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gi|117606364|ref|NP_032715.2|-----MADDDPYGTG-----* 150
gi|62644423|ref|XP_342347.2|-----MADDDPYGTG-----OMFHLNTALTHS-IF 150
gi|34577122|ref|NP_003989.2|-----MAEDDPVLRPE-----OMFHLDPDLTHL-IF 150
gi|114595421|ref|XP_001168506.1|-----MAEDDPVLRPE-----OMFHLDPDLTHL-IF 150
gi|50979190|ref|NP_001003344.1|-----MAEDDPVLRPE-----OMFHLDPDLTHL-IF 150
gi|115497302|ref|NP_001069877.1|-----MAEDDPVLRPE-----OMFHLDPDLTHL-IF 150
gi|45384086|ref|NP_990465.1|-----MAGEDPPTMVGSDP-----OMFHLDPDLTHL-IF 150
gi|118778988|ref|XP_308995.3|-----MAGEDPPTMVGSDP-----OMFHLDPDLTHL-IF 150
gi|17137094|ref|NP_477094.1|-----MAGEDPPTMVGSDP-----OMFHLDPDLTHL-IF 150
MSTLLNLDYRHELYEQOQLLGTSPIQYIVLQMDNPSPPSSSSAAAVVSGVEFTLQPGRTYASALSPSSSSASPSPPSVAIPNRRASINMSPSSASDQAAAYLQNLNLSAGLNMVYFGMGYQQQQQQQQQQHQQHQQOQLQQQHHY 150
-----MNMN-----QYDLDLN-----GKNVMFMNDASSTSGYSSSTSPNFINRSFPAHS-----FKITMELQIDFANLNLPGGNPSHPPPMANSPYQNLNNGGICOLGAINLINSTG-----VFGVANVTSFGNMTMDHGFVFPAPAIFPFSQN 150
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

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gi|117606364|ref|NP_032715.2|N-AELYSF-----EIPLSL-DGPLYLQILEOPKORGFRRFYVCEGP-SHGGLPGASSEKNNKSSYPQVKICNVGPAKVIQVLTNG-KNIHLHAHSLVKGKHCEDGCVITVAGPKDMVVGFPANLILGHVTKKKVFET 300
gi|62644423|ref|XP_342347.2|N-AELYST-----DIPLST-DGPLYLQILEOPKORGFRRFYVCEGP-SHGGLPGASSEKNNKSSYPQVKICNVGPAKVIQVLTNG-KNIHLHAHSLVKGKHCEDGCVITVAGPKDMVVGFPANLILGHVTKKKVFET 300
gi|34577122|ref|NP_003989.2|N-PEVFQP-----QMALPTADGPPYLQILEOPKORGFRRFYVCEGP-SHGGLPGASSEKNNKSSYPQVKICNVGPAKVIQVLTNG-KNIHLHAHSLVKGKHCEDGCVITVAGPKDMVVGFPANLILGHVTKKKVFET 300
gi|114595421|ref|XP_001168506.1|N-PEVFQP-----QMALPTADGPPYLQILEOPKORGFRRFYVCEGP-SHGGLPGASSEKNNKSSYPQVKICNVGPAKVIQVLTNG-KNIHLHAHSLVKGKHCEDGCVITVAGPKDMVVGFPANLILGHVTKKKVFET 300
gi|50979190|ref|NP_001003344.1|N-PELFQP-----EMPLPTADGPPYLQILEOPKORGFRRFYVCEGP-SHGGLPGASSEKNNKSSYPQVKICNVGPAKVIQVLTNG-KNIHLHAHSLVKGKHCEDGCVITVAGPKDMVVGFPANLILGHVTKKKVFET 300
gi|115497302|ref|NP_001069877.1|S-PELFQP-----EMPLPTADGPPYLQILEOPKORGFRRFYVCEGP-SHGGLPGASSEKNNKSSYPQVKICNVGPAKVIQVLTNG-KNIHLHAHSLVKGKHCEDGCVITVAGPKDMVVGFPANLILGHVTKKKVFET 300
