



MICB 405 Bioinformatics

Mini-Lab #3 – Genome Browsers

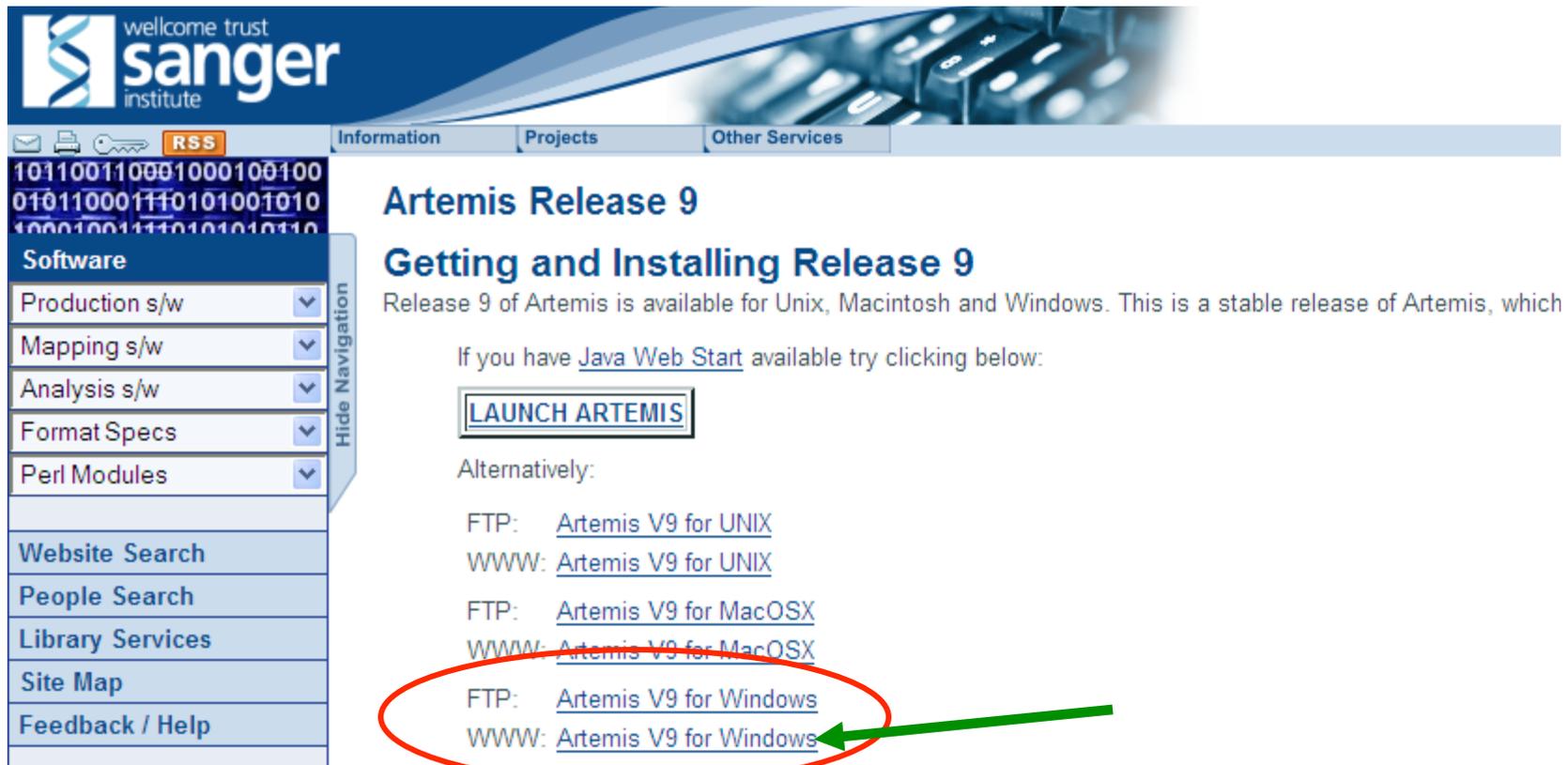
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We gratefully acknowledge the funding for the development of these teaching materials provided by UBC students through the Teaching and Learning Enhancement Fund (TLEF) from 2005-2007.

Download Artemis to Desktop

<http://www.sanger.ac.uk/Software/Artemis/v9/>

Google: “artemis v9”



The screenshot shows the Sanger Institute website. The header features the Sanger logo and navigation tabs for Information, Projects, and Other Services. A left sidebar contains a 'Software' section with dropdown menus for Production s/w, Mapping s/w, Analysis s/w, Format Specs, and Perl Modules, along with search and help links. The main content area is titled 'Artemis Release 9' and 'Getting and Installing Release 9'. It states that Release 9 is available for Unix, Macintosh, and Windows. A 'LAUNCH ARTEMIS' button is provided for users with Java Web Start. Below this, links are listed for FTP and WWW for each platform. The 'FTP: Artemis V9 for Windows' and 'WWW: Artemis V9 for Windows' links are circled in red, with a green arrow pointing to the WWW link.

wellcome trust
sanger
institute

Information Projects Other Services

101100110001000100100
010110001110101001010
100010011110101010110

Software

Production s/w

Mapping s/w

Analysis s/w

Format Specs

Perl Modules

Hide Navigation

Website Search

People Search

Library Services

Site Map

Feedback / Help

Artemis Release 9

Getting and Installing Release 9

Release 9 of Artemis is available for Unix, Macintosh and Windows. This is a stable release of Artemis, which

If you have [Java Web Start](#) available try clicking below:

LAUNCH ARTEMIS

Alternatively:

FTP: [Artemis V9 for UNIX](#)
WWW: [Artemis V9 for UNIX](#)

FTP: [Artemis V9 for MacOSX](#)
WWW: [Artemis V9 for MacOSX](#)

FTP: [Artemis V9 for Windows](#)
WWW: [Artemis V9 for Windows](#)

Objectives

- By the end of today's lecture:
 - ✓ You will practice using four different genome browsers.
 - ✓ You will navigate the genomic region for BRCA1 using three different genome browsers.
 - ✓ You will download genomic data for BRCA1
 - ✓ You will learn about the photosynthetic gene cluster of *Rhodobacter sphaeroides* using Artemis

<http://genome.cse.ucsc.edu/>

UCSC Genome Bioinformatics

Genomes - Blat - Tables - Gene Sorter - PCR - VisiGene - Proteome - Session - FAQ - Help

Genome Browser

ENCODE

Blat

Table Browser

Gene Sorter

Silico CR

Genome Graphs

Galaxy

VisiGene

Proteome Browser

Utilities

Downloads

About the UCSC Genome Bioinformatics Site

Welcome to the UCSC Genome Browser website. This site contains the reference sequence and working draft assemblies for a large collection of genomes. It also provides a portal to the ENCODE project.

We encourage you to explore these sequences with our tools. The [Genome Browser](#) zooms and scrolls over chromosomes, showing the work of annotators worldwide. The [Gene Sorter](#) shows expression, homology and other information on groups of genes that can be related in many ways. [Blat](#) quickly maps your sequence to the genome. The [Table Browser](#) provides convenient access to the underlying database. [VisiGene](#) lets you browse through a large collection of *in situ* mouse and frog images to examine expression patterns. [Genome Graphs](#) allows you to upload and display genome-wide data sets.

The UCSC Genome Browser is developed and maintained by the Genome Bioinformatics Group, a cross-departmental team within the Center for Biomolecular Science and Engineering ([CBSE](#)) at the University of California Santa Cruz ([UCSC](#)). If you have feedback or questions concerning the tools or data on this website, feel free to contact us on our [public mailing list](#). To view the results of the Genome Browser users' survey we conducted in May 2007, click [here](#).

News News Archives ►

To receive announcements of new genome assembly releases, new software features, updates and training seminars by email, subscribe to the [genome-announce](#) mailing list.

8 Jan. 2008 - Additional Job Opening with UCSC Genome Browser Project

Human (*Homo sapiens*) Genome Browser Gateway

The UCSC Genome Browser was created by the [Genome Bioinformatics Group of UC Santa Cruz](#).
 Software Copyright (c) The Regents of the University of California. All rights reserved.

clade	genome	assembly	position or search term	image width	
Vertebrate	Human	May 2004	BRCA1	620	submit

[Click here to reset](#) the browser user interface settings to their defaults.
[add your own custom tracks](#) [configure tracks and display](#) [clear session](#)

About the Human May 2004 (hg17) assembly ([sequences](#))

The May 2004 human reference sequence is based on NCBI Build 35 and was produced by the International Human Genome Sequencing Consortium.

Sample position queries

A genome position can be specified by the accession number of a sequenced genomic clone, an mRNA or EST or STS marker, a chromosomal coordinate range, or keywords from the GenBank description of an mRNA. The following list shows examples of queries for the human genome. See the [User's Guide](#) for more information.

