```
gi|31982236|ref|NP_032423.2|    ------------------------------------------------------------------------------------------------------------------------------------------------------  150
gi|109468286|ref|XP_215984.4|   ------------------------------------------------------------------------------------------------------------------------------------------------------  150
gi|11939740|ref|NP_001073286.1| ------------------------------------------------------------------------------------------------------------------------------------------------------  150
gi|114581790|ref|XP_515909.2|   MVACEELRAAAFINQFRIFQQPLQPNHQLLAEYTLQGRRSGAASPRARLRGSHVVASGQVPGWRRQSRRVRCGRCAPRARKEGREGGEGRGRRPRHLIKRLRVSREQRAHSAVASCPRGGAAGRRARPVPGVGPGAAARGGEGGCGSS  150
gi|74004608|ref|XP_535964.2|    ------------------------------------------------------------------------------------------------------------------------------------------------------  150
gi|158341672|ref|NP_001103451.1|------------------------------------------------------------------------------------------------------------------------------------------------------  150
gi|46048714|ref|NP_990620.1|    ------------------------------------------------------------------------------------------------------------------------------------------------------  150
gi|189523264|ref|XP_001923001.1|------------------------------------------------------------------------------------------------------------------------------------------------------  150
                                1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140......150


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gi|31982236|ref|NP_032423.2|    ----------------------MAVAGQLCLLYLSAGLLARLGTAFNLDTREDNVIRKSGDPGSLFGFSLAMHWQLQPEDKRLLLVGAPRAEALPLQRANRTGGLYSCDITSRGP-CTRIEFDNDADPMSESKEDQWMGVTVQSQG  300
gi|109468286|ref|XP_215984.4|   ----------------------MAVAGQLCLLYLSAGLLARLSTAFNLDTREDNVIRKSGDPGSLFGFSLAMHWQLQPEDKRLLLVGAPRAEALPLQKANRTGGLYSCDITSRGP-CTRIVFDNDADPMSESKEDQWMGVTVQSQG  300
gi|11939740|ref|NP_001073286.1| ----------------------MAAAGQLCLLYLSAGLLSRLGAAFNLDTREDNVIRKYGDPGSLFGFSLAMHWQLQPEDKRLLLVGAPRAEALPLQRANRTGGLYSCDITARGP-CTRIEFDNDADPTSESKEDQWMGVTVQSQG  300
gi|114581790|ref|XP_515909.2|   SAAASDPARSAGRPLQVPAPLPVRPPMAAAGQLCLLYLSAGLLSRLGAAFNLDTREDNVIRKYGDPGSLFGFSLAMHWQLQPEDKRLLLVGAPRAEALPLQRANRTGGLYSCDITARGP-CTRIEFDNDADPTSESKEDQWMGVTVQSQG  300
gi|74004608|ref|XP_535964.2|    ----------------------MAAAGRLWLLYLSAGLLPRLGAAFNLDTREDHVIRKAGEPGSLFGFSLAMHRQLQPEDRRLLLVGAPRAVALPLQRANRTGGLYSCDITSPGP-CTRIEFDNDADPSSESKEDQWMGVTVQSQG  300
gi|158341672|ref|NP_001103451.1|----------------------MAAAGRLWLLYLSVGLLPRLGTAFNLDTREDNVIEKTGDSGSLFGFSLAMHWQLQPEDKRLLLVGAPRAEALPLQKANRTGGLYSCDITSRGP-CTRIEFDNDADPSSESKEDQWMGVTVQSQG  300
