# Web resources for *C. elegans* studies\*

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## 1. Introduction

This chapter describes a list of core Web resources that I think are most useful to someone who is either new to studying *C. elegans* or who has not been using the Web much as a research tool. It does not contain a

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comprehensive list of Web sites and services since links to other useful Web resources can usually be readily found at the sites discussed here.

Internet is the information super highway and the World Wide Web is the easiest way to access most of the information on the internet. Although one can always find some information about anything on the Web, it is not necessarily easy to find the most relevant quickly. The Web is vast. Since its debut for internal use at CERN in 1991, the Web has grown into a global network of 60 million sites as of March 2005 (<a href="http://news.netcraft.com/archives/web\_server\_survey.html">http://news.netcraft.com/archives/web\_server\_survey.html</a>). Furthermore, the format of Web resources and information pages is divergent, prevents highly efficient queries across all sites. Thus, Web search engines are billion-dollar industries and people are being paid for their Web surfing skills, researching the Web for answers of specific questions (<a href="http://answers.google.com/answers/">http://answers.google.com/answers/</a>).

Today, it is perhaps still possible to study *C. elegans* without using the Web, but likely with much reduced efficiency. One can use the Web to place an order for a deletion mutant, to read a summary of all that is known about one's favorite gene, to perform a sequence analysis or download a sequence for local analysis, or to look up a paper and read it online anywhere there is internet access. It is true that we cannot yet have worms delivered through fiber optics cables, but anything that can be reduced to a digital form is either available on the Web today or will be tomorrow. Via fast internet and hyperlinks, all digitized information around the world about the worm can be brought to one's computer terminal in an instance.

But one needs to know where to look. To most, it probably is an easier experience using the Web for the first time than to try to find something in a brick and mortar library-that's why the Web is popular. However, to efficiently take advantage of available Web resources, it is best to know exactly where the resources are and how to use them when one gets there. I try to write this chapter as an introductory guide for those who are just starting to tap into the Web for their worm research. It is by no means a complete guide but it should make it easier for people to get started.

## 2. Portal and knowledge environment

There are two types of Web services most suitable as one's starting points: portal and knowledge environment. A portal organizes Web links relevant to the domain of interest. From a portal, a user can quickly find sites and services of potential interest and via hyperlinks be brought there. In contrast, a knowledge environment is a Web site that directly offers many different types of information and services. A knowledge environment often emphasizes the interconnection among data types, which in a way is a web within the Web. In practice, most Web sites have portal pages.

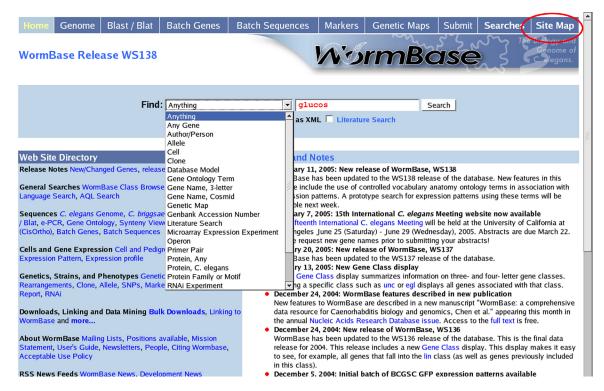
#### 2.1. WormBase

WormBase <a href="http://www.wormbase.org">http://www.wormbase.org</a> is a major repository for *C. elegans* information, including genomic, genetic, anatomy, people, and literature. WormBase is a knowledge environment. Access to information is via a set of Web pages, each of which specifically designed for a different type of biological knowledge. Further, different information types, when appropriate, are connected horizontally via hyperlinks. One can easily move from Web page of one type to another. For example, one can start by visiting a genome sequence, click a link to read about a gene that resides in this sequence on a gene page, click a link again to review an expression pattern description on an expression pattern page, click yet again to read about a cell on an anatomy page, and so on.

Some WormBase pages are complex. WormBase offers an online user guide. There is also a book chapter <a href="http://www.mrw.interscience.wiley.com/cp/cpbi/articles/bi0108/frame.html">http://www.mrw.interscience.wiley.com/cp/cpbi/articles/bi0108/frame.html</a>; although the access is restricted to subscribers of the journal. In this section I describe a few general purpose pages. In following sections, I discuss more specialized pages. Users are encouraged to visit the site and practice the most effective Web surfing technique-click and browse.

