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

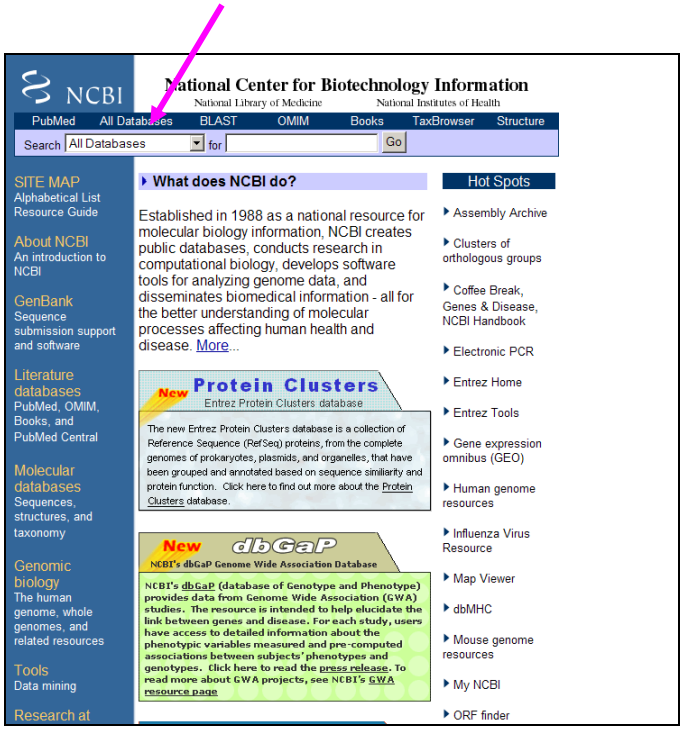
Perform a search for mammoth across all of the Entrez databases. Which databases contain records associated with the term mammoth? Link to the mammoth literature citations in the PubMed database. Identify the articles available free in PMC. Access the article "The year of the mammoth". What are the cited 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.



Example 1, Part I

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Structure of ivory.
J Morphol. 2007 Dec 21; [Epub ahead of print]
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2: Meyer M, Briggs AW, Maricic T, Höber B, Höffner B, Krause J, Weihmann A, Pääbo S, Hofreiter M. Related Articles, Links
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Mol Phylogenet Evol. 2006 Aug;40(2):620-7. Epub 2006 May 2. No abstract available.
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Australian Centre for Ancient DNA, Earth and Environmental Sciences, University of Adelaide, Adelaide, Australia. Alan.cooper@adelaide.edu.au

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- Complete mitochondrial genome and phylogeny of Pleistocene mammoth Mammuthus prim [PLoS Biol. 2006]
- A nuclear DNA phylogeny of the woolly mammoth (Mammuthus primigenius). [Mol Phylogenet Evol. 2006]
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- More than just big ears. [Curr Biol. 2002]
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Complete mitochondrial genome and phylogeny of Pleistocene Mammoth Mammuthus primigenius.

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

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

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

PMID: 16448217 [PubMed - in process]

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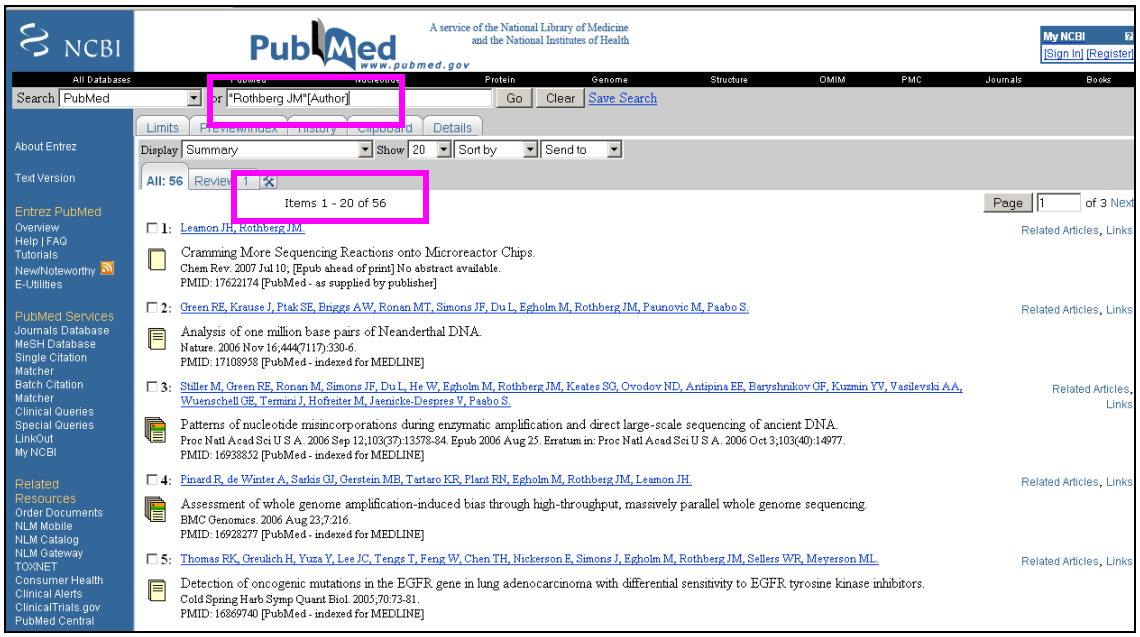
Genome sequencing in microfabricated high-density picolitre reactors.