gi|46048714|ref|NP_990620.1|    ----------------------MAAA---LLLYLP--LLPGLAGAFNLDA--ENVIGRRGEPGSLFGFSLAMHRQLQPQEKRLLLVGAPREKAFPSQQANRTGGLYSCDITSSDTRCTRVVFDEDTDPKMESKEDQWMGVTVQSQG  300
gi|189523264|ref|XP_001923001.1|----------------------MELFEKALSLNLCVFSWLVWTSASAFNLDT--QNVLRKSGQPGSLFGFSIALHRQLQPHDKTILLIGAPKARALSNQGANVTGGLYSCDITTHPNDCSRVDFDNDVDVRVENKENQWMGVTVQSQG  300
                                .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290......300


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gi|31982236|ref|NP_032423.2|    PGGKVVTCAHRYEKRQHVNTKQESRDIFGRCYVLSQNLRIED--DMDGGDWSFCDGRLRGHEKFGSCQQGVAATFTKDFHYIVFGAPGTYNWKGIVRVEQKNNTFFDMNIFEDGPYEVGGETDHDESLVPVPAN----------------  450
gi|109468286|ref|XP_215984.4|   PGGKVVTCAHRYEKRQHVNTKQESRDIFGRCYVLSQNLRIED--DMDGGDWSFCDGRLRGHEKFGSCQQGVAATFTKDFHYIVFGAPGTYNWKGIVRVEQKNNTFFDMNIFEDGPYEVGGETDHDESLVPVPAN----------------  450
gi|11939740|ref|NP_001073286.1| PGGKVVTCAHRYEKRQHVNTKQESRDIFGRCYVLSQNLRIED--DMDGGDWSFCDGRLRGHEKFGSCQQGVAATFTKDFHYIVFGAPGTYNWKGIVRVEQKNNTFFDMNIFEDGPYEVGGETEHDESLVPVPAN----------------  450
gi|114581790|ref|XP_515909.2|   PGGKVVTCAHRYEKRQHVNTKQESRDIFGRCYVLSQNLRIED--DMDGDWSFCDGRLRGHEKFGSCQQGVAATFTKDFHYIVFGAPGTYNWKGIVRVEQKNNTFFDMNIFEDGPYEVGGETEHDESLVPVPANSYLGLLFLTSVSYTDP  450
gi|74004608|ref|XP_535964.2|    PGGKVVTCAHRYEKRQHVNTKQESRDIFGRCYVLSQNLRIED--DMDGGDWSFCDGRLRGHEKFGSCQQGVAATFTKDFHYIVFGAPGTYNWKGIVRVEQKNNTFFDMNIFEDGPYEVGGETDHDESLVPVPANSYLGLLFLTSVSYTDP  450
gi|158341672|ref|NP_001103451.1|PGGKVVTCAHRYEKRQHVNTKQESRDIFGRCYVLSQNLRIED--DMDGGDWSFCDGRLRGHEKFGSCQQGVAATFTKDFHYIAFGAPGTYNWKGIVRVEQKNNTFFDMNIFEDGPYEVGGETDHDESLVPVPAN----------------  450
gi|46048714|ref|NP_990620.1|    PGGNVVTCAHRYEKRQVVNTVQETRDIIGRCYVLSQDLTIKD--DMDNGVWSFCDGRTRGHEKFGSCQQGVAATFRDYHVIVFGAPGTYNWKGVVRAEQKQTFYDLGIFDDGPYEVGDESRQDKNLVPVPAN----------------  450
gi|189523264|ref|XP_001923001.1|PGGKIVTCAHRYQRLLFPNTPQEARDITGRCYMLSQDLSIDNQSDEDGGNWKFCDGRTRGHERFGACQQGVAATFTKDYHYVIFGAPGAYNWKGIVRIEQKNNTLLEMGLFDDGPYEVDENRLDPNLVPVPAN----------------  450
                                .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......410.......420.......430.......440......450


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gi|31982236|ref|NP_032423.2|    ------------------------SYLGFSLDSGKGIVSKDDITFVSGAPRANHSGAVVLLKRD-MKSAHLLPEYIFDGEGLASSFGYDVAVVDLNADGWQDIVIGAPQYFDRDGEVGGAVYVYINQQGKWSNVKPIRLNGTKDSMFGISV  600
gi|109468286|ref|XP_215984.4|   ------------------------SYLGFSLDSGKGIVSKDDITFVSGAPRANHSGAVVLLKRD-MKSAHLLLEYIFDGEGLASSFGYDVAVVDLNADGWQDIVIGAPQYFDRDGEVGGAVYVYINQQGRWSNVKPVRLNGTKDSMFGIAV  600
gi|11939740|ref|NP_001073286.1| ------------------------SYLGFSLDSGKGIVSKDEITFVSGAPRANHSGAVVLLKRD-MKSAHLLPEHIFDGEGLASSFGYDVAVVDLNKDGWQDIVIGAPQYFDRDGEVGGAVYVYMNQQGRWNNVKPIRLNGTKDSMFGIAV  600
