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## **Module 2: Maps and Genome Sequence (NCBI)**

### **iii - Map Viewer Genome Browser**

#### **Aims**

- Introduce NCBI's Map Viewer Genome Browser
- Suggest alternative search strategies
- Provide examples of text queries
- Show examples of display options

#### **Introduction**

NCBI's Map Viewer (<http://www.ncbi.nlm.nih.gov/mapview/>) provides a graphical display of mapped genes, markers and sequences for a number of organisms including vertebrates, invertebrates, protozoa, plants and fungi. The zebrafish Map Viewer provides a graphical view of the zebrafish genome sequence (annotation of the Zv4 assembly), genetic and radiation hybrid maps.

You can submit a text based query against the whole genome, a subset of chromosomes, or a single chromosome. Query by a gene symbol, gene name, accession number, or a wild card search using an asterisk (\*) to view placement in the genomic context. Text searches can be submitted from the search bar on Map Viewer's home page, the genome view or map view pages or on the Advanced Search form. Regions of interest can also be retrieved by sequence alignment with a BLAST search.

You may also look for gene information by its position relative to other mapped markers, genes, clones, SNPs or gene models.

MapView enables you to identify genes within a candidate region, members of a gene family, genes associated with SNPs or disease related genes between two markers.

#### **Exercises**

To explore a region of a particular chromosome or the placement of an object,

try one of the follow:

- Submit a text search of a gene or marker
- Limit your search by chromosome, the type of mapped object or map name by clicking on the **“Advanced Search”** button
- Review the hits on the available maps
- Choose one or more hits and view results in the graphical viewer
- Scroll up or down the chromosome from your mapped gene to see neighboring mapped objects
- Zoom in or out to change the level of visible detail
- View connections between maps
- Change the visible maps by clicking on **“Maps and Options”**
- Examine the transcript evidence support the placement of a gene on the genome

Choose among these options and explore the Zebrafish genome in NCBI's MapViewer (<http://www.ncbi.nlm.nih.gov/mapview/>).

NCBI NCBI Map Viewer

Genome Taxonomy Entrez BLAST Help

Search  for

**Now Available!** - NCBI's annotation of the **cow** (*Bos taurus*) genome assembly (build 1.1). The cow is both an agriculturally important animal and a useful model organism for biomedical research. [Map Viewer](#) and many [other resources](#) at NCBI now provide a more comprehensive resource for cow.

Click on the organism name to go to the genome view

**Vertebrates**

**Mammals**

- [BLAST](#) *Bos taurus* (cow)
- [BLAST](#) *Canis familiaris* (dog)
- [BLAST](#) *Felis catus* (cat)
- [BLAST](#) *Homo sapiens* (human)
- [BLAST](#) *Mus musculus* (mouse)
- [BLAST](#) *Ovis aries* (sheep)
- [BLAST](#) *Pan troglodytes* (chimpanzee)
- [BLAST](#) *Rattus norvegicus* (rat)
- [BLAST](#) *Sus scrofa* (pig)

**Other Vertebrates**

- [BLAST](#) *Danio rerio* (zebrafish)
- [BLAST](#) *Gallus gallus* (chicken)

**Invertebrates**

**Insects** [BLAST](#)

- [BLAST](#) *Anopheles gambiae* (mosquito)
- [BLAST](#) *Apis mellifera* (honey bee)
- [BLAST](#) *Drosophila melanogaster* (fruit fly)

**Nematode** [BLAST](#)

- Caenorhabditis elegans* (nematode)

**Protozoa**

- [BLAST](#) *Plasmodium falciparum*

**Plants** [BLAST](#) [Search all plant maps](#)

- [BLAST](#) *Arabidopsis thaliana* (thale cress)
- [BLAST](#) *Avena sativa* (oat)
- [BLAST](#) *Glycine max* (soybean)
- [BLAST](#) *Hordeum vulgare* (barley)
- [BLAST](#) *Lycopersicon esculentum* (tomato)
- [BLAST](#) *Oryza sativa* (rice)
- [BLAST](#) *Triticum aestivum* (wheat)
- [BLAST](#) *Zea mays* (corn)

