



Геномные базы данных

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Ресурсы по анализу структуры и функции генома *Drosophila melanogaster*



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Important News:

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FlyBase A Database of the *Drosophila* Genome

Data Classes

Selected Searches & Tools

- Maps** Cytologic maps, CytoSearch, Annotated Genome: gbrowse & Apollo views
- Genes** Search Genes, Alleles, Gene Products, GadFly: Genome Annotation Database, Protein Function, Location, Process, Structure (GO), Gene Expression
- Sequences** Search & order EST project cDNAs, Genome Projects' homepages: BDGP & EDGP
- Stocks** Search & order Stocks, Stock Centers' homepages: Bloomington, Kyoto, Ehime, Szeged, Tucson, Special Stock Collections
- Transgenes & Transposons** Search Transgene Constructs or Insertions, Browse Natural Transposons
- Aberrations** Search Aberrations
- Anatomy & Images** Anatomy Images Browser and Terms
- References** Search literature References
- People** Search addresses, Update or Add your address

Search [Help?] **BLAST sequence search at BDGP, EDGP** [All Search Tools](#)

for words:

in these sections: All sections Genes References Stocks People

Symbols/Names
 Everything

**FlyBase -
Интегрированная
база данных по
структуре и
функции генов
плодовой мушки
*Drosophila
melanogaster***

<http://flybase.bio.indiana.edu/>



Ресурсы по анализу структуры и функции генома *Drosophila melanogaster*



Berkeley Drosophila Genome Project

Home

BDGP NEWS

March 11, 2003. Release 2 of the embryonic *in situ* images is now available for [query](#) and [quick search](#).

March 4, 2003: Whole genome alignment of *D. pseudoobscura* and *D. melanogaster* is now available via the [Vista Genome Browser](#) from the [Berkeley Genome Pipeline](#).

January 31, 2003. The [Release 3.1](#) annotated genomic sequence is now available for [querying](#), [sequence similarity searching](#), [browsing](#), and [download](#). Try our new [Apollo genome annotation browser](#).

Search BDGP Site

Go To FlyBase

About BDGP Contact information, [news archive](#), how to cite BDGP, and general overview

Searches

Fly BLAST Sequence similarity search of *Drosophila*-specific data sets

GadFly Search/browse the *Drosophila* genome annotations, by name, chromosomal position, molecular function or protein domain

FlyBase All Searches FlyBase, BDGP, EDGP

Analysis Tools Search sequence for patterns, splice sites, etc.

Projects

Genomic Sequencing Sequence and annotation of the *Drosophila* genome

Expression Patterns Systematic determination of patterns of gene expression in *Drosophila* embryogenesis by *RNA in situ*

BDGP -
проект по секвенированию
и аннотации генома
Drosophila melanogaster

<http://www.fruitfly.org/>



Ресурсы по анализу структуры и функции генома *Drosophila melanogaster*



Berkeley Drosophila Genome Project

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FlyBase, BDGP, EDGP

Analysis Tools

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Sequencing

cDNAs & ESTs

Transposon
Insertions

SNPs

BDGP
Resources

GadFly: Genome Annotation Database of Drosophila

Query GadFly

A fill-in-the-blank form for locating predicted Release 3 genes
[Query Release 2 annotations here](#)

FlyBase Genome Browser

Query and browse genomic sequence maps with interactive gifs

ArmView2

Browse genomic sequence maps by chromosome arm with interactive gifs

Apollo Genome Annotation Browser

Download Java application to browse genomic sequence maps interactively

Gene Ontology (GO) Browser

Search ontology terms

Protein Domain

Predicted proteins grouped by InterPro domain by EBI

Drosophila Genomic Sequence Databases

Fly BLAST

Sequence similarity searching of Drosophila-specific datasets--results hyperlink to our database reports

This page last updated on: 5/29/03

GadFly-
База данных
аннотированного
генома *Drosophila*
melanogaster

<http://www.fruitfly.org/annotation/index.html>



Ресурсы по анализу структуры и функции генома *Drosophila melanogaster*



[FlyBase](#) .. [Aberrations](#) .. [Anatomy](#) .. [Clones](#) .. [Genes](#) .. [Gene Products](#) .. [Maps](#) .. [People](#) .. [References](#) .. [Sequences](#) .. [Stocks](#) .. [Transgenes/Transposons](#) .. [cDNAs/EST's](#) .. [Help](#) .. [Searches](#) .. [News](#) .. [Images](#) .. [Preferences](#)

Drosophila ArmView2

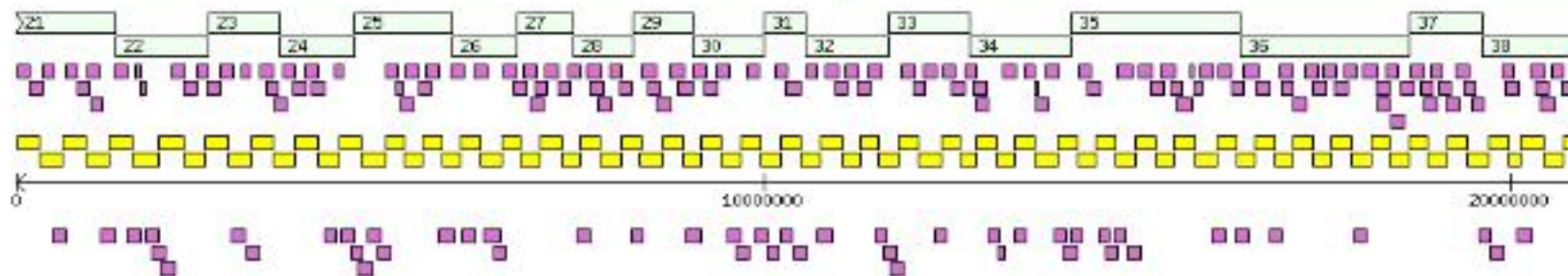
(Browse genomic sequence maps of *GadFly* Release3 version 1 (January 2003) data)
[Release Information and FAQ](#)



(WARNING: The heterochromatic contigs in U, Xh, 2h, 3h, Yh are UNORDERED and in RANDOM ORIENTATION)
 Click on a chromosome arm or scaffold to view

Display cytological numbered divisions, BAC clones, GenBank accessions that link to detailed annotated genomic sequence maps, and other features.

