

CLUSTAL FORMAT: MUSCLE (3.7) multiple sequence alignment

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gi | 7199800      -----MRLV----IAQFLLITQVF----AAQK-----NSIGPPKLLEQ-SGE
gi | 2464061      -----MWRQSTIL---AALLVALLCAG-----SAES-----KGNRPPRITKQPAPG
gi | 1136796      -----MDGKRSCSLCGGAMIMMMMMMISHMTSALEVPL-----DLPQPPTITNQ-SPK
gi | 4538399      -----MMKEKSIS-ASKASLVFFLCQMI----SALDVPLDSKLLLEELSQPPTITQQ-SPK
gi | 2978945      -----MPKKKHLS-AGGVPLILFLCQMI----SALDVPL-----DLVQPPTITQQ-SPK
gi | 4705895      -----MPKKKPLS-AGRAPLFLFLCQMI----SALDVPLDPKLLDDLVQPPTITQQ-SPK
gi | 8115822      MQLKIMPKKKRLS-AGRVPLILFLCQMI----SALEVPLDPKLLLEDLVQPPTITQQ-SPK
gi | 7661510      MQLKIMPKKKRLS-AGRAPLMLFLCQMI----SALEVPLDPKLLLEDLVQPPTITQQ-SPK

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gi | 7199800      EVWYHLDEEDLLKNR-LTLRCEADENTD-RYSWLKDGEPFVIDSEDVLWEKESQSGSIVF
gi | 2464061      ELLFKVAQQNKESDNPFIIECEADGQPEPEYSWIKNGKFDWQAYDNRMLRQPGRGTLVI
gi | 1136796      D--YIIDP----REN-INIFCEAKGKPHPSFSWTRNGTHFDVE-KDPKVVMPGTGNLVI
gi | 4538399      D--YIVDP----REN-IVIQCEAKGKPPPSFSWTRNGTHFDID-KDAQVTMKPNSGTLVV
gi | 2978945      D--YIIDP----REN-IVIQCEAKGKPPPSFSWTRNGTHFDID-KDPLVTMKPGSGTLVI
gi | 4705895      D--YIIDP----REN-IVIQCEAKGKPPPSFSWTRNGTHFDID-KDPLVTMKPGSGTLVI
gi | 8115822      D--YIIDP----REN-IVIQCEAKGKPPPSFSWTRNGTHFDID-KDPLVTMKPGTGTLLII
gi | 7661510      D--YIIDP----REN-IVIQCEAKGKPSPSFSWTRNGTHFDID-KDPLVTMKPGSGTLTI

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gi | 7199800      TK----PHASHQGYQCFASNIFGTALS NKMHLRLGSLEHFPKRDVKLLRVKEGESLTLN
gi | 2464061      TI----PKDEDRGHYQCFASNEFGTATSNSVYVRKAELNAFKDEAAKTLEAVEGEPFMLK
gi | 1136796      DI--SGEKAIEVYEGVYQCIARNEHGS AVSNNIVIRQSRSPLSWKEKNEPITVQRGTSILIQ
gi | 4538399      NIMNGVKAIEYEGVYQOCTARNERGA AISNNIVIRPSRSPLWTKEKLEPNHVREGDSLVLN
gi | 2978945      NIMSEGKAIEYEGVYQOCTARNERGA AVSNNIVVRSRSPLWTKERLEPIVLQNGQSLVLP
gi | 4705895      NIMSEGKAIEYEGVYQOCTARNERGA AVSNNIVVRSRSPLWTKERLEPIILRSGQSLVLP
gi | 8115822      NIMSEGKAIEYEGVYQOCTARNERGA AVSNNIVVRSRSPLWTKEKLEPITLQSGQSLVLP
gi | 7661510      NIMSEGKAIEYEGVYQOCTARNERGA AISNNIVIRPSRSPLWTKEKLEPIILRNGQSLVLP

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gi | 7199800      CTPPRGTPDPKIVWLYRSLDDSSVIETIRSRHITVDNEGHLHFSSVELSDGKATLV-YEC
gi | 2464061      CAAPDGFPSPTVNWMIQESIDGSI-KSINNSRMTLDPEGNLWFSNVTREDASSDF--YYA