**Fungi** [BLAST](#)

- [BLAST](#) *Candida glabrata*
- [BLAST](#) *Debaryomyces hansenii*
- [BLAST](#) *Encephalitozoon cuniculi*
- [BLAST](#) *Eremothecium gossypii*
- [BLAST](#) *Gibberella zeae*
- [BLAST](#) *Kluyveromyces lactis*
- [BLAST](#) *Magnaporthe grisea*
- [BLAST](#) *Neurospora crassa*
- [BLAST](#) *Saccharomyces cerevisiae* (baker's yeast)
- [BLAST](#) *Schizosaccharomyces pombe* (fission yeast)
- [BLAST](#) *Yarrowia lipolytica*

See more about [Bacteria](#) ([BLAST](#)), [Organelles](#) ([BLAST](#)), [Viruses](#) ([BLAST](#))

Submit a search here

Resources Workshop – Dresden 2005

Click here to view the Advanced Query options

View build statistics

Click on BLAST to submit a search

Click on a chromosome to view mapped objects

NCBI Map Viewer home

**Danio rerio genome view**  
Zv4 statistics

BLAST search Danio rerio genome

**Lineage:** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio; Danio rerio

In July 2004, the Zebrafish Genome Project, led by the [Wellcome Trust Sanger Institute](#), released [Zv4](#), a 5.7X coverage of the zebrafish genome sequence generated by whole genome shotgun and fingerprinted BAC clone sequencing. Zebrafish is an excellent vertebrate model to study human development and disease. These tiny, freshwater fish have 25 pairs of chromosomes and a genome size of 1.7 Gb.

Build 1.1 of the zebrafish reference sequence (RefSeq) genome assembly, provided by NCBI using [Zv4](#) assembly instructions from the [Sanger Institute](#) is available in NCBI's Map Viewer. Map Viewer graphically displays features on the zebrafish genome sequence assembly, including NCBI contigs (the "Contig" map), the WGS sequences (the "Component" map), and the location of genes, STSs, ESTs, and Gnomon predicted gene models.

In collaboration with [ZFIN](#) and members of the zebrafish community, Map Viewer also displays genetic maps (GAT, HS, MGH, MOP, and ZMAP) and radiation hybrid maps (LN54 and T51).

### Advanced Search:

Submit a query against Chromosomes 8 and 17 for all zgc mapped genes on the Ab initio, estDr, MGH and T51 maps.

NCBI Map Viewer home

**Danio rerio advanced search**

**Search in fields:**  
☒ no restriction  
☐ [id] ID of mapped object  
☐ [sym] symbol  
☐ [title] name of mapped object  
**Chromosome(s):** select all clear  
☐ 1 ☐ 2 ☐ 3 ☐ 4 ☐ 5 ☐ 6  
☐ 7 ☒ 8 ☐ 9 ☐ 10 ☐ 11 ☐ 12  
☐ 13 ☐ 14 ☐ 15 ☐ 16 ☒ 17 ☐ 18  
☐ 19 ☐ 20 ☐ 21 ☐ 22 ☐ 23 ☐ 24  
☐ 25 ☐ Unknown

**Type of mapped object:** select all clear  
☒ Component ☒ Contig ☒ Gene ☒ Gene Prediction ☒ Marker  
☒ STS ☒ Sequence ☒ Transcript

**Map name:** select all clear  
 Sequence Genetic RH  
☒ Ab initio ☐ GAT ☐ LN54  
☐ Component ☐ HS ☒ T51  
☐ Contig ☒ MGH  
☒ estDr ☐ MOP  
☐ GenBank DNA ☐ ZMAP  
☐ Gene  
☐ RefSeq Transcripts  
☐ STS

Try adding another term to your query with "AND" to further restrict your query.

**View the results of the query: zgc\* AND transcription, restricted to Chromosomes 8 and 17.**  
**Click on the red tick marks to go to see the placement of the objects on Chromosome 8.**

**Search for** (zgc\* AND transcriptic on chromosome(s) 8 17 **Find** **Advanced Search**

☐ Show related entries MapViewer home

**Danio rerio genome view** **Zv4 statistics** **BLAST search Danio rerio genome**

Hits: 1 2 3 4 5 6 7 8 9 10 11 12 13


Hits: 14 15 16 17 18 19 20 21 22 23 24 25 III

**Search results for query "(zgc\* AND transcription) AND (model[map\_name] OR t51[map\_name] OR mgh[map\_name] OR estDr[map\_name] OR genes[map\_name])": 2 hits**