Arm Shown: 2L (Release 3)



KEY:
 cytoband tilingpath BAC segment

Mouse over features to see name/coordinates at bottom of browser; Click on it to see details in the region (cytological numbered divisions, BACs and GB segments only)

Add Genes, and/or no other features in Size

ArmView2 – обзор генома *Drosophila melanogaster*, начиная с масштаба одного плеча хромосомы

<http://www.flybase.org>



Ресурсы по анализу структуры и функции генома *Drosophila melanogaster*



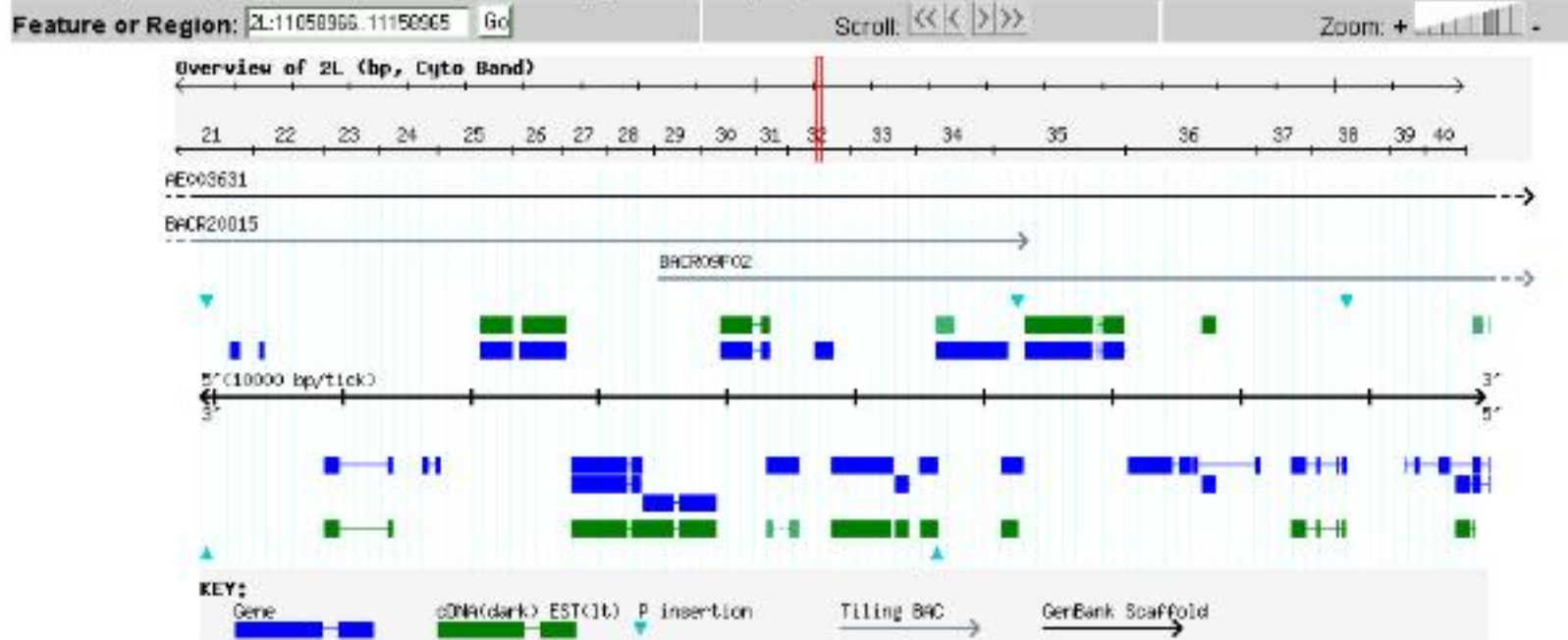
FlyBase .. Aberrations .. Anatomy .. Clones .. Genes .. Gene Products .. Maps .. People .. References .. Sequences .. Stocks .. Transgenes/Transposons .. cDNAs/ESTs .. Help .. Searches
Views .. Images .. Preferences

FlyBase Genome Browser

Search using a sequence name, gene symbol, or other feature. **Examples:** 2L, 2L:80,000..120,000, AE003622, Nrv2, Mlpp1, gene CG5682, clone: BACR31D05, cDNA: GH23250, P: P(EP)Ida[EP2537], P: EP(2)2537, SPTR: O76268

To center on a location, click the ruler. Use the Scroll/Zoom buttons to change magnification and position.

Currently showing 100,000 bp from 2L (release 3), positions 11,058,966 to 11,158,965



Display Settings:

Dump view as:

TABLE, FASTA, XML, GFF

Show features:

- | | | | | |
|--|---|--|--|--|
| <input checked="" type="checkbox"/> Gene | <input checked="" type="checkbox"/> cDNA | <input checked="" type="checkbox"/> Repeat | <input type="checkbox"/> Blastx SPTR | <input checked="" type="checkbox"/> GenBank Scaffold |
| <input type="checkbox"/> Affy Oligo | <input checked="" type="checkbox"/> P insertion | <input type="checkbox"/> Transposon | <input checked="" type="checkbox"/> Tiling BAC | |

**FlyBase -
Обзор
структурных
компонентов
генома**

<http://www.fruitfly.org/cgi-bin/annot/gbrowse>



Ресурсы по анализу структуры и функции генома *Caenorhabditis elegans*



[Home](#) | [Genome](#) | [Blast / Blat](#) | [Batch Genes](#) | [Batch Sequences](#) | [Markers](#) | [Genetic Maps](#) | [Submit](#) | [More Searches](#)

WormBase Release WS113

The biology and genome of *C. elegans*.

Search for

Detailed search |
 Exact match |
 Results as XML

Web Site Directory

- Release Notes** [New/Changed Genes](#), [release notes](#)
- General Search** [WormBase Class Browser](#), [Wormbase Query Language Search](#), [AGL Search](#)
- Sequence Search** [C. elegans Genome](#), [C. briggsae Genome](#), [Gene](#), [Blast / Blat](#), [s-PCR](#), [Gene Ontology](#), [Batch Genes](#), [Batch Sequences](#), [Syntax Viewer](#)
- Cells and Gene Expression Search** [Cell and Pedigree](#), [Neurons](#), [Expression Pattern](#), [Expression profile](#)
- Genetics, Strains, Phenotypes Search** [Genetic Interval](#), [Rearrangements](#), [Contig Interval](#), [Allele](#), [SNPs](#), [Markers](#), and [Strains](#), [Strain Report](#), [RNAi](#)
- Downloads, Linking and Data Mining** [Bulk Downloads](#), [Linking to WormBase](#), [Mining WormBase](#), [C. elegans genome annotation](#), [C. briggsae genome annotation](#), [Published data sets](#), [Download Software](#), [Download AceDB DBMS](#), [Download AceDB database](#), [WormBase CVS site](#)
- WormBase Mailing Lists** [How to subscribe](#), [WormBase-Announce](#), [WormBase/WormBase-Help](#), [WormBase-Dev](#) (password required)
- Documents** [User's Guide \(HTML\)](#), [User's Guide \(PDF\)](#), [C. elegans book \(1997\)](#), [The Mind of a Worm \(Malkin et al, 1998\)](#), [The Genetics of C. elegans \(Brenner, 1974\)](#), [Dustin Ph.D. thesis \(1997\)](#)

News and Notes

- November 9, 2003: Initial Mos insertions now available**
 845 Mos-derived transposon insertions generated in the laboratory of Laurent Segal are now available on the [Gene Browser](#) and on individual [Allele](#) pages.
- October 29, 2003: UCSC C. elegans family browser available**
 The University of California at Santa Cruz announces a [protein family browser](#) capable of finding genes based on their genomic proximity, their protein similarity, or the similarity of their expression profiles.
- October 26, 2003: Intellectual C. elegans Researcher Lineage now available**
 A list of each person's training lineage can be seen from the [Person](#) pages, for example, the [Drenner](#) page. You can add your information [here](#).
- October 27, 2003: New genome-wide RNAi data set based on RNAi-hypersensitive rrf-3 strain available**
 The results from the systematic RNAi screen reported in [Sinner et al., PLoS Biology Vol. 1, No. 1, e12 DOI: 10.1371](#) are now available for [browsing](#) and [bulk download](#).
- October 17, 2003: 2005 International C. elegans Meeting**
 Fifteenth International C. elegans Meeting will be held at the University of California at Los Angeles, June 25 (Saturday) - June 29 (Wednesday), 2005. The Genetics Society of America will be sponsoring the Meeting. Comments or questions can be addressed to [Anne Marie Mahoney](#).
- October 13, 2003: WormBase Receive 5-year NHGR Grant**
 The National Human Genome Research Institute at the US National Institutes of Health has awarded WormBase a five-year grant to continue our efforts to provide easily-accessible, comprehensive information about C. elegans. More information can be found in the [Call for press release](#).
- October 7, 2003: Negative Proteome Database adds C. elegans Proteins**
 The [Negative Proteome Database](#), which allows researchers interactively explore the differences between the protein content of different species, now carries C. elegans in addition to fruitfly, yeast, human, mouse, zebrafish, dictyostelium and a variety of prokaryotes. The database is still in beta stage: please report bugs.

