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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1 OMIM: online Mendelian Inheritance in Man
none OMIA: Online Mendelian Inheritance in Animals
609 Nucleotide: sequence database (GenBank)
173 Protein: sequence database
2 Genome: whole genome sequences
none Structure: three-dimensional macromolecular structures
2 Taxonomy: organisms in GenBank
none SNP: single nucleotide polymorphism
13 Gene: gene-centered information
1 HomoloGene: eukaryotic homology groups
none PubChem Compound: unique small molecule chemical structures
none PubChem Substance: deposited chemical substance records
1 Genome Project: genome project information
2 UniGene: gene-oriented clusters of transcript sequences
none CDD: conserved protein domain database
none 3D Domains: domains from Entrez Structure
none UniSTS: markers and mapping data
30 PopSet: population study data sets
none GEO Profiles: expression and molecular abundance profiles
none GEO DataSets: experimental sets of GEO data
none Cancer Chromosomes: cytogenetic databases
none PubChem BioAssay: bioactivity screens of chemical substances
none GENSAT: gene expression atlas of mouse central nervous system
none Probe: sequence-specific reagents
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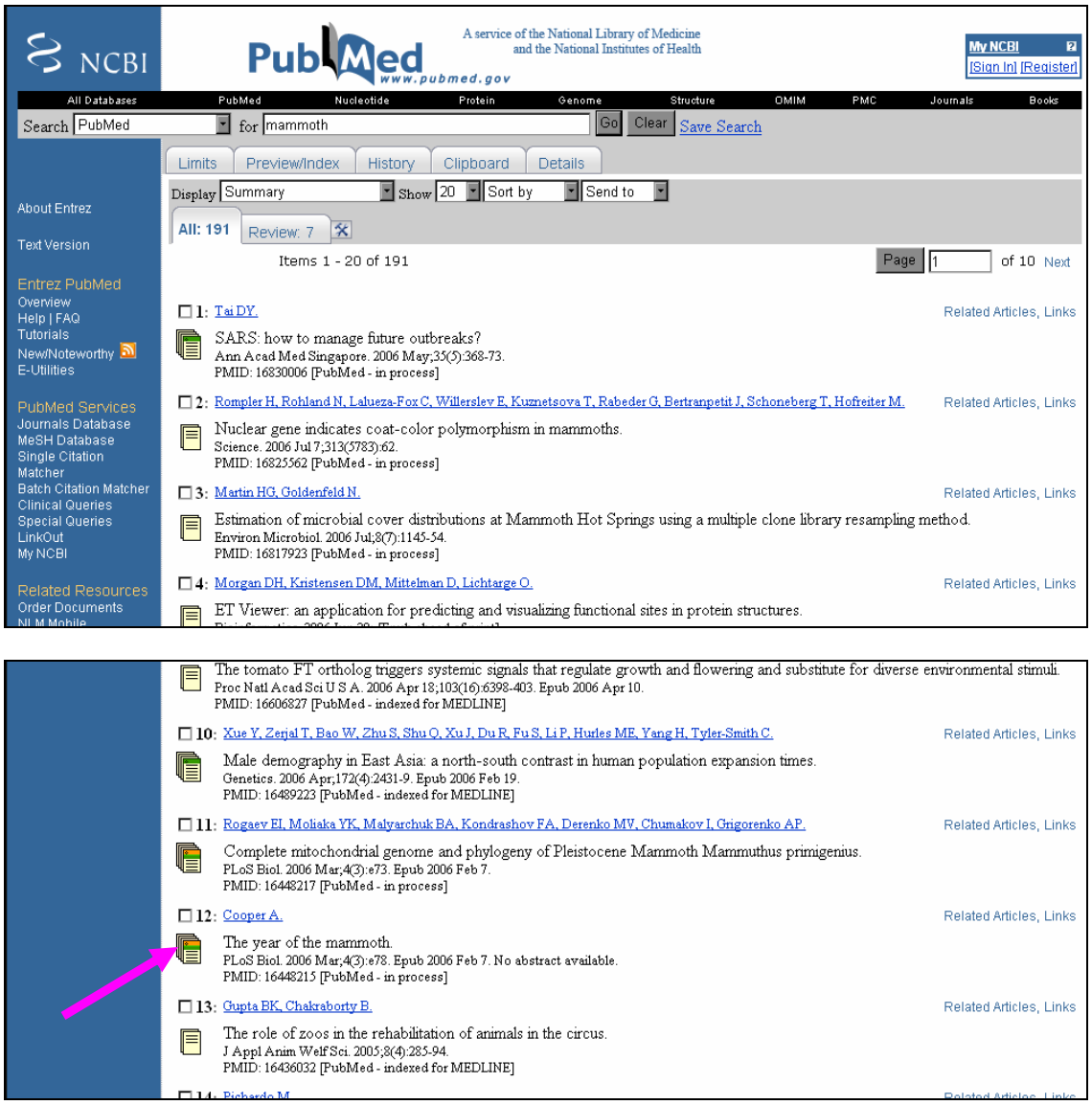
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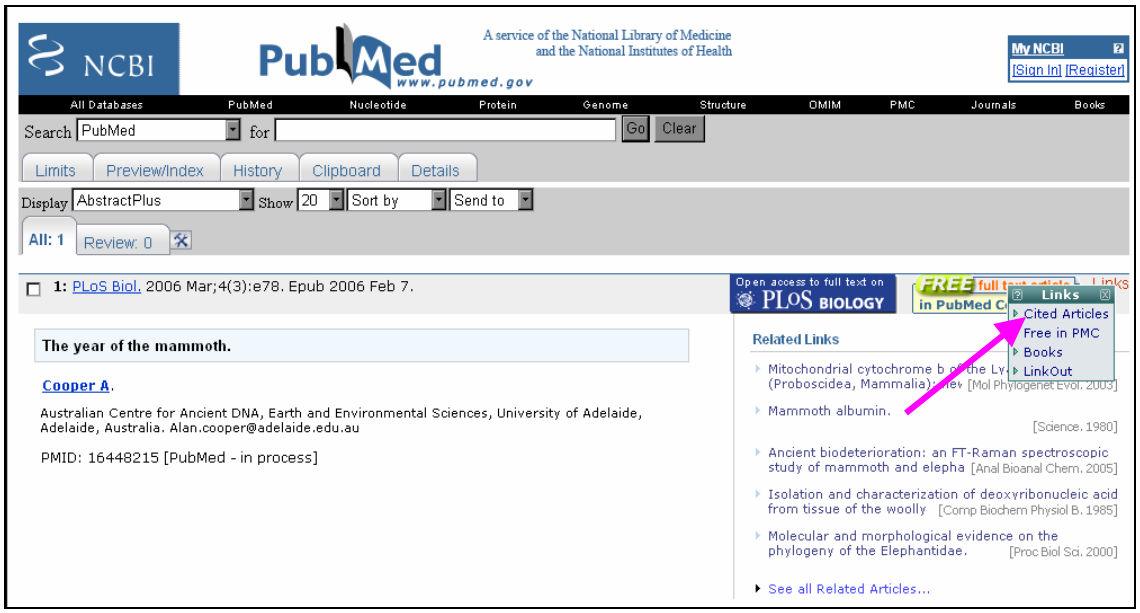
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Brudnick Neuropsychiatric Research Institute, Department of Psychiatry, University of Massachusetts Medical School, Worcester, Massachus
Evgeny.Rogaev@umassmed.edu
Phylogenetic relationships between the extinct woolly mammoth (Mammuthus primigenius), 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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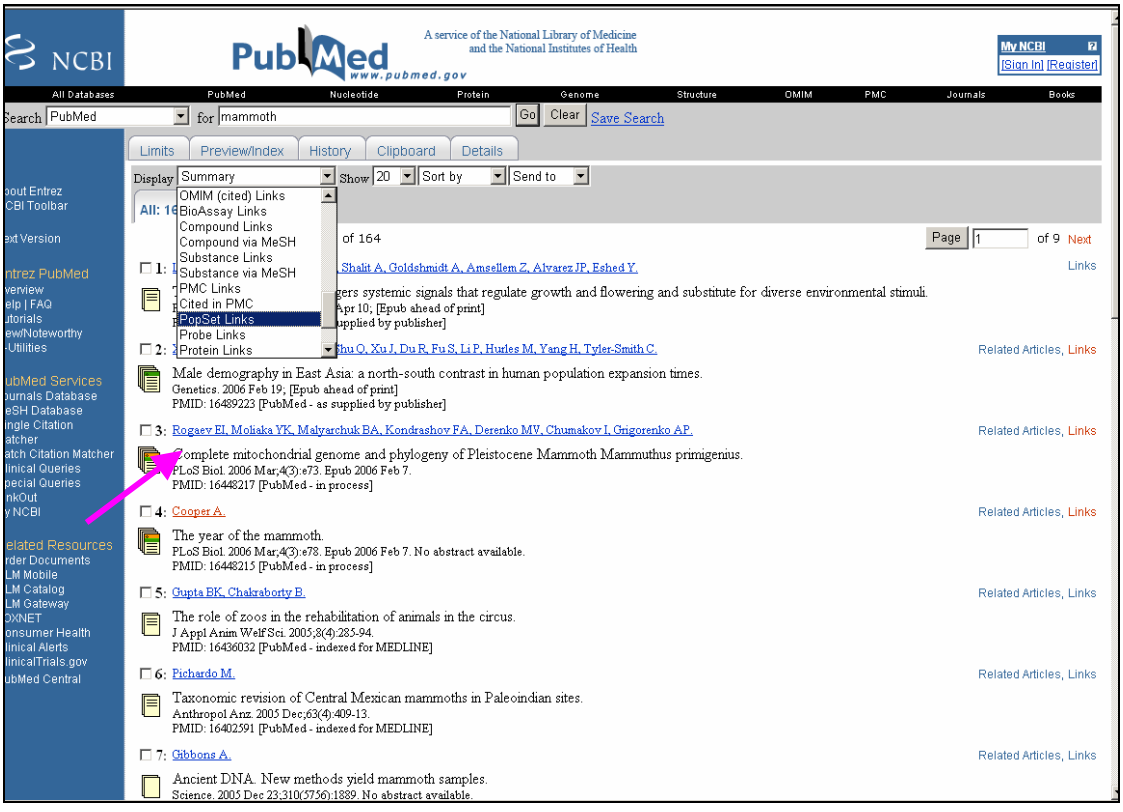
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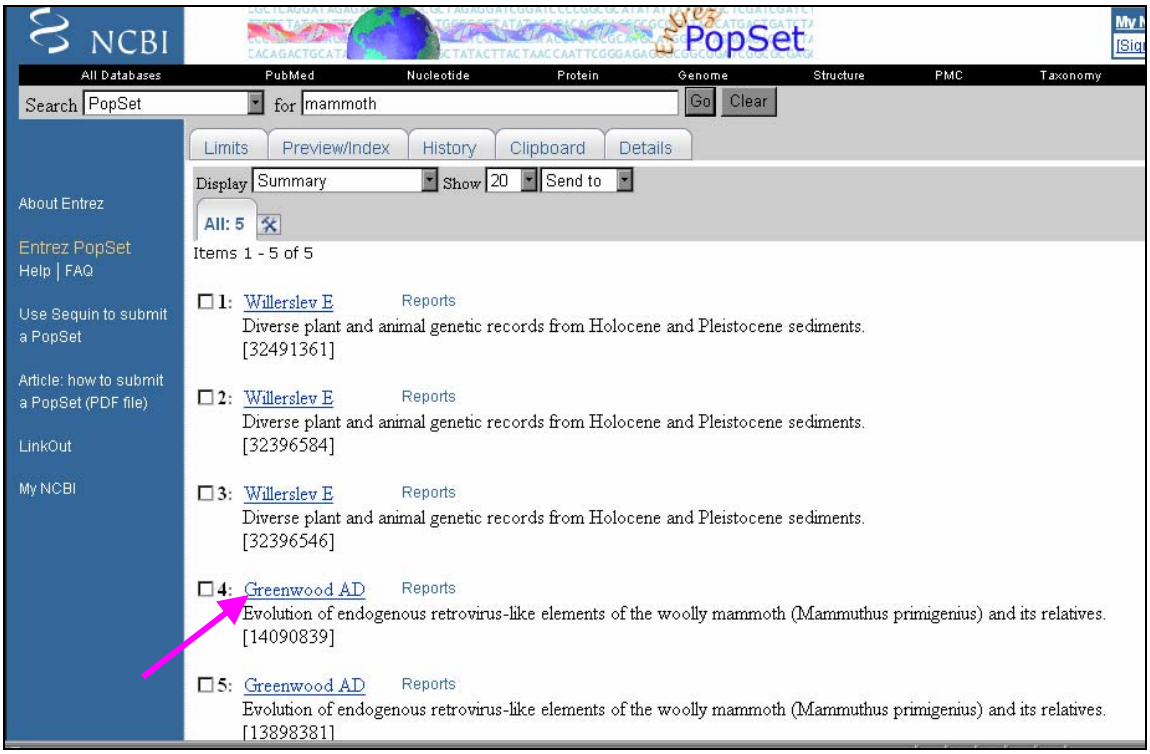
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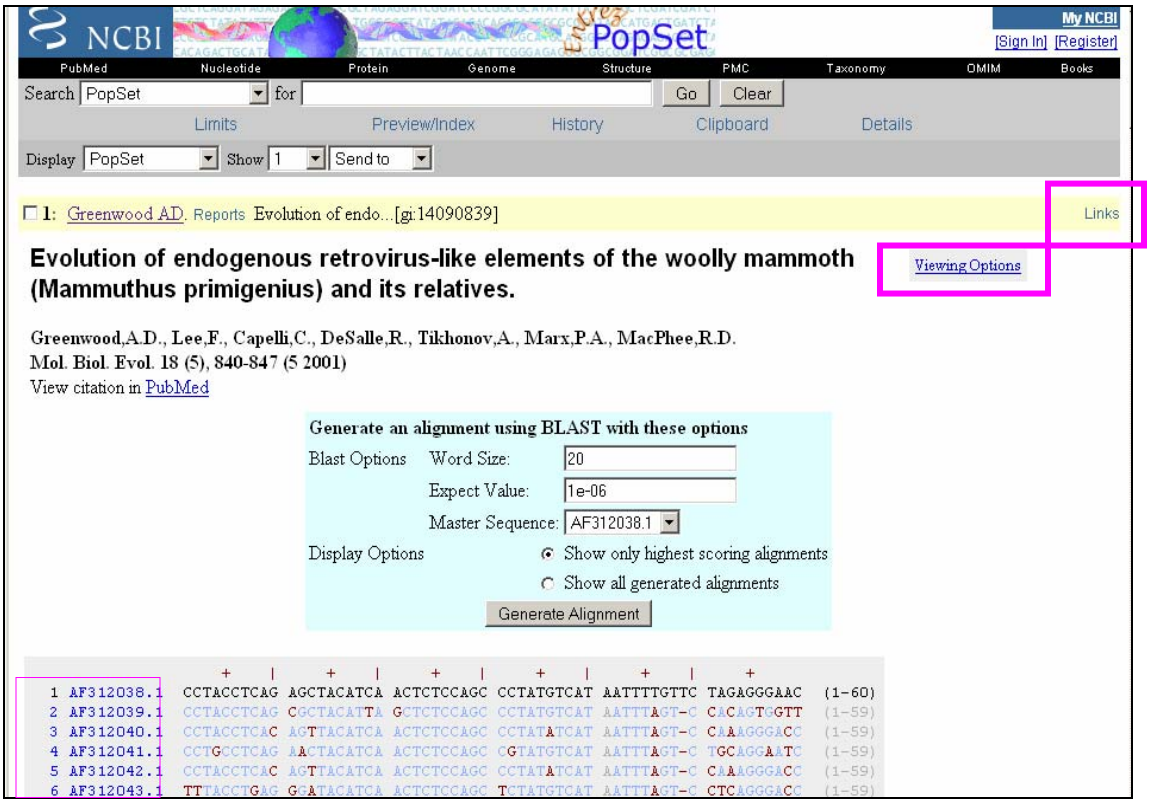
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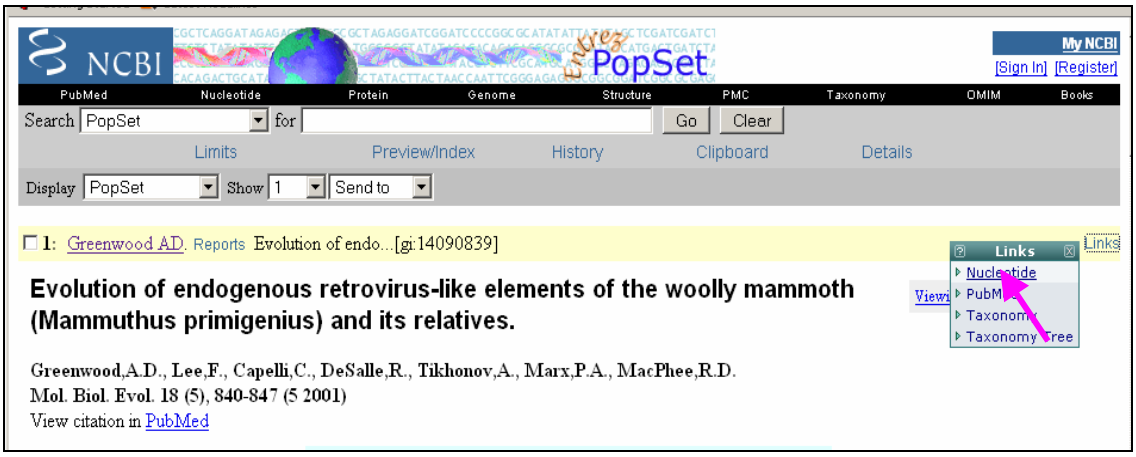
