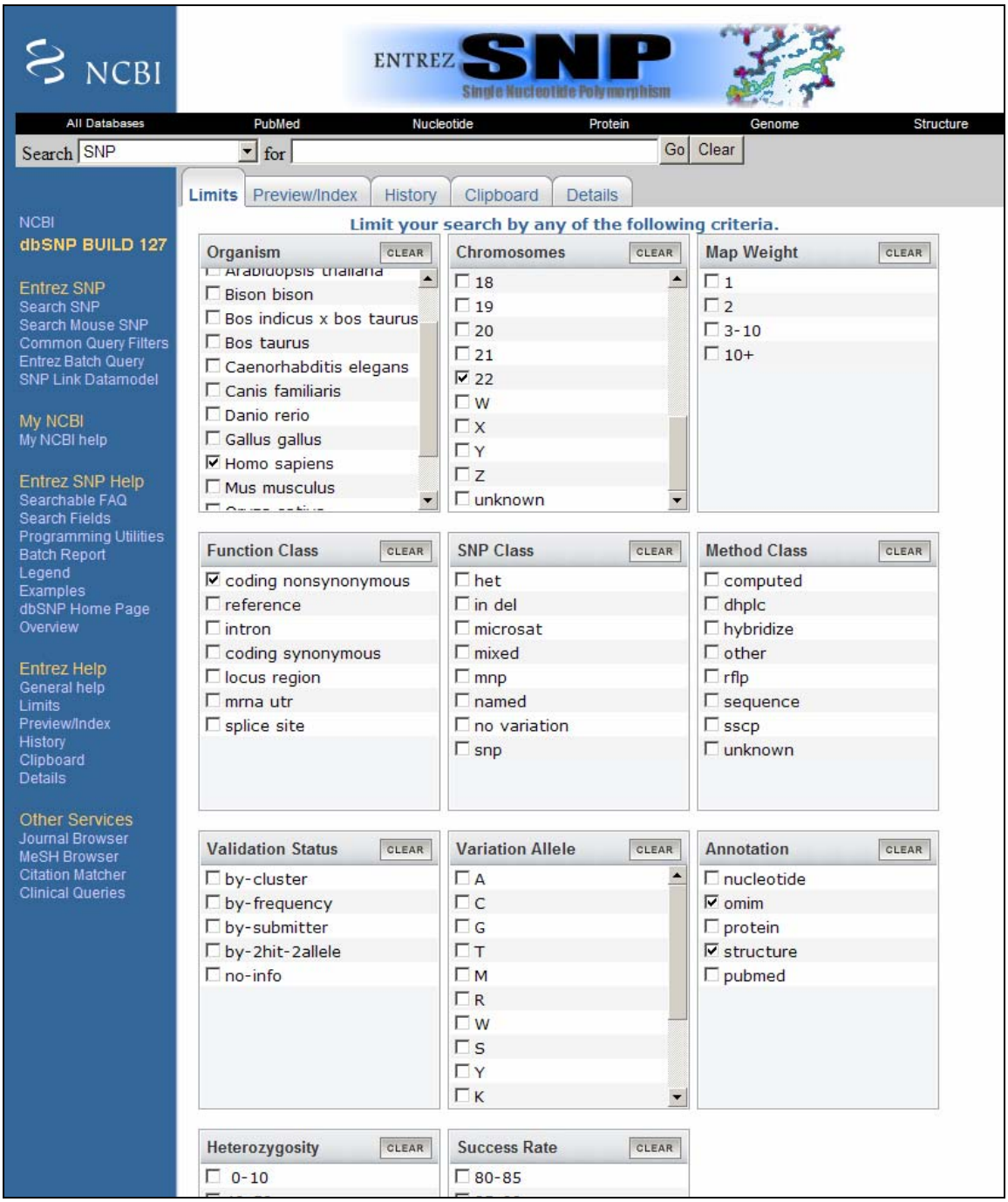
Entrez 2.0
All Databases
PubMed
Nucleotide
Protein
Genome
Structure
Map Viewer
Gene
UniGene
OMIM
Search HomoloGene for cox*[gene name] AND "txid2759"[Ancestor]
Go
Clear
Save Search
Preview/Index
History
Clipboard
Details
Show 20
Send to
Mammals: 0
Items 1 - 7 of 7
One page.