**WormBase –
 Интегрированная
 база данных по
 структуре и
 функции генов
 круглого червя -
 нематоды
*Caenorhabditis
 elegans***

<http://www.wormbase.org/>



Ресурсы по анализу структуры и функции генома *Caenorhabditis elegans*



[Home](#) | [Genome](#) | [Blast / Blat](#) | [Batch Genes](#) | [Batch Sequences](#) | [Markers](#) | [Genetic Maps](#) | [Submit](#) | [More Searches](#)

Search for Any Gene


The Biology and Genome of *C. elegans*.

[\[Switch to DasView\]](#)

Showing 11.13 kbp from II, positions 12,343,263 to 12,354,388

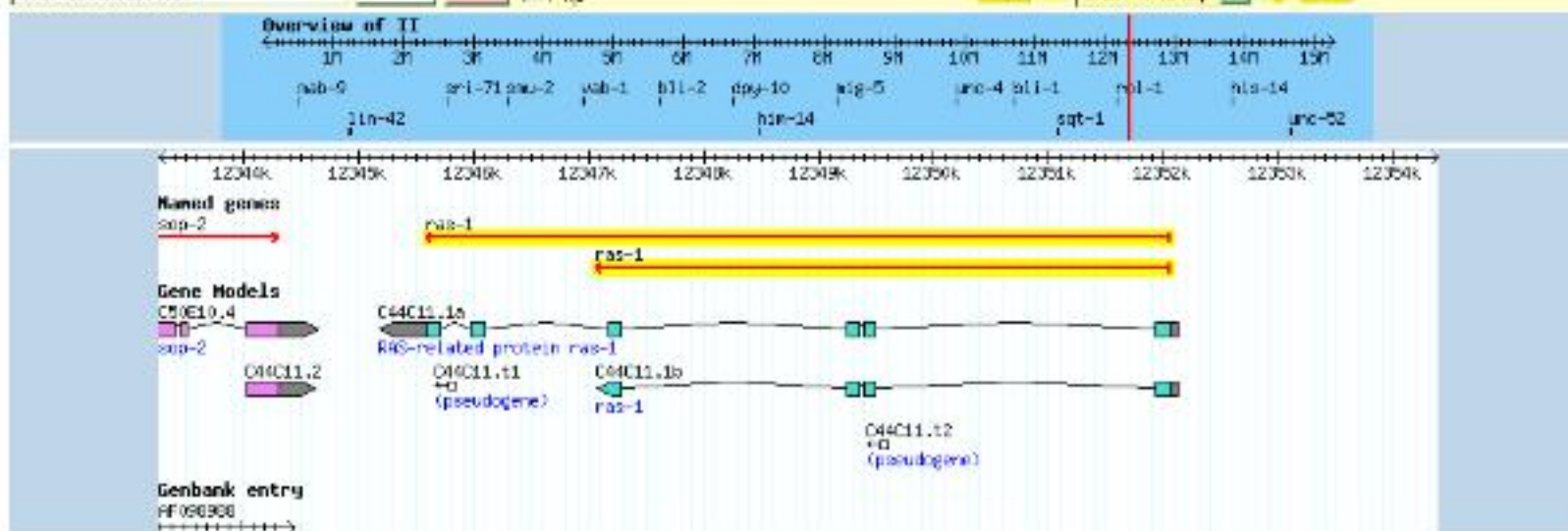
Instructions: Search using a sequence name, gene name, locus, oligonucleotide (15 bp minimum), or other landmark. The wildcard character * is allowed. To center on a location, click the ruler. Use the Scroll/Zoom buttons to change magnification and position.

Examples: *N*, rhodopsin, IV:120,000..130,000, *unc-8*, *him-7*, B0019, PCR_Product sjj_B0019.1, ttattaaacaattaa.

[\[Hide banner\]](#) | [\[Hide instructions\]](#) | [\[Bookmark this view\]](#) | [\[Link to an image of this view\]](#) | [\[Help\]](#)

Landmark or Region: Search Flip

Scroll/Zoom: Show 11.13 kbp



Manual genes: *unc-2*

Gene Models: *C04E10.4*, *unc-2*, *O44C11.2*

Genbank entry: FF08908

WormBase/
Genome -
Обзор
структурных
компонентов
генома
Caenorhabditis
elegans

<http://www.wormbase.org/db/seq/gbrowse/wormbase>



Ресурсы по анализу структуры и функции генома комаров рода *Anopheles*



The Mosquito Genomics WWW Server provides access to mosquito genomics databases and links to other genomics WWW servers and to other WWW servers around the world.

Databases and links to them are not operating currently. Other links may also be disabled or nonfunctional.

Information

[Aedes aegypti Genome Project](#)
[West Nile Info](#)
[Mosquito Control](#)
[Mosquito Fun Facts](#)
[Mosquito Information](#)
[Mosquito Genome Sizes](#)



NCBI BLAST Server
NCBI BLAST for *A. gambiae* genome



[Eusmolt Mosquito](#)

[AnoBase the Anopheles database](#)



[Mosquito Research Resource Project - Research Center](#)
[Research/Educational Mosquito Server](#)
[Other Links](#)
[Copyright Disclaimer](#)

Databases



Mosquitoes: Information across mosquito species
[Enter](#) | [About](#) | [Other mosquito information](#)



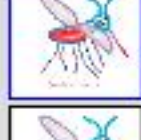
Aedes aegypti: The yellow fever mosquito
[Enter](#) | [About](#) | [Other A. aegypti information](#) | The *Aedes aegypti* Genome Project at TIGR | BLAST BAC End genomic sequences



Aedes albopictus: The Asian tiger (forest day) mosquito
[Enter](#) | [About](#) | [Other A. albopictus information](#)



Ochlerotatus (formerly Anolis) triseriatus: The Eastern tree hole mosquito
[Enter](#) | [About](#) | [Other O. triseriatus information](#)



Anopheles gambiae: The malarial mosquito
[Enter](#) | [About](#) | [Other A. gambiae information](#) | Anopheles Genetic Resource Information Project (ASGRI) prepared by Mark G. Benedict | AnoBase, the Anopheles Database at IMB | Whole genome sequence (2007 sequence: 270,253,396 bases) at NCBI or at project Ensembl



Culex pipiens: The Northern House mosquito
[Enter](#) | [About](#) | [Other C. pipiens information](#)

Геномные ресурсы других двукрылых (Diptera), имеющих медицинское значение

<http://klab.agsci.colostate.edu/>



Ресурсы по анализу структуры и функции генома *Anopheles gambiae*

AnoBase

THE ANOPHELES DATABASE

AnoBase is now presented as a "beta" form. We would like users to send their comments and suggestions to

AnoBase-comments@anbb.forth.gr.