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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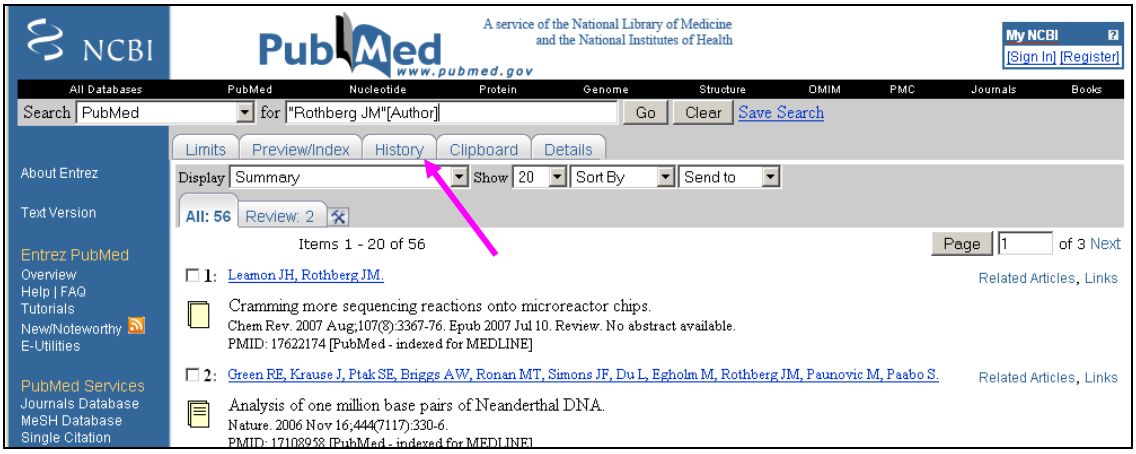
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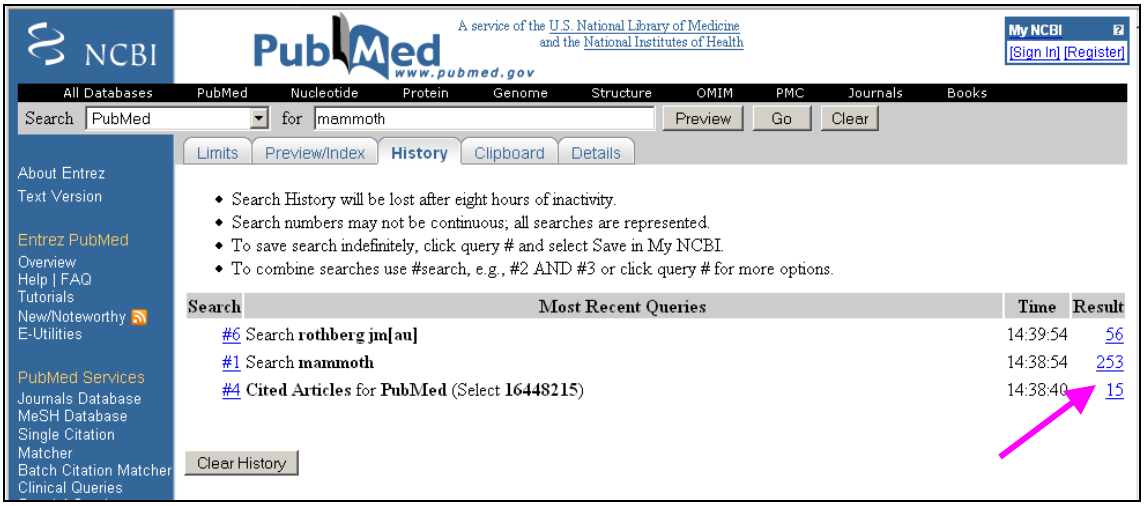
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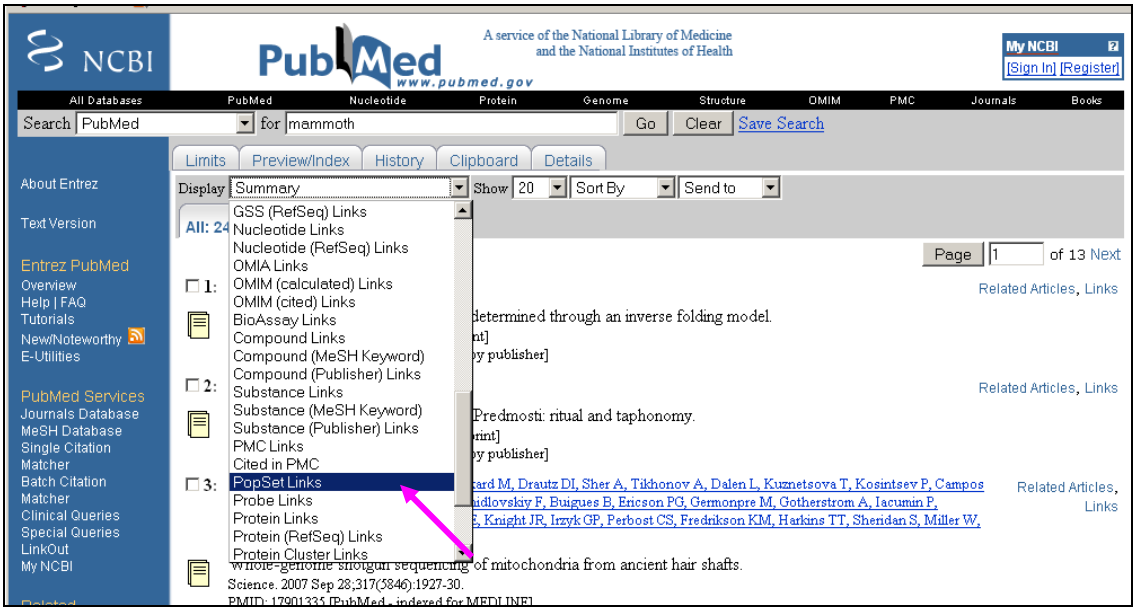
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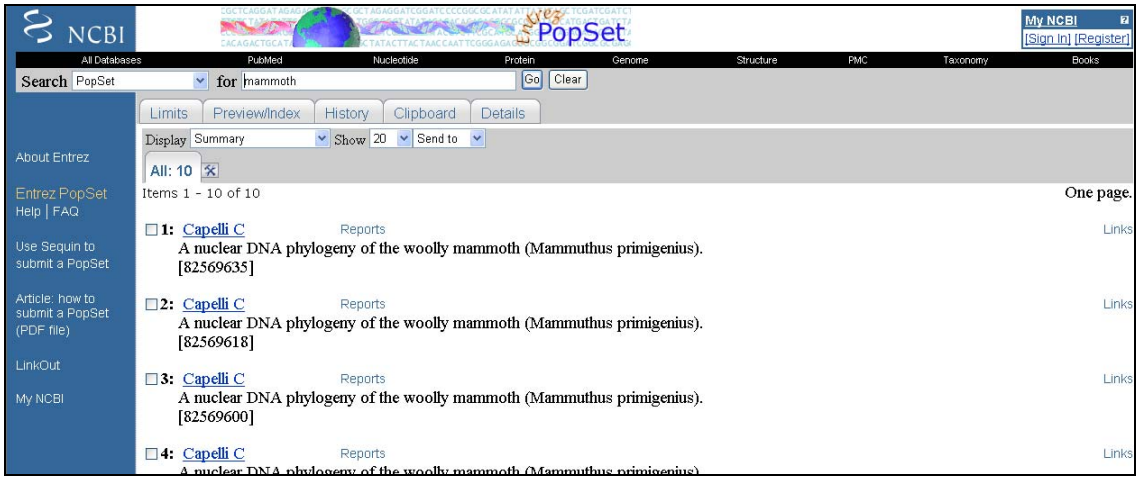
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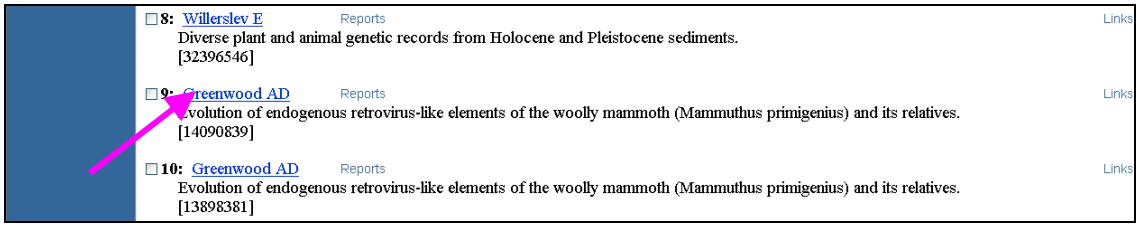
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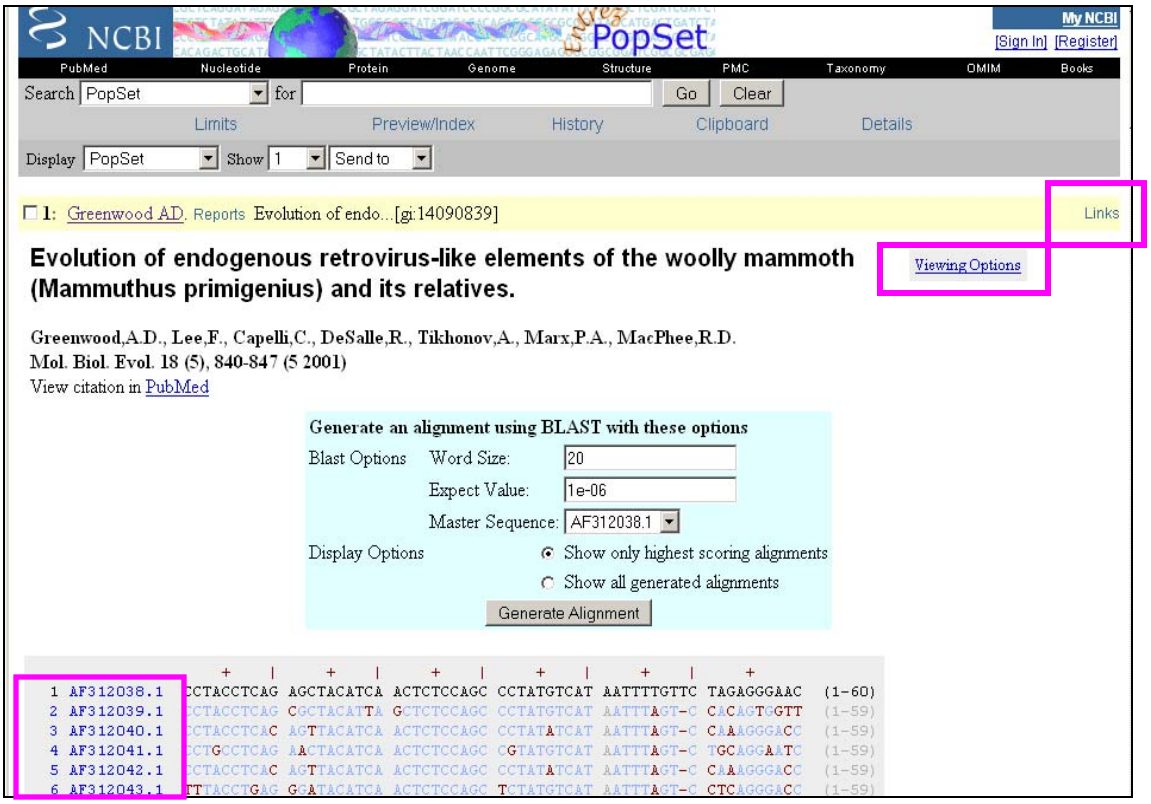
Evolution of endogenous retrovirus-like elements of the woolly mammoth (Mammuthus primigenius) and its relatives.
[13898381]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1: Greenwood AD. Reports Evolution of endo...[gi:14090839]
Links
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Evolution of endogenous retrovirus-like elements of the woolly mammoth (Mammuthus primigenius) and its relatives.
Greenwood,A.D., Lee,F., Capelli,C., DeSalle,R., Tikhonov,A., Marx,P.A., MacPhee,R.D.
Mol. Biol. Evol. 18 (5), 840-847 (5 2001)
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Expect Value: 1e-06
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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)
5 AF312042.1 CCTACCTCAC AGTTACATCA ACTCTCCAGC CCTATATCAT AATTTAGT-C CAAAGGGACC (1-59)
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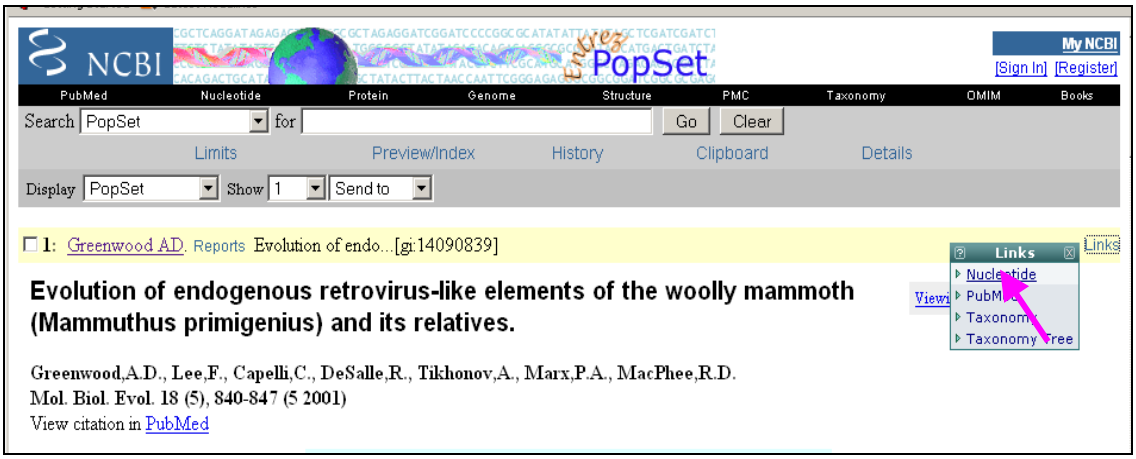
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Links
Links
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PubMed
Taxonomy
Taxonomy Tree
Evolution of endogenous retrovirus-like elements of the woolly mammoth (Mammuthus primigenius) and its relatives.
Greenwood,A.D., Lee,F., Capelli,C., DeSalle,R., Tikhonov,A., Marx,P.A., MacPhee,R.D.
Mol. Biol. Evol. 18 (5), 840-847 (5 2001)
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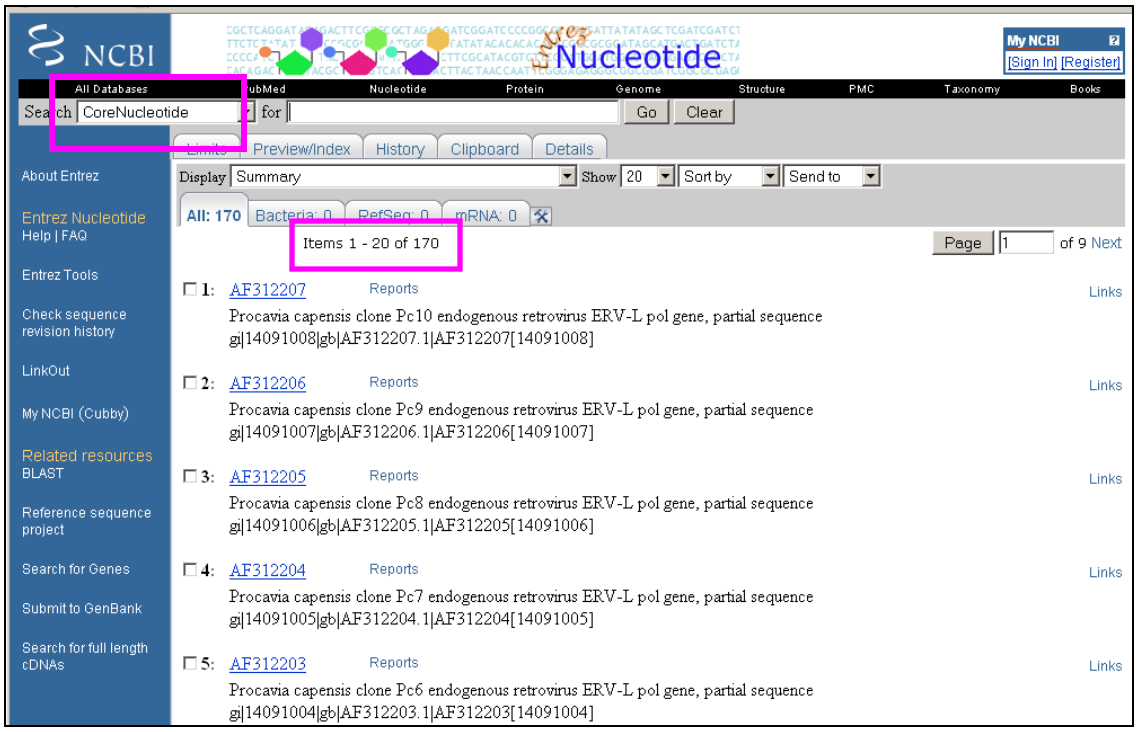
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Show 20
Sort by
Send to
All: 170
Bacteria: 0
RefSeq: 0
mRNA: 0
Items 1 - 20 of 170
Page 1 of 9 Next
1: AF312207 Reports Links
Procavia capensis clone Pc10 endogenous retrovirus ERV-L pol gene, partial sequence
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2: AF312206 Reports Links
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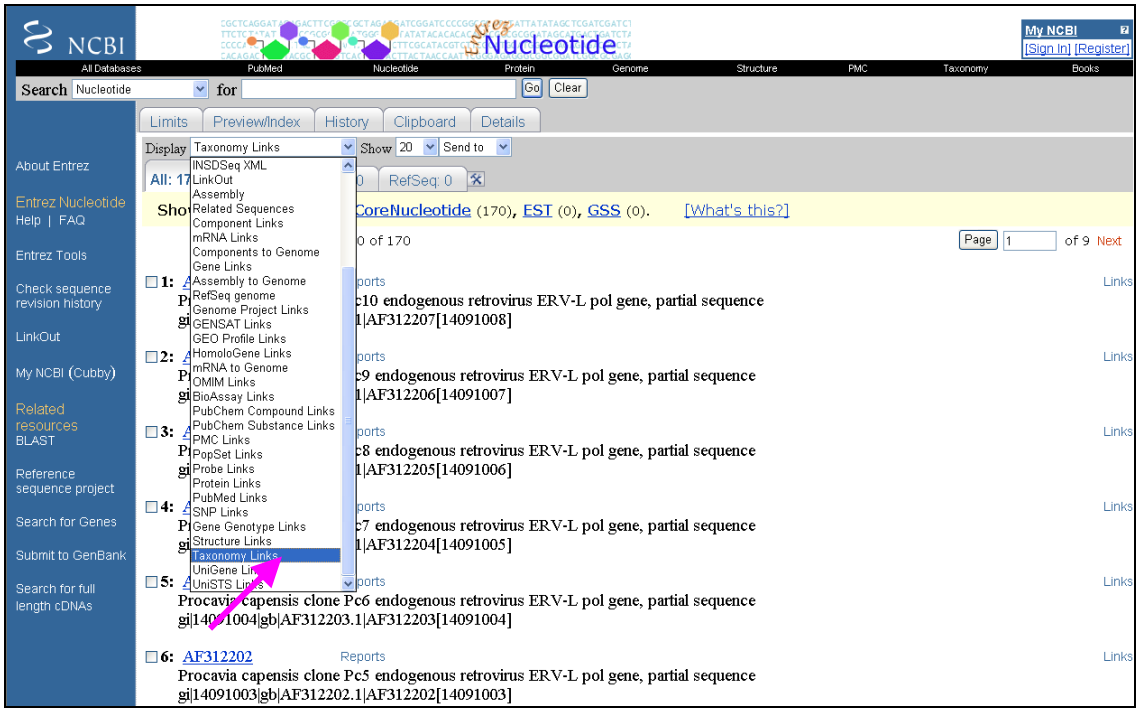
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SNP Links
Gene Genotype Links
Structure Links
Taxonomy Links
UniGene Links
UniSTS Links
CoreNucleotide (170), EST (0), GSS (0).
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Page 1 of 9 Next
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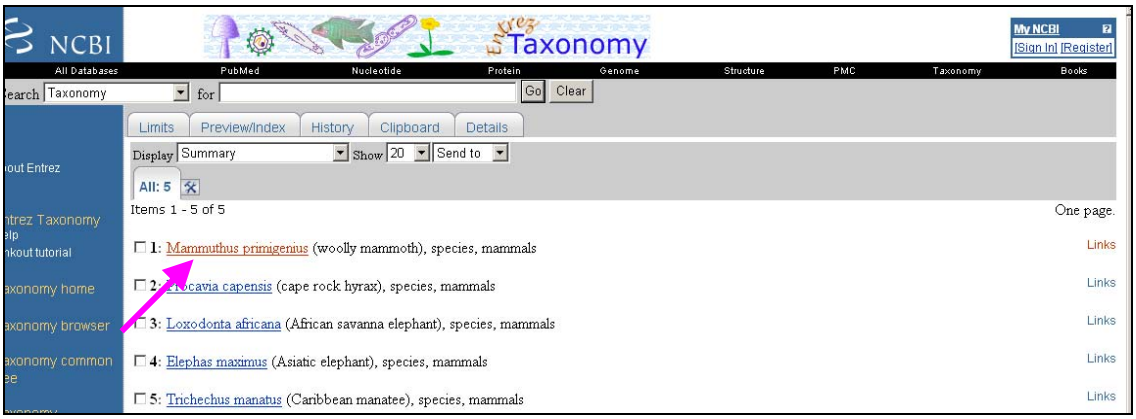
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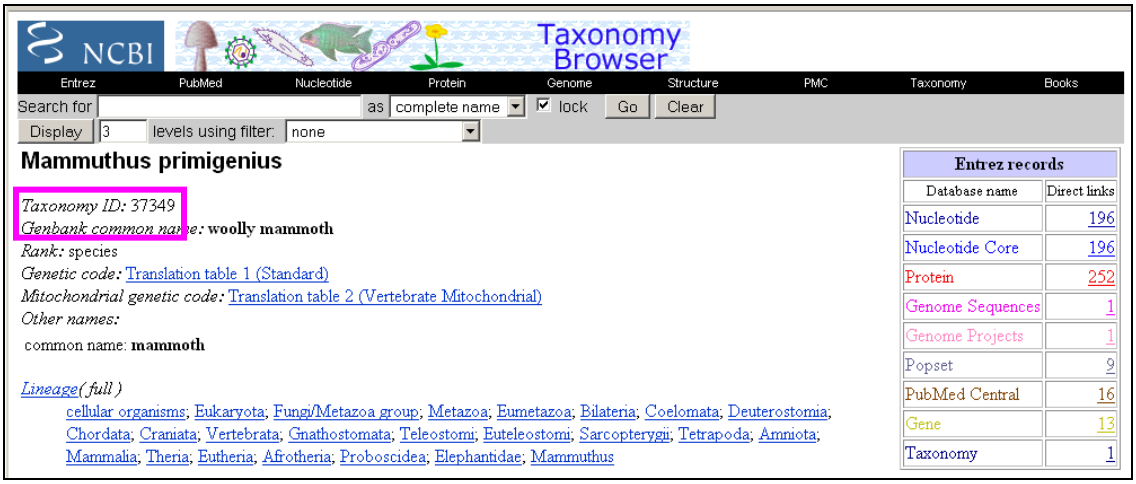
Items 1 - 5 of 5
One page.
1: Mammuthus primigenius (woolly mammoth), species, mammals
2: Procavia capensis (cape rock hyrax), species, mammals
3: Loxodonta africana (African savanna elephant), species, mammals
4: Elephas maximus (Asiatic elephant), species, mammals
5: Trichechus manatus (Caribbean manatee), species, mammals
Links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Taxonomy Browser
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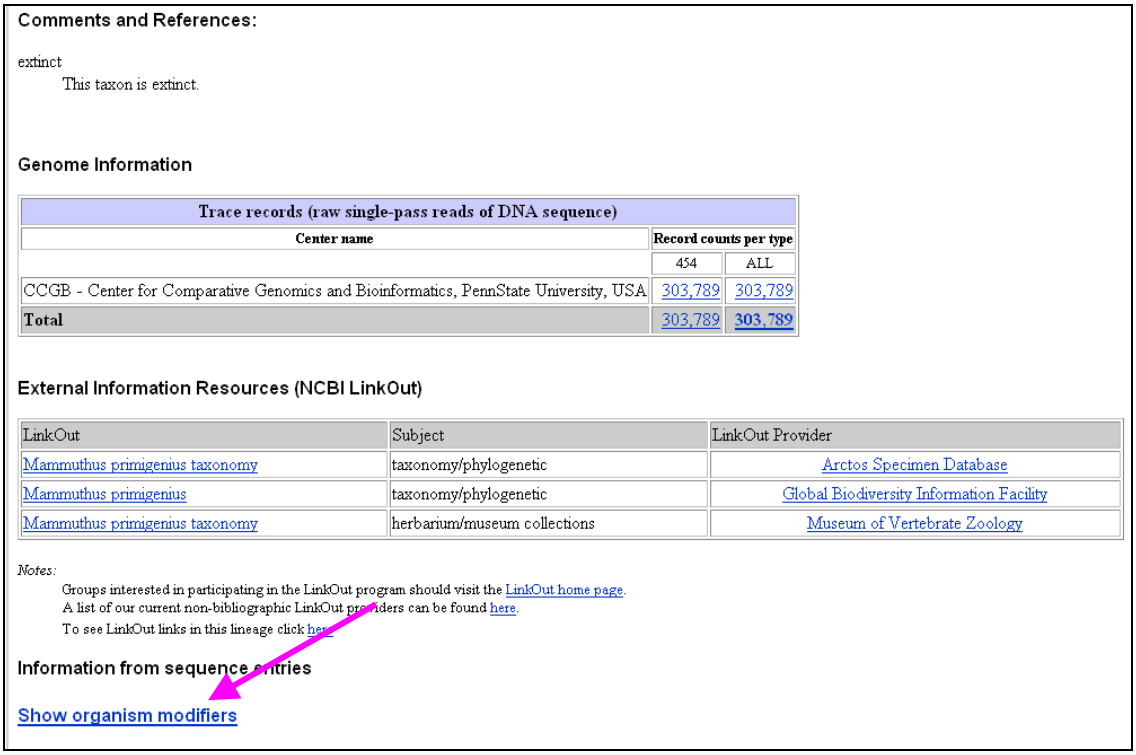
Search for as complete name lock Go Clear
Display 3 levels using filter: none
Mammuthus primigenius
Taxonomy ID: 37349
Genbank common name: woolly mammoth
Rank: species
Genetic code: Translation table 1 (Standard)
Mitochondrial genetic code: Translation table 2 (Vertebrate Mitochondrial)
Other names:
common name: mammoth
Lineage (full)
cellular organisms; Eukaryota; Fungi/Metazoa group; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Afrotheria; Proboscidea; Elephantidae; Mammuthus
Entrez records
Database name | Direct links
Nucleotide 196
Nucleotide Core 196
Protein 252
Genome Sequences 1
Genome Projects 1
Popset 9
PubMed Central 16
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
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A list of our current non-bibliographic LinkOut providers can be found here.
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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]
Wrangel Island 2 [1 1]	alaska8460 [2]	chekurovkam [1]	