LG	Match	Map element	Type	Maps
8	<a href="#">all matches</a>			
	wu:fc17f01	<a href="#">cnot6</a>	GENE	<a href="#">Genes_seq</a>
	NK2 transcription factor related 7	<a href="#">nkx2.7</a>	GENE	<a href="#">Genes_seq</a>

**Click on the gene symbol or map name to view the placement of the objects on chromosome 8**

- View the placement of *nkx2.7* on Chromosome 8.
- Follow links to ZFIN or UniSTS (sts).
- View placement information by clicking on the “Go To” blue arrow.
- Click on the chromosome or the zoom box to zoom in our out.
- Click on “Maps & Options” to change the maps displayed and other display options.

NCBI  NCBI Map Viewer

PubMed Entrez BLAST OMIM Taxonomy Structure

Search  Find Find in This View Advanced Search


Map Viewer Home

Map Viewer Help Zebrafish Maps Help Data As Table View

**Maps & Options**

Compress

Map ☐ Region Shown: 3128.36 3574.45 Go

You are here: 

**zoom box**

**Danio rerio (zebrafish) Zv4** [BLAST The Genome](#)

Chromosome: [1](#) [2](#) [3](#) [4](#) [5](#) [6](#) [7](#) [8](#) [9](#) [10](#) [11](#) [12](#) [13](#) [14](#) [15](#) [16](#) [17](#) [18](#) [19](#) [20](#) [21](#) [22](#) [23](#) [24](#) [25](#)

Query: (zgc\* AND transcription) AND (model[map\_name] OR t51[map\_name] OR mgh[map\_name] OR estDr[map\_name] OR genes[map\_name]) [\[clear\]](#)

Master Map: Goodfellow T51 [Summary of Maps](#) [Maps & Options](#)

Region Displayed: 3128.36-3574.45 cR

Genes_seq	Name	cR	Links	sts	gnt	hs	ln54	mgh	map	zmg	Go to
LOC568532	fb09c08	3171	<a href="#">ZFIN</a>								
LOC568601	bz1l10.z	3171	<a href="#">ZFIN</a>								
LOC568211	unp1170	3171	<a href="#">ZFIN</a>								
LOC568375	<b>nkx2.7</b>	3171	<a href="#">ZFIN</a>	<a href="#">sts</a>							
LOC568798	si:busm1-266f07.2	3171	<a href="#">ZFIN</a>	<a href="#">sts</a>							
LOC568240	zc117f17.za	3171	<a href="#">ZFIN</a>								
LOC568240	fj37c05	3171	<a href="#">ZFIN</a>								
LOC568751	fa93a04	3171	<a href="#">ZFIN</a>								
LOC568699	zsnp729	3171	<a href="#">ZFIN</a>								
LOC568672	zk22e2.t7	3171	<a href="#">ZFIN</a>								
LOC568946	fi73e02	3171	<a href="#">ZFIN</a>								
LOC567868	fj17g12	3171	<a href="#">ZFIN</a>								
LOC568446	<b>z7130</b>	3245	<a href="#">ZFIN</a>								
LOC568638	zc95k3.za	3245	<a href="#">ZFIN</a>								
LOC568638	zc65o18.za	3245	<a href="#">ZFIN</a>								
LOC572922	zk106c1.sp6	3245	<a href="#">ZFIN</a>								
LOC568510	fb07g06	3245	<a href="#">ZFIN</a>								
LOC568610	zsnp1982	3245	<a href="#">ZFIN</a>								

**Maps & Options**

MapView

- Recenter
- Zoom in x2
- Zoom in x4
- Zoom in x8
- Zoom out x2

Mouse over the chromosome, click and open this box.  
Choose an option to change your view.