We would also like to ask you to let us know, using the same e-mail address, of any problems that you may have identified so that we can fix them the soonest possible. AnoBase currently contains all information previously found in AnoDB, which, although no longer updated, can still be accessed at the URL

www.anobase.org/AnoDB.

The AccDB version of AnoDB has been discontinued. Full annotation of the current and older Anopheles literature is to start soon, at which time AnoBase will be presented in its "final" form.

Maps	Information about <i>cytogenetics</i> and <i>in-situ</i> hybridisations, other maps
Sequences	Information about <i>genomic</i> sequences and scaffolds
Genes & Gene products	Information about <i>genes</i> , <i>gene products</i>
Blast server	Use our local <i>blast</i> server to run your sequence versus <i>Anopheles</i> sequences
Constructs & Transposons	Information about <i>constructs</i> , <i>natural transposons</i> or <i>transposon insertions</i>
Inversions	Information about <i>inversions</i>
Markers	Information about <i>microsatellites</i> , <i>RAPDs</i> , <i>EST</i> , <i>STS</i> , etc.
Population	Information about <i>population data studies</i>
Insecticide Resistance	Information about <i>insecticide resistance studies</i> in Anophelins
References	Information about <i>published references</i>
Species	Information about <i>Anopheles</i> <i>species</i> (sequences etc.)
Community	<i>People</i> , <i>networks</i> , etc.
Documents etc.	<i>News</i> , <i>Documents</i> , <i>Conferences</i> , <i>Contributors</i> , etc.
Links	<i>Interesting links</i>

AnoBase - база данных по геномной и биологической информации об *Anopheles gambiae*, важнейшем переносчике малярии

<http://www.anobase.org/>



Ресурсы по анализу структуры и функции генома *Anopheles gambiae*



Mosquito Genome Browser

Ensembl Entry Points

Search for with

Display Chr From To

Retrieve a sequence

Advanced data retrieval tool

Search your sequence

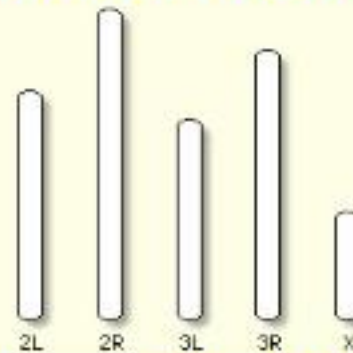
Mosquito Genome Project



This site presents the tenfold whole genome shotgun assembly of the PEST strain of *Anopheles gambiae*, as

prepared by The International *Anopheles Genome* project and funded by NIH-NIAID and the French Ministry of Research. The assembled portion of the genome is around 278 Mbp in length with a total of 8,987 unique scaffolds, the largest scaffold being 23.1 Mbp. Approximately 85% of the sequence has been assigned to chromosomal locations; chromosome arms 2L, 2R, 3L, 3R, and X are represented by 13, 49, 42, 28, and 10 large scaffolds respectively. No scaffolds have yet been assigned to the Y chromosome due to the complication of transposons or transposon fragments containing regions that are also found at the autosomal centromeres. As well as the scaffolds there are an additional 60737

Browse A Chromosome Arm



Documentation & Help

About Ensembl

For context-sensitive help on any web page click

Questions or suggestions? Try

Mosquito Genome Browser -
Обзор структурных компонентов генома *Anopheles gambiae*

http://www.ensembl.org/Anopheles_gambiae/



Ресурсы по анализу структуры и функции генома *Arabidopsis thaliana*



Home | About TAIR | Sitemap | Contact | Help | Order | Login

Search | Tools | **Arabidopsis Info** | News | Links | FTP | Stocks

TAIR Database

Genome Initiative

About Arabidopsis | Genome Initiative | Nomenclature Guide | Functional Genomics | Monsanto SNPs & Ler | Gene Expression | Education & Outreach | Gene Families | Gene Class Symbols | Ontologies | Data Submission | Arabidopsis Labs | Protocols & Manuals | Electronic Journals

The Arabidopsis Genome Initiative (AGI) is an international collaboration to sequence the genome of the model plant *Arabidopsis thaliana*. Begun in 1996 with the goal of completing the genome sequence by 2004, the genome sequencing was completed at the end of 2000.

► Arabidopsis Genome Updates UPDATE

A post-publication summary of remaining gaps and clones in progress, last updated September 30, 2003.

► Links for Arabidopsis Sequence and Annotation Information UPDATE

Kazusa, MIPS and TIGR genome annotation, tiling paths, and other resources.

► TAIR Gene Product Annotation Information NEW

Information about and bulk data files from protein annotation efforts at TAIR.

► TAIR's AGI Tools and Datasets

How to use the TAIR SeqViewer, MapViewer, BLAST, FASTA, PatMatch, and FTP to access and analyze AGI sequence data.

► Arabidopsis Genome Finished

The Arabidopsis genome has been sequenced and annotated (The Arabidopsis Genome Initiative, 2000, Nature, 408:796-815). Includes publications,

**Arabidopsis Genome Initiative (AGI) –
международный проект по
секвенированию и аннотации
генома модельного растения
резунике Таля -
*Arabidopsis thaliana***

<http://arabidopsis.org/info/agi.jsp>



Ресурсы по анализу структуры и функции генома *Arabidopsis thaliana*



tair Home | About TAIR | Sitemap | Contact | Help | Order | Login
 Search | Tools | Arabidopsis Info | News | Links | FTP | Stocks

TAIR Database Quick Search

Locus: AT4G25220

Date last modified 2003-05-02
TAIR Accession Locus 2122864
Representative Gene Model AT4G25220.1

Annotations

Category	Relationship Type	Keyword
GO Molecular Function	has	transporter activity

Annotation Detail

RNA Data

Data from Expression Microarrays	array element name	alias(es)	avg. log ratio	std. error	expression viewer	SMD spot history
	189KB	189KB.T7 189KB.XP 189KB.XP (3')	-0.017	0.024	Viewer	131659

Associated Transcripts

type	number associated
EST	(3)
cDNA clone	(2)

Description transporter, putative, similar to glycerol-3-phosphate transporter (glycerol 3-phosphate permease) (Homo sapiens) GI 7543982

Chromosome 4

Nucleotide Sequence [full length CDS](#) [full length genomic](#)

Map Locations

chrom	map	map type	coordinates	orientation	attrib
4	AGI	nuc_sequence	12920852 - 12922885 bp	forward	
4	F24A8	assembly_unit	53380 - 55311 bp	forward	details

Map Links [Map Viewer](#) [Sequence Viewer](#)

Gene Feature

type	coordinates	annotation source	date
ORF	220-1821	AGI-TIGR	2001-01-29
5' utr	1-67	AGI-TIGR	2001-01-29
5' utr	190-219	AGI-TIGR	2001-01-29
exon	1-67	AGI-TIGR	2001-01-29

