

gi | 37537522 | ref | NP_659097.2 | -MNG-QAPPHDVVVAAGTEKFIKPKIKKQGLGASTPSRP--QAAALPTTARS IAGVYVEASGQTSIYAAIKGGLLPTGLGLTLLLEAQAATGGLVLDLAAQGLLPSVEALRRGLVGLLEKELKLLAAERAVTGYDDPYGGEKLSLFAIRK 150
gi | 109480932 | ref | XP_001059215.1 | -MNG-QAPPHDVVVAAGTEKLIIVPKIMKNQSEASPSRP--QAKAALPTTARS IAGVYVEASGQTSIYDAMKQGLLPTGLGLVTLLEAQAATGGLMDLAAQGLLPSVEALRRGLVGLLEKELKLLAAERAVTGYDDPYGGEKLSLFAIRK 150
gi | 207452735 | ref | NP_112598.2 | -MSGHTLPPLPVPGTNTSTEQASVPRAMAATLGAAGPPRP-----QARS IAGVYVEASGQAQSVYAAAMEGLLPAGLQALLLEAQAATGGLVLDLARGQLLPSVEALRRGLVGLLEKELKLLAAERAVTGYDDPYGGEKLSLFAIRK 150
gi | 114622142 | ref | XP_520007.2 | -----MAATLGAAGPPRP-----QARS IAGVYVEASGQAQSVYAAAMEGLLPAGLQALLLEAQAATGGLVLDLARGQLLPSVEALRRGLVGLLEKELKLLAAERAVTGYDDPYGGEKLSLFAIRK 150
gi | 73974852 | ref | XP_532347.2 | MMNGHASPPPDALAASATLALAG-PKIMKAMAGCTSTPSRPRPQQAALSAQSKS IAGVYVEASGQAQSVYAAAMEGLLPAGLQALLLEAQAATGGLVLDLARGQLLPSVEALRRGLVGLLEKELKLLAAERAVTGYDDPYGGEKLSLFAIRK 150
gi | 292624226 | ref | XP_001922664.2 | -----MPALNNFQGP-----VAGVFLNENEIITTYQAYKKRLLNPGSCLALLEAQAATGGIIDPVKNRKTSVDEAVKGEIVGCEKELKLLAAERAVTGYDDPYGGEKLSLFAIRK 150
gi | 292624221 | ref | XP_002665585.1 | -----MPALNNFQGP-----VAGVFLNENEIITTYQAYKKRLLNPGSCLALLEAQAATGGIIDPVKNRKTSVDEAVKGEIVGCEKELKLLAAERAVTGYDDPYGGEKLSLFAIRK 150



gi | 37537522 | ref | NP_659097.2 | EVVDRITLQWRLLLEAQLATGGLVDPTQGVQVAPLACQGLLDKKTWLSLMESEFSPMGTGPFSDPNTLEQLPYSVLLGRCVQDPSGLPLLPKLTTFHLLAGAASASMLLEAGVINEEMVDRDLOEGLMUVSVVGTFRPEVRRVLEGTGGLAG 300
gi | 109480932 | ref | XP_001059215.1 | EVVDRITLQWRLLLEAQLATGGLVDPTQGVQVAPLACQGLLDKKTWLSLMESEFSPMGTGPFSDPNTLEQLPYSVLLGRCVQDPSGLPLLPKLTTFHLLAGAASASMLLEAGVINEEMVDRDLOEGLMUVSVVGTFRPEVRRVLEGTGGLAG 300
gi | 207452735 | ref | NP_112598.2 | EVVDRALQSWLVEQLATGGLVDPAQGVVLAPEPACHQGLLDRETWHLKSELEPGTGLDRFLNPTLRLERLTYHQLLERCVRAPGSGLALLPLKTIIFRSMGAVSAEELLEVLDEQAVQGLRREGRLAAVDVSARAEVRRVLEGTGSGVAG 300
gi | 114622142 | ref | XP_520007.2 | EVVDRALQSWLVEQLATGGLVDPAQGVVLAPEPACHQGLLDRETWHLKSELEPGTGLDRFLNPTLRLERLTYHQLLERCVRAPGSGLALLPLKTIIFRSMGAVSAEELLEVLDEQAVQGLRREGRLAAVDVSARAEVRRVLEGTGSGVAG 300
gi | 73974852 | ref | XP_532347.2 | EVVDRALQSWLVEQLATGGLVDPAQGVVLAPEPACHQGLLDRETWHLKSELEPGTGLDRFLNPTLRLERLTYHQLLERCVRAPGSGLALLPLKTIIFRSMGAVSAEELLEVLDEQAVQGLRREGRLAAVDVSARAEVRRVLEGTGSGVAG 300
gi | 292624226 | ref | XP_001922664.2 | DVIPKKEYGIRLLEACISAKGIYDPIEKCYLLEQAYRRGHYDENLFRGQD-----ALKVFYDPSNQNENLYPTLIKKCVAPETGLLFPYIIFKGLRRGVTSABELLASKIIDQTFENLHKKTTIQDVMLETVKEVLEGGKSIIGG 300
gi | 292624221 | ref | XP_002665585.1 | DVIPKKEYGIRLLEACISAKGIYDPIEKCYLLEQAYRRGHYDENLFRGQD-----ALKVFYDPSNQNENLYPTLIKKCVAPETGLLFPYIIFKGLRRGVTSABELLASKIIDQTFENLHKKTTIQDVMLETVKEVLEGGKSIIGG 300



gi | 37537522 | ref | NP_659097.2 | VVLLPGGHKKSFFQATVEHLVSKGIALQLEEAQAATRLVHPTTGORLWVEEAVKAGLVGPELHEQLLVAEQAVTGYDDPFSSTRIPVFCAMKKGVLVDPALRLLDAQLATGGLICPARRFRLLPEAALRFGCLDEETQRQLSCA---- 450
gi | 109480932 | ref | XP_001059215.1 | VVLLPGGHKKSFFQATVEHLVSKGIALQLEEAQAATRLVHPTTGORLWVEEAVKAGLVGPELHEQLLVAEQAVTGYDDPFSSTRIPVFCAMKKGVLVDPALRLLDAQLATGGLICPARRFRLLPEAALRFGCLDEETQRQLSCA---- 450
gi | 207452735 | ref | NP_112598.2 | VVLLPEGHKKKSFFQATVEHLLPMGTALPALLEQAATHLLVDPITGQRLWVDEAVRAGLVSPLELHEQLLVAEQAVTGHDDPFSGQIPPLFCAMKKGVLVDRPALRLLDAQLATGGLVCPARRFRLLPEAALRFGCLDEETQRQLSCA---- 450
gi | 114622142 | ref | XP_520007.2 | VVLLPEGHKKKSFFQATVEHLLPMGTALPALLEQAATHLLVDPITGQRLWVDEAVRAGLVSPLELHEQLLVAEQAVTGHDDPFSGQIPPLFCAMKKGVLVDRPALRLLDAQLATGGLVCPARRFRLLPEAALRFGCLDEETQRQLSCA---- 450
gi | 73974852 | ref | XP_532347.2 | VVQLPAGHKKKSIFQATEHLLPMGTGLLLEEAQAATCLVDPATGQWLSVDEAVRSGLLGPELHKKLLVAEQAVTGYDDPFSGQIPVPLFCAMKKELVDRPALRLLDAQLATGGLVCPARRFRLLPEAALRFGCLDEETQRQLSCA---- 450
gi | 292624226 | ref | XP_001922664.2 | VALLSTNKMSIYQAMRGGIIMPGTGLLLEEAQAATGFMDIPVENKTYSVHEAIKQKIVGPEYHAKLLAAERAVTGYDDPFTGETISLFOALKKELIVKEHGIRLLEAQAATGGIIDPINSHRVVDVAVYKRFNEMNAILEDTGDGT 450
gi | 292624221 | ref | XP_002665585.1 | VALLSTNKMSIYQAMRGGIIMPGTGLLLEEAQAATGFMDIPVENKTYSVHEAIKQKIVGPEYHAKLLAAERAVTGYDDPFTGETISLFOALKKELIVKEHGIRLLEAQAATGGIIDPINSHRVVDVAVYKRFNEMNAILEDTGDGT 450



