

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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PubMed All Databases BLAST OMIM Books TaxBrowser Structure

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Resource Guide

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GenBank
Sequence submission support and software

Literature databases
PubMed, OMIM, Books, and PubMed Central

Molecular databases
Sequences, structures, and taxonomy

Genomic biology
The human genome, whole genomes, and related resources

Tools

What does NCBI do?
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...](#)

Hot Spots

- Assembly Archive
- Clusters of orthologous groups
- Coffee Break, Genes & Disease, NCBI Handbook
- Electronic PCR
- Entrez Home
- Entrez Tools
- Gene expression omnibus (GEO)
- Human genome resources
- Influenza Virus Resource
- Map Viewer
- dbMHC
- Mouse genome resources
- My NCBI

Whole Genome Association
The NCBI Whole Genome Association (WGA) resource provides researchers with access to genotype and associated phenotype information that will help elucidate the link between genes and disease. For more information, click here to see the WGA resource page and click here to read the press release.

1 Billion Live Traces
The Trace Archive of sequencing traces has reached 1 billion live traces from over 480 organisms. For more information about the Trace Archive database click here.

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NCBI Entrez, The Life Sciences Search Engine

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Search across databases mammoth Help

192	PubMed: biomedical literature citations and abstracts	none	Books: online books
none	PubMed Central: free, full text journal articles	2	DMIM: online Mendelian Inheritance in Man
14	Site Search: NCBI web and FTP sites	none	DMIA: Online Mendelian Inheritance in Animals
73907	Nucleotide: sequence database (includes GenBank)	2	UniGene: gene-oriented clusters of transcript sequences
240	Protein: sequence database	none	CDD: conserved protein domain database Go to UniGene Result Page
2	Genome: whole genome sequences	none	3D Domains: domains from Entrez Structure
none	Structure: three-dimensional macromolecular structures	none	UniSTS: markers and mapping data
2	Taxonomy: organisms in GenBank	35	PopSet: population study data sets
none	SNP: single nucleotide polymorphism	none	GEO Profiles: expression and molecular abundance profiles
13	Gene: gene-centered information	none	GEO DataSets: experimental sets of GEO data
1	HomoloGene: eukaryotic homology groups	none	Cancer Chromosomes: cytogenetic databases
none	PubChem Compound: unique small molecule chemical structures	none	PubChem BioAssay: bioactivity screens of chemical substances
none	PubChem Substance: deposited chemical substance records	none	GENSAT: gene expression atlas of mouse central nervous system
1	Genome Project: genome project information	none	Probe: sequence-specific reagents
none	Journals: detailed information about the journals indexed in PubMed and other Entrez databases	none	MeSH: detailed information about NLM's controlled vocabulary
5	NLM Catalog: catalog of books, journals, and audiovisuals in the NLM collections		

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Search PubMed for mammoth Go Clear Save Search

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Items 1 - 20 of 192 Page 1 of 10 Next

1: Gilbert MT, Bmladen J, Miller W, Wnuf C, Willerslev E, Poinar H, Carlson JE, Leebens-Mack JH, Schuster SC. **Recharacterization of ancient DNA miscoding lesions: insights in the era of sequencing-by-synthesis.** Nucleic Acids Res. 2006 Aug 18, [Epub ahead of print] PMID: 16920744 [PubMed - as supplied by publisher] Related Articles, Links

2: Cline MG, Oh C. **A Reappraisal of the Role of Abscisic Acid and its Interaction with Auxin in Apical Dominance.** Ann Bot (Lond). 2006 Aug 1, [Epub ahead of print] PMID: 16882681 [PubMed - as supplied by publisher] Related Articles, Links

3: Tai DY. **SARS: how to manage future outbreaks?** Ann Acad Med Singapore. 2006 May;35(5):368-73. PMID: 16830006 [PubMed - in process] Related Articles, Links

4: Rompler H, Rohland N, Lalueza-Fox C, Willerslev E, Kuznetsova T, Rabeder G, Bertranpetti J, Schoneberg T, Hofreiter M. **Nuclear gene indicates coat-color polymorphism in mammoths.** Science. 2006 Jul 7;313(5783):62. PMID: 16825562 [PubMed - indexed for MEDLINE] Related Articles, Links

10: Lifschitz E, Eviatar T, Rozman A, Shalit A, Goldschmidt A, Ansellem Z, Alvarez JP, Eshed Y. **The tomato FT ortholog triggers systemic signals that regulate growth and flowering and substitute for diverse environmental stimuli.** Proc Natl Acad Sci U S A. 2006 Apr 18;103(16):6398-403. Epub 2006 Apr 10. PMID: 16606827 [PubMed - indexed for MEDLINE] Related Articles, Links

11: Xue Y, Zerial T, Bao W, Zhu S, Shu Q, Xu J, Du R, Fu S, Li P, Hurles ME, Yang H, Tyler-Smith C. **Male demography in East Asia: a north-south contrast in human population expansion times.** Genetics. 2006 Apr;172(4):2431-9. Epub 2006 Feb 19. PMID: 16489223 [PubMed - indexed for MEDLINE] Related Articles, Links

12: Rogaev EI, Moliaka YK, Malyarchuk BA, Kondrashov FA, Derenko MV, Chumakov I, Gingorenko AP. **Complete mitochondrial genome and phylogeny of Pleistocene Mammoth *Mammuthus primigenius*.** PLoS Biol. 2006 Mar;4(3):e73. Epub 2006 Feb 7. PMID: 16448217 [PubMed - in process] Related Articles, Links

13: Cooper A. **The year of the mammoth.** PLoS Biol. 2006 Mar;4(3):e78. Epub 2006 Feb 7. No abstract available. PMID: 16448215 [PubMed - in process] Related Articles, Links

14: Gupta BK, Chakraborty B. **The role of zoos in the rehabilitation of animals in the circus.** J Appl Anim Welf Sci. 2005;8(4):285-94. PMID: 16436032 [PubMed - indexed for MEDLINE] Related Articles, Links

15: Pichardo M. **Taxonomic revision of Central Mexican mammoths in Paleoindian sites.** Anthropol Anz. 2005 Dec;63(4):409-13. PMID: 16402591 [PubMed - indexed for MEDLINE] Related Articles, Links

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Related Links

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- Mammoth albumin. [Science. 1980]
- Ancient biodeterioration: an FT-Raman spectroscopic study of mammoth and elepha [Anal Bioanal Chem. 2005]
- Isolation and characterization of deoxyribonucleic acid from tissue of the woolly [Comp Biochem Physiol B. 1985]
- Molecular and morphological evidence on the phylogeny of the Elephantidae. [Proc Biol Sci. 2000]

