

Bases de datos para biólogos evolutivos

Tipos de bases de datos

- secuencias
- alineamientos
- arboles filogenéticos
- predicción de ortología/paralogia
- presión selectiva

Las secuencias

NCBI  Entrez, The Life Sciences Search Engine

HOME SEARCH SITE MAP PubMed All Databases Human Genome GenBank Map Viewer BLAST

Search across databases [Help](#)

- Result counts displayed in gray indicate one or more terms not found

6  PubMed: biomedical literature citations and abstracts	<input type="button" value="none"/>  Books: online books
24  PubMed Central: free, full text journal articles	<input type="button" value="none"/>  OMIM: online Mendelian Inheritance in Man
<input type="button" value="none"/>  Site Search: NCBI web and FTP sites	
8  Nucleotide: Core subset of nucleotide sequence records	<input type="button" value="none"/>  dbGaP: genotype and phenotype
<input type="button" value="none"/>  EST: Expressed Sequence Tag records	1  UniGene: gene-oriented clusters of transcript sequences
<input type="button" value="none"/>  GSS: Genome Survey Sequence records	<input type="button" value="none"/>  CDD: conserved protein domain database
7  Protein: sequence database	<input type="button" value="none"/>  UniSTS: markers and mapping data
1  Genome: whole genome sequences	1  PopSet: population study data sets
<input type="button" value="none"/>  Structure: three-dimensional macromolecular structures	7  GEO Profiles: expression and molecular abundance profiles
<input type="button" value="none"/>  Taxonomy: organisms in GenBank	<input type="button" value="none"/>  GEO DataSets: experimental sets of GEO data
<input type="button" value="none"/>  SNP: single nucleotide polymorphism	<input type="button" value="none"/>  Epigenomics: Epigenetic maps and data sets
<input type="button" value="none"/>  dbVar: Genomic structural variation	<input type="button" value="none"/>  Cancer Chromosomes: cytogenetic databases
3  Gene: gene-centered information	<input type="button" value="none"/>  PubChem BioAssay: bioactivity screens of chemical substances
<input type="button" value="none"/>  SRA: Sequence Read Archive	<input type="button" value="none"/>  PubChem Compound: unique small molecule chemical structures
<input type="button" value="none"/>  BioSystems: Pathways and systems of interacting molecules	<input type="button" value="none"/>  PubChem Substance: deposited chemical substance records
<input type="button" value="none"/>  HomoloGene: eukaryotic homology groups	<input type="button" value="none"/>  Protein Clusters: a collection of related protein sequences
<input type="button" value="none"/>  GENSAT: gene expression atlas of mouse central nervous system	<input type="button" value="none"/>  OMIA: online Mendelian Inheritance in Animals
<input type="button" value="none"/>  Probe: sequence-specific reagents	<input type="button" value="none"/>  BioSample: biological material descriptions
<input type="button" value="none"/>  BioProject: aggregated biological research project data	
<input type="button" value="none"/>  NLM Catalog: catalog of books, journals, and audiovisuals in the NLM collections	<input type="button" value="none"/>  MeSH: detailed information about NLM's controlled vocabulary

Las secuencias

brc-2 BRCA homolog (tumor suppressor gene Brca1) [*Caenorhabditis elegans*]

Gene ID: 175962, updated on 7-Aug-2011

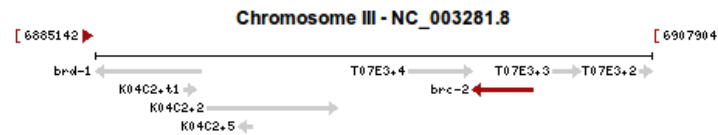
Summary

Gene symbol brc-2
Gene description BRCA homolog (tumor suppressor gene Brca1)
Primary source [WormBase:WBGene00020316](#)
Locus tag [T07E3.5](#)
Gene type protein coding
RefSeq status REVIEWED
Organism [Caenorhabditis elegans \(strain: Bristol N2\)](#)
Lineage Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis

Genomic context

Sequence : Chromosome: III; NC_003281.8 (6900523..6903043, complement)

[See brc-2 in MapViewer](#)



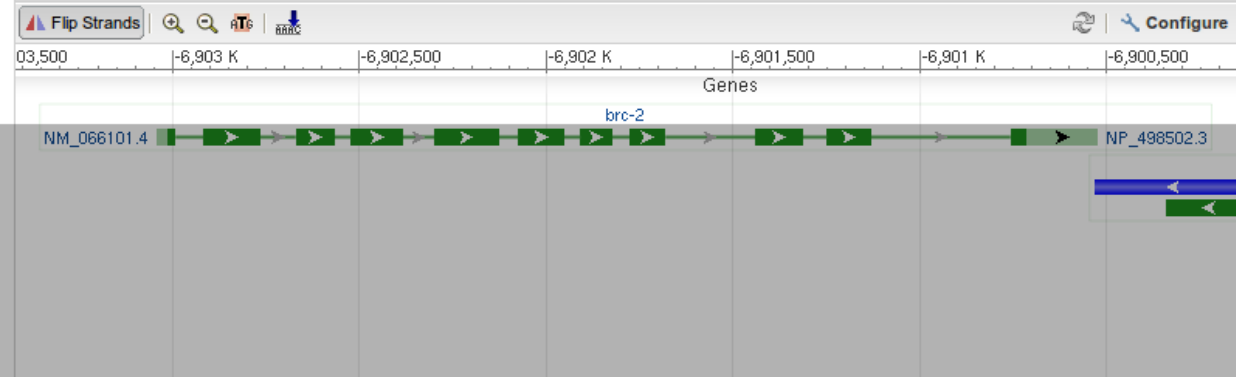
Genomic regions, transcripts, and products