gi | 1136796      CRPPAGLPPPIIFWM-----DNNFQRLPQNSRVSQALNGDLYFSNVIMEDTRNDYICYAR
gi | 4538399      CRPPVGLPPPIIFWM-----DNAFQRLPQSERVSQGLNGDLYFSNVQPEDTRVDYICYAR
gi | 2978945      CRPPIGLPPPIIFWM-----DNSFQRLPQSERVSQGLNGDLYFSNVLPEDTREDYICYAR
gi | 4705895      CRPPIGLPPPIIFWM-----DNSFQRLPQSERVSQGLNGDLYFSNVLPEDTREDYICYAR
gi | 8115822      CRPPIGLPPPIIFWM-----DNSFQRLPQSERVSQGLNGDLYFSNVLPEDTREDYICYAR
gi | 7661510      CRPPIGLPPPIIFWM-----DNSFQRLPQSERVSQGLNGDLYFSNVLPEDTREDYICYAR

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gi | 7199800      AATSPVLRGEYRSGDRI-----QLDIEPSQDKSHPVKMSVSPSEV
gi | 2464061      CSATSVFRSEYKIGNKV-----LLDVKQMGVSASQNKHPPVRQ-YVSRROS
gi | 1136796      FPHTQTIQQKQPITVKVLDIEAMNDTVLAAFLNGSDFWGDSPSGERVPSFLHPPGMESTT
gi | 4538399      FNHTQTIQQKQPISVKV-----FSTKPVTERPPVLLTPMGSTSNK
gi | 2978945      FNHTQTIQQKQPISLKVISVDELNDTI-AANLSDTEFYGAKSSKERPPTFLTPEGNESHK
gi | 4705895      FNHTQTIQQKQPISLKVISVDELNDTI-AANLSDTEFYGAKSSKERPPTFLTPEGNESHK
gi | 8115822      FNHTQTIQQKQPISVKVISVDELNDTI-AANLSDTEFYGAKSSRERPPTFLTPEGNASNK
gi | 7661510      FNHTQTIQQKQPISVKVISVDELNDTI-AANLSDTEFYGAKSHRQRPPTFLTPDGNTSRK

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gi | 7199800      TVRAGGQLKLCIFGGRPLPTIFWSKIDGELP-KSRIKDLTSHESDFGRSLIVENVHPDD
gi | 2464061      LALRGKRMELFCIYGGTPLPQTVWSKDGQRIQWSDRI-----TQGHYGKSLVIRQTNFDD
gi | 1136796      MVLKGD TLELECIADGLPTPNISWTKVNGELP-SGRF-----SFYSFQKTLKIKEVTEAD

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gi | 4538399      VELRGNVLLLECIAAGLPTPVIRWIKEGGELP-ANRT-----FFENFKKTLKI IDVSEAD
gi | 2978945      EELRGNVLSLECIAEGLPTPIIYWIKEDGMLP-ANRT-----FYRNFKKTLOI THVSEAD
gi | 4705895      EELRGNVLSLECIAEGLPTPVIYWIKEDGTLP-VNRT-----FYRNFKKTLOI IHVSEAD
gi | 8115822      EELRGNVLSLECIAEGLPTPIIYWAKEDGMLP-KNRT-----VYKNFEKTLQI IHVSEAD
gi | 7661510      EELRGNVLSLECIAEGLPTPIIYWIKEDGTLP-INRT-----FYRNFKKTLOI VQVTEAD
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gi | 7199800      AGAYECCRGRHLV-----HTVNVVRVMAAPFWEFDPPRDISLPEESTGELECLAGGQPTPII
gi | 2464061      AGTYTCDVSNVGVNAQSFSIILNVNSVPYF-TKEPEIATAAEDEEVVFE CRAAGVPEPKI
gi | 1136796      GGDYRCIAKNRMGSSQ-HTITVVVRAAPFW-ISAPQNLILAPKETGNLTC DVDGNPKPTI
gi | 4538399      SGNYKCTARNTLGSTH-HVISVTVKAAPYW-ITAPRNLVLSPGEDGTLICRANGNPKPSI
gi | 2978945      SGNYQCIAKNALGAVH-HTISVTVKAAPYW-IVAPQNLVLSPGENGT LICRANGNPKPRI
