



Zebrafish

FishMap 2.0 MANUAL

FishMap(Zv8) Genome Browser: General Help

These are general instructions for using the Generic Genome Browser. This page should be customized by the administrator of this resource to describe site-specific features.

Selecting a Region of the Genome

ZV8_v3 Database
Showing 20 kbp from chr1, positions 16,496,732 to 16,516,731

Instructions
Search using a sequence name, gene name, locus, or other landmark. The wildcard character * is allowed.
Navigation: Click one of the rulers to center on a location, or click and drag to select a region. Use the Scroll/Zoom buttons to change magnification and position.
Examples: chr1.323790..324790, myef2, Refseq_NM_199789, slc24a5, SNP_rs40663712, ENSDART00000097960, Inparanoid_ENSDARP00000076941.

Search
Landmark or Region: Search
Data Source:

Reports & Analysis:
Annotate Blast Against Displayed Sequence Configure...
Scroll/Zoom: Show 20 kbp Flip

Details
Clear highlighting

Tracks
 Analysis All on All off
 Blast Against Displayed Sequence Restriction Sites
 ERPIN All on All off
 Antizyme RNA frameshifting stimulation element GRK4 3 prime UTR element Potassium channel RNA editing signa Type II tRNA
 Arthropod 75K RNA Hairpin Ribozyme Prion pseudoknot U1 spliceosomal RNA
 Bicoid 3'-UTR regulatory element Histone 3' UTR stem-loop Pseudoknot of the domain G12) of 23S ribosomal RNA U2 spliceosomal RNA
 CsrB/RsmB RNA family Invasion gene-associated RNA Pseudoknot of upstream pseudoknot domain (UPD) of the 3'UTR 1L U4 spliceosomal RNA
 tRNA Iron response element RIT RNA U5 spliceosomal RNA
 ERPIN miRNA Predictions L-myc internal ribosome entry site (IRES) Small Nucleolar RNA Predictions from ERPIN U6atac minor spliceosomal RNA
 Eukaryotic 5S tRNA Ma3 gene ribosomal frameshift signa SRP RNA Domain IV Uua1.2 line 3
 Eukaryotic type signal recognition particle RNA Nanos 3' UTR translation control element TrkB IRES Vault RNA
 FGF-1 internal ribosome entry site (IRES) Other Predictions from ERPIN Type I tRNA Voltage-gated potassium-channel Kv1.4 IRES
 Ensembl All on All off
 Ensembl Data Ensembl Transcripts Refseq
 Ensembl Genes GC content
 Expression All on All off
 Digital Gene Expression Tags

To select a region of the genome to view, enter its name in the text field labeled "Landmark or Region". Recognized types of names are under the control of the administrator, but usually the following names are accepted:

a chromosome name

You can enter the name of a chromosome, with start and stop region, as shown in the "search" panel.

For eg., chr1:323790..324790

a gene name

You can enter the name of a gene using the standard nomenclature for *Danio rerio*.

ENSEMBL Gene Ids and Transcript Ids

The Ensembl Gene Ids and Transcript Ids.