gi | 37537522 | ref | NP_659097.2 | MGFSDPITTHDRLEHVEQLLALSVDDPETGLAFLPPLGMSHANEQGLPFIDHCRRHVLKATTSVSVGRYQGRPVSLWELLFSEAVPVKRAMLAQRHOGALSVEEALAEKKNIVEQAAATAKVTFAGLRDITVTPGELLKAEIINDDLFE 600
gi | 109480932 | ref | XP_001059215.1 | MGFSDPITTHDRLEHVEQLLALSVDDPETGLAFLPPLGMSHANEQGLPFIDHCRRHVLKATTSVSVGRYQGRPVSLWELLFSEAVPVKRAMLAQRHOGALSVEEALAEKKNIVEQAAATAKVTFAGLRDITVTPGELLKAEIINDDLFE 600
gi | 207452735 | ref | NP_112598.2 | GSFSDG-NHGGRLRVEQLLALCVDDPETGLAFLPPLSGGPRGEGPEGPPFIKYSRQALS TATATVSVGKFRGRPVSLWELLFSEAIISSEORAMLAQQYQEGTSLVEKLAELSALQAAATARVTFSGLRDITVTPGELLKAEIINDDLFE 600
gi | 114622142 | ref | XP_520007.2 | GSFSDG-NHSSLRVEQLLALCVDDPETGLAFLPPLSGGPRGEGPEGPPFIKYSRQALS TATATVSVGKFRGRPVSLWELLFSEAIISSEORAMLAQQYQEGTSLVEKLAELSALQAAATARVTFSGLRDITVTPGELLKAEIINDDLFE 600
gi | 73974852 | ref | XP_532347.2 | AGFSDFSTQESLGVQOLLARCVDDPETGLAFLPPLSHGPPGDEPQGSFPFIDHSRQALS TATATVSVGKFRGRPVSLWELLFSGVPAQRALAAQQYRDSAISVEEMAAVLTALAEQAATAVARTFAGLRDITVTPGELLKAEIINDDLFE 600
gi | 292624226 | ref | XP_001922664.2 | KGFFDPNKKENLTVLQLLDHCVIDPANGTLLPIQD-PSGN--RNETFIDYDIKKIFKGVKVKVCGKYMGMVTVSLWELLMSYFEEQORQDFIQYKSRLLTILITIKVLEIIEYSVKAKVVFEGIREKVSATLVLEADITENDLK 600
gi | 292624221 | ref | XP_002665585.1 | KGFFDPNKKENLTVLQLLDHCVIDPANGTLLPIQD-PSGN--RNETFIDYDIKKIFKGVKVKVCGKYMGMVTVSLWELLMSYFEEQORQDFIQYKSRLLTILITIKVLEIIEYSVKAKVVFEGIREKVSATLVLEADITENDLK 600



gi | 37537522 | ref | NP_659097.2 | QLREGQTSADVGSGLDSVQRYLQGTGCIAGLLLPDSQERLSIYEARKGGLLRPGTALILLEAQAATGFIIIDPKENKRYSVBEALRAGVIGPDVYAKLLSAEHAVTGYDDPYSGEQISLFAQMRDLIVRDHGIRLLEAQAATGGVIDPVH 750
gi | 109480932 | ref | XP_001059215.1 | QLREGQTSADVGSGLDSVQRYLQGTGCIAGLLLPDSQERLSIYEARKGGLLRPGTALILLEAQAATGFIIIDPKENKRYSVBEALRAGVIGPDVYAKLLSAEHAVTGYDDPYSGEQISLFAQMRDLIVRDHGIRLLEAQAATGGVIDPVH 750
gi | 207452735 | ref | NP_112598.2 | RLEHGCAAKDVGSLASQRYLQGTGCIAGLLLPDSQERLSIYEARKGGLLRPGTALILLEAQAATGFIIIDPKANKGHSVBEALRAAVIGPDVFAKLLSAEHAVTGYDDPYTGOQISLFAQMQKGLIIVREHGIRLLEAQAATGGVIDPVH 750
gi | 114622142 | ref | XP_520007.2 | RLEHGCAAKDVGSLASQRYLQGTGCIAGLLLPDSQERLSIYEARKGGLLRPGTALILLEAQAATGFIIIDPKANKGHSVBEALRAAVIGPDVFAKLLSAEHAVTGYDDPYTGOQISLFAQMQKGLIIVREHGIRLLEAQAATGGVIDPVH 750
gi | 73974852 | ref | XP_532347.2 | RLKQCGTAAQEVGRASVQKYLRLGTGCIAGVLLPDSQERLSIYEAREKGLLRPGTALILLEAQAATGFIIIDPKENKSSVBEAALRAGLIGPDVFAKLLSAEHAVTGYDDPYTGOQISLFAQMQKGLIIVREHGIRLLEAQAATGGVIDPVH 750
gi | 292624226 | ref | XP_001922664.2 | DLREGKKNVQDVTEDSEVQTYLQKPGIAGVLLPDSQ-VMSIYQARQKGLLRPGTSLVLLLEAQAATGFIIIDPANKRFSVDDAVKARVVGVDVHAKLCSAEKAVTGYDDPYTGKISLFAQMQKDLIVKDHGIRLLEAQAATGGVIDPVH 750
gi | 292624221 | ref | XP_002665585.1 | DLREGKKNVQDVTEDSEVQTYLQKPGIAGVLLPDSQ-VMSIYQARQKGLLRPGTSLVLLLEAQAATGFIIIDPANKRFSVDDAVKARVVGVDVHAKLCSAEKAVTGYDDPYTGKISLFAQMQKDLIVKDHGIRLLEAQAATGGVIDPVH 750