gi | 4705895      SGNYQCIAKNALGAVH-HTISVTVKAAPYW-IVAPHNLVLSPGENGT LICRANGNPKPRI
gi | 8115822      SGNYQCIAKNALGAIH-HTISVRVKAAPYW-ITAPQNLVLSPGEDGTLICRANGNPKPRI
gi | 7661510      SGNYQCIAKNALGAIH-HTISVTVKAAPYW-IIAPQNLVLSPEEDGT LICRANGNPKPRI
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gi | 7199800      TWSMNGKFLHELAEDSRRVLLDHGRILRVRNLNHDLDTG VYQCNASNPLGYVFANAFVHV
gi | 2464061      SWIHNGKPIEQSTPNPRRTV--TDNTIRIINL-VKGD TGNYGCNATNSLGYVYKDVYLVN
gi | 1136796      TWSVNGNPIESSHNDPSRKV--SDGVITLSDV-QTGS SAVYQCNASNDYGYLLANAFVSV
gi | 4538399      SWLTNGVP IAIAPEDPSRKV--DGDTIIFSAV-QERSSAVYQCNASNEYGYLLANAFVNV
gi | 2978945      SWLTNGVP I EIALDDPSRKI--DGDTIIFSNV-QE SSSAVYQCNASNKYGYLLANAFVNV
gi | 4705895      SWLTNGVP V EIALDDPSRKI--DGDTIMFSNV-QE SSSAVYQCNASNKYGYLLANAFVNV
gi | 8115822      SWLTNGVP I E IAPDDPSRKI--DGDTIIFSNV-QE RSSAVYQCNASNEYGYLLANAFVNV
gi | 7661510      SWLSNGVP I E IAPDDPSRKI--DGDTIIFSKV-QE RSSAVYQCNASNEYGYLLANAFVNV
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gi | 7199800      RAHAPFFRMPAARHWKVLHSTVVLDCDVDAAPEAMVRWVDADDRPLQVVEGKNKLPNH
gi | 2464061      QAEPPTI-SEAPAAVSTVDGRNVTIKRVNGSPKPLVKWLRASNW---LTGGRYNVQANG
gi | 1136796      LAEPPRVL TSLNHEYSVISNSRALLDCASFGSPLPKITWFKDSQSI--LNSDLYHIHKNG
gi | 4538399      LAEPPRIL TPANKLYQVIADSPALIDCAYFGSPKPEIEWFRGVKGS I-LRGNEYVFDHNG
gi | 2978945      LAEPPRIL TSANTLYQVIANRPALLDCAFFGSPMPTIEWFKG TKGSA-LHEDIYVLHDNG
gi | 4705895      LAEPPRIL TSANTLYQVIANRPALLDCAFFGSPMPTIEWFKG TKGSA-LHEDIYVLHDNG
gi | 8115822      LAEPPRIL TPANTLYQVIANRPALLDCAFFGSPLP TIEWFKGAKGSA-LHEDIYVLHENG
gi | 7661510      LAEPPRIL TSANTLYQVIANRPALLDCAFFGSPLP TIEWFKGAKGSA-LREDIYVLHENG
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gi | 7199800      TFMVYDVNSADEGLYYCNVSNKYGINRATNRLQVFKPTYFVRIPTPKRLILEAGETA EVF
gi | 2464061      DLEIQDVT FSDAGKYTCYAQNKFGEIQADGSLV VKEHTRITQ--EPQNYEVAAGQSATFR
gi | 1136796      TLEINVAQPQNSGKYTCIASNNLGNKENHVHLQVKEPTRIIR--QPEYKEVQRNSIAVFE
gi | 4538399      TLEIPVAQK DSTGTYT CVARNKLGKTQNEVQLEV KDP TMI IK--QPQYKVIQRSAQASFE
gi | 2978945      TLEIPVAQK DSTGTYT CVARNKLGMAKNEVHLE IKDP TRI IK--QPEYAVVQRGSKVSFE
gi | 4705895      TLEIPVAQK DSTGTYT CVARNKLGMAKNEVHLE IKDP TRFIK--QPEYAVVQRGSKVSFE
gi | 8115822      TLEIPVAQK DSTGTYT CVARNKLGMAKNEVHLE IKDP TWIVK--QPEYAVVQRGSMVSFE
gi | 7661510      TLEIPVAQK DSTGTYT CVARNKLGMAKNDVHLE IKDP TRI IK--QPEYAVVQRGSTVSFE