Additional placements for nkx2.7

assembly	map	chr	object	location	
reference	genes	8	nkx2.7	28995000—28998100 bp	<a href="#">go</a>
n/a	hs	8	nkx2.7	123.2 cM h	<a href="#">go</a>
n/a	zmap	8	nkx2.7_hs	81.5 cM z	<a href="#">go</a>
n/a	zmap	8	nkx2.7_t51	81.5 cM z	<a href="#">go</a>

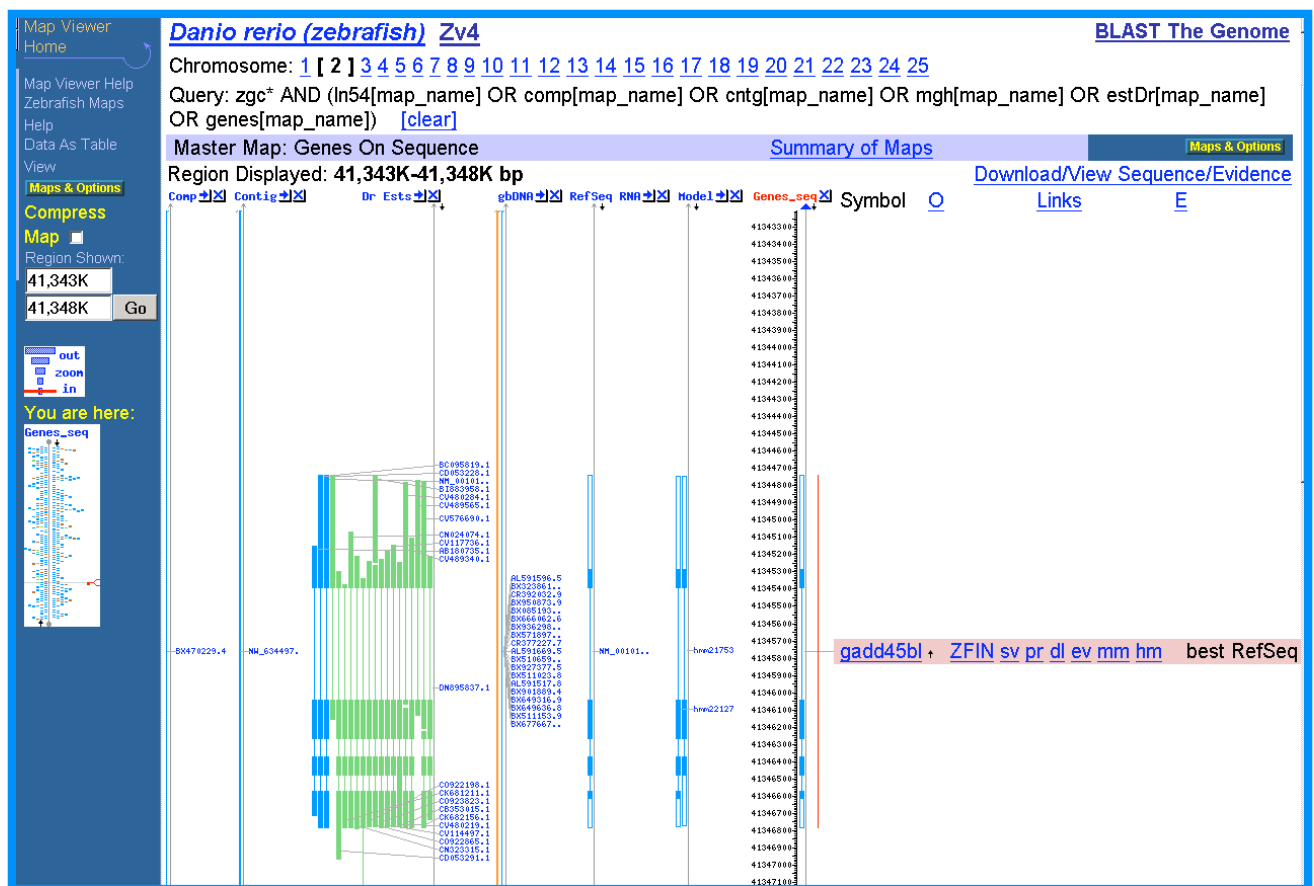
And click on 'go' to jump to the placement of nkx2.y on the other maps

