

gi | 18858477 | ref | NP_571747.1 | MFFA---LLFLIGILGQVQG---WSEPRIRLSSGALACTDVLVLESGSPLQLVCEGDGPVTFPLRLAKHKRYIKVEVGRKIRFRVEKLTVDFTGTYKCVYMNQNSN 150
gi | 189542982 | ref | XP_001918812.1 | -----GAPVIEPS-----GPVLVVEPGEIVTLRCVNSGVSVEWDGPIIPYWLDPESPFGSTLITR--NATFKNTGTYRCTLEEDPMAG 150
gi | 126723423 | ref | NP_001032948.2 | MELG---PPLVLLLA---VWHG---GAPVIEPS-----GPVLVVEPGEIVTLRCVNSGVSVEWDGPIIPYWLDPESPFGSTLITR--NATFKNTGTYRCTLEEDPMAG 150
gi | 71361659 | ref | NP_001025072.1 | MELG---APLVLLLA---AWHGCVILSGEKSRITTIHIYLLAGRRAVTEIIVLMGQRSTDVQRVNDG---GAPVIEPS-----GPVLVVEPGEIVTLRCVNSGVSVEWDGPIIPYWLDPESPFGSTLITR--NATFKNTGTYRCTLEEDPMAG 150
gi | 73954200 | ref | XP_546306.2 | MGLG---APLVLLVA---AWHV---RGVPIEPR-----GPVLVVEPGEIVTLRCVNSGVSVEWDGPIIPYWLDPESPFGSTLITR--NATFKNTGTYRCTLEEDPMAG 150
gi | 115495211 | ref | NP_001068871.1 | MGPR---LILLILLVVA---AWHG---GVPVIEPS-----GPVLVVEPGEIVTLRCVNSGVSVEWDGPIIPYWLDPESPFGSTLITR--NATFKNTGTYRCTLEEDPMAG 150
gi | 27262659 | ref | NP_005202.2 | MGPG---VLLLLLVA---AWHG---GVPVIEPS-----GPVLVVEPGEIVTLRCVNSGVSVEWDGPIIPYWLDPESPFGSTLITR--NATFKNTGTYRCTLEEDPMAG 150
gi | 118097472 | ref | XP_414597.2 | MGPGDVGPGLLLLLLTTPAVWHG---SASVIFSD---ISALVNVSDPVLRLCSGSESEVKW---YPEKFNHASSLITLIF--RTHRDGTGTYRCAYINSSDKG 150
gi | 189534206 | ref | XP_001919824.1 | MFDK---EFAAPVVKLNGTPLKDSVVLSANTSEFVLLHCDGQAEIHWKTRRRIRKQNLSEONE---LVVQ---KATAEHTGTYRCYSRSHTDIY 150
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150



gi | 18858477 | ref | NP_571747.1 | LSSSVHVFVRD SRVLFVPSISLRVVRKEGGDLLLPCLLTDPEATDFTFRMDNGSAAFGYGMNIIYDPRKGVLTIRNVHPGFNADYICARIGGAEKVKIFISINIIQLRFRPPYVYLKRNEVVKLVGERLQISCTINPNFYVNVLWTHS 300
gi | 189542982 | ref | XP_001918812.1 | -----STAIHLVVKDPAHSWN---LLAEVTVVEGQEAVALPCLITDPAALKDSVSLMRGGRQVLRKIVVFFSPWRGFIIRKAKVLDSTNTVCKIMVNGRESTTGIWLKVNVRVHPEPPQIKLEPISKLVIRGEGAAQIVCSATNAEVEGPNVILKRG 300
gi | 126723423 | ref | NP_001032948.2 | -----STAIHLVVKDPAHSWN---LLAEVTVVEGQEAVALPCLITDPAALKDSVSLMRGGRQVLRKIVVFFSPWRGFIIRKAKVLDSTNTVCKIMVNGRESTTGIWLKVNVRVHPEPPQIKLEPISKLVIRGEGAAQIVCSATNAEVEGPNVILKRG 300
gi | 71361659 | ref | NP_001025072.1 | -----SAIITHLVVKDPAHSWN---VLAEEVTVVEGQDALLPCLITDPALEAGVSLMRVGRPVLRQINYSFSWPYGFTHKAKFTETQGYCSARVGGRTVTSMGLWLVKQVVIKPPPTLILKPAELVLRVQGEAANLIESASNVVNDVDFLQHE 300
