Clustal Omega

Fast, scalable generation of high‐quality protein multiple sequence alignments using Clustal Omega 11.10.2011

Fabian Sievers, Andreas Wilm, David Dineen, Toby J Gibson, Kevin Karplus, Weizhong Li, Rodrigo Lopez, Hamish McWilliam, Michael Remmert, Johannes Söding, Julie D Thompson, Desmond G Higgins

Kalign

Very fast MSA tool that concentrates on local regions. Suitable for large alignments.

Kalign - an accurate and fast multiple sequence alignment algorithm.

Lassmann T. and Erik L.L. Sonnhammer (2005)

BMC Bioinformatics, 6:298 [pubmed]

MAFFT

MSA tool that uses Fast Fourier Transforms. Suitable for medium-large alignments.

MAFFT: a novel method for rapid multiple sequence alignment based on fast Fourier transform

Kazutaka Katoh Kazuharu Misawa Kei‐ichi Kuma Takashi Miyata

MSA Result by ClustalW