Request:	Genome Browser Response:
chr7	Displays all of chromosome 7
20p13	Displays region for band p13 on chr 20
chr3:1-1000000	Displays first million bases of chr 3, counting from p arm telomere
D16S3046	Displays region around STS marker D16S3046 from the Genethon/Marshfield maps. Includes 100,000 bases on each side as well.
RH18061;RH80175	Displays region between STS markers RH18061;RH80175. Includes 100,000 bases on each side as well.
AA205474	Displays region of EST with GenBank accession AA205474 in BRCA1 cancer gene on chr 17
AC008101	Displays region of clone with GenBank accession AC008101
AF083811	Displays region of mRNA with GenBank accession number AF083811
PRNP	Displays region of genome with HUGO Gene Nomenclature Committee identifier PRNP
NM_017414	Displays the region of genome with RefSeq identifier NM_017414
NP_059110	Displays the region of genome with protein accession number NP_059110
pseudogene mRNA	Lists transcribed pseudogenes, but not cDNAs
homologous pseudogene	Lists mRNAs for pseudohomologous genes

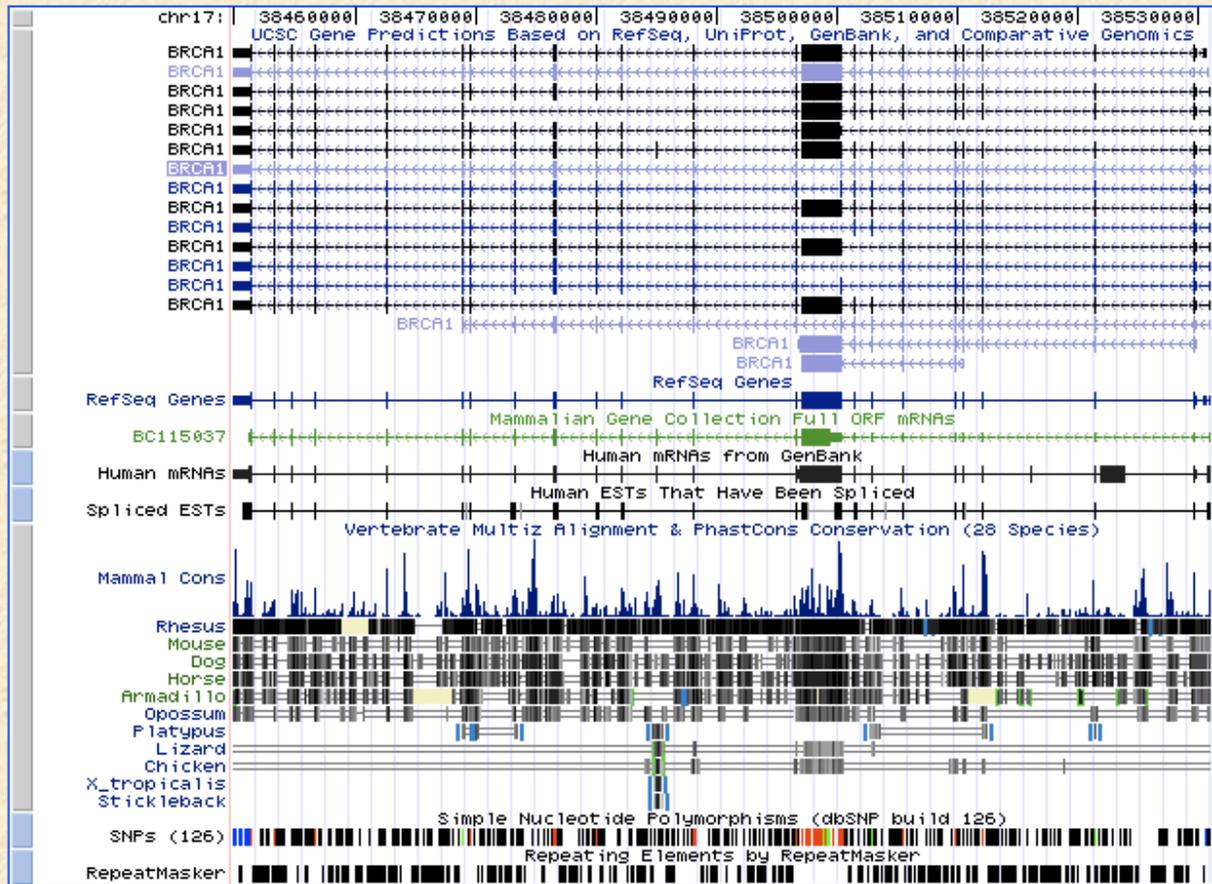
**Search for
BRCA1;
Note sample
queries**

UCSC Genome Browser on Human Mar. 2006 Assembly

move <<< << < > >> >>> zoom in 1.5x 3x 10x base zoom out 1.5x 3x 10x

position/search chr17:38,449,840-38,530,994 jump clear size 81,155 bp. configure

chr17 (q21.31) p12 p11.2 11.2 17q12 17q22 q25.3



move start

< 2.0 >

Click on a feature for details. Click on base position to zoom in around cursor. Click gray/blue bars on left for track options and descriptions.

move end

< 2.0 >

default tracks

hide all

add custom tracks

configure

refresh

Use drop-down controls below and press refresh to alter tracks displayed.

Tasks

- What genes are on either side of BRCA1 on chr 17?
- Can you figure out how to download the genomic sequence for the BRCA1 region?
- Can you figure the display to add/remove tracks that are (or are not) of interest to you?

Home Genomes Blat Tables Gene Sorter PCR **DNA** Convert Ensembl NCBI PDF/PS Help

UCSC Genome Browser on Human May 2004 Assembly

move <<< << < > >> >>> zoom in 1x 3x 10x base zoom out 1.5x 3x 10x

position/search chr17:38,423,783-38,543,782 jump clear size 120,000 bp. configure

chr17 (q21.31) p12 p11.2 q11.21 q12 22 q23.2 q25.3

Base Position 38450000 38500000 Gap Locations

UCSC Known Genes (June, 05) Based on UniProt, RefSeq, GenBank mRNA

VAT1 RND2 BRCA1 BRCA1 BRCA1 BRCA1 BRCA1 BRCA1 BRCA1 BRCA1 BC072418 U64885 BRCA1 AY354539

Click on a feature for details. Click on base position

Zoom in
Zoom out

Home Genomes Genome Browser Blat Tables Gene Sorter PCR FAQ Help

Get DNA in Window

Get DNA for

Position

Note: if you would prefer to get DNA for features of a particular track or table, try the [Table Browser](#) using the output format sequence.

Sequence Retrieval Region Options:

Add extra bases upstream (5') and extra downstream (3')

Note: if a feature is close to the beginning or end of a chromosome and upstream/downstream bases are added, they may be truncated in order to avoid extending past the edge of the chromosome.

Sequence Formatting Options:

All upper case.
 All lower case.
 Mask repeats: to lower case to N
 Reverse complement (get '-' strand sequence)

Note: The "Mask repeats" option applies only to "get DNA", not to "extended case/color options".

DNA link
Download
Sequence

collapse all Use drop-down controls below and press refresh to alter tracks displayed.
Tracks with lots of items will automatically be displayed in more compact modes. expand all

- Mapping and Sequencing Tracks refresh

Base Position dense ▾	Chromosome Band hide ▾	STS Markers hide ▾	FISH Clones hide ▾	Recomb Rate hide ▾	Map Contigs hide ▾
Assembly hide ▾	Gap hide ▾	Coverage hide ▾	BAC End Pairs hide ▾	Fosmid End Pairs hide ▾	GC Percent hide ▾
Short Match hide ▾	Restr Enzymes hide ▾				

+ Phenotype and Disease Associations refresh

- Genes and Gene Prediction Tracks refresh

UCSC Genes pack ▾	Old UCSC Genes hide ▾	Alt Events hide ▾	CCDS hide ▾	RefSeq Genes dense ▾	Other RefSeq hide ▾
MGC Genes pack ▾	ORFeome Clones hide ▾	TransMap... hide ▾	Vega Genes hide ▾	Ensembl Genes hide ▾	AceView Genes hide ▾
SIB Genes hide ▾	N-SCAN hide ▾	CONTRAST hide ▾	SGP Genes hide ▾		
Exoniphy hide ▾	Augustus hide ▾	RNA Genes hide ▾	ACEScan hide ▾		
Pos Sel Genes hide ▾					

Drop down controls
configure the data shown
in the image above

+ mRNA and EST Tracks refresh

+ Expression refresh

+ Regulation refresh

+ Comparative Genomics refresh

+ Variation and Repeats refresh

+ Pilot ENCODE Regions and Genes refresh

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

Search Ensembl

Search: for

e.g. human gene BRCA2 or rat X:100000..200000 or insulin

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.

Popular genomes [\(Log in to customize this list\)](#)

 **Human**
NCBI36

 **Mouse**
NCBIM37

 **Zebrafish**
ZFISH7

All genomes

-- Select a species --

New to Ensembl?

Did you know you can:

- [Add custom tracks](#) using our new Control Panel
- [Upload your own data](#) and save it to your Ensembl account
- [Search for a DNA or protein sequence](#) using BLAST or BLAT
- [Fetch only the data you want](#) from our public databases
- [Download data](#) in FASTA, MySQL and other formats
- [Mine Ensembl with BioMart](#) and export sequences or tables in text, html, or Excel format

Still got questions? [Try our FAQs](#)

NEW! **The new Ensembl website**
We've made some changes to our site, to make it faster and easier to use. [Find out more about what we've changed and why!](#)

Click on Human

e!Ensembl
Home > Human

Location: 6:131,533,782-131,677,240 | Gene: AKAP7 | Transcript: AKAP7-001

Search Ensembl, EBI or Sanger Institute

Jump from gene to location using tabs

Search Ensembl, EBI or Sanger Institute

Location-based displays

- Whole genome
- Chromosome summary
- Region overview
- Region in detail**
- Comparative Genomics
 - Genomic alignments (35)
 - Multi-species comp. (39)
 - Synteny (10)
- Genetic Variation
 - Resequencing (6)
 - Markers
 - Export location data

• Bookmark this page
• Configure this page
• Add custom data to page

Chromosome 6: 131,533,782-131,677,240

Assembly exceptions
chromosome 6

Assembly exceptions
COX
QBL

Click and drag the mouse to recentre the display

« Region overview | Region in detail | »

Cortigs

Ensembl/Havana gene

1.00 Mb Forward strand

131.20 Mb 131.50 Mb 131.80 Mb

EPB41L2 AKAP7 ARG1 CRSP3 ENPP3

Use the left-hand menus to navigate, export data and customise the page

About this species

- Description
 - Genome Statistics
 - Assembly and Genebuild
 - Top 40 InterPro hits
 - Top 500 InterPro hits
 - What's New
- Sample entry points
 - Karyotype
 - Location (AL032821.2)
 - Gene (BRCA2)
 - Transcript (FOXP2-203)

- Configure this page
- Add custom data to page
- Export data
- Bookmark this page

Search Ensembl Human

Search for:
 e.g. **gene BRCA2** or **AL032821.2.1.143563** or **muscular dystrophy**

Description

[Assembly and Genebuild >](#)

Assembly



This release is based on the NCBI 36 assembly of the [human genome](#) [November 2005]. The data consists of a reference assembly of the complete genome plus the Celera WGS and a number of alternative assemblies of individual haplotypic chromosomes or regions. [Full list of assemblies](#) →

The International Human Genome Sequencing Consortium have published their scientific analysis of the finished human genome.