gi | 73954200 | ref | XP_546306.2 | -----SAIITHLVVKDPAHSWN---VLAEEVTVVEGQDALLPCLITDPALEAGVSLMRVGRPVLRQINYSFSWPYGFTHKAKFTETQGYCSARVGGRTVTSMGLWLVKQVVIKPPPTLILKPAELVLRVQGEAANLIESASNVVNDVDFLQHE 300
gi | 115495211 | ref | NP_001068871.1 | -----SAIITHLVVKDPAHSWN---VLAEEVTVVEGQDALLPCLITDPALEAGVSLMRVGRPVLRQINYSFSWPYGFTHKAKFTETQGYCSARVGGRTVTSMGLWLVKQVVIKPPPTLILKPAELVLRVQGEAANLIESASNVVNDVDFLQHE 300
gi | 27262659 | ref | NP_005202.2 | -----SAIITHLVVKDPAHSWN---VLAEEVTVVEGQDALLPCLITDPALEAGVSLMRVGRPVLRQINYSFSWPYGFTHKAKFTETQGYCSARVGGRTVTSMGLWLVKQVVIKPPPTLILKPAELVLRVQGEAANLIESASNVVNDVDFLQHE 300
gi | 118097472 | ref | XP_414597.2 | -----IASVHLVVRDPNPNWY---VLFPRISVIRKGGNAEPPCFITAPEVEAGVSLVLRVGRPLMRHINYSFSWPYGFTHKAKFTETQGYCSARVGGRTVTSMGLWLVKQVVIKPPPTLILKPAELVLRVQGEAANLIESASNVVNDVDFLQHE 300
gi | 189534206 | ref | XP_001919824.1 | -----SEIHLVVKDPAHSWN---SQLRVIVIKEGSSFLLDCLLNP-AGTEFSLQMTNGSAVPPGMNYADPRRGILIPNLQPSYIGDYVCMVNSGVIKWKVVFQITVIKKAQEPSPVSLPALQVIRVIGESLIPYICQHNHYVNFVWSSP 300
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300



gi | 18858477 | ref | NP_571747.1 | SRMLPK-AEEKSTMEGDRLAIESILIFSVQLSHGNIITCTGQNEAGANBSTIQLLVVEEPIYRLSPKLSKLTIRHGLSIEVEGDDVLDGLVLEAYPPLTSEKWEPTSHNASLP---ENRFFNHNDRYEALLLLKRLNFEIEIGQYTL 450
gi | 189542982 | ref | XP_001918812.1 | -----DTKLE--IPLNSDFODNYKVKRALSLNAVDFODAGIYSCVANSNDVGTIRATMNFQVVEASAYLNLITSEOS-----LLEQVSVGNSLITVHADAYPSIHYNWTYLGPPFFEDR--KLEFIQRAIVRYTFKLVLRNVRKAEAGQVFL 450
gi | 126723423 | ref | NP_001032948.2 | -----DTKLE--IPLNSDFODNYKVKRALSLNAVDFODAGIYSCVANSNDVGTIRATMNFQVVEASAYLNLITSEOS-----LLEQVSVGNSLITVHADAYPSIHYNWTYLGPPFFEDR--KLEFIQRAIVRYTFKLVLRNVRKAEAGQVFL 450
gi | 71361659 | ref | NP_001025072.1 | -----DTKLE--IPLNSDFODNYKVKRALSLNAVDFODAGIYSCVANSNDVGTIRATMNFQVVEASAYLNLITSEOS-----LLEQVSVGNSLITVHADAYPSIHYNWTYLGPPFFEDR--KLEFIQRAIVRYTFKLVLRNVRKAEAGQVFL 450
gi | 73954200 | ref | XP_546306.2 | -----DTKLE--IPLNSDFODNYKVKRALSLNAVDFODAGIYSCVANSNDVGTIRATMNFQVVEASAYLNLITSEOS-----LLEQVSVGNSLITVHADAYPSIHYNWTYLGPPFFEDR--KLEFIQRAIVRYTFKLVLRNVRKAEAGQVFL 450
gi | 115495211 | ref | NP_001068871.1 | -----DTKLA--ISQCSDFRDNRYQKVLTELELDVVGODAGNYTCVATNARGVISTSMIFRVVESAAYLNLITSEOS-----LLEQVAVGKELRVLKVEAYPSLQSFNWTYEGPFFGSP--KLNFEITNNRYVYTKLTLRKLKPEAGRYSE 450
