

gi | 4502719 | ref | NP_001248.1 | MOPRTPPLVLCVLLSQVLLLSAEDLDCTPGFQOKVFHINQPAEFIEDOSILNLTFSDCXGNDKLRTEVSSPYFKVNSDGLVALRNIITAVGKTLFVHARTPHAEDMAELVIVGGKDIOG-SLQDIFKFARTSPVPRKRSIVVSPILPE 149
gi | 114663843 | ref | XP_001149841.1 | MOPRTPPLVLCVLLSQVLLLSAEDLDCTPGFQOKVFHINQPAEFIEDOSILNLTFSDCXGNDKLRTEVSSPYFKVNSDGLVALRNIITAVGKTLFVHARTPHAEDMAELVIVGGKDIOG-SLQDIFKFARTSPVPRKRSIVVSPILPE 149
gi | 78369244 | ref | NP_001030354.1 | MOPATPLVLCVLLSQVLLLSAEDLDCTPGFQOKVFHIDQPAEFIEDOAILNLTFSDCXGNDKLRTEVSSPYFRVNTDGLVALRNIITAVGKTLFVHARTPHAEDMAELVIVGGKDIOG-SLQDIFKFARTSPVPRKRSIVVSPILPE 149
gi | 110625609 | ref | NP_062681.2 | MOPRTPPLVLCVLLSQVLLLSAEDLDCTPGFQOKVFHINQPAEFIEDOPVNLNLTFSDCXGNDKLRTEVSSPYFKVNSDGLVALRNIITAVGKTLFVHARTPHAEDMAELVIVGGKDIOG-SLQDIFKFARTSPVPRKRSIVVSPILPE 149
gi | 20302073 | ref | NP_620244.1 | MOPRTPPLVLCVLLSQVLLLSAEDLDCTPGFQOKVFHINQPAEFIEDOPVNLNLTFSDCXGNDKLRTEVSSPYFKVNSDGLVALRNIITAVGKTLFVHARTPHAEDMAELVIVGGKDIOG-SLQDIFKFARTSPVPRKRSIVVSPILPE 149
gi | 73957267 | ref | XP_546809.2 | -----MQVEIYGIRES-----HHSAAFKKEA---GVTFSDCKGNKLLHYEVSSPYFKVNSDGLVALRNIITAVGKTLFVHARTPHAEDMAELVIVGGKDIOG-SLQDIFKFARTSPVPRKRSIVVSPILPE 119
gi | 48976117 | ref | NP_001001760.1 | MQHKQLTSLFLLSQVLLLSAEDLDCTPGFQOKVFYIEQPFETEDQPLNLTFSDCXGNDKLRTEVSSPYFKVNSDGLVALRNIITAVGKTLFVHARTPHAEDMAELVIVGGKDIOG-SLQDIFKFARTSPVPRKRSIVVSPILPE 149
gi | 189531641 | ref | XP_687082.3 | -----MDSIMVLCIQAQDEKKEVCEVPGQOKEVQVEYSGGFLKVLQVDFDDCAGNEDEFEVSNPNFLLELNLVPRRVDVIGDFMVFVGVNIIHVDDMAIILIGAPSRSPQLREILGSDMSY-RSKRLIVVPMPIE 142
1-----10-----20-----30-----40-----50-----60-----70-----80-----90-----100-----110-----120-----130-----140-----150



gi | 4502719 | ref | NP_001248.1 | NORQPPFRDVGKVVSDRPERSKFRLLTGKGVDOEPKGIIFRINENTGVSVTRILDREVIAYQLFVEITDVNGKILEGPPLELVIVIDQNDNRPIFREGPYIGHVMEGSPGTIVMRMTAFDADDPADNALLRYNIRQOTPKPSPNMF 299
gi | 114663843 | ref | XP_001149841.1 | NORQPPFRDVGKVVSDRPERSKFRLLTGKGVDOEPKGIIFRINENTGVSVTRILDREVIAYQLFVEITDVNGKILEGPPLELVIVIDQNDNRPIFREGPYIGHVMEGSPGTIVMRMTAFDADDPADNALLRYNIRQOTPKPSPNMF 299