- [Nature 431, 931 - 945 \(21 October 2004\)](#)
- [WT Sanger Institute Press Release](#)

Annotation

Since release 38 (April 2006) the gene annotation presented has been a combined Ensembl-Havana, geneset which incorporates more than 18,000 full-length protein-coding transcripts annotated by the Havana team with the Ensembl automatic gene build. The human genome sequence is now considered sufficiently stable that since 2004 the major genome browsers have come together to produce a common set of identifiers where CDS annotations of transcripts can be agreed and these identifiers are also shown.

- More information about the [CCDS project](#).

The [ENCODE](#) (ENCyclopedia Of DNA Elements) project aims to find functional elements in the human genome.

- More information about the [ENCODE resources](#) at Ensembl.



Additional manual annotation of this genome can be found in [Vega](#)

Location: 17:38,449,840-38,530,994 Gene: BRCA1

Gene: BRCA1

Gene: BRCA1 (ENSG0000012048)

Best cancer type 1 susceptibility protein (RING finger protein 53) Source: UniProtKB/Swiss-Prot P38398

Gene summary

Chromosome 17: 38,449,840-38,530,994 reverse strand.

Location

Transcripts

There are 10 transcripts in this gene: [hide transcripts](#)

BRCA1-201	ENST00000309486	ENSP00000310938	protein_coding
BRCA1-202	ENST00000346315	ENSP00000246907	protein_coding
BRCA1-203	ENST00000351666	ENSP00000338007	protein_coding
BRCA1-204	ENST00000352993	ENSP00000312236	protein_coding
BRCA1-205	ENST00000353540	ENSP00000313772	protein_coding
BRCA1-206	ENST00000354071	ENSP0000026002	protein_coding
BRCA1-207	ENST00000357654	ENSP0000030283	protein_coding
BRCA1-208	ENST00000358680	ENSP000003	
BRCA1-209	ENST0000039368	ENSP000003	
BRCA1-210	ENST00000393691	ENSP000003	

Gene Summary shows you information about the gene

click here to view genomic location

- page
- Export data
- Bookmark this page

Gene type
Prediction Method

[BRCA1](#) (HGNC (automatic))

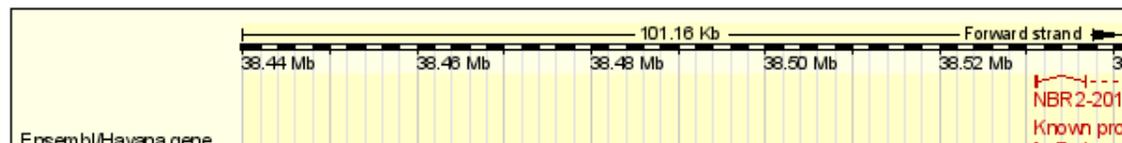
BRCC1, RNF53 [To view all Ensembl genes linked to the name [click here](#).]

This gene is a member of the Human CCDS set: [CCDS11453](#), [CCDS11454](#), [CCDS11455](#), [CCDS11456](#), [CCDS11457](#), [CCDS11458](#), [CCDS11459](#)

Known protein coding

Transcripts were annotated by the Ensembl [genebuild](#).

Transcripts



Tasks

- Explore the information presented in the Gene Summary views.
 - Can you figure out how to visualize the alternatively spliced isoforms for BRCA1?
 - What can you find out about known variations in this gene?
- Using the Location Based Displays, can you figure out how to download the genomic sequence for the BRCA1 region?

- Gene: BRCA1
- Gene summary
 - Splice variants (10)**
 - Supporting evidence
 - Sequence
 - External references (15)
 - Regulation
 - Comparative Genomics
 - Genomic alignments (3)
 - Gene Tree
 - Gene Tree (text)
 - Gene Tree (alignment)
 - Orthologues (28)
 - Paralogues (0)
 - Protein families (1)
 - Genetic Variation
 - Variation Table
 - Variation Image
 - External Data
 - ID History
 - Gene history

Gene: BRCA1 (ENSG0000012048)

Breast cancer type 1 susceptibility protein (RING finger protein 53) [Source: UniProtKB/Swiss-Prot P](#)

Location [chr17:41,273,410-41,273,530,994 reverse strand.](#)

Transcripts There are 10 transcripts in this gene: [hide transcripts](#)

BRCA1-201	ENST00000309486	ENSP00000310938	
BRCA1-202	ENST00000346315	ENSP00000246907	
BRCA1-203	ENST00000351666	ENSP00000338007	
BRCA1-204	ENST00000352993	ENSP00000312236	
BRCA1-205	ENST00000353540	ENSP00000013772	
BRCA1-206	ENST00000354071	ENSP00000326002	
BRCA1-207	ENST00000357654	ENSP00000350283	protein_coding
BRCA1-208	ENST00000393680	ENSP00000377288	protein_coding
BRCA1-209	ENST00000393683	ENSP00000377288	protein_coding
BRCA1-210	ENST00000393691	ENSP00000377294	protein_coding

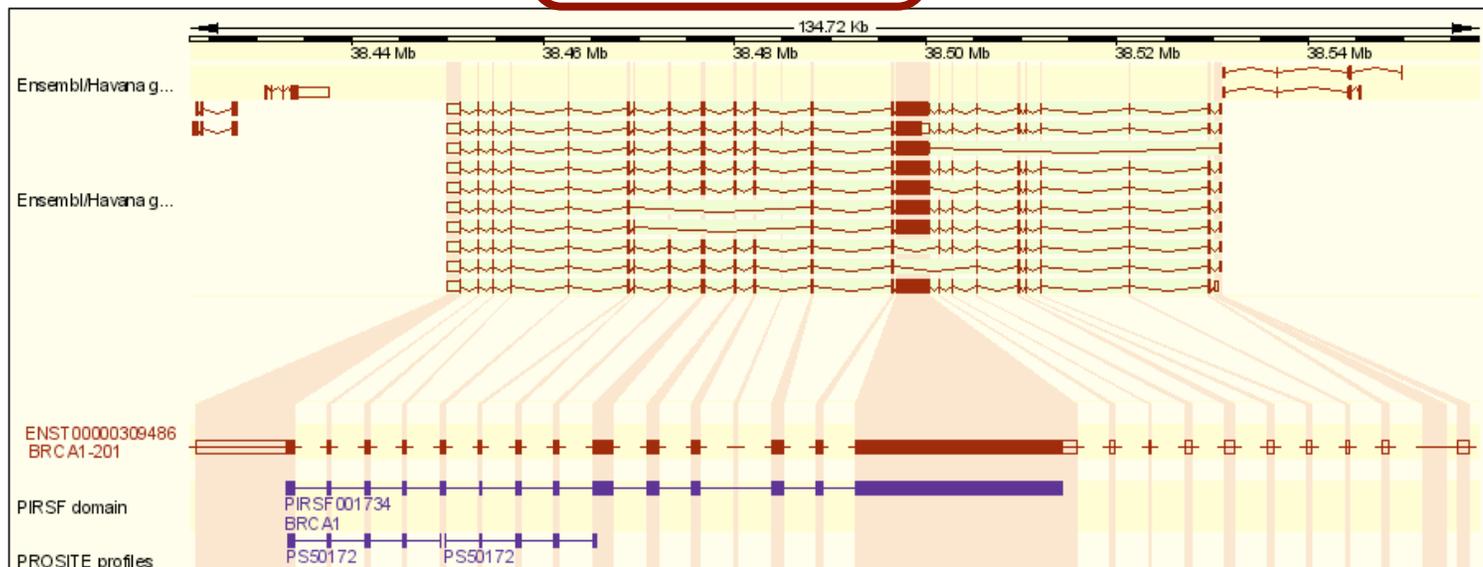
The Splice Variants page shows you information about the transcripts

- Configure this page
- Add custom data to page
- Export data
- Bookmark this page

[← Gene summary](#)

Splice variants [help](#)

[Supporting evidence ▶](#)



Gene: BRCA1

- Gene summary
- Splice variants (10)
- Supporting evidence
- Sequence
- External references (15)
- Regulation
- Comparative Genomics
 - Genomic alignments (3)
 - Gene Tree
 - Gene Tree (text)
 - Gene Tree (alignment)
 - Orthologues (28)
 - Paralogues (0)
 - Protein families (1)
- Genetic Variation
 - Variation Table
 - Variation Image**
- External Data
- ID History
- Gene history

- [Configure this page](#)
- [Add custom data to page](#)
- [Export data](#)
- [Bookmark this page](#)

Gene: BRCA1 (ENSG0000012048)

Breast cancer type 1 susceptibility protein (RING finger protein 53) [Source: UniProtKB/Swiss-Prot P38398](#)

