

Ensembl Homepage

uswest.ensembl.org/index.html

Apps | colon cancer | Chicken Salad with B | Aquaman - Injustice | Lect. 8. Intro. to mic | Gallery

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

Search all species...

Search: All species for [] Go
e.g. BRCA2 or rat 5:62797383-63627669 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.

Popular genomes

 **Human**
GRCh38

 **Mouse**
GRCm38.p3

 **Zebrafish**
Zv9

★ [Log in to customize this list](#)

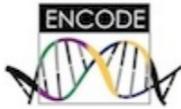
All genomes

-- Select a species --

[View full list of all Ensembl species](#)

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

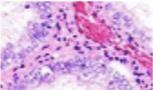
ENCODE data in Ensembl



Variant Effect Predictor



Gene expression in different tissues



Find SNPs and other variants for my gene

```
GTGTATACATTC  
CTTAAAGTCTT  
CTTCTAATTCT  
GATGATTTTCC
```

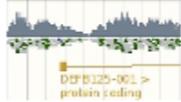
Retrieve gene sequence

```
GCCTGACTTCGGGTGG:  
GGGCTTGTGGGGGAGC  
GGGCTCTGCTGGGCT  
AGGGACAGATTTGTGA  
CACCTCTGGAGCGGTT  
CCCACTCCAGCGTGGCG
```

Compare genes across species



Use my own data in Ensembl



Learn about a disease or phenotype



What's New in Release 78 (December 2014)

- [Mouse assembly and annotation update to GRCm38.p3](#)
- [VEP: quick preview of results](#)
- [TSL, APPRIS and GENCODE basic annotations now available in Biomart](#)

[Full details](#) | [All web updates, by release](#) | [More news on our blog](#)

Latest blog posts

- 03 Dec 2014: [Ensembl 78 has been released!](#)
- 28 Nov 2014: [Retirement of archive 65](#)
- 17 Nov 2014: [Ensembl Genomes release 24 is out!](#)

