

gi | 28573920 | ref | NP_788301.1 | MASLLGSAPPAQILANQPIIVKIEPTQSFIHVDEGDRVLSLPLSDADKLGAEWIDLKDIAGLQAGGGATLLDVCFEQANEDGIIIAIVQPLENELEAELEKAEGEPEDETEPEPPAPKRLATTRPAQSRPQIQOQOQOQVQKFLSDPPA 150
gi | 158299692 | ref | XP_319750.4 | -----LRAPRRRRRR----- 11
gi | 19743907 | ref | NP_008845.2 | -----
gi | 114625040 | ref | XP_528326.2 | -----
gi | 194669369 | ref | XP_606804.4 | -----
gi | 112821692 | ref | NP_666207.3 | -----
gi | 62641935 | ref | XP_219749.3 | -----
gi | 73946789 | ref | XP_541280.2 | -----
gi | 45384158 | ref | NP_990424.1 | -----
gi | 130490232 | ref | NP_001076325.1 | -----
gi | 86560912 | ref | NP_001032971.1 | -----MVAVEQKLADARITLHAKSSLOPLSLSIETPKSKENDEESGCESSNCFPHPT 51
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

gi | 28573920 | ref | NP_788301.1 | LARSSSFSSLSFSISINISVVCKNMASNTSCGSLKRIKERTPPMPPLTTHKPAATTITATSATSAATAAATATSARENSREHSSSSSSGNGAMTAQIEIIPCKVCGDKSSGVHYGVITCEGCKGFFRRSQSSVVNVQCPRNK 300
gi | 158299692 | ref | XP_319750.4 | -----PLINTFFPIP----- 74
gi | 19743907 | ref | NP_008845.2 | -----MRAQIEVIPCKICGDKSSGIHYGVITCEGCKGFFRRSQONNASYSCPRQR 50
gi | 114625040 | ref | XP_528326.2 | -----MCENQLKIKADATAQIEVIPCKICGDKSSGIHYGVITCEGCKGFFRRSQONNASYSCPRQR 61
gi | 194669369 | ref | XP_606804.4 | -----MRAQIEVIPCKICGDKSSGIHYGVITCEGCKGFFRRSQONNASYSCPRQR 50
gi | 112821692 | ref | NP_666207.3 | -----MCENQPKIKADATAQIEVIPCKICGDKSSGIHYGVITCEGCKGFFRRSQONNASYSCPRQR 61
gi | 62641935 | ref | XP_219749.3 | -----MRAQIEVIPCKICGDKSSGIHYGVITCEGCKGFFRRSQONNASYSCPRQR 50
gi | 73946789 | ref | XP_541280.2 | -----MRAQIEVIPCKICGDKSSGIHYGVITCEGCKGFFRRSQONNASYSCPRQR 50
gi | 45384158 | ref | NP_990424.1 | -----MRAQIEVIPCKICGDKSSGIHYGVITCEGCKGFFRRSQONNASYSCPRQR 50
gi | 130490232 | ref | NP_001076325.1 | -----MRAQIEVIPCKICGDKSSGIHYGVITCEGCKGFFRRSQONNASYSCPRQR 50
gi | 86560912 | ref | NP_001032971.1 | -----IKSEPNFCFAREFKSVPPDFRIIGGDLQMGNNISKRLIKVIDINRVDMAGILPDN-----MDFRQLPENKSLLSAQIEVIPCKVCGDKSSGVHYGVITCEGCKGFFRRSQSSIVNVQCPRNK 168
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300