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Complete mitochondrial genome and phylogeny of Pleistocene Mammoth *Mammuthus primigenius*. *PLoS Biol.* 2006 Mar;4(3):e73. Epub 2006 Feb 7. PMID: 16448217 [PubMed - in process]

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

Genome sequencing in microfabricated high-density picolitre reactors. *Nature.* 2005 Sep 15;437(7057):376-80. Epub 2005 Jul 31. PMID: 16056220 [PubMed - indexed for MEDLINE]

3: [Noonan JP, Hofreiter M, Smith D, Priest JR, Rohland N, Rabeder G, Krause J, Dettler JC, Paabo S, Rubin EM.](#) Related Articles, Links

Genomic sequencing of Pleistocene cave bears. *Science.* 2005 Jul 22;309(5734):597-9. Epub 2005 Jun 2. PMID: 15933159 [PubMed - indexed for MEDLINE]

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1: [PLoS Biol.](#) 2006 Mar;4(3):e73. Epub 2006 Feb 7. Related Articles, Links

Complete mitochondrial genome and phylogeny of Pleistocene Mammoth *Mammuthus primigenius*.

[Rogaev EI, Moliaka YK, Malyarchuk BA, Kondrashov FA, Derenko MV, Chumakov I, Grigorenko AP.](#)

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

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

PMID: 16448217 [PubMed - in process]

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

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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](#), [Izzyk GP](#), [Jando SC](#), [Alenquer ML](#), [Jarvie TP](#), [Jurage 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](#), [Begelev 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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1: [Stiller M](#), [Green RE](#), [Ronan M](#), [Simons JF](#), [Du L](#), [He W](#), [Egholm M](#), [Rothberg JM](#), [Keats SG](#), [Orodov ND](#), [Antipina EE](#), [Baryshnikov GF](#), [Kuzmin YV](#), [Vasilevski AA](#), [Wuenscheil GE](#), [Termini J](#), [Hofreiter M](#), [Jaenicke-Despres V](#), [Paabo S](#). [Patterns of nucleotide misincorporations during enzymatic amplification and direct large-scale sequencing of ancient DNA](#). *Proc Natl Acad Sci U S A*. 2006 Aug 25; [Epub ahead of print] PMID: 16938852 [PubMed - as supplied by publisher]

2: [Pinard R](#), [de Winter A](#), [Sarkis GJ](#), [Gerstein MB](#), [Tartaro KR](#), [Plant RN](#), [Egholm M](#), [Rothberg JM](#), [Leamon JH](#). [Assessment of whole genome amplification-induced bias through high-throughput, massively parallel whole genome sequencing](#). *BMC Genomics*. 2006 Aug 23;7:216. PMID: 16928277 [PubMed - in process]

3: [Thomas RK](#), [Greulich H](#), [Yuza Y](#), [Lee JC](#), [Tengs T](#), [Feng W](#), [Chen TH](#), [Nickerson E](#), [Simons J](#), [Egholm M](#), [Rothberg JM](#), [Sellers WR](#), [Meyerson ML](#). [Detection of oncogenic mutations in the EGFR gene in lung adenocarcinoma with differential sensitivity to EGFR tyrosine kinase inhibitors](#). *Cold Spring Harb Symp Quant Biol*. 2005;70:73-81. PMID: 16869740 [PubMed - in process]

4: [Thomas RK](#), [Nickerson E](#), [Simons JF](#), [Janne PA](#), [Tengs T](#), [Yuza Y](#), [Garraway LA](#), [LaFramboise T](#), [Lee JC](#), [Shah K](#), [O'Neill K](#), [Sasaki H](#), [Lindeman N](#), [Wong KK](#), [Borras AM](#), [Gutmann EJ](#), [Dragnev KH](#), [DeBiasi R](#), [Chen TH](#), [Glatt KA](#), [Greulich H](#), [Desany B](#), [Lubeski CK](#), [Brockman W](#), [Alvarez P](#), [Hutchison SK](#), [Leamon JH](#), [Ronan MT](#), [Turenchalk GS](#), [Egholm M](#), [Sellers WR](#), [Rothberg JM](#), [Meyerson M](#). [Sensitive mutation detection in heterogeneous cancer specimens by massively parallel picoliter reactor sequencing](#). *Nat Med*. 2006 Jul;12(7):852-5. Epub 2006 Jun 25. PMID: 16799556 [PubMed - in process]

5: [Leamon JH](#), [Link DR](#), [Egholm M](#), [Rothberg JM](#). [Overview: methods and applications for droplet compartmentalization of biology](#). *Nat Methods*. 2006 Jul;3(7):541-3.

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Search PubMed for mammoth

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1: [W, Wuof C, Willerslev E, Poinar H, Carlson JE, Leebens-Mack JH, Schuster SC.](#) Ancient DNA miscoding lesions: insights in the era of sequencing-by-synthesis. *PLoS One* 2006 May;11(5):e7818. [Epub ahead of print] PMID: 16817923 [PubMed - indexed for MEDLINE]

2: [Morgan DH, Kristensen DM, Mittelman D, Lichtarge O.](#) Estimation of microbial cover distributions at Mammoth Hot Springs using a multiple clone library resampling method. *Environ Microbiol* 2006 Jul;8(7):1145-54. PMID: 16817923 [PubMed - indexed for MEDLINE]

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1: [Capelli C.](#) A nuclear DNA phylogeny of the woolly mammoth (*Mammuthus primigenius*). [82569635]

2: [Capelli C.](#) A nuclear DNA phylogeny of the woolly mammoth (*Mammuthus primigenius*). [82569618]

3: [Capelli C.](#) A nuclear DNA phylogeny of the woolly mammoth (*Mammuthus primigenius*). [82569600]

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8: [Willerslev E.](#) Diverse plant and animal genetic records from Holocene and Pleistocene sediments. [32396546]

9: [Greenwood AD.](#) Evolution of endogenous retrovirus-like elements of the woolly mammoth (*Mammuthus primigenius*) and its relatives. [14090839]

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1: Greenwood AD. Reports Evolution of endo...[gi:14090839] [Links](#)

Evolution of endogenous retrovirus-like elements of the woolly mammoth (*Mammuthus primigenius*) and its relatives.

