

**Muscle Multiple Protein Sequence Alignment - complete**

New Window

Edgar, Robert C. (2004), MUSCLE: multiple sequence alignment with high accuracy and high throughput, *Nucleic Acids Research* 32(5), 1792-97.

Alignment of MuscleWS alignment of Uniref50 Sequences - FASTA

Job details

** Vamsas@Dundee University Life Sciences Bioinformatics Cluster Job **

** Public Job Limits are 1 hour of CPU time and 1G of memory.

**

** All Dundee Hosted Web Services will be down between

** from 11-12-2006-17:45+GMT to 12-12-2006-09:00+GMT

** Cluster jobs will be suspended from 17:15 to 09:00

** Sorry for any inconvenience.

Started Tue Dec 12 10:38:47 2006

/gdfs/gjb_lab/software/lx24-x86/bin/muscle -maxiters 16 -anchorspacing 32 -loga

/homes/ws-dev1/NOBACK/jobs/JalviewWS/MsaWS-Jobs/muscle14280/muscle.log -nocore

-verbose -quiet -in

/homes/ws-dev1/NOBACK/jobs/JalviewWS/MsaWS-Jobs/muscle14280/inseqs.fasta -out

/homes/ws-dev1/NOBACK/jobs/JalviewWS/MsaWS-Jobs/muscle14280/inseqs_aligned.fasta

MUSCLE v3.0 (C) Copyright 2003,04 Robert C. Edgar

<http://www.drive5.com/muscle>

Profile-profile score LE

Max iterations 16

Max trees 1

Max time (No limit)