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# Fishing for Genes in the UCSC Browser

## A Tutorial

Rachel Harte <[hartera@soe.ucsc.edu](mailto:hartera@soe.ucsc.edu)>

Mark Diekhans <[markd@soe.ucsc.edu](mailto:markd@soe.ucsc.edu)>

University of California, Santa Cruz, CA

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### Abstract

This tutorial is aimed at the biologist who is interested in exploring protein-coding genes using the *University of California Santa Cruz (UCSC) Genome Browser*. It is geared towards those who have little or no experience using the *UCSC Genome Browser* and for more advanced users who are not familiar with many of the gene-oriented browser features. Using the example of a human gene, *PPP1R1B*, the reader is guided through a step-by-step process for finding and visualizing protein-coding genes in the context of the human genome and a wide variety of genomic data. The user is shown how to use the *UCSC Genome Browser* to locate a *Mammalian Gene Collection (MGC)* clone of the gene and how to order the clone from suppliers.

# 1 Accessing the UCSC Genome Browser

The *UCSC Genome Bioinformatics* website consists of a suite of tools for the viewing and mining of genomic data. The *UCSC Genome Browser* [16, 18] facilitates the viewing of clones from the *Mammalian Gene Collection (MGC)*[35, 37] in the context of other genome annotations. Various types of annotations such as *MGC Genes* are visualized in **tracks** which are graphical representations of data displayed in a genomic context on the *Genome Browser*. To view these annotation tracks, first go to the home page at <http://genome.ucsc.edu> (Figure 1).

The **blue** menu bars at the top and the left side of the *Genome Browser* home page both include following links to various tools (Figure 1):

- **Genomes** on the top **blue** bar or the *Genome Browser* link on the side **blue** menu bar allow entry to the **Gateway** page for the *Genome Browser*. From here, users may select the genomes that they wish to browse. An additional route of entry is via a **Photo Gateway** page in the *UCSC genomewiki* with photographs of each species whose genome is represented in the *UCSC Genome Browser*.
- **Blat** is a fast alignment tool[20] which allows the user to align DNA or protein sequences to the genome assemblies.
- **Tables** on the top **blue** bar or **Table Browser**[17] on the side **blue** bar link to an interface allowing the retrieval of data associated with tracks from the databases underlying the *Genome Browser*. Data added as additional tracks created by the user (**Custom Tracks**) may also be queried with this tool.
- **Gene Sorter** is a tool that displays a sorted table of genes that are related by some metric selected by the user e.g. similar expression patterns, protein homology or proximity in the genome[19].
- **Genome Graphs** on the side **blue** bar is a tool to facilitate viewing of whole genome datasets such as genome-wide SNP association studies, linkage studies and homozygosity mapping. Instructions are in the **Genome Graphs User's Guide**
- **PCR** on the top **blue** bar or **In Silico PCR** on the side **blue** bar is a fast method of searching for a pair of PCR primer sequences in a genome assembly.
- **VisiGene** is a virtual microscope for viewing *in situ* hybridization images.
- **Proteome** on the top **blue** bar and **Proteome Browser** on the side **blue** bar lead to the gateway of a tool for viewing proteins and their properties[14]. Both graphical images and links to external websites provide a rich source of protein information.
- **Utilities** on the side **blue** bar allows access to various tools to remove non-sequence-related characters from DNA or protein, for creating a gif image for a phylogenetic tree and a tool which converts genome coordinates between assemblies (**liftOver**).
- **Downloads** on the side **blue** bar allows bulk download of data including dumps from the *Genome Browser* databases.
- **Custom Tracks** is a powerful tool allowing users to add their own data for viewing and querying within the context of a genome and its associated annotation data. A **User's Guide** provides help for creating **Custom Tracks**.

## 2 Searching for a gene

Let's suppose that a user wishes to study the human *PPP1R1B* (protein phosphatase 1, regulatory (inhibitor) subunit 1B) gene, which is expressed in the brain. The protein encoded by this gene is also known as DARPP32. Its phosphorylation status is regulated by dopaminergic and glutamatergic (NMDA) receptors. Once

**UCSC Genome Bioinformatics**

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

**Gateway**

Genome Browser

ENCODE

Blat

Table Browser

Gene Sorter

In Silico PCR

Genome Graphs

Galaxy

VisiGene

Proteome Browser

Utilities

Downloads

Release Log

Custom Tracks

Archaeal Genomes

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### 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.

**26 June 2008 - New Worm Genome Available**

Along with the set of worm browser updates that we're currently releasing, we've added a new nematode to the collection: *Caenorhabditis japonica*. This genome assembly (UCSC version caeJap1, Mar. 2008) corresponds to the v. 3.0.2 assembly produced by the Genome Sequencing Center at the Washington University St. Louis (WUSTL) School of Medicine.

Bulk downloads of the sequence and annotation data are available via the Genome Browser [FTP server](#) or [Downloads](#) page. Please review the WUSTL [data use policy](#) for usage restrictions and citation information.

We'd like to thank WUSTL for providing the sequence data for this assembly. The UCSC caeJap1 browser was produced by Hiram Clawson, Ann Zweig, and Donna Karolchik. See the Genome Browser [Credits](#) page for a detailed list of the organizations and individuals who contributed to this release.

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**20 June 2008 - Two Worm Updates Released:** We've updated our browsers for the *C. remanei* and *C. brenneri* nematode genomes. [Read more.](#)

**10 June 2008 - Lamprey Browser Released:** We have released a Genome Browser for the Mar. 2007 assembly of the lamprey genome, *Petromyzon marinus*. [Read more.](#)

**10 June 2008 - Lancelet Genome Available in Browser:** The Mar.

Figure 1: UCSC Genome Browser home page. On this page, there is an introduction to the web site and postings of news of training seminars and recent additions such as new assemblies and software features. The blue menu bars at the top and left side of the page allow access to the Genome Browser for genome assemblies of a variety of organisms, data mining tools and help pages.

phosphorylated, *PPP1R1B*, is a potent protein phosphatase-1 inhibitor. To visualize this gene in the *UCSC Genome Browser* in the context of various genomic annotations, the user may take the following steps:

1. To get started, clicking on either the **Genomes** or **Genome Browser** link will take the user to the *Gateway* page where the clade, genome and assembly of interest may be selected from pull-down lists of multiple organisms and genome assemblies.
2. Below this area, there is a section describing the selected assembly which also indicates that the default assembly (at the time of writing) is known as hg18 on the *UCSC Genome Browser* website. This assembly is also known as NCBI Build 36.1. This section also contains a list of **Sample position queries**. These are a selection of queries that may be entered into the **position or search term** box adjacent to the genome and assembly controls. Examples include gene name, mRNA or EST accession and descriptive term. Such terms could be used if the gene is not a known gene with an official gene symbol. For the gene in question, the alternate name, *DARPP32*, could be used or a descriptive term such as **NMDA** which is less selective and returns a larger number of results.
3. Enter the gene symbol, *PPP1R1B* into the **position or search term** box (Figure 2).  
Clicking on the **submit** button directs the user to a page displaying the search results. For each track where there are data items containing *PPP1R1B* as their identifier or in their description, results are presented as links to the genomic positions of these items. (Figure 3).
4. Next, click on one of the links, e.g., the *RefSeq Genes PPP1R1B at chr17:35036705-*

**35046403** link. This will take you to the *PPP1R1B* locus in the human genome. Note that there are two RefSeq splice variants listed for this locus and this one is the longer transcript variant.

### 3 *Genome Browser* annotation tracks

The *Genome Browser* displays certain annotation tracks by default in the main *Browser* image. The current default display (Figure 4) shows a number of gene tracks:

- *UCSC Gene* predictions[15, 18]
- *BLAT* alignments of sequences from GenBank[2]
- *BLAT* alignments of full-length ORF *MGC Genes*.

Other visible tracks in this default display are:

- *Vertebrate Conservation*[29]
- Simple Nucleotide Polymorphisms from NCBI Build 128 of dbSNP[33] (*SNPs (128)*) track[38]
- Location of repeats found by *Repeat-Masker*

Gene structure is shown in these tracks with filled blocks representing exons; thick blocks are in the coding sequence (CDS) and thin blocks represent untranslated regions (UTRs). The lines connecting the blocks are introns. The direction of arrowheads on the lines or the blocks show the strand on which the element resides. Right-facing arrows show that it is on the sense strand while left-facing arrows show that it is on the antisense strand. To change the sense of the strand in order to more conveniently view annotation on the antisense strand, the *Genome Browser* display may be reversed using the **reverse** button underneath the *Genome Browser*

## Fishing for Genes in the UCSC Browser

The screenshot shows the UCSC Genome Browser Gateway for Human (Homo sapiens). The interface includes a navigation menu at the top with links: Home, Genomes, Blat, Tables, Gene Sorter, PCR, Session, FAQ, and Help. Below the menu is the title "Human (Homo sapiens) Genome Browser Gateway" and a copyright notice: "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."

The main search area contains several dropdown menus and input fields:

- clade:** A dropdown menu with "Vertebrate" selected.
- genome:** A dropdown menu with "Human" selected.
- assembly:** A dropdown menu with "Mar. 2006" selected.
- position or search term:** An input field containing "PPP1R1B".
- image width:** An input field containing "620".

A "submit" button is located to the right of the "position or search term" field. Below the search area are three buttons: "add custom tracks", "configure tracks and display", and "clear position". A link "Click here to reset the browser user interface settings to their defaults." is also present.

Annotations with arrows point to various parts of the interface:

- "Select Assembly Genome" points to the "genome" dropdown menu.
- "Clade" points to the "clade" dropdown menu.
- "Search box" points to the "position or search term" input field.
- "Assembly information" points to the "About the Human Mar. 2006 (hg18) assembly (sequences)" link.
- "Example queries" points to the "Sample position queries" section.

The "About the Human Mar. 2006 (hg18) assembly (sequences)" section contains the text: "The March 2006 human reference sequence (NCBI Build 36.1) was produced by the International Human Genome Sequencing Consortium."

The "Sample position queries" section provides a table of example queries and their corresponding responses:

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
chr3:1000000+2000	Displays a region of chr3 that spans 2000 bases, starting with position 1000000
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. This syntax may also be used for other range queries, such as between cytobands and uniquely-determined ESTs, mRNAs, refSeqs, etc.

Figure 2: UCSC Genome Browser Gateway page. The **position or search term** box allows the user to search for a position within the selected genome assembly or by keyword, gene symbol or other identifier. Here, a search for *PPP1R1B* is being initiated.

