

gi | 124487159 | ref | NP_001074649.1 | MKIATVPMMLLPLAFYLTDAAEGKGNODPCMFKQAQMKNGTLCPKGNNSOSLNDIIFQSEILCKRALEGAPTKIMNVKVLRSRANRATDPAKLNCSFQRKRDGDFICPDSI... 150
gi | 109506549 | ref | XP_341608.3 | MYKSELHLMRNVLEHQLSNAQ-----SSPVTNLHLHQHEDS-----ILSHREDETNKDMVMVRFSLRATRATAPAKLNCENFKQRKRDGDFICPSDASAVCGD... 132
gi | 74027261 | ref | NP_006837.2 | MKIATVSVLLPLALCLLIDAAASKNEDDEMCHFEQAFMKNGLKFCPODKKFFOSLDGIMFINCACTCKMILEK-EAKSQKRARHLARAPKATAPTELN... 149
gi | 114602636 | ref | XP_0011160674.1 | MKIATVSVLLPLALCLLIDAAASKNEDOEICHEFOAFMKNGLKFCPODKKFFOSLDGIMFINCACTCKMILEK-EAKSQKRARHLARAAKATAPTELN... 149
gi | 70794744 | ref | NP_001020568.1 | MKIAKVPMLLPLALCLLIDAAASEDENOEICNRYRALMKNGLKFCSDOKKLFOSPDGIAPINCACTCKMILEK-EAKSQKRASVLRASRAIASDKLN... 149
gi | 156120851 | ref | NP_001095572.1 | MKIITVPMMLLPLAVCLLIDAAASEDVENOETCSFYRVLKMGKGLKFCSDOKKFFOSPDGIMFVNKCAMKMLEK-EAKSQKRYRLLTRASRATA----- 91
gi | 71895337 | ref | NP_001025783.1 | -----
gi | 118097409 | ref | XP_414558.2 | -----
gi | 118097407 | ref | XP_001233107.1 | -----
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

gi | 124487159 | ref | NP_001074649.1 | ECGSSHLEETDMCSDFRAYVDGRLGCTRESDPILGPDGRTHGNRCAMCAELFLKEAENATNRRESRIRRDAAEKELCKEFENQVRNGRLFC... 300
gi | 109506549 | ref | XP_341608.3 | ECGSSHLEETDMCSDFRAYVDGRLGCTRENDPIRGPDPGRTHGNRCAMCAELFLKEAENATNRDRSRIRRDAAEELCKEFENQVRNGRLFC... 282
gi | 74027261 | ref | NP_006837.2 | ECKSSNPEDVCSAFRPFVDRGLGCTRENDPVLGPDGKTHGNRCAMCAELFLKEAENAKREGETRIRRNAEKDFCKEYEVQVRNGRLFC... 298
gi | 114602636 | ref | XP_0011160674.1 | ECKSSNPEDVCSAFRPFVDRGLGCTRENDPVLGPDGKTHGNRCAMCAELFLKEAENAKREGETRIRRNAEKDFCKEYEVQVRNGRLFC... 298
gi | 70794744 | ref | NP_001020568.1 | ECGENNPEDVCSAFRPFVDRGLGCTRENDPVLGSDGKTHGNRCAMCAELFLKEAENAKRASRARIRRSAAKDFCKEYEVQVRNGRLFC... 299
gi | 156120851 | ref | NP_001095572.1 | -----PGKDI CSDFRPFVDRGLGCTRENDPVLGPDGRTHGNRCAMCAELFLKEAENAKRENETRIRRSAAKDFCKEYEVQVRNGRLFC... 233
gi | 71895337 | ref | NP_001025783.1 | -----MIAARQFVVALALCCFA-DIAPGIEVNCSLNAGSIGKDGTSWAACPNKLDVPCGGTDSGYSNNEGICLYNREHGAVNKEYDQ... 97
gi | 118097409 | ref | XP_414558.2 | -----MRJAVFVLFVFLGDFLDAAPFGAIEVDCSRFPNATDKEGKGLVLCRNKDLRPLICGTDGVTYTDLCLLCAYSIEFGTNIKSHEDG... 87
gi | 118097407 | ref | XP_001233107.1 | -----MRGKHQQLLP-CPALSHLCSQAQSCGEYR-----LSSGRNLACSRIFFQPCGTNNVYIPNEICSLREILRSGI-VDKKHDG... 79
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300