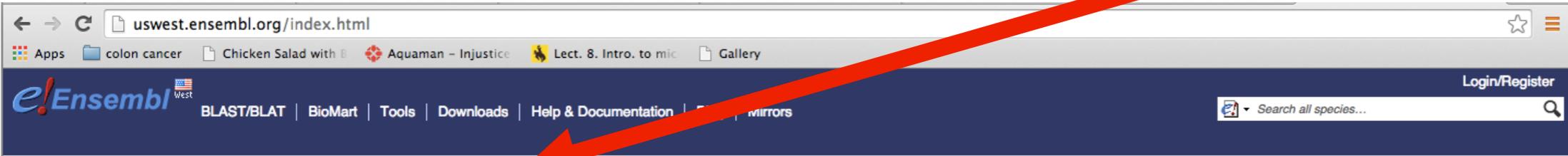
[Go to Ensembl blog](#) →

Tweets

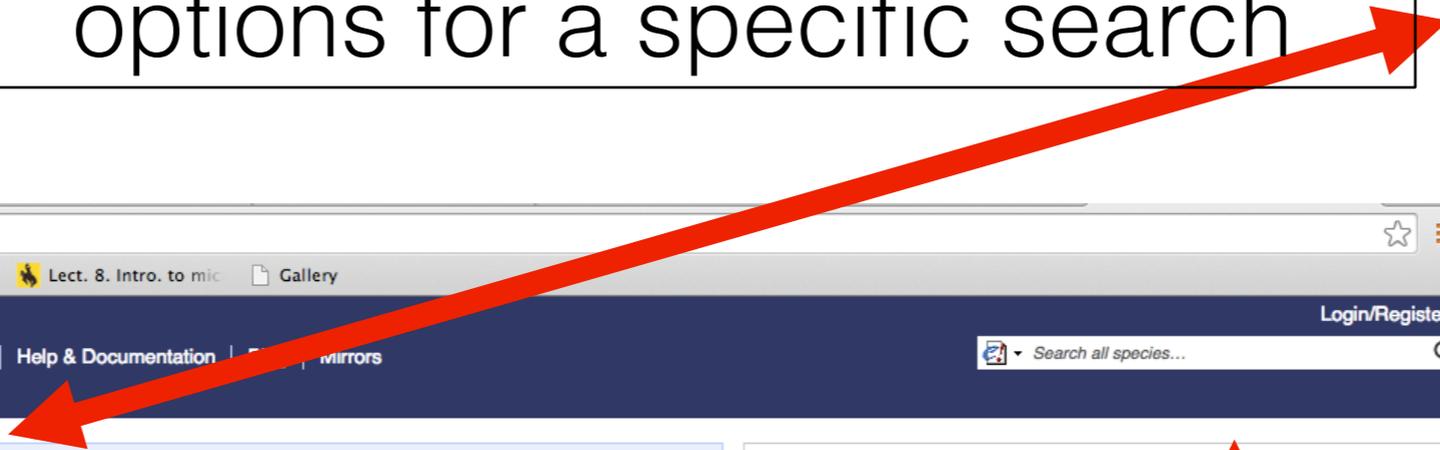
 **Ensembl** @ensembl 2h
Searching 'Christmas' on Ensembl finds one thing: Zebra finch F9 (Christmas factor), so it's our #Geneoftheweek buff.ly/1CYbz0y
Expand

 **Ensembl** @ensembl 4h
Latest paper from UCSC @GenomeBrowser, including use of Ensembl gene and regulation annotation #CitedEnsembl buff.ly/1CB3q1R
Expand

drop down menu has more options for a specific search



- ✓ All species
- Help and Documentation
-
- Favourite species
- Human
- Mouse
- Zebrafish
-
- Alpaca
- Amazon molly
- Anole lizard
- Armadillo
- Bushbaby
- C.intestinalis
- C.savignyi
- Caenorhabditis elegans
- Cat
- Cave fish
- Chicken
- Chimpanzee
- Chinese softshell turtle
- Cod
- Coelacanth
- Cow
- Dog
- Dolphin
- Duck
- Elephant
- Ferret
- Flycatcher
- Fruitfly
- Fugu
- Gibbon
- Gorilla
- Guinea Pig
- Hedgehog
- Horse
- Human
- Hyrax
- Kangaroo rat
- Lamprey
- Lesser hedgehog tenrec
- Macaque
- Marmoset
- Medaka
- Megabat
- Microbat
- Mouse
- Mouse Lemur
- Olive baboon



Search: for

e.g. BRCA2 or rat 5:62797383-63627669 or coronary heart disease

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Browse/download genome of specific species

Species Homepage: e.g Human

You can search for a gene, region, probeset or disease. in any species' home page

The screenshot shows the Ensembl Human species homepage. At the top, there is a navigation bar with links for BLAST/BLAT, BioMart, Tools, Downloads, Help & Documentation, Blog, and Mirrors. A search bar is located in the top right corner. The main header features the Ensembl logo and the text "Human Homo sapiens". A red arrow points from the text above to the search bar. The search bar contains the text "APC g" and a "Go" button. A dropdown menu is open below the search bar, showing search suggestions for "apc", "apc13p", "apca", "apcdd1", "apcl", "apcs", "apcdd1,mgc4294", and "apcdd1,stx16". Below the search bar, there are several sections: "Genome assembly" with links for more information, downloading DNA sequences, converting data, and displaying data; "Other assemblies" with a link for GRCh37 Full Feb 2014; "Comparative genomics" with links for more information and downloading alignments; "What's New in Human release 78" with a list of updates; "Gene annotation" with links for more information, downloading genes, and updating old IDs; and "Variation" with links for more information and downloading all variants. Each section includes a small icon and a brief description of the content. The search dropdown menu also includes a "Direct Links" section with a table of links to specific genes and rRNAs.