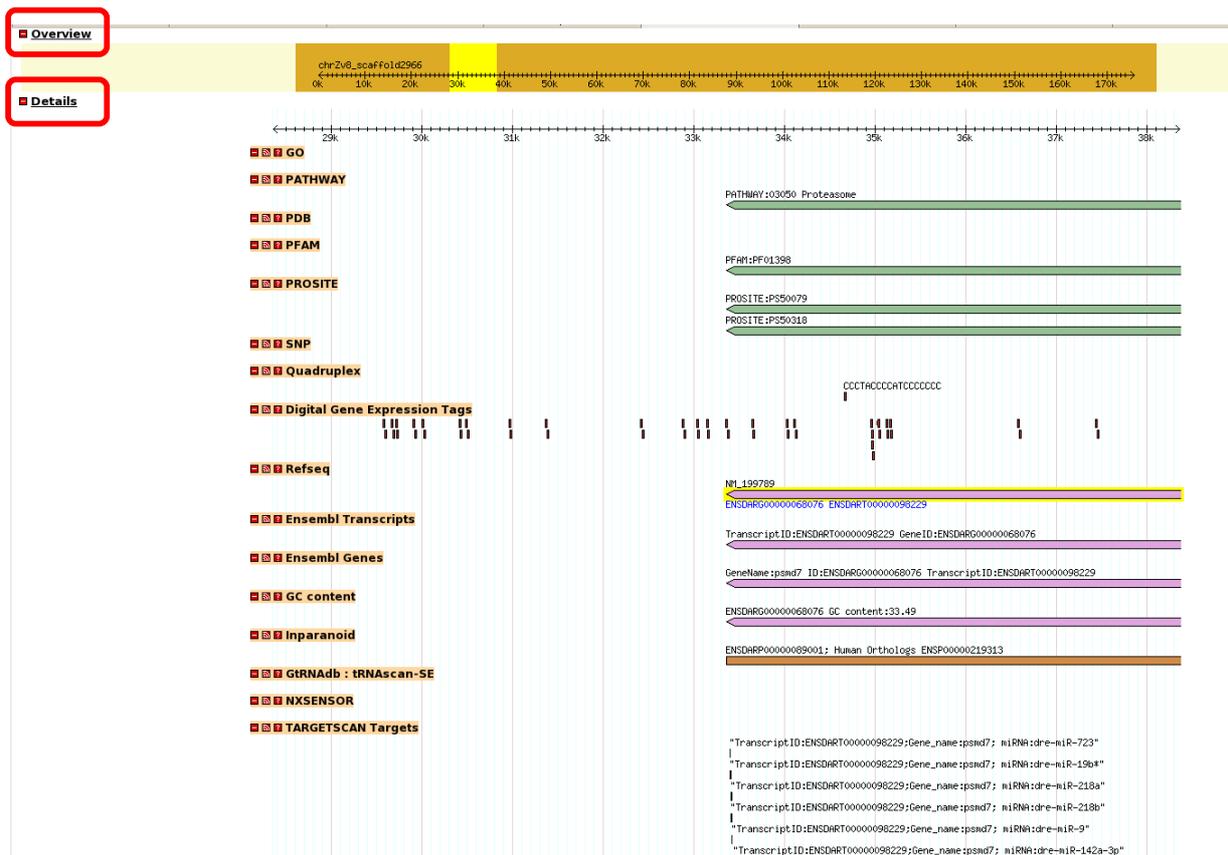
Other IDs

The RefSeq, miRNA, Inparanoid and other Ids can be used in the following format:

Refseq:NM_199789
SNP:rs40663712
Inparanoid:ENSDARP00000076941
miRNA:dre-mir-7a-2

The Overview and Detail Panels

If the landmark is found in the database, the browser will display the region of the genome it occupies. The region is displayed in two graphical panels:



Overview panel

This panel displays the genomic context, typically an entire assembled genome or a large portion of the sequence assembly such as a scaffold or contig. A yellow rectangle indicates the region of the genome that is displayed

in the Detail panel. This rectangle may appear as a single line if the detailed region is relatively small.

Detail panel

This panel displays a zoomed-in view of the genome corresponding to the overview's yellow rectangle. The detail panel consists of one or more tracks showing annotations and other features that have been placed on the genome. The Detail panel is described at length later.

If the requested landmark is not found, the browser will display a message to this effect.

Specifying the Landmark Class

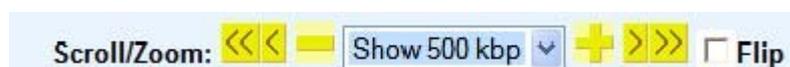
Along with the landmarks you can select "Tracks" according to your requirement.