[Viewing Options](#)

Greenwood,A.D., Lee,F., Capelli,C., DeSalle,R., Tikhonov,A., Marx,P.A., MacPhee,R.D.
Mol. Biol. Evol. 18 (5), 840-847 (5 2001)
View citation in [PubMed](#)

Generate an alignment using BLAST with these options

Blast Options Word Size: 20
Expect Value: 1e-06
Master Sequence: AF312038.1

Display Options Show only highest scoring alignments
 Show all generated alignments

[Generate Alignment](#)

1	AF312038.1	CCTACCTCAG	AGCTACATCA	ACTCTCCAGC	CCTATGTCAT	AATTTTGTTC	TAGAGGGAAC	(1-60)
2	AF312039.1	CCTACCTCAG	CGCTACAITA	GCTCTCCAGC	CCTATGTCAT	AATTTTGTTC	CACAGTGGTT	(1-59)
3	AF312040.1	CCTACCTCAG	AGTTACATCA	ACTCTCCAGC	CCTATATCAT	AATTTTGTTC	CAGAGGGAAC	(1-59)
4	AF312041.1	CCTGCTCAG	AAGTACATCA	ACTCTCCAGC	CGTATGTCAT	AATTTTGTTC	TGCAGGGAAC	(1-59)
5	AF312042.1	CCTACCTCAG	AGTTACATCA	ACTCTCCAGC	CCTATATCAT	AATTTTGTTC	CAGAGGGAAC	(1-59)
6	AF312043.1	TTTACCTGAG	GAATACATCA	ACTCTCCAGC	TCTATGTCAT	AATTTTGTTC	CTCAGGGAAC	(1-59)

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1: Greenwood AD. Reports Evolution of endo...[gi:14090839] [Links](#)

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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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- Nucleotide
- PubMed
- Taxonomy
- Taxonomy Tree

NCBI Nucleotide

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Display Summary Show 20 Send to []

All: 170 bacteria: 0 mRNA: 0 RefSeq: 0

Show only records from: [CoreNucleotide](#) (170), [EST](#) (0), [GSS](#) (0). [\[What's this?\]](#)

Items 1 - 20 of 170

1: [AF312207](#) Reports [Links](#)

Procavia capensis clone Pc10 endogenous retrovirus ERV-L pol gene, partial sequence
gi|14091008|gb|AF312207.1|AF312207[14091008]

NCBI Nucleotide

Search Nucleotide for [] Go Clear

Display Taxonomy Links Show 20 Send to [] RefSeq: 0

All: 17

Show

CoreNucleotide (170), EST (0), GSS (0). [What's this?]

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1: [Procavia capensis clone Pc6 endogenous retrovirus ERV-L pol gene, partial sequence](#) [gi|14091004|gb|AF312203.1|AF312203\[14091004\]](#) Links

2: [Procavia capensis clone Pc5 endogenous retrovirus ERV-L pol gene, partial sequence](#) [gi|14091003|gb|AF312202.1|AF312202\[14091003\]](#) Links

3: [Procavia capensis clone Pc8 endogenous retrovirus ERV-L pol gene, partial sequence](#) [gi|14091006|gb|AF312205\[14091006\]](#) Links

4: [Procavia capensis clone Pc7 endogenous retrovirus ERV-L pol gene, partial sequence](#) [gi|14091005|gb|AF312204\[14091005\]](#) Links

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6: [Procavia capensis clone Pc10 endogenous retrovirus ERV-L pol gene, partial sequence](#) [gi|14091008|gb|AF312207\[14091008\]](#) Links

NCBI Taxonomy

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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

Display Summary Show 20 Send to []

NCBI Taxonomy Browser

Entrez PubMed Nucleotide Protein Genome Structure PMC Taxonomy Books

Search for as complete name lock

Display 3 levels using filter: none

Mammuthus primigenius

Taxonomy ID: 37349
Gloabank common name: woolly mammoth

Rank: species
 Genetic code: [Translation table 1 \(Standard\)](#)
 Mitochondrial genetic code: [Translation table 2 \(Vertebrate Mitochondrial\)](#)
 Other names:
 common name: **mammoth**

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

Entrez records	
Database name	Direct links
Nucleotide	131
Protein	76
Genome Sequences	1
Genome Projects	1
Popset	5
PubMed Central	8
Gene	13
Taxonomy	1

Comments and References:

extinct
 This taxon is extinct.

Genome Information

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

External Information Resources (NCBI LinkOut)

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

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

Information from sequence entries

[Show organism modifiers](#)

Organism modifiers

To hide organism modifiers click [here](#)

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

NCBI Taxonomy Browser

Entrez PubMed Nucleotide Protein Genome Structure PMC Taxonomy Books

Search for as complete name lock

Display levels using filter:

Mammuthus primigenius

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

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

Entrez records	
Database name	Direct links
Nucleotide	131
Protein	76
Genome Sequences	1
Genome Projects	1
Popset	5
PubMed Central	8
Gene	13
Taxonomy	1

NCBI Taxonomy Browser

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Search for as complete name lock

Display levels using filter:

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](#)

NCBI Taxonomy Browser

Entrez PubMed Nucleotide Protein Genome Structure PMC Taxonomy Books

Search for as complete name lock

Display levels using filter:

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](#)
 - [Bacteria](#) (eubacteria)
 - [Eukaryota](#) (eucaryotes)

NCBI Taxonomy Browser

Entrez PubMed Nucleotide Protein Genome Structure PMC Taxonomy Books

Search for as complete name lock

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 MapView LinkOut BLAST TRACE

Lineage (full): root

- cellular organisms 33,573 *Click on organism name to get more information.*
 - Archaea 1,341
 - Bacteria (eubacteria) 12,611
 - Eukaryota (eucaryotes) 19,828

NCBI Taxonomy Browser

Entrez PubMed Nucleotide Protein Genome Structure PMC Taxonomy Books

Search for as complete name lock

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 MapView LinkOut BLAST TRACE

Lineage (full): root

- cellular organisms 33,573 *Click on organism name to get more information.*
 - Archaea 1,341
 - Bacteria (eubacteria) 12,611
 - Eukaryota (eucaryotes) 19,828

NCBI National Center for Biotechnology Information

National Library of Medicine National Institutes of Health

PubMed All Databases BLAST OMIM Books TaxBrowser Structure

Search All Databases for

GENSAT
 GEO Profiles
 GEO Datasets
 HomoloGene
 Journals
 MeSH
 NLM Catalog
 OMIA
 OMIM
 PMC
 PopSet

Assembly Archive
 Clusters of orthologous groups
 Coffee Break, Genes & Disease, NCBI Handbook