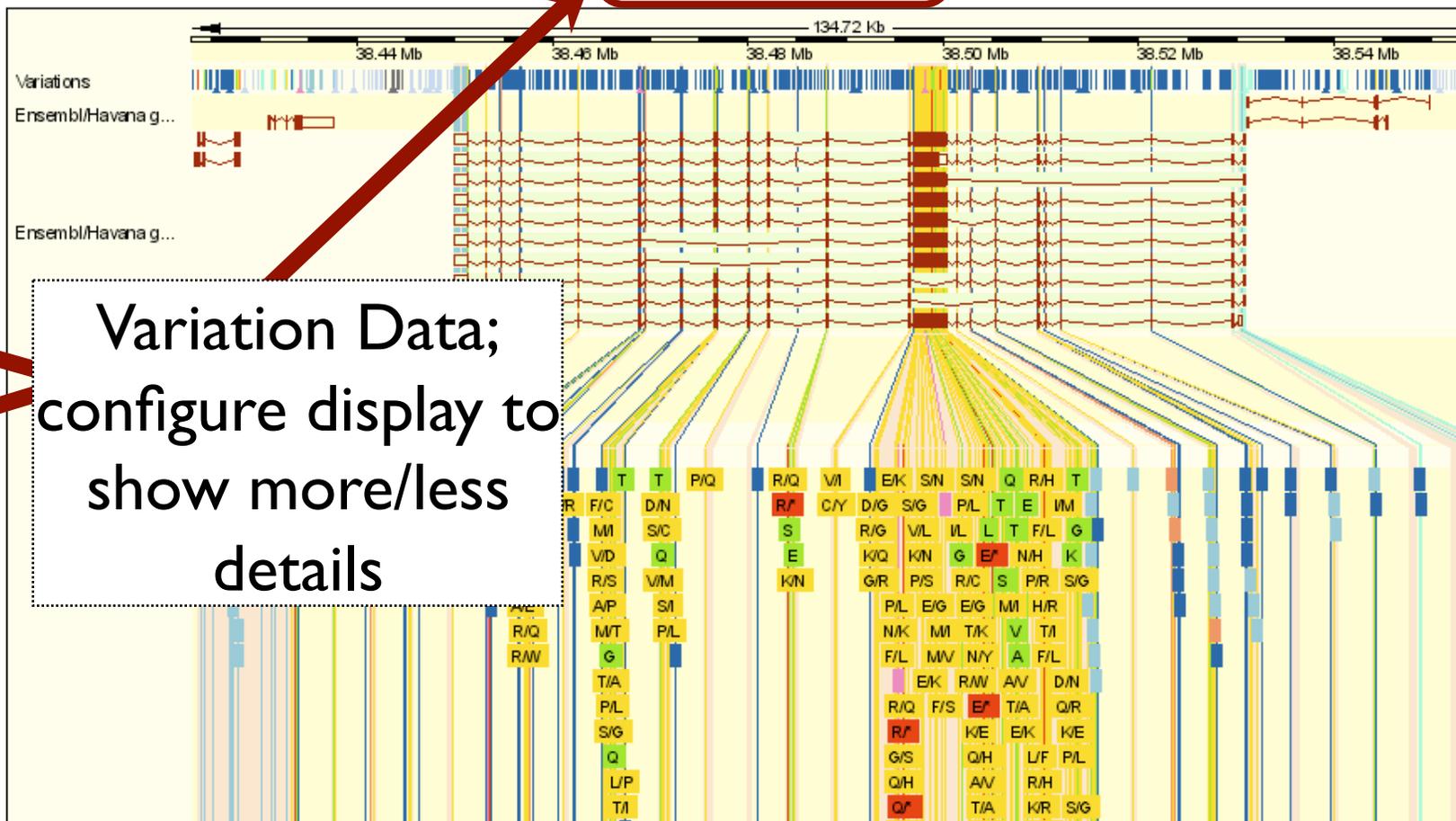
Location [Chromosome 17: 38,449,840-38,530,994 reverse strand.](#)

Transcripts There are 10 transcripts in this gene: [show transcripts](#)

« Variation Table

Variation Image [help](#)

External Data

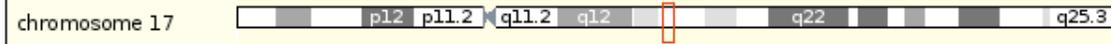


Location-based displays

- Whole genome
- Chromosome summary
- Region overview
- Region in detail**
- Comparative Genomics
 - Genomic alignments
 - Synteny (10)
- Genetic Variation
 - Resequencing (6)
 - Linkage Data
- Markers

- Configure this page
- Add custom data to page
- Export data
- Bookmark this page

Chromosome 17: 38,449,840-38,530,994

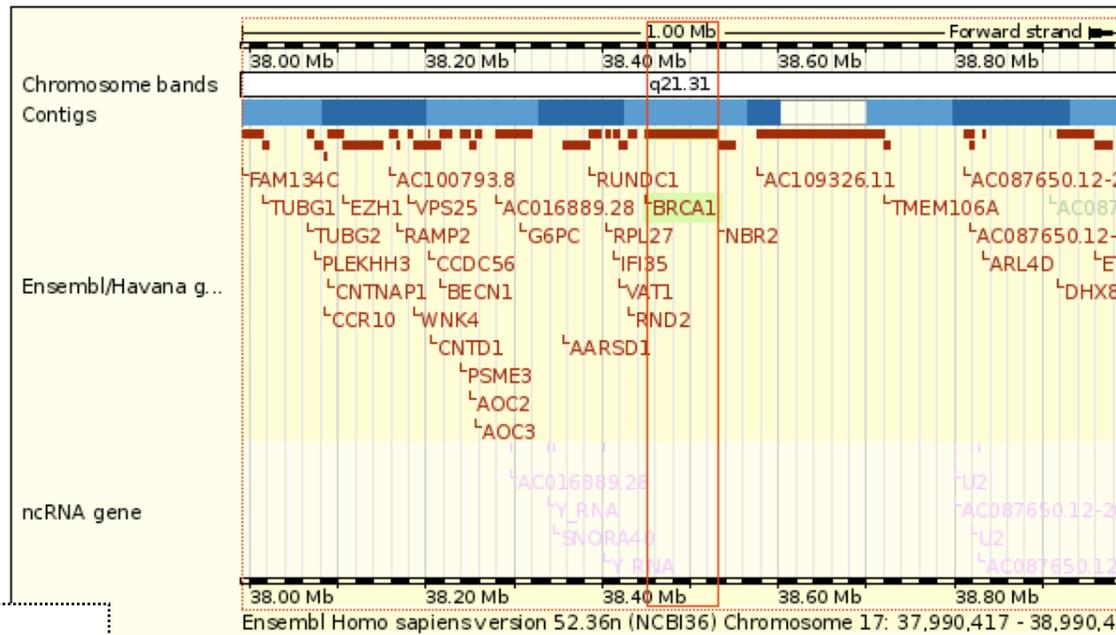


Export image

< Region overview

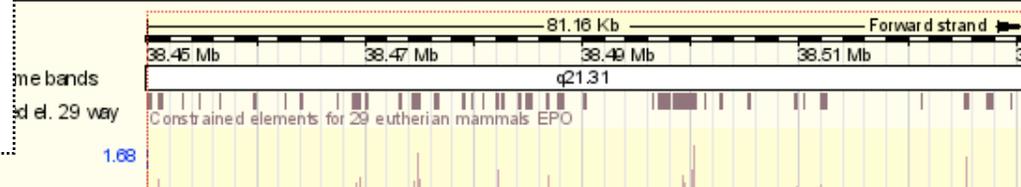
Region in detail help

Genomic alignments >



Export image

Chromosome: 17 : 38449840 - 38530994 Go>



Export options available on all pages

On your own....

Follow the next few slides to explore the genomic region for BRCA1 using the NCBI MapViewer system.

http://www.ncbi.nlm.nih.gov/mapview/

NCBI Home GenBank BLAST

Map Viewer Home > Help

The Map Viewer provides a wide variety of genome mapping and sequencing data. [More..](#)

Search

Search:

for:

Tools Legend

- Search or Browse the Genome
- BLAST
- Clone Finder
- Genome Resources page

Scientific name	Common name	Build	Tools
<i>Homo sapiens</i>	human	Build 36.3	
		Build 35.1	
<i>Macaca mulatta</i>	rhesus macaque	Build 1.1	
<i>Pan troglodytes</i>	chimpanzee	Build 2.1	

Scientific name	Common name	Build	Tools
<i>Mus musculus</i>	laboratory mouse	Build 37.1	
		Build 36.1	
<i>Rattus norvegicus</i>	rat	RGSC v3.4	

Two builds of human; Note many genomes available

News

Annotation update released for human genome build 36 Mar 23, 2010

An annotation update for the human genome (NCBI Build 36.3) ... [more](#)

[Show all](#)

Related Resources

- NCBI Home
- NCBI Web Search
- NCBI Site map
- Genome Biology
- Taxonomy
- Entrez (Global Query)
- BLAST
- Map Viewer FTP

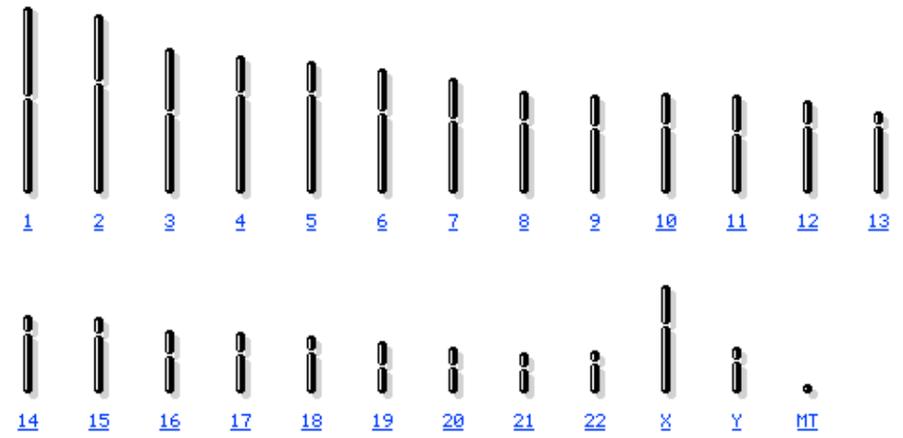
Small Genomes

- Bacteria

[Search for](#) [on chromosome\(s\)](#)