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gi | 7199800      CEAVADPRLPIRYQWTINGK--VLTESQYY-EILPDRLRFRSVRGRHSGIIDCAAITDVD
gi | 2464061      CNEAHDDTLEIEIDWWKDGQSIDFEAQPRFVK TNDNSLTI AKTMELDSGEYTCVARTRLD
gi | 1136796      CKVKHDPTLIPSMIWLKDNG--ELPDDPRF-EVGS DSLTIHDVTEDEGTYTCIRNTTLD
gi | 4538399      CVIKHDPTL IPTVIWLKDNN--ELPDDERF-LVGK DNLTIMNVTDKDDGTYTCIVNTTLD
gi | 2978945      CRVKHDHTLIPTIMWLKDNG--ELPN DERF-STDK DHLVSDVKDDGGTYTCANTTLD
gi | 4705895      CKVKHDHTLIPTILWLKDNG--ELPN DERF-SVDK DHLVSDVKDEDGGTYTCAANTTLD
gi | 8115822      CKVKHDHTLSLTVLWLKDNR--ELPS DERF-TVDK DHLVADVSDDDSGTYTCVANTTLD
gi | 7661510      CKVKHDHTLIPTVMWLKDNG--ELPN DGRF-TVDK DRLVADVNDDDGGTYTCVANTTLD
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gi | 7199800      VKLASMQLIVK-----DVPAHPV-VETAHCSEKATVKWVAASDHGDSIKKYIVE
gi | 2464061      EATARANLIVQ-----DVPNAPK-LTGITCQADKAEIHWEQOGDNRSPI LH YTIQ
gi | 1136796      QDSASATLTVV-----EQDPPTDLELTDQRERSVRLTWTTPGDEHNSPIKFLFIQ
gi | 4538399      SVSASAVLTVVAAPPTPAI IYARPNPPLDLELTGQLERSIELSWVPGEENNSPITNFVIE
gi | 2978945      SASASAVLRVVAPTPTPAPIYDVPNPPFDLELTNQLDKSVQLTWTTPGDDNNSPITKFIEE
gi | 4705895      SVSASAVLRVVAPTPTPAPIYDVPNPPFDLELTNQLDKSVQLTWTTPGDDNNSPITKFIEE
gi | 8115822      SVSASAVLSVVAPTPTPAPVYDVPNPPFDLELTDQLDKSVQLSWTPGDDNNSPITKFIEE
gi | 7661510      NVSASAVLSVVAPTPTPAPIYDVPNPPFDLELTDQLDRSVQLSWTPGDDNNSPITKFIEE
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gi | 7199800      MFTDF-KKNEWEVINEEVNVNKETFEVDITLTPWVNYTFRVAVNSHGRSDMKIDGQPK
gi | 2464061      FNTSF-TPASWDAAYEKVPNTDSSFVQMS--PWANYTFRVIAFNKIGAS-----PPSA
gi | 1136796      YEDSLHEPGVWLNMT-EVSGTSTTAQLELS--PYVYYSFRVLALNGVGLS-----ESSD
gi | 4538399      YEDGLHEPGVWHYQTE-VPGSHTTVQLKLS--PYVNYFRVIAVNEIGRS-----QPSE
gi | 2978945      YEDAMHDAGLWRHQAE-VSGTQTTAQLKLS--PYVNYFRVMAENSIGRS-----MPSE
gi | 4705895      YEDAMHEAGLWRHQAE-VSGTQTTAQLKLS--PYVNYFRVMAENSIGRS-----VPSE
gi | 8115822      YEDAMHKPGLWHHQTE-VSGTQTTAQLKLS--PYVNYFRVMAVNSIGKS-----LPSE
gi | 7661510      YEDAMHEPGLWHHQTE-VPGTQTTAQLKLS--PYVNYFRVMAENNLGRS-----LPSE
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gi | 7199800      DWLTCQTRPSFPYTNPTGVKGEGETPDNLVLSWKPLDRYYWNAAPNMQYLVRYKLDEPIHG
gi | 2464061      HSDSCTTQPDVPFKNPDNVVGGQTEPNLVI SWTPMPEIEHNAPNFHYVSWKRDIPAAA
gi | 1136796      PSRQYRTNPAKPDVNPDSVEVSGTSPDTMTISWRELSGLESNGPGLQYKVSWRMKD-AEQ