| Tracks | | | |
|--|--|---|---|
| <input type="checkbox"/> Analysis <input type="checkbox"/> All on <input type="checkbox"/> All off | | | |
| <input type="checkbox"/> Blast Against Displayed Sequence | <input type="checkbox"/> Restriction Sites | | |
| <input type="checkbox"/> ERPIN <input type="checkbox"/> All on <input type="checkbox"/> All off | | | |
| <input type="checkbox"/> Antizyme RNA frameshifting stimulation element | <input type="checkbox"/> GRIK4 3 prime UTR element | <input type="checkbox"/> Potassium channel RNA editing signa | <input type="checkbox"/> Type II tRNA |
| <input type="checkbox"/> Arthropod 75K RNA | <input type="checkbox"/> Hairpin Ribozyme | <input type="checkbox"/> Prion pseudoknot | <input type="checkbox"/> U1 spliceosomal RNA |
| <input type="checkbox"/> Bicoid 3'-UTR regulatory element | <input type="checkbox"/> Histone 3' UTR stem-loop | <input type="checkbox"/> Pseudoknot of the domain G(G1.2) of 23S ribosomal RNA | <input type="checkbox"/> U2 spliceosomal RNA |
| <input type="checkbox"/> CsrB/RsmB RNA family | <input type="checkbox"/> Invasion gene-associated RNA | <input type="checkbox"/> Pseudoknot of upstream pseudoknot domain (UPD) of the 3'UTR 11 | <input type="checkbox"/> U4 spliceosomal RNA |
| <input type="checkbox"/> cRNA | <input type="checkbox"/> Iron response element | <input type="checkbox"/> RIT RNA | <input type="checkbox"/> U5 spliceosomal RNA |
| <input type="checkbox"/> ERPIN miRNA Predictions | <input type="checkbox"/> L-myc internal ribosome entry site (IRES) | <input type="checkbox"/> Small Nucleolar RNA Predictions from ERPIN | <input type="checkbox"/> U6atac minor spliceosomal RNA |
| <input type="checkbox"/> Eukaryotic 5S rRNA | <input type="checkbox"/> Ma3 gene ribosomal frameshift signa | <input type="checkbox"/> SRP RNA Domain IV | <input type="checkbox"/> Unal.2 line 3 |
| <input type="checkbox"/> Eukaryotic type signal recognition particle RNA | <input type="checkbox"/> Nanos 3' UTR translation control element | <input type="checkbox"/> TrkB IRES | <input type="checkbox"/> Vault RNA |
| <input type="checkbox"/> FGF-1 internal ribosome entry site (IRES) | <input type="checkbox"/> Other Predictions from ERPIN | <input type="checkbox"/> Type I tRNA | <input type="checkbox"/> Voltage-gated potassium-channel Kv1.4 IRES |
| <input type="checkbox"/> Ensembl <input type="checkbox"/> All on <input type="checkbox"/> All off | | | |
| <input type="checkbox"/> Ensembl Data | <input checked="" type="checkbox"/> Ensembl Transcripts | <input checked="" type="checkbox"/> Refseq | |
| <input checked="" type="checkbox"/> Ensembl Genes | <input checked="" type="checkbox"/> GC content | | |
| <input type="checkbox"/> Expression <input type="checkbox"/> All on <input type="checkbox"/> All off | | | |
| <input checked="" type="checkbox"/> Digital Gene Expression Tags | | | |
| <input type="checkbox"/> General <input type="checkbox"/> All on <input type="checkbox"/> All off | | | |
| <input type="checkbox"/> Genes | | | |
| <input type="checkbox"/> Nucleosome Exclusion Regions <input type="checkbox"/> All on <input type="checkbox"/> All off | | | |
| <input checked="" type="checkbox"/> NXSENSOR | | | |
| <input type="checkbox"/> Orthologs <input type="checkbox"/> All on <input type="checkbox"/> All off | | | |
| <input checked="" type="checkbox"/> Inparanoid | | | |
| <input type="checkbox"/> Pathway <input type="checkbox"/> All on <input type="checkbox"/> All off | | | |
| <input checked="" type="checkbox"/> GO | <input type="checkbox"/> PDB | <input checked="" type="checkbox"/> PROSITE | |
| <input checked="" type="checkbox"/> PATHWAY | <input checked="" type="checkbox"/> PFAM | | |
| <input type="checkbox"/> Quadruplex <input type="checkbox"/> All on <input type="checkbox"/> All off | | | |
| <input checked="" type="checkbox"/> Quadruplex | | | |
| <input type="checkbox"/> TARGETS <input type="checkbox"/> All on <input type="checkbox"/> All off | | | |
| <input checked="" type="checkbox"/> miRanda Target | <input checked="" type="checkbox"/> RNAHYBRID Target | <input checked="" type="checkbox"/> TARGETSCAN Targets | |
| <input type="checkbox"/> UTR <input type="checkbox"/> All on <input type="checkbox"/> All off | | | |
| <input type="checkbox"/> Androgen receptor GU-rich element (AR_CURE) | <input type="checkbox"/> Gamma interferon activated inhibitor of Ceruloplasmin mRNA translation (GAIT element) | <input type="checkbox"/> Male specific lethal 3' UTR cis-acting element (MSL2-3UTR) | <input type="checkbox"/> TGE translational regulation element (TGE) |
| <input type="checkbox"/> AU-rich class-2 Element (ARE2) | <input type="checkbox"/> Histone 3'UTR stem-loop structure (HSL3) | <input type="checkbox"/> Mos polyadenylation response element (Mos-PRE) | <input type="checkbox"/> Upstream Open Reading Frame (uORF) |
| <input type="checkbox"/> Bruno 3' UTR responsive element (BRE) | <input type="checkbox"/> Internal Ribosome Entry Site (IRES) | <input type="checkbox"/> Selenocysteine Insertion Sequence (SECIS) - type 1 | |
| <input type="checkbox"/> Cytoplasmic polyadenylation element (CPE) | <input type="checkbox"/> Iron Responsive Element (IRE) | <input type="checkbox"/> Selenocysteine Insertion Sequence (SECIS) - type 2 | |
| <input type="checkbox"/> Variation <input type="checkbox"/> All on <input type="checkbox"/> All off | | | |
| <input checked="" type="checkbox"/> SNP | | | |
| <input type="checkbox"/> ncRNA <input type="checkbox"/> All on <input type="checkbox"/> All off | | | |

