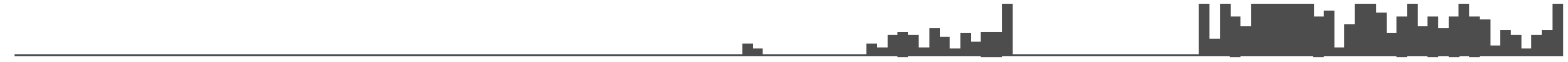


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gi|62241013|ref|NP_001014431.1|-----MS-----*-----*
gi|114655082|ref|XP_001143158.1|-----MS-----DVAIVKEGWLHKRG-----EYIKTWRPRYFLKNDGTFIGYKERPOVDVOREAP 51
gi|6753034|ref|NP_033782.1|-----MN-----DVAIVKEGWLHKRG-----EYIKTWRPRYFLKNDGTFIGYKERPOVDVOREAP 51
gi|15100164|ref|NP_150233.1|-----MN-----DVAIVKEGWLHKRG-----EYIKTWRPRYFLKNDGTFIGYKERPOVDVOREAP 51
gi|27806747|ref|NP_776411.1|-----MN-----DVAIVKEGWLHKRG-----EYIKTWRPRYFLKNDGTFIGYKERPOVDVOREAP 51
gi|73964539|ref|XP_548000.2|-----MG-----GPAASPHHAVSSG-----EYIKTWRPRYFLKNDGTFIGYKERPOVDVOREAP 52
gi|45384254|ref|NP_990386.1|-----MN-----EVAIVKEGWLHKRG-----EYIKTWRPRYFLKNDGTFIGYKERPOVDVOREAP 51
gi|189530555|ref|XP_001921993.1|MKPKPAGAMLSSEHGIHAGKAGSSQDFVGDVFLPGNAQARRPLMWKVFSLLSCLAEVNVHSLPYR--VLMTDTLYTAIFVAVVSLCTIGVEVIGDGGAVRDLVDDIKLVVVVWYEVYIKTWRPRYFLKNDGTFIGYKERPOVDVOREAP 147
gi|71983636|ref|NP_001023645.1|-----MSMSTLTKERR-----QEDVVEGWLHKRG-----EHIRNRWPRYFMIFDYGALLGFRAPKPEGPPPEP 61
gi|71988908|ref|NP_510357.3|-----MSTENAHLQ-----KEDIVTISWLHKRG-----EHIRNRWPRYFILFRDGTLLGFRSKPKEDQPLPEP 58
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

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gi|62241013|ref|NP_001014431.1|LNNFSVA---CCQLMKTERRPNTFIIRCLQWTVIERTFHVETPEEREWWTAIQTVDAGLK---KQEEEMDFRSGSPDNSGAEEMEVSLAKP-----KHRVTMNEFEYLLKLGKGTFGKV 164
gi|114655082|ref|XP_001143158.1|LNNFSVA---CCQLMKTERRPNTFIIRCLQWTVIERTFHVETPEEREWWTAIQTVDAGLK---KQEEEMDFRSGSPDNSGAEEMEVSLAKP-----KHRVTMNEFEYLLKLGKGTFGKV 164
gi|6753034|ref|NP_033782.1|LNNFSVA---CCQLMKTERRPNTFIIRCLQWTVIERTFHVETPEEREWWTAIQTVDAGLK---KQEEEMDFRSGSPDNSGAEEMEVSLAKP-----KHRVTMNEFEYLLKLGKGTFGKV 164
gi|15100164|ref|NP_150233.1|LNNFSVA---CCQLMKTERRPNTFIIRCLQWTVIERTFHVETPEEREWWTAIQTVDAGLK---KQEEEMDFRSGSPDNSGAEEMEVSLAKP-----KHRVTMNEFEYLLKLGKGTFGKV 164
gi|27806747|ref|NP_776411.1|LNNFSVA---CCQLMKTERRPNTFIIRCLQWTVIERTFHVETPEEREWWTAIQTVDAGLK---KQEEEMDFRSGSPDNSGAEEMEVSLAKP-----KHRVTMNEFEYLLKLGKGTFGKV 164
gi|73964539|ref|XP_548000.2|LNNFSVA---CCQLMKTERRPNTFIIRCLQWTVIERTFHVETPEEREWWTAIQTVDAGLK---KQEEEMDFRSGSPDNSGAEEMEVSLAKP-----KHRVTMNEFEYLLKLGKGTFGKV 165
gi|45384254|ref|NP_990386.1|LNNFSVA---CCQLMKTERRPNTFIIRCLQWTVIERTFHVETPEEREWWTAIQTVDAGLK---KQEEEMDFRSGSPDNSGAEEMEVSLAKP-----KHRVTMNEFEYLLKLGKGTFGKV 164
gi|189530555|ref|XP_001921993.1|LNNFSVARESITCXLMTERRPKNTFIIRCLQWTVIERTFHVETPEEREWWTAIQTVAESLG---KQEEEMDAS-----AEHTDMETSLSKP-----PHKVTMHDFFEYLLKLGKGTFGKV 257
gi|71983636|ref|NP_001023645.1|LNNFMIR---DAATMLFEKPRPMFMVRCLOWTVIERTFYAESAIVRWRWTHATESIKKYKGTANPQBELMENOQPKDEDESEFAGAAHATMGQSSGHGDNCSIDFRASMTIADTSEAAKRDKITMDEDFDLKVLGKGTFGKV 207
gi|71988908|ref|NP_510357.3|LNNFMIR---DAATVCLDKPRPMFIVRCLQWTVIERTFYADSADFRQMWTEAIAQVSHNR---LKENAGNLSMQ--EEDTNGNPSGESDNNMDATSTRDN---DFESTVMNIDPEEVPKNTVIMDDDFDLKVLGKGTFGKV 194
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300