Индекс генов *Arabidopsis thaliana*

<http://arabidopsis.org/servlets/TairObject?name=At4g25220>

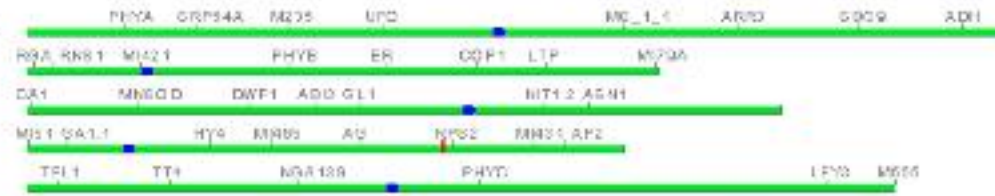


Ресурсы по анализу структуры и функции генома *Arabidopsis thaliana*



SeqViewer Close-up View | SeqViewer Home | Release Note | Print Version

- Markers
 - Polymorphisms
 - T-DNA/Tn
 - Gene Models
 - Transcripts
 - Annotation Units
-



The new view will: insert above the current view(s) or replace the view

- show 3 data rows
 - show all data [help](#)
- Some data objects may be hidden from view
 Choose "show all data" and zoom to 200kb or lower to see all objects

**Исследование структурных
компонентов генома
*Arabidopsis thaliana***

Closeup View # 1, Chromosome 4 Remove

[show legend](#)

Zoom to:

Search by name (e.g. UFO)

Select range (e.g. 1500-2500)

Click here to recenter the view

Marker: SM120_128.2, SGC5NP149, SM4

Poly: MASC08579, MASC08228, SGC5NP12989, SGC5NP12982, SGC5NP18615, SGC5NP12990, MASC08874, SGC5NP12983, SGC5NP18616, MASC08874, MASC08874

T-DNA/Tn: AL929923, AL929912, AL951409, SALK_014374, SALK_118731, 44.55.X, SALK_024739.4, AL939924, SALK_088976, 38.95.X, SALK_023202, 45.10.X, SALK_091242, 14.30.X, A, BX262473, SALK_015988, SALK_044584, 48.25.X, SALK_090845, 51.00.X, SALK_11644

Sequence ruler - click here to open 10 kb sequence window
 12,900,000 13,000,000

Gene: AT4G24930.1, AT4G25010.1, AT4G25110.1, AT4G25220.1, AT4G25320.1, AT4G25420.1, AT4G24940.1, AT4G25020.1, AT4G25130.1, AT4G25250.1, AT4G25360.1, AT4G25470.1, AT4G24950.1, AT4G25030.1, AT4G25140.1, AT4G25260.1, AT4G25370.1, AT4G25480.1

<http://arabidopsis.org/servlets/sv?action=>



Ресурсы по анализу структуры и функции генома *Danio rerio*



The Zebrafish Information Network

General Information

[Positions with ZFIN](#)
[About ZFIN](#)
[Citing ZFIN](#)
[Helpful Hints](#)
[User Support](#)
[Site News](#)
[Glossary](#)
[Download Data](#)

Genomics

[Genome Sequencing Project](#)
[Trans NIH Zebrafish Initiative](#)
[Other Genomes](#)

[Meetings / Jobs / News](#)
[The Zebrafish Book](#)
[The Zebrafish Science Monitor](#)
[Zebrafish Newsgroup](#)
[Zebrafish for K-12](#)

Nomenclature

[Laboratory Allele](#)

Mutants / Transgenics

Search for mutations / transgenic lines by gene name, map location or phenotype.

Wild-Type Stocks

Zebrafish wild-type lines.

Genes

Search for genes by name or map location.

Gene Expression

Search for gene expression patterns by gene name, developmental stage, anatomical structure, developmental or physiological process.

Map Markers

Search for mapped markers by marker type, marker name, map location or type of map.

Genetic Maps

Generate graphical views of genetic, radiation hybrid or consolidated maps.

Mapping Panels

Summary listing of zebrafish mapping panels.

Accession

Search ZFIN by data accession number.

Publications

Search for zebrafish research publications by author, title or citation.

People

Search for zebrafish researchers by name or address.

Laboratories

Search for laboratories by name, address or research interests.

Companies

Search for companies supplying zebrafish reagents.



The Zebrafish Information Network - база данных по структуре и функции генов ко стигной рыбы *Danio rerio*

http://zfin.org/cgi-bin/webdriver?Mlval=aa-ZDB_home.apg



Ресурсы по анализу структуры и функции генома *Danio rerio*



Publications People Labs Companies Acc#

Home

Mutants / Transgenics

Wild-Types

Genes

Expression

Markers

Maps

Catch of the day...

News from the zebrafish research community

Fresh Caught - April 2002

Genomic Resources for Zebrafish

Links:

- **Sanger Institute whole-genome sequence:**
This site hosts all of the efforts of the zebrafish genome sequencing project, including whole genome shotgun sequence and selective BAC shotgun sequences. In addition, the fingerprinting (physical map) of the zebrafish genome is presented in a graphic display.
- **Ensembl database of annotated zebrafish sequence:**
Provides easy access to sequence data including predicted structure and location of known genes in the genome sequence and predictions of novel genes, with supporting evidence.
- **Physical map based on fingerprinted BACs:**
A bacterial clone physical map of the genome is being constructed using restriction enzyme fingerprinting.
- **RH, meiotic and integrated maps of the genome:**
Centralized site for all meiotic and radiation hybrid maps of the zebrafish genome.
- **Washington University EST sequencing project:**
This site hosts the project in which over 200,000 ESTs have been sequenced. It offers a unigen-like set (wz' ESTs) that can be found by key word search or BLAST.
- **BLAST server for Sanger zebrafish sequence:** This site provides a BLAST search of a gene or marker of interest to the assembled sequence.

Перечень
инструментов для
анализа генома
Danio rerio

http://zfin.org/cgi-bin/webdriver?Mlval=aa-ZDB_home.apg



Ресурсы по анализу структуры и функции генома *Mus musculus*



Mouse Genome Informatics

Mouse Genome Informatics (MGI) provides integrated access to data on the genetics, genomics, and biology of the laboratory mouse.

Search Categories

- All Search Tools
- Genes and Markers
- Alleles and Phenotypes
- Strains and Polymorphisms
- Gene Expression
- Mammalian Orthology and Comparative Maps
- Mouse Maps and Mapping Data
- Mouse Tumor Biology
- Probes and Clones
- References
- Vocabulary Browsers

MouseBLAST

Search mouse, human, rat, and other sequence data

Additional Resources

Nomenclature, Lee Silver's Mouse Genetics, E-mail lists, downloads, ...

Data Submission

Instructions and tools for submitting your data

Help

User support, tutorials, FAQ, ...

About MGI

MED, CID, MDS, MFB, GO

What's New

MGI news and announcements

Search for ?

Enter term(s) or part of a term, use * as a wildcard.

In these sections:

All sections	▲	
Gene symbols/names	▼	<input type="button" value="Search"/> <input type="button" value="Reset"/>
Accession IDs	▼	
Phenotypes	▼	
Gene Expression	▼	

Mouse Genome Informatics (MGI) – интегральный доступ к информации о генетике, геномике и биологии домашней мыши *Mus musculus*

[Citing Tissue Resources](#)

[Funding Information](#)

[Warranty Disclaimer & Copyright Notice](#)

[Send overtures and comments to User Support.](#)

Last database update

11/02/2003

MGI 2.97



<http://www.informatics.jax.org/>



Ресурсы по анализу структуры и функции генома *Mus musculus*




Mouse Genome Informatics
MGI Home Help

Search for

In these sections

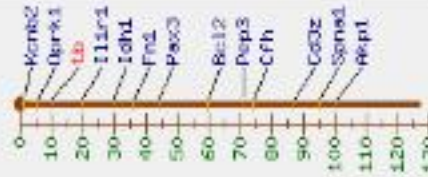
- All sections
- Gene symbols/names
- Accession IDs
- Phenotypes
- Gene Expression

Advanced search for...

