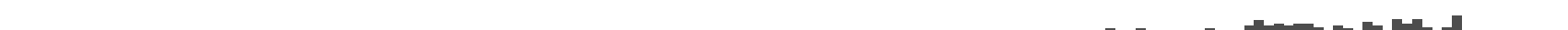


gi 50311249 |ref| XP_455649.1
gi 45198696 |ref| NP_985725.1
gi 6319448 |ref| NP_009530.1
gi 39946004 |ref| XP_362539.1
gi 32406108 |ref| XP_323667.1
gi 19112269 |ref| NP_595477.1
gi 17137132 |ref| NP_477121.1
gi 158291683 |ref| XP_313198.4
gi 33356547 |ref| NP_004517.2
gi 114589012 |ref| XP_001136645.1
gi 73984933 |ref| XP_541736.2
gi 6678826 |ref| NP_032590.1
gi 62647780 |ref| XP_232168.3
gi 194677427 |ref| XP_869445.3
gi 57524951 |ref| NP_001006139.1
gi 27545265 |ref| NP_775364.1
gi 71997752 |ref| NP_001022416.1
gi 145336465 |ref| NP_175112.2
gi 115485533 |ref| NP_001067910.1
gi 124808572 |ref| XP_001348350.1

-----MSDNDEINNGRRRRRADDDEEDLSTQPREGGANIPSSQFED--- 46
-----MASHNGMEGSHGRRRRARDENDTEQRSDSRS-QSYEHPSSQVSGRG 48
-----MSDN-----RRRRREDDSDSENELPSSQOQFRG--GMNVPVSS 38
-----MDSANRGLAAGSSNRKRARPD-DGTSIAAASSP-MPSSP 38
-----MSPLRDNPSANRG-AVPRATRKRRRNDHDCASSLPRASSVMPSSP 47
-----MDSFRKRRRDESELPFSENSLGLATPLSLPSSPPPE 39
-----MDNPSPPP-----NTPSDAERRDLRAAMTSPVGD 31
-----MCACIHLQDLPSSPAP-----NVPDMMD-RRNFRSGATSPVGD 37
-----MAESSEFTMASSPAQ-RRRGNPLTSSPGRSS--RRTDALTSPPGRD 45
-----MAESSEFTMASSPAQ-RRRGNPLTSSPGRSS--RRTDALTSPPGRD 45
MISDKKQPPDRDFEDENPKLIREISGRVPEVSRARGGHVSRFSRENWLLLRERREARWNGEPAGSTPLESARGE--ACPAPGRRLRIPDPELWGRSALLESEFTIVASSPAQ-RRR-SDPLTSSPGRSS-RRMDALTSPPGRD 142
-----MAESSEFTMASSPAQ-RRR-SDPLTSSPGRSS-RRMDALTSPPGRD 45
-----MAESSEFTMASSPAQ-RRR-SDPLTSSPGRSS-RRMDALTSPPGRD 46
RLNGERSVERGLGGASGRLGASGRAGRASGGLGGASGRPAERLLELGRRRRPPAAWAGPGGAPPAAREPSSAAGKNAVADVTSQVRFCEERGAEMAESSEFTMASSPAQ-RRR-SDPLTSSPGRSS-RRTDALTSPPGRD 146
-----MADSSSEFN-----SQAAVTSPVRSR-RRGDAFTSSPGRD 31
-----MADSSSEFN-----MATSPTRES--RRGDLTSSPGRD 30
-----MADSSSEFN-----MADRANDDVDRQFLP IADD 21
-----MADSSSEFN-----MADRANDDVDRQFLP IADD 21
MAGENSNEPSSPASPSSAGFNTDQLPSTSQ-----NSENFSDE 40
-----MDDSENNAPSTPGSPGFTDRLPNTTTSRGATDPSYEDDDDDDD 45
-----MDDKKEEDLESNKYDIDEEDLLE 26