gi|45384086|ref|NP_990465.1|NTGYIITS-----DLPLRTADGPPYLQILEOPKORGFRRFYVCEGP-SHGGLPGASSEKNNKSSYPQVKICNVGPAKVIQVLTNG-KYVHLHAHSLVKGKHCEDGCVITVAGPKDMVVGFPANLILGHVTKKKVFET 300
gi|118778988|ref|XP_308995.3|YTFQLLNLDQEQLOLQTFIVTSSNEFAAPEFNNSSEPHLVIIQEPVDK-FFRFYQSEMHGTHGSLMGSRREKSKHFFPTVELRGGGAEKRCVLSVQVDPQRAPRAPHSHHLVKSQEDLIDPHLDVGGGAAGAEPSEGVGGDGKVVVAI 300
gi|17137094|ref|NP_477094.1|FGYHQNGL-----ASDGIKIHVQPLRIVEQPEVK-FFRFYKSEMHGTHGSLMGSRKRTPKKIFPEVTLQNVLDGPAVIRCSLFTQTN-LDSEPHSHQVLRKDDRDVCPDHDLVSKER-----GVVAQ 300
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300

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gi|117606364|ref|NP_032715.2|LEARMTEACIRGYNPGLLVHSDLAYLOAEGGGDRLQDREKEIIRQAALQOTKEMDLSVVRLMFTAFLPDR-TGSFTRRLEPVVSDAIYDSKAPNASNLKIVRMDRITAGCVTGGEEIYLLCDKVKDDIQRFYEEEE-NGGVWEGFGDF 450
gi|62644423|ref|XP_342347.2|LEARMTEACIRGYNPGLLVHSDLAYLOAEGGGDRLQDREKEIIRQAALQOTKEMDLSVVRLMFTAFLPDR-TGSFTRRLEPVVSDAIYDSKAPNASNLKIVRMDRITAGCVTGGEEIYLLCDKVKDDIQRFYEEEE-NGGVWEGFGDF 450
gi|34577122|ref|NP_003989.2|LEARMTEACIRGYNPGLLVHSDLAYLOAEGGGDRLQDREKEIIRQAALQOTKEMDLSVVRLMFTAFLPDR-TGSFTRRLEPVVSDAIYDSKAPNASNLKIVRMDRITAGCVTGGEEIYLLCDKVKDDIQRFYEEEE-NGGVWEGFGDF 450
gi|114595421|ref|XP_001168506.1|LEARMTEACIRGYNPGLLVHSDLAYLOAEGGGDRLQDREKEIIRQAALQOTKEMDLSVVRLMFTAFLPDR-TGSFTRRLEPVVSDAIYDSKAPNASNLKIVRMDRITAGCVTGGEEIYLLCDKVKDDIQRFYEEEE-NGGVWEGFGDF 450
gi|50979190|ref|NP_001003344.1|LEARMTEACIRGYNPGLLVHSDLAYLOAEGGGDRLQDREKEIIRQAALQOTKEMDLSVVRLMFTAFLPDR-TGSFTRRLEPVVSDAIYDSKAPNASNLKIVRMDRITAGCVTGGEEIYLLCDKVKDDIQRFYEEEE-NGGVWEGFGDF 450
gi|115497302|ref|NP_001069877.1|LEARMTEACIRGYNPGLLVHSDLAYLOAEGGGDRLQDREKEIIRQAALQOTKEMDLSVVRLMFTAFLPDR-TGSFTRRLEPVVSDAIYDSKAPNASNLKIVRMDRITAGCVTGGEEIYLLCDKVKDDIQRFYEEEE-NGGVWEGFGDF 450
gi|45384086|ref|NP_990465.1|LETRMIDACKKGYNPGLLVHSDLAYLOAEGGGDRLQDREKEIIRQAALQOTKEMDLSVVRLMFTAFLPDR-TGSFTRRLEPVVSDAIYDSKAPNASNLKIVRMDRITAGCVTGGEEIYLLCDKVKDDIQRFYEEEE-NGGVWEGFGDF 450
gi|118778988|ref|XP_308995.3|FGCGMIIHTAKKFTAELLYKLRKRLCELN--REPTEREERQOMKEAAVMARTMNLNQVLCFRAYRVPEPTGRWVVICPEPVYVNPINNMRSALTEGKLCIRLSTIVSGVDGEGVFMFVEKVKNNKIKRFDLIDRYDQEVQEMAITF 450
gi|17137094|ref|NP_477094.1|FINMGIIHTAKKYIFTELCKKKQDRIVFQMN-RRRLSHKQLQELHGETEREAKDMNLNQVLCFAEFKIED-NGAWVPLAPPVYSNAINNRKSAQIGELRIVRLSKPIGGVMDNDELILLVEKVSNNKIKRVFEEDEDETVWEAVAKF 450