Links
Genome
Books
CancerChromosomes
Conserved Domains
dbGaP
3D Domains
Gene
Genome Project
GENSAT
GEO Profiles
GEO DataSets
HomoloGene
Journals
MeSH
NCBI Web Site
NLM Catalog
OMIA
OMIM
PMC
PopSet
Probe
Protein Clusters
PubChem BioAssay
PubChem Compound
PubChem Substance
SNP
Taxonomy
ToolKit
UniGene
UniSTS


NCBI
ENTREZ SNP
Single Nucleotide Polymorphism
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
All Databases
PubMed
Nucleotide
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NCBI
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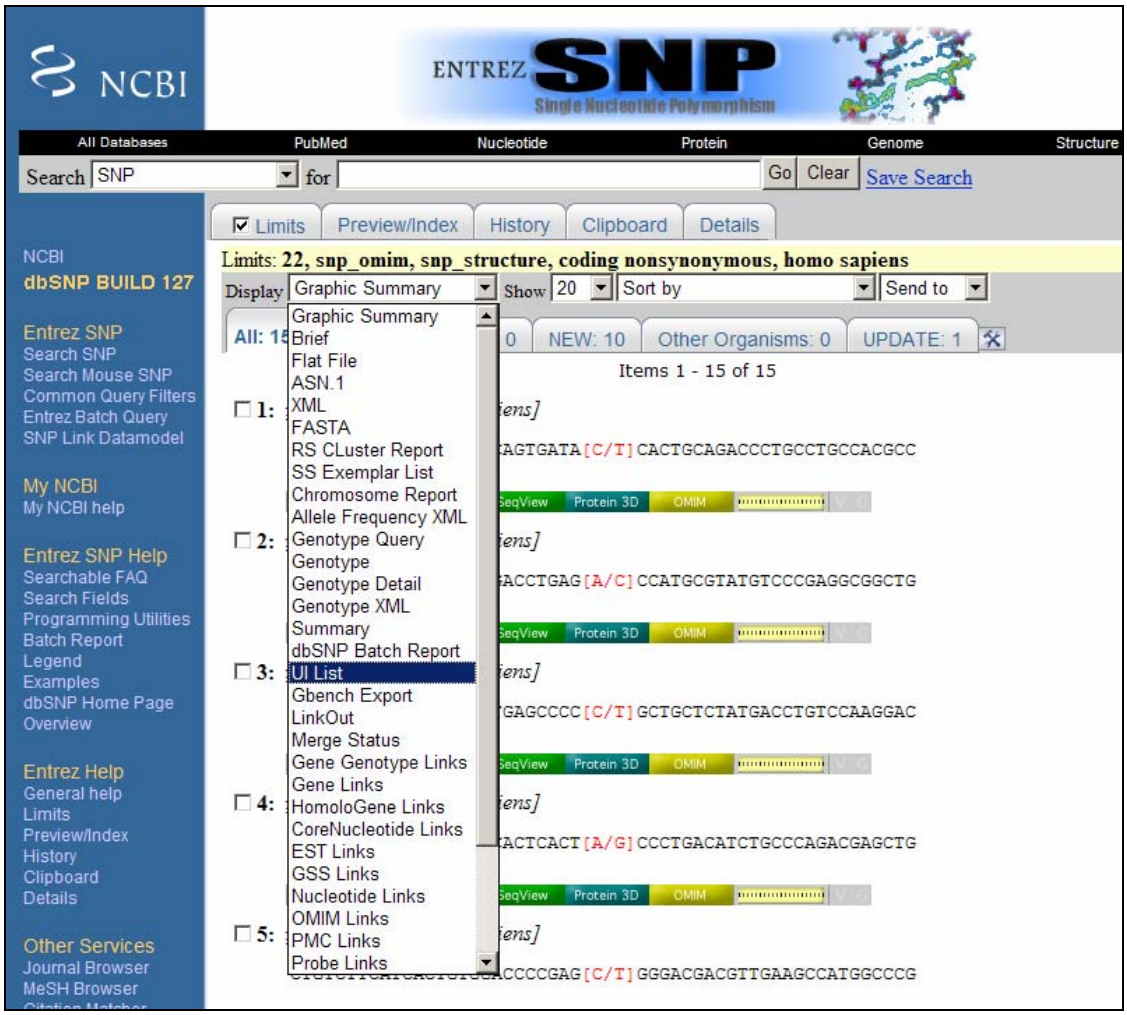
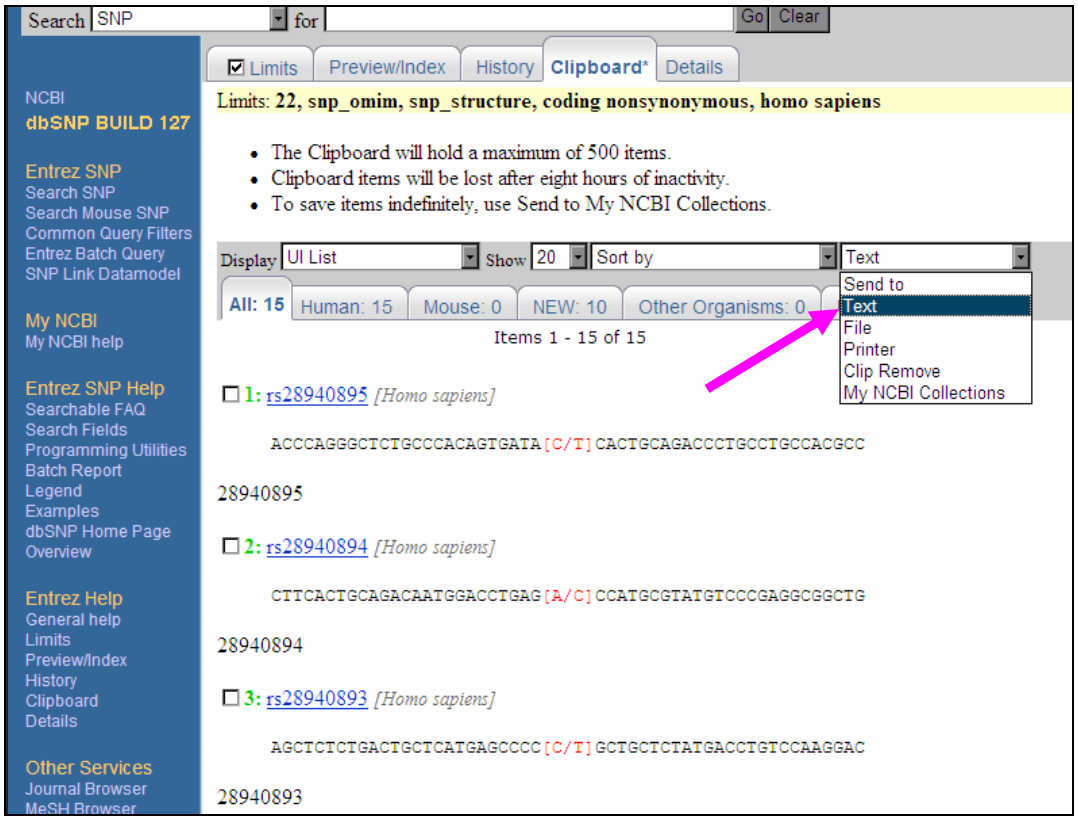
Entrez SNP
Search SNP
Search Mouse SNP
Common Query Filters
Entrez Batch Query
SNP Link Datamodel
My NCBI
My NCBI help
