Meta-MEME, Version 2.01

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TECHNOLOGY DESCRIPTION

A software toolkit for building motif-based hidden Markov models ("HMM") of families of related DNA or protein sequences. It combines multiple motif models created by MEME into a single HMM. This HMM can be trained (by the software) via expectation-maximization, and the resulting trained model can be used to produce a motif based multiple sequence alignment and search a protein database for homologs.

Further information about Meta-MEME can be found at the web address, www.sdsc.edu/Software. Click on "Molecular Biology Software".

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OTHER INFORMATION

CATEGORIZED AS

- **Biotechnology**
  - Bioinformatics
- **Computer**
  - Software

RELATED CASES

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