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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	196
Nucleotide Core	196
Protein	252
Genome Sequences	1
Genome Projects	1
Popset	9
PubMed Central	16
Gene	13
Taxonomy	1

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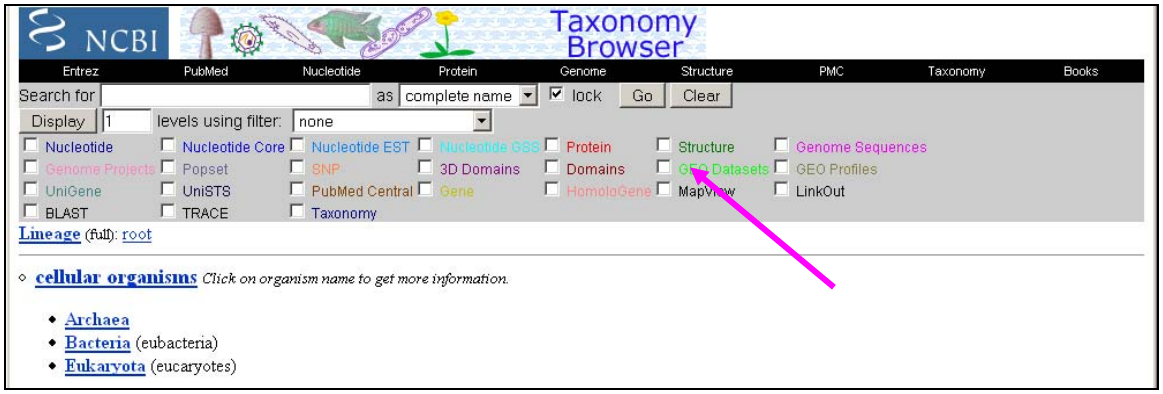
Nucleotide Protein Structure Genome Sequences Genome Projects Popset SNP
3D Domains Domains GEO Datasets GEO Expressions UniGene UniSTS PubMed Central
Gene HomoloGene MapView LinkOut BLAST TRACE

Lineage (full): root

- cellular organisms *Click on organism name to get more information.*
  - Archaea
    - Crenarchaeota (eocytes)
      - Thermoprotei
      - unclassified Crenarchaeota
      - environmental samples
    - Euryarchaeota
      - Archaeoglobi
      - Halobacteria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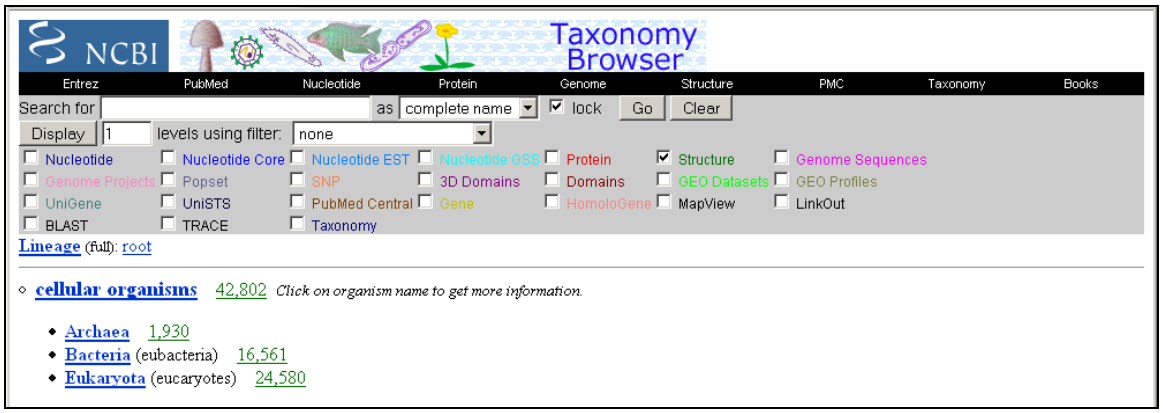
Genome Projects Popset SNP 3D Domains Domains GEO Datasets GEO Profiles
UniGene UniSTS PubMed Central Gene HomoloGene MapView LinkOut
BLAST TRACE Taxonomy
Lineage (full): root
cellular organisms Click on organism name to get more information.
Archaea
Bacteria (eubacteria)
Eukaryota (eucaryotes)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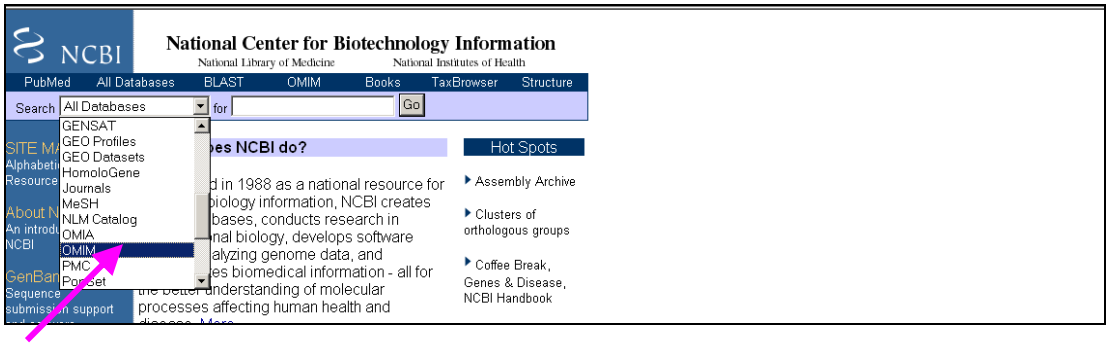
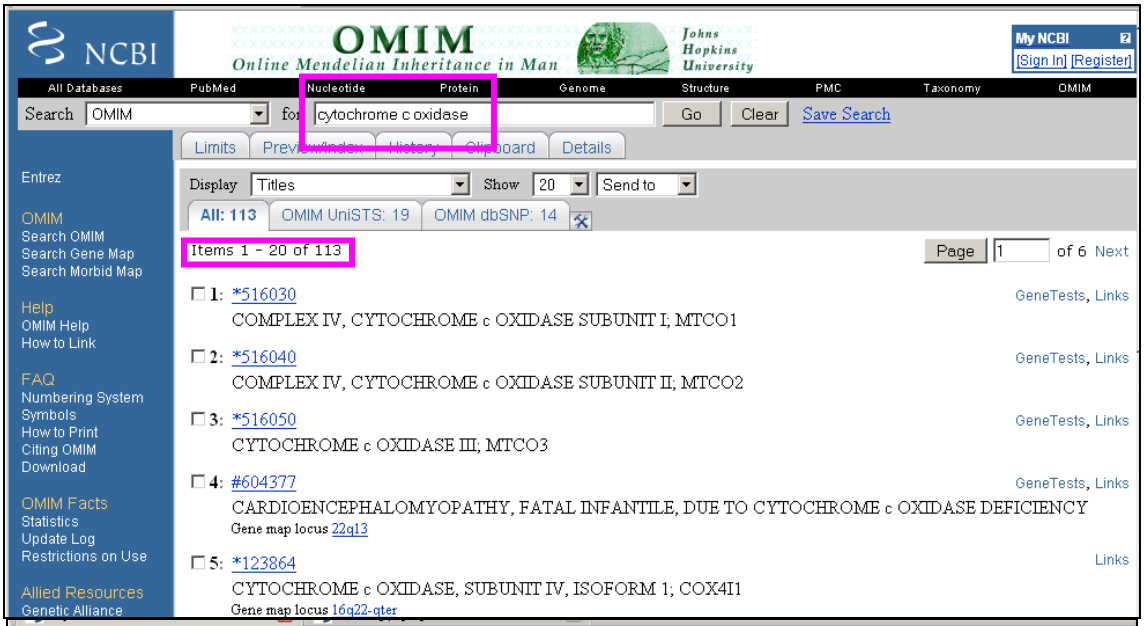
BLAST TRACE Taxonomy
Lineage (full): root
cellular organisms 42,802 Click on organism name to get more information.
Archaea 1,930
Bacteria (eubacteria) 16,561
Eukaryota (eucaryotes) 24,580

Example1, Part II





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R RefSeq
G GenBank
P 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.

