

CLUSTAL 2.1 MULTIPLE SEQUENCE ALIGNMENT

File: /media/morpheus/disk1/fst/pep_msa/NANSAps: Tue Feb 1 14:06:42 2022

Page 1 of 2

** *:***** :** ***:*****: :*:** *:***** **
 MPREFELCPGRRIGGDYPCFIIAEIGQNHQGDLDIAKRMIRMAKDCKGADCAKFQKSELEY
 MPREFELCPGRRIGGDYPCFIIAEIGQNHQGDLDIAKRMIRMAKDCKGADCAKFQKSELEY
 MPREFELCPGRRIGGDNPPCFIIAEIGQNHQGDLDIAKRMIRMAKECKGADCAKFQKSELEY
 MPREFELCPGRVGGDQPCFIIAEIGQNHQGDLDIARRMIRMAKECKGADCAKFQKSELEY
 MPLEFELCPGRRVGGADQPCFIIAEIGQNHQGDLDIAKQIMRMVKECGADCAKFQKSELEY
 MPLELELCPCRWWGGKHPCFIIAEIGQNHQGDIDVAKRMIRTAKECKGADCAKFQKSELEY
 MPLELELCPCRWWGGQHPCFIIAEIGQNHQGDLDVAKRMIRTAKECKGADCAKFQKSELEY
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 MPLELELCPCRWWGGQHPCFIIAEIGQNHQGDLDVAKRMIRMAKECKGADCAKFQKSELEY
 MPLELELCPCRWWGGQHPCFIIAEIGQNHQGDLDVAKRMIRMAKECKGADCAKFQKSELEY
 MPLELELCPCRWWGGQHPCFIIAEIGQNHQGDLDVAKRMIRMAKECKGADCAKFQKSELEY
 MPLELELCPCRWWGGQHPCFIIAEIGQNHQGDLDVAKRMIRMAKECKGADCAKFQKSELEY
 MPLELELCPCRWWGGQHPCFIIAEIGQNHQGDLDVAKRMIRTAKECKGADCAKFQKSELEY
 MPLELELCPCRWWGGQHPCFIIAEIGQNHQGDLDVAKRMIRTAKECKGADCAKFQKSELEY
 MPLELELCPCRWWGGQHPCFIIAEIGQNHQGDLDVAKRMIRTAKECKGADCAKFQKSELEY
 MPLELELCPCRWWGGQHPCFIIAEIGQNHQGDLDVAKRMIRTAKECKGADCAKFQKSELEY
 MPLEFELCPGRKIGGENPCFVIAEIGQNHQGDLEIAKKMIRMAKDSGADCAKFQKSALEY
 1.....10.....20.....30.....40.....50.....60

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***.* **.* ****:*:**:*****.* *:**: **:*:**:*:*****  
KFNKKALERPYSKHSWGKTYGEHKRHLEFSDQYRELKKYAEEVGIFFTASGMDEMAVE 120  
KFNKKALERPYSKHSWGKTYGEHKRHLEFSDQYRELKKYAEEVGIFFTASGMDEMAVE 120  
KFNKKALERPYSKHSWGKTYGEHKRHLEFSDQYRELKKYAEEVGIFFTASGMDEMAVE 120  
KFNKKALERPYSKHSWGKTYGEHKRHLEFSDQYRELKKYAEEIGIFFTASGMDEMAVE 120  
KFNKKALERPYSKHSWGKTYGEHKRHLEFSDQYRELQKYAKEIGIYFTASGMDEMAVE 120  
KFNRKALERPYSKHSWGKTYGEHKRHLEFSDQYKELOSYAQEIGIFFTASGMDEMAVE 120  
KFNRKALERPYSKHSWGKTYGEHKRHLEFSDQYKELOSYAQEIGIFFTASGMDEMAVE 120  
KFNRKALERPYSKHSWGKTYGEHKRHLEFSDQYRELQRYAEEVGIFFTASGMDEMAVE 120  
KFNRKALERPYSKHSWGKTYGEHKRHLEFSDQYRELQRYAEEVGIFFTASGMDEMAVE 120  
KFNRKALERPYSKHSWGKTYGEHKRHLEFNHDQYRELQRYAEEVGIFFTASGMDEMAVE 120  
KFNRKALARPYSKHSWGKTYGEHKRHLEFSDQYRELQKYAEEVGIFFTASGMDEMAVE 120  
KFNRKALERPYSKHSWGKTYGEHKRHLEFSHAQYKELOKYAEEVGIFFTASGMDEMAVE 120  
KFNRKALARPYTSKHSWGRTYGEHKRHLEFSDQYKELOSYAQEVGIFFTASGMDEMAVE 120  
KFNRKALERPYSKHSWGKTYGEHKRHLEFSHEQYRELQRYAQEVGIFFTASGMDEMAVE 120  
KFNRKALERPYSKHSWGKTYGEHKRHLEFSHAQYRELQRYAQEIGIFFTASGMDEMAVE 120  
KFNRKALERPYSKHSWGKTYGEHKRHLEFSHEQYKELOQYAEVGIFFFTASGMDEMAVE 120  
KFNKKALERPYNPSHSGWKTYGDHKRHLEFSDQFRELOKYAKEIGIYFTASGMDEMAVE 120  
.....70.....80.....90.....100.....110.....120
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[illegible]

