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gi |12232377 |ref |NP_073562.1|
gi |114636689 |ref |XP_001169698.1|
gi |119918885 |ref |XP_588722.3|
gi |149257287 |ref |XP_001475027.1|
gi |109458799 |ref |XP_574453.2|
gi |118091105 |ref |XP_001234315.1|
gi |125855679 |ref |XP_001331278.1|
gi |189537851 |ref |XP_001923677.1|

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-----MESLLOHLDLRFSELLAVSSTHVVSTWDPAAIV 31
MPLGISVGGKVQWPCQDKMSKQRTCKNDSSFROSSENFYLRLIFPKRKEARRRSRLASSRMWFRKFSVGCPTLSALPPLRRITSLCGETFDRGVSFHGCNPQYAEARRLQGESGIRAFAHLMESLLOHLDLRFSELLAVSSTHVVSTWDPAAIV 150
-----MDSLLEQLDRFSELLAVSSTHVVSTWDPAAIV 31
-----MEPLVQTERFSELLAVSCGSLVSTWDAEKV 31
-----MEPLVQYTERFSELLAVSCGSLVSTWDAEKV 31
-----MFSSANRMNLRPCWLGVLVPGARRVLRNRRRQCCRGVMEAVLQVAELPALLAVSRALVRDWDPPPL 72
-----MEAVLRHLNINLELLAVSRTDRVREWRDPTT 31
-----MEAVLRHLNINLELLAVSRTDRVREWRDPTT 31

1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

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gi |12232377 |ref |NP_073562.1|
gi |114636689 |ref |XP_001169698.1|
gi |119918885 |ref |XP_588722.3|
gi |149257287 |ref |XP_001475027.1|
gi |109458799 |ref |XP_574453.2|
gi |118091105 |ref |XP_001234315.1|
gi |125855679 |ref |XP_001331278.1|
gi |189537851 |ref |XP_001923677.1|

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-----RRALQWARYLRHIIHRRFGRHGPIRTALERRLHNQWRQEGGFGRGVPVPLANFQALGHCQVLLSLRLLNRRALGDAARYHLVQQLFPGPGVVRDAEETLQESLARLARRRSAVHMLRFNGYRENPNLQEDSLMKTQAEILLERLQEVGKAE 181
RRALQWARYLRHIIHRRFGRHGPIRTALERRLHNQWRQEGGFGRGVPVPLANFQALGHCQVLLSLRLLNRRALGDAARYHLVQQLFPGPGVVRDAEETLQESLARLARRRSAVHMLRFNGYRENPNLQEDSLMKTQAEILLERLQEVGKAE 300
RRALQWAGYLRHIIHRRFGRHARIRKALEQRLQNWQKQEGDSSGPAPADLANFQALGHCQVLLSLRLLNRRALGDAARYHLVQQLFPGPGVVRDAEETLQESLARLARRRSAVHMLRFNGYRENPNLQEDSLMKTQAEILLERLQEVGKAE 181
RRALQWARYLRHIIHRRFGRHGPIRTALERRLHNQWRQEGGFGRGVPVPLANFQALGHCQVLLSLRLLNRRALGDAARYHLVQQLFPGPGVVRDAEETLQESLARLARRRSAVHMLRFNGYRENPNLQEDSLMKTQAEILLERLQEVGKAE 167
RRALQWARYLHVYRRFAGRGRVREALERLH---ARGGPLG-----LRSFAALESQDARLALRLLNRRALAPAAARALPGLLFPGP--AADHRDDVPSRLVLLARRGSALRLL---CRIGGDAAPRSALRLTHAELLDARLHELGGAD 167
RRALQWARYLFHVYRRFASRGRVREALERLH---VRRGPLG-----LRSFAALESQDARLALRLLNRRALAPAAARALPGLLFPGP--AADNVDDVPSRLVLLARRGSALHLL---FRLGGDAPKGAALLRTHAELLYARLQELGGAD 167
DRALQWARYLHLDHRRFGRHGPIRTALERRLHNQWRQEGGFGRGVPVPLANFQALGHCQVLLSLRLLNRRALGDAARYHLVQQLFPGPGVVRDAEETLQESLARLARRRSAVHMLRFNGYRENPNLQEDSLMKTQAEILLERLQEVGKAE 202
QRAFKAWEYCEQLHSRYSNPTVRSRLSGLTDTNRRRLRETFP--SYSPVFESELAQCQKHLIVYLLRN---PSSPHFIIEMLFPDQ---NSPSQELLAPQNSLVTRKSAFSLLCCTVNTTSS-----YYGLQTEPEVR 157
QRAFKAWEYCEQLHSRYSNPTVRSRLSGLTDTNRRRLRETFP--SYSPVFESELAQCQKHLIVYLLRN---PSSPHFIIEMLFPDQ---NSPSQELLAPQNSLVTRKSAFSLLCCTVNTTSS-----YYGLQTEPEVR 157