Following are the track names divided, based on their categories along with number of entries in each category.

| Category | Features | Entries |
|------------------------------|--|---------|
| Erpin | AU-rich class-2 Element (ARE2), ERPIN miRNA Predictions, Other Predictions from ERPIN, Nanos 3' UTR translation control element, Bicoid 3'-UTR regulatory element, TrkB IRES, Histone 3' UTR stem-loop, Prion pseudoknot, Voltage-gated potassium-channel Kv1.4 IRES, UnaL2 line 3, Pseudoknot of upstream pseudoknot domain (UPD) of the 3'UTR 11, Ma3 gene ribosomal frameshift signal, GRIK4 3 prime UTR element , U5 spliceosomal RNA, CsrB/RsmB RNA family, Eukaryotic type signal recognition particle RNA, U4 spliceosomal RNA, Vault RNA, U2 spliceosomal RNA, U1 spliceosomal RNA, Type I tRNA, Type II tRNA, SRP RNA Domain IV, Eukaryotic 5S rRNA, RtT RNA, FGF-1 internal ribosome entry site (IRES), Antizyme RNA frameshifting stimulation element, L-myc internal ribosome entry site (IRES), ctRNA, U6atac minor spliceosomal RNA, Potassium channel RNA editing signal, Arthropod 7SK RNA, Pseudoknot of the domain G(G12) of 23S ribosomal RNA, Hairpin Ribozyme, Invasion gene-associated RNA | 7027830 |
| Ensembl | Ensembl Data, Refseq, Ensembl Transcripts, Ensembl Genes, GC Content | 710709 |
| Expression | Digital Gene Expression Tags | 6622071 |
| Nucleosome Exclusion Regions | NXSENSOR | 836955 |
| Orthologs | Inparanoid | 9070 |
| Pathway | GO, PFAM, PROSITE, Pathway, PDB | 104547 |
| Quadruplex | Quadruplex | 88639 |
| Targets | TARGETSCAN Targets, RNAHYBRID Target, miRanda Target | 3281259 |
| UTR Response Element | Iron response element, Androgen receptor GU-rich element (AR_CURE), AU-rich class-2 Element (ARE2), Bruno 3' UTR responsive element (BRE), Cytoplasmic polyadenylation element (CPE), Gamma interferon activated inhibitor of Ceruloplasmin mRNA translation (GAIT element), Histone 3'UTR stem-loop structure (HSL3), Iron Responsive Element (IRE), Internal Ribosome Entry Site (IRES), Male specific lethal 3' UTR cis-acting element (MSL2-3UTR), Mos polyadenylation response element (Mos-PRE), Selenocysteine Insertion Sequence (SECIS) - type 1, Selenocysteine Insertion Sequence (SECIS) - type 2, TGE translational regulation element (TGE), Upstream Open Reading Frame (uORF). | 153253 |
| Variation | SNP | 638032 |
| ncRNA | miRNA, Antagomirzyme | 989 |
| tRNA | GtRNAdb : tRNAscan-SE | 12292 |

Navigation



Once a region is displayed, you can navigate through it in a number of ways:

Scroll left or right with the <<, <, > and >> buttons

These buttons, which appear in the "Scroll/Zoom" section of the screen, will scroll the detail panel to the left or right. The << and >> buttons scroll an entire screen by the length of the sequence viewed, while < and > scroll a half screen, i.e., half the length of the sequence viewed.