BLAST search the human genome

Homo sapiens (human) genome view
[Build 36.2 statistics](#) [Switch to previous build](#)

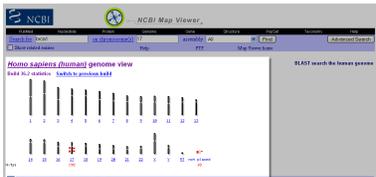


Lineage: [Eukaryota](#); [Metazoa](#); [Chordata](#); [Craniata](#); [Vertebrata](#); [Euteleostomi](#); [Mammalia](#); [Eutheria](#); [Euarchontoglires](#); [Primates](#); [Haplorrhini](#); [Catarrhini](#); [Hominidae](#); [Homo](#); [Homo sapiens](#)

September 2006: NCBI released an annotation update for the human genome (NCBI Build 36.2); this update does not change the genome assembly. The previous version of the genome assembly, [NCBI Build 35.1](#), can still be accessed for Map Viewer display and for BLAST. For additional information about changes, statistics, and the status of the CCDS project please refer to:

- [Release Notes](#)
- [Statistics](#)
- [CCDS Project](#)

The NCBI Map Viewer provides graphical displays of features on the human genome sequence assembly as well as

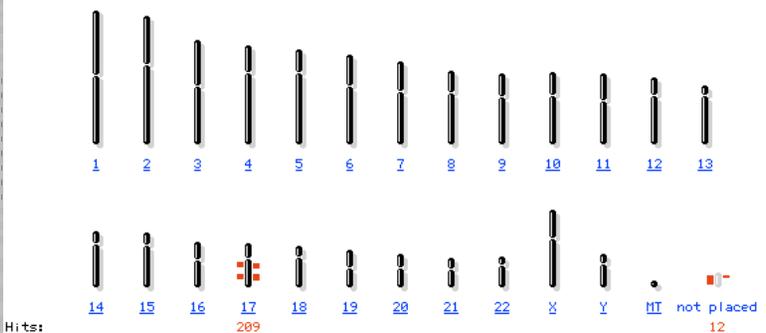


PubMed Nucleotide Protein Genome Gene Structure PopSet Taxonomy Help

Search for on chromosome(s) assembly Find

Homo sapiens (human) genome view
 Build 36.2 statistics [Switch to previous build](#)

[BLAST search the human genome](#)



Search results for query "BRCA1": 221 hits
 Hits shown: 1 - 100

Chr	Assembly	Match	Map element	Type	Maps
17	reference	all matches			
		Neighbor of Brcal1 gene 1	Rn.94975	Rn_EST_C1	Rn Un G
		BRCA1 interacting protein C-terminal helicase 1	Mm.186143	Mm_EST_C1	Mm Un G
		Neighbor of Brcal1 gene 1	Mm.784	Mm_EST_C1	Mm Un G
		Neighbor of BRCA1 gene 2 (9 hits)	Hs.559259	Hs_EST_C1	Hs Un G
		Neighbor of BRCA1 gene 1 (2 hits)	Hs.546264	Hs_EST_C1	Hs Un G
		BRCA1 interacting protein C-terminal helicase 1	Hs.532799	Hs_EST_C1	Hs Un G
		Neighbor of BRCA1 gene 1	Hs.373818	Hs_EST_C1	Hs Un G
		Neighbor of BRCA1 gene 1 (2 hits)	Hs.277721	Hs_EST_C1	Hs Un G
		BRCA1 interacting protein C-terminal helicase 1	Gga.17801	Gga_EST_C1	Gga Un G

Quick Filter

Gene

Transcript

all

RefSeq

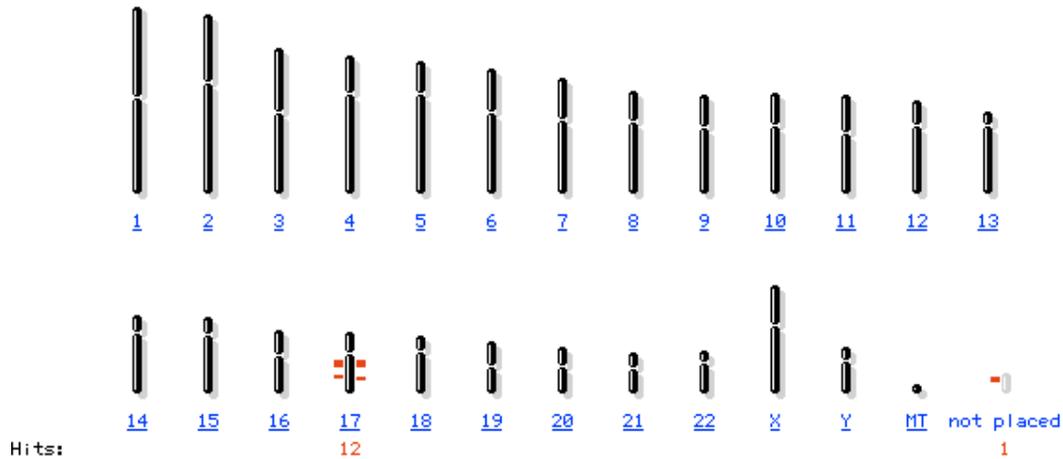
STS

Unigene

Quick Filter
 ✓ Gene

Homo sapiens (human) genome view

Build 36.2 statistics [Switch to previous build](#)



Search results for query "BRCA1 AND gene[obj_type]": 13 hits

Chr	Assembly	Match	Map element	Type	Maps
17	reference	all matches			
		similar to neighbor of BRCA1 gene 1	LOC728560	Gene	Genes cyto Genes seq
		BRCA1P1 : like BRCA1	BRCA1P1	Gene	Genes cyto Genes seq
		BRCA1 -interacting protein 1	BRIP1	Gene	Genes cyto Genes seq
		neighbor of BRCA1 gene 2	NBR2	Gene	Genes cyto Genes seq
		neighbor of BRCA1 gene 1	NBR1	Gene	Genes cyto Genes seq
		BRCA1 : breast cancer 1, early onset	BRCA1	Gene	Genes cyto Genes seq
		BRCA1 : ENSG00000012048	BRCA1	GENE	ensGenes
17	Celera	all matches			
		BRCA1P1 : like BRCA1	BRCA1P1	GENE	Genes seq
		BRCA1 -interacting protein 1	BRIP1	GENE	Genes seq
		neighbor of BRCA1 gene 2	NBR2	GENE	Genes seq
		neighbor of BRCA1 gene 1	NBR1	GENE	Genes seq
		BRCA1 : breast cancer 1, early onset	BRCA1	GENE	Genes seq
17: not placed	reference	similar to neighbor of BRCA1 gene 1	LOC727732	GENE	Genes seq

Two tasks

- Can you figure out how to LinkOut to the OMIM and/or Homologene entries for BRCA1?
- Can you figure out how to download the genomic sequence for the BRCA1 region?

Human genome overview page (Build 36.2)
 Human genome overview page (Build 35.1)
[Map Viewer Home](#)
 Map Viewer Help
 Human Maps Help
 FTP
 Data As Table View
Maps & Options
 Compress Map
 Region Shown:
 38,389K
 38,592K
 out
 zoom
 in
 You are here:
 Ideogram
 17p13
 17p12
 17p11.2
 17q11.1
 17q11.2
 17q12
 17q21
 17q22
 17q23
 17q24
 17q25
 default
 master

Master Map: Genes On Sequence

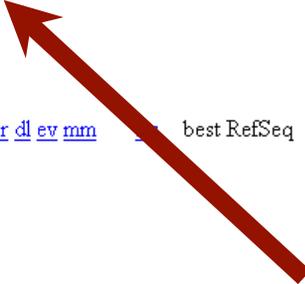
[Summary of Maps](#)

[Maps & Options](#)

Region Displayed: 38,389K-38,592K bp

[Download/View Sequence/Evidence](#)

Hs UniG	Genes_seq	Symbol	Links	E	Cyto	Description
Hs.317403 Unknown Unknown Unknown Unknown Hs.634952 Unknown Unknown Hs.175437 Unknown Unknown Unknown Unknown Unknown Hs.514199 Hs.632285 Hs.632258 Hs.514196 Unknown Hs.603111		RUNDC1 +	HGNC sv pr dl ev mm hm sts	best RefSeq	17q21.31	RUN domain containing 1
		RPL27 +	OMIM HGNC sv pr dl ev mm hm sts	best RefSeq	17q21.1-q21.2	ribosomal protein L27
		IFI35 +	OMIM HGNC sv pr dl ev mm hm sts	best RefSeq	17q21	interferon-induced protein 35
		VAT1 +	OMIM HGNC sv pr dl ev mm hm sts	best RefSeq	17q21	vesicle amine transport protein 1 homolog (T cell)
		RND2 +	OMIM HGNC sv pr dl ev mm hm sts	best RefSeq	17q21	Rho family GTPase 2
Hs.194143 Unknown Unknown		RPL21P4 +	HGNC sv dl ev mm	best RefSeq	17q21	ribosomal protein L21 pseudogene 4
Unknown Unknown		BRCA1 +	OMIM HGNC sv pr dl ev mm hm sts	best RefSeq	17q21	breast cancer 1, early onset
Unknown Hs.373818		NBR2 +	HGNC sv pr dl ev mm	best RefSeq		
Unknown Hs.601045 Hs.601912 Unknown		BRCA1P1 +	HGNC sv dl ev mm	best RefSeq		
Unknown Unknown Unknown Unknown Unknown Unknown Hs.626603		NBR1 +	OMIM HGNC sv pr dl ev mm hm sts	best RefSeq		
Hs.277721 Hs.546264						