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Evolution of endogenous retrovirus-like elements of the woolly mammoth (Mammuthus primigenius) and its relatives.
Greenwood,A.D., Lee,F., Capelli,C., DeSalle,R., Tikhonov,A., Marx,P.A., MacPhee,R.D.
Mol. Biol. Evol. 18 (5), 840-847 (5 2001)
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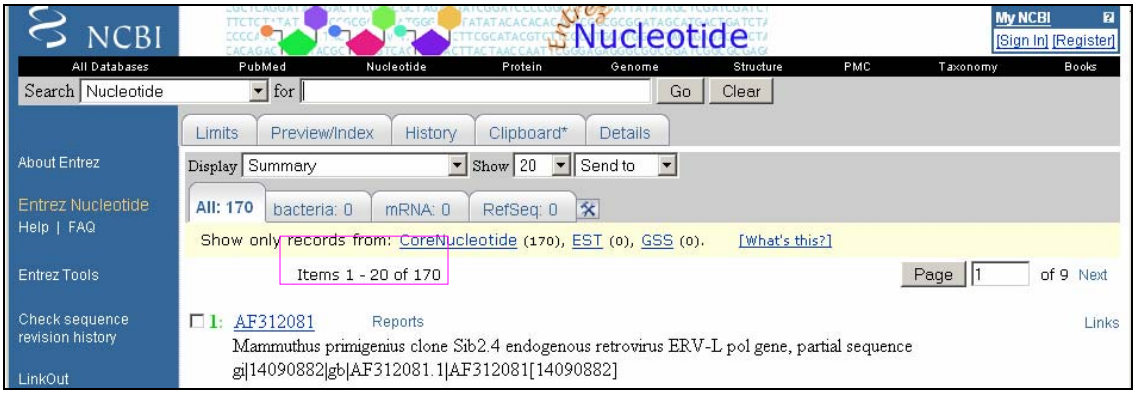
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Page 1 of 9 Next
1: AF312081 Reports Links
Mammuthus primigenius clone Sib2.4 endogenous retrovirus ERV-L pol gene, partial sequence
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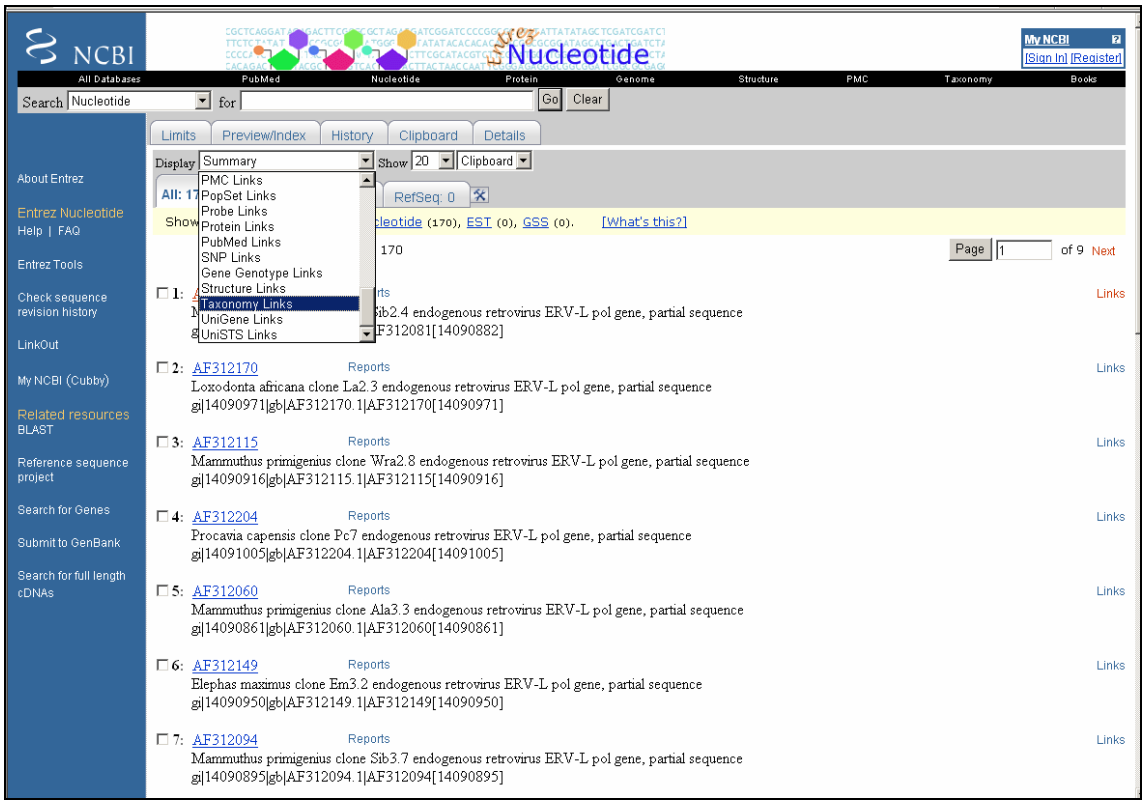
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Protein Links
PubMed Links
SNP Links
Gene Genotype Links
Structure Links
Taxonomy Links
UniGene Links
UniSTS Links
RefSeq: 0
[What's this?]
Page 1 of 9 Next
1: Links
Sib2.4 endogenous retrovirus ERV-L pol gene, partial sequence
F312081[14090882]
2: AF312170 Reports Links
Loxodonta africana clone La2.3 endogenous retrovirus ERV-L pol gene, partial sequence
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3: AF312115 Reports Links
Mammuthus primigenius clone Wra2.8 endogenous retrovirus ERV-L pol gene, partial sequence
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4: AF312204 Reports Links
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5: AF312060 Reports Links
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6: AF312149 Reports Links
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Mammuthus primigenius clone Sib3.7 endogenous retrovirus ERV-L pol gene, partial sequence
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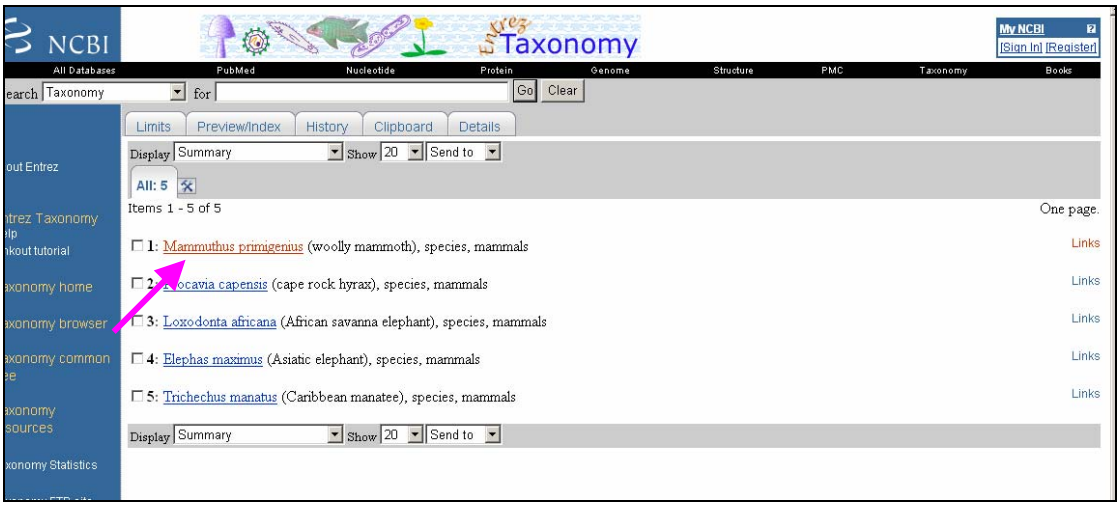
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Items 1 - 5 of 5
One page.
1: Mammuthus primigenius (woolly mammoth), species, mammals Links
2: Procavia capensis (cape rock hyrax), species, mammals Links
3: Loxodonta africana (African savanna elephant), species, mammals Links
4: Elephas maximus (Asiatic elephant), species, mammals Links
5: Trichechus manatus (Caribbean manatee), species, mammals Links
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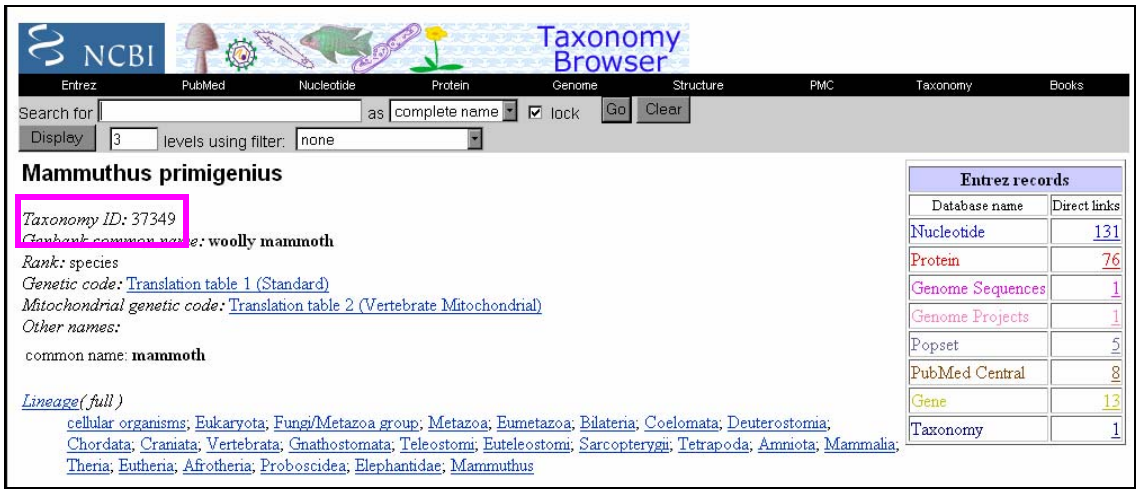