Zoom in or out using the "Show XXX Kbp" menu.

Use menu that appears in the center of the "Scroll/Zoom" section to change

the zoom level. The menu item name indicates the number of base pairs to show in the detail panel. For example, selecting the item "100 Kbp" will zoom the detail panel so as to show a region 100 Kbp wide.

Make fine adjustments on the zoom level using the "-" and "+" buttons.

Press the '-' and '+' buttons to change the zoom level by small increments (usually 10-20%, depending on how the browser is configured).

Recenter the detail panel by clicking on its scale



The scale at the top of the detail panel is live. Clicking on it will recenter the detail panel around the location you clicked. This is a fast and easy way to make fine adjustments in the displayed region.

Get information on a feature by clicking on it

Clicking on a feature in the detail view will link to a page that displays more information about it. This could be a page on the browser's web site, or a page on an external web site.

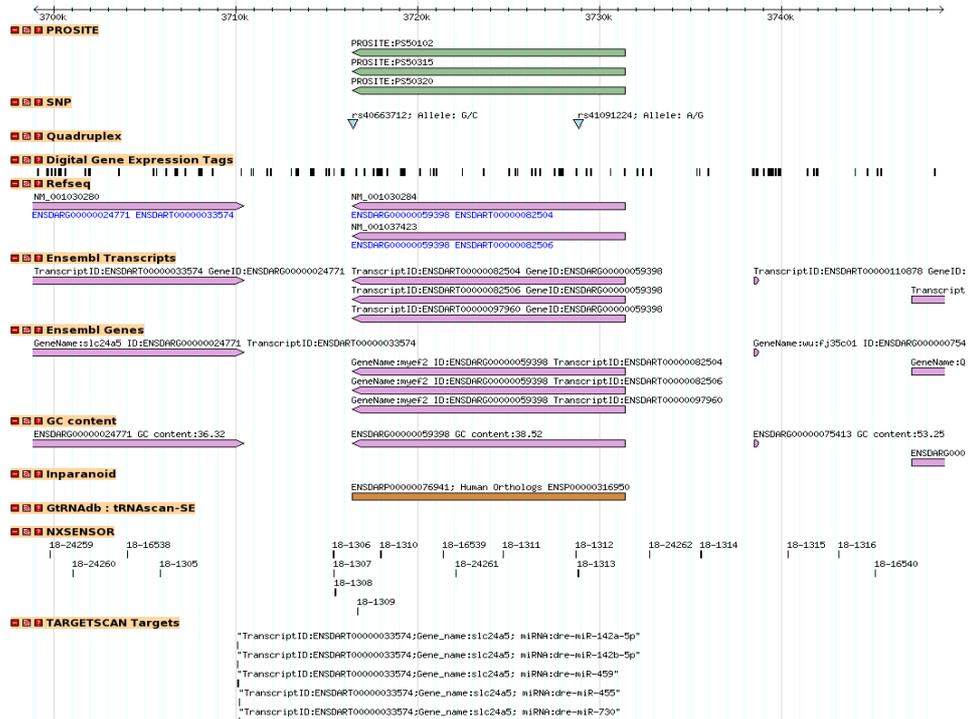
Jump to a new region by clicking on the overview panel

Click on the overview panel to immediately jump to the corresponding region of the genome.

The Detail Panel

The detailed view is composed of a number of distinct tracks which stretch horizontally from one end of the display to another. Each track corresponds to a different type of genomic feature, and is distinguished by a distinctive graphical shape and color.