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Page 2 of 2

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*****:***  ***.**:.*  :.  *****:****:****:***:*
FLQCTSAYPLQPEDVNLRVISAYQSAFPDIPIGYSGHETGIAISVAALVALGAKVVERHVT
FLQCTSAYPLQPEDVNLRVISAYQSAFPDIPIGYSGHETGIAISVAALVALGAKVVERHVT
FLQCTSAYPLQPEDVNLRVIPAYQSAFPDIPIGYSGHETGIAISVAALVALGAKVVERHV
FLQCTSAYPLQPEDVNLRVILAYQSAFPDIPIGYSGHETGIAISVAAMGAKVVERHVT
ILQCTSAYPLQPEDVNLHVITAYQSAFPDIPIGYSGHETGIAISVAAMGAKVLERHVT
FLQCTSAYPLQPEDANLRVISEYQKLFDPDIPIGYSGHETGIAISVAALVALGAKVLERHIT
FLQCTSAYPLQPEDANLRVISEYQKLFDPDIPIGYSGHETGIAISVAALVALGAKVLERHIT
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FLQCTSAYPLQPEDVNLRVISEYQKLFDPDIPIGYSGHETGIAISVAALVALGAKVLERHI
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FLQCTSAYPLQPEDVNLRVILEYQKLFDPDIPIGYSGHETGIAISVAALVALGAKVLERHIT
FLQCTSAYPLLPEDVNLRVIKEFQSTFPDIPIGYSGHETGIAITLAAMGAKVVERHVT
.....190.....200.....210.....220.....230.....240

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[illegible]

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** *: **: ***** **: *: ** *: * *: . : : : : : * : : . : :
IPEGTVLTLTDLMLTVKVGEPKGFAPAEAFIDLVGQKVRKTI EEDETITEQAVENHVKKVK- 358
IPEGTVLTLTDLMLTVKVGEPKGFAPAEAFIDLVGQKVRKTI EEDETITEQAVENHVKKVK- 358
IPEGTILTLTDLMLTVKVGEPKGFAPAEAFIDLVGQKVKKTI EEDETITEQAVENHVKKVKC 359
IPEGTVLTLTDLMLTVKVGEPKGFPPAEAFIDLVGQKVKRHIEEDETITEQAVENHVKKVKC 359
IPEGTVLTLTDLMLTVKVGEPKGYLPPEEAFIDLVGKKVKINIEEDETITEDAIENHVKKVKC 359
IPAGTILTLTDLMLTVKVGEPKGYPPEDIFNLGAKKVLVTIEEDDTVMEESVESHSKKIKA 359
IPAGTILTLTDLMLTVKVGEPKGYPPEDIFNLVGKKVLVTIEEDDTVMEESVESQSKKIKA 359
IPEGTILTMDMLTVKVGEPKGYPPEDIFNLVGKKVLVTVEEDDTIMEELVDNHGKKIKS 359
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IPEGTVLTLTDLMLTVKVGSEPKGYPPEDIFNLVGKKILVTVEEDDTILEELVDNHGKKIKS 359
IPAGTIVTLTDLMLTVKVAEPGRGFPPEEIVDLEGKTVKREIEDESVTTEAIENYNTRTK 359
310 320 330 340 350

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