

gi |113930718|ref |NP_032753.5| ---MPSGRR---VRPRLRALLLPP---LLLLRSGHAS---DLTVAVVPLPLNTSYSPWSEWARVGPVAVLALGRVKARPDLLPGWTVRMVLGSSENAAGVCSDTAA 150
gi |6981280|ref |NP_036745.1| ---MPSGRR---VRPRLRALLLPP---LLLLRSGHAS---DLTVAVVPLPLNTSYSPWSEWARVGPVAVLALGRVKARPDLLPGWTVRMVLGSSENAAGVCSDTAA 150
gi |73961665|ref |XP_547577.2| ---MLRPGRP---AGA-LPLPPPPPP---LLLLLPGSQAG---NLTVAVVPLPLNTSYSPWSEWARVGPVAVLALAAVRAQPDLLPGWTVRVLGSSENALGVCSDTAA 150
gi |194665089|ref |XP_612318.3| ---MVPAEAMPFRGPR---SGARLRLLLLLPP---LLLLLPGSYAG---NLTVAVVPLPLNTSYSPWSEWARVGPVAVLALARVKARPDLLPGWTVRVLGSSESALGVCSDTAA 150
gi |167830411|ref |NP_000897.3| ---MPSGRR---AGSRRLRLLLLLPP---LLLLLPGSHAG---NLTVAVVPLPLNTSYSPWSEWARVGPVAVLALAAQVKARPDLLPGWTVRVLGSSENALGVCSDTAA 150
gi |113678661|ref |NP_001038402.1| ---MELFQMCPRLRL---LVLLSGVSPGVVLEPVPENQPSAHASOK---NLLAVILPLHNTSYSPWSEWARVGPVAVLWALEKVDNLLAGVHLQVFNSSSENKGLCSDSVA 150
gi |221330468|ref |NP_726013.2| MELLGISIHFFFLMYVNCFAHPNRRNDITWDDLNKDISLDSITSLAGLNASDAGLEQRMYSRESKSKLSRYLEVGEKMTNRVNVGVLMASHLDSFFDLERCGPAIDLALDELVN---KVLFLKPHNITLTK---KKSYSYSCSGARA 150
gi |158293450|ref |XP_314790.4| ---MPSGRR---VRPRLRALLLPP---LLLLRSGHAS---DLTVAVVPLPLNTSYSPWSEWARVGPVAVLALGRVKARPDLLPGWTVRMVLGSSENAAGVCSDTAA 150
gi |118104469|ref |XP_429192.2| ---MPSGRR---VRPRLRALLLPP---LLLLRSGHAS---DLTVAVVPLPLNTSYSPWSEWARVGPVAVLALGRVKARPDLLPGWTVRMVLGSSENAAGVCSDTAA 150
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150



gi |113930718|ref |NP_032753.5| PAAVLDLKEHSPAVFLGPGCVVSAAPVGRFIAHWVRVPLLA---AGAPALGIGVKDEYALTRIGPSHVKLGDFVIALHRRLGWEHQALVLYADRLGDDRCFFIVEGLVMYRERLNIIVNHQEF 300
gi |6981280|ref |NP_036745.1| PAAVLDLKEHSPAVFLGPGCVVSAAPVGRFIAHWVRVPLLA---AGAPALGIGVKDEYALTRIGPSHVKLGDFVIALHRRLGWEHQALVLYADRLGDDRCFFIVEGLVMYRERLNIIVNHQEF 300
gi |73961665|ref |XP_547577.2| PAAVLDLKEHSPAVFLGPGCVVSAAPVGRFIAHWVRVPLLA---AGAPALGIGVKDEYALTRIGPSHVKLGDFVIALHRRLGWEHQALVLYADRLGDDRCFFIVEGLVMYRERLNIIVNHQEF 300
gi |194665089|ref |XP_612318.3| PAAVLDLKEHSPAVFLGPGCVVSAAPVGRFIAHWVRVPLLA---AGAPALGIGVKDEYALTRIGPSHVKLGDFVIALHRRLGWEHQALVLYADRLGDDRCFFIVEGLVMYRERLNIIVNHQEF 300