Gene	Human Gene ENSG00000134982
APC	Human Gene ENSG00000134982
5 8S rRNA	Cod Gene ENSGMOG00000020631
5 8S rRNA	Cod Gene ENSGMOG00000021622
5S rRNA	Cod Gene ENSGMOG00000020614
5S rRNA	Cod Gene ENSGMOG00000020619
5S rRNA	Cod Gene ENSGMOG00000020620

List of results



The screenshot shows the Ensembl genome browser interface. At the top, there is a navigation bar with links for BLAST/BLAT, BioMart, Tools, Downloads, Help & Documentation, Blog, and Mirrors. A search bar is located in the top right corner. Below the navigation bar, the current selection is set to 'Human (GRCh38)'. The search results are displayed in a table format, with the first result being 'APC (Human Gene)'. The left sidebar contains various filters and options, including 'Current selection', 'Restrict category to', 'Per page', and 'Layout'. The 'Best gene match' section shows a detailed view of the 'APC' gene, including its protein-coding nature and a genomic map. Below this, there is a 'Suggestions' section with a grid of related gene symbols.

Category	Count
Gene	62
Transcript	93
Variation	7027
Phenotype	1
Somatic Mutation	2214
GeneTree	3
GenomicAlignment	10
Clones & Regions	1
ProbeFeature	149
Protein Domain	1

Per page: 10 25 50 100

Layout: Standard Table

Best gene match: APC (Human Gene). Protein coding gene: adenomatous polyposis coli. HGNC Symbol; Acc:HGNC:583.

Suggestions: aapc, apca, apcl, apcs, aphe, apoc, capc, sapc, vapc, aac, abc, ac, acc, adc, aec, agc, alc, amc, ap, apa, apb, apd, ape, aph, api, apl, apm, apo, app, apr, aps, apt, apy, arc, asc, atc, apacd, apg4c, aplcc, apoc1, apoc2, apoc3, apoc4, snapc, agps, ahch, ahcp, ahcy.

Best match in detail

You can filter search results using categories on the left hand side.

Gene Summary Page

Ensembl ID: stable even if updated

ENSG = Gene
ENST = Transcript
ENSP = protein
ENSE = exon
ENSR = regulatory feature
ENSFM = protein families

Gene-based displays

- Summary
- Splice variants (10)
- Transcript comparison
- Supporting evidence
- Alt. alleles
- Sequence
 - Secondary Structure
- External references
- Regulation
- Comparative Genomics
 - Genomic alignments
 - Gene tree
 - Gene gain/loss tree
 - Orthologues (72)
 - Paralogues (2)
 - Ensembl protein families (3)
- Phenotype
- Genetic Variation
 - Variation table
 - Variation image
 - Structural variation
- External data
 - Personal annotation
- ID History
 - Gene history

Configure this page

Add your data

Export data

Bookmark this page

Share this page

Gene: APC ENSG00000134982

Description adenomatous polyposis coli [Source:HGNC Symbol;Acc:HGNC:583]

Synonyms DP2, DP2.5, DP3, PPP1R46

Location [Chromosome 5: 112,707,498-112,846,239](#) forward strand.

INSDC coordinates chromosome:GRCh38:CM000667.2:112707498:112846239:1

Transcripts This gene has 10 transcripts (splice variants) [Show transcript table](#)

Summary ⓘ

Name [APC](#) (HGNC Symbol)

CCDS This gene is a member of the Human CCDS set: [CCDS4107](#)

UniprotKB This gene has proteins that correspond to the following Uniprot identifiers: [P25054](#)

RefSeq Overlapping RefSeq Gene ID [324](#) matches and has similar biotype of protein_coding

LRG [LRG_130](#) provides a stable genomic reference framework for describing sequence variations for this gene

Ensembl version ENSG00000134982.14

GRCh37 assembly This gene maps to [112,043,195-112,181,936](#) in GRCh37 coordinates. View this locus in the GRCh37 archive: [ENSG00000134982](#)

Gene type Known protein coding

Prediction Method Annotation for this gene includes both automatic annotation from Ensembl and [Havana](#) manual curation, see [article](#).