Go to [reference sequence details](#)

Genomic Sequence

Go to nucleotide [Graphics](#) [FASTA](#) [GenBank](#)

-6,903,420 : -6,900,144 (3,277 bases shown, negative strand) [Open Full View](#)



Bibliography

Las secuencias

Caenorhabditis elegans chromosome III, complete sequence

NCBI Reference Sequence: NC_003281.8


[GenBank](#) [Graphics](#)

>gi|193211354:c6903043-6900523 Caenorhabditis elegans chromosome III, complete sequence

```
ACTTTACCAGAATATTGTGACATCGACCGATGGGTGACTCATCTAAAAAAGTGTAGTCAAGATTTATTT
TATTGTTATAGCAAGAAAATTGAGAAACATACATGAATTGCAATTCCTTTGTTTTTCAGAAAAGACAGTTTC
GACACAATATCTGAACCAGACAGCTTTGATGAGCCGAAAGGCGTACCGATATCAATGGAACCGGTTTTTT
CAACAGCGGCTGGTATCCGAATTGATGTGAAGCAGGAATCGATTGATAAATCAAAGAAGATGTTGAATGT
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AATATAAAAAATTTCAAATTCAGAGTGATCTCAAGAGCAAAATCCTCGTCTAAAGGCGGATTTTCTTCCCC
TCTCGTGCGCAAAAACAAATGGGTGCGAGCGCTTTCTGTTTCACCGTTTCGAAGAGAAGGGTAAGTTCAAAG
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TTTTCGAAGATTTCGAAGCTCCACCAGCAAAAAAATCAACCAGCAGTTCTTCTAAAAAAGTAAAAAACAT
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TGTTCTTTTATCCGTAATTCCTGTAATCCGGAGTCTTTTTTCAGAAATCCACGCCGATGTTTTGCGTGTT
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CCACTTGTAGCTACAATCGTGGCTCTGATATTAATTTGGCGACAGAATTCATGTCGACGCGGAAGTCTG
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TAGAACATTTTTAATGTTTTGGATAAATAGCCTATTTTCAGCTAAAAATCTCAAATTTTTCCGACTTGTCA
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TATGGACTTCTCCGGTCAAATGTTTATCAATGTGACTACAAAAAATATGAAGAAATTACTCGATTTGTTA
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TTTTTGTGTGTTTATTCGTTTTAACGTAGATGGTTCAAATGCTTTAATTTATTCTCAAAGAAATATCCCC
GTTCTAATTTTATATGTTCCCTTCTGTTGTTTCCATGTTAAAGAATTATTATGAAACGATGAAATCTTC
```

A

Las secuencias

 [BLAST/BLAT](#) | [BioMart](#) | [Tools](#) | [Downloads](#) | [More](#) [Account](#) · [Logout](#)




Search: for

e.g. [BRCA2](#) or [rat X:100000..200000](#) or [coronary heart disease](#)

Browse a Genome

The Ensembl project produces genome databases for vertebrates and other eukaryotic species, and makes this information freely available online. Click on a link below to go to the species' home page.



Favourite genomes ([Change favourites](#))

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GRCh37
-  **Mouse**
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All genomes

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Other species are available in [Ensembl Pre!](#) and [EnsemblGenomes](#)

Ensembl is a joint project between [EMBL - EBI](#) and the [Wellcome Trust Sanger Institute](#) to develop a software system which produces and maintains automatic annotation on selected eukaryotic genomes.

Ensembl receives major funding from the Wellcome Trust. Our [acknowledgements page](#) includes a list of additional current and previous funding bodies.


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using BLAST or BLAT
- [Fetch only the data you want](#)
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in FASTA, MySQL and other formats
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Did you know...?

 Convert old genomics coordinates to a new, updated genome using the [assembly converter](#).

What's New in Release 63 (30 June 2011)

- [Sortable tracks](#) on Region in Detail
- [Variant Effect Predictor 2.1](#)
- [Regulation configuration matrix redesign](#)

[Full details of this release](#)
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Las secuencias

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Species ▾

Search Ensembl
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Results Summary

Your search of all species with 'BRCA2' returned the following results:

By Feature type	
Total	1622
▶ Domain	248
▶ Family	210
▶ Gene	169
▶ Marker	6
▶ Somatic mutation	51
▶ Transcript	190
▶ Variation	747
▶ Variation phenotype	1

By Species	
Total	1622
▶ Alluropoda melanoleuca	12
▶ Anolis carolinensis	15
▶ Bos taurus	14
▶ Caenorhabditis elegans	12
▶ Callithrix jacchus	19
▶ Canis familiaris	14
▶ Cavia porcellus	17
▶ Choloepus hoffmanni	16
▶ Ciona intestinalis	2
▶ Ciona savignyi	6
▶ Danio rerio	20
▶ Dasypus novemcinctus	17
▶ Dipodomys ordii	17
▶ Drosophila melanogaster	7
▶ Echinops telfairi	11
▶ Equus caballus	18
▶ Erinaceus europaeus	11
▶ Felis catus	16
▶ Gallus gallus	16
▶ Gasterosteus aculeatus	12
▶ Gorilla gorilla	18
▶ Homo sapiens	828
▶ Loxodonta africana	19
▶ Macaca mulatta	17
▶ Macropus eugenii	15
▶ Meleagris gallopavo	14
▶ Microcebus murinus	17