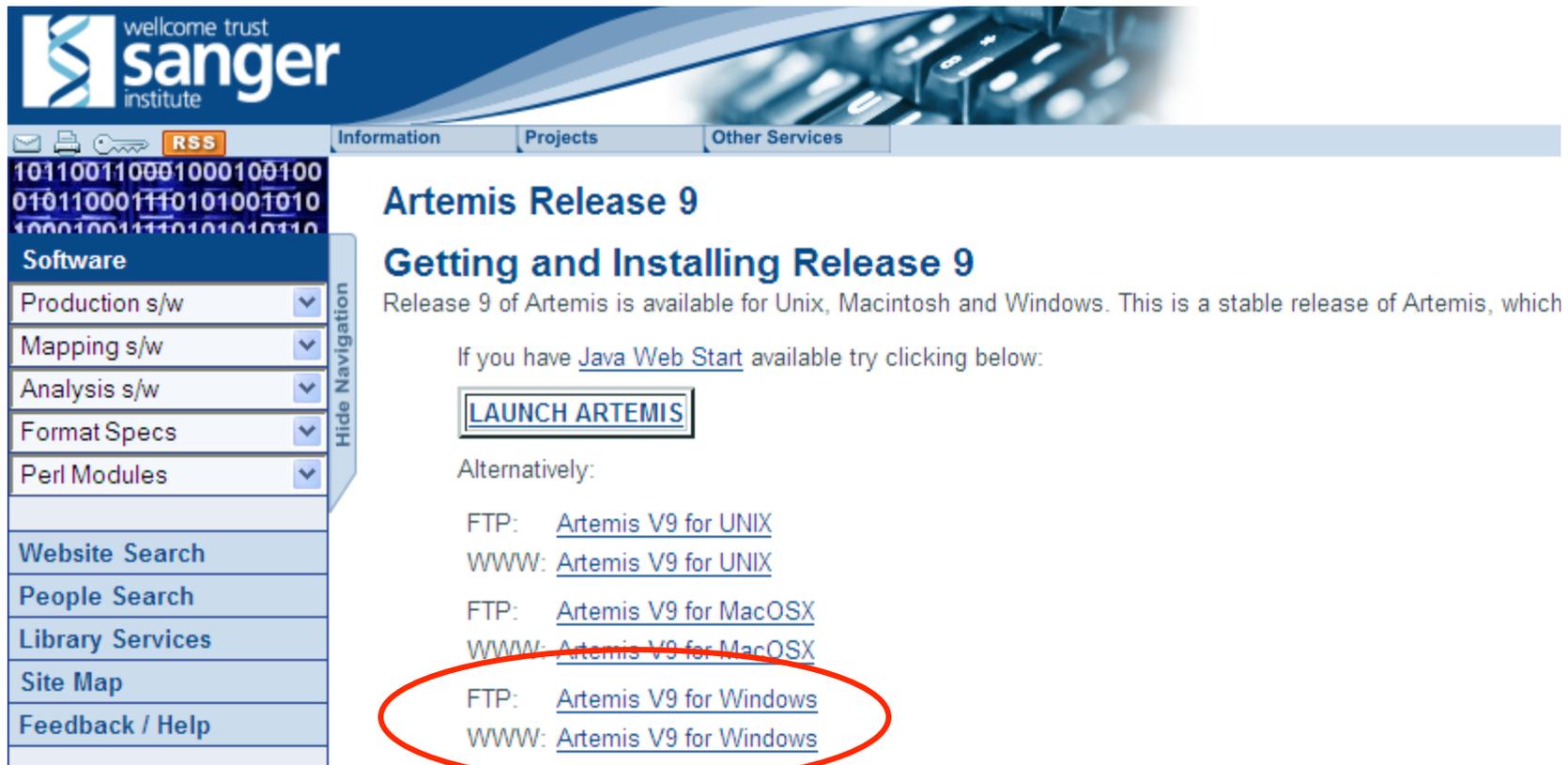
LinkOut
 OMIM = disease
 sv = sequence view
 pr = protein record
 dl = download
 hm = Homologene

Artemis genome browser for prokaryotic genomes

Download Artemis to Desktop

<http://www.sanger.ac.uk/Software/Artemis/v9/>

Google: “artemis v9”



The screenshot shows the Sanger Institute website interface. The header features the Sanger logo and navigation tabs for 'Information', 'Projects', and 'Other Services'. A left-hand navigation menu lists various software categories like 'Production s/w', 'Mapping s/w', and 'Analysis s/w'. The main content area is titled 'Artemis Release 9' and 'Getting and Installing Release 9'. It provides instructions on how to launch Artemis, including a prominent 'LAUNCH ARTEMIS' button. Below this, there are links for downloading Artemis V9 for UNIX, Mac OSX, and Windows. The Windows download links are circled in red.

wellcome trust
sanger
institute

Information Projects Other Services

101100110001000100100
010110001110101001010
100010011110101010110

Software

Production s/w

Mapping s/w

Analysis s/w

Format Specs

Perl Modules

Hide Navigation

Website Search

People Search

Library Services

Site Map

Feedback / Help

Artemis Release 9

Getting and Installing Release 9

Release 9 of Artemis is available for Unix, Macintosh and Windows. This is a stable release of Artemis, which

If you have [Java Web Start](#) available try clicking below:

LAUNCH ARTEMIS

Alternatively:

FTP: [Artemis V9 for UNIX](#)
WWW: [Artemis V9 for UNIX](#)

FTP: [Artemis V9 for MacOSX](#)
WWW: [Artemis V9 for MacOSX](#)

FTP: [Artemis V9 for Windows](#)
WWW: [Artemis V9 for Windows](#)

Rhodobacter sphaeroides

NCBI ENTREZ Genome Project connection information discovery My NCBI Welcome pjaschke. [Sign Out](#)

All Databases PubMed Nucleotide Protein Genome Structure PMC Taxonomy Books

Search Genome Project for Go Clear

Limits Preview/Index History Clipboard Details

Display Overview Show 20 Send to

All: 1 Environmental: 0 Eukaryotes: 0 Prokaryotes: 1

Genome Project > Rhodobacter sphaeroides > **Rhodobacter sphaeroides 2.4.1 project at DOE Joint Genome Institute** Links

Resource Links

NCBI Resources

- BLAST genome
- FTP
- TaxPlot

Organism data in GenBank

- Genomic
- mRNA
- Protein

Sequencing Centers

- DOE Joint Genome Institute

Related Resources

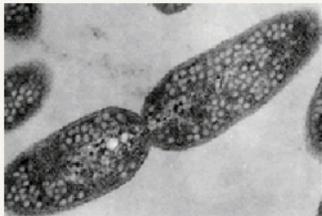
- R. sphaeroides Genome

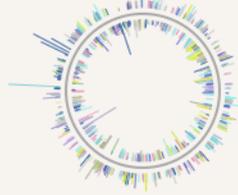
Other Databases

- GOLD

Metabolically diverse phototrophic bacterium. [Project data](#)

Lineage: *Bacteria*; *Proteobacteria*; *Alphaproteobacteria*; *Rhodobacterales*; *Rhodobacteraceae*; *Rhodobacter*; *Rhodobacter sphaeroides 2.4.1*