Entrez SNP Help
Searchable FAQ
Search Fields
Programming Utilities
Batch Report
Legend
Examples
dbSNP Home Page
Overview
Entrez Help
General help
Limits
Preview/Index
History
Clipboard
Details
Other Services
Journal Browser
MeSH Browser
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
S
Y
K
Annotation CLEAR
nucleotide
omim
protein
structure
pubmed
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
Legend
Examples
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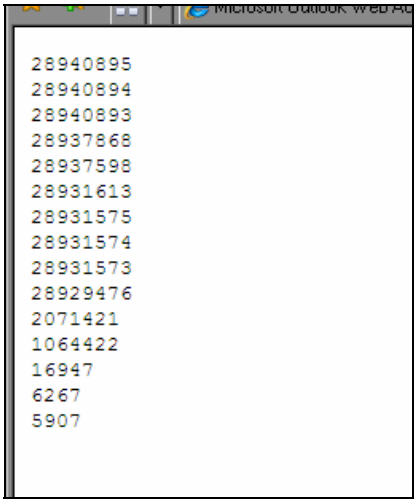
Entrez Help
General help
Limits
Preview/Index
History
Clipboard
Details
Other Services
Journal Browser
MeSH Browser
Limits: 22, snp_omim, snp_structure, coding nonsynonymous, homo sapiens
The Clipboard will hold a maximum of 500 items.