Comments and References:

extinct

This taxon is extinct.

Genome Information

Trace records (raw single-pass reads of DNA sequence)		
Center name	**Record counts per type**	
	454	ALL
CCGB - Center for Comparative Genomics and Bioinformatics, PennState University, USA	302,692	302,692
Total	302,692	**302,692**

External Information Resources (NCBI LinkOut)

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

Notes:

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

Information from sequence entries

Show organism modifiers

Organism modifiers

To hide organism modifiers click here

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

NCBI
Taxonomy Browser
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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
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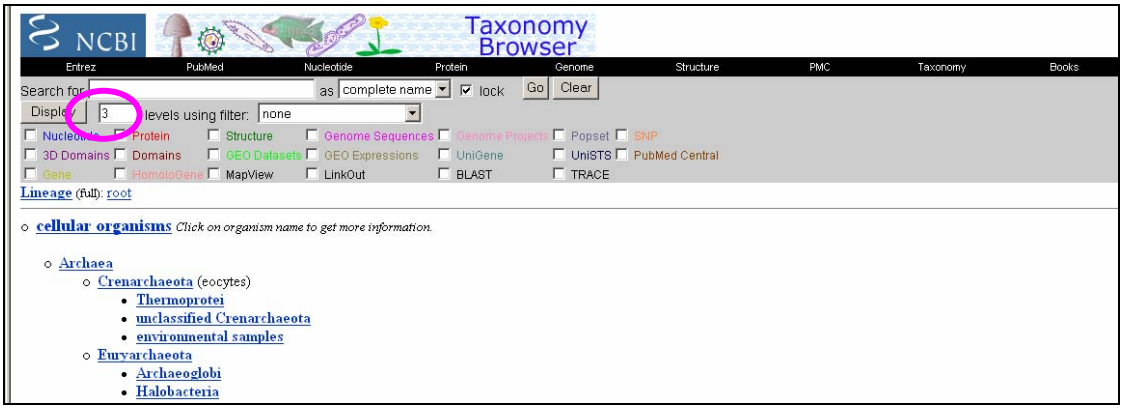
Protein 76
Genome Sequences 1
Genome Projects 1
Popset 5
PubMed Central 8
Gene 13
Taxonomy 1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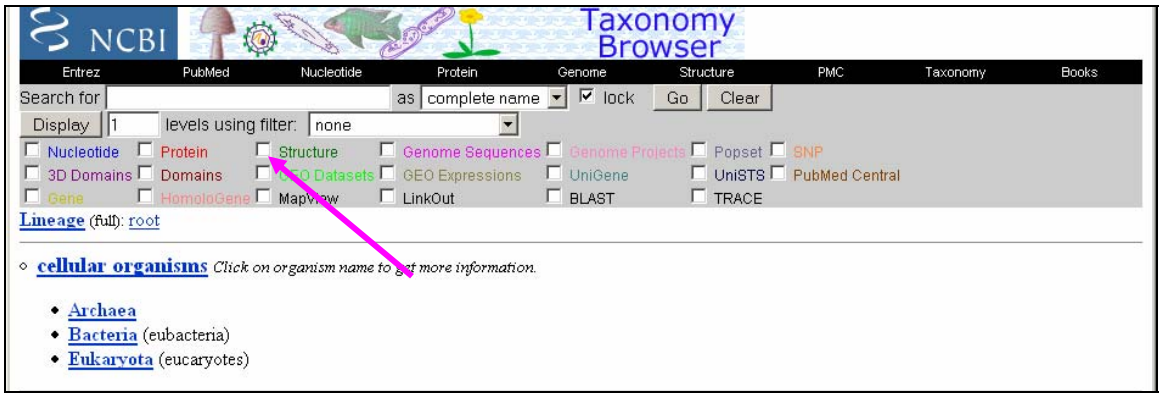
Protein Structure Genome Sequences Genome Projects Popset SNP
3D Domains Domains GEO Datasets GEO Expressions UniGene UniSTS PubMed Central
Gene HomoloGene MapViewer LinkOut BLAST TRACE
Lineage (full): root
cellular organisms Click on organism name to get more information.
Archaea
Crenarchaeota (eocytes)
Thermoprotei
unclassified Crenarchaeota
environmental samples
Euryarchaeota
Archaeoglobi
Halobacteria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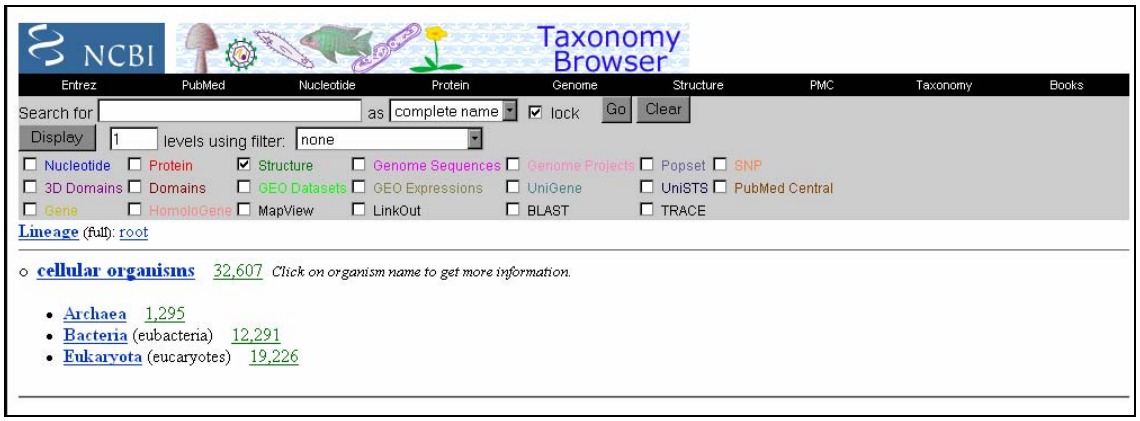
Display 1 levels using filter: none
Nucleotide Protein Structure Genome Sequences Genome Projects Popset SNP
3D Domains Domains GEO Datasets GEO Expressions UniGene UniSTS PubMed Central
Gene HomoloGene MapViewer LinkOut BLAST TRACE
Lineage (full): root
cellular organisms Click on organism name to get more information.
Archaea
Bacteria (eubacteria)
Eukaryota (eucaryotes)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Gene HomoloGene MapView LinkOut BLAST TRACE
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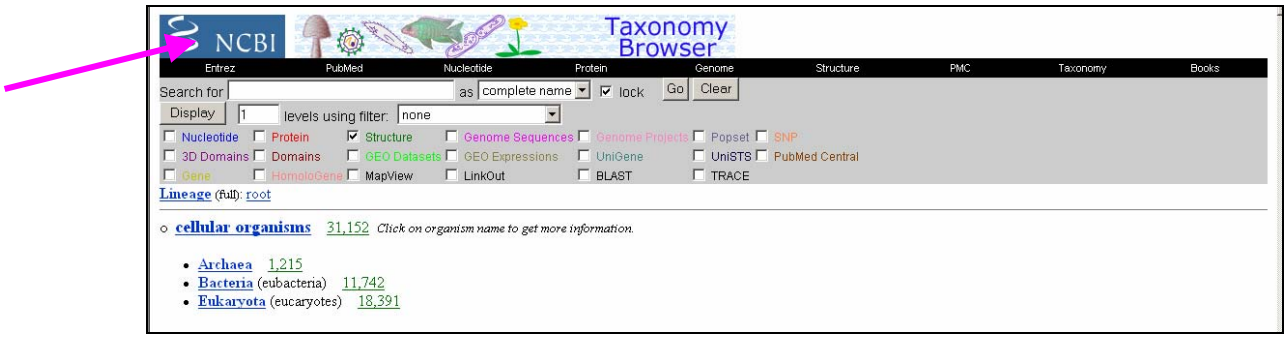
Eukaryota (eucaryotes) 19,226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3D Domains Domains GEO Datasets GEO Expressions UniGene UniSTS PubMed Central
Gene HomoloGene MapView LinkOut BLAST TRACE
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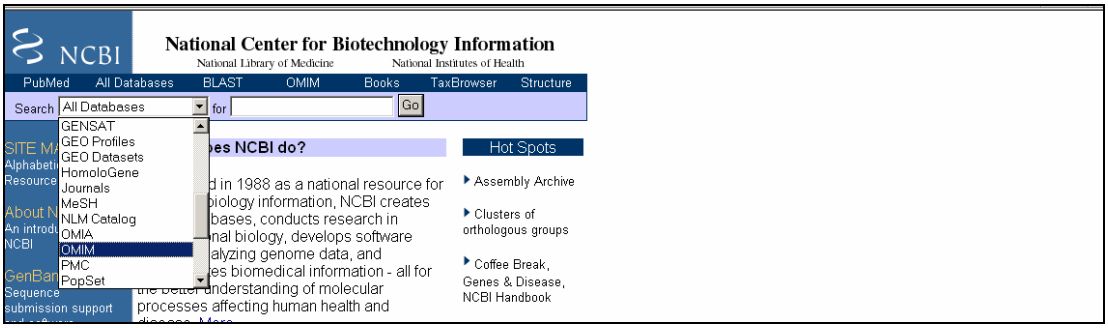
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HomoloGene
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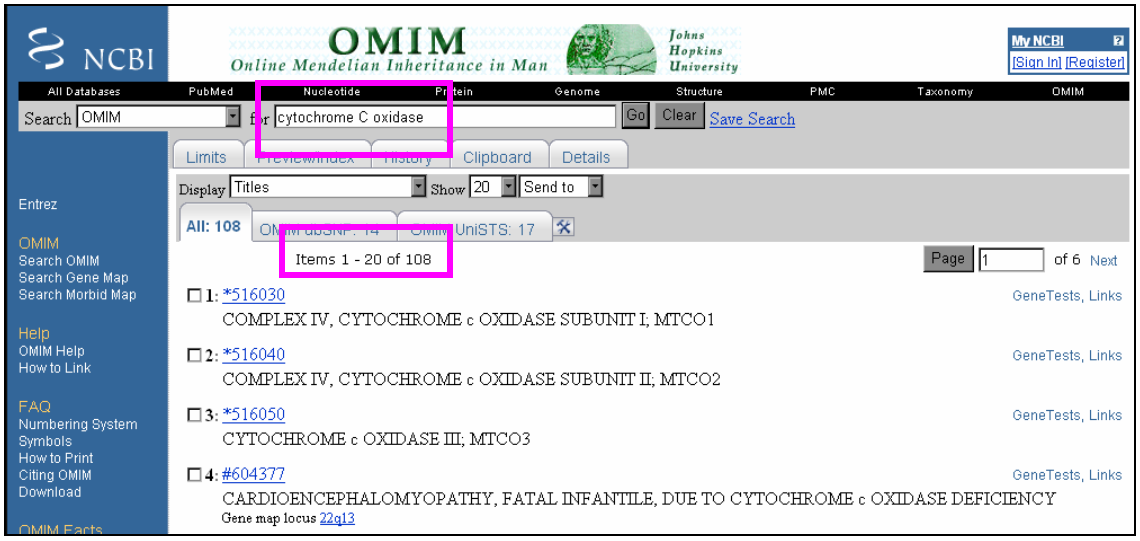
Assembly Archive
Clusters of orthologous groups
Coffee Break, Genes & Disease, NCBI Handbook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2: *516040 GeneTests, Links
COMPLEX IV, CYTOCHROME c OXIDASE SUBUNIT II; MTCO2
3: *516050 GeneTests, Links
CYTOCHROME c OXIDASE III; MTCO3
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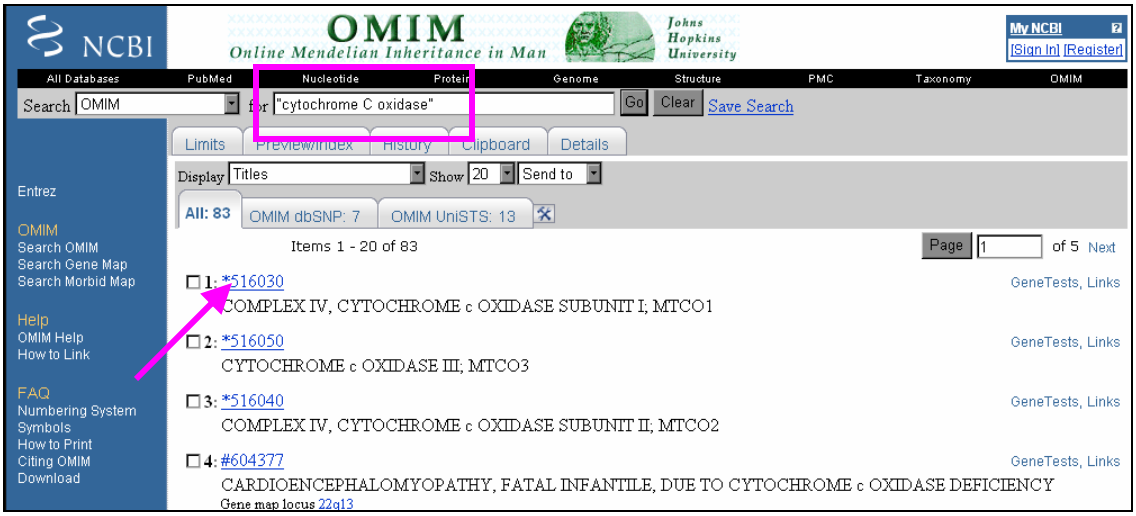
Gene map locus 22q13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Help
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CYTOCHROME c OXIDASE III; MTCO3
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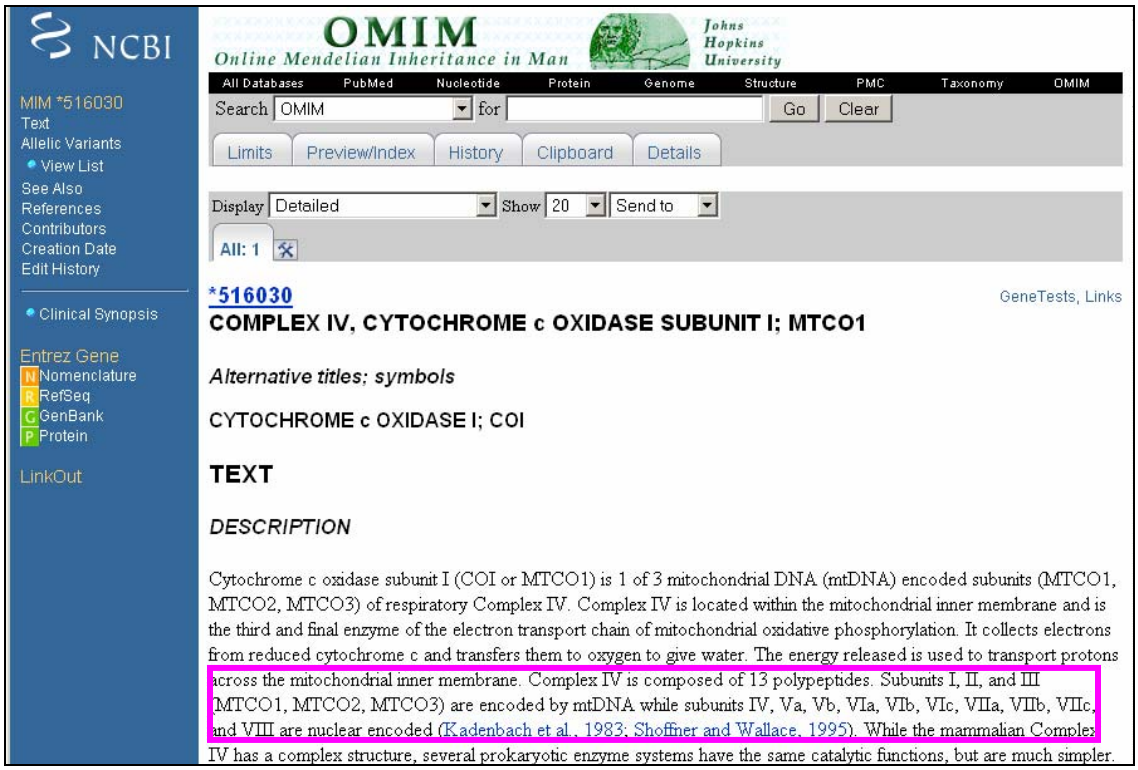
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Entrez Gene
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RefSeq
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Protein
LinkOut
*516030 GeneTests, Links
COMPLEX IV, CYTOCHROME c OXIDASE SUBUNIT I; MTCO1
Alternative titles; symbols
CYTOCHROME c OXIDASE I; COI
TEXT
DESCRIPTION
Cytochrome c oxidase subunit I (COI or MTCO1) is 1 of 3 mitochondrial DNA (mtDNA) encoded subunits (MTCO1, MTCO2, MTCO3) of respiratory Complex IV. Complex IV is located within the mitochondrial inner membrane and is the third and final enzyme of the electron transport chain of mitochondrial oxidative phosphorylation. It collects electrons from reduced cytochrome c and transfers them to oxygen to give water. The energy released is used to transport protons across the mitochondrial inner membrane. Complex IV is composed of 13 polypeptides. Subunits I, II, and III (MTCO1, MTCO2, MTCO3) are encoded by mtDNA while subunits IV, Va, Vb, VIa, VIb, VIc, VIIa, VIIb, VIIc, and VIII are nuclear encoded (Kadenbach et al., 1983; Shoffner and Wallace, 1995). While the mammalian Complex IV has a complex structure, several prokaryotic enzyme systems have the same catalytic functions, but are much simpler.