gi | 37537522 | ref | NP_659097.2 | GRFQGHVSLWDLHSEYVGAERKRELVALCGRRAAALROVIGMLTILVEAAEKPPQATFKGLRQVVSAGDLFRSOLITKQTLDELNOGKRTVQEVTEMDSVRRSLEGGNFIAAGVLIQDPEKEMSIPEALRRHILRPGTALVLLLEAQA 1650
gi | 109480932 | ref | XP_001059215.1 | GRFQGHVSLWDLHSEYVGAERKRELVALCGRRAAALROVSMVTLVEAAEKPPQATFKGLRQVVSAGDLFRSOLITKQTLDELNOGKRTVQEVTEMDSVRRSLEGGNFIAAGVLIQDPEKEMSIPEALRRHILRPGTALVLLLEAQA 1650
gi | 207452735 | ref | NP_112598.2 | GRFKGCSVSLWDLHSEYVGAERKRELVALCGRRAAALROVVSATVAVLVEAAERPLQATFRGLRQVVSARDLFRALISRRKTLDELNOGKRTVQEVTEMDSVRRSLEGGNFIAAGVLIQDPEKEMSIPEALRRHILRPGTALVLLLEAQA 1650
gi | 114622142 | ref | XP_520007.2 | GRFKGCSVSLWDLHSEYVGAERKRELVALCGRRAAALROVVSATVAVLVEAAERPLQATFRGLRQVVSARDLFRALISRRKTLDELNOGKRTVQEVTEMDSVRRSLEGGNFIAAGVLIQDPEKEMSIPEALRRHILRPGTALVLLLEAQA 1650
gi | 73974852 | ref | XP_532347.2 | GRFKGLVSLWDLHSEYVGSNKRRELVALCQSGRAATLALROVAIVAVLVAASETPSQATFRGLRQVVSASDLFRSRLIDKETLDELNOGKRTVQEVTEMDSVRRSLEGGNFIAAGVLIQDPEKEMSIPEALRRHILRPGTALVLLLEAQA 1650
gi | 292624226 | ref | XP_001922664.2 | GKFAADKRVSLWDLHSEYISAEKREKELLDQYKQN-KLSIEEITQIVTAAIIIEVTTK--RHSFKGLRQVVSASELFEAKIISKEMIGKLNNEVDDDEDINNMESIQKYLGAATCIAGVVFVQSKQKTMSEIFEAKNGLLTPTGSLVLLLEAQA 1650
gi | 292624221 | ref | XP_002665585.1 | GKFAADKRVSLWDLHSEYISAEKREKELLDQYKQN-KLSIEEITQIVTAAIIIEVTTK--RHSFKGLRQVVSASELFEAKIISKEMIGKLNNEVDDDEDINNMESIQKYLGAATCIAGVVFVQSKQKTMSEIFEAKNGLLTPTGSLVLLLEAQA 1650



gi | 37537522 | ref | NP_659097.2 | ANGFIIIDPVENRKLTVQAFQAGMFKETIYMKLLSAERAVTGYDDPYTGEQISLQAMQDLIVRDHGIRLLEAQAIGGIIDPVHSHRVPVDVAYQRYFDEEMNRILADPDDTKGFFDPNTHENLTYLQLLERCVEDPETGLVMLEI 1800
gi | 109480932 | ref | XP_001059215.1 | ANGFIIIDPVENRKLTVQAFQAGMFKETIYMKLLSAERAVTGYDDPYTGEQISLQAMQDLIVRDHGIRLLEAQAIGGIIDPVHSHRVPVDVAYQRYFDEEMNRILADPDDTKGFFDPNTHENLTYLQLLERCVEDPETGLVMLEI 1800
gi | 207452735 | ref | NP_112598.2 | ANGFIIIDPVENRKLTVQAFQAGMFKETIYMKLLSAERAVTGYDDPYTGEQISLQAMQDLIVRDHGIRLLEAQAIGGIIDPVHSHRVPVDVAYQRYFDEEMNRILADPDDTKGFFDPNTHENLTYLQLLERCVEDPETGLVMLEI 1800
gi | 114622142 | ref | XP_520007.2 | ANGFIIIDPVENRKLTVQAFQAGMFKETIYMKLLSAERAVTGYDDPYTGEQISLQAMQDLIVRDHGIRLLEAQAIGGIIDPVHSHRVPVDVAYQRYFDEEMNRILADPDDTKGFFDPNTHENLTYLQLLERCVEDPETGLVMLEI 1800
gi | 73974852 | ref | XP_532347.2 | ANGFIIIDPVENRKLTVQAFQAGMFKETIYMKLLSAERAVTGYDDPYTGEQISLQAMQDLIVRDHGIRLLEAQAIGGIIDPVHSHRVPVDVAYQRYFDEEMNRILADPDDTKGFFDPNTHENLTYLQLLERCVEDPETGLVMLEI 1800
gi | 292624226 | ref | XP_001922664.2 | ANGFVIDPVKNNKLSVEQAVAEQIVGMEWKSLLSAERAVTGYDDPYTGTITISLQALKKDLIVKEHGIRLLEAQAIGGIIDPVHSHRVPVEVAYQRYFDEEMNKILADPDDTKGFFDPNTHENLTYLQVLDRCVRDPNCLSLLLVI 1800
gi | 292624221 | ref | XP_002665585.1 | ANGFVIDPVKNNKLSVEQAVAEQIVGMEWKSLLSAERAVTGYDDPYTGTITISLQALKKDLIVKEHGIRLLEAQAIGGIIDPVHSHRVPVEVAYQRYFDEEMNKILADPDDTKGFFDPNTHENLTYLQVLDRCVRDPNCLSLLLVI 1800



gi | 37537522 | ref | NP_659097.2 | VKKGETYIYIDEATRQALTRVVKMVGKFAQTVSVWDLSSQYFTEGRRRKLREYRAONIGLENLLEVIIT-----TVBETEKQSQIFKVPGIHGDVTAELFNSGILNKKILDALRSGDRGFQDLRWLEDVVRVLEGS 1950
gi | 109480932 | ref | XP_001059215.1 | VKKGEIYVYIDEATRQVLRRTMKMHIGFAQTVSVWDLSSQYFTEGRRRKLREYRAONIGLEKLEVIIT-----TVBETEKQSQIFKVPGIHGDVTAELFNSGILDKRILDALHSGERGRQDLQLEHKKIILEG 1950
gi | 207452735 | ref | NP_112598.2 | IKKGENYVYINEARHVLQSRATAKMRVGRFADVVVFWDLSSQYFTEDRKRELIQYGAOSGGLEKLEIITIT-----TIBETEENQGIKVAAIRGEVTAADLFNSRVIDQKILHTLVRVGTGGQALSTLCEVKPYLEGR 1950
gi | 114622142 | ref | XP_520007.2 | IKKGETYVYINEARHVLQSRATAKMRVGRFADVVVFWDLSSQYFTEDRKRELIQYGAOSGGLEKLEIITIT-----TIBETEENQGIKVAAIRGEVTAADLFNSRVIDQKILHTLVRVGTGGQALSTLCEVKPYLEGR 1950
gi | 73974852 | ref | XP_532347.2 | VKKGETYIYIDEATRQVLSQTEMHVGRFAHQKISFWDLSSQYFTEERKRELVEVRAONVPLEQLLEIITIA-----TVBETEQYRGMKVAITGGEVTAELFNSGIIIDKRLDALSREKSGAQLSRMAHVRTYLEGR 1950
gi | 292624226 | ref | XP_001922664.2 | VKKGEYFFIDHHTKNILKTTTKKAGGKQFQOLVTLWDLSSQYFTEBKRRELVOQFQSGITITIEQFLEIVLVLVLOKSVTSTHITITTTTETTONNFQGIKRVDSADELLOKVIDEKIYKDLTSGKVTVDHVSQKMSVRKYLKGT 1950
gi | 292624221 | ref | XP_002665585.1 | VKKGEYFFIDHHTKNILKTTTKKAGGKQFQOLVTLWDLSSQYFTEBKRRELVOQFQSGITITIEQFLEIVLVLVLOKSVTSTHITITTTTETTONNFQGIKRVDSADELLOKVIDEKIYKDLTSGKVTVDHVSQKMSVRKYLKGT 1950



