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**Bookshelf URL:** https://www.ncbi.nlm.nih.gov/books/

NCBI News

National Center for Biotechnology Information
National Library of Medicine | National Institutes of Health
Department of Health and Human Services

# NCBI News, September 2010

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## New Databases and Tools

### Find-in-Sequence now available in nucleotide and protein databases

The new Find-in-Sequence search finds and highlights subsequences, patterns, or motifs in nucleotide or protein sequences displayed in the Entrez system. In nucleotide sequences, sub-sequences or patterns of interest may include restriction enzyme recognition sites, transcription factor binding sites and other promoter elements, poly-adenylation signals, start and stop codons, and many others. In proteins, these may include potential cleavage locations, sites of potential post-translational modification, motifs representing active sites, cofactor binding pockets, or other structural or functional signatures. The link to open the Find-in-Sequence search box appears in the Analysis Tools portlet in the right-hand Discovery column of nucleotide and protein record views. Find-in-sequence works with single and multiple sequence displays with any format that shows the sequence (GenBank, GenPept, FASTA). The search box that opens at the bottom of the display has the familiar look and feel of the find in page function of the Web browser showing all matches and providing means to jump to the next or previous match. However, unlike the simple find function, Find-in-Sequence allows matching across spaces and line breaks in the formatted sequence and can use standard nucleotide and protein ambiguity codes as well as Prosite patterns for protein sequences. Find-in-Sequence provides rapid mapping of custom features onto nucleotide and protein sequences and is a powerful addition to the suite of analysis tools now available directly from sequence records in the Entrez system.

A video demonstrating this feature is now available on the NCBI YouTube channel.

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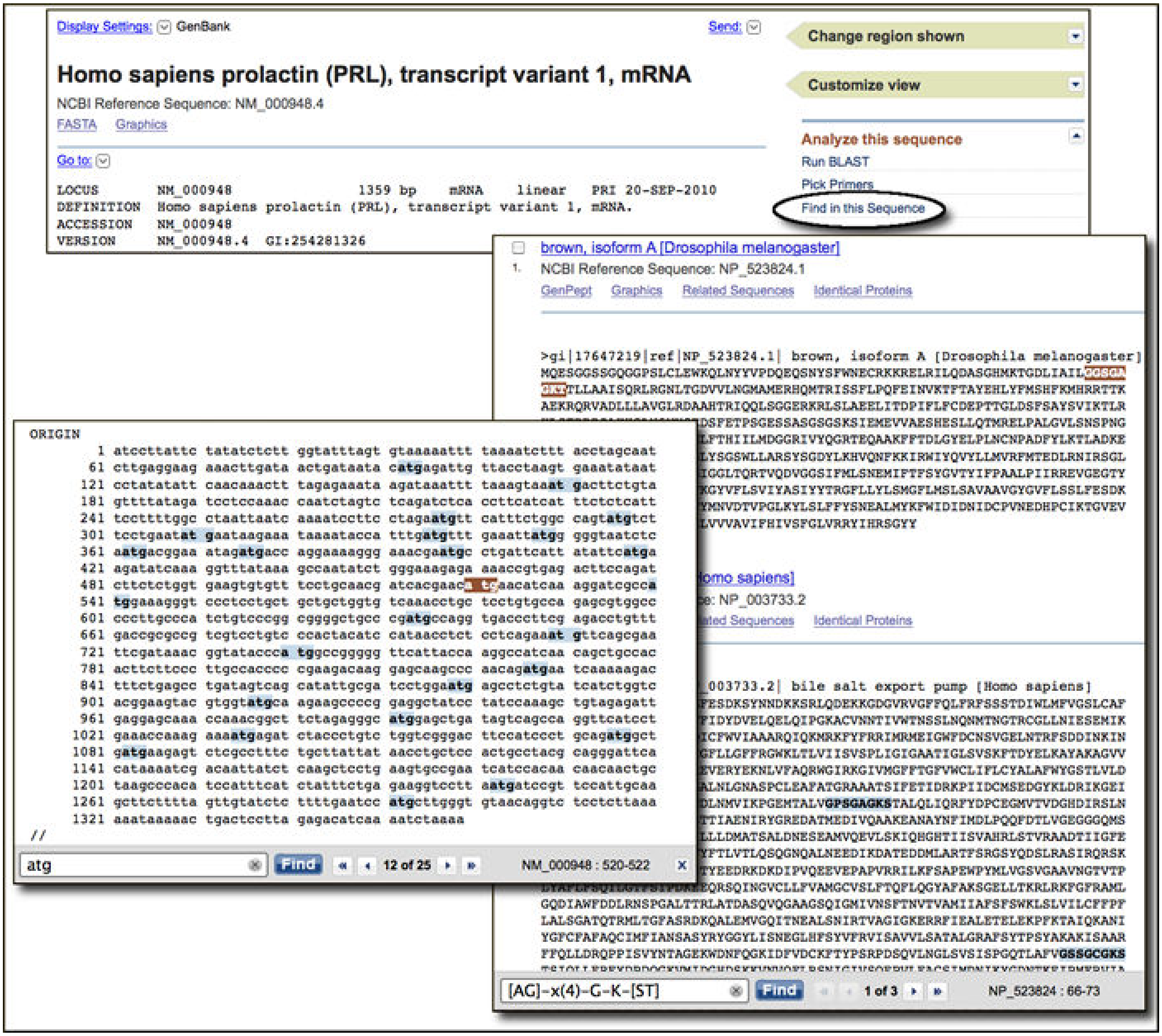