gi | 28573920 | ref | NP_788301.1 | QCVVDRVNRNRCQYCRLOKCLKLGMSRDVAVKFGFRMSKKQREKVEDEVRFHRAQMRAS---DAAPDSVVDIQTSSSDQLHH--NNYNSGGYS--NNEVG---YGSFYGYSASVTPQQTMOVDIS--ADYVDS--TYEPRSTIIDPE 435
gi | 158299692 | ref | XP_319750.4 | QCVVDRVNRNRCQYCRLOKCLKLGMSRDVAVKFGFRMSKKQREKVEDEVRFHRAQMRAN---DAAPDSVVDIQTSSSDQLHHGYNNGNSHSYVYVSNVEG---YGSFYGYSASVTPQQTMOVDIS--ADYVDS--TYEPRSTIIDPE 213
gi | 19743907 | ref | NP_008845.2 | NCLIDRTNRNRCQHCRLQKCLALGMSRDVAVKFGFRMSKKQKQDLSYAEVOKHOORLQEQRQOQSGEAEALARVYSSSISNGLSNLNNEISGTYANGHVIDLPK---SEGYYNVDSGQPPDQSGLDMTGKIKQKQEPFYDLTISVPLNFT 194
gi | 114625040 | ref | XP_528326.2 | NCLIDRTNRNRCQHCRLQKCLALGMSRDVAVKFGFRMSKKQKQDLSYAEVOKHOORLQEQRQOQSGEAEALARVYSSSISNGLSNLNNEISGTYANGHVIDLPK---SEGYYNVDSGQPPDQSGLDMTGKIKQKQEPFYDLTISVPLNFT 205
gi | 194669369 | ref | XP_606804.4 | NCLIDRTNRNRCQHCRLQKCLALGMSRDVAVKFGFRMSKKQKQDLSYAEVOKHOORLQEQRQOQSGEAEALARVYSSSISNGLSNLNNEASGTYANGHVIDLPK---SEGYYNVDSGQPPDQSGLDMTGKIKQKQEPFYDLTISVPLNFT 194
gi | 112821692 | ref | NP_666207.3 | NCLIDRTNRNRCQHCRLQKCLALGMSRDVAVKFGFRMSKKQKQDLSYAEVOKHOORLQEQRQOQSGEAEALARVYSSSISNGLSNLNNEISGTYANGHVIDLPK---SEGYYNVDSGQPPDQSGLDMTGKIKQKQEPFYDLTISVPLNFT 205
gi | 62641935 | ref | XP_219749.3 | NCLIDRTNRNRCQHCRLQKCLALGMSRDVAVKFGFRMSKKQKQDLSYAEVOKHOORLQEQRQOQSGEAEALARVYSSSISNGLSNLNNEISGTYANGHVIDLPK---SEGYYNVDSGQPPDQSGLDMTGKIKQKQEPFYDLTISVPLNFT 194
gi | 73946789 | ref | XP_541280.2 | NCLIDRTNRNRCQHCRLQKCLALGMSRDVAVKFGFRMSKKQKQDLSYAEVOKHOORLQEQRQOQSGEAEALARVYSSSISNGLSNLNNEISGTYANGHVIDLPK---SEGYYNVDSGQPPDQSGLDMTGKIKQKQEPFYDLTISVPLNFT 194
gi | 45384158 | ref | NP_990424.1 | NCLIDRTNRNRCQHCRLQKCLALGMSRDVAVKFGFRMSKKQKQDLSYAEVOKHOORLQEQRQOQSGEAEALARVYSSSISNGLSNLNNEISGTYANGHVIDLPK---SEGYYNVDSGQPPDQSGLDMTGKIKQKQEPFYDLTISVPLNFT 194
gi | 130490232 | ref | NP_001076325.1 | NCLIDRTNRNRCQHCRLQKCLALGMSRDVAVKFGFRMSKKQKQDLSYAEVOKHOORLQEQRQOQSGEAEALARVYSSSISNGLSNLNNEISGTYANGHVIDLPK---SEGYYNVDSGQPPDQSGLDMTGKIKQKQEPFYDLTISVPLNFT 200
gi | 86560912 | ref | NP_001032971.1 | NCVVDRVNRNRCQYCRLOKCLKLGMSRDVAVKFGFRMSKKQREKVEDEVRFHRAQMRAN---GLGYQALYGDYSPPPSHPSYCFDQSMYGHYPSGISTPVNG---YSLAVAATFTTPEMPCNYGATPSTNGIYVAHQATGGS 305
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450



gi | 28573920 | ref | NP_788301.1 | : * FISGHSEYRSPRDFICLPLVLYDLFVDSITFLPSPAPPASQQQQQPHHQHQQLSSAAQMVLSNGVGLGAVPFAAVVAVAAITVPTVPTVGSVAVFLGRITQKQKCFLLALPLSHYCPPEFISPSIALDGTIARLRSHRVVPGRMVLRTPH 438
gi | 158299692 | ref | XP_319750.4 | YSSFNNGQLAPG 363
gi | 19743907 | ref | NP_008845.2 | YSSFNNGQLAPG 206
gi | 114625040 | ref | XP_528326.2 | YSSFNNGQLAPG 217
gi | 194669369 | ref | XP_606804.4 | YSSFNNGQLAPG 206
gi | 112821692 | ref | NP_666207.3 | YSSFNNGQLAPG 217
gi | 62641935 | ref | XP_219749.3 | YSSFNNGQLAPG 206
gi | 73946789 | ref | XP_541280.2 | YSSFNNGQLAPG 206
gi | 45384158 | ref | NP_990424.1 | YSSFNNGQLAPG 206
gi | 130490232 | ref | NP_001076325.1 | YGSYQDSQLAPG 212
gi | 86560912 | ref | NP_001032971.1 | FPSAQ----- 310
.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600