Clipboard items will be lost after eight hours of inactivity.
To 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


28940895
28940894
28940893
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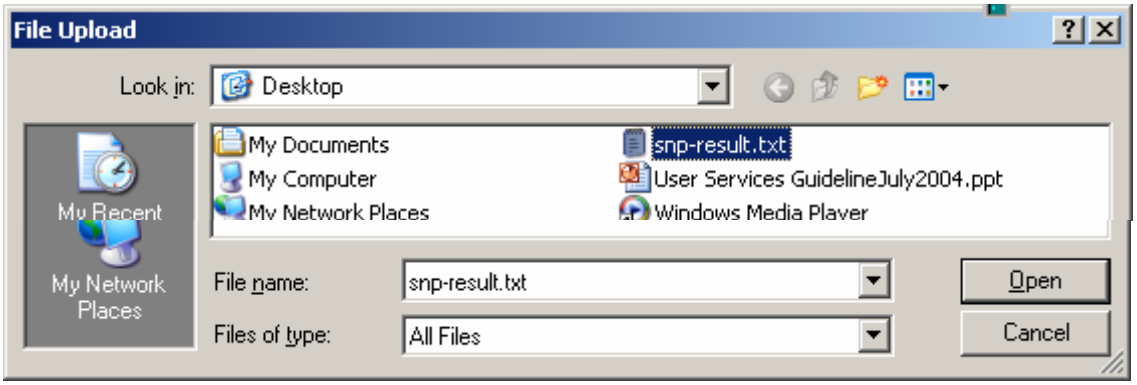
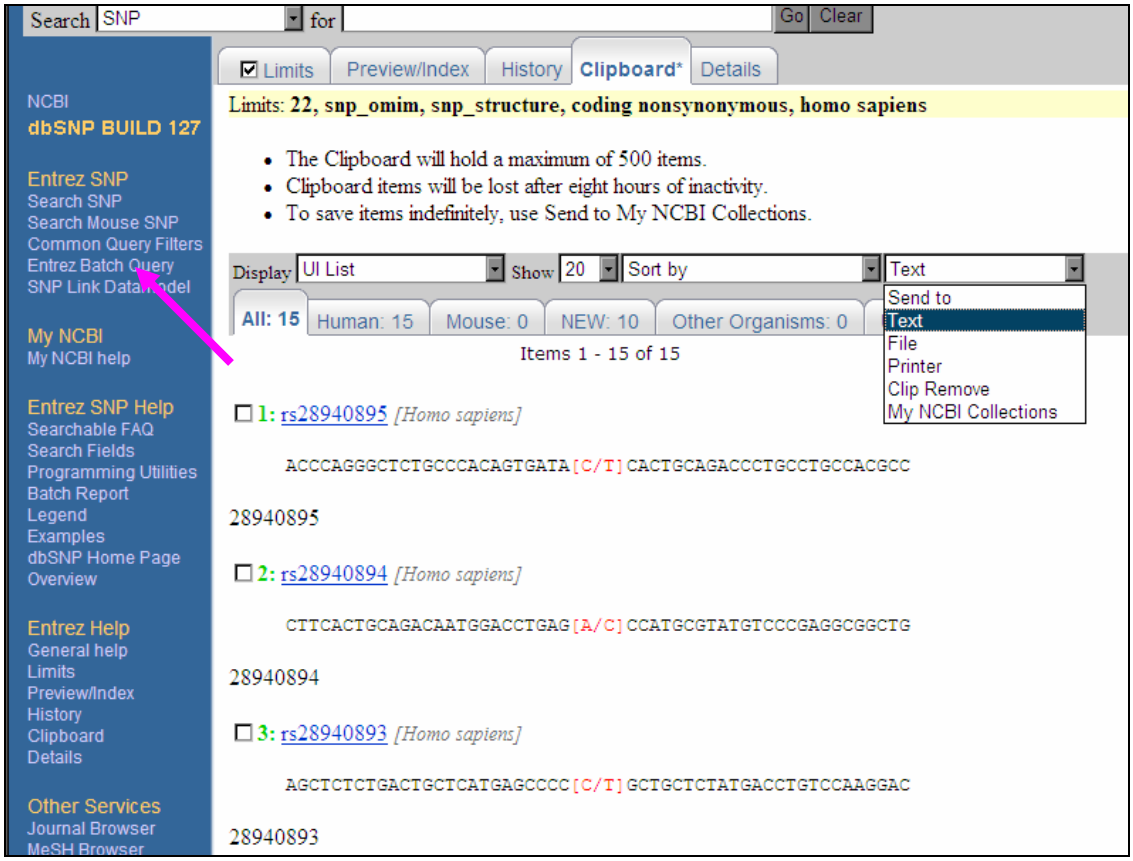