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450

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gi|117606364|ref|NP_032715.2|SPTDVRHQAIVFKTPKYKDVNIITKPASVFLRRKSDLETSEPKP-FLYYP-----EIKDKEEVQRKRQKLMNPFSDSFGGSGAGAGGGMFGSGGGGG-SGSPGPGYGSNYGFPPYGGIIFHPGVITKSNAGVTHGTINIKFKN 600
gi|62644423|ref|XP_342347.2|SPTDVRHQAIVFKTPKYKDVNIITKPASVFLRRKSDLETSEPKP-FLYYP-----EIKDKEEVQRKRQKLMNPFSDSFGGSGAGAGGGMFGSGGGGGSTGSPGPGYGFPHYGFPAVGGIIFHPGATKSNAGVTHGTINIKFKN 600
gi|34577122|ref|NP_003989.2|SPTDVRHQAIVFKTPKYKDVNIITKPASVFLRRKSDLETSEPKP-FLYYP-----EIKDKEEVQRKRQKLMNPFSDSFGGSGAGAGGGMFGSGGGGG-GTGSTGPGYGFPHYGFPTTGGIIFHPGTITKSNAGMKHGTMDTESKK 600
gi|114595421|ref|XP_001168506.1|SPTDVRHQAIVFKTPKYKDVNIITKPASVFLRRKSDLETSEPKP-FLYYP-----EIKDKEEVQRKRQKLMNPFSDSFGGSGAGAGGGMFGSGGGGG-GLRKSLETSEPKP-FLYYP-----EIKDKEEVQRKRQKLMNPFSDSFGGSGAGAGGGMFGSGGGGG 600
gi|50979190|ref|NP_001003344.1|SPTDVRHQAIVFKTPKYKDVNIITKPASVFLRRKSDLETSEPKP-FLYYP-----EIKDKEEVQRKRQKLMNPFSDSFGGSGAGAGGGMFGSGGGGG-GAGSTGPGYGFPHYGFPTTGGIIFHPGTITKSNAGMKHGTMDTESKN 600
gi|115497302|ref|NP_001069877.1|SPTDVRHQAIVFKTPKYKDVNIITKPASVFLRRKSDLETSEPKP-FLYYP-----EIKDKEEVQRKRQKLMNPFSDSFGGSGAGAGGGMFGSGGGGG-GAGSTGPGYGFPHYGFPTTGGIIFHPGTITKSNAGMKHGTMDTESKN 600
gi|45384086|ref|NP_990465.1|SPTDVRHQAIVFKTPKYKDVNIITKPASVFLRRKSDLETSEPKP-FLYYP-----EIKDKEEVQRKRQKLMNPFSDSFGGSGAGAGGGMFGSGGGGG--AGSGSTGPGYGFPHYGFPTTGGIIFHPGTITKSNAGMKHGTMDTESKN 600
gi|118778988|ref|XP_308995.3|SEADVHHQYIAIAFKTPKYKDVNIITKPASVFLRRKSDLETSEPKP-FLYYP-----EIKDKEEVQRKRQKLMNPFSDSFGGSGAGAGGGMFGSGGGGG--GGGGGGGGGGVIGSGSTRLPPLHLKPPFMLANHAGGGAIFE 600
gi|17137094|ref|NP_477094.1|RESADVHHQYIAIVCQTPPYKDKVDREVNVIILIRPSDDERSFALPFRKPK-----RSVIVSRKRRRIGSSANSSSGTESSNSLIDLKTLGLAQP-----PGLNPNLSQHQDQTITSEEFGRKHLNEFIASEDFRKLIEHNS 600
.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600

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gi|117606364|ref|NP_032715.2|GPKDCAKSDDEESTLPEKETELEGESLPMAC--TKTEPIALASTMEDKEQDMGDFDLFLEKALQARRHANALFDYAVTGDVQMLLAVQRHLTAVQDENGDSVLHLAIHLLHAQLVRLDLEVTSGLSISDDIIMNRNDLYQTPHLHAVI 750
gi|62644423|ref|XP_342347.2|PRDCAKSDDEESTLPEKETELEGESLPMAS--TKTBAIAPASTMEDKEDVDFQDNLFLKALQARRHANALFDYAVTGDVQMLLAVQRHLTAVQDENGDSVLHLAIHLLHAQLVRLDLEVTSGLSISDDIIMNRNDLYQTPHLHAVI 750