## **Basic Query** <a href="http://www.wormbase.org">http://www.wormbase.org</a>

On the front page of WormBase, type a query term (e.g. glucos) in the query box, select an information type from the pull down menu to the left and hit the "Search" botton.



The information type "Anything" gives the broadest search option and should be selected unless one wishes to restrict the search to a specific type. The search term "glucos" is deliberately left in the 'root' form of related words so that the search includes all terms that start with "glucos", such as glucose, glucosamin, glucosyl, etc.).

**Site Map** <a href="http://www.wormbase.org/db/misc/site\_map">http://www.wormbase.org/db/misc/site\_map</a>

This page is like a portal which links to pages of major searches, data viewers and resources within WormBase, providing users a general idea of what's available.

FTP Download <ftp://ftp.wormbase.org/pub/wormbase/>

Both the data and software of WormBase can be downloaded and worked with locally. This feature is not for the casual users but particularly useful for those who routinely perform large-scale data analysis. A README file <ftp://ftp.wormbase.org/pub/wormbase/README> indicates which data are available for download.

WormMart <a href="http://dev.wormbase.org/BioMart/martview">http://dev.wormbase.org/BioMart/martview</a>

Presently still under development, WormMart is an advanced query tool which allows users customize complex queries. It is also designed to run fast, expediting results returned from complex and large-scale queries. WormMart focuses on sequence-related data types.

#### 2.2. Caenorhabditis elegans WWW Server

<a href="http://elegans.swmed.edu/">http://elegans.swmed.edu/>

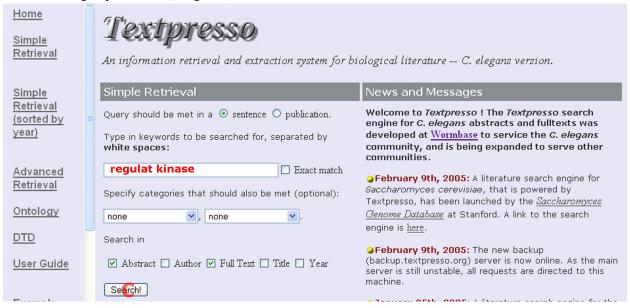
This site is a well-organized portal of many different types of information useful to *C. elegans* researchers. It is organized in two layers. The front page lists major topics or interests. Each topic has a hyperlink to a page that either offers a service (e.g. Literature Search) or is a list of links to other Web sites that offer services. Each page and link of this portal is generally self-explanatory; thus no user guide is necessary. Users can easily drill down the links to find out what is available at this site in a few minutes.



#### 3. Literature search

#### 3.1. Textpresso

Textpresso <a href="http://www.textpresso.org">http://www.textpresso.org</a> allows text searches on primarily *C. elegans* literature, including published papers, personal communications and meeting reports. Two major features distinguish Textpresso from other literature search tools: that it searches full-text contents of publications, and in addition to text strings, that it can search for groups of terms (categories).

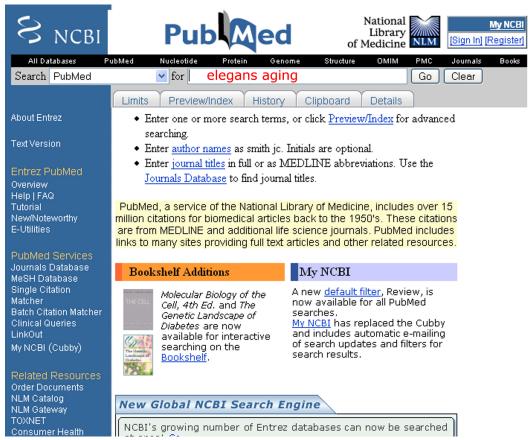


The simplest way to search using Textpresso is to start with the default settings and type into the query box a text string. For example, if one wants to learn about regulation of kinases, one can search for "regulat kinase".

Textpresso treats the words independently. The default setting automatically appends a wild card to the end of each word thus expanding the search to include any word that begins with "regulat" or "kinase". Further, the default setting is to search for sentences that simultaneously have both groups of words. Textpresso also offers category search and many other more advanced features. Users can read the user guide to learn how to use advanced features.