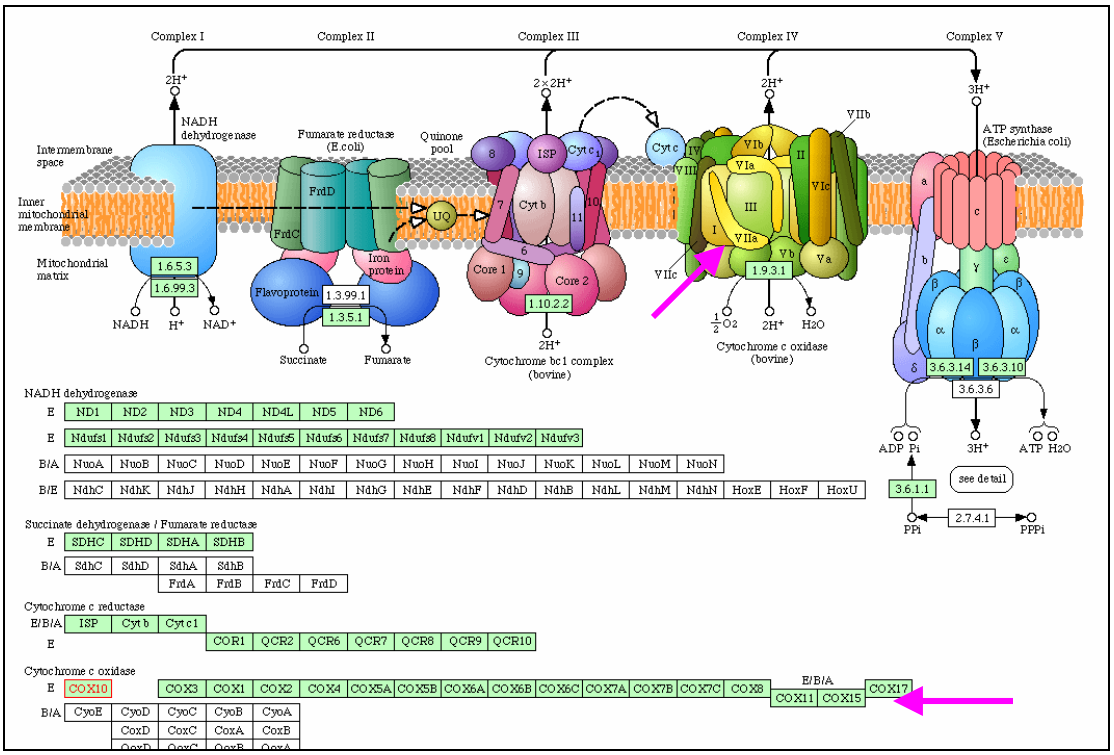

Figure from KEGG **Oxidative phosphorylation - Reference pathway (KO)**
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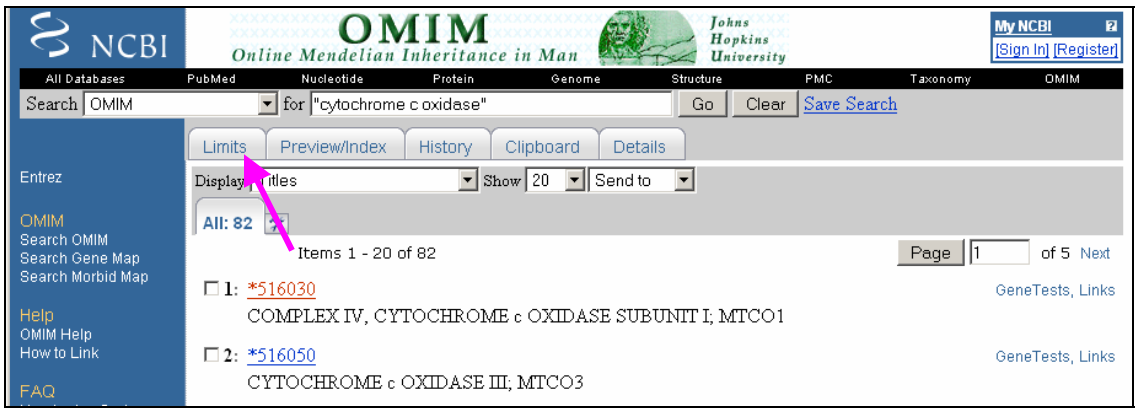

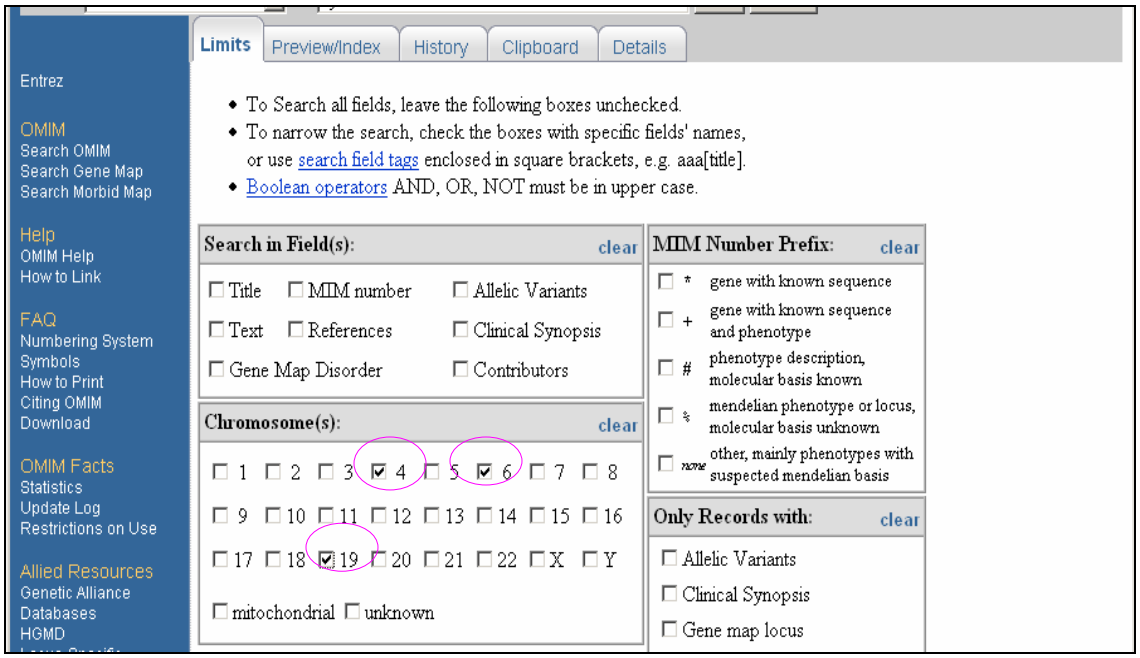
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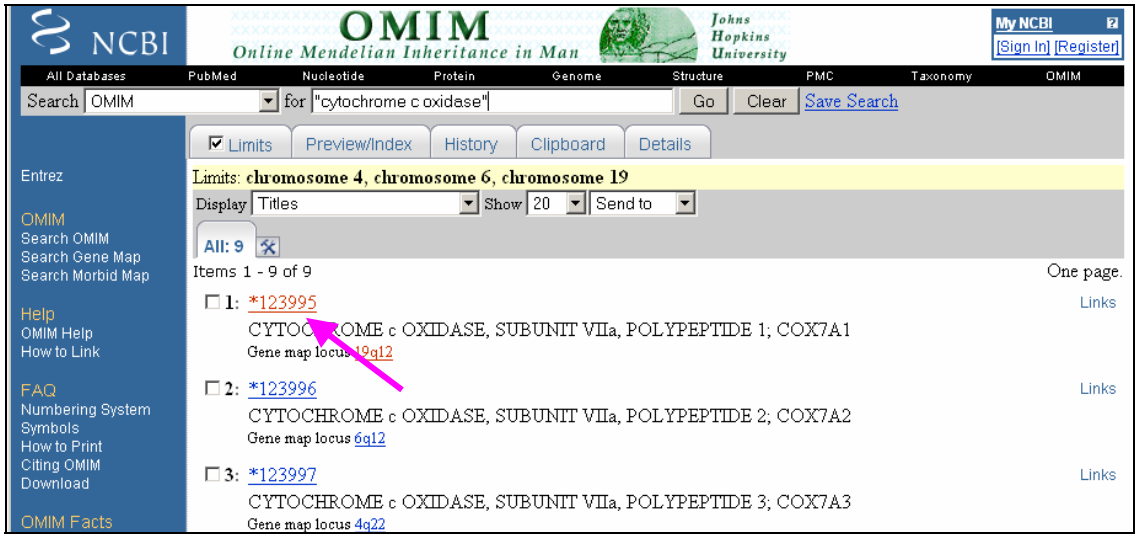
Clinical Synopsis
Gene Map Disorder
Contributors
Chromosome(s): clear
1 2 3 4 5 6 7 8
9 10 11 12 13 14 15 16
17 18 19 20 21 22 X Y
mitochondrial unknown
MIM Number Prefix: clear
* gene with known sequence
+ gene with known sequence and phenotype
# phenotype description, molecular basis known
% mendelian phenotype or locus, molecular basis unknown
none other, mainly phenotypes with suspected mendelian basis
Only Records with: clear
Allelic Variants
Clinical Synopsis
Gene map locus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3: *123997 Links
CYTOCHROME c OXIDASE, SUBUNIT VIIa, POLYPEPTIDE 3; COX7A3
Gene map locus 4q22
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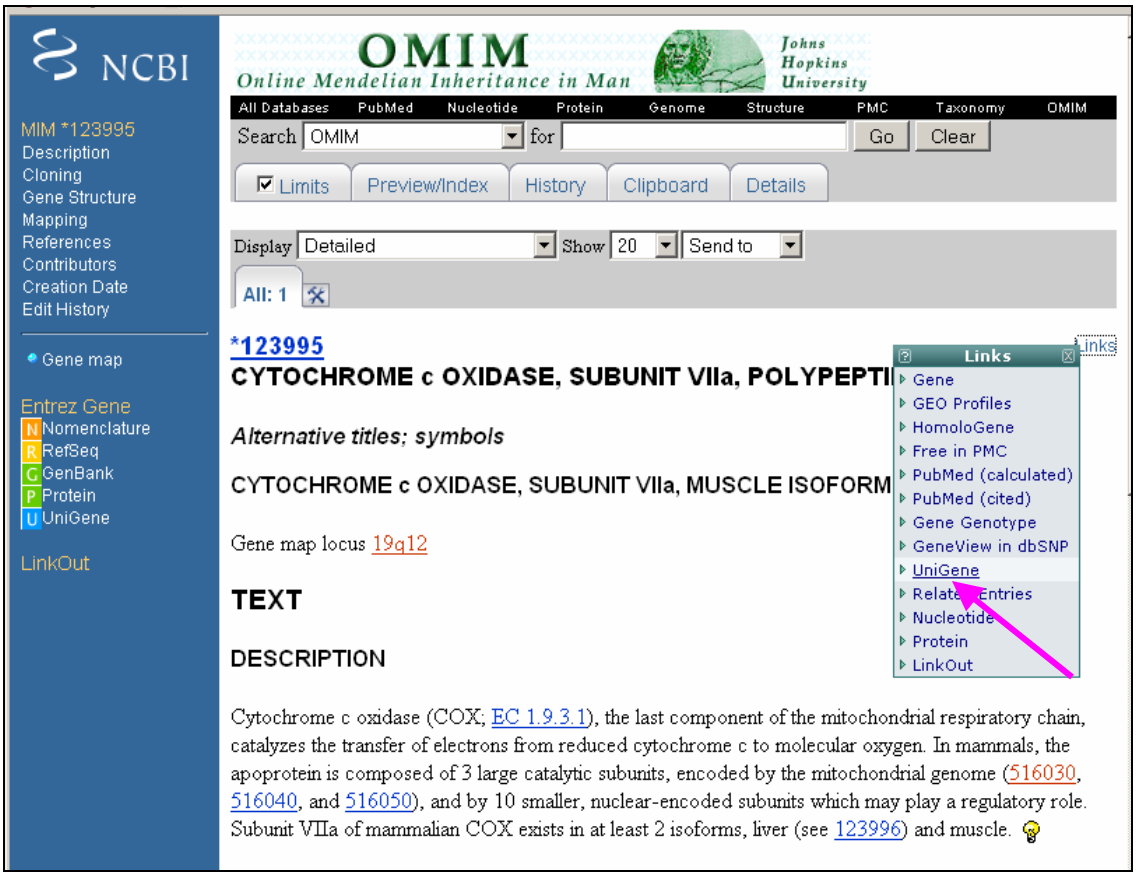
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CYTOCHROME c OXIDASE, SUBUNIT VIIa, POLYPEPTI
Alternative titles; symbols
CYTOCHROME c OXIDASE, SUBUNIT VIIa, MUSCLE ISOFORM
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DESCRIPTION
Cytochrome c oxidase (COX; EC 1.9.3.1), the last component of the mitochondrial respiratory chain, catalyzes the transfer of electrons from reduced cytochrome c to molecular oxygen. In mammals, the apoprotein is composed of 3 large catalytic subunits, encoded by the mitochondrial genome (516030, 516040, and 516050), and by 10 smaller, nuclear-encoded subunits which may play a regulatory role. Subunit VIIa of mammalian COX exists in at least 2 isoforms, liver (see 123996) and muscle.
Links
Gene
GEO Profiles
HomoloGene
Free in PMC
PubMed (calculated)
PubMed (cited)
Gene Genotype
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UniGene
Nucleotide
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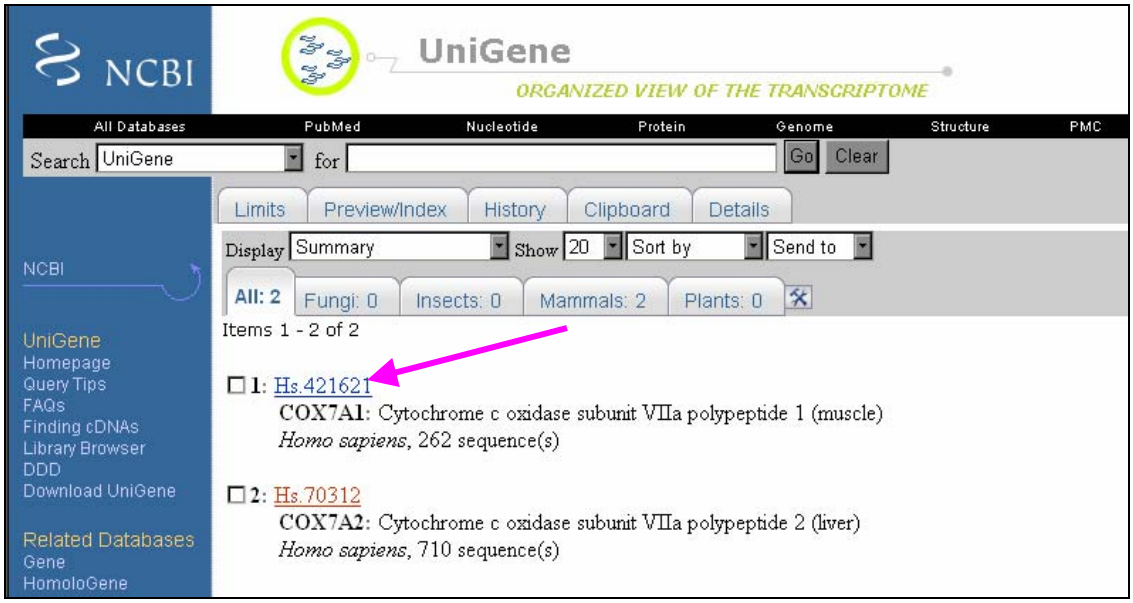
LinkOut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Finding cDNAs
Library Browser
DDD
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Related Databases
Gene
HomoloGene
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COX7A1: Cytochrome c oxidase subunit VIIa polypeptide 1 (muscle)
Homo sapiens, 262 sequence(s)
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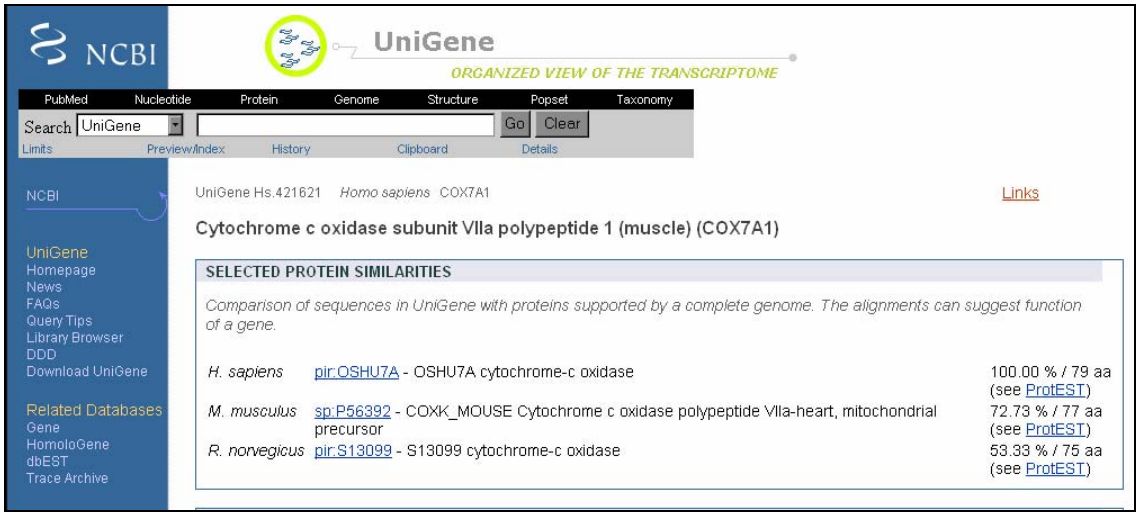
COX7A2: Cytochrome c oxidase subunit VIIa polypeptide 2 (liver)
Homo sapiens, 710 sequence(s)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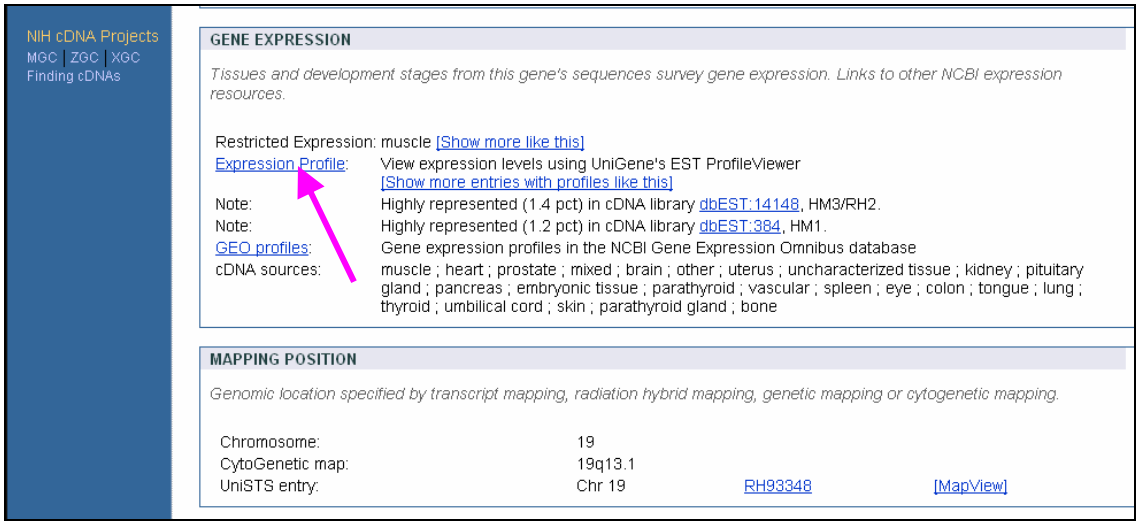
Links
Cytochrome c oxidase subunit VIIa polypeptide 1 (muscle) (COX7A1)
SELECTED PROTEIN SIMILARITIES
Comparison of sequences in UniGene with proteins supported by a complete genome. The alignments can suggest function of a gene.
H. sapiens pir:OSHU7A - OSHU7A cytochrome-c oxidase 100.00 % / 79 aa (see ProtEST)
M. musculus sp:P56392 - COXK_MOUSE Cytochrome c oxidase polypeptide VIIa-heart, mitochondrial precursor 72.73 % / 77 aa (see ProtEST)
R. norvegicus pir:S13099 - S13099 cytochrome-c oxidase 53.33 % / 75 aa (see ProtEST)