Click here to go to the location of the longer splice variant

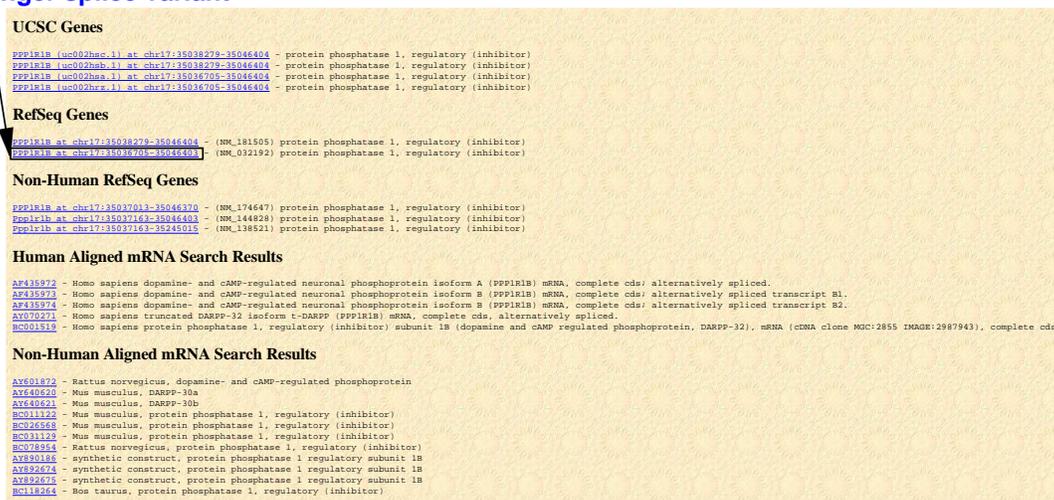


Figure 3: Results of a search for *PPP1R1B*. The results page shows all the tracks that contain data whose annotation includes the keyword “**PPP1R1B**”. This gene is found in the *UCSC Genes*, *RefSeq Genes* and *Human mRNA* tracks as well as in the tracks for *Non-human RefSeq Genes* and *Non-human mRNAs*.

image (see Figure 4). The image will then be re-drawn so that the 5' to 3' direction of transcription of the antisense gene is from left to right, which is more intuitive.

Above the *Genome Browser* image for the human genome assemblies (and for other organisms when available), there is a chromosome ideogram[13] showing a red box which indicates the position of the current viewing window within the chromosome. Navigation controls are found above and below the *Browser* image (Figure 4). Scrolling down below the *Browser* graphic allows access to the visibility controls for each track grouped by track type (see the lower part of Figure 4). These controls allow the user to select various tracks for display; display modes can be altered using the pull-down lists. Visibility options are:

- **hide** which renders the track invisible
- **dense** which collapses all the features into a single line
- **squish** which displays each features a sep-

arate line, but at 50% of the height of full mode and without labels

- **pack** which displays several features on each line with labels
- **full** which shows each feature on a separate line with labels

Such compacting of tracks is particularly useful for those tracks with large amounts of data. By altering the visibility of a number of tracks, a display such as that in Figure 5 can be achieved.

Zooming in to base level in order to examine annotations more closely can be achieved by using the navigation buttons above the *Browser* image. Clicking on the base numbers in the *Base Position* track also allows zooming. At the base level, the genome bases can be viewed below the numbering in the *Base Position* track (Figure 6). The one-letter amino acid codes for the translation of the codon triplets in all three frames for the strand being viewed will come into view as one zooms to base level (if the *Base Position* track visibility is **full**) while codons in various

# Fishing for Genes in the UCSC Browser

**UCSC Genome Browser on Human Mar. 2006 Assembly**

Home Genomes Blat Tables Gene Sorter PCR DNA Convert Ensembl UCBI PDF/PS Session Help

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

position/search chr17:35,036,705-35,046,403 jump clear size 9,699 bp. configure

chr17 (q12) 13.3 p13.1 17p12 17p11.2 q11.2 17q12 17q22 24.3 25.1 17q25.3

UCSC Gene Predictions Based on RefSeq, UniProt, GenBank, and Comparative Genomics

RefSeq Genes

Mammalian Gene Collection Full ORF mRNAs

Human mRNAs from GenBank

Human ESTs That Have Been Spliced

Spliced ESTs

Vertebrate Multiz Alignment & PhastCons Conservation (28 Species)

Mammal Cons

Rhesus Mouse Dog Horse Armadillo Opossum Platypus Lizard Chicken X\_tropicalis Stickleback

Simple Nucleotide Polymorphisms (dbSNP build 128)

Repeating Elements by RepeatMasker

move start < 2.0 > move end < 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.

default tracks hide all add custom tracks configure reverse refresh

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.

**Mapping and Sequencing Tracks** refresh

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

**Phenotype and Disease Associations** refresh

**Genes and Gene Prediction Tracks** refresh

**mRNA and EST Tracks** refresh

Human mRNAs	Spliced ESTs	Human ESTs	Other mRNAs	Other ESTs
dense	dense	hide	hide	hide
H-Inv	UniGene	Gene Bounds	SIB Alt-Splicing	Poly(A)
hide	hide	hide	hide	hide
CGAP SAGE				
hide				

**Expression and Regulation** refresh

**Comparative Genomics** refresh

**Variation and Repeats** refresh

**ENCODE Regions and Genes** refresh

Figure 4: Default tracks for the human hg18 (NCBI Build 36.1) assembly at the *PPP1R1B* gene locus.

## Fishing for Genes in the UCSC Browser

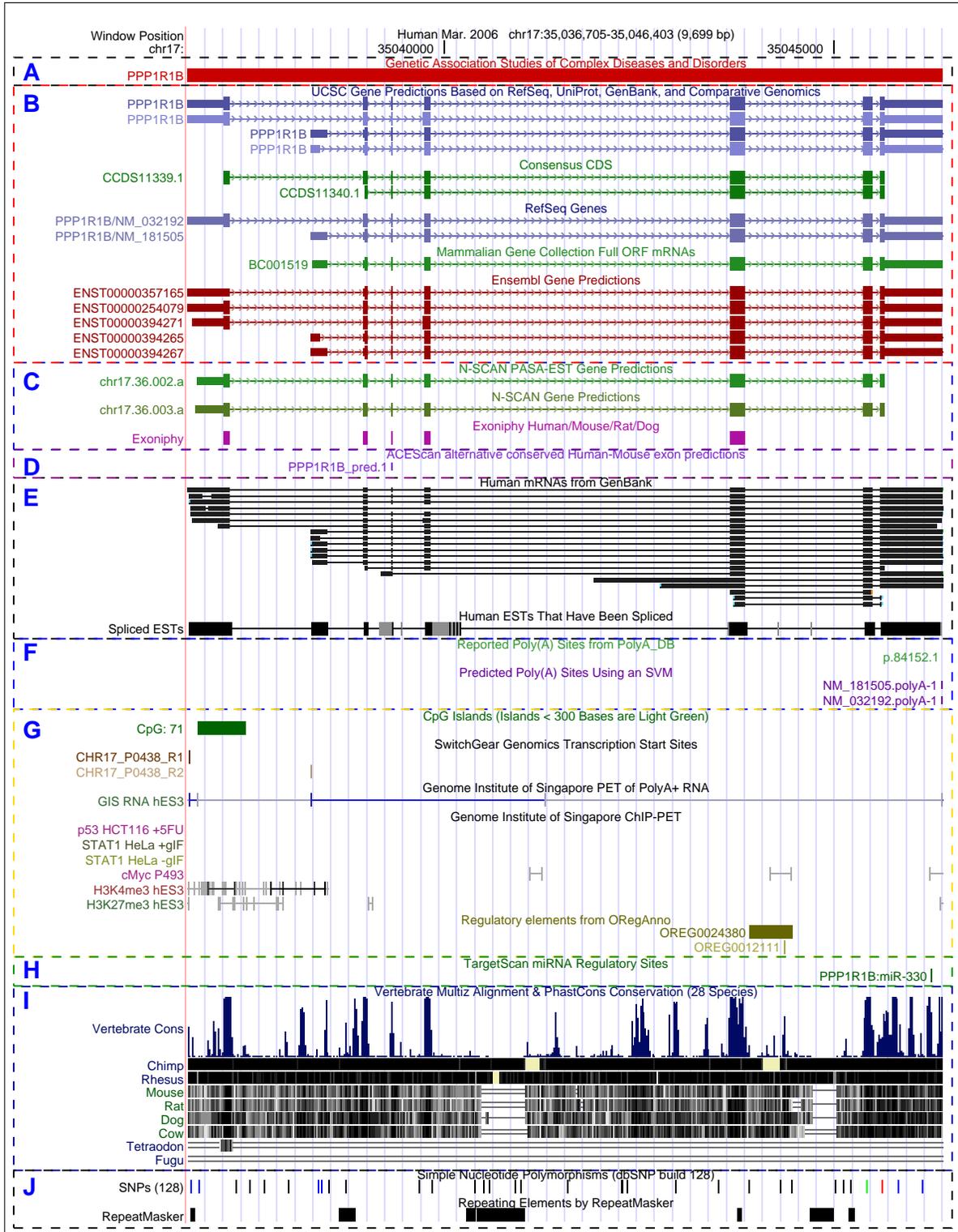


Figure 5: Human hg18 *Genome Browser* showing multiple annotations for the *PPP1R1B* gene locus. Using the track controls below the *Browser* image, the visibility has been set to display a variety of annotation types in the following tracks: (A) *Genetic Association Database (GAD) View*; (B) *UCSC, CCDS, RefSeq, MGC and Ensembl Genes*; (C) *N-SCAN predictions and ExoniPhy*; (D) *ACEScan*; (E) *Human mRNAs and Spliced ESTs*; (F) *Poly(A)*; (G) *CpG Islands, SwitchGear Transcription Start Site predictions, GIS-PET and OregAnno*; (H) *TargetScan*; (I) *Conservation*; and (J) *SNPs and RepeatMasker repeats*.

gene annotation tracks are also labeled with the one-letter amino acid code (Figure 6).

## 4 Annotation details

Each track has an associated **description page** which can be reached either by clicking on the hyperlinked name above the appropriate track control below this image or via the blue/gray bar at the side of the track. The track description details the methods and data sources used to produce the track, validation, credits and citations of relevant publications. Above the description, many tracks have configuration controls specific to the track type and some tracks also have filters. These controls allow the user to create the display that best shows the data of interest. Each item in a track also has a **details page** which may be reached by clicking on an item of interest in a track. Instead of configuration controls in the top section of the page, there are further details about the track item. These details can be extensive and may include:

- Links to external databases
- Confidence scores where applicable
- Position information
- Links to sequence
- Links to alignment information for aligned sequences, e.g., GenBank sequences.

Annotation data can be noisy, so care must be taken when using it to make interpretations. For instance, predictions can contain false positives and experimental data can be erroneous. For this reason, it is important to evaluate data from different sources in order to make an informed judgment as to the confidence that annotations should be assigned. With this in mind, examples from the different track groups will be compared for the *PPP1R1B* locus.

## 5 Phenotype and Disease Associations tracks

The *Genetic Association Database (GAD) View track*[1] has a red rectangle spanning the *PPP1R1B* locus, indicating that this gene has been associated with a disease or condition (Figure 5, Box A). The details page for this item shows that the associated condition is nicotine dependence in certain individuals. Links are provided to both the *GAD* database and to the single publication documenting evidence for the association.