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All Databases PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM

Search OMIM for cytochrome C oxidase [Save Search](#)

Limits Preview Index History Clipboard Details

Display Titles Show 20 Send to

All: 108 OMIM ORPHANS: 14 OMIM UNISTS: 17

Items 1 - 20 of 108

1: *516030
 COMPLEX IV, CYTOCHROME c OXIDASE SUBUNIT I, MTCO1
 GeneTests, Links

2: *516040
 COMPLEX IV, CYTOCHROME c OXIDASE SUBUNIT II, MTCO2
 GeneTests, Links

3: *516050
 CYTOCHROME c OXIDASE III, MTCO3
 GeneTests, Links

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

Page 1 of 6 Next

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Search OMIM for cytochrome C oxidase Go Clear Save Search

Limits Preview/Index History Clipboard Details

Display Titles Show 20 Send to

All: 83 OMIM dbSNP: 7 OMIM UniSTS: 13

Items 1 - 20 of 83 Page 1 of 5 Next

- 1: [*516030](#) GeneTests, Links
COMPLEX IV, CYTOCHROME c OXIDASE SUBUNIT I; MTCO1
- 2: [*516050](#) GeneTests, Links
CYTOCHROME c OXIDASE III; MTCO3
- 3: [*516040](#) GeneTests, Links
COMPLEX IV, CYTOCHROME c OXIDASE SUBUNIT II; MTCO2
- 4: [#604377](#) GeneTests, Links
CARDIOENCEPHALOMYOPATHY, FATAL INFANTILE, DUE TO CYTOCHROME c OXIDASE DEFICIENCY
Gene map locus 22q13

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Search OMIM for Go Clear

Limits Preview/Index History Clipboard Details

Display Detailed Show 20 Send to

All: 1

[*516030](#) GeneTests, Links
COMPLEX IV, CYTOCHROME c OXIDASE SUBUNIT I; MTCO1

Alternative titles: symbols
CYTOCHROME c OXIDASE I; COI

TEXT

DESCRIPTION

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

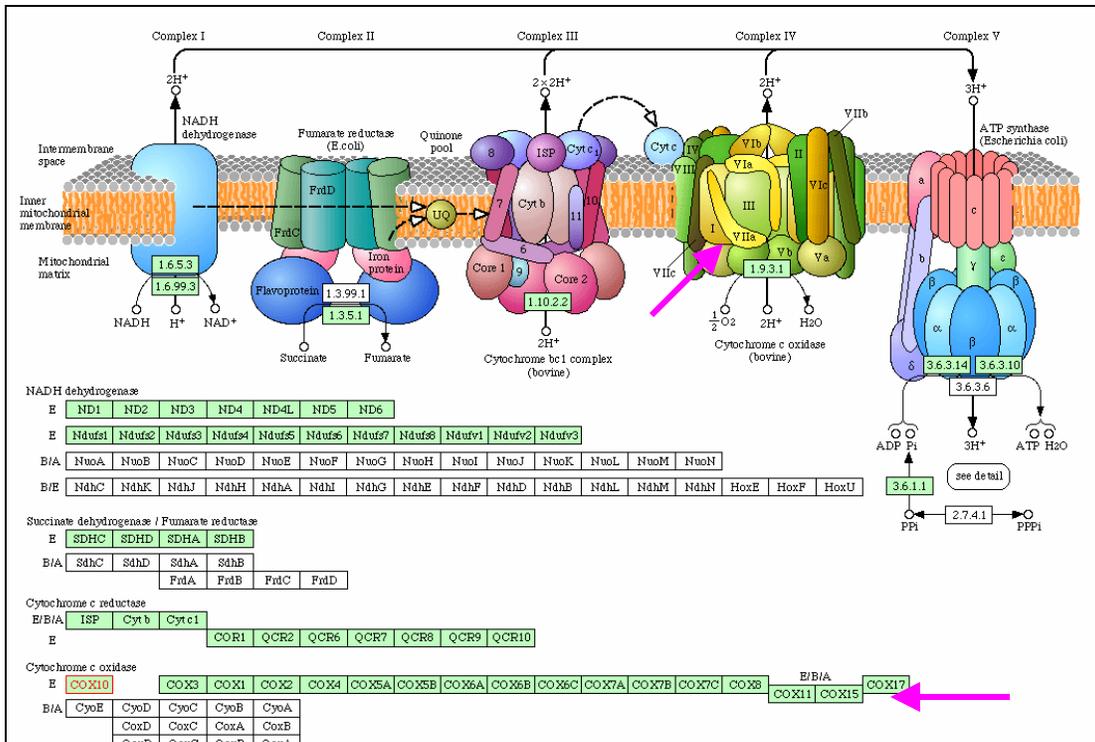


Figure from KEGG **Oxidative phosphorylation - Reference pathway (KO)**
http://www.genome.jp/dbget-in/show_pathway?ko00190+ko:K02270

The screenshot shows the OMIM database search interface. The search term "cytochrome c oxidase" has been entered, resulting in 82 items. The first two results are highlighted:

- 1: [*516030](#) COMPLEX IV, CYTOCHROME c OXIDASE SUBUNIT I; MTCO1
- 2: [*516050](#) CYTOCHROME c OXIDASE III; MTCO3

The interface includes navigation options like "Limits", "Preview/Index", "History", "Clipboard", and "Details". It also shows the number of items (82) and the current page (1 of 5).

Entrez

OMIM
Search OMIM
Search Gene Map
Search Morbid Map

Help
OMIM Help
How to Link

FAQ
Numbering System
Symbols
How to Print
Citing OMIM
Download

OMIM Facts
Statistics
Update Log
Restrictions on Use

Allied Resources
Genetic Alliance
Databases
HGMD

Limits Preview/Index History Clipboard Details

- To Search all fields, leave the following boxes unchecked.
- To narrow the search, check the boxes with specific fields' names, or use [search field tags](#) enclosed in square brackets, e.g. aaa[title].
- [Boolean operators](#) AND, OR, NOT must be in upper case.