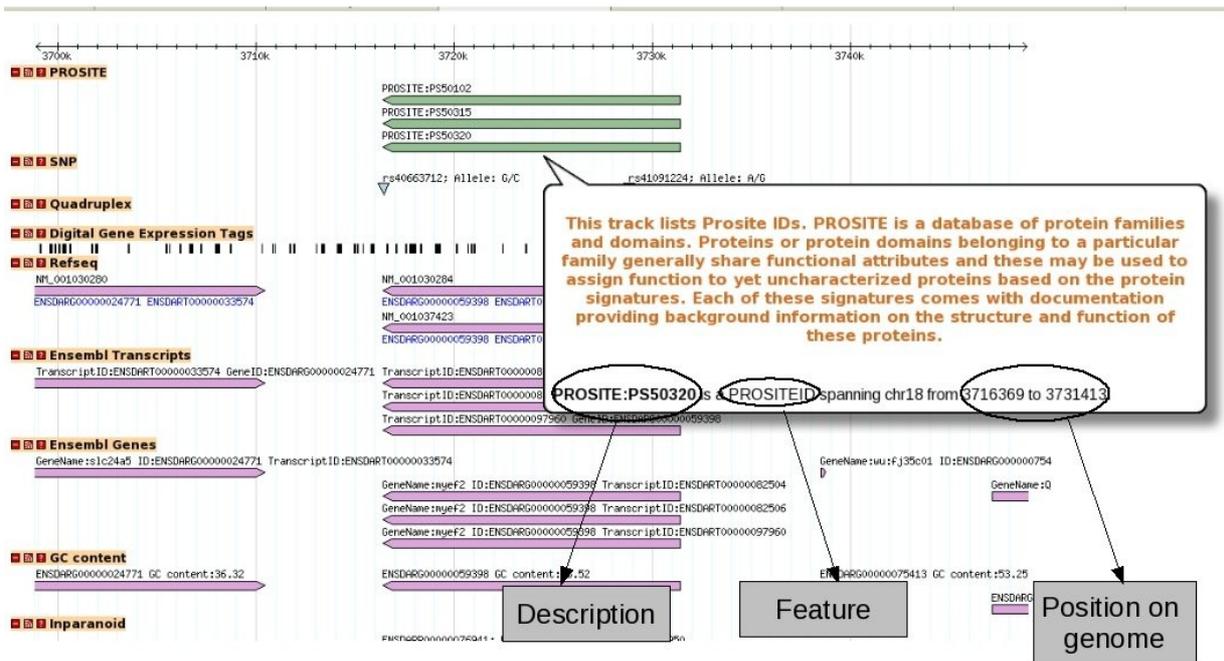
■ Details



The key to the tracks is shown at the bottom of the detail panel. For more information on the source and nature of the track, click on the track label in the "Search Settings" area (discussed below).

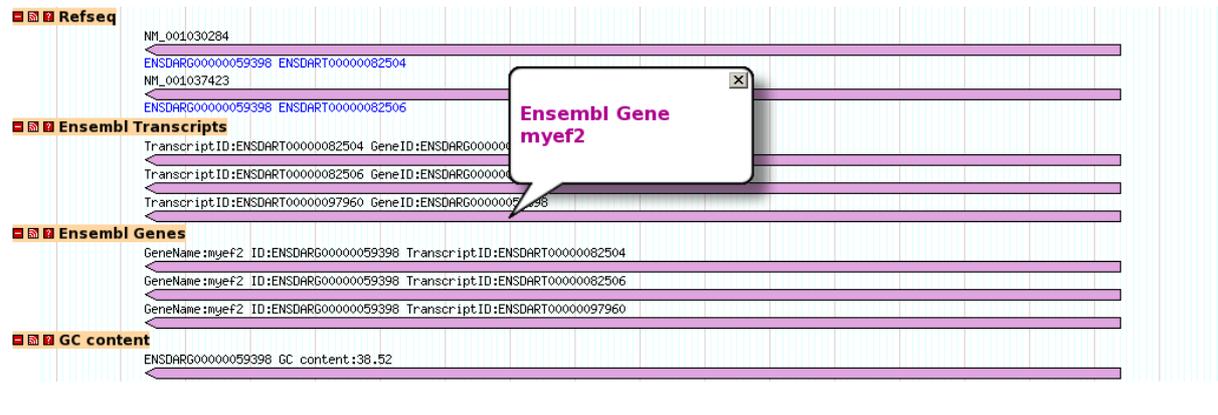
Feature description

GBrowse displays pop-up balloons when one hovers over the different data being displayed by the use of colored glyphs, or icons, to highlight the data.



On clicking this glyph, it shows a hyperlink to the resource of this data as shown below.

The balloon displays track description followed by the information for that particular region in the above format.