## 6 Gene and Gene Prediction tracks

### 6.1 UCSC Genes

The *UCSC Genes*[15, 18] track (Figure 5, Box B) consists of gene models based on data from GenBank, RefSeq and UniProt, each of which has a details page that is extremely rich in information about that gene including:

- Gene descriptions
- Database cross-reference links
- Alternate gene names
- Genetic Association data
- Chemicals interacting with the gene product
- Selected microarray data
- mRNA UTR secondary structure
- Protein domains and structure
- Orthologs from other model organisms
- Gene Ontology (GO) annotations
- Pathways involving the gene product
- Information on the gene model

The *UCSC Genes* set has four splice variants at the *PPP1R1B* locus. Two predicted transcripts encode longer proteins and differ in the

## Fishing for Genes in the UCSC Browser

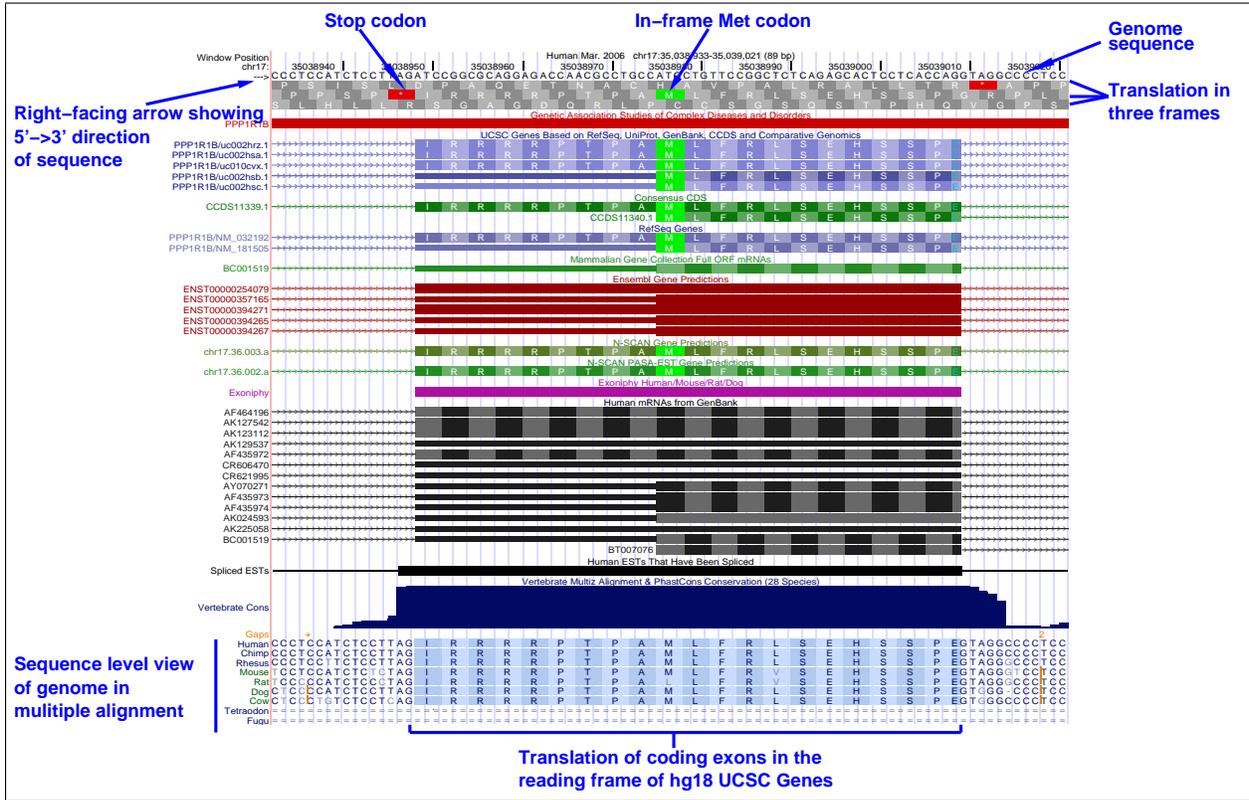


Figure 6: Multiple annotation tracks at the human hg18 *PPP1R1B* gene locus. At this zoom level, both the genome sequence and the amino acid translation in three frames are displayed in the *Base Position* track at full visibility. On the left side of this track, a right-facing arrow shows that the sequence runs from 5' to 3'. Clicking on the arrow reverse-complements the sequence so that it reads from right to left (3' to 5' prime). Various gene annotation and alignment tracks show color-coding at this zoom level; in the *mRNA* and *MGC Genes* tracks, by default, the codons are shown as alternating light and dark colored rectangles. The *UCSC Genes*, *CCDS* and *N-SCAN* tracks and the multiple alignment section of the *Conservation* track display genomic codons, by default, with the one-letter amino acids code labeling each codon in the CDS region of each transcript. *RefSeq Genes* has this feature switched off by default, but here, it is switched on together with a label for each item consisting of its gene name and RefSeq accession. At this base-level view, ATG are codons colored light green and labeled with "M" to represent potential translation start methionine codons while stop codons are colored red and are labeled with an asterisk "\*". The *Conservation* track has been configured to show a subset of species alignments and the Vertebrate conservation scores. These features can be configured using the controls at the top of the description page reached by clicking on the blue/gray mini-button at the left side of the relevant track.

size of an internal exon. The other two transcripts that encode a short protein differ in the length of the 5' UTR (Figure 5, Box B). Clicking on the first transcript (UCSC Gene **uc002hrz.1**) displays the details page which is divided into a number of collapsible sections. Selected sections are shown in the *UCSC Genes* details page figures: Figure 7 shows sections including those with gene descriptions and alternate gene names, Figure 8 shows expression data and pathways involving the gene product and Figure 9 shows a section of information about the gene model for *UCSC Gene uc002hrz.1*.

## 6.2 *TransMap* cross-species alignments

The *TransMap*[35, 36, 44] track contains cross-species alignments of GenBank[2] *mRNAs* and *Spliced ESTs*, *RefSeq Genes* and *UCSC Genes* to the genome. The more sensitive *BLASTZ* [32] alignment is used to create a base level projection of transcript alignments from different species onto a genome in order to predict orthologous genes on that genome. Mouse, human and many other vertebrate assemblies have a *TransMap* annotation track. For each genome, the vertebrate assemblies with *BLASTZ* alignments were selected. For closer evolutionary distances, the *BLASTZ* alignment nets[22] are syntenically filtered to distinguish orthologs from paralogs; for more distant species or if synteny is difficult to determine, all *BLASTZ* chains[22] are used. In this way, more genes can be mapped but with the complication that some genes are mapped to paralogous regions. Post-alignment filtering can remove some of the duplications. It is this set of chains that are used to create a base-level projection of the transcript alignments to the genome. The resulting pairwise alignments are shown in Figure 10.

## 6.3 Other *Gene and Gene Prediction* tracks

The *RefSeq*[31] transcripts are medium blue in color signifying their **Provisional** status. At this status level, a *RefSeq* is represented by a single GenBank source sequence and has not yet undergone a full review by annotators. During graduation to **Reviewed** RefSeq status, additional sequence data may be used to modify and extend the transcript structure and additional biological annotations may be added. However, users can make their own judgment by evaluating the additional evidence for a gene structure using the other annotation data.

The *Consensus Coding Sequence (CCDS)* track (Figure 5, Box B) is a high quality set of annotations consisting of a core set of protein-coding regions produced as a collaboration among NCBI, UCSC and the Havana and Ensembl groups at the Wellcome Trust Sanger Institute (WTSI) and the European Bioinformatics Institute (EBI). CCDS represent a consensus between RefSeq annotations (NCBI) and the Ensembl and Havana annotations (EBI/WTSI). At this locus, there are *CCDS* representing both splice variants in the *RefSeq Genes* track (NM.032192 and NM.181505) and also, all the predicted *UCSC Genes*. The two *CCDS* (**CCDS11339.1** and **CCDS11340.1**) represent all the coding regions that are shown in the *Gene and Gene Prediction* group annotation tracks in Figure 5, Box B.

The *MGC Genes* full-length ORF track has one MGC clone (**BC001519**) (Figure 5, Box B). MGC clone sequences have been submitted to the GenBank database so the same mRNA also appears in the *Human mRNA* track. The *mRNA* and *EST* tracks contain *BLAT* alignments of additional transcripts (see section 7 and Figure 5, Box E).

The *Gene and Gene Predictions* group of tracks also includes gene predictions based on mRNAs and ESTs such as *Ensembl Genes* [9] (Figure 5, Box B), *de novo* gene prediction

(a) Description for *UCSC Gene uc002hrz.1*

<a href="#">Home</a>	<a href="#">Genomes</a>	<a href="#">Genome Browser</a>	<a href="#">Blat</a>	<a href="#">Tables</a>	<a href="#">Gene Sorter</a>	<a href="#">PCR</a>	<a href="#">Session</a>	<a href="#">FAQ</a>	<a href="#">Help</a>
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**Human Gene PPP1R1B (uc002hrz.1) Description and Page Index**

**Description:** protein phosphatase 1, regulatory (inhibitor)

**RefSeq Summary (NM\_032192):** Midbrain dopaminergic neurons play a critical role in multiple brain functions, and abnormal signaling through dopaminergic pathways has been implicated in several major neurologic and psychiatric disorders. One well-studied target for the actions of dopamine is DARPP32. In the densely dopamine- and glutamate-innervated rat caudate-putamen, DARPP32 is expressed in medium-sized spiny neurons (Ouimet and Greengard, 1990 [PubMed 2191086]) that also express dopamine D1 receptors (Walaas and Greengard, 1984 [PubMed 6319627]). The function of DARPP32 seems to be regulated by receptor stimulation. Both dopaminergic and glutamatergic (NMDA) receptor stimulation regulate the extent of DARPP32 phosphorylation, but in opposite directions (Halpain et al., 1990 [PubMed 2153935]). Dopamine D1 receptor stimulation enhances cAMP formation, resulting in the phosphorylation of DARPP32 (Walaas and Greengard, 1984 [PubMed 6319627]); phosphorylated DARPP32 is a potent protein phosphatase-1 (see MIM 176875) inhibitor (Hemmings et al., 1984 [PubMed 6087160]). NMDA receptor stimulation elevates intracellular calcium, which leads to activation of calcineurin and dephosphorylation of phospho-DARPP32, thereby reducing the phosphatase-1 inhibitory activity of DARPP32 (Halpain et al., 1990 [PubMed 2153935]).[supplied by OMIM].