Search in Field(s): clear <input type="checkbox"/> Title <input type="checkbox"/> MIM number <input type="checkbox"/> Allelic Variants <input type="checkbox"/> Text <input type="checkbox"/> References <input type="checkbox"/> Clinical Synopsis <input type="checkbox"/> Gene Map Disorder <input type="checkbox"/> Contributors	MIM Number Prefix: clear <input type="checkbox"/> * gene with known sequence <input type="checkbox"/> + gene with known sequence and phenotype <input type="checkbox"/> # phenotype description, molecular basis known <input type="checkbox"/> ≠ mendelian phenotype or locus, molecular basis unknown <input type="checkbox"/> none other, mainly phenotypes with suspected mendelian basis
Chromosome(s): clear <input type="checkbox"/> 1 <input type="checkbox"/> 2 <input type="checkbox"/> 3 <input checked="" type="checkbox"/> 4 <input type="checkbox"/> 5 <input checked="" type="checkbox"/> 6 <input type="checkbox"/> 7 <input type="checkbox"/> 8 <input type="checkbox"/> 9 <input type="checkbox"/> 10 <input type="checkbox"/> 11 <input type="checkbox"/> 12 <input type="checkbox"/> 13 <input type="checkbox"/> 14 <input type="checkbox"/> 15 <input type="checkbox"/> 16 <input type="checkbox"/> 17 <input type="checkbox"/> 18 <input checked="" type="checkbox"/> 19 <input type="checkbox"/> 20 <input type="checkbox"/> 21 <input type="checkbox"/> 22 <input type="checkbox"/> X <input type="checkbox"/> Y <input type="checkbox"/> mitochondrial <input type="checkbox"/> unknown	Only Records with: clear <input type="checkbox"/> Allelic Variants <input type="checkbox"/> Clinical Synopsis <input type="checkbox"/> Gene map locus

NCBI

OMIM
Online Mendelian Inheritance in Man

Johns Hopkins University

All Databases PubMed Nucleotide Protein Genome Structure

Search OMIM for "cytochrome C oxidase" Go Clear Save Search

Limits Preview/Index History Clipboard Details

Limits: **chromosome 4, chromosome 6, chromosome 19**

Display: Titles Show: 20 Send to:

All: 11 OMIM dbSNP: 1 OMIM UniSTS: 2

Items 1 - 11 of 11

1: [*123995](#)
CYTOCHROME c OXIDASE, SUBUNIT VIIa, POLYPEPTIDE 1; COX7A1
Gene map locus [19q12](#)

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](#)

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Search OMIM for Go Clear

Limits Preview/Index History Clipboard Details

Display Detailed Show 20 Send to

All: 1

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

Alternative titles; symbols

CYTOCHROME c OXIDASE, SUBUNIT VIIa, MUSCLE ISOFORM

Gene map locus [19q12](#)

TEXT

DESCRIPTION

Cytochrome c oxidase (COX; [EC 1.9.3.1](#)), the last component of the mitochondrial respiratory chain, catalyzes the transfer of electrons from reduced cytochrome c to molecular oxygen. In mammals, the apoprotein is composed of 3 large catalytic subunits, encoded by the mitochondrial genome ([516030](#), [516040](#), and [516050](#)), and by 10 smaller, nuclear-encoded subunits which may play a regulatory role. Subunit VIIa of mammalian COX exists in at least 2 isoforms, liver (see [123996](#)) and muscle.

Links

- Gene
- GEO Profiles
- HomoloGene
- Free in PMC
- PubMed (calculated)
- PubMed (cited)
- Gene Genotype
- GeneView in dbSNP
- UniGene
- Related Entries
- Nucleotide
- Protein
- LinkOut

NCBI **UniGene** ORGANIZED VIEW OF THE TRANSCRIPTOME

All Databases PubMed Nucleotide Protein Genome Structure PMC

Search UniGene for Go Clear

Limits Preview/Index History Clipboard Details

Display Summary Show 20 Sort by Send to

All: 2 Fungi: 0 Insects: 0 Mammals: 2 Plants: 0

Items 1 - 2 of 2

1: [Hs.421621](#)
COX7A1: Cytochrome c oxidase subunit VIIa polypeptide 1 (muscle)
Homo sapiens, 262 sequence(s)

2: [Hs.70312](#)
COX7A2: Cytochrome c oxidase subunit VIIa polypeptide 2 (liver)
Homo sapiens, 710 sequence(s)

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PubMed Nucleotide Protein Genome Structure Popset Taxonomy

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NCBI UniGene Hs.421621 *Homo sapiens* COX7A1 [Links](#)

Cytochrome c oxidase subunit VIIa polypeptide 1 (muscle) (COX7A1)

SELECTED PROTEIN SIMILARITIES

Comparison of sequences in UniGene with proteins supported by a complete genome. The alignments can suggest function of a gene.

<i>H. sapiens</i>	pir:OSHU7A - OSHU7A cytochrome-c oxidase	100.00 % / 79 aa (see ProtEST)
<i>M. musculus</i>	sp:P56392 - COXK_MOUSE Cytochrome c oxidase polypeptide VIIa-heart, mitochondrial precursor	72.73 % / 77 aa (see ProtEST)
<i>R. norvegicus</i>	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

Hs.421621

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

NCBI UniGene EST Profile Viewer

Pubmed Nucleotide Protein Genome Structure Popset Taxonomy

Search UniGene

Limits **Index** History Details

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

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

Breakdown by Tissue

Hs.421621

blood	0	0 / 111420
bone	13	1 / 72260
bone marrow	0	0 / 48827

NCBI UniGene ORGANIZED VIEW OF THE TRANSCRIPTOME

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Search UniGene

Index History Clipboard Details

Click Preview to see only the number of search results.
Queries use # before search number, e.g., (#2 OR #3) AND asthma.
To refine a query, click query # and select Save in My NCBI.
Queries use #search, e.g., #2 AND #3 or click query # for more options.

Most Recent Queries		Time	Result
9999[Est Count]		15:03:10	45807
1502:57		15:02:57	0
21621[cid]		15:02:00	1

Query or View Index:
In the text box, use the pull-down menu to specify a search field.
To add terms to the query box and see the number of search results, or click Index to view terms within a field.

All Fields

Click to add a term to the query box.

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Search UniGene for 100:99999[Est Count] Preview Go Clear Save Search

Limits Preview/Index History Clipboard Details

- Enter terms and click Preview to see only the number of search results.
- To combine searches use # before search number, e.g., (#2 OR #3) AND asthma.
- Click on query # to add to strategy

NCBI

UniGene
 Homepage
 Query Tips
 FAQs
 Finding cDNAs
 Library Browser
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Related Databases
 Gene
 HomoloGene
 dbEST
 Trace Archive

NIH cDNA Projects

Search Most Recent Queries Time Result

Search	Time	Result
#28 Search 100:99999[Est Count]	18:14:35	45255
#27 UniGene Links for OMIM (Select 123995)	18:03:34	2

Add Term(s) to Query or View Index:

- Enter a term in the text box; use the pull-down menu to specify a search field.
- Click Preview to add terms to the query box and see the number of search results, or click Index to view terms within a field.