 Photo: DOE Joint Genome Institute

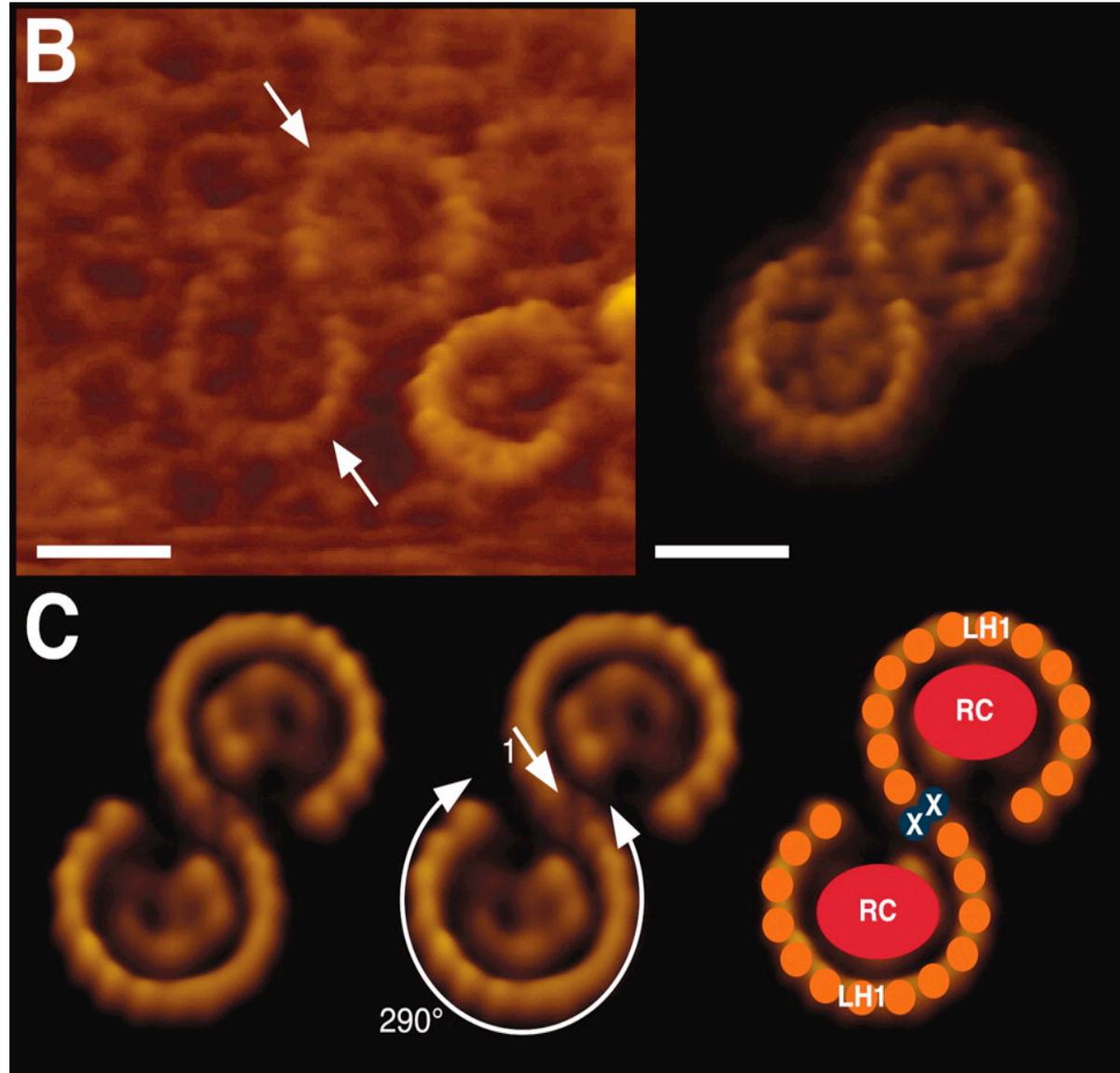
943016 nt 

Genome Projects

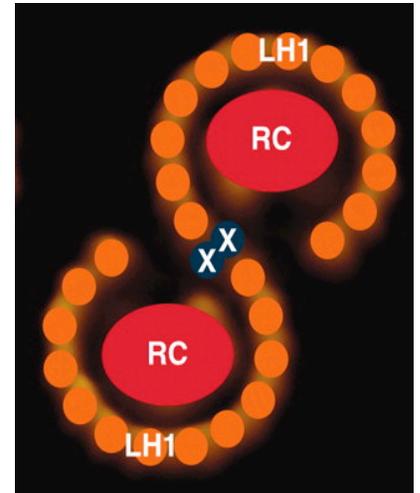
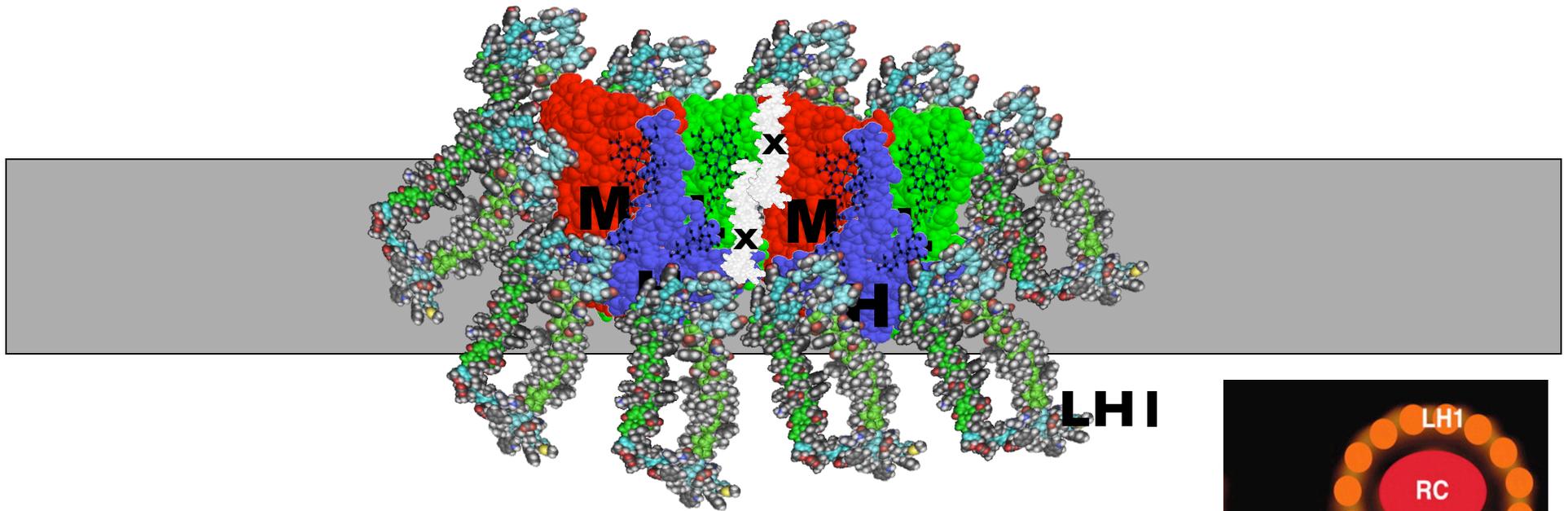
Genome sequencing:

- ▶ **Rhodobacter sphaeroides 2.4.1** (Project ID: 56) at [DOE Joint Genome Institute](#) [Complete]
Expand to show the list of Centers
- [Rhodobacter sphaeroides ATCC 17025](#) at US DOE Joint Genome Institute [Complete]
[DOE Joint Genome Institute](#)
- [Rhodobacter sphaeroides ATCC 17029](#) at US DOE Joint Genome Institute [Complete]
[DOE Joint Genome Institute](#)
- [Rhodobacter sphaeroides KD131](#) at GenoTech corp. [In progress]
[GenoTech corp.](#)

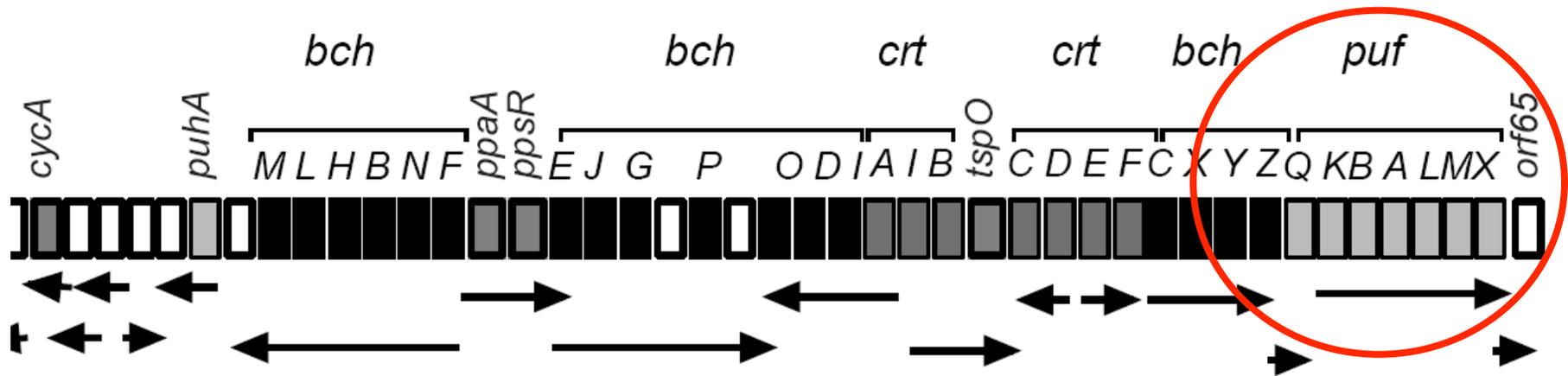
The photosynthetic co-complex



Co-complex Structure



The photosynthetic gene cluster



Chromosome I
3.11 Mbp

Download and Extract Sequence File for Chromosome I

1. Go to www.rhodobacter.org
2. Click 'Finished Genome + GenBank files'

The screenshot shows the website for *Rhodobacter sphaeroides*. The page title is "Welcome to the *Rhodobacter sphaeroides* genome project". The site is hosted by The University of Texas - Houston Health Science Center. The page is updated as of 11th May 2008. A navigation menu on the left includes links for DNA, Chro, Plasm, and Plasmid. The link "Finished Genome + Genbank Files" is circled in red. The main content area features a colorful heatmap of a bacterial cell and a circular diagram of Chromosome I. A dialog box with "OK" and "Cancel" buttons is visible in the bottom right corner.

Rhodobacter sphaeroides
Site updated: 11th May 2008

DNA

- [Contact us](#)
- [The Samuel Kaplan Lab](#)
- [About *Rhodobacter sphaeroides*](#)

Chro

- [Growing *R. sphaeroides*](#)
- [The Genome Project](#)
- [Finished Genome + Genbank Files](#)
- [DOE/JGI/MSU site](#)

Plasm

- [Draft Analysis Oak Ridge Natl. Lab](#)
- [RspCyc New!](#)

Plasm

- [Photosynthesis Genes](#)