NIH cDNA Projects
MGC | ZGC | XGC
Finding cDNAs
GENE EXPRESSION
Tissues and development stages from this gene's sequences survey gene expression. Links to other NCBI expression resources.
Restricted Expression: muscle [Show more like this]
Expression Profile: View expression levels using UniGene's EST ProfileViewer
[Show more entries with profiles like this]
Note: Highly represented (1.4 pct) in cDNA library dbEST:14148, HM3/RH2.
Note: Highly represented (1.2 pct) in cDNA library dbEST:384, HM1.
GEO profiles: Gene expression profiles in the NCBI Gene Expression Omnibus database
cDNA sources: muscle ; heart ; prostate ; mixed ; brain ; other ; uterus ; uncharacterized tissue ; kidney ; pituitary gland ; pancreas ; embryonic tissue ; parathyroid ; vascular ; spleen ; eye ; colon ; tongue ; lung ; thyroid ; umbilical cord ; skin ; parathyroid gland ; bone
MAPPING POSITION
Genomic location specified by transcript mapping, radiation hybrid mapping, genetic mapping or cytogenetic mapping.
Chromosome: 19
CytoGenetic map: 19q13.1
UniSTS entry: Chr 19 RH93348 [MapView]

Breakdown by Tissue

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bone	13	1 / 73140
bone marrow	0	0 / 49076
brain	8	7 / 832981
connective ...	0	0 / 107017
adipose tis...	0	0 / 13518
ear	0	0 / 16901
liver	0	0 / 208613
pancreas	13	3 / 218650
adrenal gland	0	0 / 31566
parathyroid	142	3 / 21097
thyroid	18	1 / 55346
pituitary g...	167	3 / 17870
placenta	9	3 / 300224
eye	28	6 / 208175
embryonic t...	10	2 / 192406
abdominal c...	0	0 / 40454
cervix	0	0 / 48394
ovary	0	0 / 107525
uterus	8	2 / 239917
prostate	70	11 / 155999
testis	0	0 / 313211
bladder	0	0 / 30662
kidney	27	6 / 214719
tongue	59	4 / 67712
larynx	0	0 / 30076
pharynx	0	0 / 14376
salivary gl...	0	0 / 20623
heart	224	20 / 89236
lymph node	0	0 / 96449
lymph	0	0 / 44866
tonsil	0	0 / 17257
spleen	18	1 / 52934
thymus	0	0 / 75154
mammary gland	8	8 / 171511
muscle	1346	154 / 114406
lung	5	2 / 351527
trachea	0	0 / 48930

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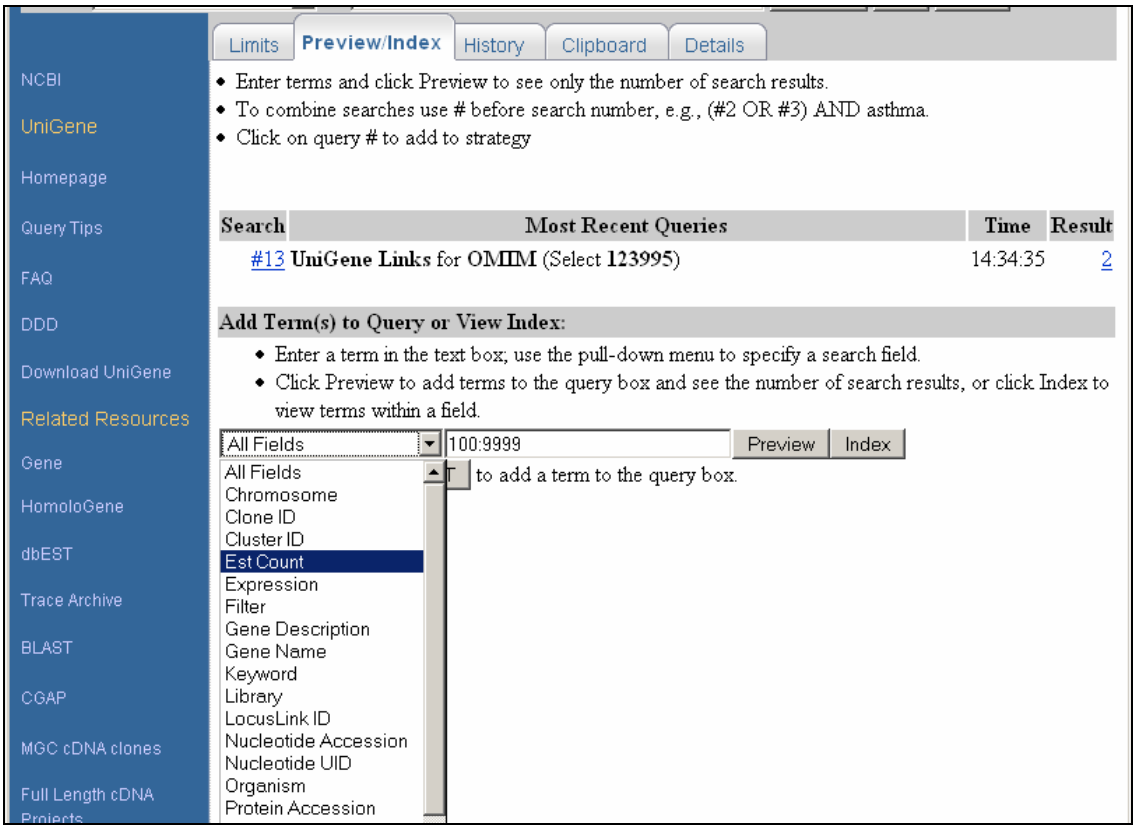
Expression profile suggested by analysis of EST counts.