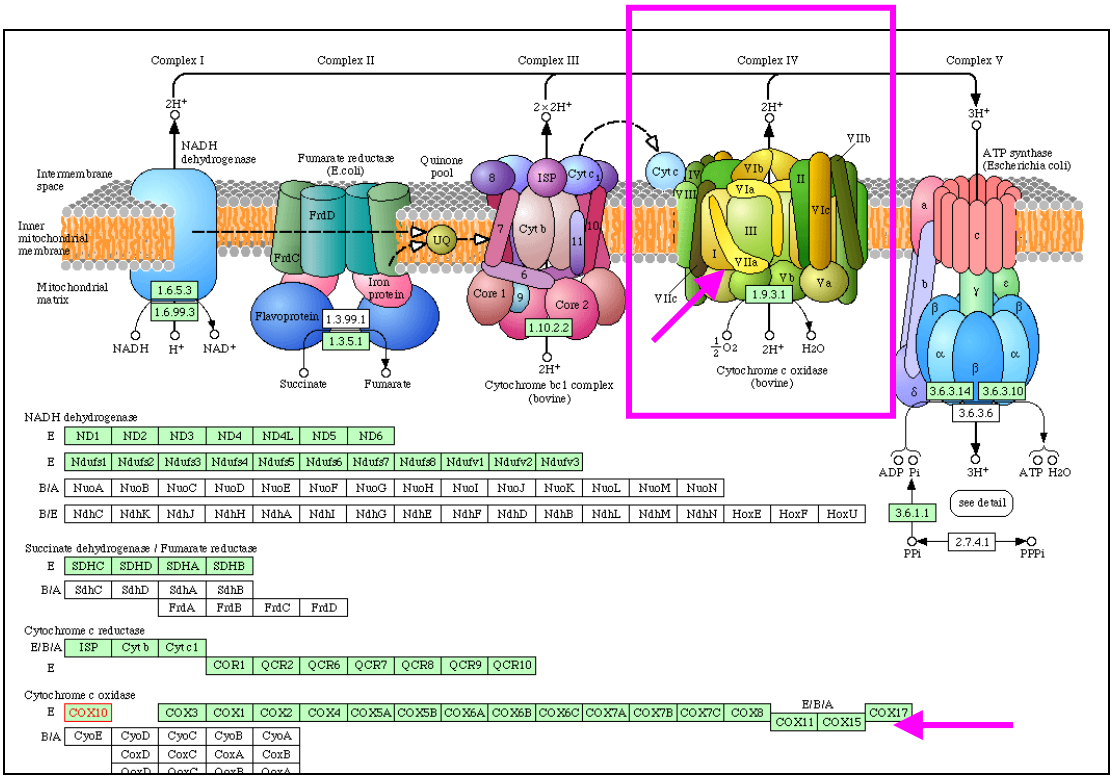

Figure from KEGG **Oxidative phosphorylation - Reference pathway (KO)**
http://www.genome.jp/dbget-bin/show_pathway?hsa00190+4512

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All: 88 OMIM UniSTS: 15 OMIM dbSNP: 8
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1: *516030
COMPLEX IV, CYTOCHROME c OXIDASE SUBUNIT I; MTCO1
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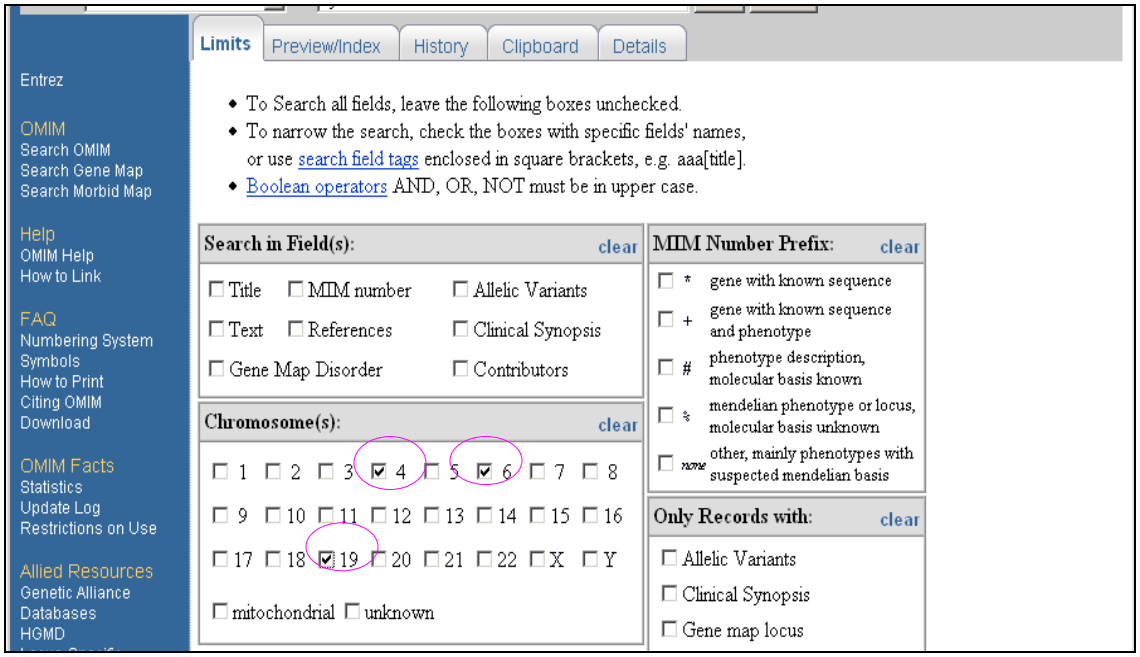
CYTOCHROME c OXIDASE III; MTCO3
GeneTests, Links
3: *516040
GeneTests, Links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1 2 3 4 5 6 7 8
9 10 11 12 13 14 15 16
17 18 19 20 21 22 X Y
mitochondrial unknown
MIM Number Prefix: clear
* gene with known sequence
+ gene with known sequence and phenotype
# phenotype description, molecular basis known
% mendelian phenotype or locus, molecular basis unknown
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Limits: **chromosome 4, chromosome 6, chromosome 19**

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Items 1 - 12 of 12 — One page.

1: *123995 — Links
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Gene map locus 9q13.12

2: *123996 — Links
CYTOCHROME c OXIDASE, SUBUNIT VIIa, POLYPEPTIDE 2; COX7A2
Gene map locus 6q12

3: *123997 — Links
CYTOCHROME c OXIDASE, SUBUNIT VIIa, POLYPEPTIDE 3; COX7A3
Gene map locus 4q22

4: *124089 — Links
CYTOCHROME c OXIDASE, SUBUNIT VIb; COX6B
Gene map locus 19q13.1

5: #256000 — GeneTests, Links
LEIGH SYNDROME; LS
LEIGH SYNDROME DUE TO MITOCHONDRIAL COMPLEX I DEFICIENCY, INCLUDED
Gene map locus 19p13, 11q13, 11q13, 11p11.11, 10q24, 9q34, 7q31-q32, 5q11.1, 5p15, 2q33

6: #607426 — GeneTests, Links
COENZYME Q10 DEFICIENCY
Gene map locus 9p13.3, 6q21, 4q21-q22

7: #157640 — GeneTests, Links
PROGRESSIVE EXTERNAL OPHTHALMOPLEGIA WITH MITOCHONDRIAL DNA DELETIONS, AUTOSOMAL DOMINANT, 1
PROGRESSIVE EXTERNAL OPHTHALMOPLEGIA WITH HYPOGONADISM, INCLUDED
Gene map locus 15q25, 4q35

8: #602473 — GeneTests, Links
ENCEPHALOPATHY, ETHYLMALONIC
Gene map locus 19q13.32

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Cloning
Gene Structure
Mapping
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Contributors
Creation Date
Edit History

Gene map

Entrez Gene
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R RefSeq
G GenBank
P Protein
U UniGene

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***123995**
CYTOCHROME c OXIDASE, SUBUNIT VIIa, POLYPEPTI

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GEO Profiles
HomoloGene
Free in PMC
PubMed (calculated)
PubMed (cited)
Gene Genotype
GeneView in dbSNP
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Alternative titles; symbols

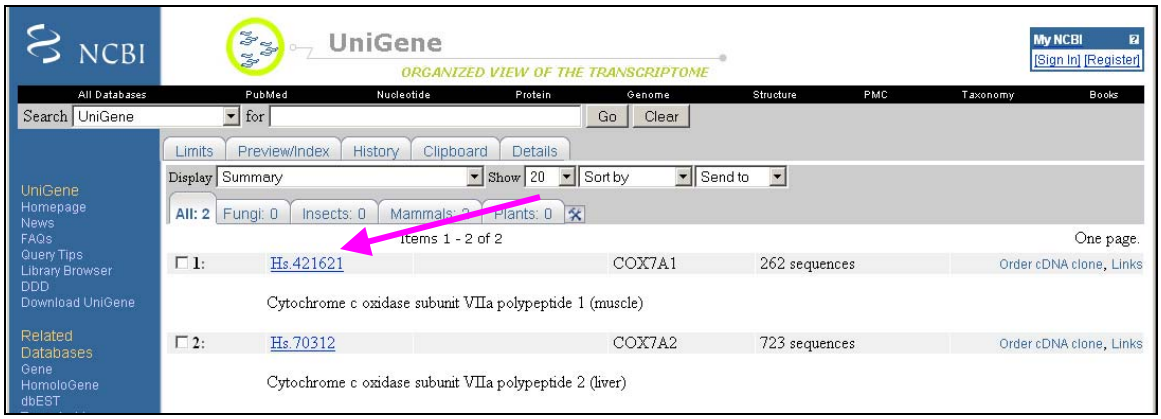
CYTOCHROME c OXIDASE, SUBUNIT VIIa, MUSCLE ISOFORM

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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2: Hs.70312 COX7A2 723 sequences Order cDNA clone, Links
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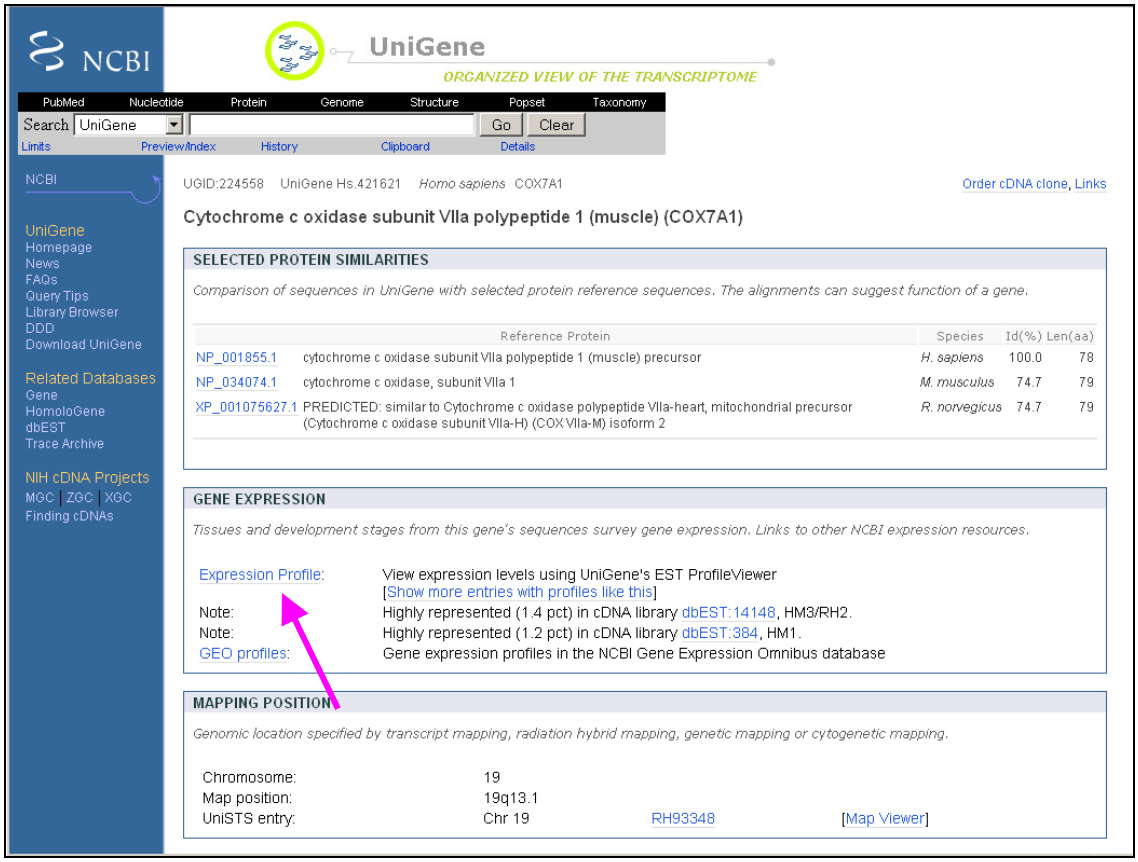
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UGID:224558 UniGene Hs.421621 Homo sapiens COX7A1
Order cDNA clone, Links
Cytochrome c oxidase subunit VIIa polypeptide 1 (muscle) (COX7A1)
SELECTED PROTEIN SIMILARITIES
Comparison of sequences in UniGene with selected protein reference sequences. The alignments can suggest function of a gene.
Reference Protein Species Id(%) Len(aa)
NP_001855.1 cytochrome c oxidase subunit VIIa polypeptide 1 (muscle) precursor H. sapiens 100.0 78
NP_034074.1 cytochrome c oxidase, subunit VIIa 1 M. musculus 74.7 79
XP_001075627.1 PREDICTED: similar to Cytochrome c oxidase polypeptide VIIa-heart, mitochondrial precursor (Cytochrome c oxidase subunit VIIa-H) (COX VIIa-M) isoform 2 R. norvegicus 74.7 79
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
[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
MAPPING POSITION
Genomic location specified by transcript mapping, radiation hybrid mapping, genetic mapping or cytogenetic mapping.
Chromosome: 19
Map position: 19q13.1
UniSTS entry: Chr 19 RH93348 [Map Viewer]
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Finding cDNAs