#### 3.2. NCBI PubMed

NCBI PubMed allows queries on articles in a large collection of biomedical journals. Coverage of PubMed is broad and usually up to date but some literature relevant to *C. elegans* studies is not covered. Also, Pubmed searches are limited to citations and abstracts.



To search, one can start by typing a term of interest in the query box and click the "Go" button. Read the tutorial to learn how to perform more sophisticated queries.

## 3.3. Caenorhabditis elegans WWW Server Worm Literature Index

Caenorhabditis elegans WWW Server Worm Literature Index <a href="http://elegans.swmed.edu/wli/">http://elegans.swmed.edu/wli/</a> offers text searches on citations and abstracts of selected publications, Worm Breeder's Gazette articles, and Worm meeting abstracts. Coverage of publications is limited to those selected by CGC (C. elegans Genetic Center). Although the coverage of search space here is only a subset of that of Textpresso, the user interface is self-explanatory, easy to use, and one can search for phrases.

## **Worm Literature Index**

Word(s) to search for:

- Partial word matches allowed
- ✓ Author ✓ Title ✓ Text

Find abstracts containing:

Any word
 All words
 Phrase

#### Find abstracts from:

- All Sources.
- Published books and papers only.
- 2004 Worm Meetings only.
- Last Worm Breeder's Gazette only.
- Any Worm Breeder's Gazette.
- Any Worm Meeting.



#### 4. Gene function

Many different aspects of biological knowledge go into the description of gene functions, including mutant phenotype, site of action, interaction with other genes, and sequence similarity to other genes. A Web resource that has descriptions of gene function usually offers a type of pages that integrate these aspects so that a user can have a holistic view of gene function at a glance.

## 4.1. WormBase Gene Summary

<a href="http://www.wormbase.org/db/gene/gene">http://www.wormbase.org/db/gene/gene>

Each gene in WormBase has a summary page which collates together several different aspects of a gene, including identification, genetic and genomic location, function, reagents and bibliography.

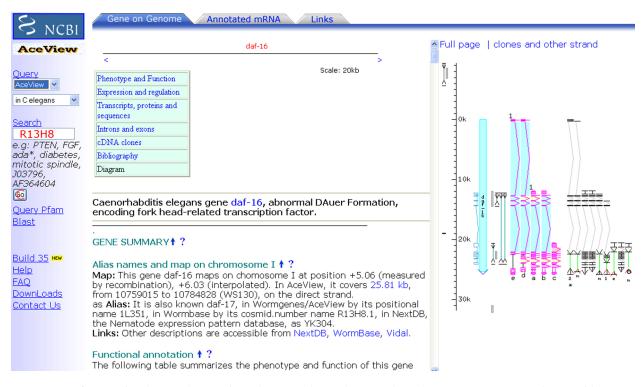
## **Gene Summary**

Specify a gene using a three letter locus-name (unc-26), a predicted gene id (R13A5.9), or a protein ID (WP:CE02711): WBGene00000481

[identification] [location] [function] [gene ontology] [reactome knowledgebase] [alleles] [similarities] [reagents] [bibliography] Identification IDs: CGC name Sequence name WB Gene ID Version ZC416.8 WBGene00000481 cha-1 - (abnormal CHoline Acetyltransferase) Concise cha-1 is part of a gene complex, in which it shares a common promoter and first (noncoding) exon with unc-17 Description: (and is thus coexpressed with unc-17), but in which the two genes encode mutationally separable functions; cha-1 encodes a choline acetyltransferase that synthesizes acetylcholine, is expressed in neurons, and is required for viability, normal growth, locomotion, and sensitivity to acetylcholinesterase inhibitors. [details] NCBI Carnitine O-acyltransferase CRAT [KOG3717] KOGs\*: Species: Caenorhabditis elegans Other L08969 (Nematode choline acetyltransferase (cha-1) mRNA, exons 1-11 and complete cds.) sequence L08970 (Nematode choline acetyltransferase (cha-1) gene, exons 1-11 and complete cds.) (s): ZC416 Gene model Gene Nucleotides Amino Protein Status Remark Swissprot (s): Model (coding/transcript) Acids C. elegans CHA-1 protein; confirmed contains similarity to Pfam ZC416.8b by cDNA domain PF00755 1884/10766 bp WP:CE17308 CLAT\_CAEEL 627 aa (Choline/Carnitine oacyltransferase) Putative Caenorhabditis briggsae: CBG08307 [syntenic alignment] (: Stein LD et al. 2003 PubMed; : best reciprocal blastp ortholog(s): match-seg-off) Caenorhabditis briggsae: CBG08305 [syntenic alignment] (: Stein LD et al. 2003 PubMed ; : best reciprocal blastp match-seq-off) Literature 108 citations citations: Notes: Cha-1 only corresponds to ZC416.8b and not ZC416.8a which instead corresponds to the unc-17 gene. ZC416.8a and ZC416.8b are different alternatively spliced forms of the same gene that both share a common 5' untranslated exon (Alfonso et al., Journal of Molecular Biology 241: 627-630, 1994). SL1 trans-spliced; see yk1344c11.5. Location Genetic Position: IV:-3.31 +/- 0.003 cM [mapping data] Genomic Position: IV:3624692..3613927 bp