**Strand:** +    **Genomic Size:** 9700    **Exon Count:** 7    **Coding Exon Count:** 7

(b) Internal and external links for *PPP1R1B*

<a href="#">Page Index</a>	<a href="#">Sequence and Links</a>	<a href="#">UniProt Comments</a>	<a href="#">Genetic Associations</a>	<a href="#">CTD</a>	<a href="#">Microarray</a>
<a href="#">RNA Structure</a>	<a href="#">Protein Structure</a>	<a href="#">Other Species</a>	<a href="#">GO Annotations</a>	<a href="#">mRNA Descriptions</a>	<a href="#">Pathways</a>
<a href="#">Other Names</a>	<a href="#">Model Information</a>	<a href="#">Methods</a>			

**Sequence and Links to Tools and Databases**

<a href="#">Genomic Sequence (chr17:35,036,705-35,046,404)</a>	<a href="#">mRNA (may differ from genome)</a>	<a href="#">Protein (204 aa)</a>
<a href="#">Gene Sorter</a>	<a href="#">Genome Browser</a>	<a href="#">Proteome Browser</a>
<a href="#">Ensembl</a>	<a href="#">Entrez Gene</a>	<a href="#">ExonPrimer</a>
<a href="#">HGNC</a>	<a href="#">HPRD</a>	<a href="#">HuGE</a>
<a href="#">Stanford SOURCE</a>	<a href="#">Treefam</a>	<a href="#">UniProt</a>

(c) UniProt Description for *PPP1R1B*

**Comments and Description Text from UniProt (Swiss-Prot/TrEMBL)**

**ID:** [IPPD\\_HUMAN](#)

**DESCRIPTION:** Dopamine- and cAMP-regulated neuronal phosphoprotein (DARPP-32).

**FUNCTION:** Inhibitor of protein-phosphatase 1.

**SUBCELLULAR LOCATION:** Cytoplasm.

**PTM:** Dopamine- and cyclic AMP-regulated neuronal phosphoprotein.

**PTM:** Phosphorylation of Thr-34 is required for activity (By similarity).

**SIMILARITY:** Belongs to the protein phosphatase inhibitor 1 family.

(d) Alternate names for *PPP1R1B*

**Other Names for This Gene**

**Alternate Gene Symbols:** DARPP32, IPPD\_HUMAN, NM\_032192, NP\_115568, Q9H7G1, Q9UD71

**UCSC ID:** uc002hrz.1

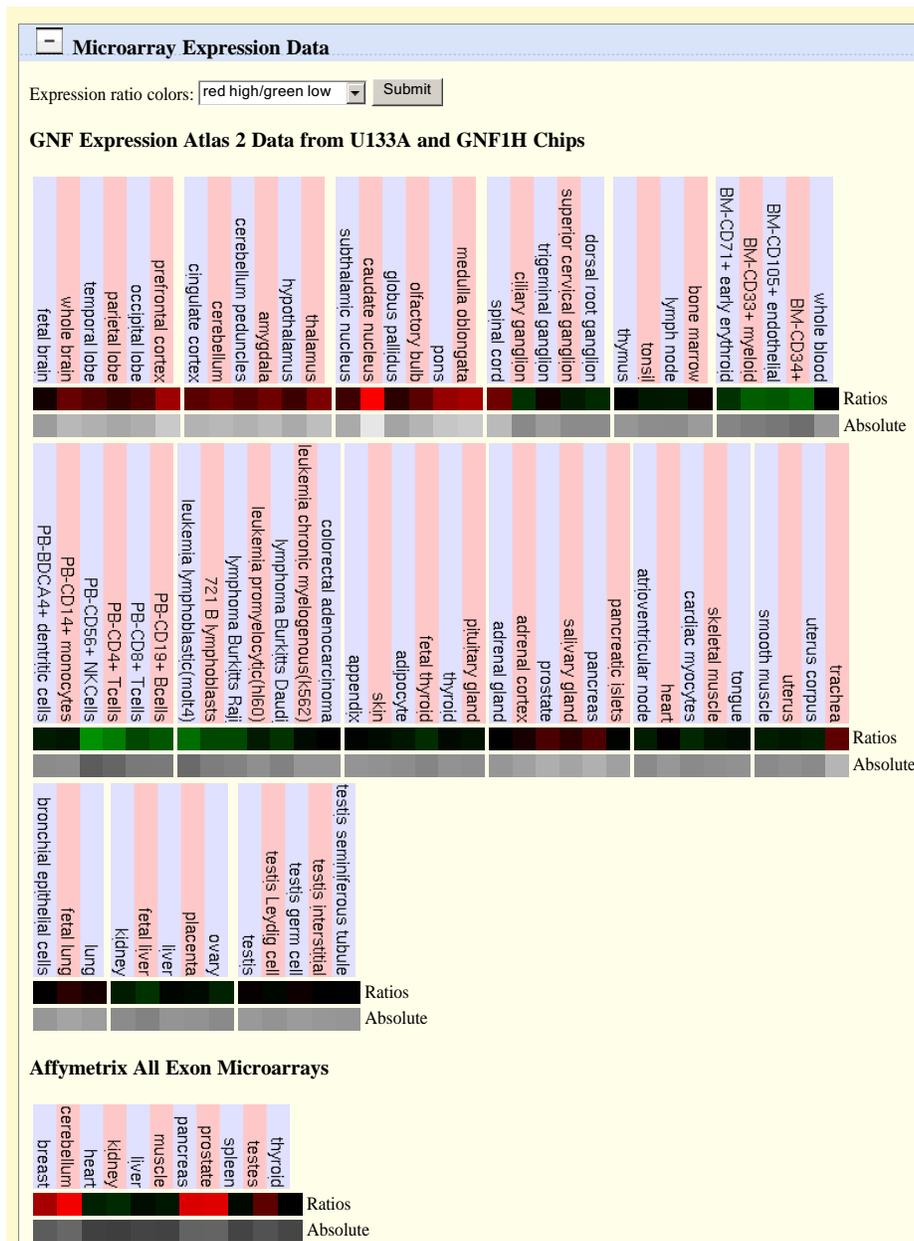
**RefSeq Accession:** [NM\\_032192](#)

**Protein:** [Q9UD71](#) (aka IPPD\_HUMAN)

**CCDS:** [CCDS11339.1](#)

Figure 7: Description, links and gene names from the details page for the human gene *PPP1R1B* (**uc002hrz.1**) in the *UCSC Genes* set. (a) shows the *RefSeq Genes* description for the gene. (b) shows links to the sections on the details page. The next section contains links to various tools and databases both at UCSC and externally. (c) shows a section containing the UniProt/SwissProt database description for the protein encoded by this gene. The UniProt ID (IPPD\_HUMAN) links to the UniProt database entry for a protein isoform produced by this gene. The UniProt record also has information about other protein isoforms represented in the database. (d) shows a section of alternate names for the *PPP1R1B* gene, some of which have links to external databases.

(a) Microarray data for *PPP1R1B*



(b) Pathways involving *PPP1R1B*

Figure 8: Expression data and pathways sections from the details page for the human gene *PPP1R1B* (**uc002hrz.1**) in the *UCSC Genes* set. (a) shows heatmap displays of microarray expression data for *PPP1R1B* in a variety of tissues and cell lines. The upper dataset is from the Genomics Institute of the Novartis Research Foundation (GNF) (<http://symatlas.gnf.org>) using Affymetrix chips. The lower dataset was provided by Affymetrix (<http://www.affymetrix.com>) and it was produced using Affymetrix Human Exon 1.0 ST arrays. (b) is the pathways section which has links to the BioCarta pathways involving the *PPP1R1B* gene product.

Gene Model Information					
category:	coding	nonsense-mediated-decay:	no	RNA accession:	NM_032192.2
exon count:	7	CDS single in 3' UTR:	no	RNA size:	1841
ORF size:	615	CDS single in intron:	no	Alignment % ID:	100.00
txCdsPredict score:	1416.67	frame shift in genome:	no	% Coverage:	100.00
has start codon:	yes	stop codon in genome:	no	# of Alignments:	1
has end codon:	yes	retained intron:	no	# AT/AC introns	0
selenocysteine:	no	end bleed into intron:	0	# strange splices:	0

Click [here](#) for a detailed description of the fields of the table above.

Figure 9: Gene model information section from the *UCSC Genes* details page for the human gene *PPP1R1B* (**uc002hrz.1**). This section shows that **uc002hrz.1** is protein-coding, has seven exons and has an open reading frame (ORF) of 615 bp among other features.

tracks such as *N-SCAN*, and exon prediction tracks such as *ExoniPhy* (Figure 5, Box C). EXONIPHY uses conservation among human, mouse, rat and dog to identify putative protein-coding exons. Computational gene predictions can provide validation for the gene and transcript structures produced by manual curation efforts such as those in the *RefSeq Genes* and *Vega Genes*[41] tracks.

## 7 GenBank mRNA and EST sequence alignments

The *mRNA and EST Tracks* group (Figure 5, Box E) show sequences from GenBank that align well to the genome using *BLAT*. In Figure 5, these tracks are compacted; the *Human mRNAs* track is shown with the visibility set to squish and the *Spliced ESTs* track is in dense mode (see the paragraph on track visibility in section 3). The transcript sequence alignments are regularly updated to keep in synchrony with GenBank; *mRNA* and *RefSeq Genes* updates are daily and *ESTs* tracks are updated weekly. The mRNA and EST transcripts may suggest the existence of additional exons and therefore additional transcript variants than those found in the gene and gene prediction tracks. The *Spliced ESTs* track shows that there are ESTs at the *PPP1R1B* locus that have two additional small

exons towards the 3' end of the gene (Figure 5). ESTs can therefore be used to predict the existence of additional splice forms not represented by mRNAs. Sequence data can be noisy; in particular, ESTs tend to have low sequence quality and were generated by single-pass sequencing. Therefore, care should be taken in interpreting these data. One caveat is that differences between transcripts and the reference genome may not be noise, but simply genetic variation between individuals. The *SNPs* track can indicate such instances (Figure 5, Box J and Figure 11). The *SNPs* track may display no known SNPs from dbSNP[33] at the position of the nonsynonymous codon. It may be that this is a SNP that has not yet been discovered or submitted to dbSNP or it could be due a sequencing error resulting in an incorrect base call. Without evidence of a SNP or viewing the sequencing quality scores, it is impossible to determine the origin of this base change.