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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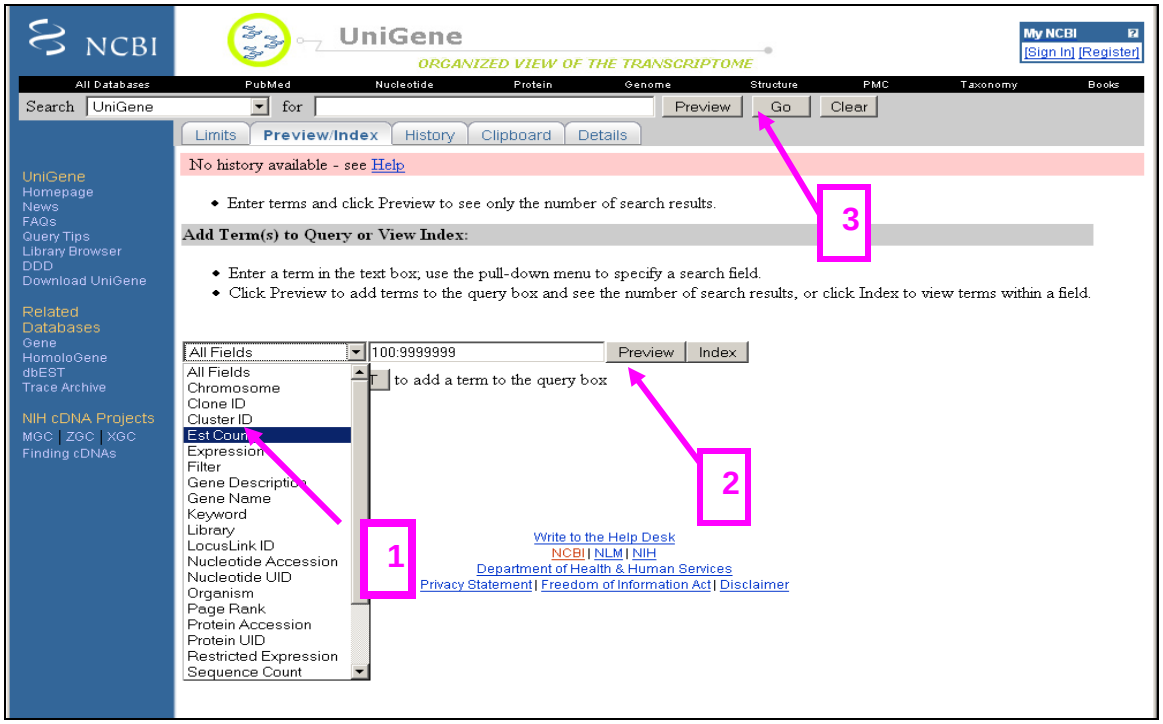
1: Hs.421621 — COX7A1 — 262 sequences — Order cDNA clone, Links
Cytochrome c oxidase subunit VIIa polypeptide 1 (muscle)