Est Count [] Preview Index

Click AND OR NOT to add a term to the query box.

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Limits Preview/Index History Clipboard Details

Display Summary Show 20 Sort by Send to

All: 45826 Fungi: 156 Insects: 1546 Mammals: 26997 Plants: 8701

Items 1 - 20 of 45826 Page 1 of 2292 Next

1: [Zm 43475](#)
 Clone Contig1011.F mRNA sequence
Zea mays, 260 sequence(s) Links

2: [Zm 43295](#)
 Clone Contig393 mRNA sequence
Zea mays, 470 sequence(s) Links

3: [Zm 43196](#)
 LOC542276: Ferredoxin III (Fd) isoprotein mRNA, pFD3
Zea mays, 296 sequence(s) Links

4: [Zm 41478](#)
 Transcribed locus
Zea mays, 100 sequence(s) Links

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Search HomoloGene for 100:99999[Est Count] Go Clear Save Search

Limits Preview/Index History Clipboard Details

Display Summary Show 20 Sort by Send to

All: 45807 Fungi: 156 Insects: 1546 Organism: 3986 Plants: 8698

Items 1 - 20 of 45807 Page 1 of 2291 Next

1: [Zm 43475](#)
 Clone Contig1011.F mRNA sequence
Zea mays, 260 sequence(s) Links

2: [Zm 43295](#)
 Clone Contig393 mRNA sequence
Zea mays, 470 sequence(s) Links

3: [Zm 43196](#)
 LOC542276: Ferredoxin III (Fd) isoprotein mRNA, pFD3
Zea mays, 296 sequence(s) Links

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Gene
Genome Project
GENSAT
GEO Profiles
GEO DataSets
HomoloGene
Journals
MeSH
NCBI Web Site
NLM Catalog
OMIA

Preview/Index History Clipboard Details

Summary Show 20 Sort by Send to

55 Fungi: 160 Insects: 1503 Mammals: 27075 Plants: 8213

Items 1 - 20 of 45255 Page 1 of 2263 Next

39421
U0062493 mRNA sequence
Zea mays, 109 sequence(s)

Links

NCBI **HomoloGene** Discover Homologs

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Search HomoloGene for [cox*[gene name]] Go Clear Save Search

Limits Preview/Index History Clipboard Details

Display Summary Show 20 Send to

All: 40 Fungi: 4 Mammals: 10

Items 1 - 20 of 40 Page 1 of 2 Next

1: HomoloGene:5017. Gene conserved in Fungi/Metazoa group Download, Links

H.sapiens	COX2	cytochrome c oxidase subunit II
P.troglodytes	COX2	cytochrome c oxidase subunit II
C.familiaris	COX2	cytochrome c oxidase subunit II
M.musculus	COX2	cytochrome c oxidase subunit II
R.norvegicus	COX2	COXII
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
E.gossypii	AM1001Wp	AM1001Wp

2: HomoloGene:5016. Gene conserved in Eukaryota Download, Links

H.sapiens	COX1	cytochrome c oxidase subunit I
P.troglodytes	COX1	cytochrome c oxidase subunit I

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All Databases PubMed Nucleotide Protein Genome Structure Map Viewer Gene UniGene OMIM

Search HomoloGene for cox*[Gene Name] Preview Go Clear

Limits Preview/Index History Clipboard Details

- Enter terms and click Preview to see only the number of search results.
- To combine searches use # before search number, e.g., (#2 OR #3) AND asthma.
- Click on query # to add to strategy

Search	Most Recent Queries	Time	Result
#33	Search cox*[Gene Name]	18:25:29	39
#32	Search cox*	18:24:58	232
#31	Search 100:99999[Est Count]	18:24:16	0

Add Term(s) to Query or View Index:

- Enter a term in the text box; use the pull-down menu to specify a search field.
- Click Preview to add terms to the query box and see the number of search results, or click Index to view terms within a field.
- Multiple terms selected from Index will be ORed, click AND to add to search.

Ancestor Taxonomy ID:2759 Preview Index

Click AND OR NOT to add terms selected from Index to the query box.

txid207598(621) Up
 txid222544(2)
 txid2759(6140)
 txid28985(7)
 txid314145(77)
 txid41454(159)

NCBI HomoloGene Discover Homologs

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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

Display Summary Show 20 Send to

All: 5 Fungi: 0 Mammals: 0

Items 1 - 5 of 5

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.familiaris	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	Subunit I of cytochrome c oxidase, which i...
K.lactis	COX1	cytochrome c oxidase subunit 1
E.gossypii	AM1002W	AM1002Wp
P.falci-parum	col	Plasmodium falci-parum col gene

2: HomoloGene:5014. Gene conserved in Eukaryota

H.sapiens	COX3	cytochrome c oxidase subunit III
P.troglodytes	COX3	cytochrome c oxidase subunit III
C.familiaris	COX3	cytochrome c oxidase subunit III
M.musculus	COX3	cytochrome c oxidase subunit III
G.gallus	COX3	cytochrome c oxidase subunit III

Links

- Conserved Domains
- Gene
- GEO Profiles
- Related HomoloGene
- Full text in PMC
- Protein
- PubMed
- Gene Genotype
- Taxonomy
- UniGene
- Taxonomy Tree

Download, 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
 - Euarctontoglires
 - Murinae
 - Mus musculus
 - Rattus norvegicus
 - Homo/Pan/Gorilla group
 - Homo sapiens
 - Pan troglodytes
 - Gallus gallus
 - Diptera
 - Anopheles gambiae
 - Drosophila melanogaster

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Search HomoloGene for COX*[Gene Name] AND "txid2759"[Ancestor] Go Clear Save Search

Gene Genome Project GENSAT GEO Profiles GEO DataSets HomoloGene Journals MeSH NCBI Web Site NLM Catalog OMIA OMIM PMC PopSet Probe PubChem BioAssay PubChem Compound PubChem Substance SNP Taxonomy

