



"MUSCLE: multiple sequence alignment with high accuracy and high throughput"
Nucleic Acids Res. 32(5):1792 (2004)

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

Alignment of <http://www.jalview.org/examples/uniref50.fa>
Job details

Job Output:

Started Wed Dec 7 20:14:16 2016

/homes/www-jws2/servers/tomcat-7.0.53_jaba-2.1/webapps/jabaws/binaries/src/muscle/musc
le -clwstrict -quiet -verbose -nocore -log stat.log -in input.txt -out result.txt

Alphabet Amino

MUSCLE v3.8.31 by Robert C. Edgar
<http://www.drive5.com/muscle>

Profile-profile score	LE
Max iterations	8
Max trees	1
Max time	(No limit)
Max MB	4294966874
Gap open	-2.9
Gap extend (dimer)	0
Gap ambig factor	0
Gap ambig penalty	-0
Center (LE)	-0.52
Term gaps	Half