## 4.2. NCBI AceView

NCBI AceView <a href="http://www.ncbi.nlm.nih.gov/IEB/Research/Acembly/index.html?worm">http://www.ncbi.nlm.nih.gov/IEB/Research/Acembly/index.html?worm</a> shows clustering of EST sequences, their alignments to the genome, and annotation of genes, including gene structure, biological function, and bibliography.



To perform a simple search, type into the query box a key word (such as R13H8, a genomic cosmid name), click the "Go" button. Many navigation links are there on the result page. To get at the most information, users should click and browse around.

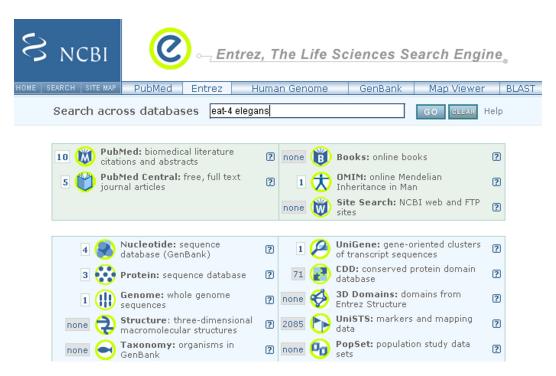
## 5. Sequence analysis-retrieval

## 5.1. NCBI GenBank

NCBI GenBank <a href="http://www.ncbi.nlm.nih.gov/Genbank/index.html">http://www.ncbi.nlm.nih.gov/Genbank/index.html</a> is a repository of sequences from many phylogenetically diverse organisms including the worm.



Search by a simple text string match; follow the appropriate links (Nucleotide or Protein) to download sequences.

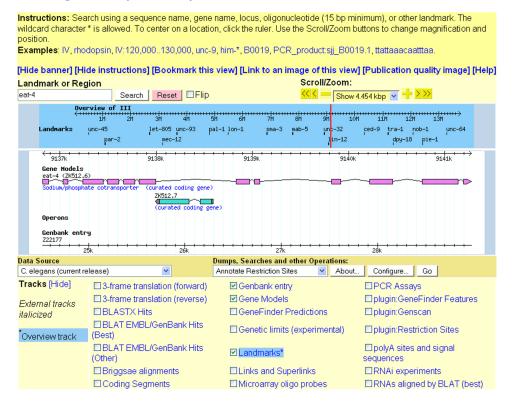


Notice the extensive links to other types of information here. Browse and click to explore.

#### 5.2. WormBase Genome Browser

WormBase Genome Browser <a href="http://www.wormbase.org/db/seq/gbrowse/wormbase">http://www.wormbase.org/db/seq/gbrowse/wormbase</a> is a physical map browser. Using Genome Browser, one can search and display sequences and sequence-related features; one can also zoom in or out and move along on a chromosome.

Showing 4.454 kbp from III, positions 9,136,822 to 9,141,275

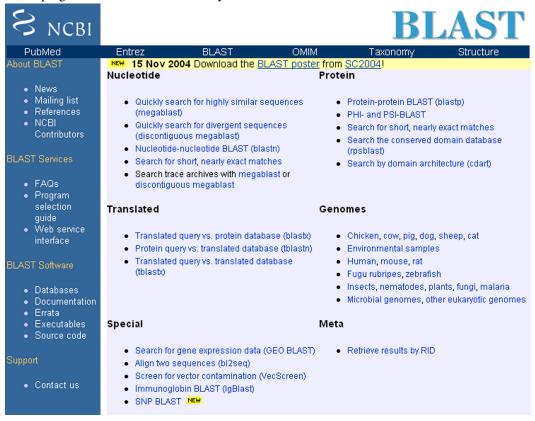


With Genome Browser, one can search for sequences by name or sequence (restricted to oligo size pieces) match, display and explore selected tracks of sequence and sequence features, and export sequences, features and images. Interested users can either explore around the page or read the user guides (<a href="http://www.its.caltech.edu/~wormbase/userguide/Menu/Sequence/index.html">http://www.mrw.interscience.wiley.com/cp/cpbi/articles/bi0108/frame.html</a>).