**Another option is to view one of the genes in the results set: gad45bl**

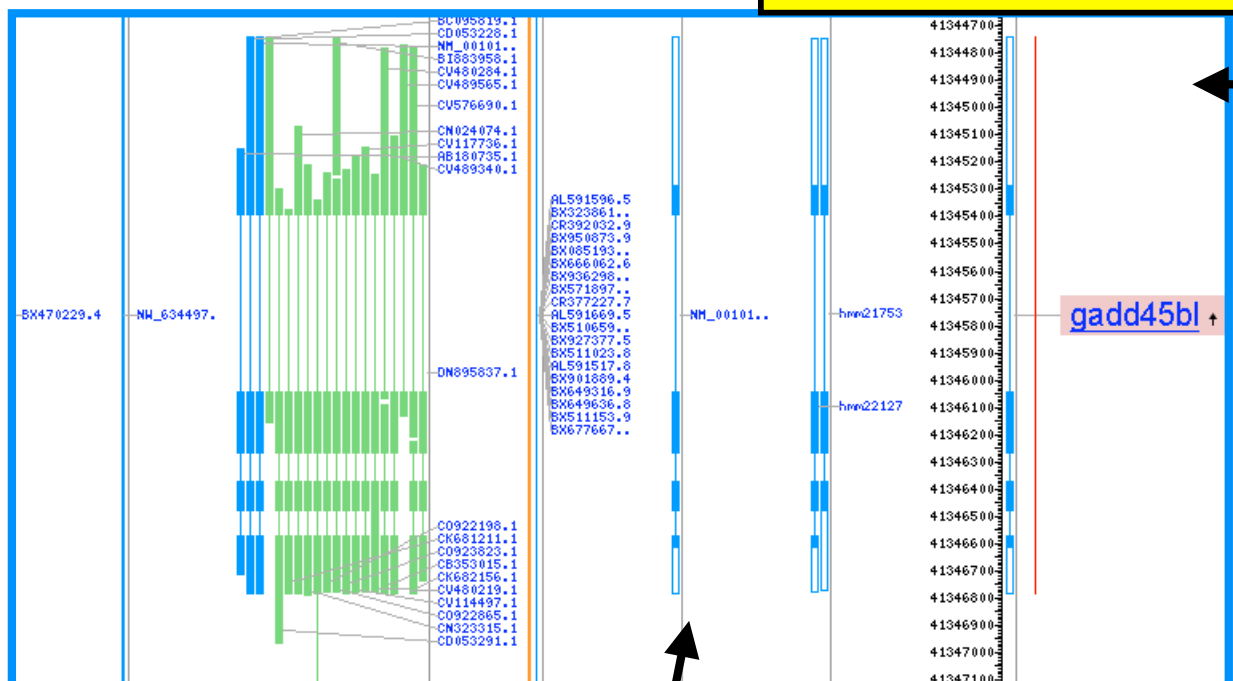
- Click on maps and options
- Select from the Available Maps, click Add, to add these maps to the Maps Displayed list
- Click Apply to make these changes in the display

The screenshot shows a web browser window titled "Map Viewer - Mozilla". The interface is for configuring gene maps for the organism **Danio rerio**. At the top, there are fields for **Chromosome: 2** and **Region Shown: 41343202.7: 41348320.2**, with a **Help** link. Below this, there are two main sections: **Available Maps:** and **Maps Displayed (left to right):**. The **Available Maps:** section contains a list of map types: ---Sequence Maps---, Ab initio, Component, Contig, estDr, GenBank DNA, Gene, RefSeq Transcripts, and STS. There are **ADD>>** and **<<REMOVE** buttons between the two lists. The **Maps Displayed (left to right):** section contains a list of selected maps: [ ] Component, [ ] Contig, [ ] estDr, [ ] GenBank DNA, [ ] RefSeq Transcripts, [ ] Ab initio, and [R] Gene. To the right of this list are buttons for **Move UP**, **Move DOWN**, **Make Master/Slave**, **Toggle Ruler**, and a checkbox for **([R] before map set')**. Below these sections is a **More Options:** section with checkboxes for **Show Connections** (unchecked) and **Verbose Mode** (checked). There is a **Compress Map:** dropdown set to **off** and a field for **Auto Compress if > 350 px**. The **Page Length:** is set to **35**. At the bottom are **OK**, **Apply**, and **Close** buttons.

**View the transcript evidence in the Dr ESTs map or the Gnomon models representing supported alternative transcripts in the Model map (<http://tinyurl.com/doqvo> ).**



or in zoomed in a bit ...



Contig NW\_634497

Gnomon models

RefSeq: NM\_001012386