Customizing the Detail Panel

You can customize the detailed display in a number of ways:

Turn tracks on and off

The figure shows the "Tracks" panel in the FishMap interface. It contains a list of tracks with checkboxes to turn them on or off. The tracks are organized into several categories:

- Analysis:** Blast Against Displayed Sequence, Restriction Sites
- ERPIN:** Antizyme RNA frameshifting stimulation element, GRIK4 3 prime UTR element, Potassium channel RNA editing signa, Type II tRNA, Arthropod 75K RNA, Hairpin Ribozyme, Prion pseudoknot, U1 spliceosomal RNA, Bicoid 3'-UTR regulatory element, Histone 3' UTR stem-loop, Pseudoknot of the domain GIG12 of 23S ribosomal RNA, U2 spliceosomal RNA, CsrB/RsmB RNA family, Invasion gene-associated RNA, Pseudoknot of upstream pseudoknot domain (UPD) of the 3'UTR 11, U4 spliceosomal RNA, cRNA, Iron response element, RTT RNA, U5 spliceosomal RNA, ERPIN miRNA Predictions, L-myc internal ribosome entry site (IRES), Small Nucleolar RNA Predictions from ERPIN, U6atac minor spliceosomal RNA, Eukaryotic 5S rRNA, Ma3 gene ribosomal frameshift signa, SRP RNA Domain IV, Unal2 line 3, Eukaryotic type signal recognition particle RNA, Nanos 3' UTR translation control element, TrikB IRES, Vault RNA, FGF-1 internal ribosome entry site (IRES), Other Predictions from ERPIN, Type I tRNA, Voltage-gated potassium-channel Kv1.4 IRES
- Ensembl:** Ensembl Data, Ensembl Transcripts, Refseq, Ensembl Genes, GC content
- Expression:** Digital Gene Expression Tags
- General:** Genes
- Nucleosome Exclusion Regions:** NXSENSOR
- Orthologs:** Inparanoid
- Pathway:** GO, PDB, PROSITE, PATHWAY, PFAM
- Quadruplex:** Quadruplex
- TARGETS:** miRanda Target, RNAHYBRID Target, TARGETSCAN Targets
- UTR:** Androgen receptor GU-rich element (AR_CURE), Gamma interferon activated inhibitor of Ceruloplasmin mRNA translation (GAIT element), Male specific lethal 3' UTR cis-acting element (MSL2-3UTR), TGE translational regulation element (TGE), AU-rich class-2 Element (ARE2), Histone 3'UTR stem-loop structure (HSL3), Mos polyadenylation response element (Mos-PRE), Upstream Open Reading Frame (uORF), Bruno 3' UTR responsive element (BRE), Internal Ribosome Entry Site (IRES), Selenocysteine Insertion Sequence (SECIS) - type 1, Cyttoplasmic polyadenylation element (CPE), Iron Responsive Element (IRE), Selenocysteine Insertion Sequence (SECIS) - type 2
- Variation:** SNP
- McRNA:** McRNA

The panel labeled "Tracks" contain a series of check-boxes. Each check-box

corresponds to a track type. Selecting the check-box activates its type. Select the label to the right of the check-box to display a window that provides more detailed information on the track, such as the algorithm used to generate it, its author, or citations.

Change the properties of the tracks using the "Configure Tracks" button

Settings for ZV8_v3 Database

| Undo Changes | | Revert to Defaults | Refresh | Track Options | | | Cancel Changes and Return... | Accept Changes and Return... |
|--|-------------------------------------|--------------------|----------|--------------------|--|--|------------------------------|------------------------------|
| Track | Show | Format | Limit | Change Track Order | | | | |
| Track 1 PROSITE | <input checked="" type="checkbox"/> | Auto | No limit | | | | | |
| Track 2 Unal2 line 3 | <input type="checkbox"/> | Auto | No limit | | | | | |
| Track 3 SNP | <input checked="" type="checkbox"/> | Auto | No limit | | | | | |
| Track 4 Quadruplex | <input checked="" type="checkbox"/> | Auto | No limit | | | | | |
| Track 5 Histone 3'UTR stem-loop structure (HSL3) | <input type="checkbox"/> | Auto | No limit | | | | | |
| Track 6 Iron Responsive Element (IRE) | <input type="checkbox"/> | Auto | No limit | | | | | |
| Track 7 Selenocysteine Insertion Sequence (SECIS) - type 1 | <input type="checkbox"/> | Auto | No limit | | | | | |
| Track 8 Selenocysteine Insertion Sequence (SECIS) - type 2 | <input type="checkbox"/> | Auto | No limit | | | | | |
| Track 9 Cytoplasmic polyadenylation element (CPE) | <input type="checkbox"/> | Auto | No limit | | | | | |
| Track 10 TGE translational regulation element (TGE) | <input type="checkbox"/> | Auto | No limit | | | | | |