28937598
28931613
28931575
28931574
28931573
28929476
2071421
1064422
16947
6267
5907


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
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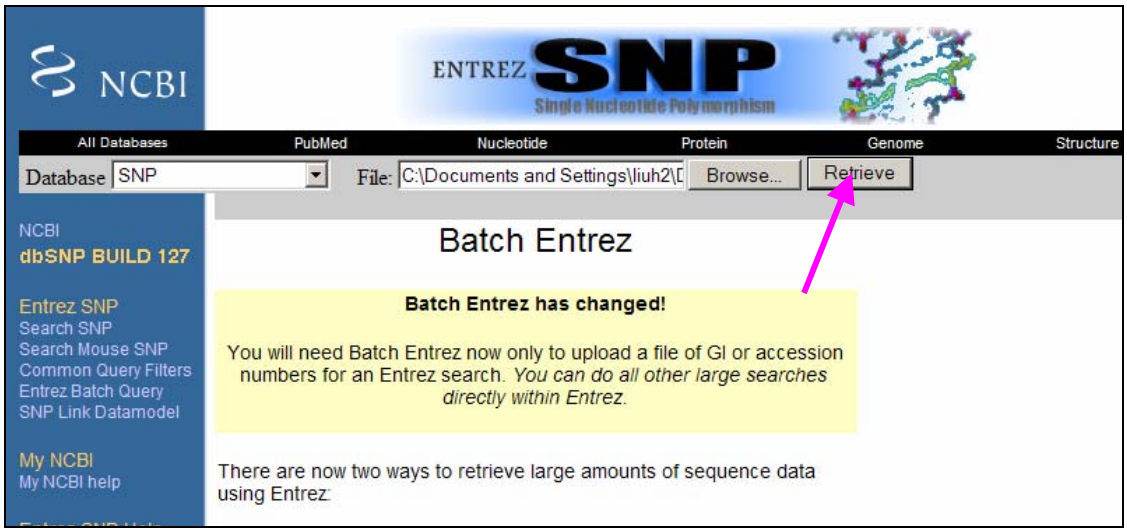
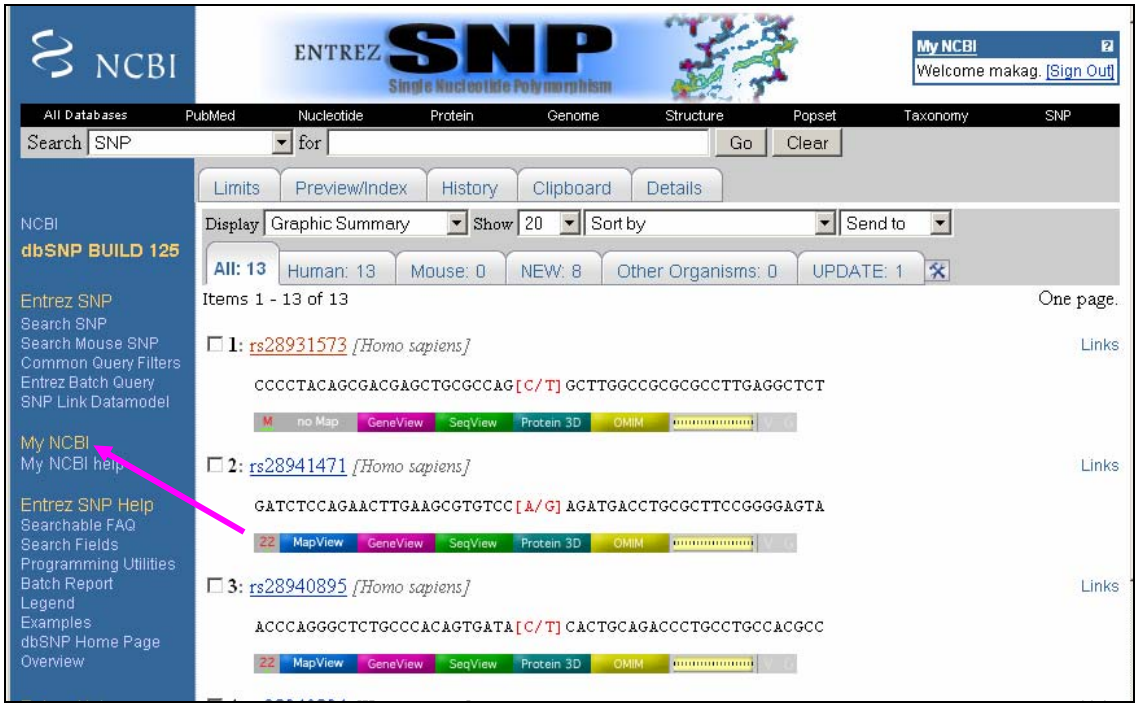