gi |167830411|ref |NP_000897.3| PAAVLDLKEHSPAVFLGPGCVVSAAPVGRFIAHWVRVPLLA---AGAPALGIGVKDEYALTRIGPSHVKLGDFVIALHRRLGWEHQALVLYADRLGDDRCFFIVEGLVMYRERLNIIVNHQEF 300
gi |113678661|ref |NP_001038402.1| PLVAVDLKFSNPNWAFIGPCDSSSPVAFRITWHEVPMII---SGARLGFV---NLYVSSINIGETPKKLGDFVIALHRRLGWEHQALVLYADRLGDDRCFFIVEGLVMYRERLNIIVNHQEF 300
gi |221330468|ref |NP_726013.2| PGLAADMYFDVDDVLAFIGPACAFALFEPVARLAAYNKNPIIIGMDQPPSEGEGLTVISGILGRIRIKWKNENGMFKDKSKYVILIRMSYCCORLILVFSISIQFNWNVHVALVDR---SFLSWVYGNKLEYGLRQKDELLKFKVELN 300
gi |158293450|ref |XP_314790.4| PGLAADLHFKEHSPAVFLGPGCVVSAAPVGRFIAHWVRVPLLA---AGAPALGIGVKDEYALTRIGPSHVKLGDFVIALHRRLGWEHQALVLYADRLGDDRCFFIVEGLVMYRERLNIIVNHQEF 300
gi |118104469|ref |XP_429192.2| PAAVLDLKEHSPAVFLGPGCVVSAAPVGRFIAHWVRVPLLA---AGAPALGIGVKDEYALTRIGPSHVKLGDFVIALHRRLGWEHQALVLYADRLGDDRCFFIVEGLVMYRERLNIIVNHQEF 300
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300



gi |113930718|ref |NP_032753.5| VEGD-PDHYTKLLRITVQRKGRVIYICSSPDARFRLMMLLALDAGLIGEDYVFFHLDVFGQSLKSAAGLVPQKPRWERGDDRSARQAFQAAKIIITYKEPDNPEYLEFLKOLKLLADKKNFTMEDG-LKNIIPASFHDGLLLYVQAVTEIL 450
gi |6981280|ref |NP_036745.1| VEGD-PDHYTKLLRITVQRKGRVIYICSSPDARFRLMMLLALDAGLIGEDYVFFHLDVFGQSLKSAAGLVPQKPRWERGDDRSARQAFQAAKIIITYKEPDNPEYLEFLKOLKLLADKKNFTMEDG-LKNIIPASFHDGLLLYVQAVTEIL 450
gi |73961665|ref |XP_547577.2| AEGD-LDQYALLLHTVRRKGRVIYICSSPDARFRLMMLLALDAGLIGEDYVFFHLDVFGQSLKSAAGLVPQKPRWERGDDRSARQAFQAAKIIITYKEPDNPEYLEFLKOLKLLADKKNFTMEDG-LKNIIPASFHDGLLLYVQAVTEIL 450
gi |194665089|ref |XP_612318.3| AEGD-RDHYTMLLRTVRRKGRVIYICSSPDARFRLMMLLALDAGLIGEDYVFFHLDVFGQSLKSAAGLVPQKPRWERGDDRSARQAFQAAKIIITYKEPDNPEYLEFLKOLKLLADKKNFTMEDG-LKNIIPASFHDGLLLYVQAVTEIL 450
gi |167830411|ref |NP_000897.3| AEGD-LDHYTMLLRTVRRKGRVIYICSSPDARFRLMMLLALDAGLIGEDYVFFHLDVFGQSLKSAAGLVPQKPRWERGDDRSARQAFQAAKIIITYKEPDNPEYLEFLKOLKLLADKKNFTMEDG-LKNIIPASFHDGLLLYVQAVTEIL 450
gi |113678661|ref |NP_001038402.1| NDEEPLRYDELLRDISHKARVIVYVCKWEIKRKLMEVFWRQGFQBEYAFFIDLFGSLQSGGAPAPRPRWERGDDRSARQAFQAAKIIITYKEPDNPEYLEFLKOLKLLADKKNFTMEDG-LKNIIPASFHDGLLLYVQAVTEIL 450