By Help	
Total	15
▶ Docs	15

Las secuencias

e!Ensembl BLAST/BLAT | BioMart | Tools | Downloads | Help & Documentation | Blog | Mirrors

Human (GRCh37) | Location: 16:23,614,483-23,652,678 | Gene: PALB2 | Transcript: PALB2-201

Gene-based displays

- Gene summary
- Splice variants (1)
- Supporting evidence
- Sequence**
- External references
- Regulation
- Comparative Genomics
 - Genomic alignments
 - Gene Tree (image)
 - Gene Tree (text)
 - Gene Tree (alignment)
- Orthologues (44)
- Paralogues
- Protein families (1)
- Genetic Variation
 - Variation Table
 - Variation Image
 - Structural Variation
- External Data
 - Personal annotation
- ID History
 - Gene history

Configure this page | **Manage your data** | Export data | Bookmark this page

Gene: PALB2 (ENSG00000083093)

Description partner and localizer of BRCA2 [Source:HGNC Symbol;Acc:26144]
Location [Chromosome 16: 23,614,483-23,652,678](#) reverse strand.
Transcripts There is 1 transcript in this gene

Name	Transcript ID	Length (bp)	Protein ID	Length (aa)	Biotype	CCDS
PALB2-201	ENST00000261584	4058	ENSP00000261584	1186	Protein coding	CCDS32406

Gene summary [help](#)

Name [PALB2](#) (HGNC Symbol)
Synonyms FANCN, FLJ21816 [To view all Ensembl genes linked to the name [click here](#).]
CCDS This gene is a member of the Human CCDS set: [CCDS32406](#)
Gene type Known protein coding
Prediction Method Annotation produced by the Ensembl [genebuild](#).

Ensembl/Havana.g... 23.61 Mb 23.62 Mb 23.63 Mb 23.64 Mb 23.65 Mb 23.66 Mb

Contigs < AC008870.8

Ensembl/Havana.g... < NDUFA B1-001 protein coding < PALB2-201 protein coding < NDUFA B1-002 processed transcript

58.20 Kb Forward strand

Reverse strand

[Export Image](#)

Configuring the display

Tip: use the "Configure this page" link on the left to show additional data in this region.

Las secuencias

e!Ensembl BLAST/BLAT | BioMart | Tools | Downloads | More ▾ Login · Register

New | Count | Results | ★ URL | XML | Perl | Help

Dataset
Homo sapiens genes (GRCh37.p3)
Filters [None selected]
Attributes
Protein
Ensembl Gene ID
Ensembl Transcript ID

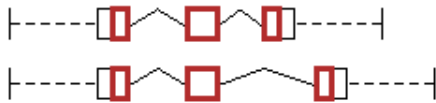
Dataset
[None Selected]

Please select columns to be included in the output and hit 'Results' when ready

Features **Homologs**
 Structures **Variation**
 Transcript Event **Sequences**

SEQUENCES:

Sequences (max 1)



Unspliced (Transcript) 5' UTR
 Unspliced (Gene) 3' UTR
 Flank (Transcript) Exon sequences
 Flank (Gene) cDNA sequences
 Flank-coding region (Transcript) Coding sequence
 Flank-coding region (Gene) Protein

Upstream flank
 Upstream flank

Downstream flank
 Downstream flank

Las secuencias

Species	DNA (FASTA)	cDNA (FASTA)	ncRNA (FASTA)	Protein sequence (FASTA)	Annotated sequence (EMBL)	Annotated sequence (GenBank)	Gene sets	Whole databases	Variation (EMF)	Variation (GVF)	Regulation (GFF)	Data files
<i>Alluopoda melanoleuca</i> (Panda)	FASTA	FASTA	FASTA	FASTA	EMBL	GenBank	GTF	MySQL	-	-	-	-
<i>Anolis carolinensis</i> (Anole Lizard)	FASTA	FASTA	FASTA	FASTA	EMBL	GenBank	GTF	MySQL	-	-	-	-
<i>Bos taurus</i> (Cow)	FASTA	FASTA	FASTA	FASTA	EMBL	GenBank	GTF	MySQL	-	GVF	-	-
<i>Caenorhabditis elegans</i> (C. elegans)	FASTA	FASTA	FASTA	FASTA	EMBL	GenBank	GTF	MySQL	-	-	-	-
<i>Callithrix jacchus</i> (Marmoset)	FASTA	FASTA	FASTA	FASTA	EMBL	GenBank	GTF	MySQL	-	-	-	-
<i>Canis familiaris</i> (Dog)	FASTA	FASTA	FASTA	FASTA	EMBL	GenBank	GTF	MySQL	-	GVF	-	-
<i>Cavia porcellus</i> (Guinea Pig)	FASTA	FASTA	FASTA	FASTA	EMBL	GenBank	GTF	MySQL	-	-	-	-
<i>Choloepus hoffmanni</i> (Sloth)	FASTA	FASTA	FASTA	FASTA	EMBL	GenBank	GTF	MySQL	-	-	-	-
<i>Ciona intestinalis</i> (C. intestinalis)	FASTA	FASTA	FASTA	FASTA	EMBL	GenBank	GTF	MySQL	-	-	-	-
<i>Ciona savignyi</i> (C. savignyi)	FASTA	FASTA	FASTA	FASTA	EMBL	GenBank	GTF	MySQL	-	-	-	-
<i>Danio rerio</i> (Zebrafish)	FASTA	FASTA	FASTA	FASTA	EMBL	GenBank	GTF	MySQL	-	GVF	-	-
<i>Dasyus novemcinctus</i> (Armadillo)	FASTA	FASTA	FASTA	FASTA	EMBL	GenBank	GTF	MySQL	-	-	-	-
<i>Dipodomys ordii</i> (Kangaroo rat)	FASTA	FASTA	FASTA	FASTA	EMBL	GenBank	GTF	MySQL	-	-	-	-
<i>Drosophila melanogaster</i>	FASTA	FASTA	FASTA	FASTA	EMBL	GenBank	GTF	MySQL	-	GVF	-	-