gi | 37537522 | ref | NP_659097.2 | NYIAGVIAPLQKVMSEYKASREELIPAGFAAQMLEAQAATGYLMDPCINQRLCVDEATAAGLVGEDLRERLVNAEAKAGYKDPATGETIPLVQAMERKLVGREEARLLEVOVATGGVIDPRLHHRVPLDTCORGCMDDSLVLIAID 2100
gi | 109480932 | ref | XP_001059215.1 | NCIAGVTAPLQKVMSEYKASKEELIPAGFAAQMLEAQAATGYLMDPCSRRLRCVDEATAAGLVGEDLRERLVSAEAKAGYEDPATGETIPLVQAMEKLVGREEARLLEVOVATGGVIDPRLHHRVPLDTCORGCMDDSLVLIAID 2100
gi | 207452735 | ref | NP_112598.2 | DCIAGVTVPSIREVMSLHEASRKELIPAAFAFWLLEAQAAGFLLDPCITRQKLSVDEAVDVGLVNEELRERLKAERAAAGYRDPATGDTIPLFQAMQKQLIEKAEALRLEVOVATGGVIDPQHHRPLLETAYRRGCLHKDIYALISD 2100
gi | 114622142 | ref | XP_520007.2 | GCIAGVTVPLQEVMSLYDASRKELIPMGFAFWLLEAQAAGFLLDPCITRQKLSVDEAVDVGLVNEELRERLKAERAAAGYRDPATGDTIPLFQAMQKQLIEKAEALRLEVOVATGGVIDPQHHRPLLETAYRRGCLHKDIYALISD 2100
gi | 73974852 | ref | XP_532347.2 | GCIAGVTVPLQEVMSLYDASRKELIPMGFAFWLLEAQAAGFLLDPCITRQKLSVDEAVDVGLVNEELRERLKAERAAAGYRDPATGDTIPLFQAMQKQLIEKAEALRLEVOVATGGVIDPQHHRPLLETAYRRGCLHKDIYALISD 2100
gi | 292624226 | ref | XP_001922664.2 | NSIAGVFVQSKQKTMSEIFEAKNGLLTPTGSLVLLLEAQAAGGFVIDPVKNNKLSVEQAVSEQIVGVEWKNKLLSAERAVTGYDDPYTGTITISLQALKKDLIVKEHGIRLLEAQAIGGIIDPVHSHRVPVEVAYQRYFDEEMNKILAD 2100
gi | 292624221 | ref | XP_002665585.1 | NSIAGVFVQSKQKTMSEIFEAKNGLLTPTGSLVLLLEAQAAGGFVIDPVKNNKLSVEQAVSEQIVGVEWKNKLLSAERAVTGYDDPYTGTITISLQALKKDLIVKEHGIRLLEAQAIGGIIDPVHSHRVPVEVAYQRYFDEEMNKILAD 2100



gi | 37537522 | ref | NP_659097.2 | QKH----- 2250
gi | 109480932 | ref | XP_001059215.1 | QKH----- 2250
gi | 207452735 | ref | NP_112598.2 | QKH----- 2250
gi | 114622142 | ref | XP_520007.2 | QKH----- 2250
gi | 73974852 | ref | XP_532347.2 | QKH----- 2250
gi | 292624226 | ref | XP_001922664.2 | PDDDKKCFDPNTHENLTYLQVLDRCVRDPNCLSLLLVIVKKGEEYFFIDHHTKNILKTTTKKAGGKQFQOLVTLWDLSSQYFTEBKRRELVOQFQSGITITIEQFLEIVLVLVLOKSVTSTHITITTTTETTONNFQGIKRVDSAD 2250
gi | 292624221 | ref | XP_002665585.1 | PDDDKKCFDPNTHENLTYLQVLDRCVRDPNCLSLLLVIVKKGEEYFFIDHHTKNILKTTTKKAGGKQFQOLVTLWDLSSQYFTEBKRRELVOQFQSGITITIEQFLEIVLVLVLOKSVTSTHITITTTTETTONNFQGIKRVDSAD 2250



gi | 37537522 | ref | NP_659097.2 | ----- 2400
gi | 109480932 | ref | XP_001059215.1 | ----- 2400
gi | 207452735 | ref | NP_112598.2 | ----- 2400
gi | 114622142 | ref | XP_520007.2 | ----- 2400
gi | 73974852 | ref | XP_532347.2 | ----- 2400
gi | 292624226 | ref | XP_001922664.2 | ----- 2400
gi | 292624221 | ref | XP_002665585.1 | ----- 2400

.....2260.....2270.....2280.....2290.....2300.....2310.....2320.....2330.....2340.....2350.....2360.....2370.....2380.....2390.....2400

gi | 37537522 | ref | NP_659097.2 | ----- 2550
gi | 109480932 | ref | XP_001059215.1 | ----- 2550
gi | 207452735 | ref | NP_112598.2 | ----- 2550
gi | 114622142 | ref | XP_520007.2 | ----- 2550
gi | 73974852 | ref | XP_532347.2 | ----- 2550
gi | 292624226 | ref | XP_001922664.2 | ----- 2550
gi | 292624221 | ref | XP_002665585.1 | ----- 2550

.....2410.....2420.....2430.....2440.....2450.....2460.....2470.....2480.....2490.....2500.....2510.....2520.....2530.....2540.....2550

gi | 37537522 | ref | NP_659097.2 | ----- 2700
gi | 109480932 | ref | XP_001059215.1 | ----- 2700
gi | 207452735 | ref | NP_112598.2 | ----- 2700
gi | 114622142 | ref | XP_520007.2 | ----- 2700
gi | 73974852 | ref | XP_532347.2 | ----- 2700
gi | 292624226 | ref | XP_001922664.2 | ----- 2700
gi | 292624221 | ref | XP_002665585.1 | ----- 2700

.....2560.....2570.....2580.....2590.....2600.....2610.....2620.....2630.....2640.....2650.....2660.....2670.....2680.....2690.....2700

gi | 37537522 | ref | NP_659097.2 | ----- 2850
gi | 109480932 | ref | XP_001059215.1 | ----- 2850
gi | 207452735 | ref | NP_112598.2 | ----- 2850
gi | 114622142 | ref | XP_520007.2 | ----- 2850
gi | 73974852 | ref | XP_532347.2 | ----- 2850
gi | 292624226 | ref | XP_001922664.2 | ----- 2850
gi | 292624221 | ref | XP_002665585.1 | ----- 2850

.....2710.....2720.....2730.....2740.....2750.....2760.....2770.....2780.....2790.....2800.....2810.....2820.....2830.....2840.....2850

gi | 37537522 | ref | NP_659097.2 | ----- 3000
gi | 109480932 | ref | XP_001059215.1 | ----- 3000
gi | 207452735 | ref | NP_112598.2 | ----- 3000
gi | 114622142 | ref | XP_520007.2 | ----- 3000
gi | 73974852 | ref | XP_532347.2 | ----- 3000
gi | 292624226 | ref | XP_001922664.2 | ----- 3000
gi | 292624221 | ref | XP_002665585.1 | ----- 3000