gi | 124487159 | ref | NP_001074649.1 | EFQDRARNGILFCITRENDPIRGLDGRTHGNLCSMCAFFKTEAEKK- AEAGSRNRGSESEYALG-----EPRALRFLGKRSTTELN----- 376
gi | 109506549 | ref | XP_341608.3 | EFQDRAKNGILFCITRENDPIRGLDGRTHGNLCSMCAFFKTEAEKK- AEAGTRNRGSEKSEYALG-----EPRALRFLGKRSTTELN----- 425
gi | 74027261 | ref | NP_006837.2 | QYONQAKNGILFCITRENDPIRGPDPGKTHGNLCSMCAFFKTEAEKK- AEAGSRNRGSESEYALG-----EPRALRFLGKRSTTELN----- 445
gi | 114602636 | ref | XP_0011160674.1 | QYONQAKNGILFCITRENDPIRGPDPGKTHGNLCSMCAFFKTEAEKK- AEAGSRNRGSESEYALG-----EPRALRFLGKRSTTELN----- 445
gi | 70794744 | ref | NP_001020568.1 | EYQDHAKNGILFCITRENDPIRGPDPGKTHGNLCSMCAFFKTEAEKK- AEAGSRNRGSESEYALG-----EPRALRFLGKRSTTELN----- 446
gi | 156120851 | ref | NP_001095572.1 | EYQDRAKNGILFCITRENDPIRGPDPGKTHGNLCSMCAFFKTEAEKK- AEAGSRNRGSESEYALG-----EPRALRFLGKRSTTELN----- 380
gi | 71895337 | ref | NP_001025783.1 | LQVVRDGMTVACPRILKPCVGSDFSTYDNECGICAYNAEHTNISKLHDGECKLEIGVDCSKYPS----- 164
gi | 118097409 | ref | XP_414558.2 | -----ETVPMNCSSVAN----- 99
gi | 118097407 | ref | XP_001233107.1 | -----VDCIGYMR----- 87
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450

gi | 124487159 | ref | NP_001074649.1 | NGOLYCTRENAPIRGPDGKIHGNLCSMCAFFKTEAEKK- AEAGSRNRGSESEYALG-----EPRALRFLGKRSTTELN----- 480
gi | 109506549 | ref | XP_341608.3 | NGOLYCTRENAPIRGPDGKIHGNLCSMCAFFKTEAEKK- AEAGSRNRGSESEYALG-----EPRALRFLGKRSTTELN----- 531
gi | 74027261 | ref | NP_006837.2 | NGRLLCTRENAPIRGPDGKIHGNLCSMCAFFKTEAEKK- AEAGSRNRGSESEYALG-----EPRALRFLGKRSTTELN----- 550
gi | 114602636 | ref | XP_0011160674.1 | NRRLLCTRENAPIRGPDGKIHGNLCSMCAFFKTEAEKK- AEAGSRNRGSESEYALG-----EPRALRFLGKRSTTELN----- 550
gi | 70794744 | ref | NP_001020568.1 | NGOLYCTRENAPIRGPDGKIHGNLCSMCAFFKTEAEKK- AEAGSRNRGSESEYALG-----EPRALRFLGKRSTTELN----- 552
gi | 156120851 | ref | NP_001095572.1 | NGOLYCTRENAPIRGPDGKIHGNLCSMCAFFKTEAEKK- AEAGSRNRGSESEYALG-----EPRALRFLGKRSTTELN----- 530
gi | 71895337 | ref | NP_001025783.1 | -----TVSKDGRITLVAAPRILSPVCGTDGFTVDNECGICAHNAEQRTH----- 207
gi | 118097409 | ref | XP_414558.2 | -----TTSDEGKVMVLCNRAFNPCVCGTDGFTVDNECGICAHNAEQRTH----- 142
gi | 118097407 | ref | XP_001233107.1 | -----HTDGLG-----TAGIQQYSPLYATNGLVSNKCTFCS-AVANGED----- 126
.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600