## 6. Sequence analysis-search for homologous sequences

#### 6.1. NCBI Blast

NCBI Blast <a href="http://www.ncbi.nlm.nih.gov/BLAST/">http://www.ncbi.nlm.nih.gov/BLAST/</a> offers a very extensive set of blast services. Here, different types of blast searches can be performed against all available sequences in GenBank database. One can even download programs to install and run locally.



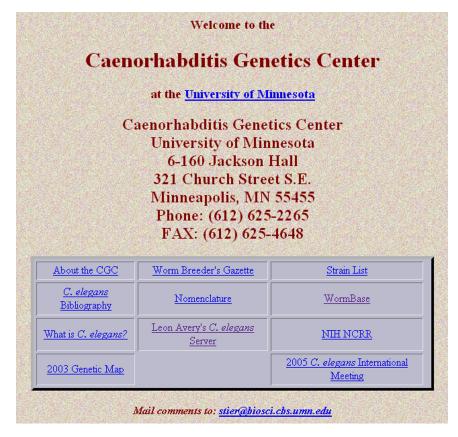
## 6.2. WormBase Blat Server

WormBase Blat Server <a href="http://www.wormbase.org/db/searches/blat">http://www.wormbase.org/db/searches/blat</a> is limited to basic Blast or Blat searches against *C. elegans* and C. Briggsae sequences. However, WormBase already stores information of homologous sequences from other species in its database. Such sequences may be displayed in Genome Browser under feature tracks.

#### 7. Genetics

## 7.1. Caenorhabditis Genetics Center (CGC)

Caenorhabditis Genetics Center (CGC) <a href="http://biosci.umn.edu/CGC/CGChomepage.htm">http://biosci.umn.edu/CGC/CGChomepage.htm</a> is a resource center for *C. elegans* genetics. It is responsible for gene nomenclature, strain collection and distribution, and genetic map construction. CGC homepage is a portal that has links to these and some other related services useful to *C. elegans* geneticists.



## 7.2. Genetic mapping analysis

WormBase integrates genetic map information with that of physical map. Two search tools are particular useful for genetic mapping analysis.

## **Genetic Interval Search**

- This page will list genes inside a genetically-defined interval.
- Specify a genetic interval using the names of two genes (for example evi-7 to sup-23).
- Alternatively, define the endpoints using the notation chromosome:position, as in II:-4.3 to II:-4.0.
- Entering a single value into the start position will center the search on a window 0.3 cM wide
- Interval size is currently limited to 2 cM. Longer intervals may take some time to collate.

From position/landmark: II:-4.3 To: III:-4.0 Search

#### Displaying genetic interval II:-4.3 to II:-4.0

Name	Мар	Pos	Type	Description
B0304.3 / cyp-23A1	II	-4.2541	nane	The B0304.3 gene encodes a homolog of the human gene CYP7B1, which when mutated leads to giant cell hepatitis (OMIM:231100). RNAi: WT [WBRNAi00009688]
B0304.1 / hlh-1		-4.2322	named gene	hlh-1 is orthologous to the human gene MYOGENIC FACTOR 6 (HERCULIN) (MYF6; OMIM:159991), which when mutated leads to disease. [C.elegansII] cc450am: recessive lethal, arrest at varying stages as lumpy dumpy with some muscle differentiation, disorganized myofilaments. Encodes member of MyoD family. Transcripts present transiently in MS descendants, stably in D daughters and C and MS lineages leading to body wall muscle. Antibody staining similar (nuclear staining, persists through development of body wall muscle cells). [Krause et al. 1990, 1994; Chen et al. 1992; KM; PD] RNAi: WT [WBRNAi00009686]; Unc [WBRNAi00024379]; Unc [WBRNAi00027142]
B0304.4	II	-4.2233	predicted	No molecular description available.