gi | 27262659 | ref | NP_005202.2 | -----DTKLA--ISQCSDFRDNRYQKVLTELELDVVGODAGNYTCVATNARGVISTSMIFRVVESAAYLNLITSEOS-----LLEQVAVGKELRVLKVEAYPSLQSFNWTYEGPFFGSP--KLNFEITNNRYVYTKLTLRKLKPEAGRYSE 450
gi | 118097472 | ref | XP_414597.2 | -----NPKLA--IPLQCSDFHNNRYQKVLTELELDVVGODAGNYTCVATNARGVISTSMIFRVVESAAYLNLITSEOS-----LIQEVTVGELNKLQVHIEAYPKLILHWHHEHDSLKNSSGN--KLNSEMVPEKNNVNNLFDLHLEGEERGLYTF 450
gi | 189534206 | ref | XP_001919824.1 | -----TKSVK--SNGKPDIDYQYIINDLIPAVTMEBSGKTCIANNSAGFRNASMLRVRVREGVILVPLQAA--INQVEAGDSPLKLQVHIEAYPKLILHWHHEHDSLKNSSGN--KLNSEMVPEKNNVNNLFDLHLEGEERGLYTF 450
KVVLFNPREIKKKKKCEQVCAIYLLFQQLKMSDTEMLTCTAMNEAGRNBSIAVLRVVEKPYLELPTLSSVYKGNENNVVRMHGQDELGVHIDAYPDVEAWKWKPPSNHSYSET---FHKIHDIDIMAIRLKNVGAQDYGDYIF 450
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450



gi | 18858477 | ref | NP_571747.1 | NVKNSMKSASITFDIKMYKPVARVKWENVT---LSCRSYGYPAISILWYQCTGIRTTCPENTDLOPIQIQTVEFOKE-SFGAVGVESVLTVGP-NRRMTIVCVAFNLVCGQSDIFS-----MEVSDQIFISAMCGSTVAMVVLG 600
gi | 189542982 | ref | XP_001918812.1 | -----MAQNKAGWNNLTFELTLRYPPVEVSVTWMPVNGSDVLFCDVSGYPOPSVTWMECRGHTDRCDDEAQAQVWVNDTHPEVLSQR--PFDKVVIISQLPIGTLKHNMTYVCKTHNSVGNSSQVFRVAVSLGQSKQLPDESLFPTVVVACSVMSLLV 600
gi | 126723423 | ref | NP_001032948.2 | -----MAQNKAGWNNLTFELTLRYPPVEVSVTWMPVNGSDVLFCDVSGYPOPSVTWMECRGHTDRCDDEAQAQVWVNDTHPEVLSQR--PFDKVVIISQLPIGTLKHNMTYVCKTHNSVGNSSQVFRVAVSLGQSKQLPDESLFPTVVVACSVMSLLV 600
gi | 71361659 | ref | NP_001025072.1 | -----LARNRGGDSLTFELTLRYPPVEVSVTWMPVNGSDVLFCDVSGYPOPSVTWMECRGHTDRCDDEAQAQVWVNDTHPEVLSQR--PFDKVVIISQLPIGTLKHNMTYVCKTHNSVGNSSQVFRVAVSLGQSKQLPDESLFPTVVVACSVMSLLV 600
gi | 73954200 | ref | XP_546306.2 | -----LARNRGGDSLTFELTLRYPPVEVSVTWMPVNGSDVLFCDVSGYPOPSVTWMECRGHTDRCDDEAQAQVWVNDTHPEVLSQR--PFDKVVIISQLPIGTLKHNMTYVCKTHNSVGNSSQVFRVAVSLGQSKQLPDESLFPTVVVACSVMSLLV 600
gi | 115495211 | ref | NP_001068871.1 | -----QARNARGEDLTFELTLRYPPVEVSVTWMPVNGSDVLFCDVSGYPOPSVTWMECRGHTDRCDDEAQAQVWVNDTHPEVLSQR--PFDKVVIISQLPIGTLKHNMTYVCKTHNSVGNSSQVFRVAVSLGQSKQLPDESLFPTVVVACSVMSLLV 600
gi | 27262659 | ref | NP_005202.2 | -----LARNRGGDSLTFELTLRYPPVEVSVTWMPVNGSDVLFCDVSGYPOPSVTWMECRGHTDRCDDEAQAQVWVNDTHPEVLSQR--PFDKVVIISQLPIGTLKHNMTYVCKTHNSVGNSSQVFRVAVSLGQSKQLPDESLFPTVVVACSVMSLLV 600
gi | 118097472 | ref | XP_414597.2 | -----LARNRGGDSLTFELTLRYPPVEVSVTWMPVNGSDVLFCDVSGYPOPSVTWMECRGHTDRCDDEAQAQVWVNDTHPEVLSQR--PFDKVVIISQLPIGTLKHNMTYVCKTHNSVGNSSQVFRVAVSLGQSKQLPDESLFPTVVVACSVMSLLV 600