gi | 124487159 | ref | NP_001074649.1 | -----EKVDAGKAKKEAVQELCRKVTHTQLRNGP-----LRCSTRNPIEGLDGMKYNACFMCAFFFOEAK-KSAGFRPKVKREVK-VDCSEYLALSKRGEIFCTRENDPVRGPDGKTHGNKCAMCA 598
gi | 109506549 | ref | XP_341608.3 | -----EKAEAGTKRREAVQELCSKVTHTLLKNGR-----LPCTKKNDPIEGLDGIYASTCSMCAFFFOEAK-KNEAGFGAKAKREVKVDCSEFLILLRGGELFCITRENDPVRGPDGKTHGNKCAMCA 650
gi | 74027261 | ref | NP_006837.2 | -----GKVEAEKVKREAVQELCSEYRHYVNRGR-----LPCITRENDPIEGLDGIHGNLCSMCAFFFOEAKKEKERAEPRAKVKREAEKETCDFEFRLLQNGKLFCTRENDPVRGPDGKTHGNKCAMCA 670
gi | 114602636 | ref | XP_0011160674.1 | -----LPCITRENDPIEGLDGIHGNLCSMCAFFFOEAKKEKERAEPRAKVKREAEKETCDFEFRLLQNGKLFCTRENDPVRGPDGKTHGNKCAMCA 670
gi | 70794744 | ref | NP_001020568.1 | -----EKVKAEEKSKREAVQELCSEYRHYVNRGR-----LPCITRENDPIEGLDGIHGNLCSMCAFFFOEAKKEKERAEPRAKVKREAEKETCDFEFRLLQNGKLFCTRENDPVRGPDGKTHGNKCAMCA 672
gi | 156120851 | ref | NP_001095572.1 | -----MNVNKCAMCASLFLREBEKKNVKKEENEKAEFEKVKRAAAGELCSEYRHYVNRGR-----LPCITRENDPIEGLDGIHGNLCSMCAFFFOEAKKEKERAEPRAKVKREAEKETCDFEFRLLQNGKLFCTRENDPVRGPDGKTHGNKCAMCA 676
gi | 71895337 | ref | NP_001025783.1 | -----VSKKHGDKCRQRIPIIDCDQYPTKRTGGKLLVRCPRILLPCVCGDGFVYDNECGICAHNAHGTEVKKSHDGRCKERSTLDCQYLNQNGEAITACPFILQVCGTDGVTYSNDCSLCA 331
gi | 118097409 | ref | XP_414558.2 | -----VDRRHDDGCRKELAVDCSEYPK----- 165
gi | 118097407 | ref | XP_001233107.1 | -----IDLLAVGKE-----PEICKEFLNR----- 145
.....610.....620.....630.....640.....650.....660.....670.....680.....690.....700.....710.....720.....730.....740.....750

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gi |124487159|ref|NP_001074649.1|VFKEEERKRKEGENQRIISGESSGGNP----KAKDECAQVRESMKHGQLSCTRESDPVRGVDGEHYNNKCVMKKELLQKEMEETKNSASRSNGTGAIGKDVCDQFRNQMKNGKLLCTRESDPTRGPDGAMHGKNCAMCKERLEK 743
gi |109506549|ref|XP_341608.3|VFKEEERKRKEGENQRIISGESSGGNP----KAKDECAQVRESMKNGELSCCTRESDPVRGADGKPYNNKCVMKKELLRREMEETKNSASRSNGT--ETRKDVCDQFRNQMKNGKLLCTRESDPTRGPDGKTHGNKCAMCKERLEK 793
gi |74027261|ref|NP_006837.2|VFKEEERKRKEEEDRNAAGHSSGGGG---GNTQDECAEYREQMKNGRLSCTRESDPVRDADGKSYNNQCTMCKAKLREAEERKNEYERSRSNGTGESGKDTCDQFRNQMKNGKLLCTRESDPVVRGPDGKTHGNKCTMCKEKLER 816
gi |114602636|ref|XP_001160674.1|VFKEEERKRKEEEDRNAAGHSSGGGG---GNTQDECAEYREQMKNGRLSCTRESDPVRDADGKSYNNQCTMCKAKLREAEERKNEYERSRSNGTGESGKDTCDQFRNQMKNGKLLCTRESDPVVRGPDGKTHGNKCTMCKEKLER 816
gi |70794744|ref|NP_001020568.1|VFKEEERKRKEEEDRNAAGHSSGGGGSGGEGKADQCAEFRDKLQNGKLSCTRESDPVRDADGKSYNNKCTMCKEILREAEERKNEYERSRSNGTGESGKDTCDQFRNQMKNGKLLCTRESDPVVRGPDGKTHGNKCAMCKDKLER 822
gi |156120851|ref|NP_001095572.1|VFKEEERKRKEEEDRNAAGHSSGGG---RGKAKDQCAEYREKMKDKGLSCTRESDPVRDADGKSYNNKCTMCKEILREAEERKNEYERSRSNGTGESGKDVCDQFRNQMKNGKLLCTRESDPVVRGSDGKTHGNKCAMCKERLEK 822
gi |71895337|ref|NP_001025783.1|NIELGTSVAKKHDGRCEEVPELDCSKYKT-----STLKDGRQVVACIMYDPCANGVVYASECTLCAHNLGRINLNGKRRNG-----RCEEDITKEHCRFQKVSPICTIMYVYPHCGSDGVTYSNRKCFNAYVVS 460
gi |118097409|ref|XP_414558.2|-----PDCIADRLPLCGSDNKTGNKCNFCNAVVS 196
gi |118097407|ref|XP_001233107.1|-----SVFQRESNPHCGTDGVTYGNKCAFCKAVL-- 175
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.....760.....770.....780.....790.....800.....810.....820.....830.....840.....850.....860.....870.....880.....890.....900

