



Show results of job:

Show results

Recent jobs:

22

8401389

Select all Deselect all

Clear sel. Jobs

Delete sel. Jobs

queued

running

done

error

Max-Planck Institute for Developmental Biology

Quickfinder

Utils

AlignmentViewer	Blammer	Clustal Omega	HHalign	Kalign	MAFFT	MSAProbs	MUSCLE	ProbCons	TCoffee
New job	Resubmit	Log	Input-params	Delete					

Date: 10:50 on Oct 12 2015

Help

Results

Forward Save Export

Select all Deselect all Select the best ten

Number of sequences: 2

MSAPROBS version 0.9.7 multiple sequence alignment

☒ 26998 E-KPKFAIQDNHHITKV TENLFSKEEVCQMGEGTVDLALFGSPFFILEYDLMAPNG-HIS

☒ nmr RVKPSASLKLHH-----DLKLCLGDHSSVPVALKGQGPFTLTVDIIETFSSKRK

. ** . : : : : *

☒ 26998 TKKI-QVATKYASLKLPN-QIPGEYITTIKAIFDGNYGESDIHFREHOSELI IKOTVHPI

☒ nmr TFEIKEIKTNEYVIKTPVFTTGGDYILSLVSIKDSTGC--VVGLSOPDAKIOVRR----

* : * :: * : : * * * : * * :: : * * . : : : : : : : :

☒ 26998 PDV☒ nmr --D

Yongchao Liu, Bertil Schmidt and Douglas L. Maskell MSAProbs: multiple sequence alignment based on pair hidden Markov models and partition function posterior probabilities. *Bioinformatics* (2010) 26 (16): 1958-1964.