

gi | 289629261 | ref | NP_001164491.1 | MESEYVLCNWKDLWPAKVLRSRSETSNKRKKAFLSLEVOILSLDEKIKLSDTETKILNKSQIEAIAASLGLQSEDAPPPEETAYGRSLKVALGILNERTNLSQASTSDEBEITMLSONVPOKQSDSPPHKKYRKDEG---DLPGLCEE 147
gi | 114689712 | ref | XP_001142672.1 | MESEYVLCNWKDLWPAKVLRSRSETSNKRKKAFLSLEVOILSLDEKIKLSDTETKILNKSQIEAIAASLGLQSEDAPPPEETAYGRSLKVALGILNERTNLSQASTSDEBEITMLSONVPOKQSDSPPHKKYRKDEG---DLPGLCEE 147
gi | 74008509 | ref | XP_852784.1 | MEAEYVLCNWKDLWPAKVLRSRSETSNKRKKAFLSLEVOILSLDEKIKVVESTAKILSKSQIEAALASSLAAQSEGLDPIEETAYERSLKVALLDILNERTNVQASSSDEEATTLSONDPOKLSDSPPRKKYRKHEGEGDGLKCPPE 150
gi | 119923736 | ref | XP_586767.3 | MDAEYVLCNWQDLWPAKVLRSSEASSNKRKKAFLSLEVOILSLDEKIQMESTETKILNKSQVEAIAASSLAAQSEVDPPEETAYERSLKMALDILNERTNLIQVSSSDEEETILSONIPKQPSDPPRKKYRKHEG---EGDLPKCLEE 149
gi | 29789431 | ref | NP_780750.1 | -----MALEMVKEGTLNLSQESMSEEPATASENVPEQPPDPPPHKKFRKLES-----NT 50
gi | 109511143 | ref | XP_577028.2 | MDGEYVLCGWKDLWPAKVLDRSESPDSSKRKKLTSVEVEILSLDEKIVESKDTKVLKSAVEAIMSSLTVOSEVFTPEETAYERSLKMALDILNERTNLIQVSSSDEEETILSONIPKQPSDPPHKKFRKLES-----NL 141
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150



gi | 289629261 | ref | NP_001164491.1 | RENSAACLLAS--SEDDSLYDDKSOAPTMDVTLPSVEVTKSLQNSWCEVTPPSLSEDNDEKKNKIDISAVMSVHSAVKEESACVCKDEKFAFPLSPLSSDMLIMPALKKEESEDTCLELILAVPSECSAFSEN--IEDPGEGPSN--PCLD 292
gi | 114689712 | ref | XP_001142672.1 | RENSAACLLAS--SEDDSLYDDKSOAPTMDVTLPSVEVTKSLQNSWCEVTPPSLSEDNDEKKNKIVISAVMSVHSAVKEESACVCKDEKFAFPLSPLSSDMLIMPALKKEESEDTCLELILAVPSECSAFSEN--IEDPGEGPSN--PCLD 292
gi | 74008509 | ref | XP_852784.1 | SENAAALLVAVLENNDQYDDKSOVHATIDALPSEMETKLEENPWCEVTPPSLSEDDDEKESKKKIDISTIMPLHSTIKKEEDAVIKDEKFTPLLL---SDFTVVPKAVKEETPDVCPETM--AVSTESSTFSEN--IEDPGEGPSN--PCSD 293
gi | 119923736 | ref | XP_586767.3 | NENSTILLVSE--SEDDSLDDDKSOVHAMIDNIPNETETKSONLSWCQVTPPSLLEDEDEKESKKKIDLS--ILPLLSITKEEDVYVKEEFKSPPLP---SDGFTVVPKALKEEPEIDVPEAL--AASSECFAFSEN--IEDPGEGPSN--PCSV 290
gi | 29789431 | ref | NP_780750.1 | QSDSASILLC--SEDDSMTDKLVQVHTTGESMPSMDTKATEENLGCCTDPSLADDDDKKEKKKIDISAIMSVNLSLKEESEYIKKEEFVPSSE-----DLTVP---KEESQDILPEAPLAVSSECSIVSENNMEDPGEGPSNONLVSY 191
gi | 109511143 | ref | XP_577028.2 | QSDSASMLLC--SEDDSLSEKLVQVHTTSENMPSEVEMKS--ENLSCCOTVPSFSDDDDKKEKKKIDISAIMSVNLSLKEESEYIKKEEFVPSSE-----DLVAVP---KEESQDILPEAPLAVSSECFIVSENNMEDPGEGPSNONLVSY 280
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300



