

# Overview of WormBase Tools

## [The Top Search Box](#)

This is the primary route into the content of the WormBase database. From here you can type in a vast array of identifiers or search strings to find what you are looking for. The indexing of the database continues to be developed to make it easier to find the data our users require. If you have any ideas or notice that you can't get to data that you know is in the database, please drop us an email ([help@wormbase.org](mailto:help@wormbase.org)) so that we can continue this effort.

## [Blast/Blat](#)

This tool allows you to BLAST or BLAST nucleotide or peptide sequence against a selection of nematode genomes hosted by WormBase.

## [e-PCR](#)

This search uses Greg Schuler's e-PCR program to search for STSs in the current *C. elegans* genome. Enter a list of primer pairs or chromosomal positions to find PCR products. Users can also enter a list of PCR product names already in WormBase to see what genes they intersect.

## [JBrowse and GBrowse](#)

The Generic Genome Browser (GBrowse) is a genome viewer and is GMOD's most popular component that allows users to see all sequence features on the chromosomes, like introns, exons, alleles etc. JBrowse is new genome browser that is faster and more powerful than GBrowse.

## [Nucl. Aligner and Protein Aligner](#)

Enter a WormBase gene ID to see the alignment of various types of data (EST mRNA etc.) in a genomic context.

## [Synteny Viewer](#)

A sequence comparison tool for visualizing genome alignments both within and between species.

## [Ontology Browser](#)

WormBase uses ontologies to describe anatomy, developmental life stages, and phenotypes. The Ontology Browser allows users to find genes with a specific phenotype, expression pattern, biological process, molecular function or cellular component.

## [Textpresso](#)

Query the WormBase and PubMed Central full-text literature collection with keywords or phrases.

## [WormMine](#)

WormMine is an advanced data mining and bulk query tool. Users can perform queries for with single or lists of entities, constrain searches using powerful filters and boolean queries, download results in a variety of formats, publish search parameters for easier replication, and save searches for further analyses. WormMine currently compromises approximately 90% of the WormBase corpus of data. multiple genes or other entities at the same time, and analyze/filter the results.

## [SimpleMine](#)

SimpleMine allows users to enter a list of genes to get an Excel file for their phenotypes, expression patterns, interacting genes, genetic map position, orthologs, disease association, and more. SimpleMine also allows users to convert gene names among WormBase Gene ID, Entrez PubMed names, Transcript, WormPep, Uniprot, TreeFam, and RefSeq.

## [WormBase SPELL](#)

SPELL (Serial Pattern of Expression Levels Locator) is a query-driven search engine for microarray, RNAseq and Proteomics data. Given a small set of query genes, SPELL identifies which datasets are most informative for these genes, then within those datasets, additional genes are identified with expression profiles most similar to the query set. WormBase SPELL collected >6,000 experiments for 9 nematode species. Users can also download these datasets for their own analysis.

## [Parasite BioMart](#)

WormBase Parasite hosts sequence curation for over 100 nematode species. Parasite BioMart allows users to perform multi-gene queries for sequence features, filter and download the results.

## [Gene Sets Enrichment](#)

Enter a list of genes, find their enriched tissues, phenotype, biological processes, molecular functions and cellular localizations.

## [Query Language Search](#)

This searches the underlying ACeDB database using either the old-style WormBase Query Language (WQL) or the "new" Ace Query Language (AQL).

## [Livechat](#)

This tool is available on every page from within WormBase via a tab on the right hand side of your browser. If any curators/developers are online you will be able to initiate a live chat to try and immediately resolve any issues you are having with the site.