.....2860.....2870.....2880.....2890.....2900.....2910.....2920.....2930.....2940.....2950.....2960.....2970.....2980.....2990.....3000

gi|37537522|ref|NP_659097.2| NRRRLSVEEVAAGVVGGEIQEKLLEAERAVTGYTDPYTGDIISLFOAMORDLIVRDEHGIRLLEAQIATGGVIDPVHSHRVPVDVAYQRYFDEDMNSILADPGDDTKGFFDPNTHENLTYLQLLRRCVRDPETGFYMLQLAGKGSVHH 3900
gi|109480932|ref|XP_001059215.1| HNRRLSVEEVAAGVVGGEIREEKLLSAERAVTGYTDPYTGEOISLFOAMORDLIVKNGIRLLEAQIATGGVIDPVHSHRVPVDVAYKRGYFDEEMNSILADPGDDTKGFFDPNTHENLTYLQLLQRAIVPEPETGLLFLSLLKG----- 3900
gi|207452735|ref|NP_112598.2| RNLRLSVEEVAAGVVGGEIQEKLLEAERAVTGYTDPYTGQIISLFOAMOKDLIVREHGIRLLEAQIATGGVIDPVHSHRVPVDVAYRRGYFDEEMNRVLADPSDDTKGFFDPNTHENLTYVQLLRRCVDPDPTGLYMLQLAGRGSVAVHQ 3900
gi|114622142|ref|XP_520007.2| ----- 3900
gi|73974852|ref|XP_532347.2| ----- 3900
gi|292624226|ref|XP_001922664.2| KKKLISVEQAVSEGIQVVEWKNKLLSAERAVTGYTDPNTGKIIISLFOALKKDLIVKEHGIRLLEAQIATGGIIDPVYSHRVPVEVAYQRYFDEEMNKILADPDDTKGFFDPNTOENLTYLQVLRVCRVDPNTGLSLLVIVKKGEEYFF 3900
gi|292624221|ref|XP_002665585.1| KKKLISVEQAVSEGIQVVEWKNKLLSAERAVTGYTDPNTGKIIISLFOALKKDLIVKEHGIRLLEAQIATGGIIDPVYSHRVPVEVAYQRYFDEEMNKILADPDDTKGFFDPNTOENLTYLQVLRVCRVDPNTGLSLLVIVKKGEEYFF 3900
.....3760.....3770.....3780.....3790.....3800.....3810.....3820.....3830.....3840.....3850.....3860.....3870.....3880.....3890.....3900

gi|37537522|ref|NP_659097.2| LSEELRRLREARVTPGTGDFGQGISVWELLFYREVPESLRDILLRRYAGGLTVHDVTTLTLSLLARAKDGSPRX-----DPOGALGKATMEVKRGLHRGHXVPVWDILTNSYVSRDTRKELLAQFSSGLLPLMKRRLTITIE 4050
gi|109480932|ref|XP_001059215.1| LSEELRRLREARVTPGTGDFGQGISVWELLFYREVPESLRDILLRRYAGGLTVHDVTTLTLSLLARAKDGSPRX-----DPOGALGKATMEVKRGLHRGHXVPVWDILTNSYVSRDTRKELLAQFSSGLLPLMKRRLTITIE 4050
gi|207452735|ref|NP_112598.2| LSEELRRLREARVTPGTGDFGQGISVWELLFYREVPESLRDILLRRYAGGLTVHDVTTLTLSLLARAKDGSPRX-----DPOGALGKATMEVKRGLHRGHXVPVWDILTNSYVSRDTRKELLAQFSSGLLPLMKRRLTITIE 4050
gi|114622142|ref|XP_520007.2| ----- 4050
gi|73974852|ref|XP_532347.2| ----- 4050
gi|292624226|ref|XP_001922664.2| IDEHTKNIKSTTTKKAGGKYGQGLVTLWDLLYSSYIIEKKRRELVOQFKSGITITIEQFLIIVLILVSG 4050
gi|292624221|ref|XP_002665585.1| IDEHTKNIKSTTTKKAGGKYGQGLVTLWDLLYSSYIIEKKRRELVOQFKSGITITIEQFLIIVLILVSG 4050
.....3910.....3920.....3930.....3940.....3950.....3960.....3970.....3980.....3990.....4000.....4010.....4020.....4030.....4040.....4050

gi|37537522|ref|NP_659097.2| EAEEIQESKPKPRDASLKOQDYG-----ARGSGTSPDEGDAQDSSEARQQEQTLRAITMQVHRGQFRDQOVVWVKVLFSSYLSERREELLAQHLGKLGVMELVSLAQIIEEIEERLSEKVFPGLRRLQVASELCTSGIIL 4200
gi|109480932|ref|XP_001059215.1| EAEEIQESKPKPRDASLKOQDYG-----ARGSGTSPDEGDAQDSSEARQQEQTLRAITMQVHRGQFRDQOVVWVKVLFSSYLSERREELLAQHLGKLGVMELVSLAQIIEEIEERLSEKVFPGLRRLQVASELCTSGIIL 4200
gi|207452735|ref|NP_112598.2| EAEEAPGARPQLQDAWRGPRPFGPAGRGDGDGCRSQRGQEGEETQEAASAAAAARRQEQTLRDAITMEVQRGQGRPVVWVLFSSYLSERREELLAQHAAGALGLDPLVAVLIRVIEEIEERLSEKVFPGLRRLQVASELCTSGIIL 4200
gi|114622142|ref|XP_520007.2| ----- 4200
gi|73974852|ref|XP_532347.2| ----- 4200
gi|292624226|ref|XP_001922664.2| -----KSVTSTHTITSTTITETQNTNFOGIRKRDVSADELLQSKVI 4200
gi|292624221|ref|XP_002665585.1| -----KSVTSTHTITSTTITETQNTNFOGIRKRDVSADELLQSKVI 4200
.....4060.....4070.....4080.....4090.....4100.....4110.....4120.....4130.....4140.....4150.....4160.....4170.....4180.....4190.....4200

gi|37537522|ref|NP_659097.2| DRDITMRELAQCTKIIEVTEMDSVKRYLGGSSCIAGVLVFPVGEPRGQEKMSIYQAMWKGVLKPGTALVLLLEAQAATGFVIDPVNRRLSVEEVAAGVVGGEIQEKLLEAERAVTGYTDPYTGDIISLFOAMORDLIVRDEHGIRLLEAQ 4350
gi|109480932|ref|XP_001059215.1| DRDITMRELAQCTKIIEVTEMDSVKRYLGGSSCIAGVLVFPVGEPRGQEKMSIYQAMWKGVLKPGTALVLLLEAQAATGFVIDPVNRRLSVEEVAAGVVGGEIQEKLLEAERAVTGYTDPYTGDIISLFOAMORDLIVRDEHGIRLLEAQ 4350
gi|207452735|ref|NP_112598.2| GPEILRDLAQCTKIIEVTEMDSVKRYLGGSSCIAGVLVPAKDPGRQEKMSIYQAMWKGVLKPGTALVLLLEAQAATGFVIDPVNRRLSVEEVAAGVVGGEIQEKLLEAERAVTGYTDPYTGDIISLFOAMOKDLIVREHGIRLLEAQ 4350
gi|114622142|ref|XP_520007.2| ----- 4350
gi|73974852|ref|XP_532347.2| ----- 4350
gi|292624226|ref|XP_001922664.2| DEKIYKDLTSGKVVVDHVKMDSVRRYKLGINSIAGVFVQ-----KQITMSIFEAKNKGLLTPGTSLVLLLEAQAATGFVIDPVNRRLSVEEVAAGVVGGEIQEKLLEAERAVTGYTDPNTGKIIISLFOALKKDLIVKEHGIRLLEAQ 4350
gi|292624221|ref|XP_002665585.1| DEKIYKDLTSGKVVVDHVKMDSVRRYKLGINSIAGVFVQ-----KQITMSIFEAKNKGLLTPGTSLVLLLEAQAATGFVIDPVNRRLSVEEVAAGVVGGEIQEKLLEAERAVTGYTDPNTGKIIISLFOALKKDLIVKEHGIRLLEAQ 4350
.....4210.....4220.....4230.....4240.....4250.....4260.....4270.....4280.....4290.....4300.....4310.....4320.....4330.....4340.....4350

