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gi|4758250|ref|NP_004084.1|    --MA-VRRDSVWKYCWGVLMLVC-----RVAIS-----KSIIVLEP-----150
gi|114650617|ref|XP_001134800.1|  --MA-VRRDSVWKYCWGVLMLVC-----RVAIS-----KSIIVLEP-----150
gi|31542597|ref|NP_034241.2|     MAMARSRRDSVWKYCWGLLMVLC-----RVAIS-----RSIVLEP-----150
gi|109503590|ref|XP_225050.4|     MAMARSRRDSVWKYCWGLLMVLC-----RVAIS-----RSIVLEP-----150
gi|73989471|ref|XP_854550.1|      --MA-ARRDSVWKYCWGVLMLVC-----RVAIS-----RSIVLEP-----150
gi|194671926|ref|XP_001787972.1|  MVTTPRPRGSLRRLRPRPLCAAGRARGVLAAGGFRGGRGARRPAASGRCGFAEAAAARRGAPGARAPKGLGEKNARLPSASLSPSPPRFAVILGRRCERVPIKEIVRRRRARGEALPFWGQGLGARPPRRIPGRRALPLFAPVHWDRAFRPA150
gi|45382249|ref|NP_990155.1|     MAARRRDASACKYCWGALMVLW-----RVALA-----KSIIVLEP-----150
gi|18858593|ref|NP_571098.1|     ---MGGDSLWRYYFGVLIAC-----KVNLE-----RALLILDS-----150
gi|71984507|ref|NP_501955.2|     MGIATFILLSLFPFIG-----WARKIIPD-----150
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150
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gi|4758250|ref|NP_004084.1|    ---IYWNSSNSKFLPG--QGLVLYPQIGDKLDIICPKVDSKTIVGOYEEYKVMVDKDAQDRCTIKKENTPLLNCAPKPDQDKFTIKFOEFSPNLWGLEFQKNKDYIIISTNSGLEGLDNOEGGVCOTRAMKILMKVGDASSAGSTRNK300
gi|114650617|ref|XP_001134800.1|  ---IYWNSSNSKFLPG--QGLVLYPQIGDKLDIICPKVDSKTIVGOYEEYKVMVDKDAQDRCTIKKENTPLLNCAPKPDQDKFTIKFOEFSPNLWGLEFQKNKDYIIISTNSGLEGLDNOEGGVCOTRAMKILMKVGDASSAGSTRNK300
gi|31542597|ref|NP_034241.2|     ---IYWNSSNSKFLPG--QGLVLYPQIGDKLDIICPKVDSKTIVGOYEEYKVMVDKDAQDRCTIKKENTPLLNCARPDQDKFTIKFOEFSPNLWGLEFQKNKDYIIISTNSGLEGLDNOEGGVCOTRAMKILMKVGDASSAGSARNH300
gi|109503590|ref|XP_225050.4|     ---IYWNSSNSKFLPG--QGLVLYPQIGDKLDIICPKVDSKTIVGOYEEYKVMVDKDAQDRCTIKKENTPLLNCARPDQDKFTIKFOEFSPNLWGLEFQKNKDYIIISTNSGLEGLDNOEGGVCOTRAMKILMKVGDASSAGSTRNN300
gi|73989471|ref|XP_854550.1|      ---IYWNSSNSKFLPG--QGLVLYPQIGDKLDIICPKVDSKTIVGOYEEYKVMVDKDAQDRCTIKKENTPLLNCARPDQDKFTIKFOEFSPNLWGLEFQKNKDYIIISTNSGLEGLDNOEGGVCOTRAMKILMKVGDASSAGSARNH300
gi|194671926|ref|XP_001787972.1|  FGAEISWNSSNSKFLPG--QGLVLYPQIGDKLDIICPKVDSKTIVGOYEEYKVMVDKDAQDRCTIKKENTPLLNCARPDQDKFTIKFOEFSPNLWGLEFQKNKDYIIISTNSGLEGLDNOEGGVCOTRAMKILMKVGDASSAGSTRHS300
gi|45382249|ref|NP_990155.1|     ---IYWNSSNSKFLPG--QGLVLYPQIGDKLDIICPKVDSKTIVGOYEEYKVMVDKDAQDRCAIRKDNTPLLNCAPKPDQDKFTIKFOEFSPNLWGLEFQKNKDYIIISTNSGLEGLDNOEGGVCOTKTKMKILMKVGDASSAGLPRST300
gi|18858593|ref|NP_571098.1|     ---IYWNNTNITKFPQ--QGLVLYPQIGDKMDIVCPVVEGSGMEGVYKLYMVEQLKSCQVTKADTPLLNCVKKPDQDKFTIKFOEFSPNLWGLEFFRQKDYIIISTNSGLEGLDNOEGGVCIKTKSMKILMKVGNPFDPISEPKD-300