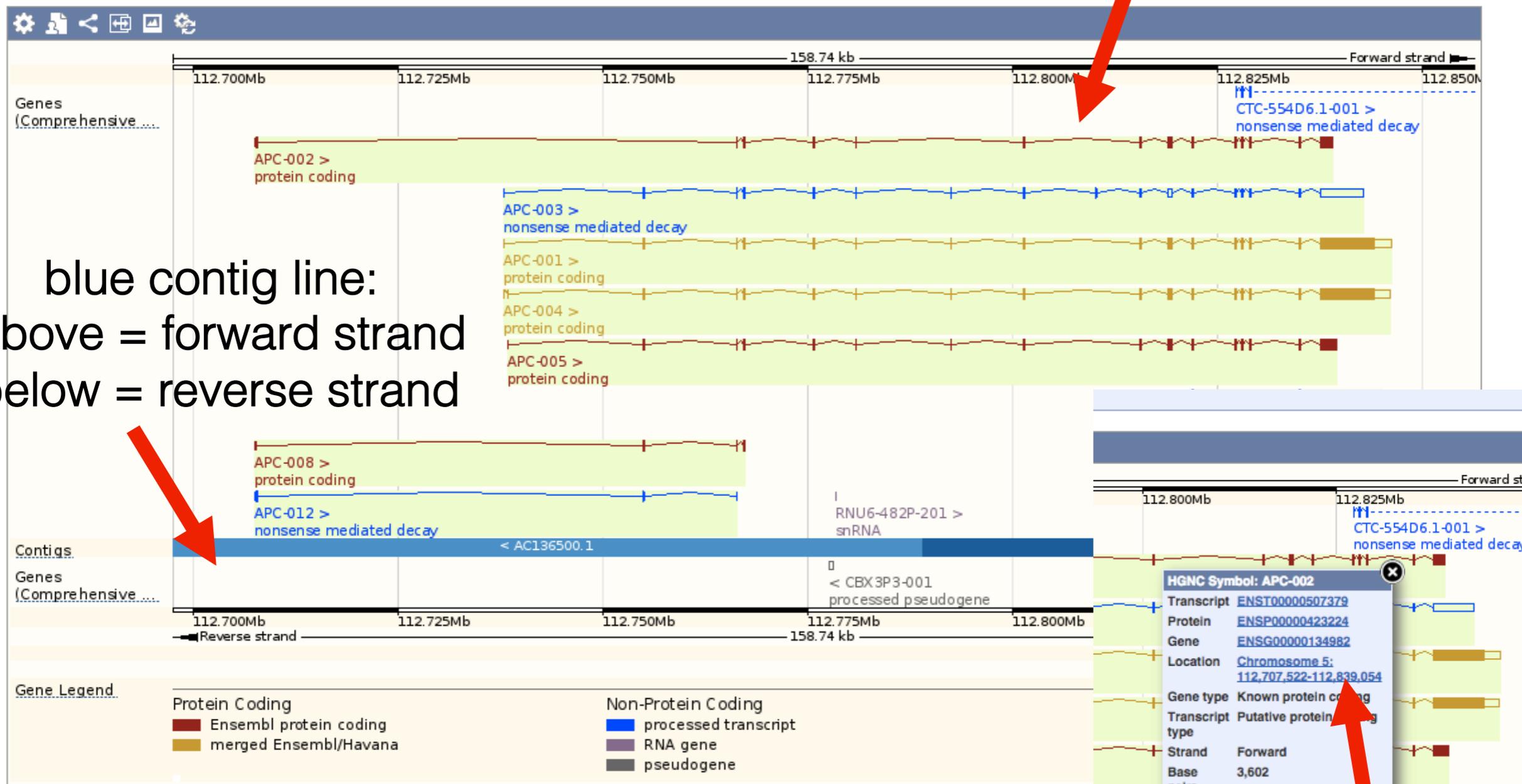
Alternative genes This gene corresponds to the following database identifiers:
Havana gene: [OTTHUMG00000128806](#)