gi|34577122|ref|NP_003989.2|DPEGCDKSDDKNTVNLFGKVIETTEQDQPSAEAVGNSEVNLVYATGTEESAGVDNLFLKAMQLAKRANALFDYAVTGDVQMLLAVQRHLTAVQDENGDSVLHLAIHLLHAQLVRLDLEVTSGLSISDDIIMNRNDLYQTPHLHAVI 750
gi|114595421|ref|XP_001168506.1|DPEGCDKSDDKNTVNLFGKVIETTEQDQPSAEAVGNSEVNLVYATGTEESAGVDNLFLKAMQLAKRANALFDYAVTGDVQMLLAVQRHLTAVQDENGDSVLHLAIHLLHAQLVRLDLEVTSGLSISDDIIMNRNDLYQTPHLHAVI 750
gi|50979190|ref|NP_001003344.1|DSEGCCKNVDREAVNLGKVIETTEQDQPSAEAVGNSEVNLVYATGTEESAGVDNLFLKAMQLAKRANALFDYAVTGDVQMLLAVQRHLTAVQDENGDSVLHLAIHLLHAQLVRLDLEVTSGLSISDDIIMNRNDLYQTPHLHAVI 750
gi|115497302|ref|NP_001069877.1|DSEGCCKSDREVNLSQVETETTEQDQDQSS--KRGTAAANLITCVGVKEENRSFQDNLFLKAMQLAKRANALFDYAVTGDVQMLLAVQRHLTAVQDENGDSVLHLAIHLLHAQLVRLDLEVTSGLSISDDIIMNRNDLYQTPHLHAVI 750
gi|45384086|ref|NP_990465.1|DESSDKQSDKWDIKKDVKIVETVEKNECRTSGHNEEKEDALCLCKDREKPKCCQDGLFLKAMQLAKRANALFDYAVTGDVQMLLAVQRHLTAVQDENGDSVLHLAIHLLHAQLVRLDLEVTSGLSISDDIIMNRNDLYQTPHLHAVI 750
gi|118778988|ref|XP_308995.3|QLEPSTSLTTSAPHDIMSIGI-----STTINSKELTKASIIDILNIFPTIASDVAFDSDFKNSSEFNKLIQEIQQDVLKLETDAAEAGGCAAD--ESVLRGAIADLVASGDSRQEGMLRKLKLLALIKLFGAD 750
gi|17137094|ref|NP_477094.1|DLEKICQLDMLQHDGHNRAEIVP-----SHRNRTIKCLDDELPEIKQDRISPKISHRKWEKIFSHALNINNRD--LLEVEISHKDKLKLALIQQLQVMNYPNLKVDVNSLNADGSS-----ALHVACQ 750
.....610.....620.....630.....640.....650.....660.....670.....680.....690.....700.....710.....720.....730.....740.....750

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gi | 117606364 | ref | NP_032715.2 | TKQEDVVEDLLRVGADLSLLDRWGNSVLHLAAEGHDRILSILLK-SRKAAPLIDHPNGEGLNAHIAVMSNSLPCLLLVAAG-AEVNAOEQSGRTALHLAVEYDNISLAGCLLEG-----DAHVDSTTYDGTTPLHIAAGRGSTRLA 900
gi | 62644423 | ref | XP_342347.2 | TKQEDVVEDLLRVGADLSLLDRWGNSVLHLAAEGHDRILSILLK-NSKAALLINHPNGEGLNAHIAVMSNSLPCLLLVAAG-AEVNAOEQSGRTALHLAVEYDNISLAGCLLEG-----DALVDSTTYDGTTPLHIAAGRGSTRLA 900
gi | 34577122 | ref | NP_003989.2 | TKQEDVVEDLLRVGADLSLLDRLGNSVLHLAAEGHDRKVLSILLK-HKKAALLLDHPNGDGLNAHIAMMSNSLPCLLLVAAG-ADVNAOEQSGRTALHLAVEHDNISLAGCLLEG-----DAHVDSTTYDGTTPLHIAAGRGSTRLA 900
gi | 114595421 | ref | XP_001168506.1 | TKQEDVVEDLLRVGADLSLLDRLGNSVLHLAAEGHDRKVLSILLK-HKKAALLLDHPNGDGLNAHIAMMSNSLPCLLLVAAG-ADVNAOEQSGRTALHLAVEHDNISLAGCLLEG-----DAHVDSTTYDGTTPLHIAAGRGSTRLA 900