## Homo sapiens prolactin (PRL), transcript variant 1, mRNA

NCBI Reference Sequence: NM_000948.4

```
LOCUS       NM_000948               1359 bp    mRNA    linear   PRI 20-SEP-2010
DEFINITION  Homo sapiens prolactin (PRL), transcript variant 1, mRNA.
ACCESSION   NM_000948
VERSION     NM_000948.4  GI:254281326
```

```
ORIGIN
        1 atccttattc tatatctctt ggtatttagt gtaaaaattt taaaatcttt acctagcaat
       61 cttgaggaag aaacttgata actgataata catgagattg ttacctaagt gaaatataat
      121 cctatatatt caacaaactt tagagaaata agataaattt taaagtaaat gacttctgta
      181 gttttataga tcctccaaac caatctagtc tcagatctca ccttcatcat ttctctcatt
      241 tccttttggc ctaattaatc aaaatccttc ctagaatgtt catttctggc cagtatgtct
      301 tcctgaatat gaataagaaa taaaatacca tttgatgttt gaaattatgg gggtaatctc
      361 aatgacggaa atagatgacc aggaaaaggg aaacgaatgc ctgattcatt atattcatga
      421 agatatcaaa ggtttataaa gccaatatct gggaaagaga aaaccgtgag acttccagat
      481 cttctctggt gaagtgtgtt tcctgcaacg atcacgaaca tgaacatcaa aggatcgcca
      541 tggaaagggt ccctcctgct gctgctggtg tcaaacctgc tcctgtgcca gagcgtggcc
      601 cccttgccca tctgtcccgg cggggctgcc cgatgccagg tgacccttcg agacctgttt
      661 gaccgcgccg tcgtcctgtc ccactacatc cataacctct cctcagaaat gttcagcgaa
      721 ttcgataaac ggtatacccа tggccggggg ttcattacca aggccatcaa cagctgccac
      781 acttcttccc ttgccacccc cgaagacaag gagcaagccc aacagatgaa tcaaaaagac
      841 tttctgagcc tgatagtcag catattgcga tcctggaatg agcctctgta tcatctggtc
      901 acggaagtac gtggtatgca agaagccccg gaggctatcc tatccaaagc tgtagagatt
      961 gaggagcaaa ccaaacggct tctagagggc atggagctga tagtcagcca ggttcatcct
     1021 gaaaccaaag aaaatgagat ctaccctgtc tggtcgggac ttccatccct gcagatggct
     1081 gatgaagagt ctcgcctttc tgcttattat aacctgctcc actgcctacg cagggattca
     1141 cataaaatcg acaattatct caagctcctg aagtgccgaa tcatccacaa caacaactgc
     1201 taagcccaca tccatttcat ctatttctga gaaggtcctt aatgatccgt tccattgcaa
     1261 gcttctttta gttgtatctc ttttgaatcc atgcttgggt gtaacaggtc tcctcttaaa
     1321 aaataaaaac tgactcctta gagacatcaa aatctaaaa
//
```

brown, isoform A [Drosophila melanogaster]