Arboles filogenéticos

- Gene-based displays
- Gene summary
 - Splice variants (6)
 - Supporting evidence
 - Sequence
 - External references
 - Regulation
 - Comparative Genomics
 - Genomic alignments
 - Gene Tree (Image)**
 - Gene Tree (text)
 - Gene Tree (alignment)
 - Orthologues (46)
 - Paralogues
 - Protein families (2)
 - Genetic Variation
 - Variation Table
 - Variation Image
 - Structural Variation
 - External Data
 - Personal annotation
 - ID History
 - Gene history

- Configure this page
- Manage your data
- Export data
- Bookmark this page

Gene: BRCA2 (ENSG00000139618)

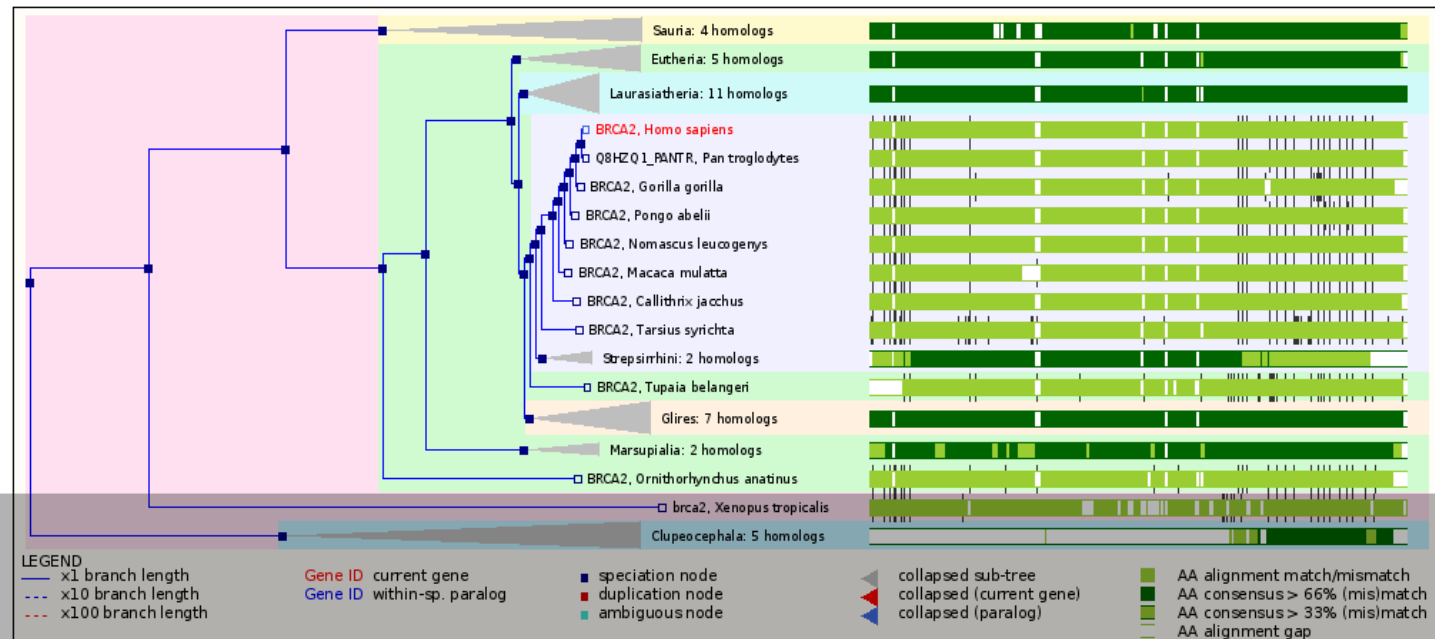
Description breast cancer 2, early onset [Source:HGNC Symbol;Acc:1101]
Location [Chromosome 13: 32,889,611-32,973,805](#) forward strand.
Transcripts There are 6 transcripts in this gene

Name	Transcript ID	Length (bp)	Protein ID	Length (aa)	Biotype	CCDS
BRCA2-001	ENST00000380152	10930	ENSP00000369497	3418	Protein coding	CCDS9344
BRCA2-003	ENST00000530893	2009	ENSP00000435699	602	Protein coding	-
BRCA2-201	ENST00000544455	10984	ENSP00000439902	3418	Protein coding	CCDS9344
BRCA2-002	ENST00000470094	842	ENSP00000434898	186	Nonsense mediated decay	-
BRCA2-005	ENST00000528762	495	ENSP00000433168	64	Nonsense mediated decay	-
BRCA2-006	ENST00000533776	523	No protein product	-	Retained intron	-