1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150



gi 50311249 |ref| XP_455649.1
gi 45198696 |ref| NP_985725.1
gi 6319448 |ref| NP_009530.1
gi 39946004 |ref| XP_362539.1
gi 32406108 |ref| XP_323667.1
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gi 114589012 |ref| XP_001136645.1
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gi 6678826 |ref| NP_032590.1
gi 62647780 |ref| XP_232168.3
gi 194677427 |ref| XP_869445.3
gi 57524951 |ref| NP_001006139.1
gi 27545265 |ref| NP_775364.1
gi 71997752 |ref| NP_001022416.1
gi 145336465 |ref| NP_175112.2
gi 115485533 |ref| NP_001067910.1
gi 124808572 |ref| XP_001348350.1

-----PLGSPDEIDFENPDNDGDEAVNVEEDLSDVBERMN-EVDLMGDDMYRDYASNTEEDTERRGVDDQ-EQOELSLA-----ERRRIDAQLNERDRLVHR-----NTAVLDDDDGEGAGAHNLDAMGLPVQRRRRRQVYEAD--- 175
SRMGNSPLGSPDEIDFENPDNDGDERIEFADDDDDAEEERID-EVDLVGDDMYADYANRNDKDFYENEGVDDA-EHEELSLA-----DRRIDAQLNARDRLMHD-----SQVFLDD-EMDADKMGVDMAMPVQRRRRRQVDEADY--- 184
-----PLGSPDMINPEGDNDVDD-----VDDIDVEEQQN-EVDLMDNMYEDYAADHNRDRDQDOVDD-EQOELSLA-----ERRRIDAQLNERDRLR-----NVAVLDDDEEGEGAGAHNLDAMGLPVQRRRRRQVDELENS 165
PAFHMAHGADDNDDIRED-AEIQDDIDIDEMAEEDVDLFRDGYERDQQ-DENRDRDGDIDDEENYEGLODIA-----ERRRIDAQLNRRDRVARRQ--RIPAAFLPGDEEDGD-----IDLTAQRRRRRQVDEMD--- 165
PAFFVAHGADE-DDDIREDVAEIEDDDDLDELAEEDVDLFRGFERDVRERDENADYEGDIDDD-EYEALDPA-----ARRRLEAKLARDRQVVR--M--GMCTTLPGLDDEDDGD-----IDLTLNERRRRRRQVDEMD--- 173
FSDEAAEALVEEDIEDLDD-----GALDVEDEEGE-----DLFGEGMERDYQONLELDRDIEELDDDDNLELDIG-----ARRAVDARLRDRRRIELDAAAGRTKPAAFLOQEDDDDDLSN-----LGTGTRHRHR--I-DEYSP 163
FEPFENEDEILGDQTVRDAEAE-----DGEELFGDMENDYRPPELDDHDPALLD-DEDDFSEMSQ-----GDRFAAESEMERRRRDRAG--IHRDRLDGLFGQSDDEDDVVG-----PRAKRIRAGE 141