Hs.421621- COX7A1: Cytochrome c oxidase subunit VIIa polypeptide 1 (muscle)

See Legend

Breakdown by Tissue

	Hs.421621	
blood	0	0 / 109832
bone	13	1 / 73140
bone marrow	0	0 / 49076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14:34:35
2
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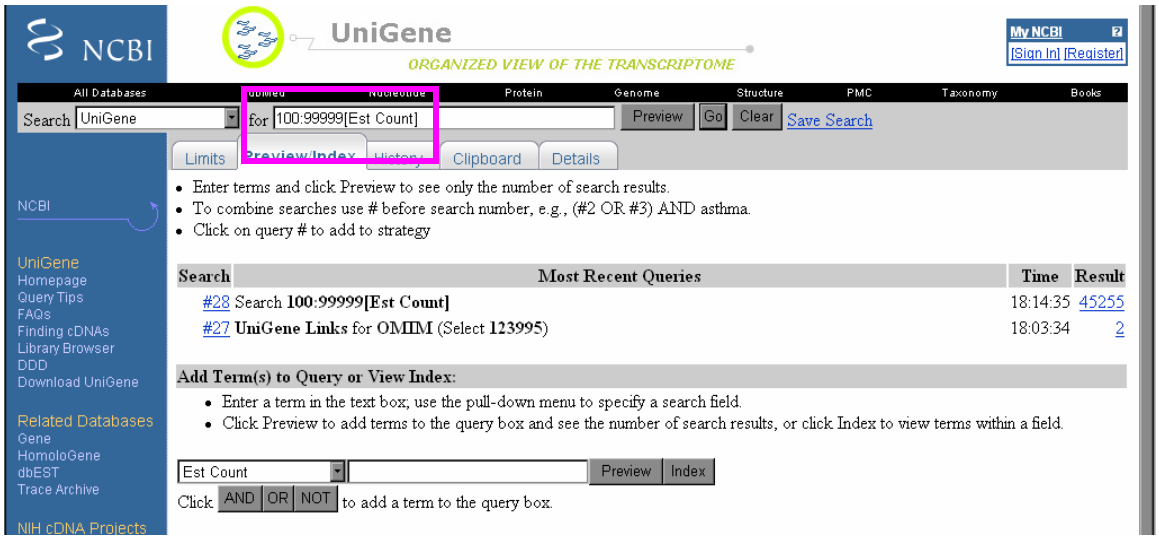
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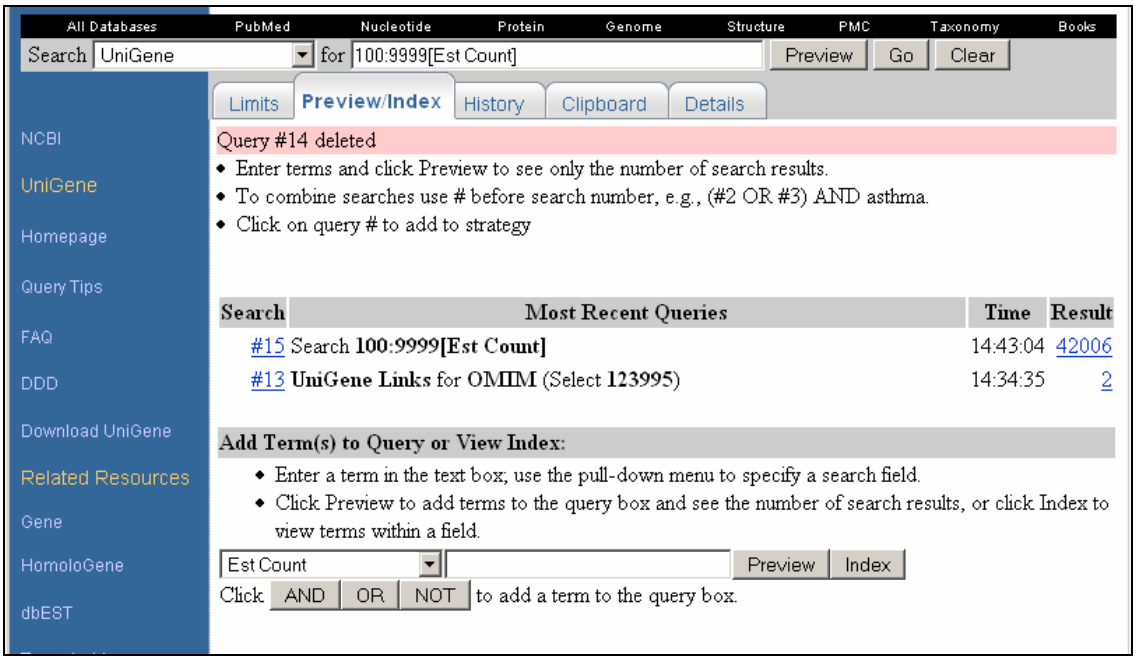
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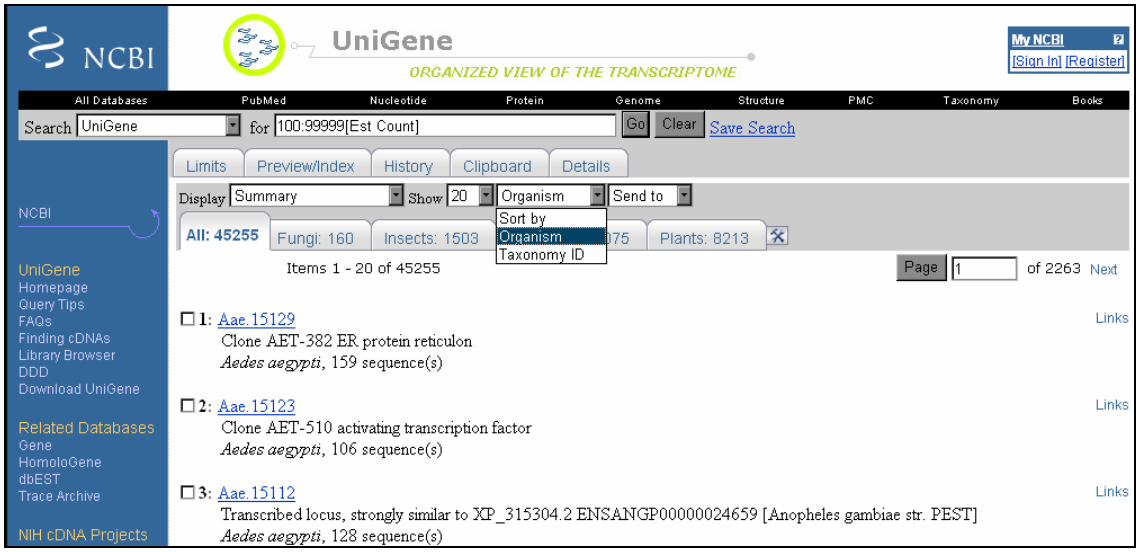
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2: Aae.15123 Links
Clone AET-510 activating transcription factor
Aedes aegypti, 106 sequence(s)
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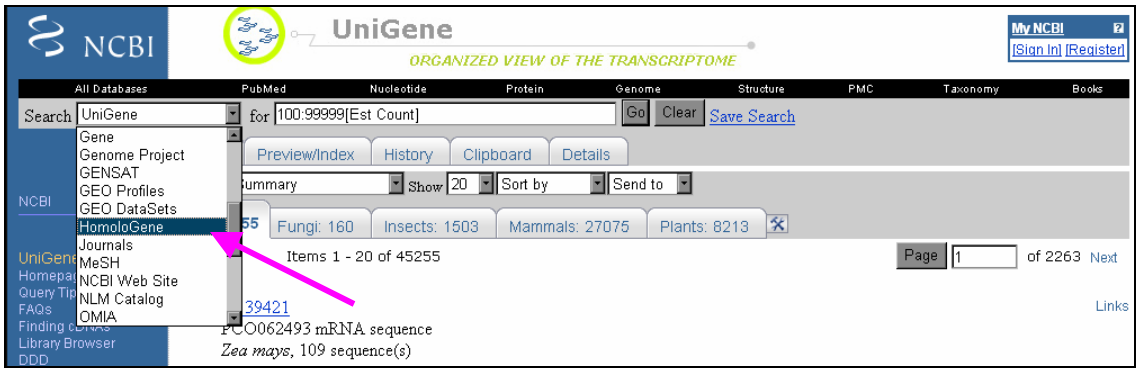
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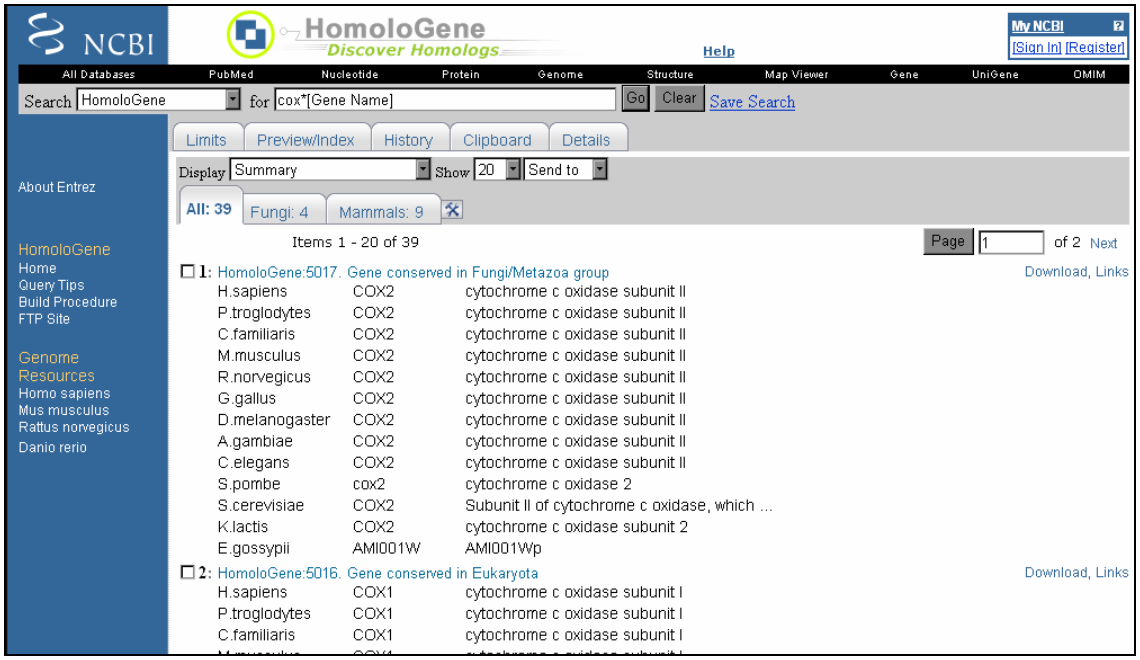
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1: HomoloGene:5017. Gene conserved in Fungi/Metazoa group
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C.familiaris COX2 cytochrome c oxidase subunit II
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R.norvegicus COX2 cytochrome c oxidase subunit II
G.gallus COX2 cytochrome c oxidase subunit II
D.melanogaster COX2 cytochrome c oxidase subunit II
A.gambiae COX2 cytochrome c oxidase subunit II
C.elegans COX2 cytochrome c oxidase subunit II
S.pombe cox2 cytochrome c oxidase 2
S.cerevisiae COX2 Subunit II of cytochrome c oxidase, which ...
K.lactis COX2 cytochrome c oxidase subunit 2
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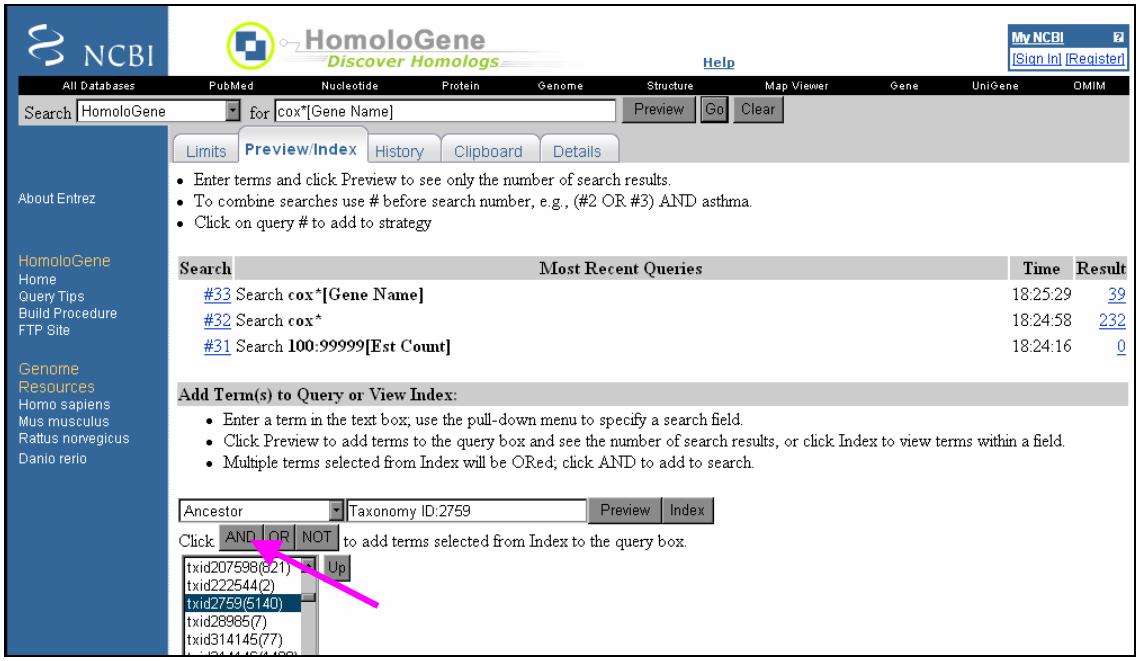
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#31 Search 100:99999[Est Count] 18:24:16 0