This will bring up a window that has detailed settings for each of the tracks. Toggle the check-box in the "Show" column to turn the track on and off (this is the same as changing the check-box in the Search Settings area). Change the pop-up menu in the "Format" column to alter the appearance of the corresponding track. Options include:

- *Compact* which forces all items in the track onto a single overlapping line without labels or descriptions;
- *Expand*, which causes items to bump each other so that they don't collide; and
- *Expand & Label*, which causes items to be labeled with their names and a brief description. The default, *Auto* will choose compact mode if there are too many features on the track, or one of the expanded modes if there is sufficient room. Any changes you make are remembered the next time you visit the browser. **Press Accept Changes and Return...** when you are satisfied with the current options. One may restore defaults by clicking on *Revert to Defaults* and undo changes by clicking *Undo Changes*.

Change the order of tracks using the "Configure Tracks" button.

The last column of the track options window allows you to change the order of the tracks. The pop-up menu lists all possible feature types in alphabetic order. Select the feature type you wish to assign to the track. The window should refresh with the adjusted order automatically, but if it doesn't, select the "Refresh" button to see the new order.

Uploading Your Own and 3rd Party Annotations

This browser supports third party annotations, both your own private annotations and published annotations contributed by third parties.

Uploading Your Own Annotations

■ [Add your own tracks](#)

Upload your own data: [\[Help\]](#)

Upload a file

To view your own annotations on the displayed genome, go to the bottom of the screen and click on the **Browse...** button in the file upload area. This will prompt you for a text file containing your annotations. See the annotation format help document for information on how to create this file.

Once loaded, tracks containing these annotations will appear on the detailed display and you can control them just like any of the built-in tracks. In addition, new **Edit**, **Delete** and **Download** buttons will appear in the file upload area. As their names imply, these buttons allow you to edit the uploaded file, download it, or delete it completely.

■ [Add your own tracks](#)

Upload your own data: [\[Help\]](#)

Upload a file

Add remote annotations: [\[Help\]](#)

The date at which the uploaded file was created or last modified is printed next to its name. If there are a manageable number of annotated areas, GBrowse will create links that allow you to jump directly to them.

You may upload as many files as you wish, but be advised that the performance of the browser may decrease if there are many large uploads to process.

Viewing 3rd Party Annotations

To view 3rd party annotations, the annotations must be published on a reachable web server and you must know the annotation file's URL.

Add remote annotations: [\[Help\]](#)

Enter Remote Annotation URL

At the bottom of the browser window is a text box labeled "Enter Remote Annotation URL". Type in the URL and then press "Update URLs". The system will attempt to upload the indicated URL. If successful, the data will appear as one or more new tracks. Otherwise you will be alerted with an error message.

You may add as many remote URLs as you wish. To delete one, simply erase it and press "Update URLs" again.

Quick Uploads

Another way to upload your own features is by adding an "add" argument to the gbrowse URL. For example, this URL will create a track named "MyGff" containing a feature named "Trial". Trial occupies the region on the genome between 323790 and

324790.

http://fishmap.igib.res.in/cgi-bin/gbrowse/ZV8_v3/?add=chr1+MyGff+Trial+323790..324790

You can have as many "add" options as you like:

http://fishmap.igib.res.in/cgi-bin/gbrowse/ZV8_v3/?add=chr1+MyGff+Trial+323790..324790;add=chr1+MyGFF+Trial2+323790..324790

The format is:

reference+trackName+featureName+start..stop,start..stop,start..stop ...

where "reference" is the name of the landmark that start and stop are relative to. You can use a chromosome name, a gene name, or anything else that this browser recognizes in the search box. "trackName" is the name of the track to upload, "featureName" is the name of the feature you are uploading, and "start..stop" are the start and end coordinates relative to "reference". For multisegmented features, specify multiple start..stop pairs separated by commas.

See the uploaded annotation help file for more details

Software Bugs

As always, this software may contain bugs. Please report any that you suspect to the author, along with whatever information that you can provide as to what you were doing when the bug appeared.

AUTHOR

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