gi | 189534206 | ref | XP_001919824.1 | -----SAGSISVNASIIFVHVYQKPTIVIKWEN---GVVSGAAGYPIPIISNFOQVNRALGSDNR--SGVELMANQISIEGSEGEPEPVLKPSALPETINADLIFECVATNAGDDCDFYTFISGPRPSTVQST--VLSLISGALSVAIT 600
.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600



gi | 18858477 | ref | NP_571747.1 | LLLIFMIYKYKOKPKYQVRWKIIEAINGNNYTFIDPTQLPNEYKWEFPRDKLKGKTLGAGAFGKVVEATAYGLGKEDNITRVAVKMLKASAHPPDEREALMSLKLIMSHLGHQHNIVNLLGACTHGGPVLVITEYCCYGDLLNFLRRAE 750
gi | 189542982 | ref | XP_001918812.1 | -----LLLIFMIYKYKOKPKYQVRWKIIEAINGNNYTFIDPTQLPNEYKWEFPRDKLKGKTLGAGAFGKVVEATAYGLGKEDNITRVAVKMLKASAHPPDEREALMSLKLIMSHLGHQHNIVNLLGACTHGGPVLVITEYCCYGDLLNFLRRAE 750
gi | 126723423 | ref | NP_001032948.2 | -----LLLIFMIYKYKOKPKYQVRWKIIEAINGNNYTFIDPTQLPNEYKWEFPRDKLKGKTLGAGAFGKVVEATAYGLGKEDNITRVAVKMLKASAHPPDEREALMSLKLIMSHLGHQHNIVNLLGACTHGGPVLVITEYCCYGDLLNFLRRAE 750
gi | 71361659 | ref | NP_001025072.1 | -----LLLIFMIYKYKOKPKYQVRWKIIEAINGNNYTFIDPTQLPNEYKWEFPRDKLKGKTLGAGAFGKVVEATAYGLGKEDNITRVAVKMLKASAHPPDEREALMSLKLIMSHLGHQHNIVNLLGACTHGGPVLVITEYCCYGDLLNFLRRAE 750
gi | 73954200 | ref | XP_546306.2 | -----LLLIFMIYKYKOKPKYQVRWKIIEAINGNNYTFIDPTQLPNEYKWEFPRDKLKGKTLGAGAFGKVVEATAYGLGKEDNITRVAVKMLKASAHPPDEREALMSLKLIMSHLGHQHNIVNLLGACTHGGPVLVITEYCCYGDLLNFLRRAE 750
gi | 115495211 | ref | NP_001068871.1 | -----LLLIFMIYKYKOKPKYQVRWKIIEAINGNNYTFIDPTQLPNEYKWEFPRDKLKGKTLGAGAFGKVVEATAYGLGKEDNITRVAVKMLKASAHPPDEREALMSLKLIMSHLGHQHNIVNLLGACTHGGPVLVITEYCCYGDLLNFLRRAE 750
gi | 27262659 | ref | NP_005202.2 | -----LLLIFMIYKYKOKPKYQVRWKIIEAINGNNYTFIDPTQLPNEYKWEFPRDKLKGKTLGAGAFGKVVEATAYGLGKEDNITRVAVKMLKASAHPPDEREALMSLKLIMSHLGHQHNIVNLLGACTHGGPVLVITEYCCYGDLLNFLRRAE 750
gi | 118097472 | ref | XP_414597.2 | -----LLLIFMIYKYKOKPKYQVRWKIIEAINGNNYTFIDPTQLPNEYKWEFPRDKLKGKTLGAGAFGKVVEATAYGLGKEDNITRVAVKMLKASAHPPDEREALMSLKLIMSHLGHQHNIVNLLGACTHGGPVLVITEYCCYGDLLNFLRRAE 750
gi | 189534206 | ref | XP_001919824.1 | -----LWMLLILLYKRNKAQKYEIQKIIIVNDGNNYTFIDPTQLPNEYKWEFPRDKLKGKTLGAGAFGKVVEATAYGLGKEDNITRVAVKMLKASAHPPDEREALMSLKLIMSHLGHQHNIVNLLGACTHGGPVLVITEYCCYGDLLNFLRRAE 750
.....610.....620.....630.....640.....650.....660.....670.....680.....690.....700.....710.....720.....730.....740.....750