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gi|62241013|ref|NP_001014431.1|LLVKEKATGRYYAMKILKKEVIVAKDEVAHTLTENRVLQNSRRPFLTALKYSFQTHDRLCFVMEYANGGELFFHLSRERVFSEDRARFYGAEIVSALDYLHSEKNVYVRDLKLENLMLDKDGHIKITDFGLCKEGIKDGAITMFCGTP 314
gi|114655082|ref|XP_001143158.1|LLVKEKATGRYYAMKILKKEVIVAKDEVAHTLTENRVLQNSRRPFLTALKYSFQTHDRLCFVMEYANGGELFFHLSRERVFSEDRARFYGAEIVSALDYLHSEKNVYVRDLKLENLMLDKDGHIKITDFGLCKEGIKDGAITMFCGTP 314
gi|6753034|ref|NP_033782.1|LLVKEKATGRYYAMKILKKEVIVAKDEVAHTLTENRVLQNSRRPFLTALKYSFQTHDRLCFVMEYANGGELFFHLSRERVFSEDRARFYGAEIVSALDYLHSEKNVYVRDLKLENLMLDKDGHIKITDFGLCKEGIKDGAITMFCGTP 314
gi|15100164|ref|NP_150233.1|LLVKEKATGRYYAMKILKKEVIVAKDEVAHTLTENRVLQNSRRPFLTALKYSFQTHDRLCFVMEYANGGELFFHLSRERVFSEDRARFYGAEIVSALDYLHSEKNVYVRDLKLENLMLDKDGHIKITDFGLCKEGIKDGAITMFCGTP 314
gi|27806747|ref|NP_776411.1|LLVKEKATAAYAMKILKKEVIVAKDEVAHTLTENRVLQNSRRPFLTALKYSFQTHDRLCFVMEYANGGELFFHLSRERVFSEDRARFYGAEIVSALDYLHSEKNVYVRDLKLENLMLDKDGHIKITDFGLCKEGIKDGAITMFCGTP 314
gi|73964539|ref|XP_548000.2|LLVKEKATGRYYAMKILKKEVIVAKDEVAHTLTENRVLQNSRRPFLTALKYSFQTHDRLCFVMEYANGGELFFHLSRERVFSEDRARFYGAEIVSALDYLHSEKNVYVRDLKLENLMLDKDGHIKITDFGLCKEGIKDGAITMFCGTP 314
gi|45384254|ref|NP_990386.1|LLVKEKATGRYYAMKILKKEVIVAKDEVAHTLTENRVLQNSRRPFLTALKYSFQTHDRLCFVMEYANGGELFFHLSRERVFSEDRARFYGAEIVSALDYLHSEKNVYVRDLKLENLMLDKDGHIKITDFGLCKEGIKDGAITMFCGTP 314
gi|189530555|ref|XP_001921993.1|LLVKEKATGRYYAMKILKKEVIVAKDEVAHTLTENRVLQNSRRPFLTALKYSFQTHDRLCFVMEYANGGELFFHLSRERVFSERACFYGAEIVSALHYLHSEKNVYVRDLKLENLMLDKDGHVITDFGLCKEGITDGAITMFCGTP 407
gi|71983636|ref|NP_001023645.1|LLCKEKR---QKLYATKILKQVITAREEVAHTLTENRVLQRCCKHPFLTELKYSFOEQHYICFVMOFANGGELFTVVRKCGTFSEPRARFYGAEIVLALGYLHR-CDIVYRDMKLENLLDKDGHIKITDFGLCKEISFQDKTISFCGTP 356
gi|71988908|ref|NP_510357.3|LLCREKSSDKLYATKIRKEMVVDREVAHTLTENRVLVYACVHPFLILLKYSFOAQYHICFVMEFANGGELFTLQRCCKTFSEARTRFYGSEITLALGYLHR-RNIVYRDMKLENLLDRDGHIKITDFGLCKEIEIYQDKTISFCGTP 343
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450