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gi |124487159|ref|NP_001074649.1|EAAEKKKKEDEKRNTEIKSDK-----EDKCHEYRSMQLDGRLICITRENDPVRDADGKMHVVKCAMCOMMFEREANERKMR--EENRSOPTNEAKDQCGEVHNSVEDAKPRPARSSLPSIRGISKDECFEONLMKNEKLIQPETDDP 886
gi |109506549|ref|XP_341608.3|EAAEKKKKEDEKRNTEIKSDK-----EDKCHEYRSMQLDGRLICITRENDPIRGPDGKTHVVKCAMCOMMFEREANERKMR--EENRSOPTNEAKDQCGEVHNSVEDAKPRPARSSLPSIRGISKDECFEONLMKNEKLIQPETDDP 913
gi |74027261|ref|NP_006837.2|EAAEKKKKEDEDRSNTGERENTGERENDKEDLCREFRSMQRNGKLICTRENNPVRGPYKMHINKCAMCOSIFDREANERKKNDEEKSSEKPSNNAKDEC-----SEFRNYIRNNELICPRENDP 936
gi |114602636|ref|XP_001160674.1|EAAEKKKKEDEDRSNTGERENTGERENDKEDLCREFRSMQRNGKLICTRENNPVRGPYKMHINKCAMCOSIFDREANERKKNDEEKSSEKPSNNAKDEC-----SEFRNYIRNNELICPRENDP 936
gi |70794744|ref|NP_001020568.1|EAAEKKKKEEDNLRNTG-----EKSNNEDQCHEFRSMVRNGKLICTRENNPVRGPDGKMHVVKCAMCOSIFDREANERKKNDEEKSSEKPSNNAKDEC-----SEFRNYIRNNELICPRENDP 936
gi |156120851|ref|NP_001095572.1|EAAEKKKKEEGEYTRNT-----GKDKKEDQCHEFRNMVRDGLICTKENNPVRGPYKTYANKCAMCOSIFEREAKERKKNDEEKSSEKPSNNAKDEC-----SEFRNYIRNNELICPRENDP 966
gi |71895337|ref|NP_001025783.1|NRLLNLVSMAC----- 472
gi |118097409|ref|XP_414558.2|NGLLTLSHFGKC----- 208
gi |118097407|ref|XP_001233107.1|----- 175
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.....910.....920.....930.....940.....950.....960.....970.....980.....990.....1000.....1010.....1020.....1030.....1040.....1050

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gi |124487159|ref|NP_001074649.1|VRCADGTFYQNKCHMCRDVLKNEAMKRSGLQESQDIRSTKE-GDPEFSSSSLDSEMCNRYRILPRMGYLCPKNLNVPVCGDDGQTYSNPCMLCHENLMROTNRIHKQGACESSNLKIVSITGPASEKMMG 1017
gi |109506549|ref|XP_341608.3|VRCADGTFYQNKCHMCRDVLKNEAMKRSGLQESQDIRSTKE-GDPEFSSSSLDSEMCNRYRILPRMGYLCPKNLNVPVCGDDGQTYSNPCMLCHENLMROTNRIHKQGACESSNLKIVSITGPASEKMMG 1009
gi |74027261|ref|NP_006837.2|VHGADGKFYTNKCYMCRVFLTEALERAKLQEKPSHVRASQEEEDSPDS-FSSLDSEMCNRYRILPRMGYLCPKNLNVPVCGDDGQTYSNPCMLCHENLMROTNRIHKQGACESSNLKIVSITGPASEKMMG 1064
gi |114602636|ref|XP_001160674.1|VHGADGKFYTNKCYMCRVFLTEALERAKLQEKPSHVRASQEEEDSPDS-FSSLDSEMCNRYRILPRMGYLCPKNLNVPVCGDDGQTYSNPCMLCHENLMROTNRIHKQGACESSNLKIVSITGPASEKMMG 1064
gi |70794744|ref|NP_001020568.1|VSGADGVEYKNCYMCRAVLIKEALERARYREKPSHVRFMEE-NSPTSSSSLDSEMCNRYRILPRMGYLCPKNLNVPVCGDDGQTYSNPCMLCHENLMROTNRIHKQGACESSNLKIVSITGPASEKMMG 1063
gi |156120851|ref|NP_001095572.1|VLCADGKLYKNCYMCRSIFKEALDRIRLEBEKPSHFRSSSEEDSSSSISSLSNSEMCKHYRILPRMGYLCPKNLNVPVCGDDGQTYSNPCMLCHENLMROTNRIHKQGACESSNLKIVSITGPASEKMMG 1091
gi |71895337|ref|NP_001025783.1|----- 472
gi |118097409|ref|XP_414558.2|----- 208
gi |118097407|ref|XP_001233107.1|----- 175
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.....1060.....1070.....1080.....1090.....1100.....1110.....1120.....1130.....1140.....1150.....1160.....1170.....1180...

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