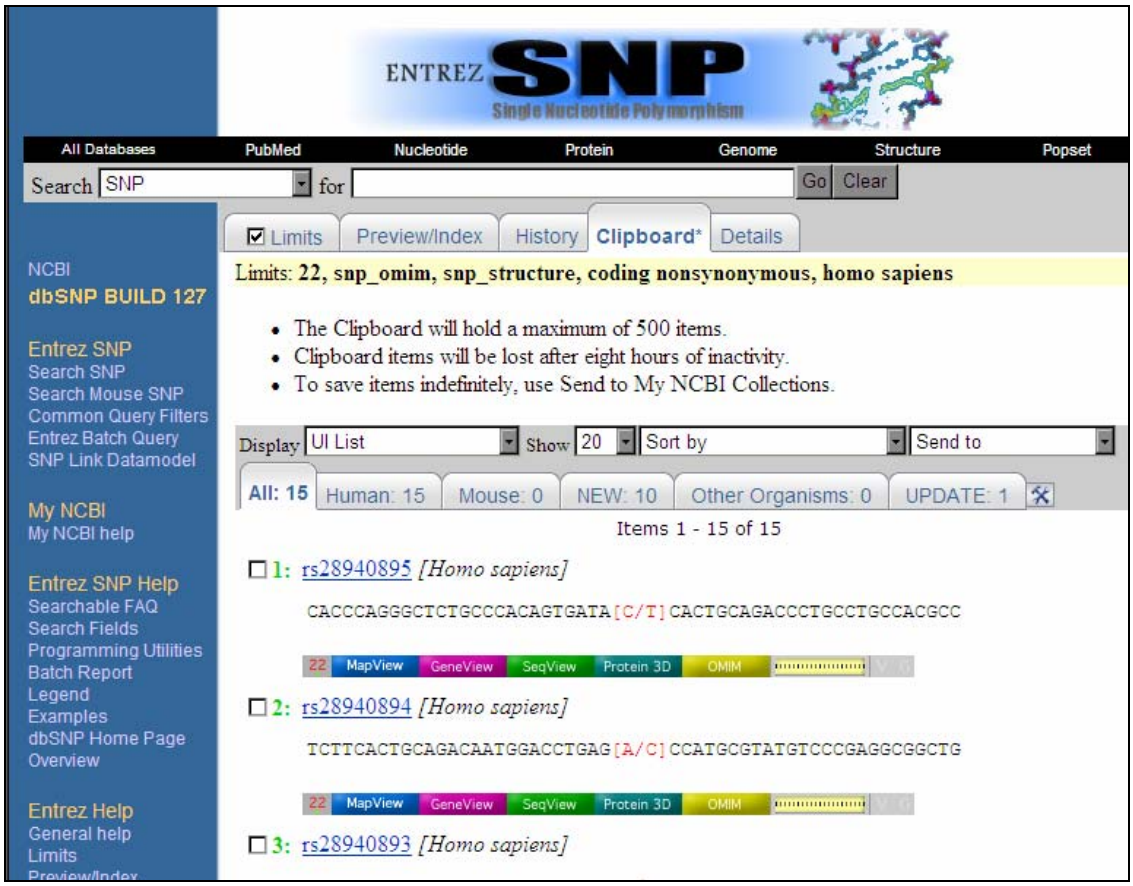
dbSNP Home Page
Overview
Entrez Help
General help
Limits
Preview/Index
History
Clipboard
Details
Other Services
Journal Browser
MeSH Browser
Limits: 22, snp_omim, snp_structure, coding nonsynonymous, homo sapiens
The Clipboard will hold a maximum of 500 items.