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txid222544(2)
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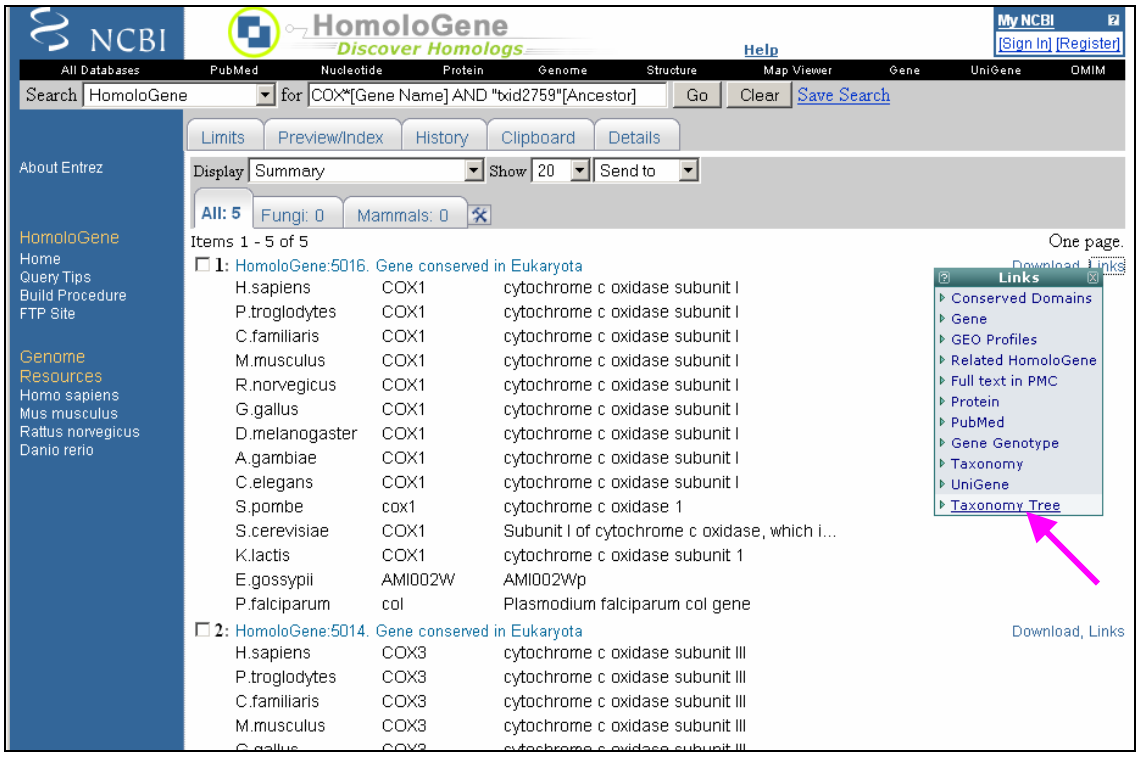
txid28985(7)
txid314145(77)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1: HomoloGene:5016. Gene conserved in Eukaryota
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C.familiaris COX1 cytochrome c oxidase subunit I
M.musculus COX1 cytochrome c oxidase subunit I
R.norvegicus COX1 cytochrome c oxidase subunit I
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C.elegans COX1 cytochrome c oxidase subunit I
S.pombe cox1 cytochrome c oxidase 1
S.cerevisiae COX1 Subunit I of cytochrome c oxidase, which i...
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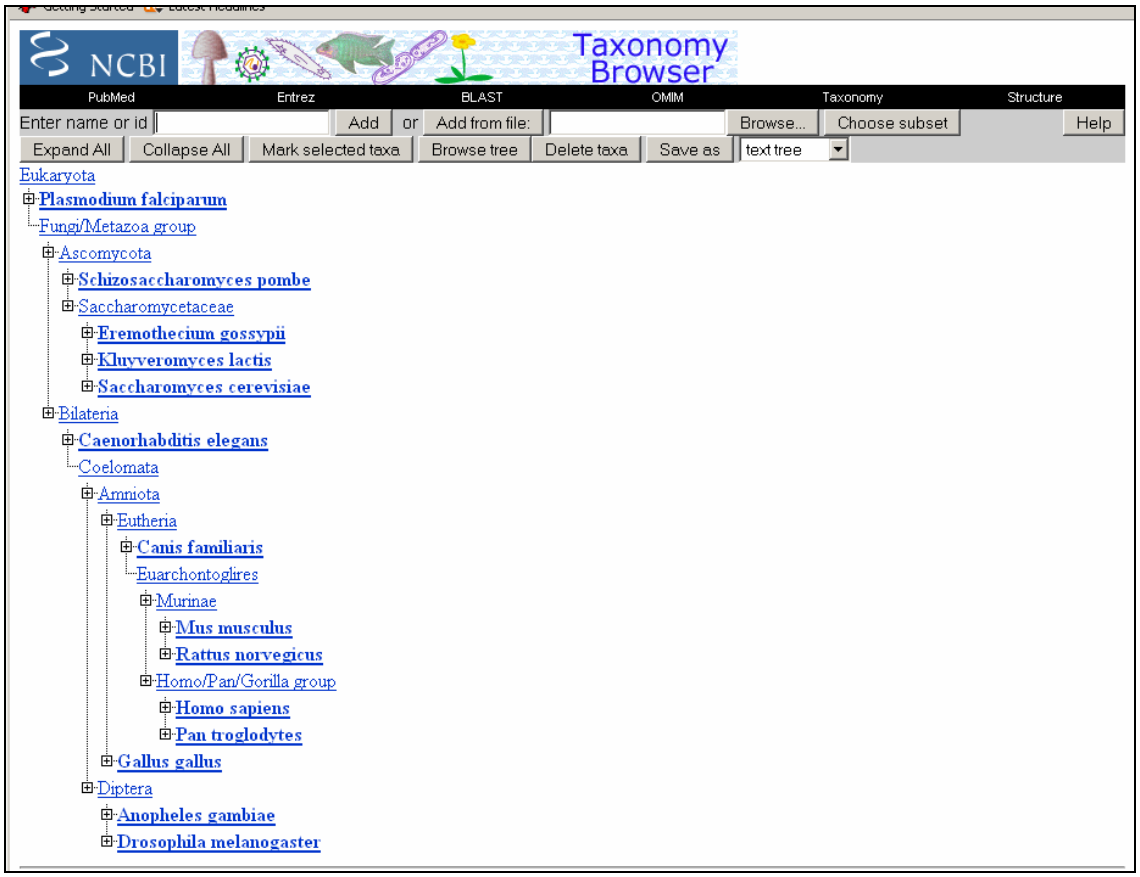
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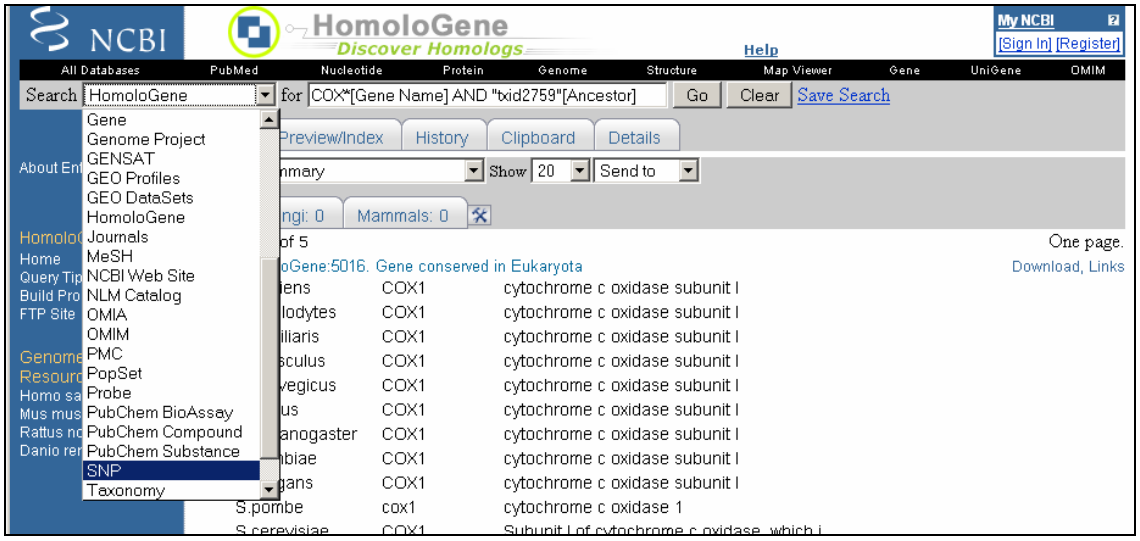
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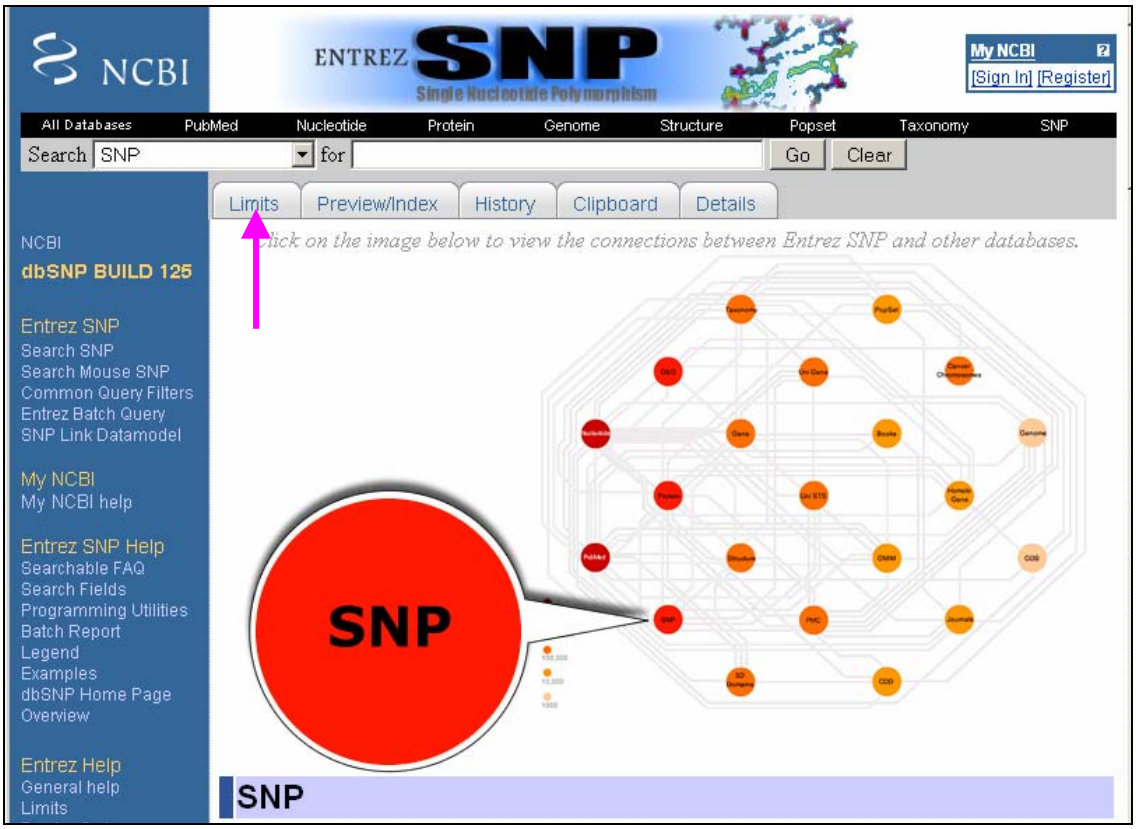
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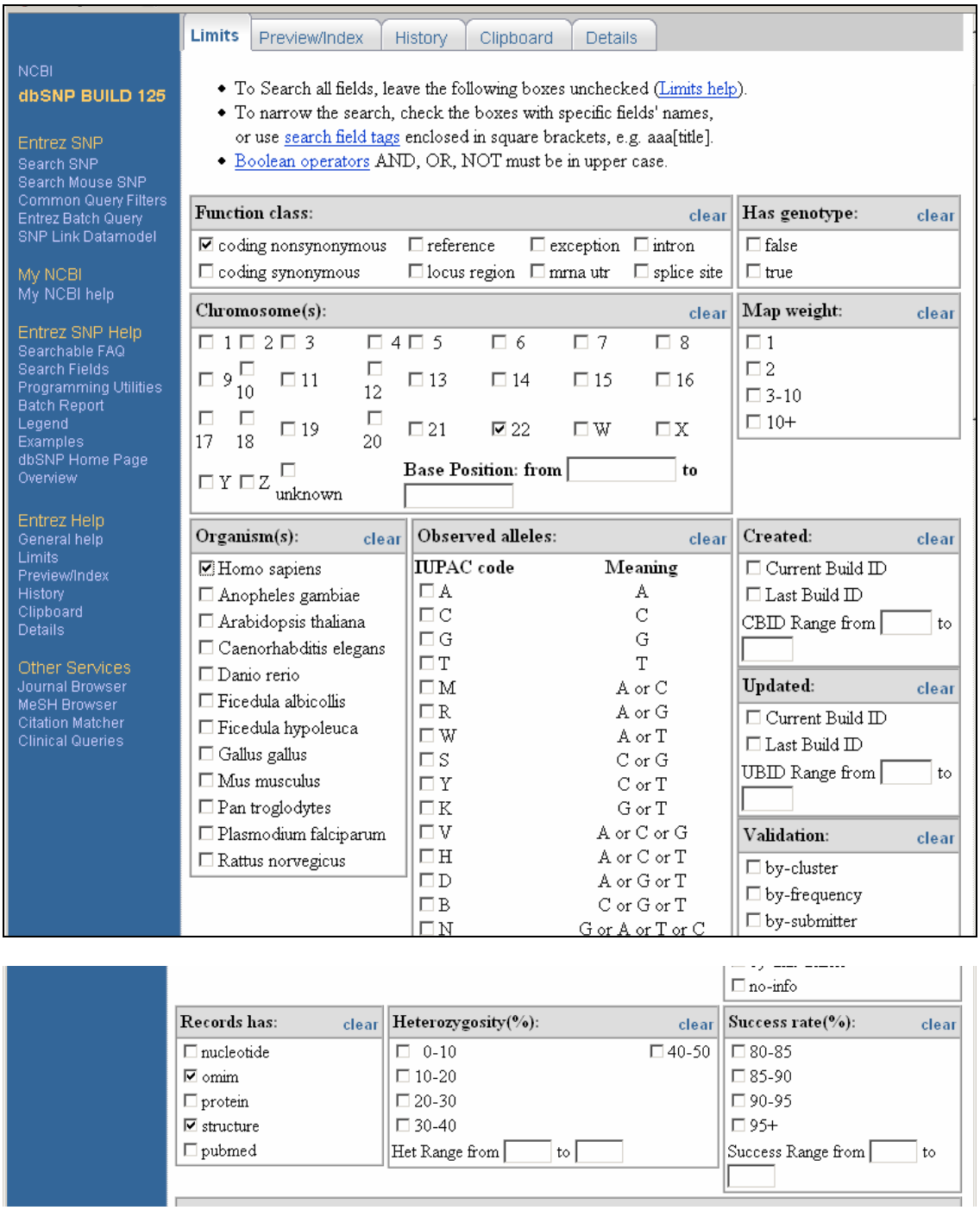
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reference
locus region
exception
mrna utr
intron
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false
true
Chromosome(s): clear
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 W X Y Z unknown
Base Position: from to
Map weight: clear
1
2
3-10
10+
Organism(s): clear
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Anopheles gambiae
Arabidopsis thaliana
Caenorhabditis elegans
Danio rerio
Ficedula albicollis
Ficedula hypoleuca
Gallus gallus
Mus musculus
Pan troglodytes
Plasmodium falciparum
Rattus norvegicus
Observed alleles: clear
IUPAC code / Meaning
A A
C C
G G
T T
M A or C
R A or G
W A or T