1. NCBI Reference Sequence: NP_523824.1

```
>gi|17647219|ref|NP_523824.1| brown, isoform A [Drosophila melanogaster]
MQESGGSSGQGGPSLCLEWKQLNYYVPDQEQSNYSFWNECRKKRELRILQDASGHMKTGDLIAILGGSGA
GKTTLLAAISQRLRGNLTGDVVLNGMAMERHQMTRISSFLPQFEINVKTFTAYEHLYFMSHFKMHRRTTK
AEKRQRVADLLLAVGLRDAAHTRIQQLSGGERKRLSLAEELITDPIFLFCDEPTTGLDSFSAYSVIKTLR
DSFETPSGESSASGSGSKSIEMEVVAESHESLLQTMRELPALGVLSNSPNG
LFTHIILMDGGRIVYQGRTEQAAKFFTDLGYELPLNCNPADFYLKTLADKE
LYSGSWLLARSYSGDYLKHVQNFKKIRWIYQVYLLMVRFMTEDLRNIRSGL
IGGLTQRTVQDVGGSIFMLSNEMIFTFSYGVTYIFPAALPIIRREVGEGTY
KGYVFLSVIYASIYYTRGFLLYLSMGFLMSLSAVAAVGYGVFLSSLFESDK
YMNVDTVPGLKYLSLFFYSNEALMYKFWIDIDNIDCPVNEDHPCIKTGVEV
LVVVAVIFHIVSFGLVRRYIHRSGYY
```

omo sapiens]

e: NP_003733.2

```
_003733.2| bile salt export pump [Homo sapiens]
FESDKSYNNDKKSRLQDEKKGDGVRVGFFQLFRFSSSTDIWLMFVGSLCAF
FIDYDVELQELQIPGKACVNNTIVWTNSSLNQNMTNGTRCGLLNIESEMIK
ICFWVIAAARQIQKMRKFYFRRIMRMEIGWFDCNSVGELNTRFSDDINKIN
GFLLGFFRGWKLTLVIISVSPLIGIGAATIGLSVSKFTDYELKAYAKAGVV
EVERYEKNLVFAQRWGIRKGIVMGFFTGFVWCLIFLCYALAFWYGSTLVLD
ALNLGNASPCLEAFATGRAAATSIFETIDRKPIIDCMSEDGYKLDRIKGEI
DLNMVIKPGEMTALVGPSGAGKSTALQLIQRFYDPCEGMVTVDGHDIRSLN
TTIAENIRYGREDATMEDIVQAAKEANAYNFIMDLPQQFDTLVGEGGGQMS
LLLDMATSALDNESEAMVQEVLSKIQHGHTIISVAHRLSTVRAADTIIGFE
YFTLVTLQSQGNQALNEEDIKDATEDDMLARTFSRGSYQDSLRASIRQRSK
TYEEDRKDKDIPVQEEVEPAPVRRILKFSAPEWPYMLVGSVGAAVNGTVTP
LYAFLFSQILGTFSIPDKEQRSQINGVCLLFVAMGCVSLFTQFLQGYAFAKSGELLTKRLRKFGFRAML
GQDIAWFDDLRNSPGALTTRLATDASQVQGAAGSQIGMIVNSFTNVTVAMIIAFSFSWKLSLVILCFFPF
LALSGATQTRMLTGFASRDKQALEMVGQITNEALSNIRTVAGIGKERRFIEALETELEKPFKTAIQKANI
YGFCFAFAQCIMFIANSASYRYGGYLISNEGLHFSYVFRVISAVVLSATALGRAFSYTPSYAKAKISAAR
FFQLLDRQPPISVYNTAGEKWDNFQGKIDFVDCKFTYPSRPDSQVLNGLSVSISPGQTLAFVGSSGCGKS
```

## Recent NCBI Publication on dbVar

The NCBI Database of Genomic Structural Variation (dbVar) announced in the February 2010 issue of the NCBI News was described in a recent correspondence article in *Nature Genetics*.