gi | 4538399      PSEQYLTKSANPDENPSNVQIGSEPDNLVITWESLKGFSNGPGLQYKVSWRQKDVDE
gi | 2978945      ASEQYLTKAAEPDQNPMAVEGLGTEPDNLVITWKPLNGFQSNPGLQYKVSWRQKDGDE
gi | 4705895      ASEQYLTKAAEPDQNPMAVEGLGTEPDNLVITWKPLNGFQSNPGLQYKVSWRQKDGDE
gi | 8115822      ASEQYLTKASEPDKNPTAVEGLGSEPDNLVITWKPLNGFESNGPGLQYKVSWRQKDGDE
gi | 7661510      ASEQYLTKAAEPDKNPTAVEGLGSEPDNLVITWKPLNGFESNGPGLQYKVSWRQKDGDE
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gi | 7199800      WTEFLVEDSLANFTIIRDQPTFRKYLIQVQSVNSVGP SIVEPEIHHGWSGEDVPDEAPRD
gi | 2464061      WENNNIFDWRQNNIADIADQPTFVKYLIKVVAINDRGESNVAAEEVVGYSGEDRPLDAPT
gi | 1136796      WTTVTLAN--VSQHVVGTPTFTLYEVTVQAVNDYGE GP-RPEVVLGYSGENSP TVAPEN
gi | 4538399      WTSVVAN--VSKYIVSGTPTFVPEIKVQALNDLGYAP-EPSEVIGHSGEDLPMVAPGN
gi | 2978945      WTSVVAN--VSKYIVSGTPTFVYLIKVQALNDVGFAP-EPAAVMGHSGEDLPMVAPGN
gi | 4705895      WTSVVAN--VSKYIVSGTPTFVYLIKVQALNDVGFAP-EPAAVMGHSGEDLPMVAPGN
gi | 8115822      WTSVVAN--VSKYIVSGTPTFVYLIKVQALNDMGFAP-EPAVVMGHSGEDLPMVAPGN
gi | 7661510      WTSVVAN--VSKYIVSGTPTFVYLIKVQALNDAGFAP-EPAAVMGHSGEDLPMVAPGN
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gi | 7199800      FHIDTQINFTTINFTWNPVDANTVNGHFVGYEIEYW-----KAENTIRKYSIKIPANS
gi | 2464061      FTMRQITSSTSGYMAWTPVSEESVRGHFKGYKIQTW-----TENEGEEGLREIHKVGD
gi | 1136796      VKV-SVQSGTEAEVHWAVPLSSVRGLKGYKVTYQMRSLHKQDYDRENPOVLIFSGEE
gi | 4538399      VQV-HVINSTLAKVHWDVPVPLKSVRGLHQGYKVIYWKVQSLSRRSKRHVEKKILTFRGNK
gi | 2978945      VRV-SVVNSTLAEVHWDPVPPKSVRGLHQGYRIYYWKTQSSSKRNRRIEKKILTFQGTK
gi | 4705895      VRV-SVVNSTLAEVHWDPVPPKSVRGLHQGYRIYYWKAQSSSKRNRRIEKKILTFQGSK
gi | 8115822      VRV-NVVNSTLAEVHWDPVPLKSVRGLHQGYRIYYWKTQSSSKRNRRIEKKILTFQGSK
gi | 7661510      VRV-NVVNSTLAEVHWDPVPLKSVRGLHQGYRIYYWKAQSSSLTRNRRIEKKILTFQGSK
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gi | 7199800      TYKVINSFHAVTNYSAHIRTRNKRLRSAPSDYVSFAMPEGPPGKVHNLRVY SVGSTAILL
gi | 2464061      HNALVTQFKPDSKNYARILAYNGRFRNGPPSAVIDFDFTPEGVPSPVQGLDAYPLGSSAFML
gi | 1136796      TVGRLPDLHPYSHYRLNIRAFNGHGDGPSSTDOQFQTPEGVPGPPTNVNIRNLNLD SLLV
gi | 4538399      TFGMLPGLPEYSSYKLNVRVVNGKGE GPASPDKVFKTPEGVPSPPSFLKITNPTLDSLTL
gi | 2978945      THGMLPGLQPYSHYALNVRVVNGKGE GPASTDRGFHTPEGVPSAPSSLKIVNPTLDSLTL
gi | 4705895      THGMLPGLQPYSHYVNLNVRVVNGKGE GPASADRGFHTPEGVPSAPSSLKIVNPTLDSLTL