gi | 78369244 | ref | NP_001030354.1 | NORQPPFRDVGKVVSDRPERSGKFRLLTGKGVDOEPKGIIFRINENTGVSVTRILDREVIAYQLFVEITDVNGKILEGPPLELVIVIDQNDNRPIFREGPYIGHVMEGSPGTIVMRMTAFDADDPADNALLRYNIRQOTPKPSPNMF 299
gi | 110625609 | ref | NP_062681.2 | NORQPPFRDVGKVVSDRPERSGKFRLLTGKGVDOEPKGIIFRINENTGVSVTRILDREVIAYQLFVEITDVNGKILEGPPLELVIVIDQNDNRPIFREGPYIGHVMEGSPGTIVMRMTAFDADDPADNALLRYNIRQOTPKPSPNMF 299
gi | 20302073 | ref | NP_620244.1 | NORQPPFRDVGKVVSDRPERSGKFRLLTGKGVDOEPKGIIFRINENTGVSVTRILDREVIAYQLFVEITDVNGKILEGPPLELVIVIDQNDNRPIFREGPYIGHVMEGSPGTIVMRMTAFDADDPADNALLRYNIRQOTPKPSPNMF 299
gi | 73957267 | ref | XP_546809.2 | NORQPPFRDVGKVVSDRPERSGKFRLLTGKGVDOEPKGIIFRINENTGVSVTRILDREVIAYQLFVEITDVNGKILEGPPLELVIVIDQNDNRPIFREGPYIGHVMEGSPGTIVMRMTAFDADDPADNALLRYNIRQOTPKPSPNMF 269
gi | 48976117 | ref | NP_001001760.1 | NORPPFRSVDGKVVSDRPERSGKFRLLTGKGVDOEPKGIIFRINENTGVSVTRILDREVIAYQLFVEITDVNGKILEGPPLELVIVIDQNDNRPIFREGPYIGHVMEGSPGTIVMRMTAFDADDPADNALLRYNIRQOTPKPSPNMF 299
gi | 189531641 | ref | XP_687082.3 | NORAPFRRLIGKVVSSDMKEHFHFRLLTGKGVDOEPKGVFSINRLSGDVAVSRALDREALAYHQLQVSTDLISGKLVGPPVLDLVSVIDQNDNRPIFREKPRYSGEVLRGSPGTIVMRMTAFDADDPADNALLRYNIRQOTPKPSPNMF 292
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300



gi | 4502719 | ref | NP_001248.1 | YIDPEKGDIVTVVSPALLDREITLENPKYELIIEAQMAGLVDGLTGATATIMIDDKNDHSPKFKKEFOATVEEGAVGIVNLTVEDKDDPPTGAWRAAYTIINGNPGQSFETHNPQINEGMLSVVKPLDYEISAFHLLIKVENEDP 449
gi | 114663843 | ref | XP_001149841.1 | YIDPEKGDIVTVVSPALLDREITLENPKYELIIEAQMAGLVDGLTGATATIMIDDKNDHSPKFKKEFOATVEEGAVGIVNLTVEDKDDPPTGAWRAAYTIINGNPGQSFETHNPQINEGMLSVVKPLDYEISAFHLLIKVENEDP 449
gi | 78369244 | ref | NP_001030354.1 | YIDPEKGDIVTVVSPALLDREITLENPKYELIIEAQMAGLVDGLTGATATIMIDDKNDHSPKFKKEFOATVEEGAVGIVNLTVEDKDDPPTGAWRAAYTIINGNPGQSFETHNPQINEGMLSVVKPLDYEISAFHLLIKVENEDP 449