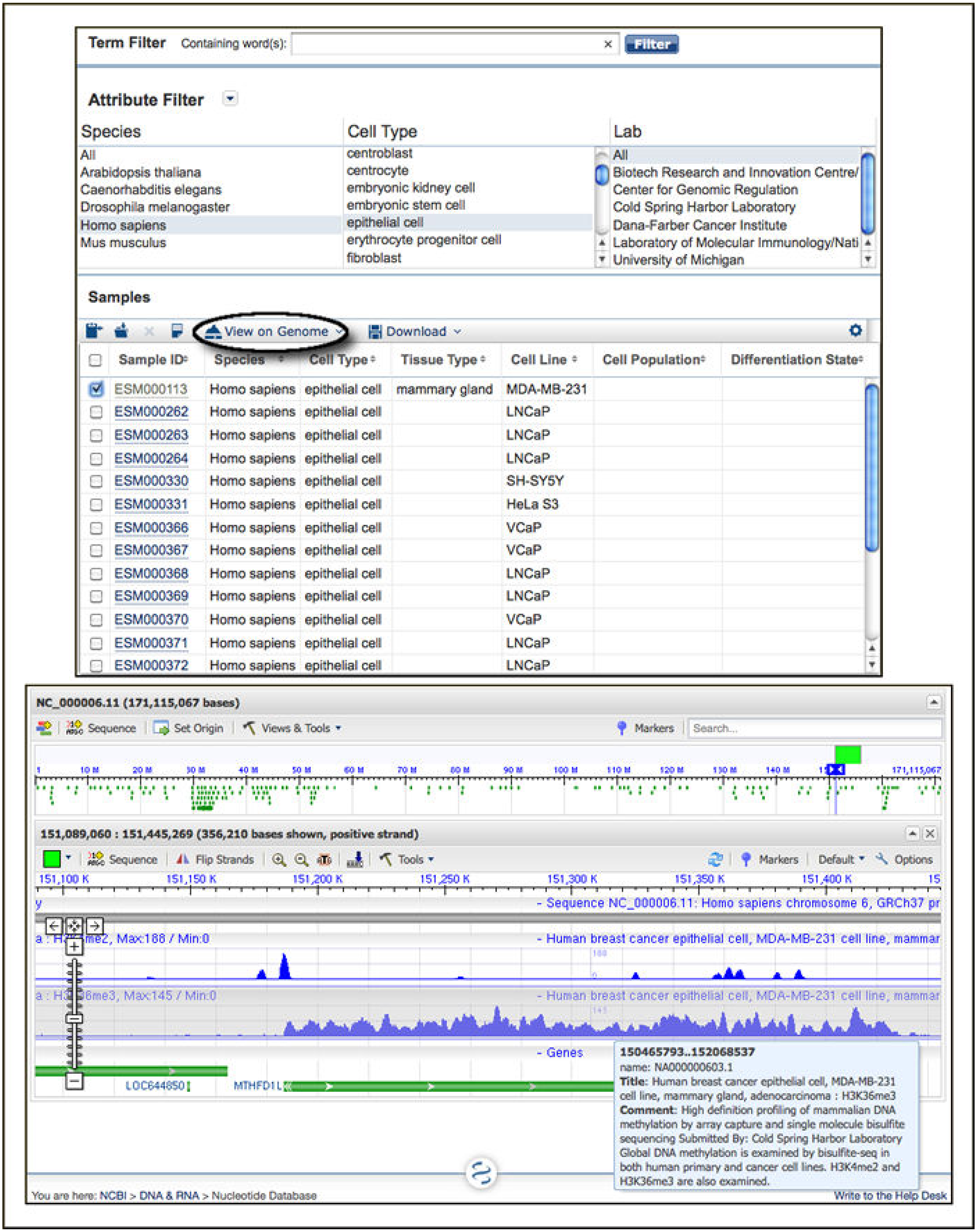
Church DM, Lappalainen I, Sneddon TP, Hinton J, Maguire M, Lopez J, Garner J, Paschall J, DiCuccio M, Yaschenko E, Scherer SW, Feuk L, Flicek P. **Public data archives for genomic structural variation**. *Nat Genet*. 42, 813-814 (2010). PMID: 20877315