gi | 50979190 | ref | NP_001003344.1 | TKQEAVVDDLLRAGADLSLLDRLGNSVLHLAAEGQDRKILSILLK-HKKAALLMDHPNGEGLNAHIAVMSNSMPCLLLLVAAG-ADVNAOERKSGRTALHLAVEHDNISLAGCLLEG-----DAHVDSTTYDGTTPLHIAAGRGSTRLA 900
gi | 115497302 | ref | NP_001069877.1 | TKQEAVVEDLLRAGADLSLLDRLGNSVLHLAAEGHDRKILSILLK-HKKAAQLIDHPNGEGLNAHIAVMSNSLPCLLLMAAG-ADVNAOERKSGRTALHLAVEHDNISLAGCLXLEG-----DAHVDSTTYDGTTPLHIAAGRGSTRLA 900
gi | 45384086 | ref | NP_990465.1 | TKQEAVVEDLLKAGANVNLLDRHCNSVLHLAAEGHDRKILSILLK-HQKASSMIDLSNGEGLSAHIMVYNANSLCLKLLTAAG-VDVAAOERKSGRTALHLAVEQENIPLAGCLLEG-----DVDADSTTYDGTTPLHIAAGRGFKKLA 900
gi | 118778988 | ref | XP_308995.3 | VNRSRQLLASHWTAANQQLN-CLHAIRRNDTTACKLILLHE-NQLAELLDLFNDRNTGLHLAVSCNSEFIVKALLGAG-AKLHCDYR-GNTPLHRAVENVPDMVRLLLLGG-----GLRLCINDDGLTLQAVARNLKII 900
gi | 17137094 | ref | NP_477094.1 | QDRAHIRPLLGMCNPNLKNNAGNTPLHVAVKEHLSCVESFLNGVPTVQLDLSLTTDDGLTPLHMAIRQNKDVAKLLSDRRSISVANTMDGNNALHMAVLEQSVELLVLLDAQENLTDILQANAGHTPLELAERKANDRVV 900
.....760.....770.....780.....790.....800.....810.....820.....830.....840.....850.....860.....870.....880.....890.....900
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gi | 117606364 | ref | NP_032715.2 | ALLKAAGADPLVENFEPLYDLDDSWEKAGED-----EGVVPGTPLDMAANWVFDILNGKPYEP-VFTSDDILPOGDMKOLTEDTRLQLCKLLEIPDPDKNWATLAOKLG-----LGILNAFRLSPASKTLMDNYEVSGGTIKEL 1050
gi | 62644423 | ref | XP_342347.2 | ALLKAAGADPLVENFEPLYDLDDSWEKAGED-----EGVVPGTPLDMAANWVFDILNGKPYEP-VFTSDDILPOGDIRQLTEDTRLQLCKLLEIPDPDKNWATLAOKLG-----LGILNAFRLSPASKTLMDNYEVSGGTIKEL 1050
gi | 34577122 | ref | NP_003989.2 | ALLKAAGADPLVENFEPLYDLDDSWENAGED-----EGVVPGTPLDMATSWQVFDILNGKPYEP-EFTSDDLLAOGDMKQLAEDVKLOLYKLLEIPDPDKNWATLAOKLG-----LGILNAFRLSPASKTLMDNYEVSGGTVREL 1050
gi | 114595421 | ref | XP_001168506.1 | ALLKAAGADPLVENFEPLYDLDDSWENAGED-----EGVVPGTPLDMATSWQVFDILNGKPYEP-EFTSDDLLAOGDMKQLAEDVKLOLYKLLEIPDPDKNWATLAOKLG-----LGILNAFRLSPASKTLMDNYEVSGGTVREL 1050
gi | 50979190 | ref | NP_001003344.1 | ALLKAAGADPLVENFEPLYDLDDSWEKDGED-----EGVVPGTPLDMATNWQVFDILNGKPYEP-EFTSDDLLAOGDMKOLTEDAKLOLYKLLEIPDPDKNWATLAOKLG-----QGILNAFRLSPASKTLMDNYEVSGGTIKEL 1050
gi | 115497302 | ref | NP_001069877.1 | ALLKAAGADPLVENFEPLYDLDDSWDEDGED-----EGVVPGTPLDMASSWQVFDILNGKPYEP-EFTSDDLLAOGDMKOLTEDAKLOLYKLLEIPDPDKNWATLAOKLG-----LGILNAFRLSPASKTLMDNYEVSGGTIKEL 1050