gi | 110625609 | ref | NP_062681.2 | YIDPEKGDIVTVVSPALLDREITLENPKYELIIEAQMAGLVDGLTGATATIMIDDKNDHSPKFKKEFOATVEEGAVGIVNLTVEDKDDPPTGAWRAAYTIINGNPGQSFETHNPQINEGMLSVVKPLDYEISAFHLLIKVENEDP 449
gi | 20302073 | ref | NP_620244.1 | YIDPEKGDIVTVVSPALLDREITLENPKYELIIEAQMAGLVDGLTGATATIMIDDKNDHSPKFKKEFOATVEEGAVGIVNLTVEDKDDPPTGAWRAAYTIINGNPGQSFETHNPQINEGMLSVVKPLDYEISAFHLLIKVENEDP 419
gi | 73957267 | ref | XP_546809.2 | YIDPEKGDIVTVVSPALLDREITLENPKYELIIEAQMAGLVDGLTGATATIMIDDKNDHSPKFKKEFOATVEEGAVGIVNLTVEDKDDPPTGAWRAAYTIINGNPGQSFETHNPQINEGMLSVVKPLDYEISAFHLLIKVENEDP 449
gi | 48976117 | ref | NP_001001760.1 | YIDPEKGDIVTVVSPVLLDREITMETPKYELVIEAKDMGGHDVGLTGATATILIDDKNDHPEFKKEFOATVEEGAVGIVNLTVEDKDDPPTGAWRAAYTIINGNPGQSFETHNPQINEGMLSVVKPLDYEISAFHLLIKVENEDP 449
gi | 189531641 | ref | XP_687082.3 | YIDPERGDIVTVIAPQLDREITLPTTQVLEIIVAKDMAGSEVGLTGATATIIITDRNDHAFEPHSLFQASVNEGSTGVVNLTVDDRDPATGAWRAAYTIINGNPGQSFETHNPQINEGMLSVVKPLDYEISAFHLLIKVENEDP 442
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450



gi | 4502719 | ref | NP_001248.1 | LVPDVSYGPSSTAVVHITVLDVNEGPFVFPDPMVTRQEDLSVGSVLLTVNADDPDSLQHOIIRYSVYKDPAGWLNINPINGVTDITAVLDRESPPFVNSVYALFLAIDSGNPPATGCTGLLITLEDVNDNAPFIPTVAEVCDDAKNL 599
gi | 114663843 | ref | XP_001149841.1 | LVPDVSYGPSSTAVVHITVLDVNEGPFVFPDPMVTRQEDLSVGSVLLTVNADDPDSLQHOIIRYSVYKDPAGWLNINPINGVTDITAVLDRESPPFVNSVYALFLAIDSGNPPATGCTGLLITLEDVNDNAPFIPTVAEVCDDAKNL 599
gi | 78369244 | ref | NP_001030354.1 | LVPDVSYGPSSTAVVHITVLDANESPVFVFPDPMVTKQENISVGSVLLTVNADDPDSLQHOIIRYSVYKDPAGWLNINPINGVTDITALLDRESPPFVNSVYALFLAIDSGNPPATGCTGLLITLEDVNDNAPFIPTVAEVCDDAKNL 599
gi | 110625609 | ref | NP_062681.2 | LVPDVSYGPSSTAVVHITVLDVNEGPFVFPDPMVTKQENISVGSVLLTVNADDPDSLQHOIIRYSVYKDPAGWLNINPINGVTDITAVLDRESPPFVNSVYALFLAIDSGNPPATGCTGLLITLEDVNDNAPFIPTVAEVCDDARNL 599
gi | 20302073 | ref | NP_620244.1 | LVPDVSYGPSSTAVVHITVLDVNEGPFVFPDPMVTKQENISVGSVLLTVNADDPDSLQHOIIRYSVYKDPAGWLNINPINGVTDITAVLDRESPPFVNSVYALFLAIDSGNPPATGCTGLLITLEDVNDNAPFIPTVAEVCDDARNL 599