The publication and resource are also announced in a recent NIH press release.

dbVAR provides information on large scale (> 1Kb) variations in genome sequences and includes copy number variants and other deletions and insertions.

## Epigenomics Resource

A new Epigenomics resource (www.ncbi.nlm.nih.gov/epigenomics) is part of the Entrez search and retrieval system. Epigenomics is a new field of research with the goal of understanding how different cell types and lineages acquire distinct patterns of gene expression. The Epigenomics database contains results of genome-wide studies on modifications of chromatin (histone modification, DNA methylation, DNAase footprinting) in various cell types. These studies assay programmable changes that affect gene expression (epigenetics). A Sample Browser provides access to experimental data. Data can be filtered based on biological attributes such as cell type, differentiation stage, health status, and others. Data may be displayed on the genome using either the UCSC genome browser or NCBI graphical sequence viewer as shown below.



**Term Filter** Containing word(s): × Filter

**Attribute Filter**

Species
All
Arabidopsis thaliana
Caenorhabditis elegans
Drosophila melanogaster
Homo sapiens
Mus musculus

Cell Type
centroblast
centrocyte
embryonic kidney cell
embryonic stem cell
epithelial cell
erythrocyte progenitor cell
fibroblast

Lab
All
Biotech Research and Innovation Centre/
Center for Genomic Regulation
Cold Spring Harbor Laboratory
Dana-Farber Cancer Institute
Laboratory of Molecular Immunology/Nati
University of Michigan

**Samples**

| □ | Sample ID | Species | Cell Type | Tissue Type | Cell Line | Cell Population | Differentiation State |
|---|---|---|---|---|---|---|---|
| ☑ | ESM000113 | Homo sapiens | epithelial cell | mammary gland | MDA-MB-231 | | |
| □ | ESM000262 | Homo sapiens | epithelial cell | | LNCaP | | |
| □ | ESM000263 | Homo sapiens | epithelial cell | | LNCaP | | |
| □ | ESM000264 | Homo sapiens | epithelial cell | | LNCaP | | |
| □ | ESM000330 | Homo sapiens | epithelial cell | | SH-SY5Y | | |
| □ | ESM000331 | Homo sapiens | epithelial cell | | HeLa S3 | | |
| □ | ESM000366 | Homo sapiens | epithelial cell | | VCaP | | |
| □ | ESM000367 | Homo sapiens | epithelial cell | | VCaP | | |
| □ | ESM000368 | Homo sapiens | epithelial cell | | LNCaP | | |
| □ | ESM000369 | Homo sapiens | epithelial cell | | LNCaP | | |
| □ | ESM000370 | Homo sapiens | epithelial cell | | VCaP | | |
| □ | ESM000371 | Homo sapiens | epithelial cell | | LNCaP | | |
| □ | ESM000372 | Homo sapiens | epithelial cell | | LNCaP | | |

**NC_000006.11 (171,115,067 bases)**

**151,089,060 : 151,445,269 (356,210 bases shown, positive strand)**

- Sequence NC_000006.11: Homo sapiens chromosome 6, GRCh37 pr

a : H3K4me2, Max:188 / Min:0 - Human breast cancer epithelial cell, MDA-MB-231 cell line, mammar

a : H3K36me3, Max:145 / Min:0 - Human breast cancer epithelial cell, MDA-MB-231 cell line, mammar

- Genes

**150465793..152068537**
name: NA000000603.1
**Title**: Human breast cancer epithelial cell, MDA-MB-231 cell line, mammary gland, adenocarcinoma : H3K36me3
**Comment**: High definition profiling of mammalian DNA methylation by array capture and single molecule bisulfite sequencing Submitted By: Cold Spring Harbor Laboratory Global DNA methylation is examined by bisulfite-seq in both human primary and cancer cell lines. H3K4me2 and H3K36me3 are also examined.