gi|114581790|ref|XP_515909.2|   DQFVYKTRPPREQPDTFPDVMMNSYLGFSLDSGKGIVSKDEITFVSGAPRANHSGAVVLLKRD-MKSAHLLPEHIFDGEGLASSFGYDVAVVDLNKDGWQDIVIGAPQYFDRDGEVGGAVYVYINQQGRWNNVKPIRLNGTKDSMFGIAV  600
gi|74004608|ref|XP_535964.2|    DQFVYKTQPPREKPNTSPDVMMNSYLGFSLDSGKGIVSKDEITFVSGAPRANHSGAVVLLKRD-MKSAHLLPEYIFDGEGLASSFGYDVAVADLNKDGWQDIVIGAPQYFDRDGEVGGAVYVYINQQGRWNNVKPIRLNGTKDSMFGIAV  600
gi|158341672|ref|NP_001103451.1|------------------------SYLGFSLDSGKGIVSKDEITFVSGAPRANHSGAVVLLKRD-LKSAHLLPEHIFDGEGLASSFGYDVAVVDLNKDGWQDIVIGAPQYFDRSGEVGGAAYVYINQQGRWNNVKPIRLNGTKDSMFGIAV  600
gi|46048714|ref|NP_990620.1|    ------------------------SYLGFSLDSGKGIVSQDEMTFVSGAPRANHSGAVVLLKKE-KNQRALSLEHMFDGEGLASSFGYDVAVVDLNSDGWQDIVVGAPQYFDRSGDIGGAVYIYINQRGKWEGIKPIRLNGTADSMFGIAV  600
gi|189523264|ref|XP_001923001.1|------------------------SYLGFSLDSGHSITEKGKLIIVSGAPRANHSGAVVFLRKEGELSSMLTPEHILEGPGLASSFGYDVAVVDLNGDGWQDVVVGAPQFFQRDEEVGGAVYVINKAGRWRDVTPVRLNGTKDSMFGLSV  600
                                .......460.......470.......480.......490.......500.......510.......520.......530.......540.......550.......560.......570.......580.......590......600


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gi|31982236|ref|NP_032423.2|    KNIGDINQDGYPDIAVGAPYDD--LGKVFIYHGSPTGIITKPTQVLEGT---SPYFGYSIAGNMDLDRNSYPDLAVGSLSDSVTIFRSRPVINILKTITVTPNRIDLRQKSMCGSPSGICLKVKACFEYTAKPSGYNPPISILGILEAEK  750
gi|109468286|ref|XP_215984.4|   KNIGDINQDGYPDIAVGAPYDD--LGKVFIYHGSPTGIITKPTQVLEGT---TPFFGYSIAGNMDLDRNSYPDVAVGSLSDSVTIFRSRPVINILKTITVTPSRIDLRQKSMCGSPSGICLKVKACFEYTAKPSGYNPPISILGILEAEK  750
gi|11939740|ref|NP_001073286.1| KNIGDINQDGYPDIAVGAPYDD--LGKVFIYHGSANGINTKPTQVLKGI---SPYFGYSIAGNMDLDRNSYPDVAVGSLSDSVTIFRSRPVINIQKTITVTPNRIDLRQKTACGAPSGICLQVKSCFEYTANPAGYNPSISIVGTLEAEK  750
gi|114581790|ref|XP_515909.2|   KNIGDINQDGYPDIAVGAPYDD--LGKVFIYHGSANGINTKPTQVLKGI---SPYFGYSIAGNMDLDRNSYPDVAVGSLSDSVTIFRSRPVINIQKTITVTPNRIDLRQKTACGAPSGICLQVKSCFEYTANPAGYNPSISIVGTLEAEK  750
gi|74004608|ref|XP_535964.2|    KNIGDINQDGYPDIAVGAPYDD--MGKVFIYHGSPNGINTKPTQVILEGK---SPYFGYSIAGNMDLDRNSYPDVAVGSLSDSVTVFRSRPVINIRSRPVINIQKIILCGAPSGICLKVKACFEYTAKPTGYNPSISILGTLEAEK  750
gi|158341672|ref|NP_001103451.1|KNIGDINQDGYPDIAVGAPYDG--KGKVFIYHGSANINTKPTQVLKGI---SPFFGYSIAGNMDLDRNSYPDVAVGSLSDSVTIFRSRPVINIQQTITVTPNRIDLRQKTLCGAPSGICLKVKACFEYTAKPTGYNPSITIVGTLEAEK  750
gi|46048714|ref|NP_990620.1|    ENVGDINQDGYPDIAVGAPYDG--FGKVYIYHGSKNGINTEPAQILDGEKTGTNFFGYSIAGNMDLDKNSYPDLAVGSLSDSVSVFRSRPVISITKSITVQPDKLDLKKKNPED-PSEIWMDVKACFQYTANPRNLNPRIKINYTFEAEN  750
gi|189523264|ref|XP_001923001.1|ENIGDVNLDSFEDIAVGAPYADSGPFGSVIYHGSADGISTKPAQILEGKQHNKMFGYSIAGNMDLDHNSYPDLAVGSLSDTVFIYRSKNVISIKKDIKVTPKEIDLTKKTCGN---SICLTVEACFSYRANPTTYNPKITISCTFEAEW  750
                                .......610.......620.......630.......640.......650.......660.......670.......680.......690.......700.......710.......720.......730.......740......750
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