[Go to Region in Detail](#) for more tracks and navigation options (e.g. zooming)

Use to customize what you see

Gene Summary Page (scroll down)

Hover to see ID and more information, click to go to specific page with more details



blue contig line:
Above = forward strand
below = reverse strand

Boxes are exons & lines are introns. Filled boxes are coding sequences, unfilled represent UTRs (non coding sequence)

click on location for sequence

Gene Location

Location of this gene

Chromosome view:
click on location to zoom in and out

The screenshot displays the Ensembl genome browser interface for the APC gene. The top navigation bar shows the human genome (GRCh38) and the specific location on Chromosome 5: 112,706,746-112,838,278. The main view is divided into several tracks: 'Chromosome 5: 112,706,746-112,838,278' showing the chromosome map, 'Region in detail' showing a 1.00 Mb zoomed-in view of the gene structure with various transcripts and exons, and 'Human cDNAs (R...)' showing the full-length cDNA sequence. A sidebar on the left provides navigation options like 'Whole genome', 'Chromosome summary', and 'Region overview'. At the bottom, there are search fields for 'Location' and 'Gene', and a zoom slider. Red arrows highlight key features: one points to the 'Export the sequence' button in the sidebar, another points to the 'Region in detail' track, a third points to the 'Location of this gene' label at the top, and a fourth points to the zoom slider at the bottom right.

Export the sequence

shows the region where the gene is in detail shows the location of gene

zoom in and out of the 'region in detail'

Ensembl BLAST/BLAT search

Search Tickets are saved, so you can revisit your results, to see old tickets, scroll down.

The screenshot shows the Ensembl BLAST/BLAT search page. At the top, the Ensembl logo and navigation menu are visible. The main content area is titled "BLAST/BLAT search" and includes a "Create new ticket:" section. Below this, there is a "Sequence data:" section with a text input field for "Maximum of 30 sequences (type in plain text, FASTA or sequence ID)", an "Or upload sequence file" button, and radio buttons for "DNA" (selected) and "Protein". The "Search against:" section features a dropdown menu currently set to "Human (Homo sapiens)", with a search input field below it. Further down, there are options for "DNA database" (set to "Genomic sequence") and "Protein database" (set to "Proteins (GENCODE/Ensembl)"). At the bottom, there is a "Method:" dropdown set to "BLAT" and an optional "Description" field.

Add either DNA or Protein sequence, Automatically updates to FASTA format

You can change the species to search in a different Genome for homology

BLAST/BLAT search results

Web Tools

- Web Tools
 - BLAST/BLAT
 - Ticket
 - BLAT against Mouse (Genomic sequence)**
 - Variant Effect Predictor
 - Assembly Converter

Configure this page

Add your data

Export data

Bookmark this page

Share this page

Results for BLAT against Mouse (Genomic sequence)

Job details

Job name: BLAT against Mouse (Genomic sequence)

Species: Mouse (Mus musculus)