S C or G
Y C or T
K G or T
V A or C or G
H A or C or T
D A or G or T
B C or G or T
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CBID Range from to
Updated: clear
Current Build ID
Last Build ID
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by-submitter
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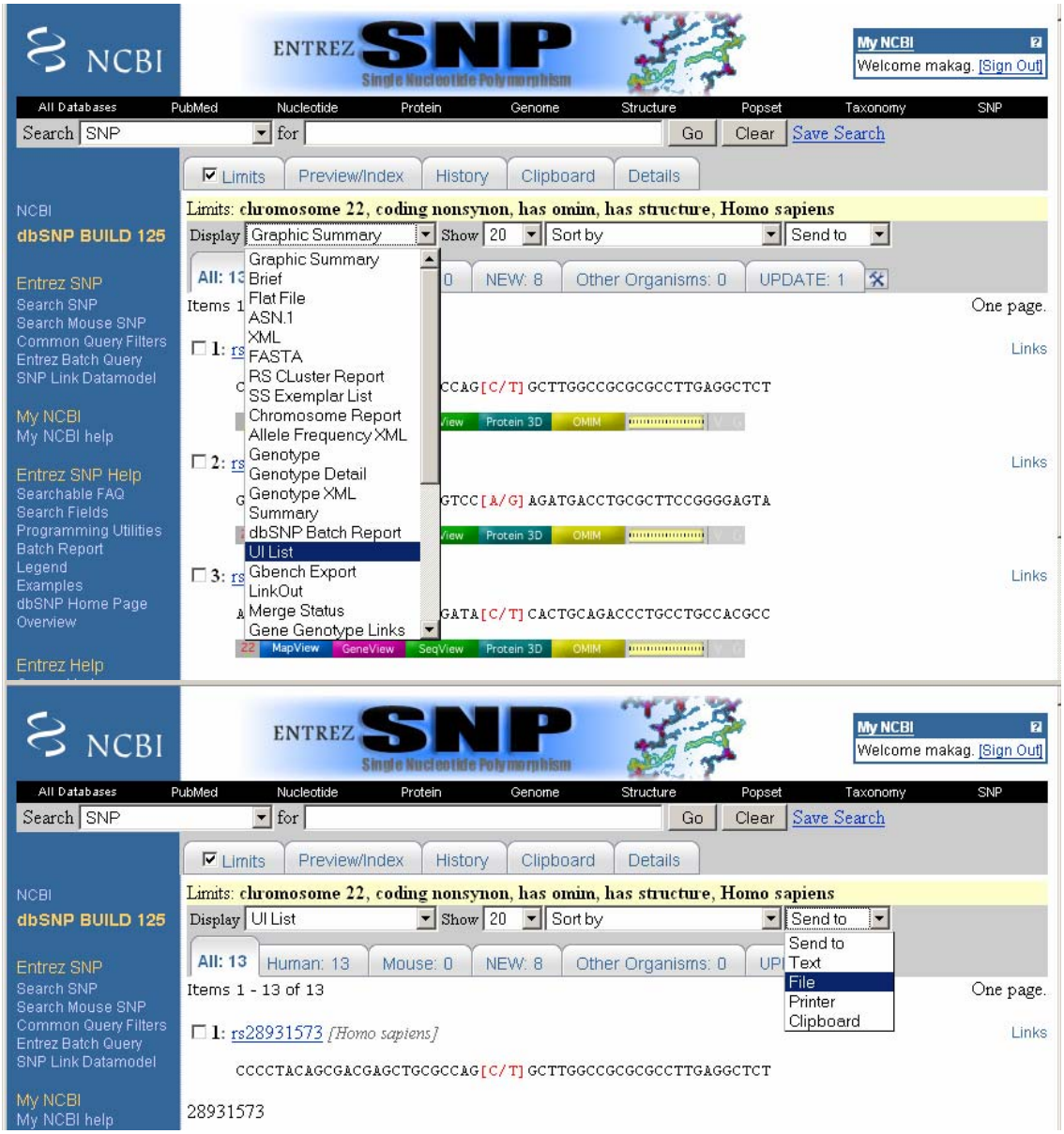
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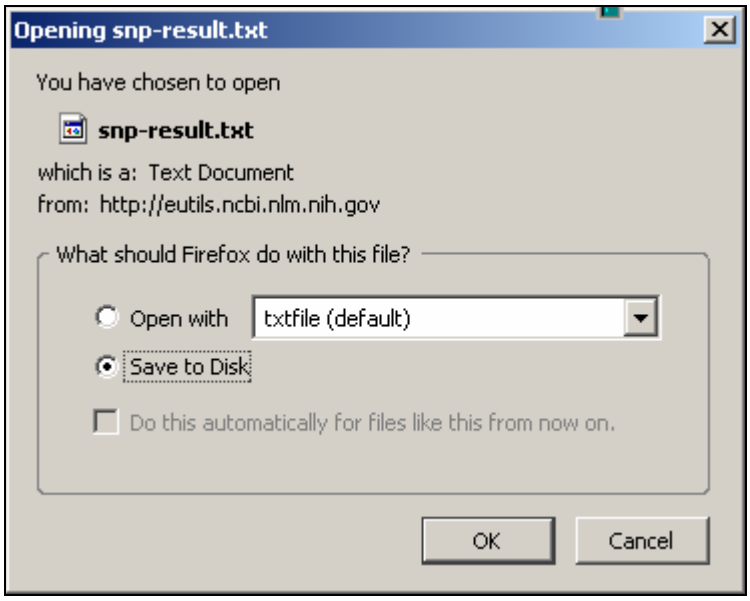
28931573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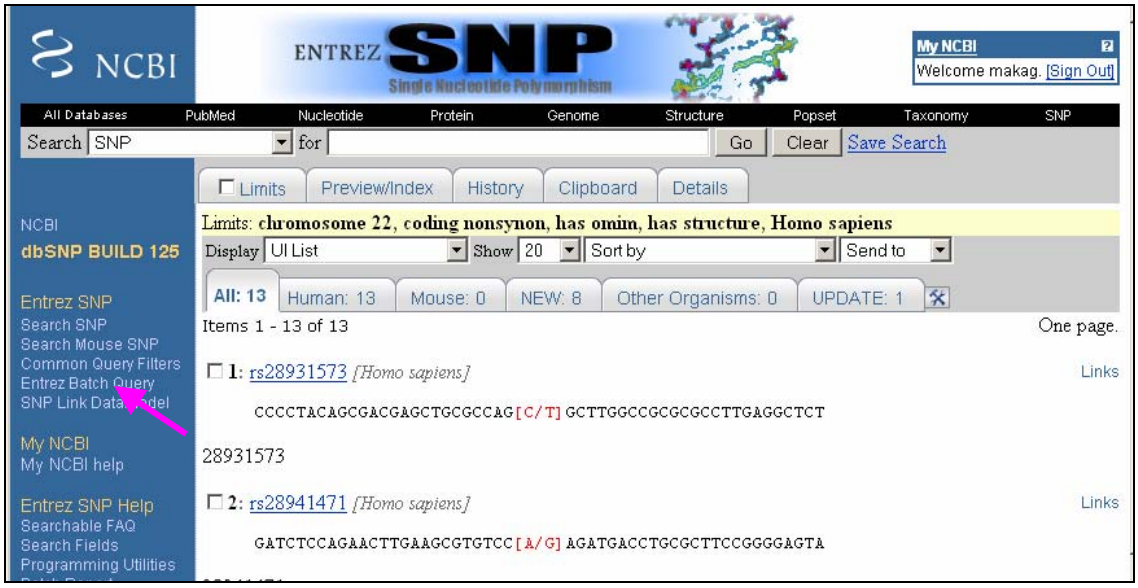
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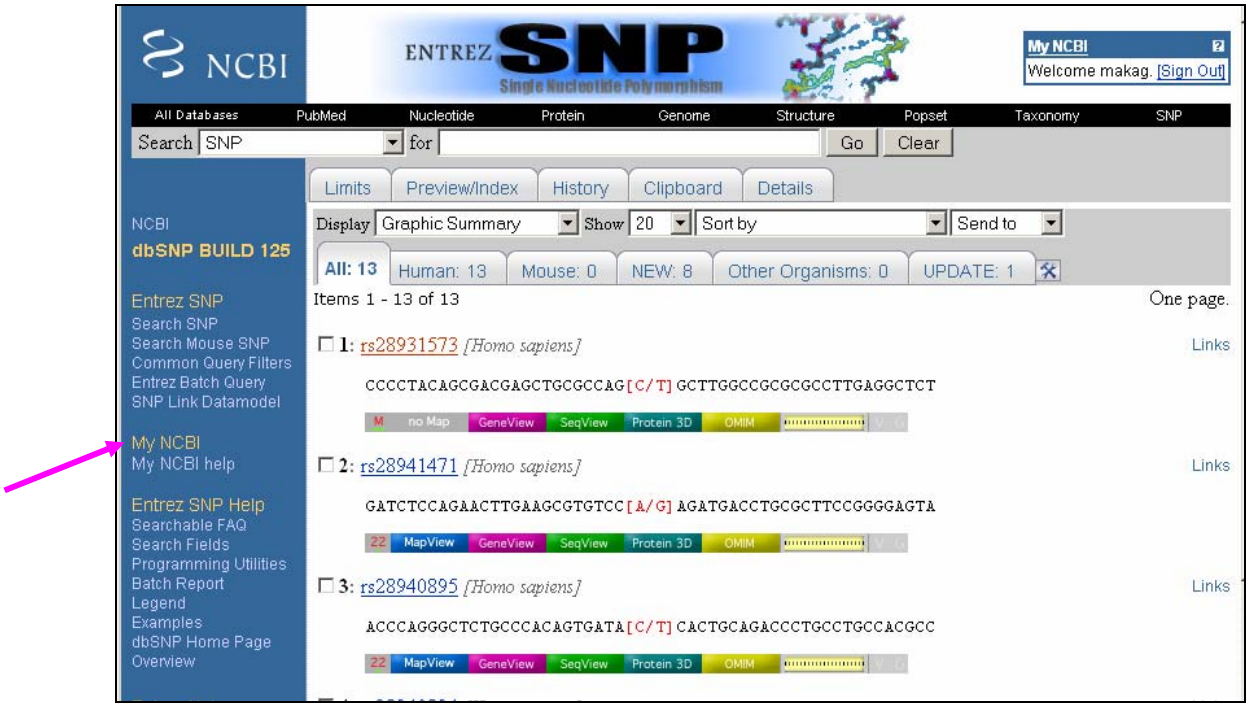
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Overview
1: rs28931573 [Homo sapiens] Links
CCCCTACAGCGACGAGCTGCGCCAG[C/T]GCTTGGCCGCGCGCCTTGAGGCTCT
no Map GeneView SeqView Protein 3D OMIM
2: rs28941471 [Homo sapiens] Links
GATCTCCAGAACTTGAAGCGTGTCC[A/G]AGATGACCTGCGCTTCCGGGGAGTA
22 MapView GeneView SeqView Protein 3D OMIM
3: rs28940895 [Homo sapiens] Links
ACCCAGGGCTCTGCCCACAGTGATA[C/T]CACTGCAGACCCTGCCTGCCACGCC
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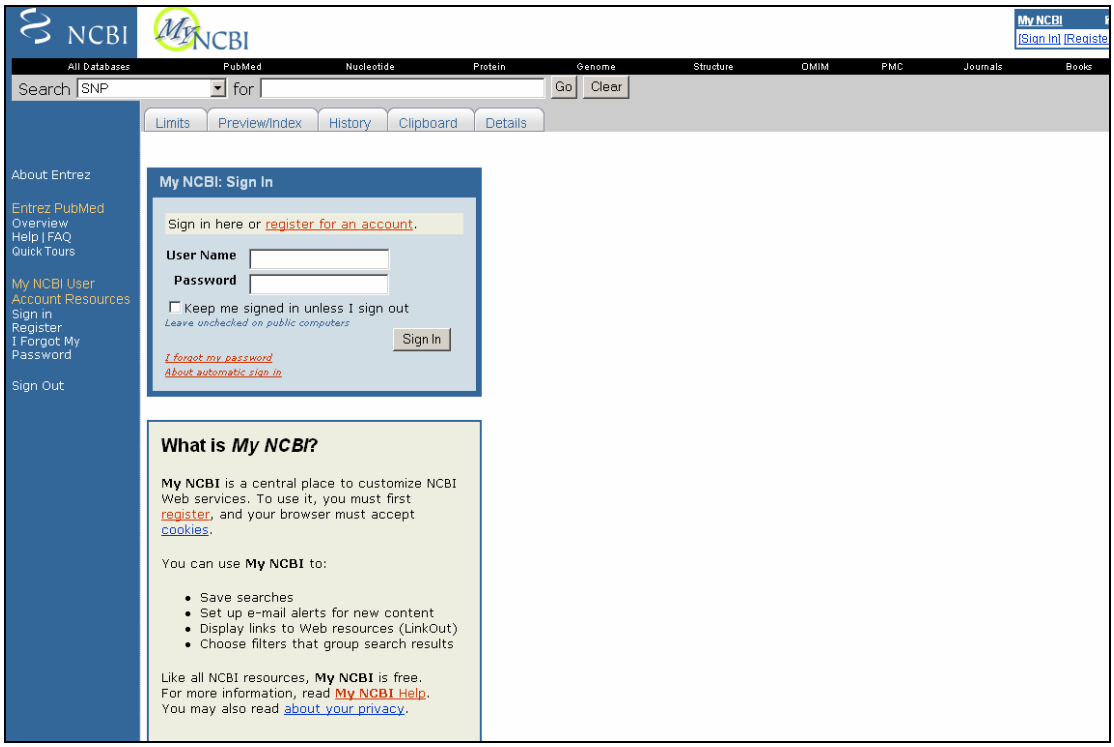
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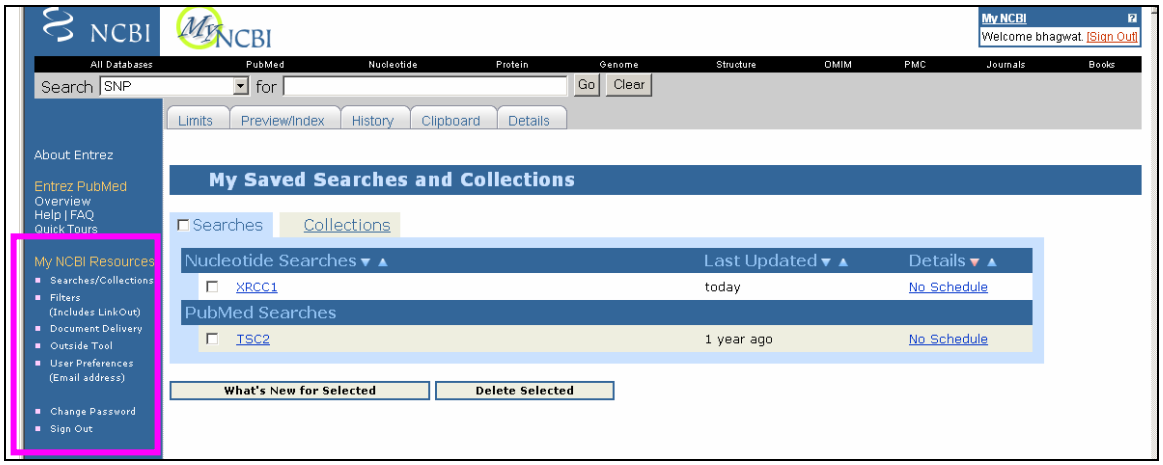
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Last Updated
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XRCC1
today
No Schedule
PubMed Searches
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1 year ago
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What's New for Selected
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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.

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