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Primary Show 20 Send to

Angi: 0 Mammals: 0

of 5 One page. Download, Links

Gene	Protein	Gene
HomoloGene:5016. Gene conserved in Eukaryota		
Canis familiaris	COX1	cytochrome c oxidase subunit I
Drosophila melanogaster	COX1	cytochrome c oxidase subunit I
Eremothecium gossypii	COX1	cytochrome c oxidase subunit I
Kluyveromyces fragilis	COX1	cytochrome c oxidase subunit I
Mus musculus	COX1	cytochrome c oxidase subunit I
Rattus norvegicus	COX1	cytochrome c oxidase subunit I
Schizosaccharomyces pombe	COX1	cytochrome c oxidase subunit I
Saccharomyces cerevisiae	COX1	Subunit I of cytochrome c oxidase, which i

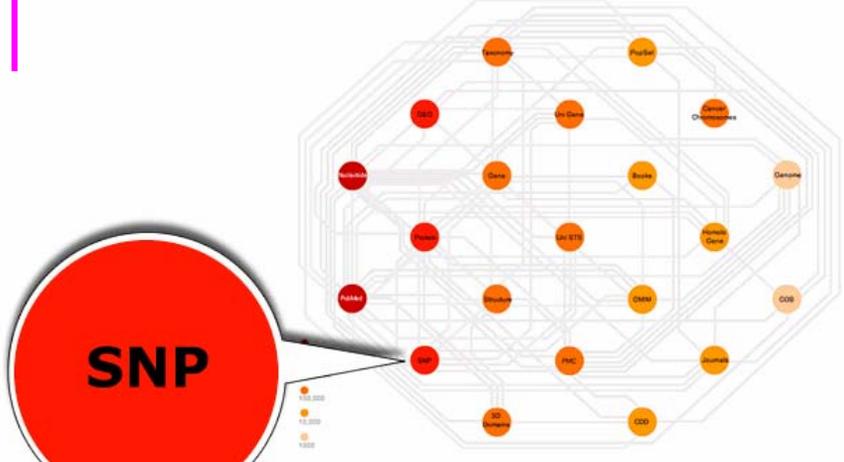

ENTREZ **SNP**
Single Nucleotide Polymorphism
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 Common Query Filters
 Entrez Batch Query
 SNP Link Datamodel
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 Limits

Click on the image below to view the connections between Entrez SNP and other databases.



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Other Services
 Journal Browser
 MeSH Browser
 Citation Matcher
 Clinical Queries

Limits Preview/Index History Clipboard Details

- To Search all fields, leave the following boxes unchecked ([Limits help](#)).
- To narrow the search, check the boxes with specific fields' names, or use [search field tags](#) enclosed in square brackets, e.g. aaa[title].
- [Boolean operators](#): AND, OR, NOT must be in upper case.

Function class: clear		Has genotype: clear	
<input checked="" type="checkbox"/> coding nonsynonymous	<input type="checkbox"/> reference	<input type="checkbox"/> exception	<input type="checkbox"/> intron
<input type="checkbox"/> coding synonymous	<input type="checkbox"/> locus region	<input type="checkbox"/> mrna utr	<input type="checkbox"/> splice site
Chromosome(s): clear		Map weight: clear	
<input type="checkbox"/> 1	<input type="checkbox"/> 2	<input type="checkbox"/> 3	<input type="checkbox"/> 4
<input type="checkbox"/> 5	<input type="checkbox"/> 6	<input type="checkbox"/> 7	<input type="checkbox"/> 8
<input type="checkbox"/> 9	<input type="checkbox"/> 10	<input type="checkbox"/> 11	<input type="checkbox"/> 12
<input type="checkbox"/> 13	<input type="checkbox"/> 14	<input type="checkbox"/> 15	<input type="checkbox"/> 16
<input type="checkbox"/> 17	<input type="checkbox"/> 18	<input type="checkbox"/> 19	<input type="checkbox"/> 20
<input type="checkbox"/> 21	<input checked="" type="checkbox"/> 22	<input type="checkbox"/> W	<input type="checkbox"/> X
<input type="checkbox"/> Y	<input type="checkbox"/> Z	<input type="checkbox"/> unknown	
Base Position: from <input type="text"/> to <input type="text"/>			
Organism(s): clear		Observed alleles: clear	
<input checked="" type="checkbox"/> Homo sapiens	<input type="checkbox"/> Anopheles gambiae	<input type="checkbox"/> Arabidopsis thaliana	<input type="checkbox"/> Caenorhabditis elegans
<input type="checkbox"/> Danio rerio	<input type="checkbox"/> Ficedula albicollis	<input type="checkbox"/> Ficedula hypoleuca	<input type="checkbox"/> Gallus gallus
<input type="checkbox"/> Mus musculus	<input type="checkbox"/> Pan troglodytes	<input type="checkbox"/> Plasmodium falciparum	<input type="checkbox"/> Rattus norvegicus
IUPAC code	Meaning		
<input type="checkbox"/> A	A		
<input type="checkbox"/> C	C		
<input type="checkbox"/> G	G		
<input type="checkbox"/> T	T		
<input type="checkbox"/> M	A or C		
<input type="checkbox"/> R	A or G		
<input type="checkbox"/> W	A or T		
<input type="checkbox"/> S	C or G		
<input type="checkbox"/> Y	C or T		
<input type="checkbox"/> K	G or T		
<input type="checkbox"/> V	A or C or G		
<input type="checkbox"/> H	A or C or T		
<input type="checkbox"/> D	A or G or T		
<input type="checkbox"/> B	C or G or T		
<input type="checkbox"/> N	G or A or T or C		
Created: clear		Updated: clear	
<input type="checkbox"/> Current Build ID		<input type="checkbox"/> Current Build ID	
<input type="checkbox"/> Last Build ID		<input type="checkbox"/> Last Build ID	
CBID Range from <input type="text"/> to <input type="text"/>		UBID Range from <input type="text"/> to <input type="text"/>	
Validation: clear			
<input type="checkbox"/> by-cluster		<input type="checkbox"/> by-frequency	
<input type="checkbox"/> by-submitter			

Records has: clear		Heterozygosity(%): clear		Success rate(%): clear	
<input type="checkbox"/> nucleotide	<input checked="" type="checkbox"/> omim	<input type="checkbox"/> 0-10	<input type="checkbox"/> 10-20	<input type="checkbox"/> 20-30	<input type="checkbox"/> 30-40
<input type="checkbox"/> protein	<input checked="" type="checkbox"/> structure	<input type="checkbox"/> 40-50	Het Range from <input type="text"/> to <input type="text"/>		
<input type="checkbox"/> pubmed		<input type="checkbox"/> 80-85	<input type="checkbox"/> 85-90	<input type="checkbox"/> 90-95	<input type="checkbox"/> 95+
		Success Range from <input type="text"/> to <input type="text"/>			