gi | 45384086 | ref | NP_990465.1 | AVLKAAGADPHVENFELFDVEDVKDDDD-----EGIVPGTPLDMAANWEYDILNGKPYIAAAVSEDLSGPLRELNESSKQLYKLLEIPDPDSKNSLAKKLG-----LGILNAFRLSPASKILLDNYKISGGTVOEL 1050
gi | 118778988 | ref | XP_308995.3 | RILLEAGASVREKLKHGNNILHIAVDNDALDIVHYILEVKELRERNAGYTPLQLADAKSHTG-QNNKLIVRELLRHVDLQLKEVKKEVDAAEDEEEEEEEEEEEEEEDEDEEGGEHQREASAPSSVLDSMDLINGERASI 1050
gi | 17137094 | ref | NP_477094.1 | QLLKNVYPEKGELAMTWIPCVKVEEIDSSD-----ESSDAQLEIKEEMDEIEKDESVELDLSGPRROKDESSRDEMDNNKLQLLKNKFIVDRLCSLLNDPLG-----HGSDFQDRKMQLARQHLKQFAIIWLGAED 1050
.....910.....920.....930.....940.....950.....960.....970.....980.....990.....1000.....1010.....1020.....1030.....1040.....1050
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gi | 117606364 | ref | NP_032715.2 | MEALQMGYTEAIEVIQAAFRPEATASSP-VITAQVECLPLSSSTROH-----IDELRDSDVCDSGVETSFRKLSFTESLTGDE-PLLSLNKMPHYGOEGPIEGKI----- 1167
gi | 62644423 | ref | XP_342347.2 | VEALROMGYTEAIEVIQAAFRTPETASSP-VITAQAHLLPLSSSTROH-----IDELRDNDSDVCDSGVETSFRKLSFSESLTGDG-PLLSLNKMPHNYGDGPIEGKI----- 1167
gi | 34577122 | ref | NP_003989.2 | VEALROMGYTEAIEVIQ-----AASSPVKTSQAHSLPLSPASTROQ-----IDELRDSDVCDSGVETSFRKLSFTESLTSGA-SLLTLNKMPHDYGOEGPLEGKI----- 1167
gi | 114595421 | ref | XP_001168506.1 | VEALROMGYTEAIEVIQ-----AASSPVKTSQAHSLPLSPASTROQ-----IDELRDSDVCDSGVETSFRKLSFTESLTSGA-SLLTLNKMPHDYGOEGPLEGKI----- 1167
gi | 50979190 | ref | NP_001003344.1 | VEALROMGYTEAIEVIQAAFCAPEIAAPSPGKAPOLLSLPLSASTRSP-----VDEVRD-DSICDSGVETSFRRLSFTESLTSGE-SLLTLNKAPHEYGOEGPIEGKI----- 1167
gi | 115497302 | ref | NP_001069877.1 | VEALROMGYTEAIDVIQAAFC---ADTSPAKTSQAHSLPFAPASTRPQ-----IDELRD-DSICDSGVETSFRKLSFTESLTSGH-SLLTLNKVPHDYGOEGPIEGKI----- 1167
gi | 45384086 | ref | NP_990465.1 | IAALTMDHTEAIEVIQALSSSRQIYQEDNIEAFPSLSPSFAKETGE---LYNHKFODESTCDSGVETSFRKLSFTYSDLNKSSILLSKITLGYGOSSVGSSIPEN----- 1167
gi | 118778988 | ref | XP_308995.3 | ARLLEHEFEAEPQRKATKRDSGPDREPDTLLDEQLEELCRLLDAGSGWRELSLLDFHSFFVNEQAPSPARMLLGYFEMQLHLDRLIDMLRVLELRDFIRSIDEMICRRMK----- 1167
gi | 17137094 | ref | NP_477094.1 | LDHVRKGASVEFSTEAR-----ALQAVDPQAVALLVNPT----- 1167
.....1060.....1070.....1080.....1090.....1100.....1110.....1120.....1130.....1140.....1150.....1160.....
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