Search Categories

- All Search Tools
- Genes/Markers
- Alleles/Phenotypes
- Strains/Polymorphisms
- Expression

Gene Detail Your Input Welcome

Symbol Name ID	tb tumbler MGI:98489		Nomenclature History
Map position	Chromosome 1 10.0 cM Detailed Map = 1 cM Mapping data(1)		
Phenotypes	All phenotypic alleles(1) : Spontaneous(1) Mouse Locus Catalog		
References	(Earliest) J:13434 Dickie MM, "Tumbler, tb" <i>Mouse News Lett</i> 1965,31():45 (Latest) J:30778 Sweet HO et al., "Mutations at The Jackson Laboratory (Update to Mouse Genome 1993, 91:862-5 - J16313)" <i>Mouse Genome</i> 1995,93(4):1030-4 All references(5)		
Other accession IDs	MGD-MRK-14723		

Индекс генов *Mus musculus*

<http://www.informatics.jax.org/>



Ресурсы по анализу структуры и функции генома *Mus musculus*



The screenshot shows the MGI Mouse Genome Informatics search page. At the top is the MGI logo with a mouse icon. Below it is a search bar with a 'Go' button. A dropdown menu is open, showing search categories: 'All sections', 'Gene symbols/frames', 'Accession IDs', 'Phenotypes', and 'Gene Expression'. Below the search bar is an 'Advanced search for...' dropdown.

Search Categories

- All Search Tools
- Genes/Markers
- Alleles/Phenotypes
- Strains/Polymorphisms
- Expression
- Comparative Maps/Data
- Mouse Maps/Data
- Mouse Tumor Biology
- Probes/Clones
- References
- Vocabulary Browsers
 - Gene Ontology (GO)
 - Anatomical Dictionary
 - Phenotype Classifications

MouseBLAST

Additional Resources

Genome Analysis Tools

[MGS Home]

Introduction

This document provides links to external genomic sequence analysis servers and software applications. The tools are organized in these groups.

- Comprehensive sequence analysis servers
- Sequence analysis pipeline software
- Results visualization and curation tools
- Large-scale comparative methods
- Genomic sequence analysis servers

Comprehensive Sequence Analysis Servers

These are analysis servers that run multiple gene prediction and analysis programs with a given query sequence.

- **Genome Analysis Pipeline (ORNL)** - Predicts exons (GRAIL, GRAIL-EXP), gene-structures (GENSCAN), GRAIL feature tools: CpG islands, BAC end hits, PolyA, Trna, Simple Repeats, Complex Repeats, homology searches (BLAST).
- **CGG Nucleotide Sequence Analysis launcher (Sanger Institute)** - Predicts gene structure (FGENESH+, BESTORF, FGENE, FEX, SPL), promoter and transcription start sites (TSSG, TSSW), polyadenation site (POLYAH), and other features (CDSB, RNASPL, HBR).
- **RUMMAGE (The Genome Sequencing Center at the Institute of Molecular Biotechnology in Jena, Germany)**- A High-Throughput Sequence Annotation Server. The following functional and organizational elements have been addressed so far: Repetitive elements (RepeatMasker, SST, CENSOR and XNUM), promoters (ProScanID), exons (GRAIL, FEXHB, MZEF, Xpound and GENSCAN), gene-structures (GENSCAN, DPS and ExonSampler), tRNA coding (tRNA), CpG islands (LCP and CPG), GC-profiling (LCP) and homology and motif searches against sequence data base (BLAST, and FASTA). (This site requires registration.)
- **NIX (The UK Human Genome Mapping Project Resource Center)**- A high-throughput sequence annotation server. For genomic sequences, the functional and organizational elements addressed include: Repetitive elements (RepeatMasker), exons (GRAIL, GeneFinder, GeneMark, FEX, HEXON, FGENE), tRNA coding (tRNAscan), and sequence similarity (BLAST versus DNA and protein sequence databases).

**Инструменты
анализа генома
*Mus musculus***

http://www.informatics.jax.org/mgihome/MGS/genome_analysis.shtml



Ресурсы по анализу структуры и функции генома *Mus musculus*



Genome Exploration
Research Group
RIKEN Genomic Sciences Center
Genome Science Lab
RIKEN Tsukuba Life Science Center

[FANTOM top page](#)

[About FANTOM](#)

[Viewer Help](#)

[Annotation Viewer](#)

[Reference](#)

[FANTOM meeting](#)

[Link](#)

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FANTOM

FUNCTIONAL ANNOTATION OF MOUSE

The FANTOM is a collection of functional annotations for the RIKEN full-length cDNA clones and provides not simply the gene functions themselves, but also many other informative and useful data describing functional information about the clones.

Announcements

-Updated FANTOM data were available at [FANTOM DB](#).

[About FANTOM](#)

[Viewer Help](#)

[FANTOM DB](#)

[Annotation viewer](#)

[Reference](#)

[FANTOM meeting](#)

[Link](#)

[FAQ](#)

[Information](#)

**Функциональная
аннотация генома *Mus
musculus***

<http://www.gsc.riken.go.jp/e/FANTOM/>



Ресурсы по анализу структуры и функции генома *Homo sapiens*

HUGO Gene Nomenclature Committee

Home | About HGNC | Database | Guidelines | Submissions | Downloads | Gene Families

Giving unique and meaningful names to every human gene

Commercial Users

Contact Us

Database Links

FAQs

IAC (International Advisory Committee)

Journal Links

Meetings

Newsletter

Public Engagement

Publications

Specialist Advisors

Symbol Checklist

Workshops

Current Committee:

- Dr Sue Povey
- Dr Hester Wain
- Dr Elspeth Bruford
- Dr Ruth Lovering
- Dr Matthew Wright
- Dr Versha Khodiyar
- Mr Connie Talbot Jr.

Search Approved Symbols

We have approved symbols for nearly one half of the genes in the human genome and, with an estimated 15,000 more genes to name, we still have plenty to do! Use the Genev database to search for your gene.

Quick Gene Search

Gene Symbol Submission

Obtaining a gene symbol before publication will avoid any possible conflicts with existing symbols and will ensure that your gene is promptly recorded in our database and others. Any information that you provide will be treated in the strictest confidence. For bulk data submissions please follow the Sequence Project Submission Format

Gene Families and Groupings

We strongly encourage the use of a stem (or root) symbol as a basis for a hierarchical series that allows the easy identification of other related members in both database searches and the literature. Please contact us as soon as possible with new members of gene families, as some symbols may be reserved in our database.

Genome Database

NCBI

BLAST
Entrez
LocusLink
OMM

Ensembl
Interpro
SWISS-PROT

ArkDB (other species)
FlyBase
MGI (Mouse Genome Informatics)
RGD (Rat Genome Database)
Ratmap
SGD (Saccharomyces Genome Database)
ZFIN (Zebrafish Information Network)

Перечень индексов генов человека разумного – *Homo sapiens*, занятых сбором, систематизацией и форматизацией данных по названию, структуре и функции генов.