gi|37537522|ref|NP_659097.2| IATGGVIDPVHSHRVPVDVAYQRYFDEDMNSILADPGDDTKGFFDPNTHENLTYLQLLRRCVRDPEIGFYMLQLAGKGSVHHLSEELRRLREARVTPGTGDFGQGISVWELLFYREVPESLRDILLRRYAGGLTVHDVTTLTLSL 4500
gi|109480932|ref|XP_001059215.1| IATGGVIDPVHSHRVPVDVAYQRYFDEDMNSILADPGDDTKGFFDPNTHENLTYLQLLRRCVRDPEIGFYMLQLAGKGSVHHLSEELRRLREARVTPGTGDFGQGISVWELLFYREVPESLRDILLRRYAGGLTVHDVTTLTLSL 4500
gi|207452735|ref|NP_112598.2| IATGGVIDPVHSHRVPVDVAYRRGYFDEEMNRVLADPSDDTKGFFDPNTHENLTYVQLLRRCVDPDPTGLYMLQLAGRGSVAVHQLSEELRRLREARVTPGTGDFGQGISVWELLFYREVPESLRDILLRRYAGGLTVHDVTTLTLSL 4500
gi|114622142|ref|XP_520007.2| ----- 4500
gi|73974852|ref|XP_532347.2| ----- 4500
gi|292624226|ref|XP_001922664.2| IATGGIIDPVYSHRVPVEVAYQRYFDEEMNKILADPDDTKGFFDPNTOENLTYLQVLRVCRVDPNTGLSLLVIVKKGEEYFFIDEHTKNIKSTTTKKAGGKYGQGLVTLWDLLYSSYIIEKKRRELVOQFKSGITITIEQFLIIVLIL 4500
gi|292624221|ref|XP_002665585.1| IATGGIIDPVYSHRVPVEVAYQRYFDEEMNKILADPDDTKGFFDPNTOENLTYLQVLRVCRVDPNTGLSLLVIVKKGEEYFFIDEHTKNIKSTTTKKAGGKYGQGLVTLWDLLYSSYIIEKKRRELVOQFKSGITITIEQFLIIVLIL 4500
.....4360.....4370.....4380.....4390.....4400.....4410.....4420.....4430.....4440.....4450.....4460.....4470.....4480.....4490.....4500

gi|37537522|ref|NP_659097.2|LARAKDGS PRX-----DPOGALGKATMEVKRGLRHXVPVVDILTSNYVSRDTRKELLAQFSSGSLTLPMLKRRLLTITIEEAEETQESKPKPRDASLKO DDTG-----ARGSGTSPDEGDA DSSSEAROOEQTLRAIT 4650
gi|109480932|ref|XP_001059215.1| 4650
gi|207452735|ref|NP_112598.2|LAQAQAARAEAEAGSPRPDPREALRAATMEVKVGRLRGRAVPVVDVLAAGYVSRAREELLAEFSGSCTLDLPALTRRLTAITIEEAEAPGARPLQDQAWRGPREFPGPAGRGDDEGRSQRREGQGEGETOEAATAAARRQEQTLRDAI 4650
gi|114622142|ref|XP_520007.2| 4650
gi|73974852|ref|XP_532347.2| 4650
gi|292624226|ref|XP_001922664.2|VSC 4650
gi|292624221|ref|XP_002665585.1|VSC 4650
.....4510.....4520.....4530.....4540.....4550.....4560.....4570.....4580.....4590.....4600.....4610.....4620.....4630.....4640.....4650

gi|37537522|ref|NP_659097.2|MQVHRGQFRDQVSVWKVLFSSYLSERREELLAQHLAGKLGVMELVLLTQIIEETEEERLQKVSFPGLRRQVASELCTSGILDRTMRELAQGKTIHEVTEMDSVKRYLGGSSCIAGVLVVPVGEFGRDEKMSIYQAMWKGVLRRPGI 4800
gi|109480932|ref|XP_001059215.1| 4800
gi|207452735|ref|NP_112598.2|MEVQRGQFQGRPVVVDVLFSSYLSERREELLAQHAAGALGLPDLVAVLIRVIEETEEERLQKVSFRGLRRQVASELHSTGILGPETLRDLAQGKTIHQEVTEMDSVKRYLGGSSCIAGVLVPAKDPGRDEKMSIYQAMWKGVLRRPGI 4800
gi|114622142|ref|XP_520007.2| 4800
gi|73974852|ref|XP_532347.2| 4800
gi|292624226|ref|XP_001922664.2|-----KSVTSTHTITTTTTETQNTNFGIRKDVSADELLQSKVIDEKIKDLSGKVTVDHVSKMDSVRKYLRGTNSIAGVVFQ-----KQTMSTIFEAKNKGLLTPGI 4800
gi|292624221|ref|XP_002665585.1|-----KSVTSTHTITTTTTETQNTNFGIRKDVSADELLQSKVIDEKIKDLSGKVTVDHVSKMDSVRKYLRGTNSIAGVVFQ-----KQTMSTIFEAKNKGLLTPGI 4800
.....4660.....4670.....4680.....4690.....4700.....4710.....4720.....4730.....4740.....4750.....4760.....4770.....4780.....4790.....4800

gi|37537522|ref|NP_659097.2|ALVLLLEAQAATGFVIDPVNRRLSVEEAVAAQVVGGEIQEKLLSAERAVTGYTDPYIGDQISLFAQMKDLIVREHGIRLLEAQAATGGVIDPVHSHRVPVDVAYRQYFDEEMNSILADPGDDTKGFFDPNTHENLYVLLRRCVDP 4950
gi|109480932|ref|XP_001059215.1| 4950
gi|207452735|ref|NP_112598.2|ALVLLLEAQAATGFVIDPVRNRLLSVEEAVAAQVVGGEIQEKLLSAERAVTGYTDPYIGDQISLFAQMKDLIVREHGIRLLEAQAATGGVIDPVHSHRVPVDVAYRQYFDEEMNRLADPSDDTKGFFDPNTHENLYVLLRRCVDP 4950
gi|114622142|ref|XP_520007.2| 4950
gi|73974852|ref|XP_532347.2| 4950
gi|292624226|ref|XP_001922664.2|SLVLLLEAQAATGFVIDPVKNKLLSVEQAVSEGIVGVWKNKLLSAERAVTGYTDPNTGKIIISLFAQMKDLIVREHGIRLLEAQAATGGVIDPVYSHRVPVEVAYRQYFDEEMNKILSDPDDTKGFFDPNTHENLYVLLRRCVDP 4950
gi|292624221|ref|XP_002665585.1|SLVLLLEAQAATGFVIDPVKNKLLSVEQAVSEGIVGVWKNKLLSAERAVTGYTDPNTGKIIISLFAQMKDLIVREHGIRLLEAQAATGGVIDPVYSHRVPVEVAYRQYFDEEMNKILSDPDDTKGFFDPNTHENLYVLLRRCVDP 4950
.....4810.....4820.....4830.....4840.....4850.....4860.....4870.....4880.....4890.....4900.....4910.....4920.....4930.....4940.....4950