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Limits: **chromosome 22, coding nonsynon, has omin, has structure, Homo sapiens**

Display Graphic Summary Show 20 Sort by Send to

All: 13 Items 1 - 13 of 13

- 1: rs28931573 [Homo sapiens]
 - Graphic Summary
 - Brief
 - Flat File
 - ASN.1
 - XML
 - FASTA
 - RS Cluster Report
 - SS Exemplar List
 - Chromosome Report
 - Allele Frequency XML
 - Genotype
 - Genotype Detail
 - Genotype XML
 - Summary
 - dbSNP Batch Report
 - UI List
 - Gbench Export
 - LinkOut
 - Merge Status
 - Gene Genotype Links

CCAG [C/T] GCTTGCCGCGCGCCTTGAGGCTCT

GTCC [A/G] AGATGACCTGCGCTTCCGGGAGTA

GATA [C/T] CACTGCAGCCCTGCCTGCCACGCC

22 MapView GeneView SeqView Protein 3D OMM

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Limits: **chromosome 22, coding nonsynon, has omin, has structure, Homo sapiens**

Display UI List Show 20 Sort by Send to

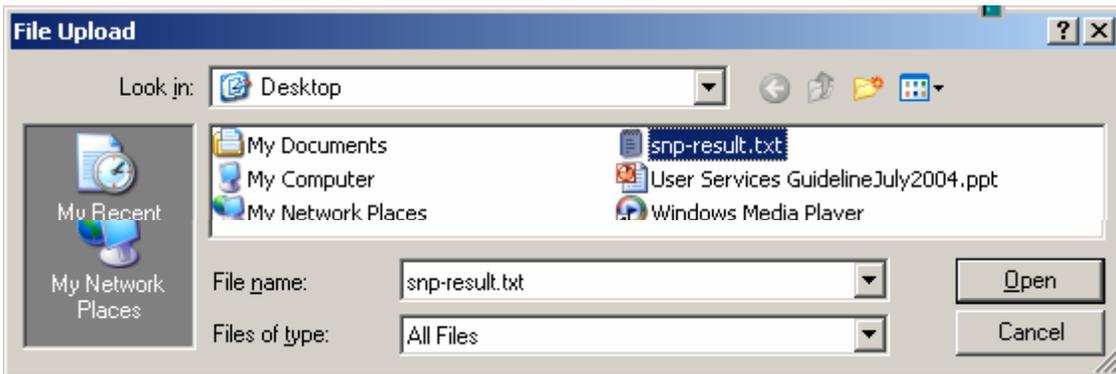
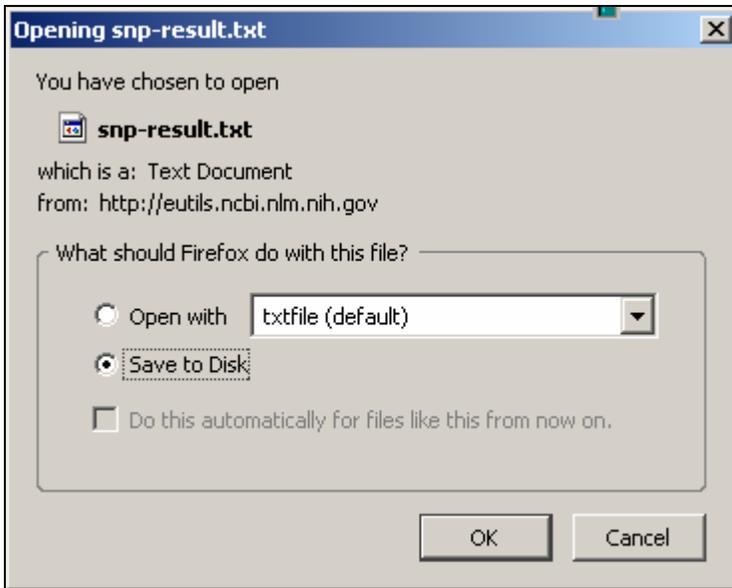
All: 13 Human: 13 Mouse: 0 NEW: 8 Other Organisms: 0 UP

Items 1 - 13 of 13

- 1: rs28931573 [Homo sapiens]
 - Send to
 - Text
 - File
 - Printer
 - Clipboard

CCCTACAGCGACGAGCTGCGCCAG [C/T] GCTTGCCGCGCGCCTTGAGGCTCT

28931573



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Limits Preview/Index History Clipboard Details

Limits: **chromosome 22, coding nonsynon, has omin, has structure, Homo sapiens**

Display UI List Show 20 Sort by Send to

All: 13 Human: 13 Mouse: 0 NEW: 8 Other Organisms: 0 UPDATE: 1

Items 1 - 13 of 13 One page.

1: rs28931573 [*Homo sapiens*] Links

CCCCCTACAGCGACGAGCTGCCCCAG [C/T] GCTTGGCCGCGCCCTTGAGGGCTCT

28931573

2: rs28941471 [*Homo sapiens*] Links

GATCTCCAGAACTTGAAGCGTGTCC [A/G] AGATGACCTGCGCTTCCGGGGAGTA

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Database: SNP File: C:\Documents and Settings\gratia Browse... Retrieve

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 Search Mouse SNP
 Common Query Filters
 Entrez Batch Query
 SNP Link Datamodel

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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.

1: [rs28931573](#) [*Homo sapiens*] Links

CCCCTACAGCGACGAGCTGCGCCAG[C/T]GCTTGGCCGCGCGCCTTGAGGCTCT

no Map GeneView SeqView Protein 3D OMIM

2: [rs28941471](#) [*Homo sapiens*] Links

GATCTCCAGA AACTTGAAGCGTGTC[C/A/G]AGATGACCTGCGCTTCCGGGGAGTA

MapView GeneView SeqView Protein 3D OMIM

3: [rs28940895](#) [*Homo sapiens*] Links

ACCCAGGGCTCTGCCACAGTGATA[C/T]CACTGCAGACCCTGCCTGCCACGCC

MapView GeneView SeqView Protein 3D OMIM

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Searches Collections

Nucleotide Searches ▼ ▲	Last Updated ▼ ▲	Details ▼ ▲
<input type="checkbox"/> XRCG1	today	No Schedule
<input type="checkbox"/> TSC2	1 year ago	No Schedule

What's New for Selected Delete Selected

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- Filters (Includes Link-Out)
- Document Delivery
- Outside Tool
- User Preferences (Email address)
- Change Password
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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.

Course developed by:

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