Gene Tree (image) [help](#)

GeneTree ENSGT00390000003602

Number of genes 47
 Number of duplication nodes 0
 Number of ambiguous nodes 1



[Export Image](#)

Arboles filogenéticos



[Login] Home

Search in PhylomeDB

(i.e. YBL058W, holA, Phy00085K5_HUMAN)

Go Fuzzy Search

You can also use a BLAST search

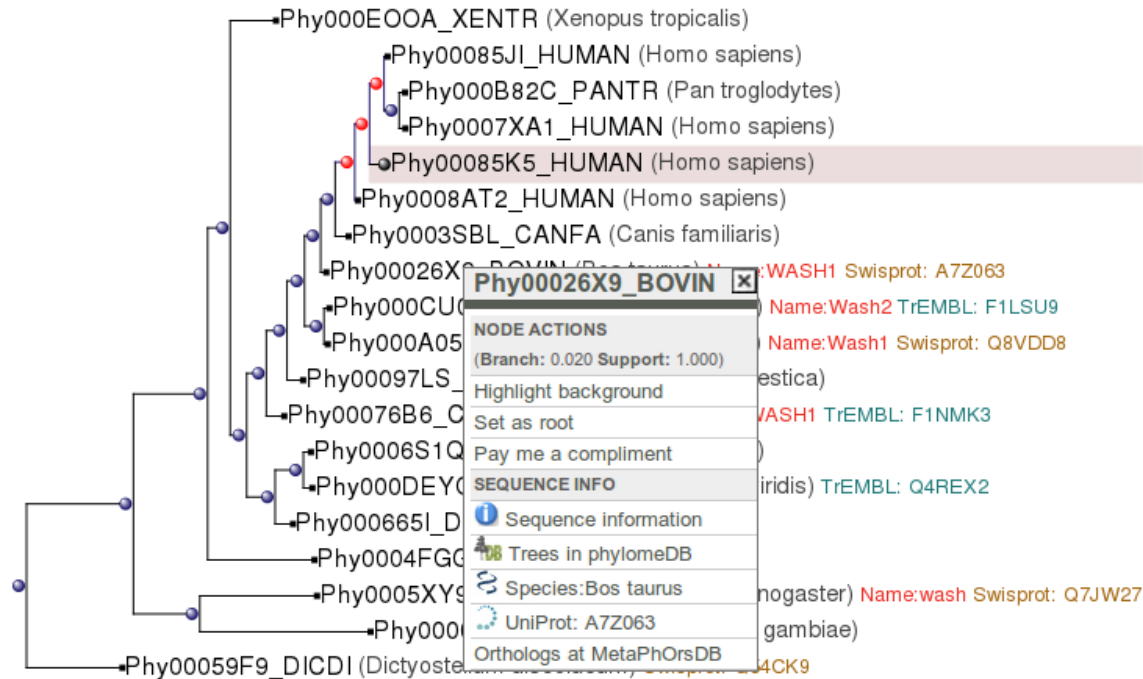
Latest Phylomes

A. thaliana	2011
A. melifera	2010
T. castaneum	2010
C. albicans	2009

[see all phylomes](#)

Phy00085K5_HUMAN (trees)

Human phylome (1) Method: Blosum62 -- jump to collateral tree -- See alignments Download data.tar.gz



0.60

ete_dev

- Speciation events.
- Duplication events.
- seed sequence

(Note that default labeling colors in phylomeDB have been changed to be consistent with other related databases)

MetaPhOrs homology predictions

Predicción de ortología/paralogía

- Gene-based displays**
- Gene summary
 - Splice variants (6)
 - Supporting evidence
 - Sequence
 - External references
 - Regulation
 - Comparative Genomics
 - Genomic alignments
 - Gene Tree (image)
 - Gene Tree (text)
 - Gene Tree (alignment)
 - Orthologues (46)**
 - Paralogues
 - Protein families (2)
 - Genetic Variation
 - Variation Table
 - Variation Image
 - Structural Variation
 - External Data
 - Personal annotation
 - ID History
 - Gene history

Gene: BRCA2 (ENSG00000139618)

Description breast cancer 2, early onset [Source:HGNC Symbol;Acc:1101]

Location [Chromosome 13: 32,889,611-32,973,805](#) forward strand.

Transcripts There are 6 transcripts in this gene






Show/hide columns		Filter				
Name	Transcript ID	Length (bp)	Protein ID	Length (aa)	Biotype	CCDS
BRCA2-001	ENST00000380152	10930	ENSP00000369497	3418	Protein coding	CCDS9344
BRCA2-003	ENST00000530893	2009	ENSP00000435699	602	Protein coding	-
BRCA2-201	ENST00000544455	10984	ENSP00000439902	3418	Protein coding	CCDS9344
BRCA2-002	ENST00000470094	842	ENSP00000434898	186	Nonsense mediated decay	-
BRCA2-005	ENST00000528762	495	ENSP00000433168	64	Nonsense mediated decay	-
BRCA2-006	ENST00000533776	523	No protein product	-	Retained intron	-

Orthologues [help](#)

Summary of orthologues of this gene

Click on 'Show' to display the orthologues for one or more groups, or click on 'Configure this page' to choose a custom list of species