Genetic Interval Search <a href="http://wormbase.org/db/searches/interval">http://wormbase.org/db/searches/interval</a> can return a list of genes that have the potential to map within a specified genetic interval.

It should be noted that the genetic and physical map correlation is often solely based on statistical inferences thus should not be taken literally as factual.

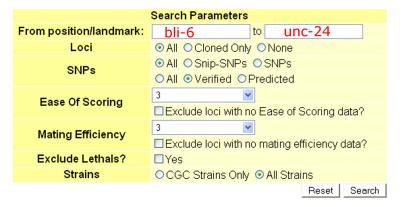
### 7.3. Small interval genetic mapping

SNP, Visible Marker, And Strain Search <a href="http://wormbase.org/db/searches/strains">http://wormbase.org/db/searches/strains</a> is particularly useful for finding markers for genetic mapping experiments in a small interval.

### SNP, Visible Marker, And Strain Search

This page is designed to assist in the selection of SNPS and visible genetic markers for mapping experiments. Provided with a genetic interval, it will display all visible markers and SNPs within that interval, as well as strains carrying those SNPs. The severity of markers can be restricted to avoid conflicts with the mutation of interest. To simplify in the acquisition of strains, strains can be restricted to those directly available from the CGC.

- Specify the interval using the names of two genetically defined loci (unc-70), or predicted genes (JC8.10a).
- Alternatively, you may provide genetic map positions using chromosome:position notation (III:-0.685).
- Please note: intervals are restricted to 2 cM.
- Entering a single value into the start position will center the search on a window 0.3 cM wide.
- · Learn more about how this script works.



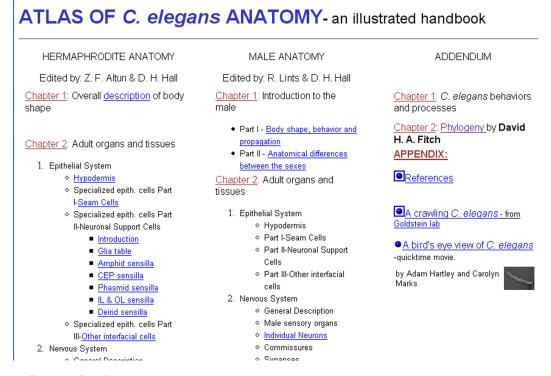
## 8. Cell and anatomy

#### 8.1. WormAtlas

WormAtlas <a href="http://www.wormatlas.org/">http://www.wormatlas.org/</a> provides anatomical information of *C. elegans*. The front page lists several useful entry points.



One can use the simple text search tool to search the site for information that relates to anatomical terms (e.g. PVT, name of a neuron). Another good way to use this site is to read sections of the "handbook".



### 8.2. Gene Expression Pattern

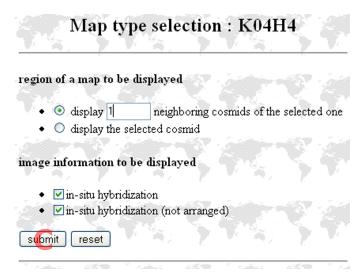
Summary of published gene expression data can be found at WormBase, or *C. elegans* AceView. Two Web sites offer primary, sometimes unpublished expression data.

The Nematode Expression Pattern Database (NEXTDB) <a href="http://nematode.lab.nig.ac.jp/db2/">http://nematode.lab.nig.ac.jp/db2/</a> provides access to *C. elegans* EST sequences obtained by Yuji Kohara's laboratory and some other experimental results derived from them, such as expression patterns determined by *in situ* hybridization, which can be searched via a text query tool.

	Advanced searc	h by keywords
		help
key	value	example
YK clone		yk48g3, YK48G3, yk48g3.3, 48g3
cosmid	К04Н4	K04H4, k04h4
gene name		pos-1, POS-1
product name		K04H4.2a, k04h4.2a
CELK group	- 1000	CELK02199, 2199
homologous protein		kinase, homeobox
motif or domain	ξ.	transmembrane receptor
chromosome	all 💌	
clone size	to	
To collect and the second	submit reset	

As an example, let's query for cosmid K04H4. On the result page, one can either click on a group, such as CELK02617, to go to the summary page for this EST cluster group (roughly equivalent to a gene) directly, or one can select the cosmid K04H4 link to jump to a map view to begin browsing along the chromosome, gene-by-gene, for *in situ* data.