<http://www.gene.ucl.ac.uk/nomenclature/>



Ресурсы по анализу структуры и функции генома *Homo sapiens*

Symbol Report: HSBP1

[Back To Search](#)

Approved Gene Symbol: HSBP1
Approved Gene Name: heat shock factor binding protein 1
HGNC ID: 5203
Location: reserved
Sequence Accession ID: [AF068754](#)
PMIDs: [9649501](#)
Status: Approved

Synonyms

Aliases:
Previously Approved Symbols:
Previous Gene Names:

Other Database Links

- Ensembl: [HSBP1](#)
- Enzyme ID:
- GENATLAS: [HSBP1](#)
- GeneCards: [HSBP1](#)
- GeneClinics/GeneTests: [HSBP1](#)
- IMGT:
- LocusLink ID: [3281](#)
- MGI:
- OMIM: [604553](#)
- RefSeq ID: [NM_001537](#)
- Swiss-Prot ID: [O75506](#)

Структурно-
функциональная
информация о генах
Homo sapiens в индексе
HUGO Gene
Nomenclature
Committee
(HGNC)

http://www.gene.ucl.ac.uk/cgi-bin/nomenclature/get_data.pl?hgnc_id=5203



Ресурсы по анализу структуры и функции генома *Homo sapiens*



GeneCards™ an academic web site of the **WEIZMANN INSTITUTE OF SCIENCE** in association with **XENNEX**

[Terms of Use](#) | [GeneCards Homepage](#) | [Search Examples](#) | [Comment Form](#)

Notice - Please read carefully prior to linking to any third-party site.

Nov 5, 2003: [Release of Version 2.28](#) - Commercial usage now requires a license from [XenneX Inc.](#)

GeneCards™ is a database of human genes, their products and their involvement in diseases. It offers concise information about the functions of all human genes that have an approved symbol, as well as selected others.

[\[complete gene list\]](#) [\[disease genes\]](#) [\[hot genes\]](#) -

SEARCH **Notice** - Please read carefully prior to linking to any third-party site.

| [Quick Start](#) | [Guided Tour](#) | [More search examples](#) |

Search/Display GeneCards™ by

For example, you can display the GeneCard for the (case-sensitive) symbol [RAP1B](#) for a random gene, for a random [HUGO approved gene](#), or search GeneCards™ for the keyword(s):

- [p53](#)
- [apolipoprotein](#) AND (hyper* OR Alzheimer*)
- [GC21M032](#) region on chromosome 16band
- [U85287](#) GenBank accession No.
- [Hs_1288](#) UniGene cluster

[About GeneCards](#)
[What's New](#)
[Data Sources](#)
[Data Extraction](#)
[Citing This Resource](#)
[Publications](#)

[Mirror sites](#)

Индекс генов *Homo sapiens* **GeneCards**

<http://bioinformatics.weizmann.ac.il/cards/>



Ресурсы по анализу структуры и функции генома *Homo sapiens*



an academic web site of the
in association with

[Terms of Use](#) | [GeneCards Homepage](#) | [Search Examples](#) | [Comment Form](#)

GeneCard for gene **HSBP1** Approved UCL/HGNCHUGO Human Gene Nomenclature database symbol
GC16P083580 HSBP1 (heat shock factor binding protein 1)

Aliases and Additional Descriptions <small>(According to GDB, OMIM, HUGO, LocusLink, SWISS-PRCT, and/or GeneLoc)</small>	<ul style="list-style-type: none"> HSF1BP heat shock factor binding protein 1 Heat shock factor binding protein 1 <p style="font-size: small;">Previous GC Identifiers: GC15P074690 GC16P084506</p>
Chromosomal Location <small>(According to GeneLoc and/or HUGO and/or LocusLink (NCBI))</small>	<p>Chromosome: 16 GeneLoc gene densities</p> <p>LocusLink cytogenetic band: 16q23.3 Ensembl cytogenetic band: 16q23.3</p> <p>Gene in genomic location: bands according to Ensembl, locations according to GeneLoc (and/or LocusLink)</p>

Структурно-функциональная информация о генах *Homo sapiens* в индексе GeneCards

<http://bioinformatics.weizmann.ac.il/cards-bin/carddisp?HSBP1>



Ресурсы по анализу структуры и функции геномов ВЫСШИХ ПОЗВОНОЧНЫХ



MGI
Mouse Genome Informatics
MGI Home Help

Search for:

In these sections:

- All sections
- Gene symbols/names
- Accession IDs
- Phenotypes
- Gene Expression

Advanced search for...

Search Categories

- All Search Tools
- Genes/Markers
- Alleles/Phenotypes
- Strains/Polymorphisms

Mammalian Orthology and Comparative Maps

Searches

- Mammalian Orthology**
Search by species, gene symbol, name, or map position.
- Oxford Grid**
Display a two-species orthology comparison, including links to comparative maps.
- Comparative Maps**
Build a comparative map using the Linkage Map tool.

Orthology Map Views

- Mouse and Human Orthology Map**
View orthologies between mouse and human at the whole genome level.
- Mouse and Rat Orthology Map**
View orthologies between mouse and rat at the whole genome level.

Один из инструментов сравнительных исследований геномов высших позвоночных

MGI
Mouse Genome Informatics
MGI Home Help

Search for:

In these sections:

- All sections
- Gene symbols/names
- Accession IDs
- Phenotypes
- Gene Expression

Advanced search for...

Search Categories

- All Search Tools
- Genes/Markers
- Alleles/Phenotypes
- Strains/Polymorphisms
- Expression
- Comparative Maps/Data

Mammalian Orthology Query Results

Query Summary

Organism: equals *mouse, laboratory*
Marker Symbol/Name: contains *tl* searching current symbols/names and synonyms.
Comparison Organism: equals *human* searching only selected species.
Sort: by *Marker in primary species*
Display Limit: equals *500*

129 matching items displayed

Species	Symbol	Chr	AccID	Criteria		
				AA	NS	NT
human	CTLA4	2 (q33)	GDB:119818 (GDB-Australia) 1493 (LocusLink)	●	●	●
mouse, laboratory	Ctla4	1 (30.1 cM)	MGI:88556	●	●	●
Number of References				8	2	4

Comparative Map: Display 2 cM around mouse Ctla4 vs (human)

http://www.informatics.jax.org/searches/homology_report.cgi



Ресурсы по анализу структуры и функции геномов ВЫСШИХ ПОЗВОНОЧНЫХ



VISTA Genome Browser

VISTA Genome Browser · GenomeVISTA · VISTA / rVISTA · Contact · About Us · Cite Us

To browse whole-genome alignments produced by the [Berkeley Genome Pipeline](#) please select a pair of genomes and enter a RefSeq gene name or a position (e.g. chrX1-100000) on the first (base) genome:

Base genome	Aligned genome	Position	
Mouse Feb. 2003	Rat Jun. 2003 (LAGAN)	chr4:52196047-52313394	Go

Vista Genome Browser 1.0 (pairwise alignments) [Help](#)
 Vista Genome Browser 2.0 (multiple alignments) [Help](#)

Description: Feb. 2003 Mouse Genome Assembly vs Rat Jun. 2003. Aligned using LAGAN.