Species set	Show details	1:1	1:many	many:many	No orthologues
Primates Human and 8 other primates	<input type="checkbox"/>	9	0	0	0
Rodents Mouse, rat and 6 other rodents	<input type="checkbox"/>	8	0	0	0
Laurasiatheria Carnivores, ungulates and insectivores	<input type="checkbox"/>	11	0	0	0
Placental Mammals 33 placental mammalian species	<input type="checkbox"/>	33	0	0	0
Sauropsida Birds and Reptiles	<input type="checkbox"/>	4	0	0	0
Fish Zebrafish and 4 other ray-finned fish	<input type="checkbox"/>	5	0	0	0
All All species, including invertebrates	<input type="checkbox"/>	46	0	0	0

-  Configure this page
-  Manage your data
-  Export data
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-  Download view as CSV

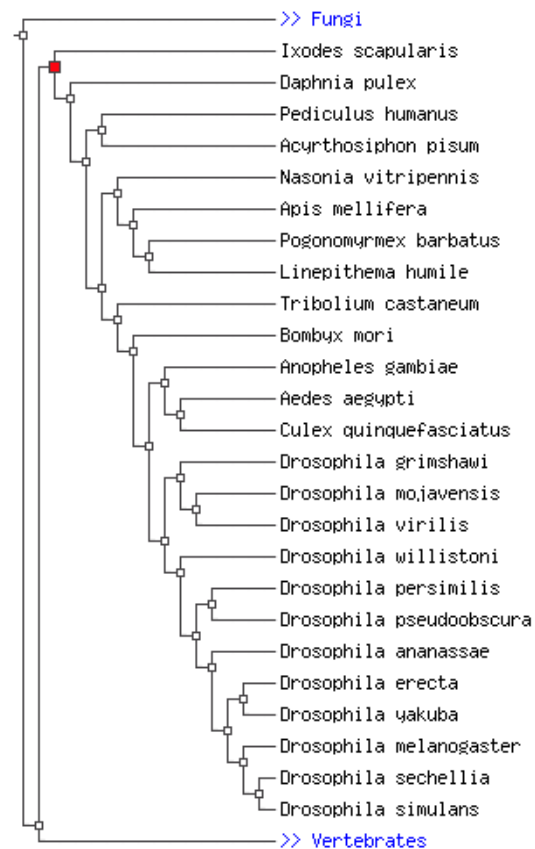
Predicción de ortología/paralogia

OrthoDB: Database of Orthologous Groups

Wed, 09/01/2010 - 16:03

[Show Help](#)

[Fungi](#) **Arthropods** [Vertebates](#) [Metazoa](#)



[Show/Hide copy-number selectors](#)

OrthoDB

The Hierarchical Catalog of Eukaryotic Orthologs

OrthoDB presents a catalog of eukaryotic orthologous protein-coding genes across 44 vertebrates, 25 arthropods, and 46 fungi. Orthology refers to the last common ancestor of the species under consideration, and thus OrthoDB explicitly delineates orthologs at each radiation along the species phylogeny. The database of orthologs presents available protein descriptors, together with Gene Ontology and InterPro attributes, which serve to provide general descriptive annotations of the orthologous groups, and facilitate comprehensive orthology database querying.

Search OrthoDB: ["Cytochrome P450"](#) [protease](#) | [peptidase](#) [kinase -serine](#) [FBqn0036816](#) [IPR017981](#)
[GO:0006950](#)

For detailed instructions on OrthoDB search functions, data sources, and further information, please see [Help](#).

The previous release of OrthoDB (2009, 40 vertebrates, 23 arthropods, and 32 fungi) can be accessed [here](#). The original release of OrthoDB (2008, 15 vertebrates, 20 arthropods, and 23 fungi) can be accessed [here](#).

Please Cite:

Waterhouse RM, Zdobnov EM, Tegenfeldt F, Li J, Kriventseva EV.
OrthoDB: the hierarchical catalog of eukaryotic orthologs in 2011.
NAR, Jan 2011, PMID:[20972218](#)

Downloads



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Predicción de ortología/paralogia

OrthoDB Results

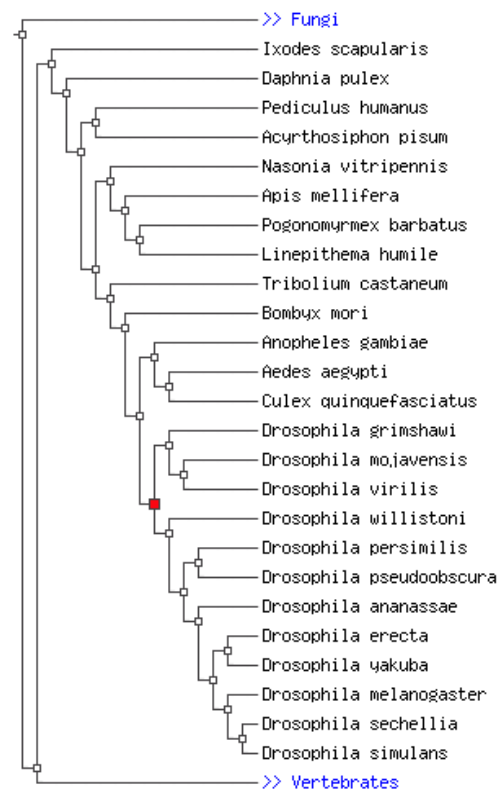
Your search for: ["Cytochrome P450"] returned 82 orthologous groups

[Get all as Fasta](#) | [All Tab Delimited](#) | [Print Tables](#)

[Show Help](#) | [Show History](#)