	Re	esult of k	eywoi	rd sea	rch		
clone	group	chromosome	cosmid (	CDS No.	product	gene	size
1029f07	CELK02617	<b>1</b> G3	K04H4	1	K04H4.1	emb-9	2.50
1053c02	CELK 02617	LG3	K04H4	1	K04H4.1	emb-9	2.68
1062a05	CELK02617	LG3	K04H4	1	K04H4.1	emb-9	2.22
1068c10	CELK02617	LG3	K04H4	1	K04H4.1	emb-9	2.13
1068f08	CELK 01842	LG3	K04H4	1	K04H4.1	emb-9	3.71
1071d10	CELK 10298	LG3	K04H4	4	K04H4.5	x	2.61
108f8	CELK02617	LG3	K04H4	1	K04H4.1	emb-9	1.89
1113c11	CELK02617	LG3	K04H4	1	K04H4.1	emb-9	2.24
1202a01	CELK 02617	LG3	K04H4	1	K04H4.1	emb-9	2.94
1278a06	CELK02617	LG3	K04H4	1	K04H4.1	emb-9	5.49
1285a06	CELK02617	LG3	K04H4	1	K04H4.1	emb-9	2.08
1285d05	CELK02617	LG3	K04H4	1	K04H4.1	emb-9	2.14
1313a04	CELK02617	LG3	K04H4	1	K04H4.1	emb-9	5.04
1317c06	CELK 11193	LG3	K04H4	4	K04H4.5	x	1.92
133d11	CELK02199	LG3	K04H4	3	K04H4.2b	X	1.66
134e1	CELK 02199	LG3	K04H4	3	K04H4.2b	X	2.58
1415g03	CELK02199	LG3	K04H4	2	K04H4.2b	X	2.85



To go to the map view, select "display neighboring cosmids". Note here that it is best to start with one cosmid on either side because more will be too crowded for the physical map display. Click on the "submit" button brings up an "Area map" page. On the left hand side of this page is a physical map which is actually an interactive graphical Java application.

## Area map (around the cosmid K04H4) New window for : shift precise CELK04818 zoom CELK08839 5000 10000 150000<mark>99-</mark>10-40 CEL 7-1818 20**0/E)**LK0878<mark>9</mark> CELK02617 CELF00903 30000 35000 CELK0261702199 40000 CELK02199 45000 CELF02762 50000 CELK11193 CELK10298 55000 60000 65000 CELK08719 70000 75000 CELK03670 80000 85000 CELF00878 CELK00826

On this page, clicking on any thumbnail will bring up links to full size in situ images. To move 'downward' on the physical map, select the pink bar representing the lower cosmid; then click on the "shift" button on top of this page to effect the move. To move by more than one cosmid at a time, one can change the number (defaulted to 1) next to the "shift" button. To adjust the viewable area of the physical map display, one needs to resize the map. "Change map size" control strip is at the very bottom of the web page (not in view here). A warning here is that this Java application may not be stable at all times. Be gentle.

## 8.3. BCGSC Expression Pattern

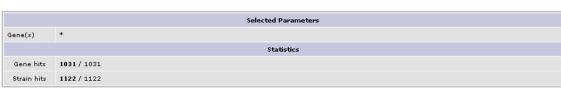
BCGSC Expression Patterns <a href="http://elegans.bcgsc.ca/perl/eprofile/browse">http://elegans.bcgsc.ca/perl/eprofile/browse</a> lists GFP expression data which can be browsed directly or searched by gene name, tissue pattern or life stage.

## **Expression Patterns**

for C. elegans promoter::GFP fusions

BROWSE -- Any stage -- 🔻 Tissue: -- Any tissue -Genes/Pg: 10 🗸 Page: 1.(AC7 - B00) Page 1/104 >> >| Go

Browse Gene Search Pattern Search Contact Disclaimer Home





For each expression pattern, there are text annotations, images or even animations of series of images.

## 9. Concluding remark

The Web is still growing rapidly, both in terms of technology and content. We can expect that C. elegans Web resources will also grow and improve. As more people become accustomed to using the Web in their research, existing resources will improve and more will be made available. It will be a challenge for this chapter to keep up with future changes so that it remains to be useful.

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