gi | 289629261 | ref | NP_001164491.1 | TSONQPSMSEEMGAAACPGSCSRECEVFSASNPVWDYSHLMSERNFORLDFEELBEEGQASDKSLSPRINLSLLDDDEED--EELPRFILHYETHPFETGMIVWFYKQKYPFWPAVIKSIIRKERRKASVLLVPEANMNSSEKKGIRVNF 440
gi | 114689712 | ref | XP_001142672.1 | TSONQPSMSEEMGAAACPGSCSRECEVFSASNPVWDYSHLMSERNFORLDFEELBEEGQASDKSLSPRINLSLLDDDEED--EELPRFILHYETHPFETGMIVWFYKQKYPFWPAVIKSIIRKERRKASVLLVPEANMNSSEKKGIRVNF 440
gi | 74008509 | ref | XP_852784.1 | TSONQP--VEEAGISASSQPCSECCVFSASNHALDYSLLVNNERLQRLDFEELGEELOASDKSAQVNSLS--ILDDNEED--EELPRFVFNVEPRSFETGMIVWFYKQKYPFWPAVVIKSIIRKERRKASVLLVPEANMNEKRGIRVNF 439
gi | 119923736 | ref | XP_586767.3 | ASONQP--VEEEMDAEAFQPPSSQEQVFSASNSHSSGDDYSLLSGNSERNLQRLDFEELGEELOASDKSARISIAAAILDDDEED--EELPRFVFNVEPRSFETGMIVWFYKQKYPFWPAVVIKSIIRKERRKASVLLVPEANMNEKRGIRVNF 438
gi | 29789431 | ref | NP_780750.1 | ANQNSVSESDVGAETSTAGCSGDFVSLPRD-----IVNSDLLLQRLDLEDEBEARASGKLLSLNPACAAALENDDDDDELPRFILRYETRAFETGMIVWFYKQKYPFWPAVIKSIIRKERRKASVLLVPEADMSPQKKGVRVSL 334
gi | 109511143 | ref | XP_577028.2 | GSGSSTVSESDVGAETSTAGCSGDFVSLPRD-----IVNSDLLLQRLDLEDEBEARASGKLLSLNPACAAALENDDDDDELPRFILRYETRAFETGMIVWFYKQKYPFWPAVIKSIIRKERRKASVLLVPEADMSPQKKGVRVSL 423
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450



gi | 289629261 | ref | NP_001164491.1 | RRLKKFDCKEKQMLVDKAREDYSESIDWCISLICYRVRIGCGSFTGSLLEYAADISYVPRKKEKQDIFRNKFKPLHNEEDAREPMAVTSQTKKMSFQKILPDRMKAARDRANKNLVDFIVNAKGTENHLLAIVNGTKGSRWLKSFNLNA 590
gi | 114689712 | ref | XP_001142672.1 | RRLKKFDCKEKQMLVDKAREDYSESIDWCISLICYRVRIGCGSFTGSLLEYAADISYVPRKKEKQDIFRNKFKPLHNEEDAREPMAVTSQTKKMSFQKILPDRMKAARDRANKNLVDFIVNAKGTENHLLAIVNGTKGSRWLKSFNLNA 590
gi | 74008509 | ref | XP_852784.1 | RRLKKFDCKEKQALVEKAREDYSESIDWCISLICYRVRIGCGSFTGSLLEYAADISYVPRKKEKQDIFRNKFKPLHNEEDAREPMAVTSQTKKMSFQKILPDRMKAARDRANKNLVDFIVNAKGTENHLLAILNGTKASRWLKSFLNAN 589
gi | 119923736 | ref | XP_586767.3 | RRLKKFDCKEKQALVEKAREEYSESIDWCISLICYRVRIGCGSFTGSLLEYAADISYVPRKKEKQDIFRNKFKPLHNEEDAREPMAVTSQTKKMSFQKILPDRMKAARDRANKNLVDFIVNAKGTESHLLAILNGTKGSRWLKSFNLNAH 588
gi | 29789431 | ref | NP_780750.1 | RRLKKYDCKEKQALVEKAREEYRESIDWCISLICYRVRIGCGSFTGSLFEYAAADISYVPRKKEKQDIFRNKFKPLHNEEDAREPMAVTSQTKKMSFQKILPDRMKAARDRANKNLVDFIVNAKGTEDHLLGILKGTGKSKWLKSFNLNAK 484
gi | 109511143 | ref | XP_577028.2 | RRLKKYDCKEKQALVEKAREEYRESIDWCISLICYRVRIGCGSFTGSLFEYAAADISYVPRKKEKQDIFRNKFKPLHNEEDAREPMAVTSQTKKMSFQKILPDRMKAARDRANKNLVDFIVNAKGTEDHLLGILKGTGKSKWLKSFNLNAK 573
.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600



gi | 289629261 | ref | NP_001164491.1 | RFTPCIEYFDEDEDLDEVVKYLQEVNQLIDIMPWIKDDKIKFILEVLLPEAIIICSIASVDGLDYEAABAKYKGLPCLGYRERELFPAKILFEKRRKAPLNEAH 696
gi | 114689712 | ref | XP_001142672.1 | RFTPCIEYFDEDEDLDEVVKYLQEVNQLIDIMPWIKDDKIKFILEVLLPEAIIICSIASVDGLDYEAABAKYKGLPCLGYRERELFPAKILFEKRRKAPLNEAH 696
gi | 74008509 | ref | XP_852784.1 | RFTPCIEYFDEDEDLDEVVKYLQEVNQLIDIMPWIKDDKIKFILEVLLPEAIIICSIASVDGLDYEAABAKYKGLPCLGYRERELFPAKILFEKRRKAPLNEAH 695
gi | 119923736 | ref | XP_586767.3 | RFTPCIEYFDEDEDLDEVVKYLQEVNQLIDIMPWIKDDKIKFILEVLLPEAIIICSIASVDGLDYEAABAKYKGLPCLGYRERELFPAKILFEKRRKAPLNEAH 694
gi | 29789431 | ref | NP_780750.1 | SFTPCIEYFDEDEDLDEVVKYLQEVNQLIDIMPWIKDDKIKFILEVLLPEAIIICSIASVDGLDYEAABAKYKGLPCLGYRERELYDSKILFEKRRRSLPNEH 590
gi | 109511143 | ref | XP_577028.2 | SFTPCIEYFDEDEDLDEVVKYLQEVNQLIDIMPWIKDDKIKFILEVLLPEAIIICSIASVDGLDYEAABAKYKGLPCLGYRERELYDSKILFEKRRRSLPNEH 679
.....610.....620.....630.....640.....650.....660.....670.....680.....690.....700.....