There are configurable signals in the alignment displays for the *mRNAs* and *ESTs* track that denote certain features in the sequences and may aid in the identification of noise in the sequences:

- By default, the *mRNAs* tracks display red or yellow lines in aligned blocks where a base difference between a transcript and the reference genome results in a nonsynonymous codon (Figures 11(b) and (c)). At

## Fishing for Genes in the UCSC Browser

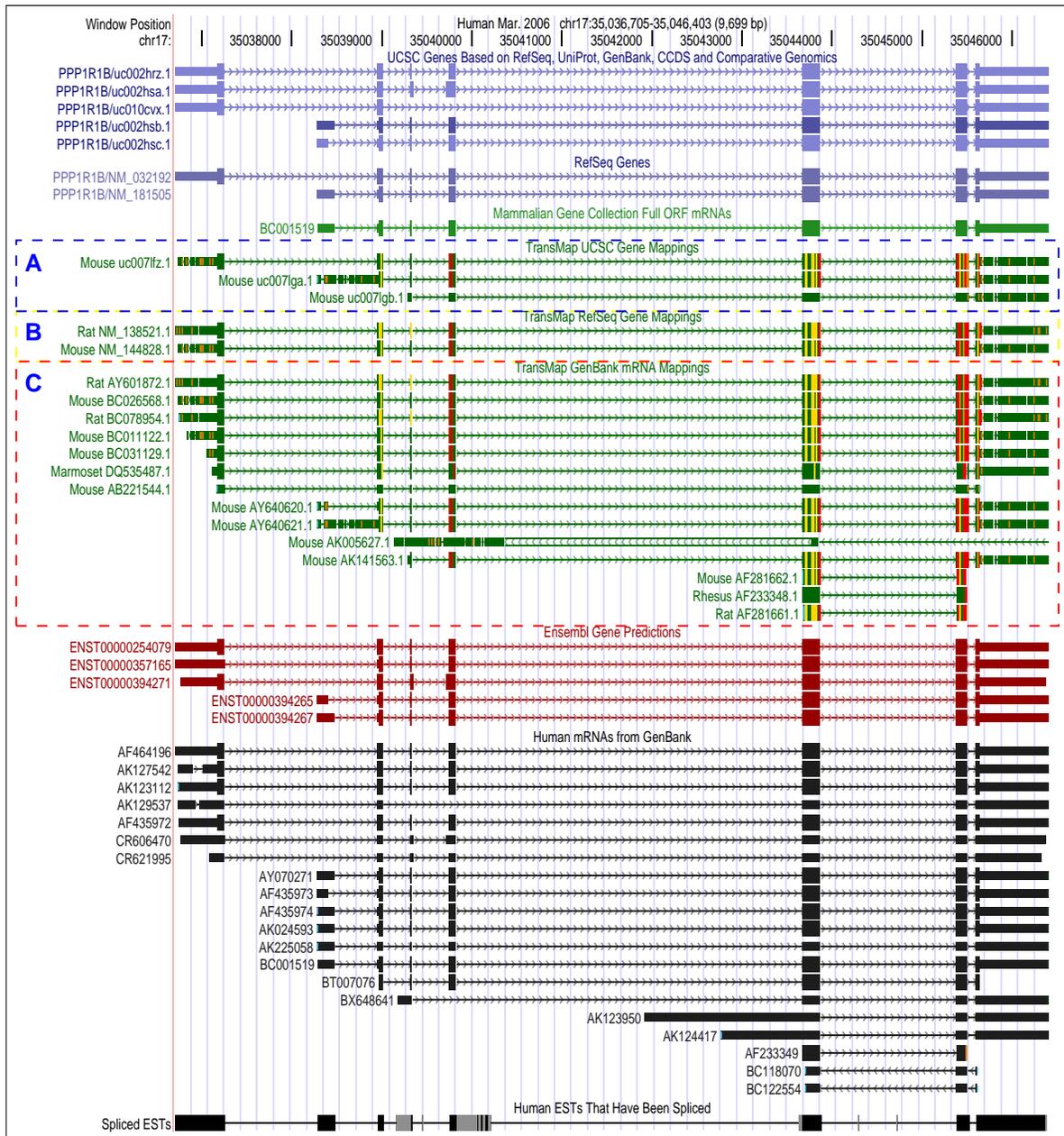
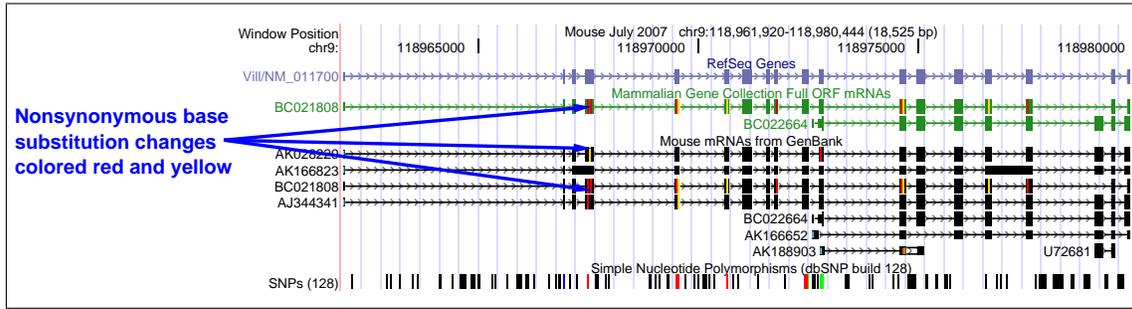


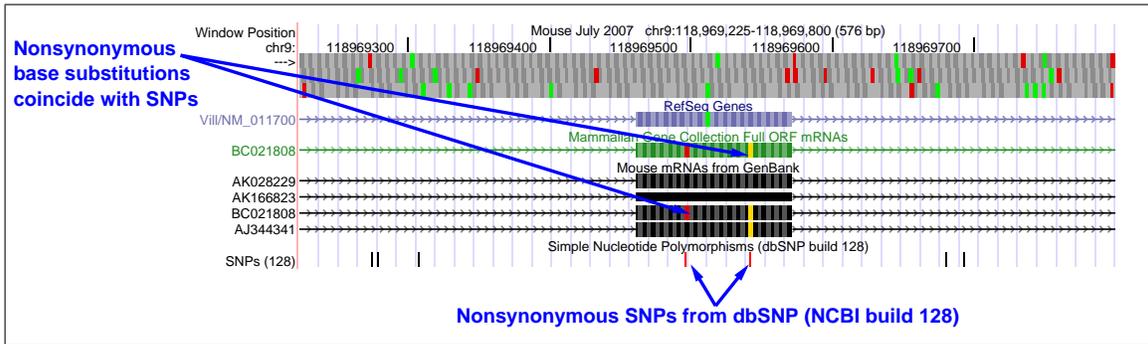
Figure 10: *TransMap* track at the human hg18 *PPP1R1B* gene locus. (A) *UCSC Genes*; (B) *RefSeq Genes* and (C) *GenBank mRNAs* alignments from other species are projected on to the human genome via *BLASTZ* alignment chains and nets. The *TransMap ESTs* and *human mRNAs* are shown in squish visibility mode since there are large numbers of these transcripts. For the same reason, human *Spliced ESTs* are shown with dense visibility. Colored lines on the alignments represent nonsynonymous codons in aligned transcripts compared to the reference genome sequence; red signifies that amino acids differ in physicochemical properties and yellow signifies similar amino acids. *TransMap* alignments show that the exons towards the 3' end of the *PPP1R1B* gene appear to be fast evolving in human whereas those at the 5' end are evolving at a slower rate.

## Fishing for Genes in the UCSC Browser

(a) Full view of mouse *Vill* gene with nonsynonymous base changes in MGC and mRNA tracks



(b) Exon 5 showing genomic codons and known SNPs resulting in nonsynonymous base changes



(c) Base-level view of exon 5 showing amino acid substitutions caused by nonsynonymous base changes

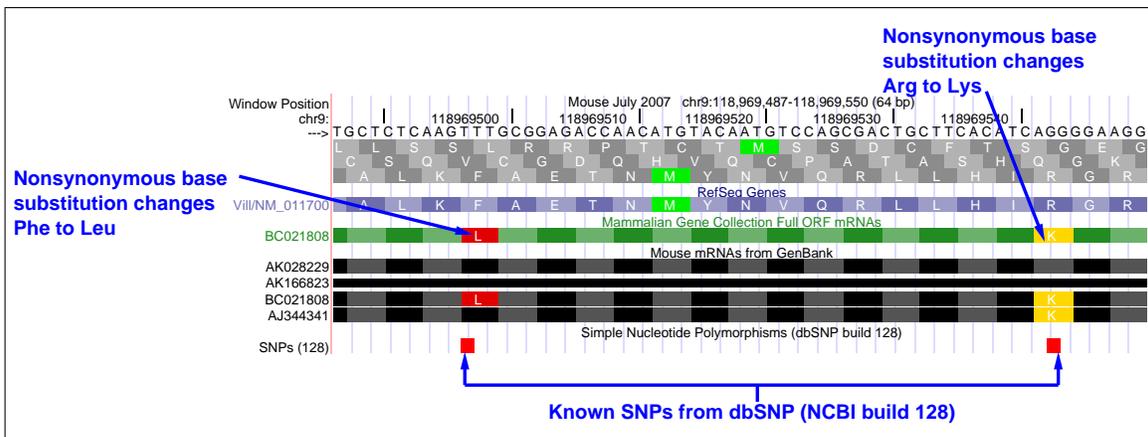


Figure 11: *Genome Browser* transcript rendering modes: Non-synonymous base changes. Various signals can be incorporated into the track displays that can aid in identifying noise in the data. The mouse (mm9, NCBI Build 37 assembly) *Vill* gene is shown at different zoom levels. Colored tick marks (zoomed out) or rectangles (base level view) represent nonsynonymous amino acid changes due to substitutions in *MGC Genes* and *mRNA* transcripts compared to the reference genome. Similar amino acids are colored yellow and amino acids that differ in physicochemical properties are colored red. Zooming in to a specific region can be achieved by clicking at the top of the *Base Position* track or using the zoom controls. (a) shows the entire *Vill* gene. (b) shows exon 5 with genomic codons appearing in the *Base Position* track and the *RefSeq Genes*, *MGC* and *mRNA* tracks. The nonsynonymous base changes in **BC021808** and in the **AJ344341** are due to known polymorphisms colored red in the *SNP* track. (c) shows the base level view of exon 5.

the base level display, the nonsynonymous codons in the transcripts display the one letter amino acid codes (Figure 11(c)).

- By default, the *ESTs* tracks display red lines in aligned blocks showing a base difference between a transcript and the reference genome; this signal can also be turned on for *mRNAs* and *MGC Genes*.
- Vertical blue lines indicate an insertion at the beginning or the end of a transcript relative to the reference genome (Figure 12(a)).
- Green lines indicate the presence of a polyA tail at the 3' end of a transcript (Figure 12(a)).
- Orange lines indicate insertions in the middle of a transcript relative to the reference genome (Figure 12(b)).
- Double horizontal lines indicate that both the genome and the transcript have an insertion. This may be due to poor sequence quality in a subregion of the transcript (Figures 12(a) and (b)).

Due to technical reasons, cloned sequences are often incomplete especially at the ends of the UTRs. Therefore, it is difficult to determine whether differences in UTR length are due to "real" variation between transcripts. Genomic data displayed in the *Genome Browser* can help the user to make an informed decision regarding the completeness of mRNAs. A vertical green line at the 3' end of a transcript indicates the presence of a polyA tail, confirming that the sequence is complete at the 3' end. Both reported and predicted polyadenylation (polyA) sites are shown in the *Poly(A)* track[4, 24]; data in this track may suggest alternative polyadenylation sites whose use would result in variation of the 3' UTR length (Figure 5, Box F). For *PPP1R1B*, both predicted and reported sites are in agreement and coincide with the 3' ends of the transcripts at this locus.