News News archive >>

August 28, 2003
We released Vista Genome Browser (Version 2.0) to display results of multiple whole-genome human, mouse, and rat alignments as well as results of multiple alignments of specific genomic regions. You can select the new browser in the VISTA Browser Gateway on this page

**VISTA –
Просмотр
результатов
выравнивания и
оценки сходства
двух геномов**

<http://pipeline.lbl.gov>



Ресурсы по анализу структуры и функции геномов ВЫСШИХ ПОЗВОНОЧНЫХ

allgenes.org

[news](#) [statistics](#) [credits](#) [BLAST](#) [query](#)

**Allgenes.org –
Индекс генов и их
транскриптов у
человека и мыши**

Quick Search for DoTS Transcripts

DoTS Transcript ID (DT.104964): [GO!](#)

By External ID:

GeneCards: [GO!](#)

By Function:

Human or Mouse Transcript Descrip Keyword (Actin) [GO!](#)

Quick Search for DoTS Genes

DoTS Gene ID (DG.61706): [GO!](#)

Advanced Search for DoTS Transcripts

Query for DoTS Transcripts by: [GO!](#)

Note: queries marked with an asterisk() allow you to provide a dataset as input.*

Advanced Query Facilities

Compose Boolean Queries:

Use the [Boolean Query Composer](#) to build complex boolean queries based on the simple queries listed above.

<http://www.allgenes.org/query.html>



Ресурсы по анализу структуры и функции геномов ВЫСШИХ ПОЗВОНОЧНЫХ



allgenes.org

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Human DoTS Transcript DT.313524

RNA last modified May 2

100% identity to 100% of Breast cancer type 1 susceptibility protein
6308 bp RNA containing 29 sequence(s) review status=unreviewed

ON THIS PAGE: [Gene](#) [GO Function](#) [Links](#) [RH Map](#) [Gene Traps](#) [NRDB\(G\)](#) [Motifs\(G\)](#)

OTHER VIEWS: [Summary](#) [Genome mRNA seq](#) [Assembly](#) [Assembly alignment](#) [Input seqs](#) [EST](#) [Ibs](#) [EST anatomy](#) [Motifs](#) [NRDB hits](#) [Protein features](#) [Protein seq](#)

DoTS Gene to which this DoTS Transcript belongs

Gene	Symbol	Description
DG 35732838	null	

Predicted GO function(s) [\[more information\]](#)

GO_ID	name	review status
GO:0008369	obsolete	needs re-review
GO:0003677	DNA binding activity	unreviewed
GO:0003723	RNA binding activity	unreviewed
GO:0004553	hydrolase activity, hydrolyzing O-glycosyl compounds	unreviewed
GO:0005524	ATP binding activity	unreviewed

Links to LocusLink, GeneCards(TM), MGI and the GNF Gene Expression Atlas (GEA)

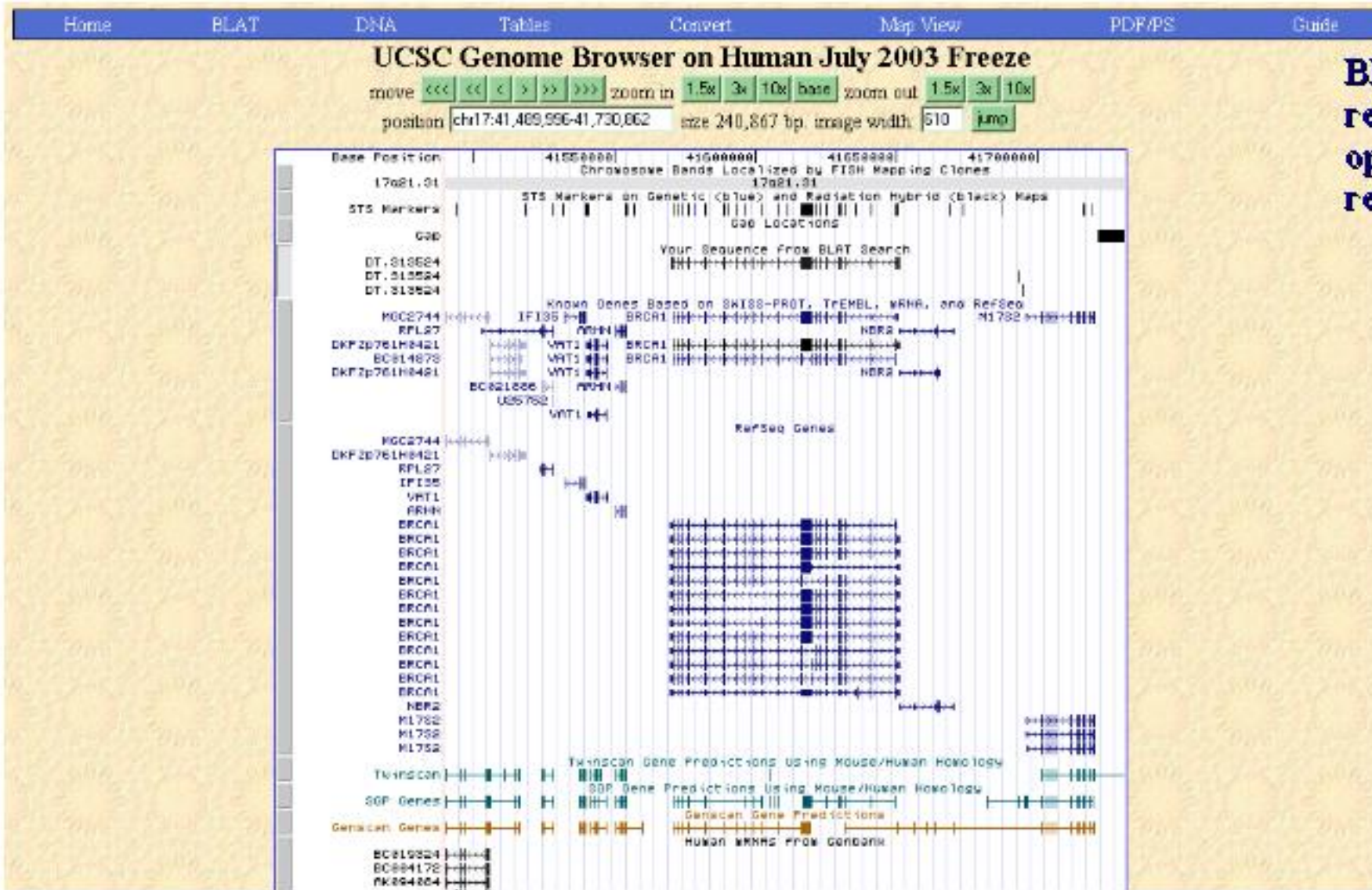
Database	Link	Locus name	Chromosome
GeneCards	BRCA1		
GEA U95A	604_at		
GEA U95A	1993_s_at		
GEA U95A	33724_at		
LocusLink	672		

**Allgenes.org –
Карточка для гена и
его транскрипта**

<http://www.allgenes.org/allgenes/servlet?page=ma&id=DT.313524>



Ресурсы по анализу структуры и функции геномов ВЫСШИХ ПОЗВОНОЧНЫХ



BLAT обзор
геномной
организации
гена

<http://genome.ucsc.edu/cgi-bin/hgTracks?hgid=27022227&...>