Search type: BLAT

Download results file

click to see sequence that found a match

customize what you see

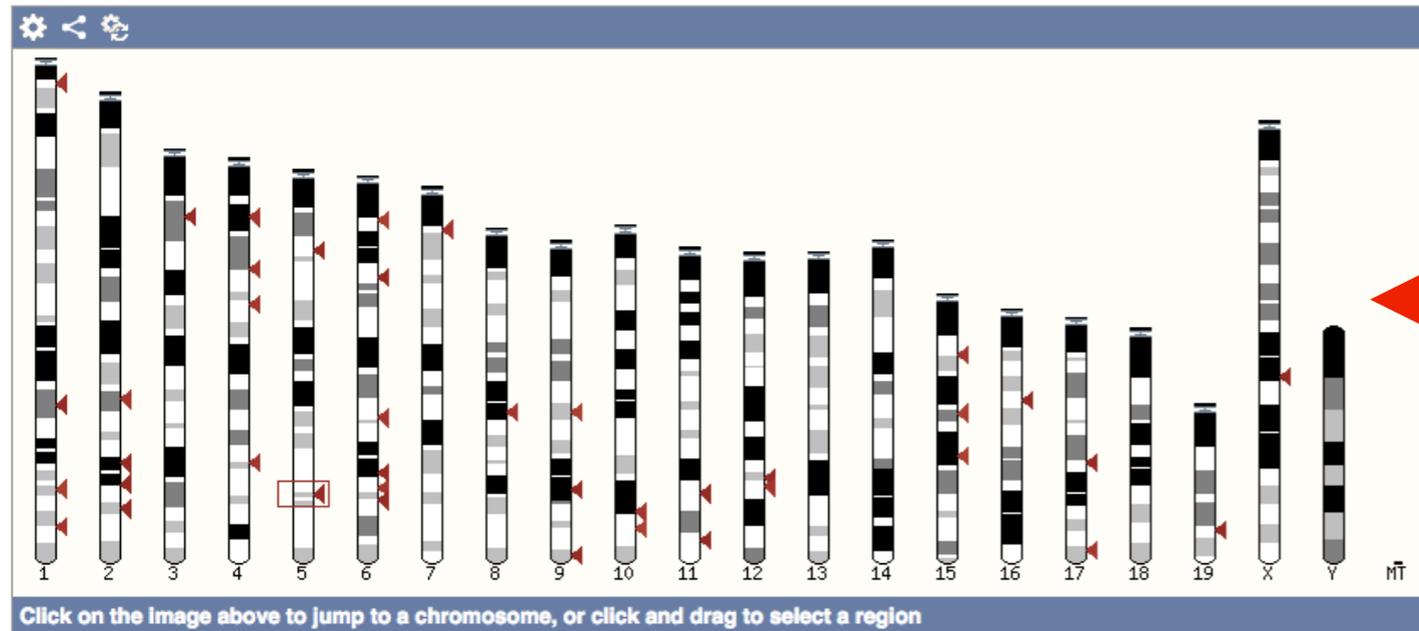
download text file of this page

Results table

Show All entries Show/hide columns Filter

Genomic Location	Orientation	Query name	Query start	Query end	Query ori	Length	Score	E-val	%ID
4:22889421-22889531 [Sequence]	Forward	[Sequence]	603	709	Forward	113	173.0	3.1e-43	89.38 [Alignment]
5:125240915-125240976 [Sequence]	Forward	[Sequence]	554	615	Forward	62	119.0	5.2e-27	100.00 [Alignment]
1:134238486-134238540 [Sequence]	Forward	[Sequence]	607	661	Forward	55	101.0	9.7e-22	96.36 [Alignment]
1:9858829-9858878 [Sequence]	Forward	[Sequence]	315	364	Forward	50	78.0	1.4e-14	88.00 [Alignment]
2:143640763-143640808 [Sequence]	Forward	[Sequence]	674	720	Forward	47	77.0	1.9e-14	95.74 [Alignment]
15:62661589-62661642 [Sequence]	Forward	[Sequence]	721	788	Forward	68	76.0	5.5e-14	76.47 [Alignment]
2:118795489-118795532 [Sequence]	Forward	[Sequence]	632	675	Forward	44	75.0	6.0e-14	90.91 [Alignment]
4:56497665-56497706 [Sequence]	Forward	[Sequence]	746	787	Forward	42	75.0	9.6e-14	92.86 [Alignment]
1:166837108-166837164 [Sequence]	Forward	[Sequence]	608	656	Forward	57	75.0	1.0e-13	80.70 [Alignment]
				781	Forward	55	72.0	5.8e-13	87.27 [Alignment]
				287	Forward	39	70.0	2.4e-12	94.87 [Alignment]
				345	Forward	35	66.0	2.9e-11	97.14 [Alignment]
				807	Forward	47	64.0	1.8e-10	82.98 [Alignment]
				733	Forward	41	63.0	4.1e-10	92.68 [Alignment]

HSP distribution on genome:



Scroll down to see results location on genome

click on Alignment to see alignment of that particular result