FEPFEDAEAILGDTTVRDIYDEEADGEEELFGDMENDYRPPAPHLDRDMDDDL-T-BEYSDTSQ-----ADRAAAEEMRRRRDRAG--VHRDHRDLFVYKSDDEDDI-----PRAKRIRAGE 148
LPPFDESEGLLGTGPLEEEEE-----DGEELIGDMERYDRAIPELDAYEAGLALDDDEVEELTA-----SOREAAERAMRORDREAGRGLGRMRGGLLYSDDEDEERP-----A-KRKRQVER 156
LPPFDESEGLLGTGPLEEEEE-----DGEELIGDMERYDRAIPELDAYEAGLALDDDEVEELTA-----SOREAAERAMRORDREAGRGLGRMRGGLLYSDDEDEERP-----A-KRKRQVER 156
LPPFDESEGLLGTGPLEEEEE-----DGEELIGDMERYDRAIPELDAYEAGLALDDDEVEELTA-----SOREAAERAMRORDREAGRGLGRMRGGLLYSDDEDEERP-----A-KRKRQVER 254
LPPFDESEGLLGTGPMEEEE-----DGEELIGDMERYDRAIPELDAYEAGLALDDDEVEELTA-----SOREAAERTMRORDREAGRGLGRMRGGLLYSDDEDEERP-----A-KRKRQVER 156
LPPFDESEGLLGTGPEVEEEE-----DGEELIGDMERYDRAIPELDAYEAGLALDDDEVEELTA-----SOREAAERAMRORDREAGRGLGRMRGGLLYSDDEDEERP-----A-KRKRQVER 157
LPPFDESEGLLGTGPLEEEEE-----DGEELIGDMERYDRAIPELDAYEAGLALDDDEVEELTA-----SOREAAERVMRORDREAGRGLGRMRGGLLYSDDEDEERP-----S-KRKRQVER 257
LPPFDESEGLLGTGPLEDEE-----EGEELIGDMERYDRAIPELDAYEAGLALDDDEVEELTA-----SOREAAERVMRORDRELEQMGMRMRGGLLYSDDEDEERP-----L-KRKRQVER 142
LPPFDESEGLLGTLPDEEDD-----DGEELIGDMERYDRAIPELDAYEAGLALDDDEVEELTA-----SAREAAEAAMRRRRDREQLGMGRIGRGLLYSDDEDDKRP-----TKRORVLAER 141
ADDDVGDIDEMFNDEEDPEDE-----EGENLFGDMERYDRAIPELDAYEAGLALDDDEVEELTA-----SARRAAEAEMRQD-----QLLDDDALYEDGDEEEDVTD-----RRRGRGRGR 126
EEAAVDTVIRDEPDEAEDEEEE-----EGEDLFDNDFMNDYRKMNDNDQYSESGMD-DASDVGLSLV-----SARRAAEAEMRQD-----QLLDDDALYEDGDEEEDVTD-----RRRGRGRGR 126
VVGAEAEAVDNNVLPEDDGVAAAEDEE-----EGEDLFDNDFMNDYRKMNDNDQYSESGMD-DASDVGLSLV-----SARRAAEAEMRQD-----QLLDDDALYEDGDEEEDVTD-----RRRGRGRGR 169
EGRLNEERQAELESGSLEFEEGIFGADDEKEMQKLRNLGLDNDDDDDFIDDELDYEDNLKA-----RRAAEHRMQMQRKQEKYKKNFKWLTLEDQLEGGDEEEDIFDKVAEKVAKRRNHLHTAETDI 156