gi | 8115822      THGMLPGLPEFSHYTLNVRVVNGKGE GPASDRVFNTPEGVPSAPSSLKIVNPTLDSLTL
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gi | 7661510      THGMLPGLEPF SHYTLNVRVVNGKGE GPASPDKVFNTPEGVPSAPSSLKIVNPTLDSLTL
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gi | 7199800      QWDAPLQPNGRIRGYFISFQNEKNETE----ETYVIHRQK----HYLHEKSEPDTGYKVS
gi | 2464061      HWKKPLYPNGKLTGYKIYYEEVKESY-VGERREYDPHITDPRVTRMKMAGLKPNSKYRIS
gi | 1136796      EWTPPLEDNHGLTGYLLKYQPINTTEEAGLLKEVLLPANE---TSYTLDKLTHSTHYKFF
gi | 4538399      EWGSPTHPNGVLTSYILKFQPINNTHELGPLVEIRIPANE---SSLILKLNLYSTRYKFF
gi | 2978945      EWDPSPHPNGILTEYILQYQPINSTHELGLPLVDLKIPANK---TRWTLKLNLFSTRYKFF
gi | 4705895      EWDPSPHPNGILTEYILKYQPINSTHELGLPLVDLKIPANK---TRWTLKLNLFSTRYKFF
gi | 8115822      EWDPSPHPNGILTEYTLKYQPINSTHELGLPLVDLKIPANK---TRWTLKLNLFSTRYKFF
gi | 7661510      EWEPSPHPNGILTEYTLKYQPINSTHELGLPLVDLKIPANK---TRWILKLNLFSTRYKFF
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gi | 7199800      VWAETRAGEGPVTLRPVRTWPARI-----PDAPIFR----VKNISLDSFVVE
gi | 2464061      ITATTKMGEGSEHYIEKTTLKDAVN-----VAPATPSFSWEQLPSDNGLAKFRIN
gi | 1136796      LNAMTETGSGPAVTKEAFTEVDEALIRHPAVEAGKAPPAGPMFG--NVNSSVKEDHAVIS
gi | 4538399      FNAQTSVSGSGSQITEEA VTIMDEVQ-----PLYPRIR--NVT TAAA ETYANIS
gi | 2978945      FYAQTSVGP GSGQITEEAITTVDEAG-----IPP-----
gi | 4705895      FYAQTSVSGSGSQITEEAITTVDEAGILPPDVGAGKVRVAVSPRIG--NVTAAA ETYANIS
gi | 8115822      FYAQTSAGSGSQITEEA VTTVDEAGILPPDVGAGKVQAVNPRIS--NL TAAA ETYANIS
gi | 7661510      FYAQTAAGSGIQITEEAITTVDEAGILPPDVGAGK--AVYPGIS--KL TAAA ETSANIS
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gi | 7199800      WQPNNH SVWKMPGA AFFVNYTAESSKTWFQSEI IYLPYTEITIRNLKEDQKYFMQGI AK-
gi | 2464061      WLPSTEGH---PGTHFFTMHRIKGETQ-WIRENEEKNSDYQEVGGLDPETAYEFRVVSVD
gi | 1136796      WEYLGPDG-----NVYVEYVVDNSKEPWKTEFVNGTRTFQ-IRGLKPGMSYRVRLVAKD
gi | 4538399      WEYEGPDH-----ANFYVEYGVAGSKEDWKKEIVNGSRSFFVLKGLTPGTAYKVRVGAE-
gi | 2978945      -----PDV-----GAGKGKEEWRKEIVNGSRSFFGLKGLMPGTAYKVRVGAE-
gi | 4705895      WEYEGPEH-----VKFYVEYGVAGSKEEWRKEIVNGSRSFFGLKGLMPGTAYKVRVGAE-
gi | 8115822      WEYEGPEH-----VNFYVEYGVAGSKEEWRKEIVNGSRSFFGLKGLMPGTAYKVRVGAV-
gi | 7661510      WEYEGPEL-----VNFYVEYGVAGSKEEWRREIVNGSRSFFGLKGLMPGTAYKVRVGAE-
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gi | 7199800      ---DGPRRSESV---FLPIKTLNRD YANRLKEDSLRSAAWFIAVLGVLGIGLFTICLTFC