OrthoDB Home

[Fungi](#) [Arthropods](#) [Vertebates](#) [Metazoa](#)



Show/Hide copy-number selectors

Copy-Number Searches

A) Select radiation node and define profile on the tree above then

Group [EOG46DKDS](#): 13 genes in 12 species

[Get Fasta](#) | [Tab Delimited](#)

Gene Ontologies

Molecular Function: 13 genes with [GO:0009055](#): electron carrier activity; 13 genes with [GO:0004497](#): monoxygenase activity; 13 genes with [GO:0020037](#): heme binding;

Biological Process: 1 gene with [GO:0055114](#): oxidation reduction;

Cellular Component: 1 gene with [GO:0005789](#): endoplasmic reticulum membrane; 1 gene with [GO:0005792](#): microsome;

InterPro Domains

13 genes with [IPR001128](#): Cytochrome P450;

Phyletic Profile: Genes in 12/12 species: single-copy in 11 species and multi-copy in 1 species.

Evolutionary Rate 1.02



Organism	Protein ID	InterPro
DGRIM	1. FBqn0118522 (B4JC58) GH11041	IPR001128
DMOJA	1. FBqn0140302 (B4KGY6) GI17558	IPR001128
DVIRI	1. FBqn0202777 (B4LR14) GJ15584	IPR001128
	2. FBqn0203880 (B4M7Y4) GJ16699	IPR001128
DWILL	1. FBqn0227384 (B4NDR2) GK25425	IPR001128
DPERS	1. FBqn0153487 (B4H0X7) GL15883	IPR001128
DPSEU	1. FBqn0245684 (B5DNJ0) GA24287	IPR001128
DANAN	1. FBqn0098035 (B3MU69) GF21030	IPR001128
DEREC	1. FBqn0116043 (B3NAA0) GG23904	IPR001128
DYAKU	1. FBqn0236384 (B4P0H5) GE19017	IPR001128
DMELA	1. FBqn0028940 (Q9V419) ✔ Probable cytochrome P450 28a5	IPR001128
DSECH	1. FBqn0170359 (B4HXD4) GM15441	IPR001128
DSIMU	1. FBqn0195309 (B4Q5G1) GD23944	IPR001128

Related Groups:

Group	Hit E-value	Hit Identity
EOG49S5KR	1.00e-200	61.29 %
EOG4PG5C0	1.00e-200	49.17 %
EOG4Z09K1	1.00e-200	45.08 %
EOG4R4ZDV	1.00e-200	41.49 %
EOG4VDP98	1.00e-40	28.65 %

Top 5 of 103
[View All 103](#)

Presión selectiva

Gene-based displays

- Gene summary
- Splice variants (6)
- Supporting evidence
- Sequence
- External references
- Regulation
- Comparative Genomics
 - Genomic alignments
 - Gene Tree (image)
 - Gene Tree (text)
 - Gene Tree (alignment)
 - Orthologues (46)**
 - Paralogues
 - Protein families (2)
- Genetic Variation
 - Variation Table
 - Variation Image
 - Structural Variation
- External Data
 - Personal annotation
- ID History
 - Gene history

- Configure this page
- Manage your data
- Export data
- Bookmark this page
- Download view as CSV

Gene: BRCA2 (ENSG00000139618)

Description breast cancer 2, early onset [Source:HGNC Symbol;Acc:1101]
Location [Chromosome 13: 32,889,611-32,973,805](#) forward strand.
Transcripts There are 6 transcripts in this gene
[Click the plus to show the transcript table](#)

Orthologues [help](#)

Summary of orthologues of this gene

Click on 'Show' to display the orthologues for one or more groups, or click on 'Configure this page' to choose a custom list of species

Species set	Show details	1:1	1:many	many:many	No orthologues
Primates Human and 2 other primates	<input type="checkbox"/>	3	0	0	0
Rodents Mouse, rat and -2 other rodents	<input type="checkbox"/>	0	0	0	0
Laurasiatheria Carnivores, ungulates and insectivores	<input type="checkbox"/>	0	0	0	0
Placental Mammals 3 placental mammalian species	<input type="checkbox"/>	3	0	0	0
Sauropsida Birds and Reptiles	<input type="checkbox"/>	0	0	0	0
Fish Zebrafish and -1 other ray-finned fish	<input type="checkbox"/>	0	0	0	0
All All species, including invertebrates	<input type="checkbox"/>	3	0	0	0

Selected orthologues

[View sequence alignments of these homologues.](#)

Show/hide columns		Filter					
Species	Type	dN/dS	Ensembl Identifier & gene name	Compare	Location	Target %id	Query %id
Chimpanzee (<i>Pan troglodytes</i>)	1-to-1	0.28906	ENSPTRG00000005766 Q8HZQ1_PANTR Breast cancer 2 Fragment [Source: UniProtKB/TrEMBL; acc: Q8HZQ1]	<ul style="list-style-type: none"> Multi-species view Alignment (protein) Alignment (cDNA) Gene Tree (image) 	Region: Chromosome 13 Start: 32082480 End: 32166147 Strand: 1	99	99
Macaque (<i>Macaca mulatta</i>)	1-to-1	0.53226	ENSMMUG00000007197 BRCA2 breast cancer 2, early onset [Source:HGNC Symbol;Acc:1101]	<ul style="list-style-type: none"> Multi-species view Alignment (protein) Alignment (cDNA) Gene Tree (image) 	Region: Chromosome 17 Start: 11687584 End: 11777925 Strand: 1	93	91
Orangutan (<i>Pongo abelii</i>)	1-to-1	0.62121	ENSPPYG00000005264 BRCA2 breast cancer 2, early onset [Source:HGNC Symbol;Acc:1101]	<ul style="list-style-type: none"> Multi-species view Alignment (protein) Alignment (cDNA) Gene Tree (image) 	Region: Chromosome 13 Start: 31850770 End: 31940736 Strand: 1	96	96