gi|37537522|ref|NP_659097.2|ETCFYMLQLACKGSSVHHLSEELRRALREARVTPGTGDFQGSISVWELLFYREVPESLRQDLRRYQAGGLTVHDVITLITSLARAKDGS PRX-----DPOGALGKATMEVKRGLRHXVPVVDILTSNYVSRDTRKELLAQFS 5100
gi|109480932|ref|XP_001059215.1| 5100
gi|207452735|ref|NP_112598.2|DTGLYMLQLAGRGSAVHQLSEELRRCALRDARVTPGSGALQGSISVWELLFYREVSEDRRQDLRVRAGLITVEELGAILTSLLAQAQAARAEAEAGSPRPDPREALRAATMEVKVGRLRGRAVPVVDVLAAGYVSRAREELLAEF 5100
gi|114622142|ref|XP_520007.2| 5100
gi|73974852|ref|XP_532347.2| 5100
gi|292624226|ref|XP_001922664.2|KTFGLSLLVLKK----- 5100
gi|292624221|ref|XP_002665585.1|KTFGLSLLVLKK----- 5100
.....4960.....4970.....4980.....4990.....5000.....5010.....5020.....5030.....5040.....5050.....5060.....5070.....5080.....5090.....5100

gi|37537522|ref|NP_659097.2|SGSLTLPMLKRRLLTITIEEAEETQESKPKPRDASLKO DDTG-----ARGSGTSPDEGDA DSSSEAROOEQTLRAITMQVHRGQFRDQVSVWKVLFSSYLSERREELLAQHLAGKLGVMELVLLTQIIEETEEERLQKVSF 5250
gi|109480932|ref|XP_001059215.1| 5250
gi|207452735|ref|NP_112598.2|SGTLDLPALTRRLTAITIEEAEAPGARPLQDQAWRGPREFPGPAGRGDDEGRSQRREGQGEGETOEAATAAARRQEQTLRDAIMEVQRGQFQGRPVVVDVLFSSYLSERREELLAQHAAGALGLPDLVAVLIRVIEETEEERLQKVSF 5250
gi|114622142|ref|XP_520007.2| 5250
gi|73974852|ref|XP_532347.2| 5250
gi|292624226|ref|XP_001922664.2| 5250
gi|292624221|ref|XP_002665585.1| 5250
.....5110.....5120.....5130.....5140.....5150.....5160.....5170.....5180.....5190.....5200.....5210.....5220.....5230.....5240.....5250

gi|37537522|ref|NP_659097.2|PGLRRQVSAELCTSGILDRDTRMRELAQCTKIHEVTEMDSVKRYLGGSSCIAGVLPVVGEPGRQEKMSIYQAMWKGVLKPGTALVLLAQAAATGFVIDPVRNRLSVEEVAAGVVGGEIQEKLLEAERAVTGYTDPYTGDIISLFOA 5400
gi|109480932|ref|XP_001059215.1| 5400
gi|207452735|ref|NP_112598.2|RGLRRQVSAELHTSGILGPELRLDRAQCTKIHEVTEMDSVKRYLGGSSCIAGVLPVPAKDPGRQEKMSIYQAMWKGVLKPGTALVLLAQAAATGFVIDPVRNRLSVEEVAAGVVGGEIQEKLLEAERAVTGYTDPYTGDIISLFOA 5400
gi|114622142|ref|XP_520007.2| 5400
gi|73974852|ref|XP_532347.2| 5400
gi|292624226|ref|XP_001922664.2| 5400
gi|292624221|ref|XP_002665585.1| 5400
.....5260.....5270.....5280.....5290.....5300.....5310.....5320.....5330.....5340.....5350.....5360.....5370.....5380.....5390.....5400

gi|37537522|ref|NP_659097.2|MQRDLIVRDEHGIRLLEAQTATGGVIDPVHSHRVPVDVAYQRGYFDEDMNSILADPGDDTKGFFDPNTHENLTYLQLLRRCVDRDPEYGFYMLQIAGKGSVHHLSEELRRLREARVTPGTGDFGQSIIVWELLFYREVPELRODLLRR 5550
gi|109480932|ref|XP_001059215.1| 5550
gi|207452735|ref|NP_112598.2|MQRDLIVRDEHGIRLLEAQTATGGVIDPVHSHRVPVDVAYRQGYFDEEMNRVLADPGDDTKGFFDPNTHENLTYLQLLRATLDPEYGLLFLSLSLG 5550
gi|114622142|ref|XP_520007.2| 5550
gi|73974852|ref|XP_532347.2| 5550
gi|292624226|ref|XP_001922664.2| 5550
gi|292624221|ref|XP_002665585.1| 5550
.....5410.....5420.....5430.....5440.....5450.....5460.....5470.....5480.....5490.....5500.....5510.....5520.....5530.....5540.....5550

gi|37537522|ref|NP_659097.2|YQAGGLVVDVITLITSLARAKDGSFPRXDPQCALGKATMEVVKRGLRGRHXVPVVDILTSNYVSRDTRKELLAQFSSGSLALPMLKRRLLTIEEAETQESKPKPRDASLKKQDTGARGSGTSPDEGDAQDSSESARQQEQTLRATIM 5700
gi|109480932|ref|XP_001059215.1| 5700
gi|207452735|ref|NP_112598.2| 5700
gi|114622142|ref|XP_520007.2| 5700
gi|73974852|ref|XP_532347.2| 5700
gi|292624226|ref|XP_001922664.2| 5700
gi|292624221|ref|XP_002665585.1| 5700
.....5560.....5570.....5580.....5590.....5600.....5610.....5620.....5630.....5640.....5650.....5660.....5670.....5680.....5690.....5700

gi|37537522|ref|NP_659097.2|QVHRGQFRDQCVSVKVLFSYLSSETRREELLAQHLGKLVMEVLSLLTQIIEETEEERLSKVSFPGLRRQVSAELCTSGILDRDTRMRELAQCTKIHEVTEMDSVKRYLGGSSCIAGVLPVVGEPGRQEKMSIYQAMWKGVLKPGTAL 5850
gi|109480932|ref|XP_001059215.1| 5850
gi|207452735|ref|NP_112598.2| 5850
gi|114622142|ref|XP_520007.2| 5850
gi|73974852|ref|XP_532347.2| 5850
gi|292624226|ref|XP_001922664.2| 5850
gi|292624221|ref|XP_002665585.1| 5850
.....5710.....5720.....5730.....5740.....5750.....5760.....5770.....5780.....5790.....5800.....5810.....5820.....5830.....5840.....5850

