

# Lasergene®

## MegAlign

### MULTIPLE AND PAIRWISE SEQUENCE ALIGNMENT

MegAlign offers researchers a choice of four pairwise and four multiple sequence alignment methods for aligning nucleic acid or polypeptide sequences. Users can enter their own sequences or load public data directly from NCBI. To find more related sequences for alignment, a BLAST query can be run or the Entrez text query interface can be utilized, followed by dropping in the sequences wanted from the list of matches.

Alignments views can be customized to highlight the similarities or differences of the sequences. Differences in chemical, structural, or functional characteristics between sequences, researchers' groupings or consensi can be displayed. Researchers can construct phylogenetic trees, generate detailed worktables, or export data of sequence comparisons. MegAlign provides valuable tools permitting comparisons of gene families or sequence pairs that can be customized for presentations and publications.

### MAIN MegAlign WINDOW

Palette tools for showing protein, DNA or layout customization

Consensus bar showing degree of similarity in each alignment column

Protein sequence display

GammaTubulins.meg

Sequence Name < Pos = 1 < Pos = 436

Consensus 10 Sequences

Sequence Name	10	20	30	40	440	450
Frog	MP--REIITLQGGCCGQIGFEPWQLCAENGISPDGILEDFATDC				DESREIVQSLVDEYHAAESP DY	
Fission Yeas	MP--REIITLQGGCCGQIGFEPWQLCAENGISPEGIVEEFPATEG				DNSREIVQOLIDEYHAATRPDY	
Fruitfly	MP--SEIITLQGGCCGQIGFEPWQLCAENGISPDGTLSEFATEG				DSSRDVVDLINEYEACEDPNY	
Human	MP--REIITLQGG				DESRETVDCLVQYEAAATREY	
Feen	MP--REIITLQGG					
Mustard	MP--REIITLQGG					
SeaUrchin	MP--REIITLQGG					
SlimeMold	MP--REIITLQGG					
Trypanosome	MP--REIITLQGG					
Worm	MSGTGALHTVMVGG					

Alignment Report of GammaTubulins.meg ClustaW (Slow/Accura...)

G N G S Y L L E R L N D R Y P K K L I Q T Y S V F P N Q

160 170

148 G L G S Y L L E R L N D R Y P K K L V Q T Y S V F P N Q

148 G L G S F L L E R L N D R Y P K K L I Q T Y S V F P N S

148 G N G S F I K E R L A D R Y P K K L I Q T F S V F P N Q

148 G L G S Y L L E R L N D R Y P K K L V Q T Y S V F P N Q

148 G N G S Y L L E A L N D R Y S K K L V Q T Y S V F P N Q

148 G N G S Y L L E T L N D R Y S K K L V Q T Y S V F P N Q

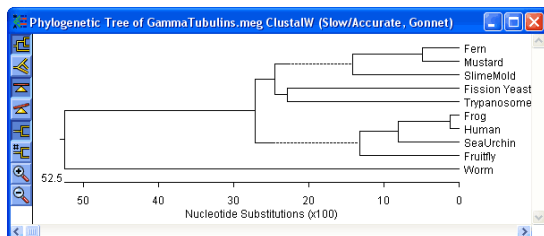
148 G N G S Y L L E K L N D R Y F P K K L I Q T Y S V F P N Q

148 G N G S F L L E Q L N D R Y F P K K L I Q T Y S V F P N E

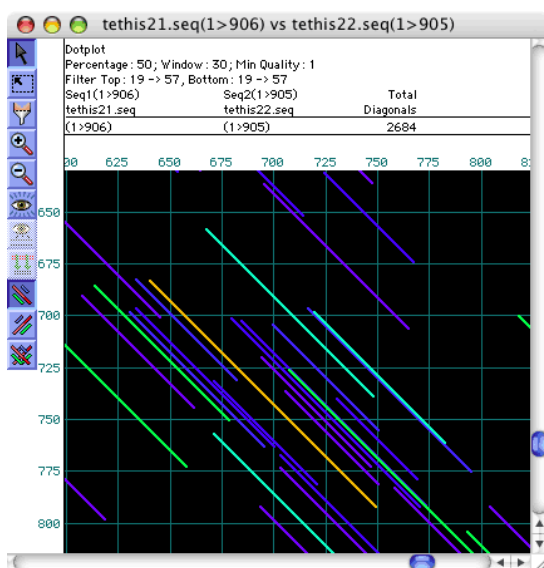
148 G N G S Y L L E N L N D R Y F P K K L I Q T Y S V F P N Q

150 F L L E R L R E A F P K K L V I Q T Y S V F A N S

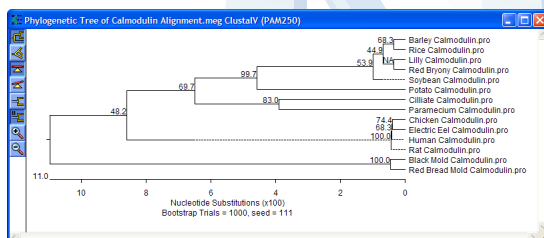
## MegAlign FEATURES



View phylogenetic trees



Compare all regions of two sequences using Dotplot



Optimal tree structure is validated through bootstrapping

## Sequence Entry

- Import data from many popular file formats
- Read sequences and features from other Lasergene project files
- Edit template sequence and share newly created features through integration with SeqBuilder and other Lasergene modules
- Download sequences from NCBI using accession number, BLAST or text search

## Alignments and Analyses

- Align DNA, protein and DNA+protein sequences
- Perform multiple sequence alignments using
  - Jotun Hein
  - Clustal V
  - Clustal W - both Fast and Slow algorithms
- Perform pairwise sequence alignments using
  - Wilbur-Lipman
  - Martinez Needleman-Wunsch
  - Lipman-Pearson
  - Dotplot analysis
- Create subalignments from selected ranges of longer alignments
- Reconstruct phylogeny
- Calculated sequence similarity and distance
- Edit and adjust final alignment manually if desired
- Export data and alignments into popular formats

## Graphical Displays and Tools

- Customize alignment displays
- Highlight matches or mismatches to the consensus or other sequence with distinct colors or shading
- Define the consensus by residue or by chemical, structural or charge characteristics
- Create a custom consensus based on user's own residue classification scheme
- Display consensus strength as color-coded histograms
- Copy selected sections of alignment report and paste into other applications

## Bootstrapping

- Bootstrapping compares trees generated from similar alignments and counts the number of times a specific branching pattern occurs
- Counts appear on the branches expressed in percentage terms. Branch patterns with higher values are statistically more likely to appear
- Bootstrapping provides a measure of the robustness of a feature of the data dependent upon the chosen criterion for comparison