gi |221330468|ref |NP_726013.2| GNDE--EYENYLKSDASMYARVILSVRGLVVRKFMALAAHSLGMEVWVFLDVEIFQSEYWG---DKGWEMKDEHDAKARAYEALLRVSLLOPTSPKQDFADNVRENALYDNYTFEGEVEVNFYGAFFDGVLLGMALNDEL 450
gi |158293450|ref |XP_314790.4| GNDE--EDTEAVLKDASMYARVILSVRGLVVRKFMALAAHSLGMEVWVFLDVEIFQSEYWG---DKGWEMKDEHDAKARAYEALLRVSLLOPTSPKQDFADNVRENALYDNYTFEGEVEVNFYGAFFDGVLLGMALNDEL 450
gi |118104469|ref |XP_429192.2| PPET---AVSGEFFNVIVAVFASDGFYQAVYVQNGILSHQNTNAAAKEFCEHECHP---ASWKDANGENCCVHHANIHSCPLAFMGRG---GICGPWIPDDGIFITHL 450
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450



gi |113930718|ref |NP_032753.5| AQQGVITDGENITQRMNRRSFGVTVGKIDRNGDRDIDFSLWDM-DPEGAFRVVNLNFGTSQELMAVSEHKLWYPLGY---PPPDIPKCGFDNEDPACNDHFSSTLEVLAALVGSLSLVSFLIVSFFIYRKMOLKELVSELWRVWEDL 600
gi |6981280|ref |NP_036745.1| AQQGVITDGENITQRMNRRSFGVTVGKIDRNGDRDIDFSLWDM-DPEGAFRVVNLNFGTSQELMAVSEHKLWYPLGY---PPPDIPKCGFDNEDPACNDHFSSTLEVLAALVGSLSLVSFLIVSFFIYRKMOLKELVSELWRVWEDL 600
gi |73961665|ref |XP_547577.2| AHGGAVTDGEAITQRMNRRSFGVTVGKIDRNGDRDIDFSLWDM-DPEGAFRVVNLNFGTSQELMAVSEHKLWYPLGY---PPPDIPKCGFDNEDPACNDHFSSTLEVLAALVGSLSLVSFLIVSFFIYRKMOLKELVSELWRVWEDL 600
gi |194665089|ref |XP_612318.3| AHGGAVTDGEAITQRMNRRSFGVTVGKIDRNGDRDIDFSLWDM-DPEGAFRVVNLNFGTSQELMAVSEHKLWYPLGY---PPPDIPKCGFDNEDPACNDHFSSTLEVLAALVGSLSLVSFLIVSFFIYRKMOLKELVSELWRVWEDL 600
gi |167830411|ref |NP_000897.3| AHGGAVTDGEAITQRMNRRSFGVTVGKIDRNGDRDIDFSLWDM-DPEGAFRVVNLNFGTSQELMAVSEHKLWYPLGY---PPPDIPKCGFDNEDPACNDHFSSTLEVLAALVGSLSLVSFLIVSFFIYRKMOLKELVSELWRVWEDL 600
gi |113678661|ref |NP_001038402.1| DRSGSRPPGVDVNVKRMNRRSFGVTVGKIDRNGDRDIDFSLWDM-DPEGAFRVVNLNFGTSQELMAVSEHKLWYPLGY---PPPDIPKCGFDNEDPACNDHFSSTLEVLAALVGSLSLVSFLIVSFFIYRKMOLKELVSELWRVWEDL 600
gi |221330468|ref |NP_726013.2| TEGGDIRDGVNITRRMNRIFEGITGHVRIDNDRDADYIILDL-DPEGAFRVVNLNFGTSQELMAVSEHKLWYPLGY---PPPDIPKCGFDNEDPACNDHFSSTLEVLAALVGSLSLVSFLIVSFFIYRKMOLKELVSELWRVWEDL 600
gi |158293450|ref |XP_314790.4| NEGGDIRDGVNITRRMNRIFEGITGHVRIDNDRDADYIILDL-DPEGAFRVVNLNFGTSQELMAVSEHKLWYPLGY---PPPDIPKCGFDNEDPACNDHFSSTLEVLAALVGSLSLVSFLIVSFFIYRKMOLKELVSELWRVWEDL 600