You are here: NCBI > DNA & RNA > Nucleotide Database

Write to the Help Desk

## Microbial Genomes

Eleven finished microbial genomes were released during September 2010. The original sequence data files submitted to GenBank/EMBL/DDBJ are available on the FTP site: ftp.ncbi.nih.gov/genbank/genomes/Bacteria/. The RefSeq provisional versions of these genomes are also available: ftp.ncbi.nih.gov/genomes/Bacteria/.

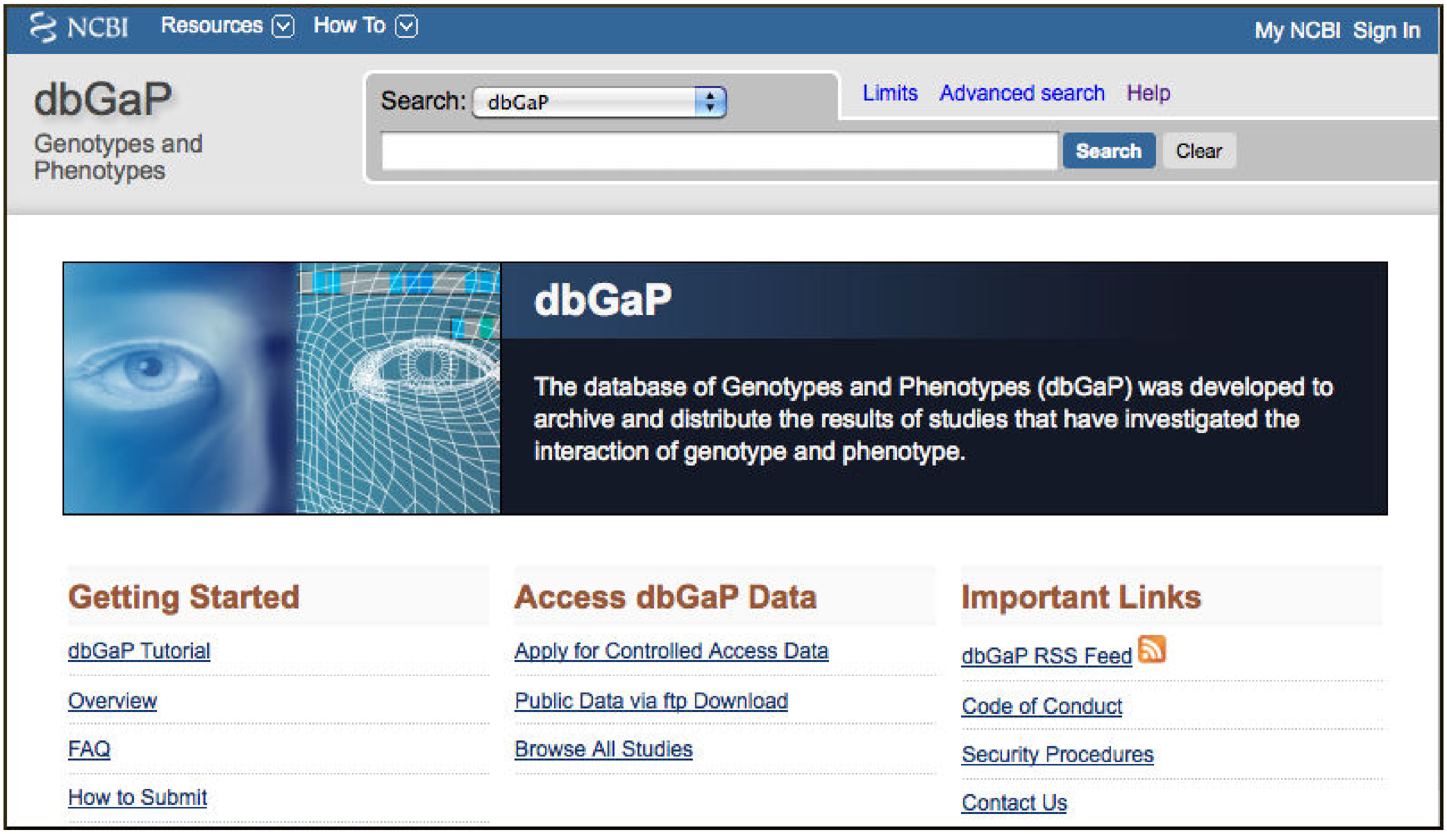
# GenBank News

GenBank release 179.0 is available via web and FTP. The current release includes information available as of August 16, 2010. Release notes are available on the on the NCBI ftp site: ftp.ncbi.nih.gov/genbank/gbrel.txt

# Updates and Enhancements

## dbGaP

The Entrez dbGaP resource has migrated to the streamlined discovery-oriented design that has been in service in PubMed for nearly a year, described fully in the November 2009 issue of the NCBI News. Included in the re-design is a new home page (www.ncbi.nlm.nih.gov/gap), Limits and Advanced Search page. The image of the human face on the homepage, shown immediately below, is a composite of faces from approximately 10,000 people.



The database of Genotypes and Phenotypes (dbGaP) was developed to archive and distribute the results of studies that have investigated the interaction of genotype and phenotype.

## PubMed DTDs

PubMed E-Utility 2011 DTDs will be updated in mid-December, approximately on December 13. The new DTDs can be found:

http://eutils.ncbi.nlm.nih.gov/corehtml/query/DTD/pubmed_110101.dtd

## RefSeq

RefSeq Release 43 is now available through the Entrez system and can be downloaded from the FTP site (ftp.ncbi.nlm.nih.gov/refseq/release). This full release incorporates genomic, transcript, and protein data available as of September 16. It includes 11,223,078 records from 10,854 different species and strains. Changes since the last release are desciribed in the release notes (ftp.ncbi.nlm.nih.gov/refseq/release/release-notes/RefSeq-release43.txt). More information on the RefSeq project is available on the RefSeq Homepage (www.ncbi.nlm.nih.gov/RefSeq/).