.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300

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gi |12232377 |ref |NP_073562.1|
gi |114636689 |ref |XP_001169698.1|
gi |119918885 |ref |XP_588722.3|
gi |149257287 |ref |XP_001475027.1|
gi |109458799 |ref |XP_574453.2|
gi |118091105 |ref |XP_001234315.1|
gi |125855679 |ref |XP_001331278.1|
gi |189537851 |ref |XP_001923677.1|

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-----AERPAPFLSLWLERLPNNFLKVIAVALLQPPLSRRPQHE--LEPGIHKSPGEGSC--VLVHMLLGNSEVFAAFCRALPAGLLTIVTSRHPALSPVVLGLLTDWQRLHYDLDKGIWVGTESE--DVPWEELHNRFSQSLCOAPPPLKDKVLI 327
AERPAPFLSLWLERLPNNFLKVIAVALLQPPLSRRPQHE--LEPSIHKSPGEGSC--VLVHMLLGNSEVFAAFCRALPAGLLTIVTSRHPALSPVVLGLLTDWQRLHYDLDKGIWVGTESE--DVPWEELHNRFSQSLCOAPPPLKDKVLI 446
AEGPGRLLSRWLERLPNDNFKVVAALLLPQASRRLQEEELGVGSPKTPGDGRC--ELLRWLLGKSDIVVAFCRNLPAELLISVVGRRPELSPVVLGLLTDWQRLHYDLDKGIWVGTESE--DVPWEELHNRFSQSLCOAPPPLKDKVLI 328
SAAARKLLDRLWTRGPREHVLDTAEALLREEDPEPAQA---DPAAGADETC--KLLRWLLESPEVLAFAFCRHLPAKRLASVAGCHHALSRAYLDLLTAWARLHYDLDKGIWVGTESE--DMPWEELCLRLOSCHAOFPLOEVLV 309
STAARKLLDRLWTRGPREHVLDTAEALLREEDPEPAQA---ADSAGADETC--KLLRWLLESPEVLAFAFCRHLPAKRLASVAGCHHALSRAYLDLLTAWARLHYDLDKGIWVGTESE--DMPWEELCLRLOSCHAOFPLOEVLV 308
AGAALGWLGPVLEQLPQRAFQVVAEALLRQCCGGGDSSAGQAGGAEAGSVA GALLSWLLEDLHRFSACSLLLPGTLLASLAGRYAQLSRRVLDLLAEWGSHELLYDPLQGRVVKSRSEBAKLCWEELRERFGLCOGQSVQLRQTA 352
GKLLGKLLNSILARPQNEEHAKECLLDLSDRCDSSAGKVDGFYDVIAGALLCSSDESQRFIITWLKESDGGNLFCTVISPVECAVISRQSPFRKLYWGALKQWASCLEYDVTKSVVWVTESEGA---VSEFDVLADRLDLNSGESLKEETE 304
GKLLGKLLNSILARPQNEEHAKECLLDLSDRCDSSAGKVDGFYDVIAGALLCSSDESQRFIITWLKESDGGNLFCTVISPVECAVISRQSPFRKLYWGALKQWASCLEYDVTKSVVWVTESEGA---VSEFDVLADRLDLNSGESLKEETE 304

.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450

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gi |12232377 |ref |NP_073562.1|
gi |114636689 |ref |XP_001169698.1|
gi |119918885 |ref |XP_588722.3|
gi |149257287 |ref |XP_001475027.1|
gi |109458799 |ref |XP_574453.2|
gi |118091105 |ref |XP_001234315.1|
gi |125855679 |ref |XP_001331278.1|
gi |189537851 |ref |XP_001923677.1|

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-----ALETCKAAGDGFVEVPLSIWTDLLLALRSQAFRKRQVLGLSAGLSSV 374
ALETCKAAGDGFVEVPLSIWTDLLLALRSQAFRKRQVLGLSAGLSSV 493
ALKSVKAAGDGFVEVPLSIWTDLLLALRSQAFRKRQVLGLSAGLSSV 359
ILRSRKALDGDGFVEVPLSIWTDLLLALRSQAFRKRQVLGLSAGLSSV 343
ILRSCKALDGDGFVEVPLSIWTDLLLALRSQAFRKRQVLGLSAGLSSV 339
ALKLTLQDGDGFVEVPLSIWTDLLLALRSQAFRKRQVLGLSAGLSSV 391
ALKLTLQDGDGFVEVPLSIWTDLLLALRSQAFRKRQVLGLSAGLSSV 333
ALKLTLQDGDGFVEVPLSIWTDLLLALRSQAFRKRQVLGLSAGLSSV 333

.....460.....470.....480.....490.....