gi | 2464061      GHFNTE SATQEIDTNTVEGPIMVA-----NET-VANAGWFIGMMLALAF-I IILFIIIC
gi | 1136796      HSDATI HSTQEM---LITVPAMTN-----RQAEIATQGWFIGLMCAIAL-LILVLLIVC
gi | 4538399      -GLSGFRSSEDL---FETGPAMAS-----RQVDIATQGWFIGLMCAVAL-LILILLIVC
gi | 2978945      -GDSGFVSSSE DV---FETGPAMAS-----RQVDIATQGWFIGLMCAVAL-LILILLIVC
gi | 4705895      -GDSGFVSSSE DV---FETGPAMAS-----RQVDIATQGWFIGLMCAVAL-LILILLIVC
gi | 8115822      -GDSGFVSSSE DV---FETGPAMAS-----RQVDIATQGWFIGLMCAVAL-LILILLIVC
gi | 7661510      -GDSGFVSSSE DV---FETGPAMAS-----RQVDIATQGWFIGLMCAVAL-LILILLIVC
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gi | 7199800      CGNKNRQEKFAVRRKEIEIGH---QODNEEEKQFLEY-----
gi | 2464061      IIRNRGK KYDVHDRELANG---RRDYPEEGGFHEYSQPLDNKSAGRQSVSSANKPGVE
gi | 1136796      FIKRNKGGKYPVKEKEDAHADPEIQPMKEDDGT FGEYS DTEDHKPL-KGSRTPSNGTVKK
gi | 4538399      FIRRKNKGGKYPVKEKEDAHADPEIQPMKEDDGT FGEYS DAE DHKPLKKGSRTPSDRTVKK
gi | 2978945      FIRRKNKGGKYPVKEKEDAHADPEIQPMKEDDGT FGEYS DAE DHKPLKKGSRTPSDRTVKK
gi | 4705895      FIRRKNKGGKYPVKEKEDAHADPEIQPMKEDDGT FGEYS DAE DHKPLKKGSRTPSDRTVKK
gi | 8115822      FIRRKNKGGKYPVKEKEDAHADPEIQPMKEDDGT FGEYS DAE DHKPLKKGSRTPSDRTVKK
gi | 7661510      FIRRKNKGGKYPVKEKEDAHADPEIQPMKEDDGT FGEYS DAE DHKPLKKGSRTPSDRTVKK
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gi | 7199800      -----QYG-----FKN-----
gi | 2464061      SDT-DSMAEYGDGDTGQFTEDGSGFIGQYVPGKLQPPVSPQPLNNSAAA HQAAPTAGGSGA
gi | 1136796      DDSDDSLVDYEGEGD GQFNEDGSGFIGQYS GKKEKDT-----
gi | 4538399      EDSDDSLVDYEGEGVNGQFNEDGSGFIGQYS GKKEKEP-----

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gi | 2978945      EDSDDSLVDYGEGVNGQFNEDGSFIGQYSGKKEKEP-----  
gi | 4705895      EDSDDSLVDYGEGVNGQFNEDGSFIGQYSGKKEKEP-----  
gi | 8115822      EDSDDSLVDYGEGVNGQFNEDGSFIGQYSGKKEKEP-----  
gi | 7661510      EDSDDSLVDYGEGVNGQFNEDGSFIGQYSGKKEKEP-----
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          : **          * . :
```

```
gi | 7199800      -----  
gi | 2464061      AGSAAAAGASGGASSAGGAAASNGGAAAGAVATYV  
gi | 1136796      -----AEGNESSEAPSPVAMNSFV  
gi | 4538399      -----AEGNESSEAPSPVAMNSFV  
gi | 2978945      -----AEGNESSEAPSPVAMNSFV  
gi | 4705895      -----AEGNESSEAPSPVAMNSFV  
gi | 8115822      -----AEGNESSEAPSPVAMNSFV  
gi | 7661510      -----AEGNESSEAPSPVAMNSFV
```