gi|37537522|ref|NP_659097.2|LVLLAQAAATGFVIDPVRNRLSVEEVAAGVVGGEIQEKLLEAERAVTGYTDPYTGDIISLFOAMQRDLIVRDEHGIRLLEAQTATGGVIDPVHSHRVPVDVAYQRGYFDEDMNSILADPGDDTKGFFDPNTHENLTYLQLLRRCVDRDPE 6000
gi|109480932|ref|XP_001059215.1| 6000
gi|207452735|ref|NP_112598.2| 6000
gi|114622142|ref|XP_520007.2| 6000
gi|73974852|ref|XP_532347.2| 6000
gi|292624226|ref|XP_001922664.2| 6000
gi|292624221|ref|XP_002665585.1| 6000
.....5860.....5870.....5880.....5890.....5900.....5910.....5920.....5930.....5940.....5950.....5960.....5970.....5980.....5990.....6000

gi|37537522|ref|NP_659097.2| TGFVMLQLAGKGSVHHLSEELRRALREARVTPGTGDFQGQSIQVWELLFYREVPESLRQDLLRRYQAGGLVVDVTTILTSLLARAKDGSPRXDPQALGKATMEVVRGHLRGHXVPVVDILTSNYVSRDTRKELLAQFSSGSLILPML 6150
gi|109480932|ref|XP_001059215.1| 6150
gi|207452735|ref|NP_112598.2| 6150
gi|114622142|ref|XP_520007.2| 6150
gi|73974852|ref|XP_532347.2| 6150
gi|292624226|ref|XP_001922664.2| 6150
gi|292624221|ref|XP_002665585.1| 6150
.....6010.....6020.....6030.....6040.....6050.....6060.....6070.....6080.....6090.....6100.....6110.....6120.....6130.....6140.....6150

gi|37537522|ref|NP_659097.2| KRRLTTIIEEAEETQESKPKPRDASLKOQDTGARGSGTSPDEGDAQDSSSEARQQEQTLRATIMQVHRGQFRDQQVSVWKVLFSSYLSERREELLAQHLAGKLGVMELVSLTQIIEETEERLSKVSFPGLRROVSASELCTSGILDR 6300
gi|109480932|ref|XP_001059215.1| 6300
gi|207452735|ref|NP_112598.2| 6300
gi|114622142|ref|XP_520007.2| 6300
gi|73974852|ref|XP_532347.2| 6300
gi|292624226|ref|XP_001922664.2| 6300
gi|292624221|ref|XP_002665585.1| 6300
.....6160.....6170.....6180.....6190.....6200.....6210.....6220.....6230.....6240.....6250.....6260.....6270.....6280.....6290.....6300

gi|37537522|ref|NP_659097.2| DIMRELAQCTKIHEVTEMDSVKRYLGGSSCIAGVLVFPVQGEPRQEKMSIYQAMWGVLRPGTALVLLAQAAATGFIIIDPVNNRRLSVEEVAAGVVGGEIQEKLLSAERAVTGYTDPYTGDIISLFCAMQRDLIVRDHGIRLLEAQTIA 6450
gi|109480932|ref|XP_001059215.1| 6450
gi|207452735|ref|NP_112598.2| 6450
gi|114622142|ref|XP_520007.2| 6450
gi|73974852|ref|XP_532347.2| 6450
gi|292624226|ref|XP_001922664.2| 6450
gi|292624221|ref|XP_002665585.1| 6450
.....6310.....6320.....6330.....6340.....6350.....6360.....6370.....6380.....6390.....6400.....6410.....6420.....6430.....6440.....6450

gi|37537522|ref|NP_659097.2| TGGVIDPVHSHRVFVDVAYQRGFDNMSILADPGDDTKGFFDPNTHENLTYLQLLRRCVRDPEITGFVMLQLAGKGSVHHLSEELRRALREARVTPGTGDFQGQSIQVWELLFYREVPESLRQDLLRRYQAGGLVVDVTTILTSLLA 6600
gi|109480932|ref|XP_001059215.1| 6600
gi|207452735|ref|NP_112598.2| 6600
gi|114622142|ref|XP_520007.2| 6600
gi|73974852|ref|XP_532347.2| 6600
gi|292624226|ref|XP_001922664.2| 6600
gi|292624221|ref|XP_002665585.1| 6600
.....6460.....6470.....6480.....6490.....6500.....6510.....6520.....6530.....6540.....6550.....6560.....6570.....6580.....6590.....6600

gi|37537522|ref|NP_659097.2| RAKDGSPPREDPQALGKATMEVVRGHLRGHVVPVVDILTSNYVSRDTRKELLAQFSSGSLILPMLKRRLTTIIEEAEETQESKPKPRDASLKOQDTGARGSGTSPDEGDAQDSSSEARQQEQTLRATIMQVHRGQFRDQQVSVWKVLFSS 6750
gi|109480932|ref|XP_001059215.1| 6750
gi|207452735|ref|NP_112598.2| 6750
gi|114622142|ref|XP_520007.2| 6750
gi|73974852|ref|XP_532347.2| 6750
gi|292624226|ref|XP_001922664.2| 6750
gi|292624221|ref|XP_002665585.1| 6750
.....6610.....6620.....6630.....6640.....6650.....6660.....6670.....6680.....6690.....6700.....6710.....6720.....6730.....6740.....6750

gi		37537522		ref		NP_659097.2		SYLSETRREELLAQHLAGKLGVMELVSLLTQIIEETEEERLESKVSFPGLRRQVASELCTSGILDRDTMRELAQGTKEIHEVTEMDQVKRYLGGSSCIAGVLPVQGEFGRQEKMSIYQAMWKGVLKPGTALVLLLEAQAATCFIIDPVNNR	6900
gi		109480932		ref		XP_001059215.1		-----	6900
gi		207452735		ref		NP_112598.2		-----	6900
gi		114622142		ref		XP_520007.2		-----	6900
gi		73974852		ref		XP_532347.2		-----	6900
gi		292624226		ref		XP_001922664.2		-----	6900
gi		292624221		ref		XP_002665585.1		-----	6900
							6760.....6770.....6780.....6790.....6800.....6810.....6820.....6830.....6840.....6850.....6860.....6870.....6880.....6890.....6900	

gi		37537522		ref		NP_659097.2		RLSVEEVAAGVVGGEIQEKLLEAERAVTGYTDPYTGDOIISLFQAMORDLIVKNEGIRLLEAQIAAGGVIDPVHSHRVPVDVAYQRYFDQEMNSILADPGDDIKGFFDPNTHENLYLQLLQRAIIDPETGLLFLSLSKG	7041
gi		109480932		ref		XP_001059215.1		-----	7041
gi		207452735		ref		NP_112598.2		-----	7041
gi		114622142		ref		XP_520007.2		-----	7041
gi		73974852		ref		XP_532347.2		-----	7041
gi		292624226		ref		XP_001922664.2		-----	7041
gi		292624221		ref		XP_002665585.1		-----	7041
							6910.....6920.....6930.....6940.....6950.....6960.....6970.....6980.....6990.....7000.....7010.....7020.....7030.....7040.	