gi |118104469|ref |XP_429192.2| STAG---KMSQRNFKSIVLVHVG---VSLIAHRIVRGMQVLEAKTILVPAVVCGGPFCHEESGICFADCGECLPLSARAIATAPICLVCTAFIMVVMWFYCKRMLWDESWIETFTCI 600
.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600



gi |113930718|ref |NP_032753.5| QPSS-----LERHLRSAGSRLILSGRSNYG---SLLITTEG--QFVFAKTAAYKGNLVAVKRVNRKRIELTRKVLFLKHMARDVNEHLTRFVGACDPP---NICILTEYCPRGSLDILENESITLDWMFRYSLINDIVKGMFLPHNG 750
gi |6981280|ref |NP_036745.1| QPSS-----LERHLRSAGSRLILSGRSNYG---SLLITTEG--QFVFAKTAAYKGNLVAVKRVNRKRIELTRKVLFLKHMARDVNEHLTRFVGACDPP---NICILTEYCPRGSLDILENESITLDWMFRYSLINDIVKGMFLPHNG 750
gi |73961665|ref |XP_547577.2| QPSS-----LERHLRSAGSRLILSGRSNYG---SLLITTEG--QFVFAKTAAYKGNLVAVKRVNRKRIELTRKVLFLKHMARDVNEHLTRFVGACDPP---NICILTEYCPRGSLDILENESITLDWMFRYSLINDIVKGMFLPHNG 750
gi |194665089|ref |XP_612318.3| QPSS-----LERHLRSAGSRLILSGRSNYG---SLLITTEG--QFVFAKTAAYKGNLVAVKRVNRKRIELTRKVLFLKHMARDVNEHLTRFVGACDPP---NICILTEYCPRGSLDILENESITLDWMFRYSLINDIVKGMFLPHNG 750
gi |167830411|ref |NP_000897.3| QPSS-----LERHLRSAGSRLILSGRSNYG---SLLITTEG--QFVFAKTAAYKGNLVAVKRVNRKRIELTRKVLFLKHMARDVNEHLTRFVGACDPP---NICILTEYCPRGSLDILENESITLDWMFRYSLINDIVKGMFLPHNG 750
gi |113678661|ref |NP_001038402.1| QMSN-----TEKVLRRACKSLILSGRSNYG---SLLITTEG--NFCIYAKTYGKGNITAIKYVNRKRIELTRKVLFLKHMARDVNEHLTRFVGACDPP---NICILTEYCPRGSLDILENESITLDWMFRYSLINDIVKGMFLPHNG 750
gi |221330468|ref |NP_726013.2| LIEMGCMFGSKGGLQRLDVENISLQDFGLHSGRASIAFSTSLPPVYITIGQFKGERVAIKKVVKKVVDLTPQLLWEIKQARDVSHENVRFVGCACIDLPRTVLLITTEYCSRGSLKDVLENEALQDWNFRMSLIHDIVKGMFLPHNG 750
gi |158293450|ref |XP_314790.4| LIEMGCMFGSKGGLQRLDVENISLQDFGLHSGRASIAFSTSLPPVYITIGQFKGERVAIKKVVKKVVDLTPQLLWEIKQARDVSHENVRFVGCACIDLPRTVLLITTEYCSRGSLKDVLENEALQDWNFRMSLIHDIVKGMFLPHNG 750
gi |118104469|ref |XP_429192.2| KQDHILWAKGVMSPGPPAEPSENASCTIRLSSCAAANAS--KKQHFOTQGRYDGRVAIKKIMKKAFTLSKIRVEIKQARDVSHENVRFVGCACIDLPRTVLLITTEYCSRGSLKDVLENEALQDWNFRMSLIHDIVKGMFLPHNG 750
.....610.....620.....630.....640.....650.....660.....670.....680.....690.....700.....710.....720.....730.....740.....750