Presión selectiva

[New Search](#)

HUMAN PAML BROWSER

Query On ID	None ▾	<input type="text"/>	(Examples)	Submit
Query On Significance	None ▾	Threshold for Significance (e.g. 0.01)		Submit
		<input type="text"/>		
Reset				
Use * as wild character				

The Human PAML Browser provides access to the results of tests for positive selection in 14,000 human genes. Multiple alignments of protein-coding regions of genes from human and other mammals were extracted from whole-genome alignments available from [UC-Santa Cruz](#). Each gene was analyzed using the maximum likelihood tests of selection using [PAML](#). Branch, site, and branch+site tests were performed, each with at least one matching null model. For a full description of the evolutionary models, click [HERE](#)

Presión selectiva

HUMAN PAML BROWSER

BREAST CANCER 2, EARLY ONSET

Experiment: UCSC alignments plus Ppy

Gene Symbol	BRCA2
Lab Data	
Entrez Gene	675
# of Codons	3418

Organism	% Coverage	% Identity	Accession
Hsa	100.00	100.00	U43746
Ptr	96.54	99.44	
Ppy	98.68	98.15	
Mmu	98.01	96.59	
Ocu	78.99	80.62	

LRT Results	
p = chidist(2x(lnL1-lnL2), (np1-np2))	
Test	p
modelA vs. model1a	1.00000
modelA vs. modelAnull	1.00000
modelH vs. modelHnull	0.01020

[DNA Alignment](#)

[Site Models](#)

[DNA Fasta](#)

[Branch and Site Models](#)

[Protein Alignment](#)

[Protein Fasta](#)

Presión selectiva

Pupasuite 3

home | help | tutorial | contact

prioritization of SNPs in genotyping experiments based on functional properties

Upload Data | SNP prioritization | Functional haplotypes | SNP viewer and filter

anonymous working on project default 0 Kb of 1.00 Gb (0.00%) no active jobs logout

SNP prioritization

▶ [Online examples \(test the form with example data\)](#)

Select your organism

Homo sapiens
 Mus musculus
 Rattus norvegicus

Define your data

SNP list
 Gene/Transcript list
 Genomic

Select your gene/transcript list

Select gene file (this data format is [idlist:gene](#))

Non-synonymous SNPs

All non-synonymous SNPs
 Mutations affecting protein structure and dynamics (SNPeffect)
 Mutations affecting protein cellular processing (SNPeffect)
 Mutations affecting functional sites (SNPeffect)
 Pathological mutations predicted by selective constraints (dN/dS)

Omega values from to

Transcription factor binding site

TRANSFAC/Match predictions
 JASPAR/MatScan predictions
 ORegAnno

microRNA

Job list

no jobs found

Data list

Presión selectiva

SNP ID	SNP location	alleles	transcript stable ID	aminoacid change	aminoacid envlroment	aminoacid relative position	wSIr	siR p-value	wBayesian	bayesianModel	extrapolated
rs1804387	21:34911561(+)	G/A	ENST00000361093	L/F	KLA	21	0	p>0.05	0.081	M8	yes
rs1804387	21:34911561(+)	G/A	ENST00000381815	L/F	KLA	21	0	p>0.05	0.081	M8	yes
rs1804387	21:34911561(+)	G/A	ENST00000381831	L/F	KLA	21	0	p>0.05	0.081	M8	yes
rs1804387	21:34911561(+)	G/A	ENST00000381839	L/F	KLA	21	0	p>0.05	0.081	M8	no
rs11908823	21:34924145(+)	A/G	ENST00000290239	T/A	GTM	870	0	-	0.0	-	no
rs11908823	21:34924145(+)	A/G	ENST00000300278	T/A	GTM	870	0	-	0.0	-	no
rs11908823	21:34924145(+)	A/G	ENST00000321758	T/A	GTM	832	0	-	0.0	-	no
rs11908823	21:34924145(+)	A/G	ENST00000356577	T/A	GTM	870	0	-	0.0	-	no
rs11908823	21:34924145(+)	A/G	ENST00000381679	T/A	GTM	870	0	-	0.0	-	no
rs11908823	21:34924145(+)	A/G	ENST00000381729	T/A	GTM	870	0	-	0.0	-	no

Enlaces/ayuda

- NCBI: <http://www.ncbi.nlm.nih.gov/guide/>
- Ensembl: <http://www.ensembl.org/index.html>
- Phylomedb: <http://phylomedb.org/>
- phyleasProg: <http://phyleasprog.inra.fr/>
- phylogeny.fr: <http://www.phylogeny.fr/>
- orthodb: <http://cegg.unige.ch/orthodb4>
- Pupasuite: <http://pupasuite.bioinfo.cipf.es/>
- Human PAML browser: <http://mendel.gene.cwru.edu/adamslab/cgi-bin/paml/pbrowser.py>
- Felsenstein list of phylogeny programs: <http://evolution.genetics.washington.edu/phylip/software.html>

preguntas?