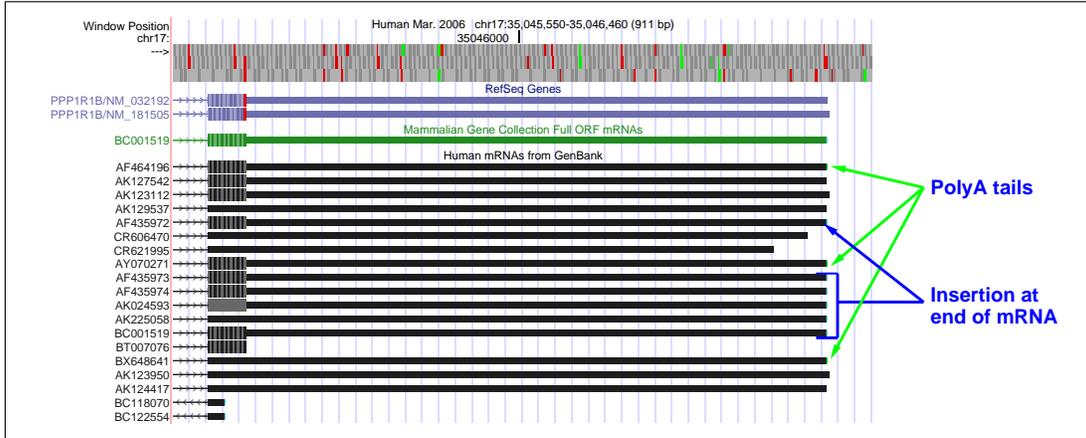
The completeness of the 5' UTR is more difficult to assess. To aid in this evaluation, there are computationally predicted sites

for transcription start sites (TSS) (*Eponine TSS* [8] and *SwitchGear TSS* (<http://www.switchgeargenomics.com/>) tracks). In Figure 5, Box G, the *SwitchGear Genomics TSS* track predicts the transcription start sites of both the longer and shorter splice variants in the *RefSeq Genes* and *Ensembl Genes* tracks (Box B). Experimental data such as ditags can be used to support and verify the 5' and 3' ends of a transcript. *Gene Identification Signature Paired-End Tags (GIS-PET)* [5, 6, 30, 40, 43] involves the sequencing of 5' and 3' signatures of full-length cDNAs that are subsequently concatenated to form ditags, sequenced and then mapped to the genome of origin to mark the boundaries of the transcripts (Figure 5, Box G and Figure 14). Ditags offer a much more efficient way of obtaining such data than traditional cDNA sequencing with the limitation that the internal exon structure is not determined. *GIS-PET* data from human embryonic stem cells (hES3) confirm the existence of transcripts whose 5' end is coincident with both the 5' end of the longer and shorter *PPP1R1B* transcripts (NM\_181505) and with the 5' end of some of the longer mRNAs (Figure 14). At the 3' end, there are ditags that are coincident with the 3' end of the RefSeq transcripts and many mRNA transcripts of the *PPP1R1B* gene (Figure 14) as well as the computationally predicted *SwitchGear TSSs*.

## 8 Conservation and regulation data

The *Conservation* track shows a 28-way multiple alignment of vertebrate genomes[29] created using the *MULTIZ* alignment program[3] and a histogram (wiggle type track) of conservation scores[34] associated with the alignment (Figure 5, Box I). Conservation tends to peak in coding regions of the gene and falls off in non-coding parts (introns and intergenic regions) so

(a) Insertions at the end of transcripts and polyA tails



(b) Internal transcript insertions

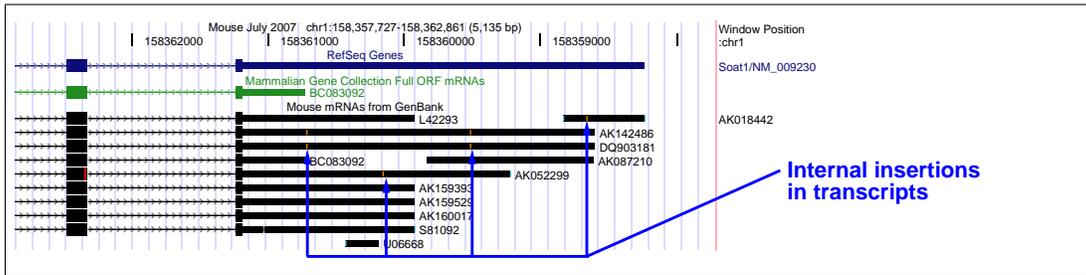
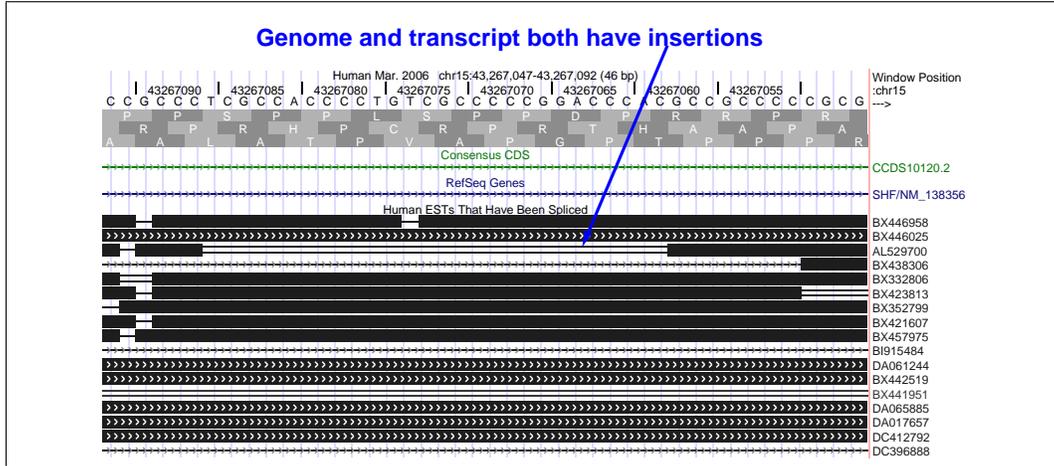


Figure 12: *Genome Browser* transcript rendering modes: Insertions and polyA tails. Various signals can be incorporated into the track displays for GenBank *mRNAs* and *ESTs* that can aid in identifying noise in the data. (a) shows the human *PPP1R1B* gene locus with vertical, colored lines at the 3' ends of mRNAs; blue indicates insertions (at the 5' or 3' transcript end) in the transcript alignment relative to the genome and green lines indicate the presence of polyA tails. (b) shows the mouse (mm9, NCBI Build 37 assembly) *Soat1* gene locus showing orange lines in aligned mRNAs which indicate insertions that occur in the middle of the mRNA sequences in their alignments to the genome. Note that *Soat1* is on the reverse strand and the image has been reversed using the **reverse** button below the *Genome Browser* graphic (see Figure 4) so the gene can be viewed in the 5' to 3' orientation. Track element labels are now shown on the right side of the image.

(a) Insertion in both transcript and genome



(b) EST sequence indicating sequence that is unalignable to the genome

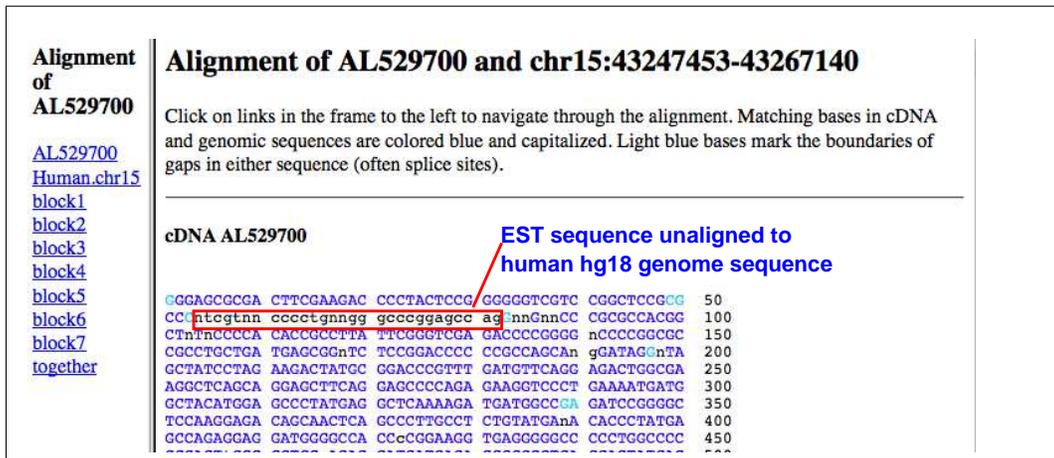


Figure 13: *Genome Browser* transcript rendering modes: Insertions in both sides of the alignment. Various signals can be incorporated into the track displays for GenBank *mRNAs* and *ESTs* that can aid in identifying noise in the data. (a) shows the human (hg18, NCBI Build 36.1) *SHF* gene locus at a position where the human EST, **AL529700**, has double horizontal lines between the black rectangles representing sequence aligned to the genome. The double lines indicate that there are insertions in the alignment in both the EST sequence and the genome. This is shown in (b) where the **AL529700** sequence is blue if it aligns to the genome where black text shows unaligned regions. The unaligned sequence in the red box corresponds to the double lines in image in (a) where it can also be noted that the genome sequence in this region is different from that in the human EST sequence whereas the flanking regions from both sequences are similar, hence the insertion in both transcript and genome in the sequence alignment. This region of the EST is likely to be an erroneous sequence as a result of poor quality sequencing.