gi|71984507|ref|NP_501955.2|     ---INWTSSNPIFDVSTNDHVISVHIGDRVSIKCPKSD--EIGKYEYSYIYMVSDDEYDHCFLSKP--RLVGAQDNQTIINASINIVFRSFLPTPGGFEPFGPKNYFLISTSDGILEGIDRKKDGLCTAKQMKIKFEVGDORRRGIENPKFA300
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300
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gi|4758250|ref|NP_004084.1|    DPTRRPELEAGTNGRSSTTSP-----FVKPNP-----GSSTDGNSAGHSGNNILGSEVALFAGIASGCIIFIVIIIILVVLKLYRRRHRKHSPOHTTLTSLSTLATPKRSG---NNGSEPSDIIIPLRITADSVFCPHYEKV450
gi|114650617|ref|XP_001134800.1|  DPTRRPELEAGTNGRSSTTSP-----FVKPNP-----GSSTDGNSAGHSGNNILGSEVALFAGIASGCIIFIVIIIILVVLKLYRRRHRKHSPOHTTLTSLSTLATPKRSG---NNGSEPSDIIIPLRITADSVFCPHYEKV450
gi|31542597|ref|NP_034241.2|     DPTRRPELEAGTNGRSSTTSP-----FVKPNP-----GSSTDGNSAGHSGNNLLGSEVALFAGIASGCIIFIVIIIILVVLKLYRRRHRKHSPOHTTLTSLSTLATPKRGG---NNGSEPSDVIIPLRITADSVFCPHYEKV450
gi|109503590|ref|XP_225050.4|     DPTRRPELEAGTNGRIISDAPPDRFSLADAGSRSLPLPSQ-----SSSTDGNSAGHSGNNLLGSEVALFAGIASGCIIFIVIIIILVVLKLYRRRHRKHSPOHTTLTSLSTLATPKRGG---NNGSEPSDVIIPLRITADSVFCPHYEKV450
gi|73989471|ref|XP_854550.1|      DPTRRPELEAGTNGRSSTTSP-----FVKPNP-----SSSTDGSSAGHSGNNILGSEVALFAGIASGCIIFIVIIIILVVLKLYRRRHRKHSPOHTTLTSLSTLATPKRGG---NNGSEPSDIIIPLRITADSVFCPHYEKV450
gi|194671926|ref|XP_001787972.1|  DPTRRPELEAGTNGRSSTTSP-----FVKPNP-----SSSTDGSSAGHSGNNILGSEVALFAGIASGCIIFIVIIIILVVLKLYRRRHRKHSPOHTTLTSLSTLATPKRGG---NNGSEPSDIIIPLRITADSVFCPHYEKV450
gi|45382249|ref|NP_990155.1|     DPTRRPELEAGTNGRSSTTSP-----FVKDHS-----GSSTDGSKAGHS--SILGSEVALFAGIASGCIIFIVIIIILVVLKLYRRRHRKHSPOHTTLTSLSTLATPKRSG---NNGSEPSDIIIPLRITADSVFCPHYEKV450
gi|18858593|ref|NP_571098.1|     YPTSYPPKRPDLGKDKSNE-----VLKPDA-----SPHGDKGDGDKRSSSVIGSEVALFACIASASVIVIIIIMLVFLLKLYRRRHRKHSPOHTTLTSLSTLATPKRSGGGNNGSEPSDIIIPLRITADSVFCPHYEKV450
gi|71984507|ref|NP_501955.2|     ARLLKQRDAEHSFVPMVYVD-----EDIDDDDDGNSN-----ACSVFVSIIVVLLASRYLL-----450
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450
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gi|4758250|ref|NP_004084.1|    SGDYGHPVYIVQEMPPQSPANIYYKV 476
gi|114650617|ref|XP_001134800.1|  SGDYGHPVYIVQEMPPQSPANIYYKV 476
gi|31542597|ref|NP_034241.2|     SGDYGHPVYIVQEMPPQSPANIYYKV 476
gi|109503590|ref|XP_225050.4|     SGDYGHPVYIVQEMPPQSPANIYYKV 476
gi|73989471|ref|XP_854550.1|      SGDYGHPVYIVQEMPPQSPANIYYKV 476
gi|194671926|ref|XP_001787972.1|  SGDYGHPVYIVQEMPPQSPANIYYKV 476
gi|45382249|ref|NP_990155.1|     SGDYGHPVYIVQEMPPQSPANIYYKV 476
gi|18858593|ref|NP_571098.1|     SGDYGHPVYIVQEMPPQSPANIYYKV 476
gi|71984507|ref|NP_501955.2|     .....460.....470.....476
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