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gi|62241013|ref|NP_001014431.1|YLAPAEVLLEDNDYGRAVDWVGLGVVYEMMCGRLPFYNDHEKLFELILMEEIRFPRTLGP EAKSLLSGLLKKDPKQRLGGGSEDAKEIMQHRFFAGIVWQDVYEKLLSPPFKPQVTSETDRYFDEEFTAQMIITIPPDQDMSMECVDS- 463
gi|114655082|ref|XP_001143158.1|YLAPR-----SCLCR-----GLVACCSLTVLPGDP-----LEIQLSPPFKPQVTSETDRYFDEEFTAQMIITIPPDQDMSMECVDS- 387
gi|6753034|ref|NP_033782.1|YLAPAEVLLEDNDYGRAVDWVGLGVVYEMMCGRLPFYNDHEKLFELILMEEIRFPRTLGP EAKSLLSGLLKKDPKQRLGGGSEDAKEIMQHRFFAGIVWQDVYEKLLSPPFKPQVTSETDRYFDEEFTAQMIITIPPDQDMSMECVDS- 463
gi|15100164|ref|NP_150233.1|YLAPAEVLLEDNDYGRAVDWVGLGVVYEMMCGRLPFYNDHEKLFELILMEEIRFPRTLGP EAKSLLSGLLKKDPKQRLGGGSEDAKEIMQHRFFAGIVWQDVYEKLLSPPFKPQVTSETDRYFDEEFTAQMIITIPPDQDMSMECVDS- 463
gi|27806747|ref|NP_776411.1|YLAPAEVLLEDNDYGRAVDWVGLGVVYEMMCGRLPFYNDHEKLFELILMEEIRFPRTLGP EAKSLLSGLLKKDPKQRLGGGSEDAKEIMQHRFFAGIVWQDVYEKLLSPPFKPQVTSETDRYFDEEFTAQMIITIPPDQDMSMECVDS- 463
gi|73964539|ref|XP_548000.2|YLAPAEVLLEDNDYGRAVDWVGLGVVYEMMCGRLPFYNDHEKLFELILMEEIRFPRTLGP EAKSLLSGLLKKDPKQRLGGGSEDAKEIMQHRFFAGIVWQDVYEKLLSPPFKPQVTSETDRYFDEEFTAQMIITIPPDQDMSMECVDS- 464
gi|45384254|ref|NP_990386.1|YLAPAEVLLEDNDYGRAVDWVGLGVVYEMMCGRLPFYNDHEKLFELILMEEIRFPRTLGP EAKSLLSGLLKKDPKQRLGGGSEDAKEIMQHRFFAGIVWQDVYEKLLSPPFKPQVTSETDRYFDEEFTAQMIITIPPDQDMSMECVDS- 463
gi|189530555|ref|XP_001921993.1|YLAPAEVLLEDNDYGRAVDWVGLGVVYEMMCGRLPFYNDHEKLFELILMEEIRFPRTLGP EAKSLLSGLLKKDPKQRLGGGSEDAKEIMQHRFFAGIVWQDVYEKLLSPPFKPQVTSETDRYFDEEFTAQMIITIPPDQDMSMECVDS- 556
gi|71983636|ref|NP_001023645.1|YLAPAEVLDDHDYGRCDWVGLGVVYEMMCGRLPFYSKDNKLFELIMAGDLRFPKLSQEARLLTGLLVKDPTRLGGGPEADALEICRADFFRTVDWEAIVRKEIETPPYKPNVQSETDTSYDFNEFTSIPVQLTTPPSRSGALAVDE 506
gi|71988908|ref|NP_510357.3|YLAPAEVIDIDYDREVDWVGLGVVYEMMCGRLPFAKENGKLFELIICDLKFFNRLSPEAVTLLSGLLERPAKRLGAGPDAAREVRAEFFKVDVDEAALRKEVEPPFKPNVSETDTSFFDFREFTSMPEVQLTTPRRGELPVDE 493
.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600

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gi|62241013|ref|NP_001014431.1| -ERRPHFPQFS-YASGTA----- 480
gi|114655082|ref|XP_001143158.1| -ERRPHFPQFS-YASGTA----- 404
gi|6753034|ref|NP_033782.1| -ERRPHFPQFS-YASGTA----- 480
gi|15100164|ref|NP_150233.1| -ERRPHFPQFS-YASGTA----- 480
gi|27806747|ref|NP_776411.1| -ERRPHFPQFS-YASGTA----- 480
gi|73964539|ref|XP_548000.2| -ERRPHFPQFS-YASGTA----- 481
gi|45384254|ref|NP_990386.1| -ERRPHFPQFS-YASGTA----- 480
gi|189530555|ref|XP_001921993.1| -ERRPHFPQFS-YASGTA----- 573
gi|71983636|ref|NP_001023645.1| EEMGSNFTQFSFHNVMGSLNRIHEAEDNEDYDMG 541
gi|71988908|ref|NP_510357.3| EELQANFIQFASYVVSGLERSYDINRSADKYEIR 528
.....610.....620.....630.....

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