## Fishing for Genes in the UCSC Browser

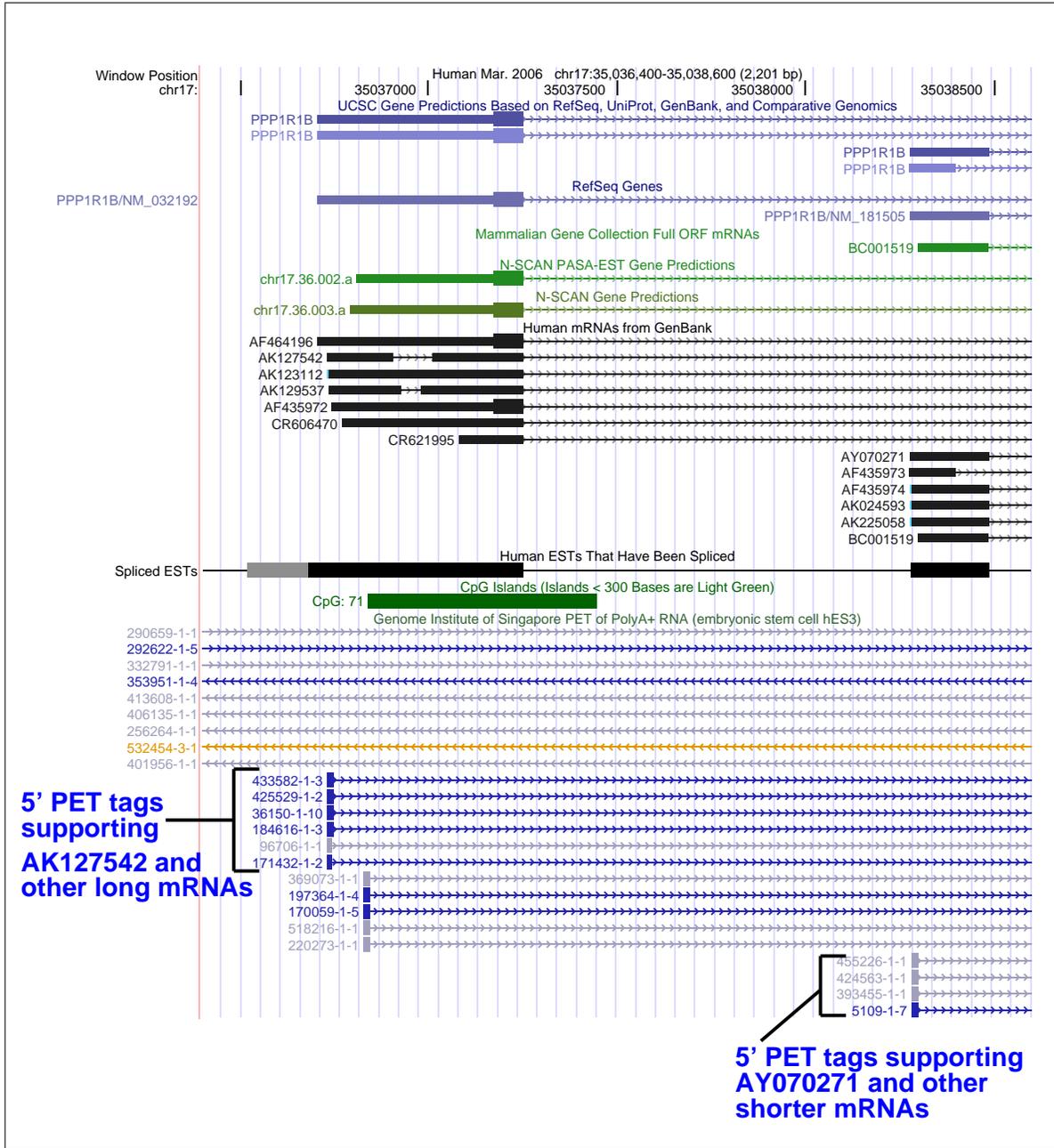


Figure 14: *PPP1R1B* locus showing the *GIS-PET PolyA+ RNA* ditags from the human embryonic cell line (hES3). The *GIS-Pet (Gene Identification Signature Paired End Ditags) RNA* track can be considered in evaluating the 5' completeness of transcripts. By clicking on the zoom buttons above the *Browser* image or by clicking above the base numbers at the top of the image, a zoomed-in genome view can be created. The *GIS-Pet RNA* track shows ditags from the 5' and 3' ends of full-length polyA+ mRNA. In this view, it can be seen that there are ditags whose 5' end coincide with the 5' end of some of the longer mRNAs e.g. **AK127542** and **AK123112** and ditags that coincide with the 5' end of the shorter mRNAs, e.g., **AY070271** and **AF435973** and the RefSeq, **NM\_181505**. There is a longer mRNA (**AF464196**) and ESTs that have been used to extend the RefSeq, **NM\_181505**, further upstream, but there are no ditags that represent this transcript.

it is a strong signal for a protein-coding gene (Figure 15). Conservation of sequence implies functional significance and can also occur where there are regulatory elements in the genome.

The *ACEScan*[42] track predicts conserved alternative exons that are present in some transcripts and skipped by others in both human and mouse (Figure 5, Box D). Enrichment of splicing regulatory motifs occurs in intron regions close to alternative exons, which also show a greater degree of conservation than those close to constitutive exons. *ACEScan* uses this information to predict the constitutive exon that is skipped in the human mRNA, **AK129537**.

Transcriptional regulatory elements tend to be enriched near the first exon [27]. Evidence of such motifs are the *CpG island* [10] at the 5' end of the *PPP1R1B* gene locus and the *SwitchGear TSS* prediction[7, 39] which is color-coded according to confidence level (a darker color implies a higher score) (Figure 5, Box G). The *ORegAnno*[11] track displays hand-curated regulatory regions extracted from the literature (Figure 5, Box G). The darker green rectangle represents a regulatory region, located in an intron of the *PPP1R1B*, bound by the CCCTC-binding factor (zinc finger protein) (CTCF) transcription factor. The lighter green item below represents the actual location of the CTCF binding site. This binding site was determined by ChIP (Chromatin Immunoprecipitation)-chip experiments (details are found by clicking on these track items). Histone modifications and multiple transcription factor binding sites for a variety of cell types are shown in the *GIS-PET* track (the GIS-PET method is described in section 7). Tri-methylation of lysine4 and lysine27 on histone H3 is indicated at the 5' end of the *PPP1R1B* gene (Figure 5, Box G). Such signals for regulatory elements may be misleading; CpG islands are frequently found in or near promoters of genes but not all genes have them, TSS predictions may contain false positives and transcription factor binding site measurements can be noisy.

*TargetScan*[12, 25, 26] predicts the presence of a microRNA binding site in a conserved region at the 3' end of the transcript (Figure 5, Box H). The prediction is based partially on conservation so the *TargetScan* annotation and conservation are not independent evidence of a regulatory region.

The *Conservation* track shows peaks of conservation that correspond to the coding sequence of the gene (Figure 5, Box I). Conservation falls off at the exon/intron boundaries as illustrated in Figures 15(a) and (b) which show a close-up view of the 5' and 3' ends of the *PPP1R1B* gene.

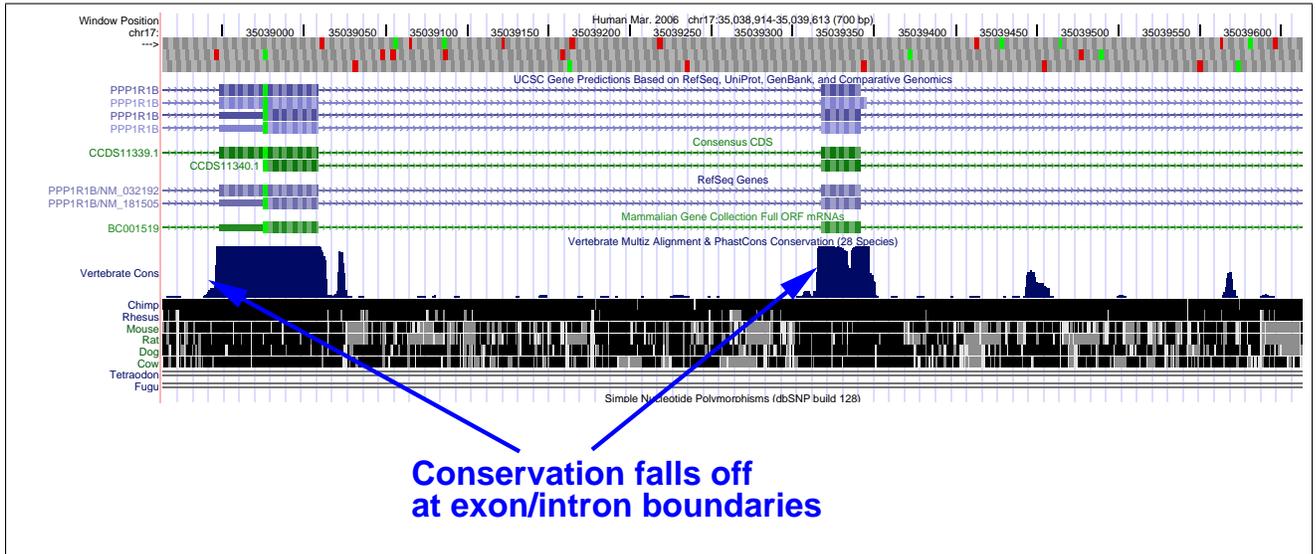
At this zoom level, by default, the *Conservation* track shows the nucleotide sequence of the aligned genomes, and, in coding regions based on the longest *UCSC Genes* transcript at this locus, the codon translation can be seen for each of the genomes. This enables the user to see not only the conservation at the amino acid level but also where there are differences at the amino acid level between proteins encoded by orthologous protein-coding genes. In Figure 15(b), it is possible to see that there is a SNP (**rs35797948**) in the *SNPs (128)* track which is colored red, indicating a nonsynonymous mutation in the coding region. Clicking on the SNP in this track displays further information about this SNP and a link out to the entry for the SNP in dbSNP at NCBI (<http://www.ncbi.nlm.nih.gov/SNP/>). This reveals that there are two known alleles (A/G) which code for either an arginine (CGC codon) or a histidine (CAC) amino acid in the translation of this last coding exon of *PPP1R1B*. Histidine and arginine are both positively charged making this a conservative substitution; histidine is an aromatic structure.

## 9 Ordering an MGC clone

Having used the *Genome Browser* to explore the *PPP1R1B* gene, the user may now desire to order a clone for this gene for experimental re-

## Fishing for Genes in the UCSC Browser

(a) 5' view



(b) 3' view

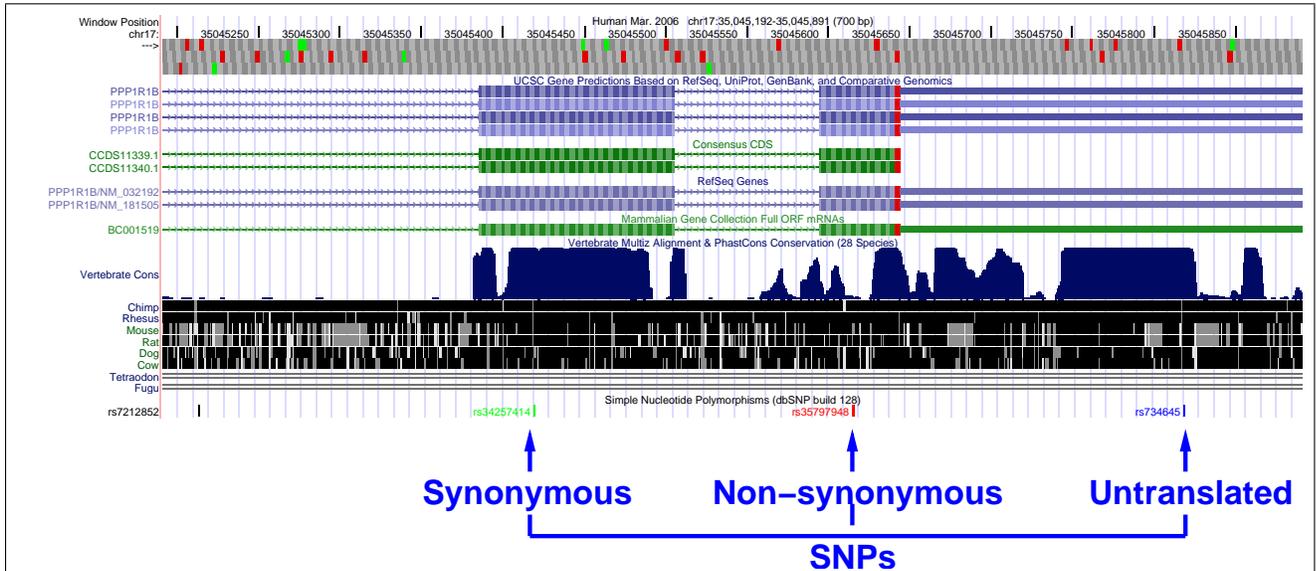


Figure 15: Zoomed in view of the 5' and 3' ends of the *PPP1R1B* gene. Conservation is high in the exons in the coding region and falls off at the boundaries of exons.

search. An MGC clone can be ordered by following links from the *Genome Browser* to vendors. The *MGC Genes* track shows the alignment of one full-length MGC clone (BC001519) for *PPP1R1B*. As mentioned previously (section 6.3), it is also shown in the *Human mRNAs* track since MGC clones are in the GenBank database (Figure 5, Box B).