2: Hs.70312 — COX7A2 — 723 sequences — Order cDNA clone, Links
Cytochrome c oxidase subunit VIIa polypeptide 2 (liver)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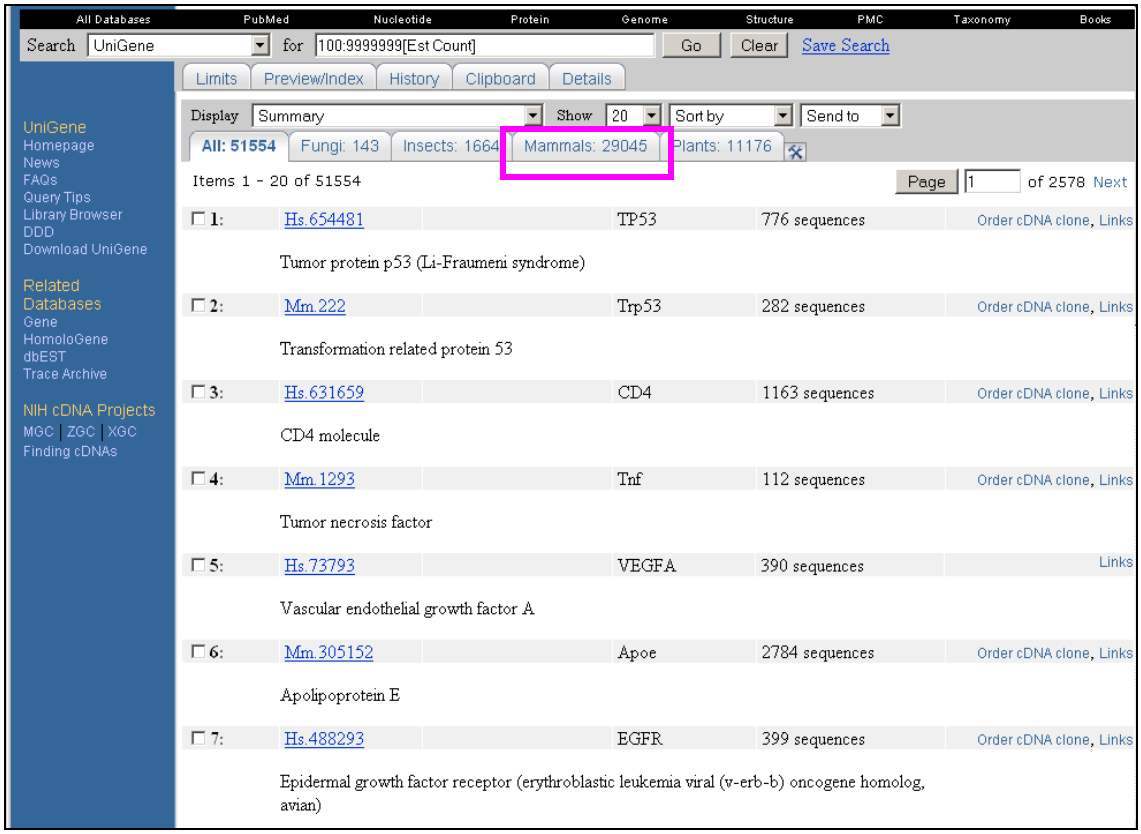
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1: Hs.654481 TP53 776 sequences Order cDNA clone, Links
Tumor protein p53 (Li-Fraumeni syndrome)
2: Mm.222 Trp53 282 sequences Order cDNA clone, Links
Transformation related protein 53
3: Hs.631659 CD4 1163 sequences Order cDNA clone, Links
CD4 molecule
4: Mm.1293 Tnf 112 sequences Order cDNA clone, Links
Tumor necrosis factor
5: Hs.73793 VEGFA 390 sequences Links
Vascular endothelial growth factor A
6: Mm.305152 Apoe 2784 sequences Order cDNA clone, Links
Apolipoprotein E
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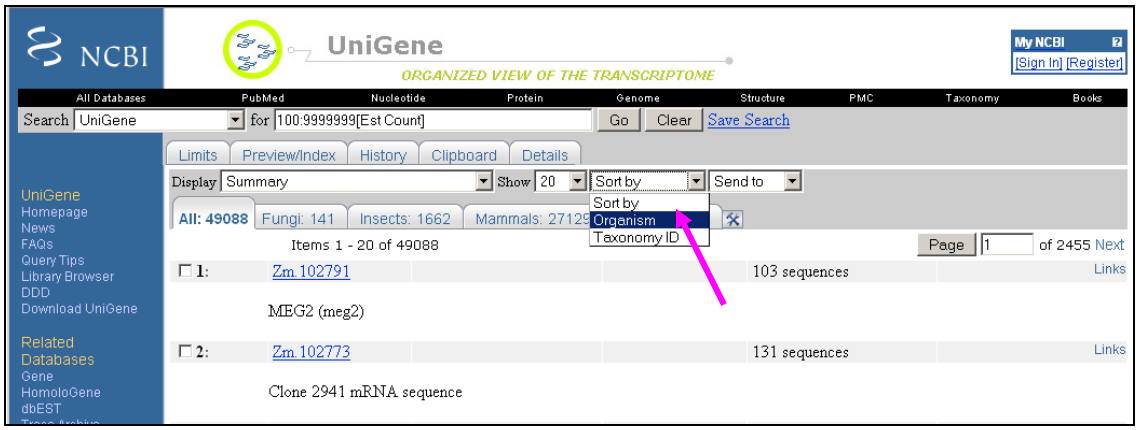
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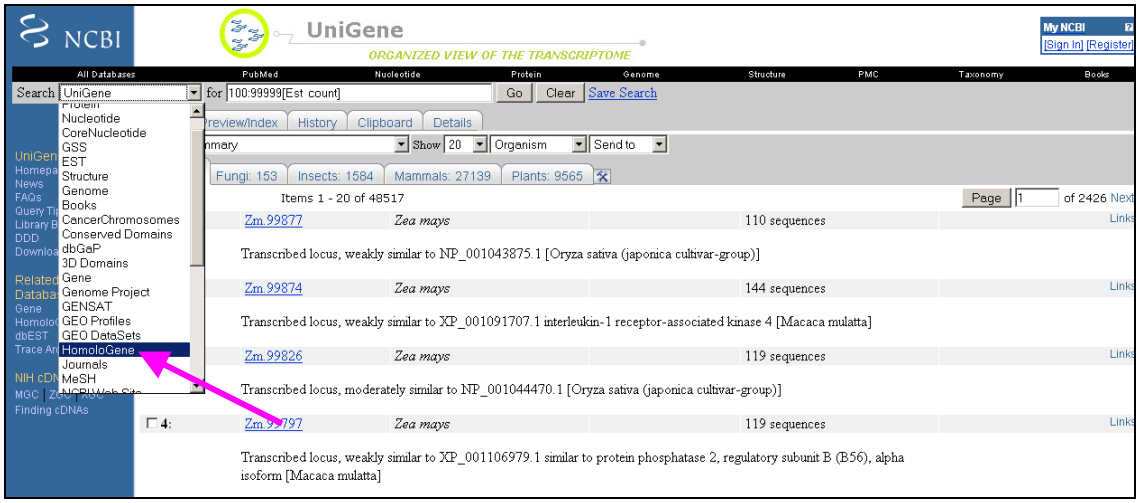
MEG2 (meg2)
2: Zm.102773 131 sequences Links
Clone 2941 mRNA sequence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Zm.99874 Zea mays 144 sequences Links
Transcribed locus, weakly similar to XP_001091707.1 interleukin-1 receptor-associated kinase 4 [Macaca mulatta]
Zm.99826 Zea mays 119 sequences Links
Transcribed locus, moderately similar to NP_001044470.1 [Oryza sativa (japonica cultivar-group)]
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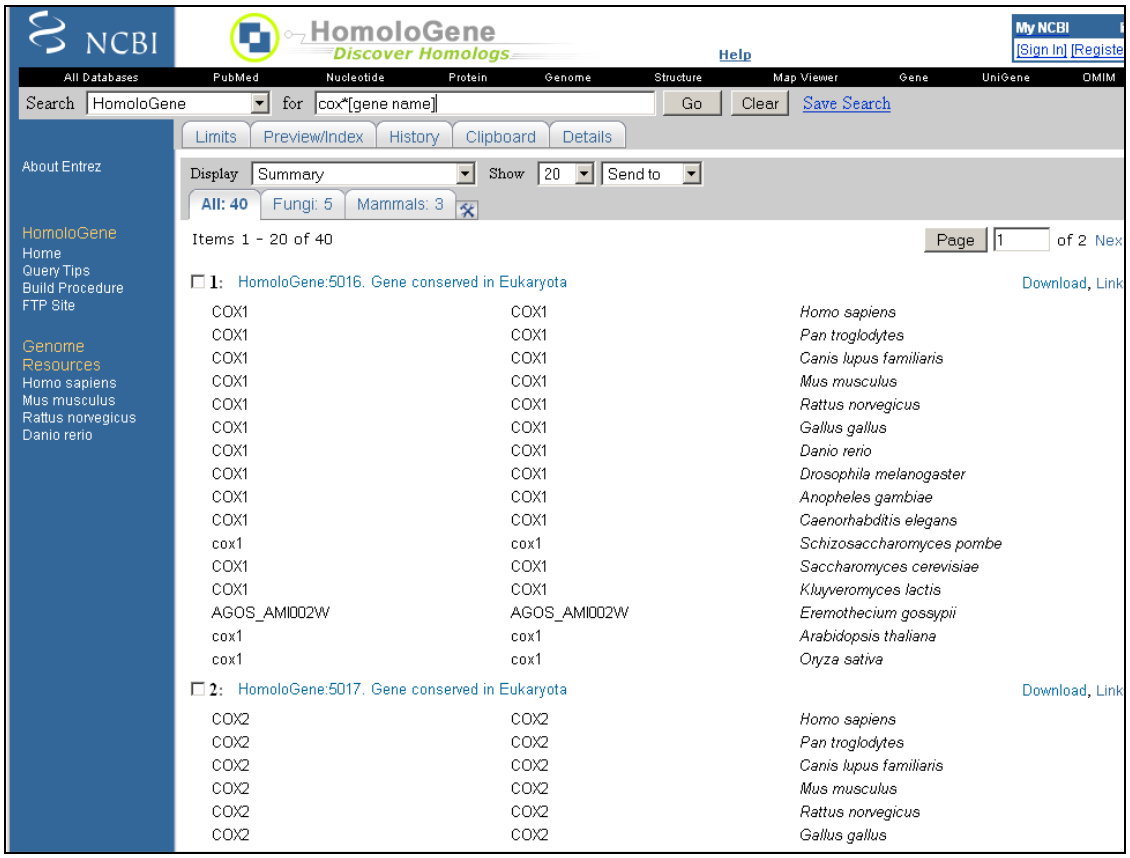
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COX1 COX1 Saccharomyces cerevisiae
COX1 COX1 Kluyveromyces lactis
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cox1 cox1 Oryza sativa
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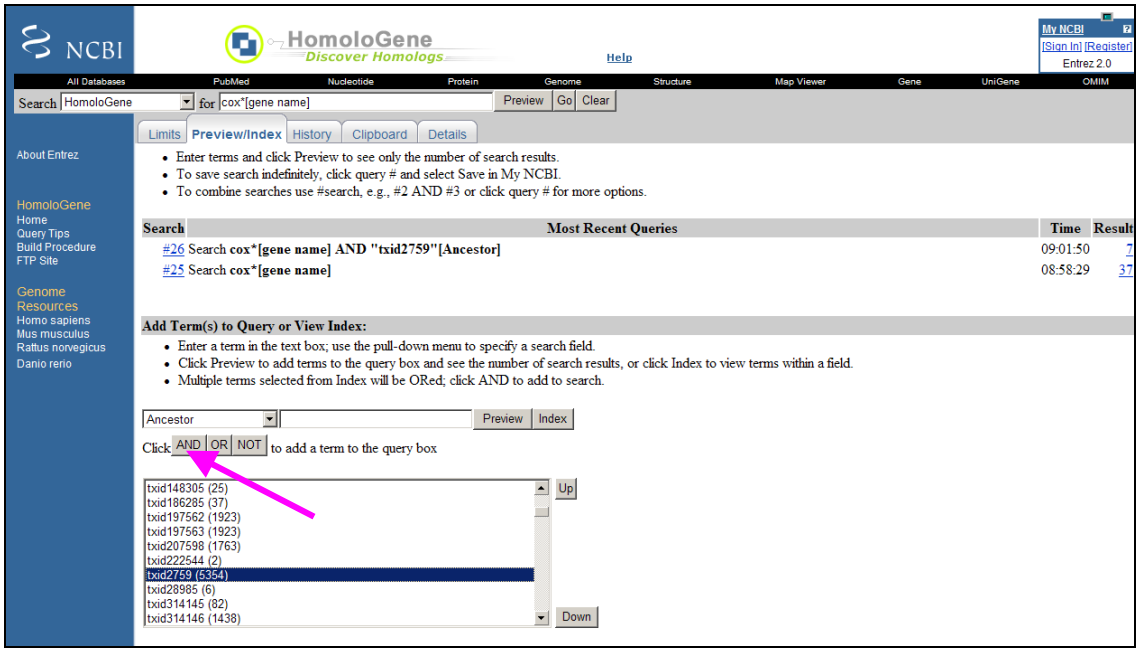
COX2 COX2 Gallus gallus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txid207598 (1763)
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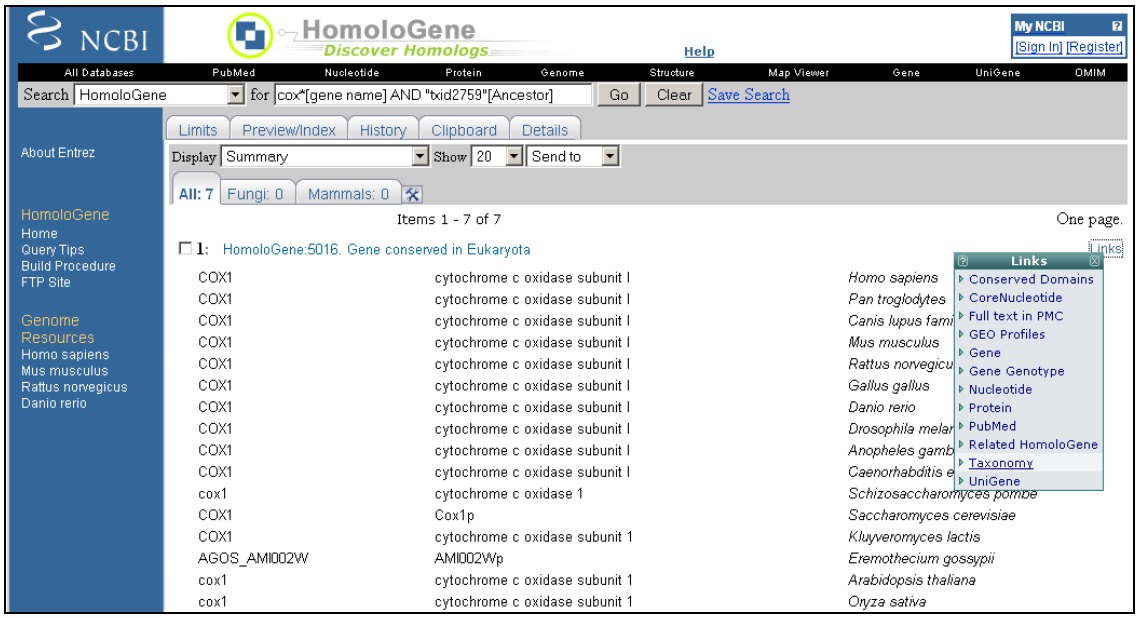
Down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COX1 Cox1p Saccharomyces cerevisiae
COX1 cytochrome c oxidase subunit 1 Kluyveromyces lactis
AGOS_AMI002W AMI002Wp Eremothecium gossypii
cox1 cytochrome c oxidase subunit 1 Arabidopsis thaliana
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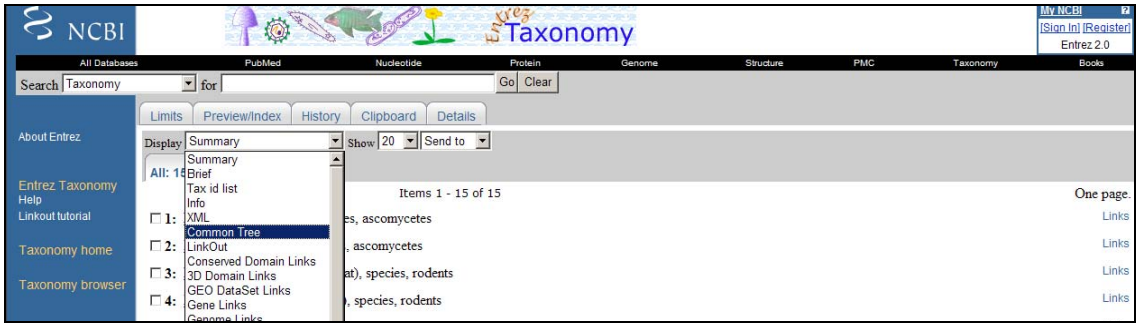
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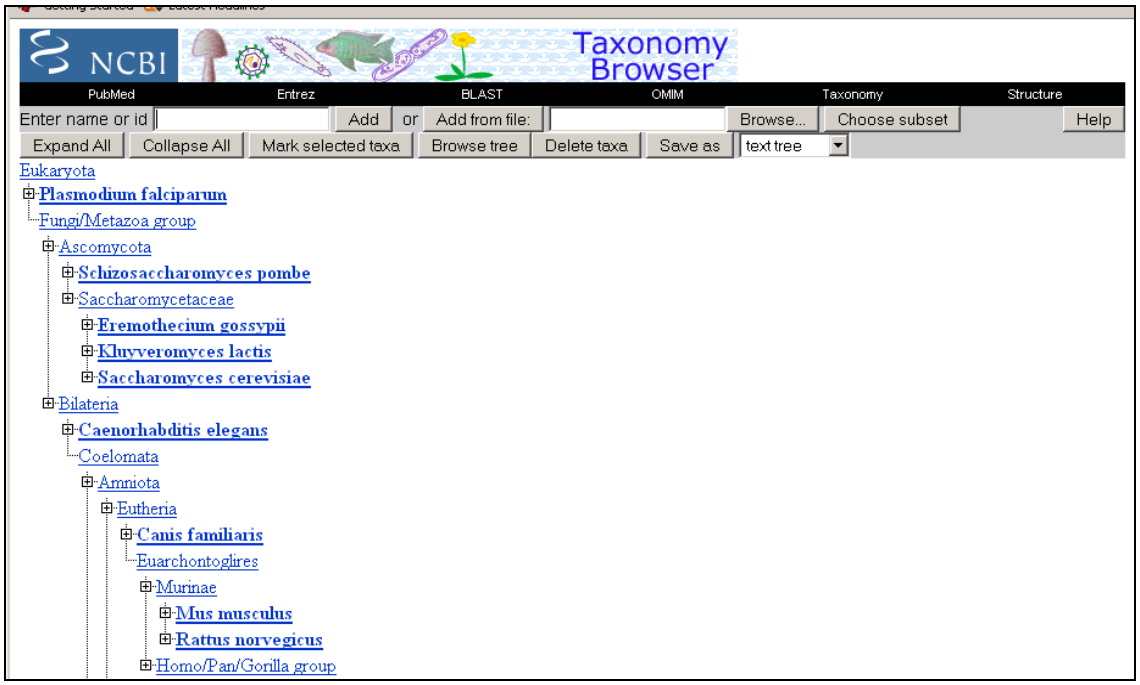
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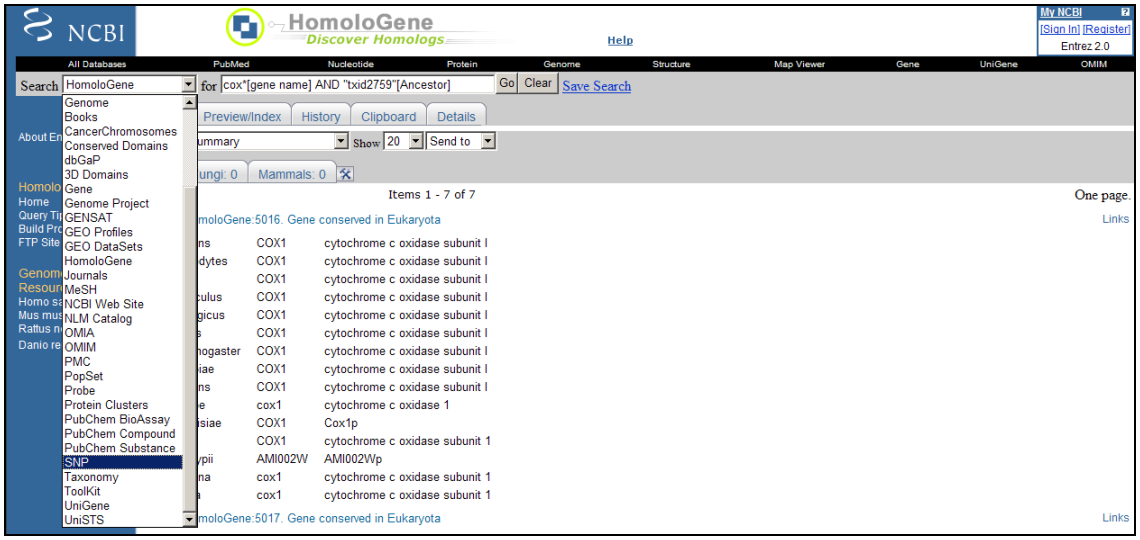
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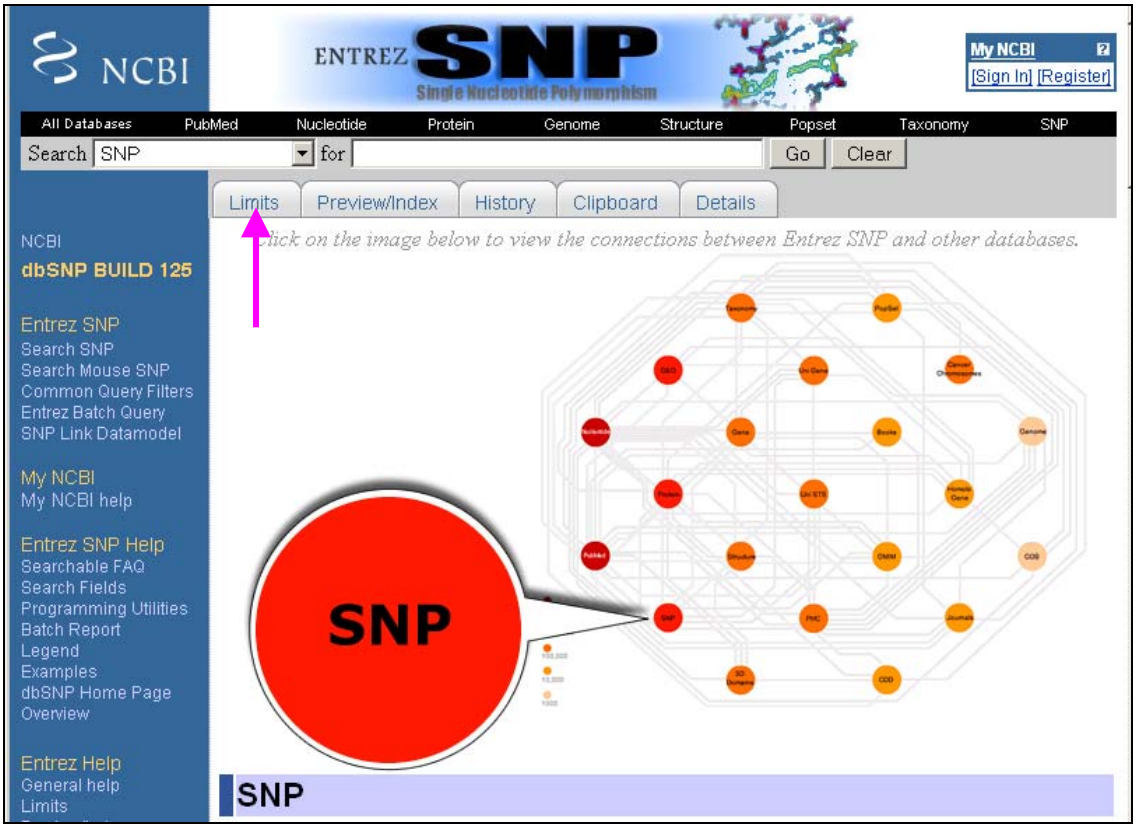