Clipboard items will be lost after eight 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
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dbSNP Home Page
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General help
Limits
Limits: 22, snp_omim, snp_structure, coding nonsynonymous, homo sapiens
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All: 15 Human: 15 Mouse: 0 NEW: 10 Other Organisms: 0 UPDATE: 1
Items 1 - 15 of 15
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CACCCAGGGCTCTGCCCACAGTGATA[C/T]CACTGCAGACCCTGCCTGCCACGCC
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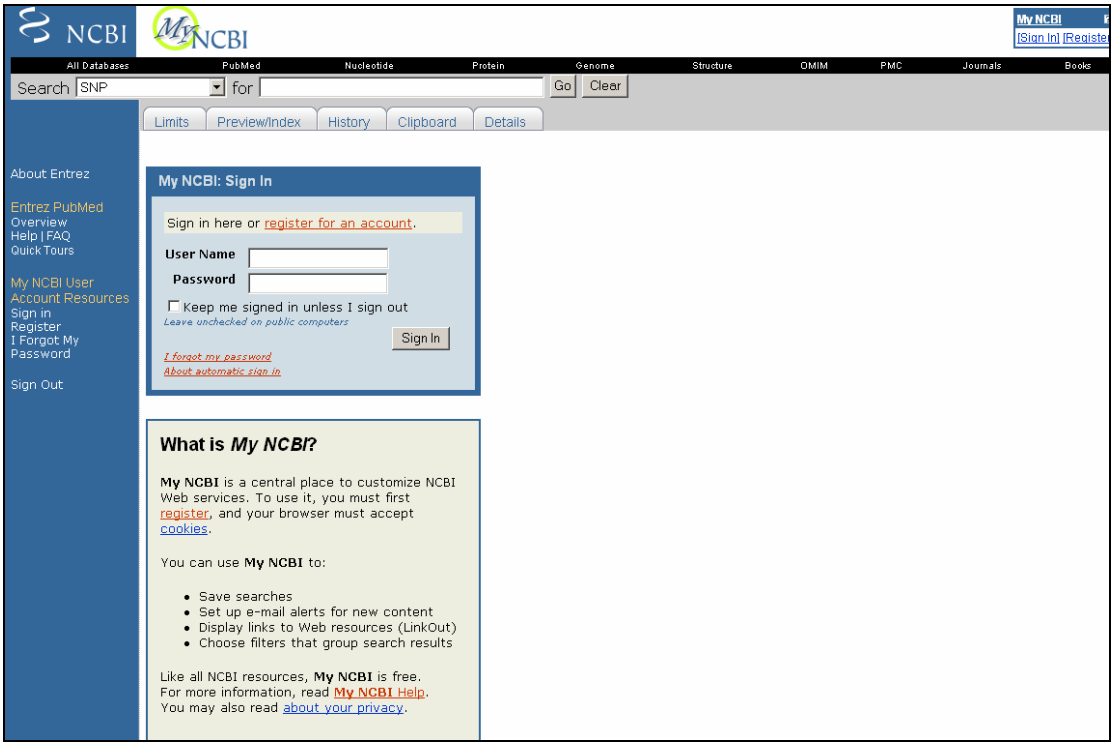
TCTTCACTGCAGACAATGGACCTGAG[A/C]CCATGCGTATGTCCCGAGGCGGCTG
22 MapView GeneView SeqView Protein 3D OMIM
3: rs28940893 [Homo sapiens]


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)