A click on the alignment for the **BC001519** sequence in the *MGC Genes* track takes the user to the details page for this MGC transcript (Figure 16). The details page displays a gene description, the RefSeq accession and RefSeq description. Additionally, there is information about the clone, links for downloading protein, mRNA and genomic sequences, the alignment to the human reference genome sequence, NCBI clone validation information and links to various external databases including an MGC clone validation report and links to the MGC website. The CDS annotation of the MGC clone is frozen, but the RefSeq transcripts are continually being updated by NCBI manual annotators as more transcript and other experimental evidence becomes available. The RefSeq CDS similarity table on the MGC clone details page shows users how the RefSeq annotations differ to that of the MGC clone.

To order a clone, the user should follow the first link in the **Links** box, **Order MGC clone**, which directs the user to a portal where clone distributors are listed. In some cases, there is a direct ordering link to facilitate the ordering process as seen in Figure 17.

## 10 Summary

The *Genome Browser* is a very effective tool for the integration and analysis of biological data in a genomic context. It provides an easy method of rapidly locating an MGC clone for a gene of interest with direct links for ordering the clone. Many tools are built into the *Genome Browser*; their use is beyond the scope

of this tutorial but there is extensive documentation to help users to navigate use of the *Genome Browser* and its integrated tools. To read the documentation, click on the **Help** link on the top blue menu bar found on the *Genome Browser* website. Links are also provided on the user interface for each tool. Additionally, questions regarding the website and *Genome Browser* use are welcome. Users may search the mailing list archives (<http://genome.ucsc.edu/contacts.html>) and may also send questions via e-mail to the mailing list: [genome@soe.ucsc.edu](mailto:genome@soe.ucsc.edu).

## 11 FAQ

**Question 1:** How do I do a batch search for all the genes that lie in a specified region of a human chromosome?

**Answer 1:** The **Table Browser** is an extremely useful tool for querying the database tables that underlie the *Genome Browser*. The **Table Browser** can be reached by clicking on the **Tables** link on the top blue bar of the *UCSC Genome Bioinformatics* web pages. To retrieve a set of genes from the *UCSC Genes* set, these steps may be followed:

1. Make sure that the correct assembly is selected. For the hg18 human assembly (NCBI Build 36.1), select *Vertebrate* as the **clade**, *Human* as the **genome** and *Mar. 2006* as the **assembly**.
2. For the **group**, select *Genes and Gene Prediction Tracks* and for the **track**, select *UCSC Genes*.
3. Select *knownGene* as the **table**.
4. Select *position*. To find genes in a region of the chromosome, type the genomic location in the text box in the format, chr1:10000-100000. This example will find genes on chromosome 1 between base 10,000 and base 100,000. Then press the **lookup** button.

## Fishing for Genes in the UCSC Browser

<a href="#">Home</a>	<a href="#">Genomes</a>	<a href="#">Genome Browser</a>	<a href="#">Blat</a>	<a href="#">Tables</a>	<a href="#">Gene Sorter</a>	<a href="#">PCR</a>	<a href="#">Session</a>	<a href="#">FAQ</a>	<a href="#">Help</a>
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**MGC Clone BC001519.2**

**PPP1R1B**  
 Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 1B, mRNA (cDNA clone MGC:2855 IMAGE:2987943), complete cds.  
**RefSeq:** NM\_181505.2

**RefSeq Summary:** Midbrain dopaminergic neurons play a critical role in multiple brain functions, and abnormal signaling through dopaminergic pathways has been implicated in several major neurologic and psychiatric disorders. One well-studied target for the actions of dopamine is DARPP32. In the densely dopamine- and glutamate-innervated rat caudate-putamen, DARPP32 is expressed in medium-sized spiny neurons (Ouimet and Greengard, 1990 [PubMed 2191086]) that also express dopamine D1 receptors (Walaas and Greengard, 1984 [PubMed 6319627]). The function of DARPP32 seems to be regulated by receptor stimulation. Both dopaminergic and glutamatergic (NMDA) receptor stimulation regulate the extent of DARPP32 phosphorylation, but in opposite directions (Halpain et al., 1990 [PubMed 2153935]). Dopamine D1 receptor stimulation enhances cAMP formation, resulting in the phosphorylation of DARPP32 (Walaas and Greengard, 1984 [PubMed 6319627]); phosphorylated DARPP32 is a potent protein phosphatase-1 (see MIM 176875) inhibitor (Hemmings et al., 1984 [PubMed 6087160]). NMDA receptor stimulation elevates intracellular calcium, which leads to activation of calcineurin and dephosphorylation of phospho-DARPP32, thereby reducing the phosphatase-1 inhibitory activity of DARPP32 (Halpain et al., 1990 [PubMed 2153935]).[supplied by OMIM]. Sequence Note: removed 1 base from the 5' end that did not align to the reference genome assembly. Publication Note: This RefSeq record includes a subset of the publications that are available for this gene. Please see the Entrez Gene record to access additional publications.  
**Clone Source:** [Mammalian Gene Collection](#)

**MGC Clone Information and Links**

Gene	PPP1R1B	Links	<a href="#">Order MGC clone</a>
Product	protein phosphatase 1, regulatory (inhibitor)	MGC clone database	<a href="#">MGC clone database</a>
Tissue	colon, adenocarcinoma	IMAGE clone 2987943	<a href="#">IMAGE clone 2987943</a>
Library	NIH_MGC_15	Genbank BC001519	<a href="#">Genbank BC001519</a>
Development	n/a	RefSeq NM_181505.2	<a href="#">RefSeq NM_181505.2</a>
CDS	214..720	CCDS11340.1	<a href="#">CCDS11340.1</a>
Modification date	2008-07-04	UCSC Gene uc002hsc.1	<a href="#">UCSC Gene uc002hsc.1</a>
		Brent Lab Clone Validation	<a href="#">Brent Lab Clone Validation</a>

**RefSeq CDS similarity with MGC clone BC001519**

RefSeq	Position	CDS similarity
<a href="#">NM_181505.2</a>	<a href="#">chr17:35038279-35046404</a>	100.00%
<a href="#">NM_032192.2</a>	<a href="#">chr17:35036705-35046403</a>	90.37%

**Sequences**

mRNA	Protein	Genomic
<a href="#">Reference genome mRNA</a>	<a href="#">Reference genome protein</a>	

**Alignments**

genomic (browser)	span	mRNA (alignment details)	identity	aligned
<a href="#">chr17:35038300-35046401</a>	8102	<a href="#">+ BC001519:1-1477</a>	100.0%	97.0%

**NCBI Clone Validation**

mRNA start	mRNA end	Gene	Notes
1481	1522	PPP1R1B	polyA tail: 42 bases do not align to the human genome.

**Description and Methods**

Click [here](#) for details

Figure 16: Details page for the *PPP1R1B* MGC clone. The details page for the MGC full-length ORF mRNA (**BC001519**) shows information about the gene, this MGC clone and its sequence, similarity between the the RefSeq CDS and the annotated MGC CDS region, alignments, clone validation information and links to external databases.

**Order cDNA clones for Homo sapiens gene PPP1R1B**  
 PPP1R1B: protein phosphatase 1, regulatory (inhibitor) subunit 1B (dopamine and cAMP regulated phosphoprotein, DARPP-32)

The following clone(s) can be purchased through any of the IMAGE distributors. Some of them have provided direct order link(s) for your convenience.

Clone: MGC:2855 (IMAGE:2987943)  
 Clone Sequence: BC001519.2  
 Vector: pOTB7  
 Corresponding RefSeq mRNA: NM\_181505.2

from American Type Culture Collection  
 from RZPD German Resource Center for Genome Research  
 from Geneservice Ltd  
 from Harvard Institute of Proteomics  
 from Open Biosystems

Other clone(s) for the corresponding gene

**I.M.A.G.E. Distributors**

The I.M.A.G.E Consortium, headquartered at Lawrence Livermore National Laboratory, has handled clone arraying, archiving, and distribution for a number of large-scale projects, including MGC and The ORFeome Collaboration.

**I.M.A.G.E. Homepage**

Distribution of the physical reagents, either individual clones or entire collections, is handled by the following U.S. and European suppliers:

- American Type Culture Collection
- Invitrogen, Inc
- Open Biosystems
- Gene Service, Ltd.
- RZPD German Resource Center

Figure 17: NCBI page for ordering *PPP1R1B* cDNA clones. The page displays links to vendors for cDNA clones. In this case, there is only one clone listed for this gene. GenBank and RefSeq accessions, and the name of the vector containing the clone are shown. The clone can be obtained from distributors of Integrated Molecular Analysis of Genomes and their Expression (I.M.A.G.E) Consortium clones and links to some of the vendors are provided. For this clone, direct ordering links are for American Type Culture Collection (ATCC), RZPD German Resource Center for Genome Research, Geneservice Ltd., Harvard Institute of Proteomics and Open Biosystems.

5. Finally select the **output format**. The default will provide the *UCSC Gene* identifier and the genomic location for each *UCSC Gene*. Press the **get output** button to perform the search.

A similar batch search can be done for *RefSeq Genes* (**table**: *refGene*), *Ensembl Genes* (**table**: *ensGene*) or other gene set.

**Question 2:** How do I do a batch search for genes on an entire human chromosome, for example, chr21?

**Answer 2:** To carry out this search, follow the

instructions in the answer to **Question 1**, except at step 4, type the name of the chromosome into the **position** box in the format, chr21.

**Question 3:** How do I do batch retrievals for full-CDS MGC cDNA clones?

**Answer 3:** Use the **Table Browser**. See **Question 1** and **Question 2** for guidance on batch retrieval using this tool. To search for full-CDS MGC cDNA clones, the **track** to select is *MGC Genes* and the **table** to select is *mgcGenes*.

## 12 Other resources

- UCSC Genome Browser help at <http://genome.ucsc.edu/training>
- UCSC Genome Browser updates in the Nucleic Acids Research (NAR) Database issues[13, 16, 18, 23]
- The original UCSC Genome Browser publication[21]
- UCSC genome browser tutorial[45]
- UCSC Genome Browser: Deep support for molecular biomedical research.[28]
- Chapter 1, Unit 1.4 of Using Biological Databases in “Current Protocols in Bioinformatics”
- “Genomes, Browsers and Databases: Data-Mining Tools for Integrated Genomic Databases”, Peter Schattner (first edition, 2008).

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