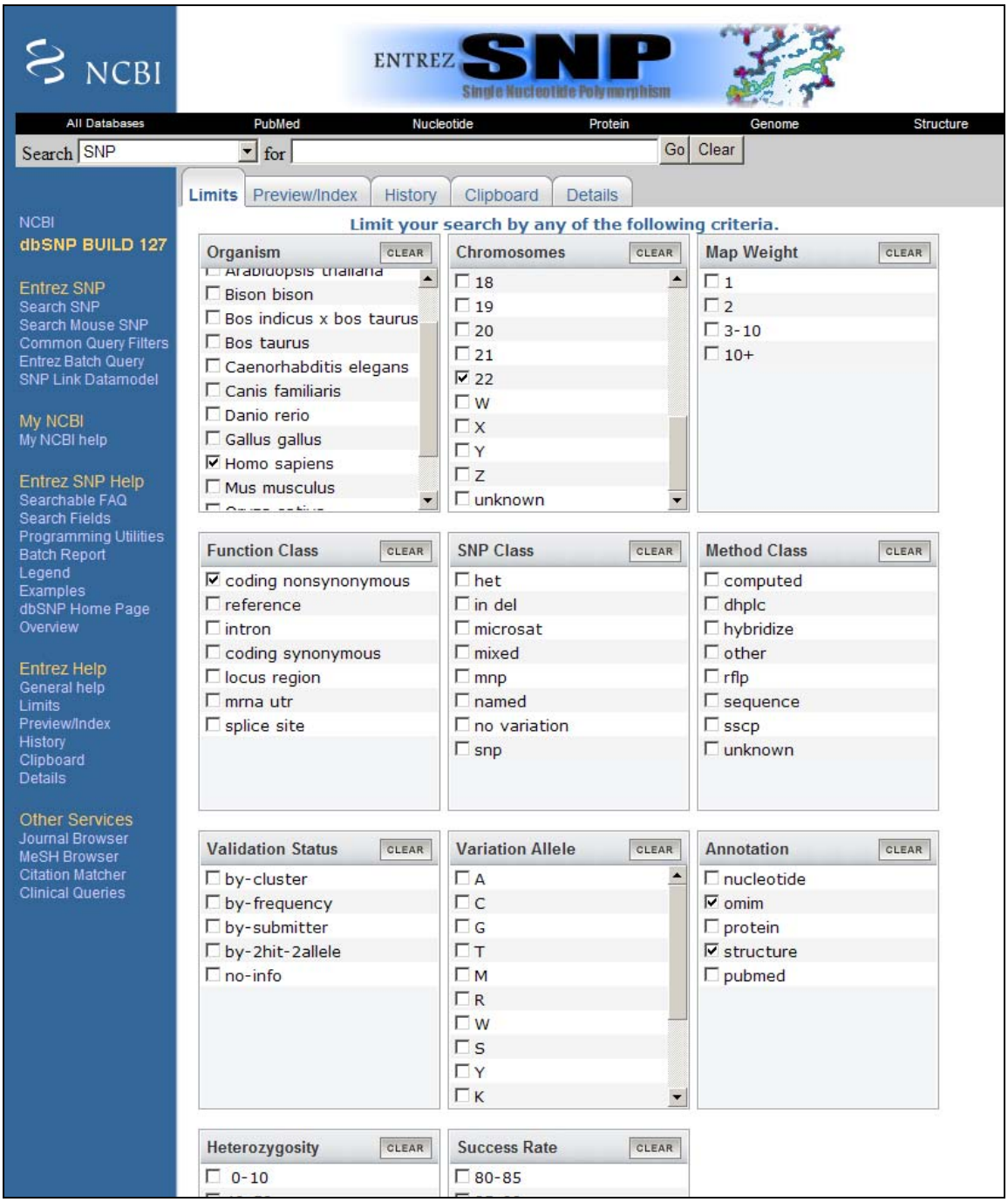
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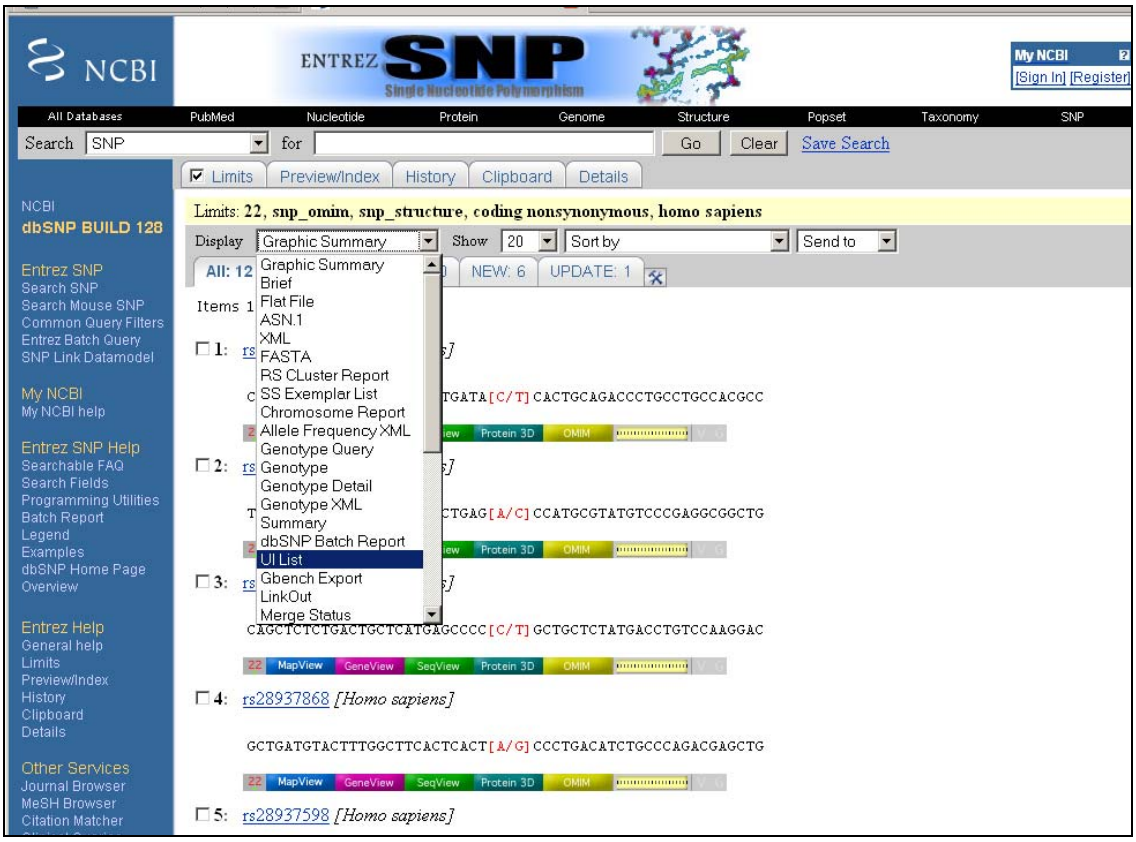
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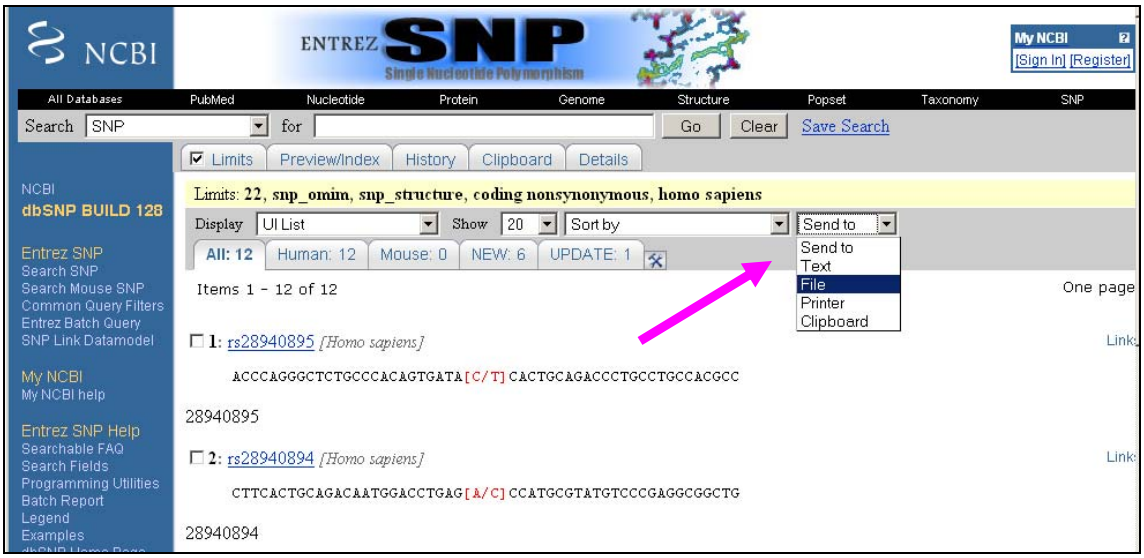
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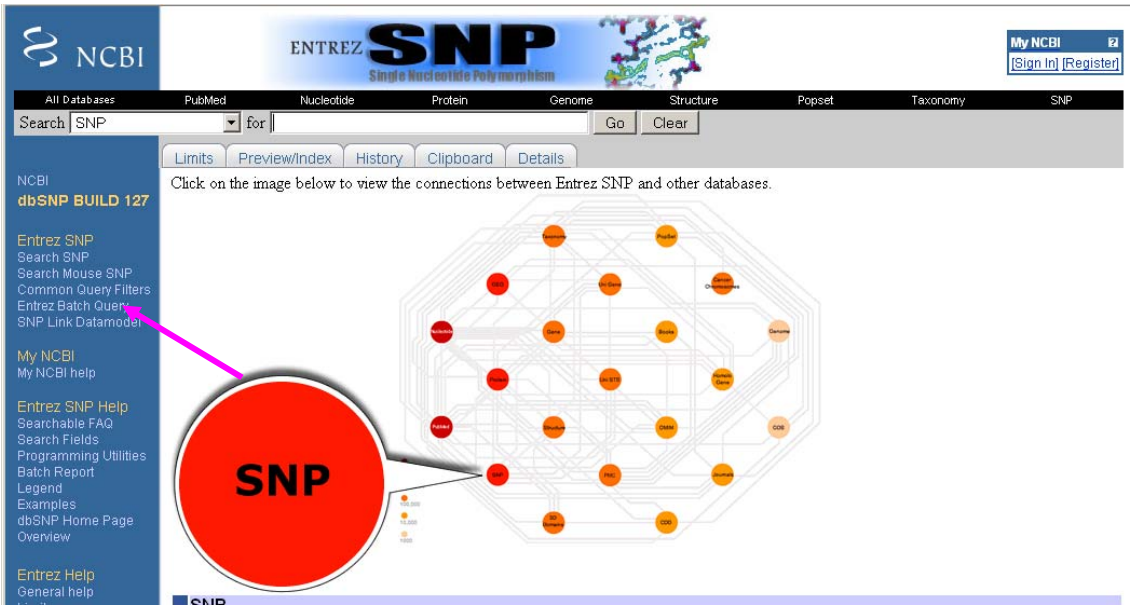
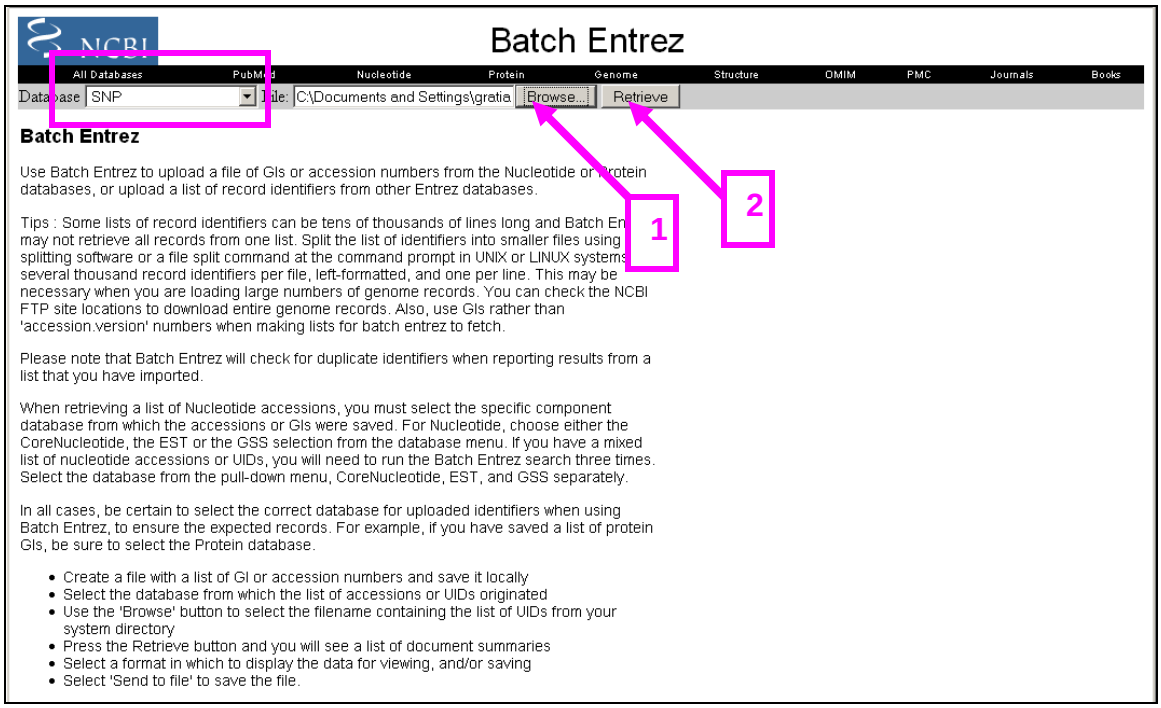
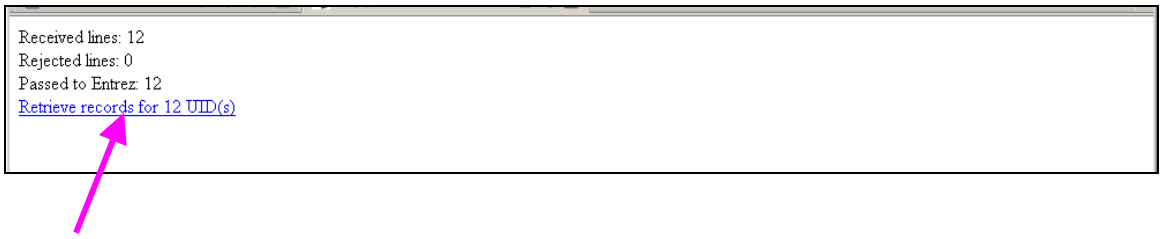
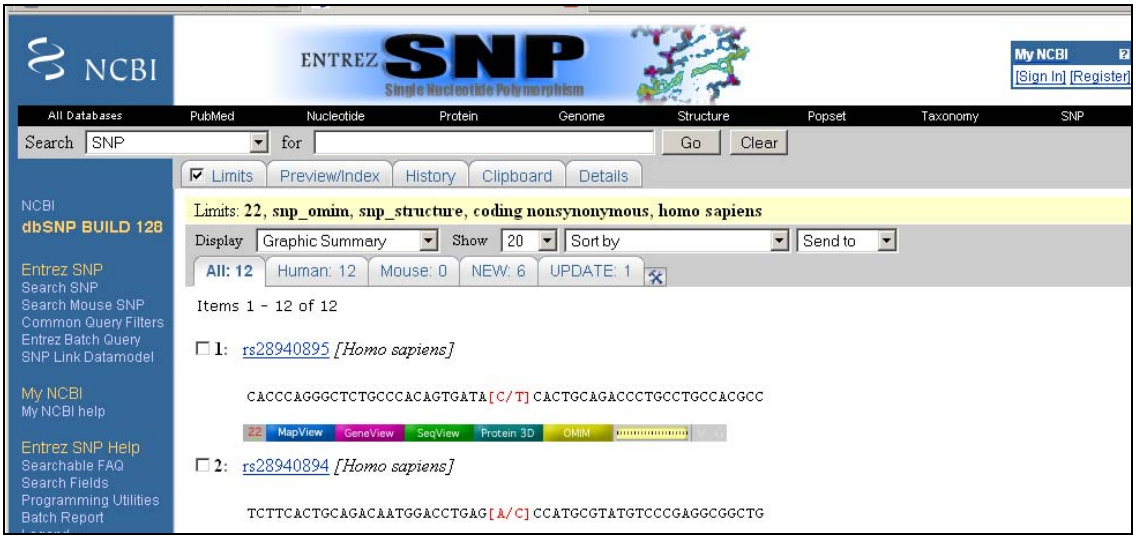
Limits: 22, snp_omim, snp_structure, coding nonsynonymous, homo sapiens
Display UI List Show 20 Sort by Send to
All: 12 Human: 12 Mouse: 0 NEW: 6 UPDATE: 1
Send to
Text
File
Printer
Clipboard
Items 1 - 12 of 12
One page
1: rs28940895 [Homo sapiens]
ACCCAGGGCTCTGCCCACAGTGATA[C/T]CACTGCAGACCCTGCCTGCCACGCC
28940895
2: rs28940894 [Homo sapiens]
CTTCACTGCAGACAATGGACCTGAG[A/C]CCATGCGTATGTCCCGAGGCGGCTG
28940894
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

```
28940895
28940894
28940893
28937868
28937598
28931613
5030865
2071421
1064422
16947
6267
5907
```