gi | 73957267 | ref | XP_546809.2 | LVPDVSYGPSSTAVVHITVLDVNEGPFVFPDPMVTKQENISVGSVLLTVNADDPDSLQHOIIRYSVYKDPAGWLNINPINGVTDITAVLDRESPPFVNSVYALFLAIDSGNPPATGCTGLLITLEDVNDNAPFIPTVAEVCDDAKNL 569
gi | 48976117 | ref | NP_001001760.1 | LIPDIAYGPSSTAVVITVEDVNEGPFVFPDPMVTKQENIPGSIIVLTVNADDPDSLQHOIIRYSVYKDPASWLNINPINGVTDITAVLDRESPPHVDNRYTALFLAIDSGNPPATGCTGLLITLEDVNDNAPFIPTVAEVCDDAKDL 599
gi | 189531641 | ref | XP_687082.3 | LVPDIVYGPSSTAVVITVLDVNEGPFVFPDPLVIRRENIPGSEFVAMNADDPDYLQSIRFAVLRDPADWLVNPKGNVTIRAILDRESPPHVDNRYTALFLAIDSGNPPATGCTGLLITLEDVNDNAPFIPTVAEVCDDAKDM 592
.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600



gi | 4502719 | ref | NP_001248.1 | SVVILGASDKDLHPNTDPFKFEIHKQAVDPKVKIKSKINNTHALVSLLOLNKANYNLPIMVTDGKPPMNIIDLRVQVCSCKNSKVCNAGALRFSLPSVLLLSLFLACL---- 713
gi | 114663843 | ref | XP_001149841.1 | SVVILGASDKDLHPNTDPFKFEIHKQAVDPKVKIKSKINNTHALVSLLOLNKANYNLPIMVTDGKPPMNIIDLRVQVCSCKNSKVCNAGALRFSLPSVLLLSLFLACL---- 713
gi | 78369244 | ref | NP_001030354.1 | SVVILGADKDLHPNTDPFKFEIHKQAVDPKVKIKSKINNTHALVSLLOLNKANYNLPIMVTDGKPPMNIIDLRVQVCSCKNSKVCNAGALRFSLPSVLLLSLFLACL---- 713
gi | 110625609 | ref | NP_062681.2 | SVVILGASDKDLHPNTDPFKFEIHKQAVDPKVKIKSKINNTHALVSLLOLNKANYNLPIMVTDGKPPMNIIDLRVQVCSCKNSKVCNAGALRFSLPSVLLLSLFLACL---- 714
gi | 20302073 | ref | NP_620244.1 | SVVILGASDKDLHPNTDPFKFEIHKQAVDPKVKIKSKINNTHALVSLLOLNKANYNLPIMVTDGKPPMNIIDLRVQVCSCKNSKVCNAGALRFSLPSVLLLSLFLACL---- 714
gi | 73957267 | ref | XP_546809.2 | SVVILGASDKDLHPNTDPFKFEIHKQAVDPKVKIKSKINNTHALVSLLOLNKANYNLPIMVTDGKPPMNIIDLRVQVCSCKNSKVCNAGALRFSLPSVLLLSLFLACL---- 683
gi | 48976117 | ref | NP_001001760.1 | RVVILGASDKDLHPNTDPFKFELSKQSGPEKILWRINKLNTHALVSLLOLNKANYNLPISVTDGKPPMNIIDLRVQVCSCKNSKVCNAGALRFSLPSVLLLSLFLACL---- 717
gi | 189531641 | ref | XP_687082.3 | NVVILGGRDKDIRNTPDFKIELGKQGLKPKWIKSRINDTHSQIMLLHSLKANYNLPVLDVSGVPPISNNIELKVOVCTCKNRMDCSRAASVQINVLVLLGLLILCL---- 706
.....610.....620.....630.....640.....650.....660.....670.....680.....690.....700.....710.....