## Entrez Gene Record Status

Entrez Gene (www.ncbi.nlm.nih.gov/gene) has two new properties field terms to identify the status of records that are no longer current (alive). Replaced records, retrieved with the search term "replaced"[Properties], are those that have been made secondary to (merged with) another gene record while discontinued records, retrieved with "discontinued"[Properties], are no longer current but not identified with another record. As before, current records can be retrieved with the term "alive"[properties] or by using "current only"[Filter].

## NCBI Workshop at ASHG Annual Meeting

NCBI scientists will present a special workshop at the American Society for Human Genetics meeting on November 4 at 7:15 p.m. The workshop entitled, "A Practical Guide to Genome-Scale Data at NCBI", will provide information on genome-scale resources available at NCBI including finding and downloading data, analysis, and management of data sets. NCBI will also staff an exhibit booth at the meeting.

**Announce Lists and RSS Feeds**

Eighteen topic-specific mailing lists are available which provide email announcements about changes and updates to NCBI resources including dbGaP, BLAST, GenBank, and Sequin. The various lists are described on the Announcement List summary page: www.ncbi.nlm.nih.gov/Sitemap/Summary/email_lists.html. To receive updates on the *NCBI News*, please see: www.ncbi.nlm.nih.gov/About/news/announce_submit.html.

Twelve RSS feeds are now available from NCBI including news on PubMed, PubMed Central, NCBI Bookshelf, LinkOut, HomoloGene, UniGene, and NCBI Announce. Please see: www.ncbi.nlm.nih.gov/feed/.

Users can also stay updated on NCBI's resources on Facebook and Twitter: twitter.com/NCBI.

Send comments and questions about NCBI resources to: info@ncbi.nlm.nih.gov, or by calling 301-496-2475 between the hours of 8:30 a.m. and 5:30 p.m. EST, Monday through Friday.