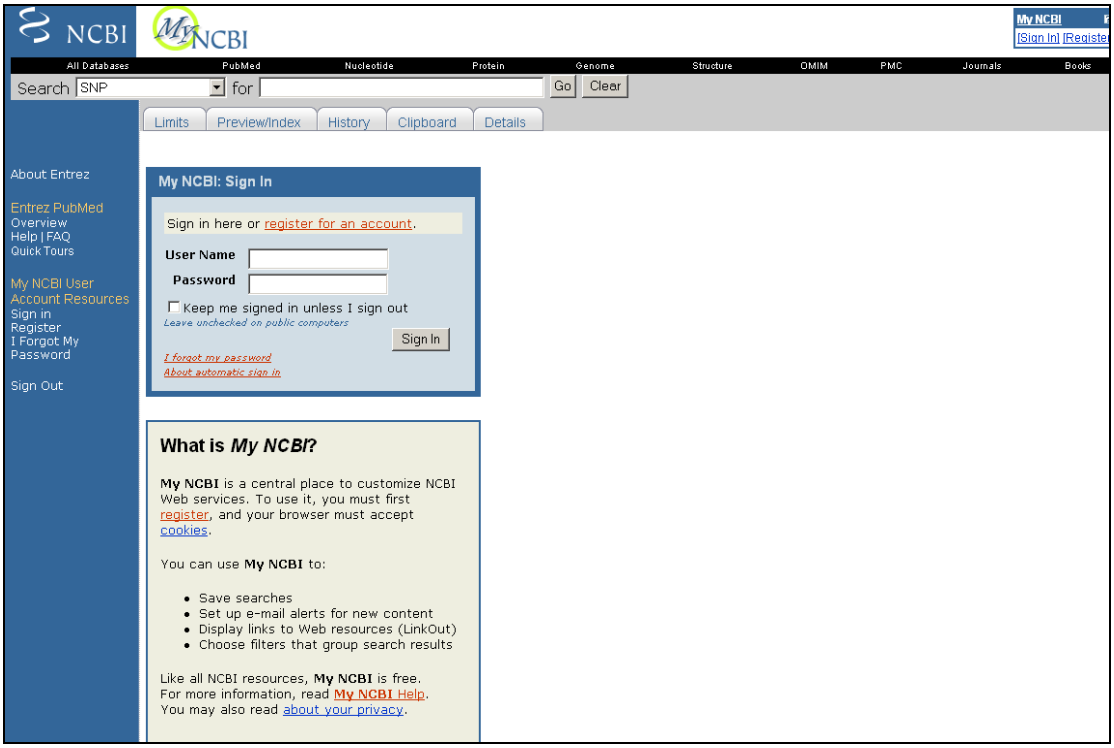


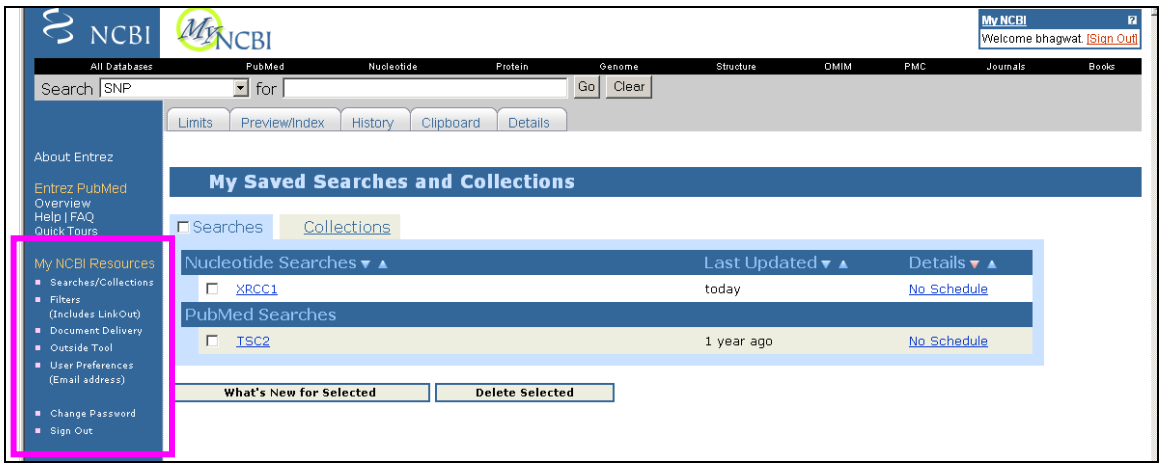

NCBI
Batch Entrez
All Databases
PubMed
Nucleotide
Protein
Genome
Structure
OMIM
PMC
Journals
Books
Database SNP
File: C:\Documents and Settings\gratia
Browse...
Retrieve
1
2
Batch Entrez
Use Batch Entrez to upload a file of GIs or accession numbers from the Nucleotide or Protein databases, or upload a list of record identifiers from other Entrez databases.
Tips : Some lists of record identifiers can be tens of thousands of lines long and Batch Entrez may not retrieve all records from one list. Split the list of identifiers into smaller files using splitting software or a file split command at the command prompt in UNIX or LINUX systems several thousand record identifiers per file, left-formatted, and one per line. This may be necessary when you are loading large numbers of genome records. You can check the NCBI FTP site locations to download entire genome records. Also, use GIs rather than 'accession.version' numbers when making lists for batch entrez to fetch.
Please note that Batch Entrez will check for duplicate identifiers when reporting results from a list that you have imported.
When retrieving a list of Nucleotide accessions, you must select the specific component database from which the accessions or GIs were saved. For Nucleotide, choose either the CoreNucleotide, the EST or the GSS selection from the database menu. If you have a mixed list of nucleotide accessions or UIDs, you will need to run the Batch Entrez search three times. Select the database from the pull-down menu, CoreNucleotide, EST, and GSS separately.
In all cases, be certain to select the correct database for uploaded identifiers when using Batch Entrez, to ensure the expected records. For example, if you have saved a list of protein GIs, be sure to select the Protein database.
• Create a file with a list of GI or accession numbers and save it locally
• Select the database from which the list of accessions or UIDs originated
• Use the 'Browse' button to select the filename containing the list of UIDs from your system directory
• Press the Retrieve button and you will see a list of document summaries
• Select a format in which to display the data for viewing, and/or saving
• Select 'Send to file' to save the file.


Received lines: 12
Rejected lines: 0
Passed to Entrez: 12
Retrieve records for 12 UID(s)

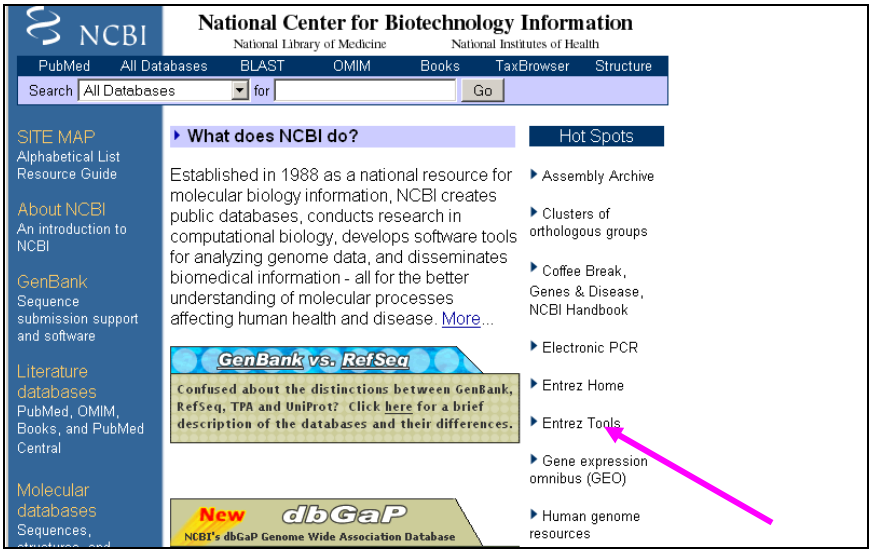

NCBI
ENTREZ SNP
Single Nucleotide Polymorphism
My NCBI
[Sign In] [Register]
All Databases
PubMed
Nucleotide
Protein
Genome
Structure
Popset
Taxonomy
SNP
Search SNP for
Go
Clear
Limits
Preview/Index
History
Clipboard
Details
NCBI
dbSNP BUILD 128
Entrez SNP
Search SNP
Search Mouse SNP
Common Query Filters
Entrez Batch Query
SNP Link Datamodel
My NCBI
My NCBI help
Entrez SNP Help
Searchable FAQ
Search Fields
Programming Utilities
Batch Report
Limits: 22, snp_omim, snp_structure, coding nonsynonymous, homo sapiens
Display Graphic Summary
Show 20
Sort by
Send to
All: 12
Human: 12
Mouse: 0
NEW: 6
UPDATE: 1
Items 1 - 12 of 12
1: rs28940895 [Homo sapiens]
CACCCAGGGCTCTGCCCACAGTGATA[C/T]CACTGCAGACCCTGCCTGCCACGCC
MapView
GeneView
SeqView
Protein 3D
OMIM
2: rs28940894 [Homo sapiens]
TCTTCACTGCAGACAATGGACCTGAG[A/C]CCATGCGTATGTCCCGAGGCGGCTG

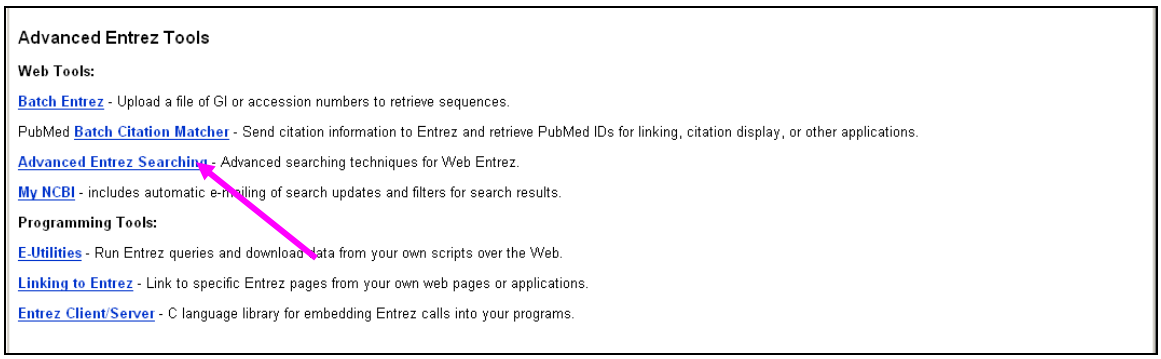
Customized searches:





Documentation:





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.. Navigate to Fig 2 in the Results and Discussion section, 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". Combine the result of the search with the six 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 (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.

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