Plasmid pRS241c

Plasmid pRS241d

Plasmid pRS241c

Plasmid pRS241d

Welcome to the *Rhodobacter sphaeroides* genome project

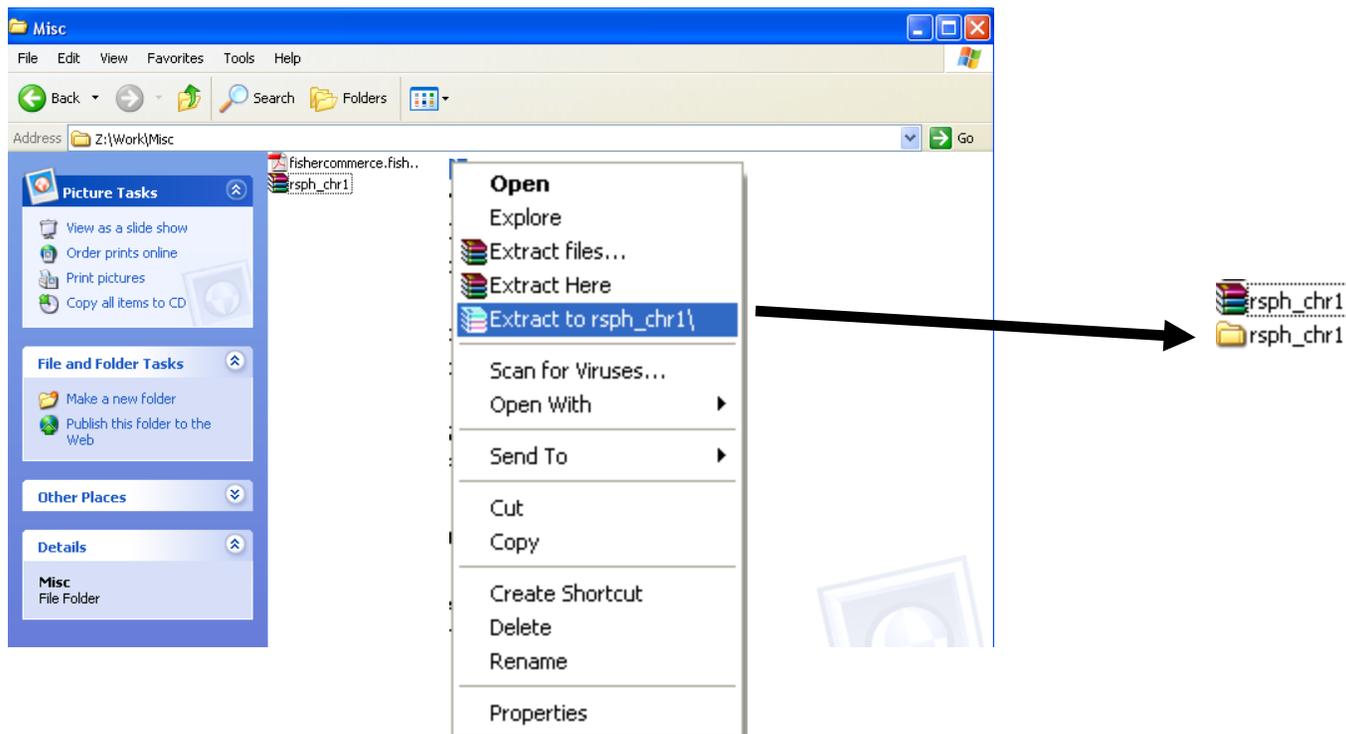
The University of Texas - Houston Health Science Center

Chromosome I

OK Cancel

Download and Extract Sequence File for Chromosome I

3. Find 'rsph_chr1.zip' file.
4. Right click on file and then choose **'Extract to rsph_chr1\'**

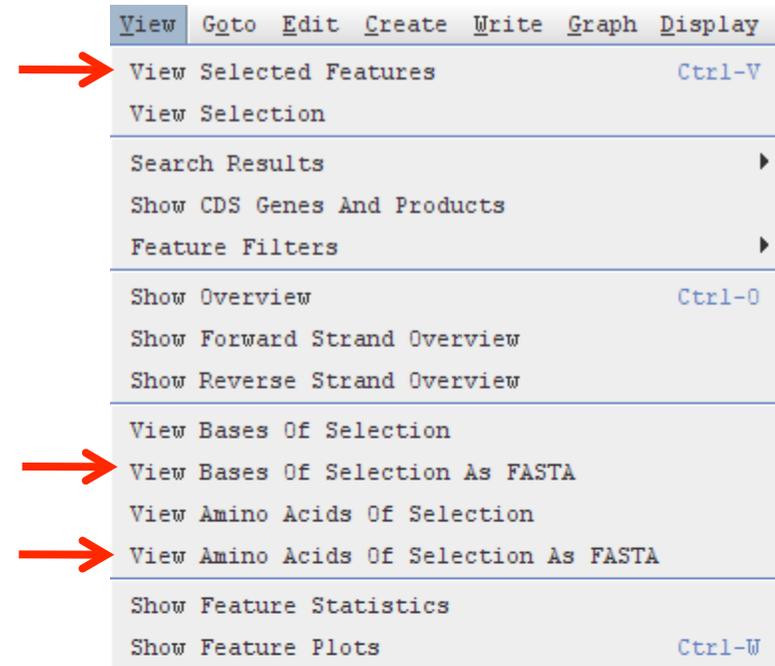
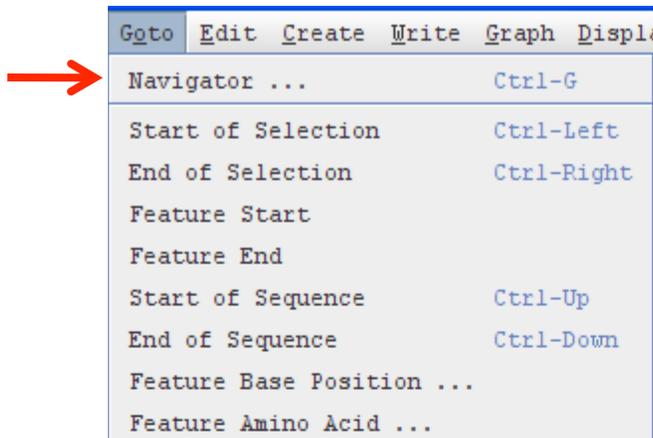
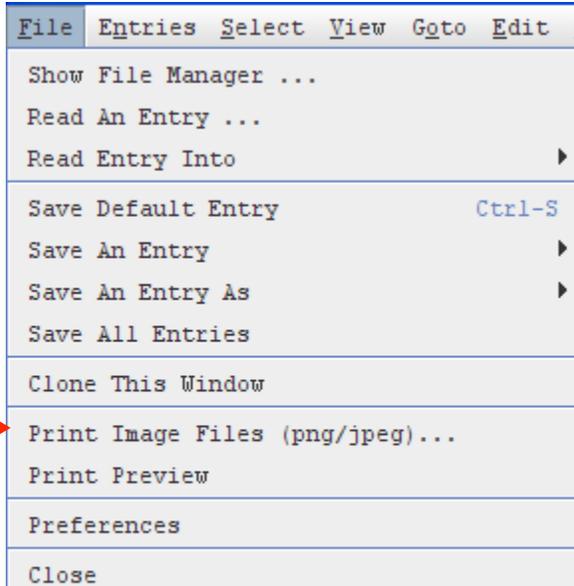


Start Artemis and Load Chromosome I File



Menu Bar

File Entries Select View Goto Edit Create Write Graph Display



Top Pane: Overview

3 Forward strand reading frames

3 Reverse strand reading frames

File Entries Select
Nothing selected
Entry: esph_chrl.art

RNA_42 RNA_43 RNA_3

800 1600 2400 3200 4000 4800 5600 6400 8800 9600 10400 11200

RSP1426 RSP1427 RSP1428

Gene

Zoom

Move window along DNA

'Special feature'

Stop codons

The image shows a screenshot of a genome browser interface. At the top, there is a menu bar with 'File', 'Entries', and 'Select'. Below it, a status bar indicates 'Nothing selected' and 'Entry: esph_chrl.art'. The main area displays a DNA sequence with three forward reading frames (top) and three reverse reading frames (bottom). A scale at the bottom indicates positions from 800 to 11200. Several genes are annotated: RNA_42, RNA_43, RNA_3, RSP1426, RSP1427, and RSP1428. A red bar highlights a region between RSP1427 and RSP1428, labeled 'Gene'. A 'Zoom' button is located on the right side. A 'Move window along DNA' button is at the bottom left. Two callout boxes, 'Special feature' and 'Stop codons', point to specific regions in the sequence. A bracket on the left indicates the '3 Forward strand reading frames', and another bracket at the bottom indicates the '3 Reverse strand reading frames'.

Middle Pane: Sequence Detail

The image shows a screenshot of a sequence viewer interface. It displays two DNA strands: the forward strand (5' to 3') and the reverse strand (3' to 5'). Each strand is accompanied by its 3-frame translation. The forward strand translation shows amino acids: P S G F R G G A P A N G S A W V G A, L R G S G A E P Q R T A A R G + G, and A F G V Q G R S P S E R Q R V G R G. The reverse strand translation shows: R R P E P A S G W R V A A R P Y P G, K P T * P R L G L S R C R T P L P, and G E P N L P P A G A F P L A H T P A. A 'Genome Coordinates' box with an arrow points to a scale below the strands, with markers at 7800, 7820, and 7840. A scroll bar is visible at the bottom of the sequence viewer, with an arrow pointing to it from the text 'Scroll & Zoom'.

Forward Strand
3 Frame Translation

Forward Strand (5'→3')

Genome Coordinates

Reverse Strand (3'←5')

Reverse Strand
3 Frame Translation

Scroll & Zoom

Four Tasks

- Find the *pufM* and *pufL* genes of the reaction center (part of the *puf* operon)
- How many nucleotides overlap between the coding sequence of these genes?
- Are the genes in the same frame?
- Export a picture of the *puf* operon (*pufQBALMX*)

Bottom Pane: Feature List

CDS	1976931	1978313		COG0665: Glycine/D-amino acid oxidases (DadA)
CDS	1978340	1980286	c	Experimental evidence in Rhodobacter capsulatu
CDS	1980460	1980708	c	Citation: McGlynn P, Hunter CN, Jones MR. (199
CDS	1980721	1981647	c	pfam: Photosynthetic reaction center protein,
CDS	1981640	1982488	c	pfam: Photosynthetic reaction center protein,
CDS	1982612	1982788	c	pfam: Antenna complex alpha/beta subunit,
CDS	1982802	1982951	c	pfam: Antenna complex, alpha/beta subunit
CDS	1982953	1983015	c	Citation: Gong L, Kaplan S. (1996) Microbiolog
CDS	1983082	1983315	c	Citation: Bauer CE, Moxre BI. (1988) Proc Natl

Links

- UCSC Genome Browser

<http://genome.cse.ucsc.edu/>

- Ensembl Genome Browser

<http://www.ensembl.org/index.html>

- NCBI MapViewer

<http://www.ncbi.nlm.nih.gov/mapview/index.html>

- Artemis

<http://www.sanger.ac.uk/Software/Artemis/>