.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300



gi 50311249 |ref| XP_455649.1
gi 45198696 |ref| NP_985725.1
gi 6319448 |ref| NP_009530.1
gi 39946004 |ref| XP_362539.1
gi 32406108 |ref| XP_323667.1
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gi 73984933 |ref| XP_541736.2
gi 6678826 |ref| NP_032590.1
gi 62647780 |ref| XP_232168.3
gi 194677427 |ref| XP_869445.3
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gi 71997752 |ref| NP_001022416.1
gi 145336465 |ref| NP_175112.2
gi 115485533 |ref| NP_001067910.1
gi 124808572 |ref| XP_001348350.1

-----DDLLSDMDIDPLADELLESLSLADVKAAS-SYSEWITQPNVSRITARELKSFLLEYTD-----ESGKSVVGARIRTLGEMNSSELEVNRYHLVES--KAILALFLAKSPEMLKIFDVTVAME 287
-----DDLLSDMDVDPLEELLESLSLADVKAAS-SYSEWITQPNVSRITARELKSFLLEYTD-----EYKSVVGARIRTLGEMNSSELEVNRYHLVES--KAILALFLARCPPEMLKIFDVTVAME 296
-----DDLLSDMDIDPLREELLESLSLADVKAAS-SYSEWITQPNVSRITARELKSFLLEYTD-----ETGRSVVGARIRTLGEMNSSELEVNRYHLVES--KAILALFLAKSPEMLKIFDVTVAME 277
EDMDADIMAEELSLAALHDVKAAS-SLTDWVSNPAVQRTIKREFKAFLEFYTD-----EHGSSVVGNRIKTLGEMNSSELEVNRYHLVES--KAILALFLANAPTEMLKIFDVTVAME 273
VMDGDDIMDSPLAALMDVKAAS-TLSEWISVPAVQRTIKREFKAFLEFYTD-----ESGSSVVGNRIKTLGEMNSSELEVNRYHLVES--KAILALFLANAPTEMLKIFDVTVAME 281
NVGALDESSELPLESIADVKAAS-SIAEWITQPNVSRITARELKSFLLEYTD-----ENGTSVVGNRIKTLGEMNSSELEVNRYHLVES--KAILALFLANAPTEMLKIFDVTVAME 270
AAVG-----EVEDTEMVESIENLEDLKGH-SIKEWWSMLGPRTEIANRFQSFLLRFVD-----ERGAITVYRDRIRRMCEQNSMSSFFVSVYDLANK--EHLVAYFLPEAPFOMLIDKVAKD 250
AAEIGAEETEDASMVESIENLEDLKGH-SIKEWWSMLGPRTEIANRFQSFLLRFVD-----DKGHVYVYRIRRMCEQNSMSSFFVSVYDLANK--EHLVAYFLPEAPFOMLIDKVAKE 260
ATE-----DGEEDBEMIESIENLEDLKGH-SVREWWSMAGPRLIEHHRFKNFLRTHVD-----SHGHNVFKERISDMCKENRESLVVNYEDLAAR--EHLVAYFLPEAPFOMLIDKVAKE 265
ATE-----DGEEDBEMIESIENLEDLKGH-SVREWWSMAGPRLIEHHRFKNFLRTHVD-----SHGHNVFKERISDMCKENRESLVVNYEDLAAR--EHLVAYFLPEAPFOMLIDKVAKE 265
ATE-----DGEEDBEMIESIENLEDLKGH-SVREWWSMAGPRLIEHHRFKNFLRTHVD-----SHGHNVFKERISDMCKENRESLVVNYEDLAAR--EHLVAYFLPEAPFOMLIDKVAKE 363
ATE-----DGEEDBEMIESIENLEDLKGH-SVREWWSMAGPRLIEHHRFKNFLRTHVD-----SHGHNVFKERISDMCKENRESLVVNYEDLAAR--EHLVAYFLPEAPFOMLIDKVAKE 265
ATE-----DGEEDBEMIESIENLEDLKGH-SVREWWSMAGPRLIEHHRFKNFLRTHVD-----SHGHNVFKERISDMCKENRESLVVNYEDLAAR--EHLVAYFLPEAPFOMLIDKVAKE 266
ATE-----DGEEDBEMIESIENLEDLKGH-SVREWWSMAGPRLIEHHRFKNFLRTHVD-----GRGHNVFKERISDMCKENRESLVVNYEDLAAR--EHLVAYFLPEAPFOMLIDKVAKE 365
AADG-----VEEEDBEMIESIENLEDLKGH-SVREWWSMAGPRLIEHHRFKNFLRTHVD-----DHGHNVFKERISDMCKENRESLVVNYEDLAAR--EHLVAYFLPEAPFOMLIDKVAKE 252
AAGGAGAMEGDEBEMIESIENLEDLKGH-SVREWWSMAGPRLIEHHRFKNFLRTHVD-----EHGHNVFKERISDMCKENRESLVVNYEDLWLR--ACVG-VFSTKAPAEMLKIFDEAAKE 251
GDAADQDVSMPEREDIPVLDIENIRGR--HIRDVSDEAVAKIERLRFKFLRTHVD-----GNKQTKKIKMKSMAADNRESLEVSFTDLSDDNGONISYFLPEAPFOMLIDKVAKE 241
GNGGDDPCNPPSSPGVSP-----DISMTDQTDYEDDDNDEAEFEMIRYQGLREWVMRDEVRFAIKKFKDPLLYVVKPK--NENGDIENVRLINEMVANKSLEIDYKEFIHV--HPNIAIWLADAPQVFLVMEVSEK 291
PRTIPREDDDGDGAPSSPGRSQRGMYSGGDVPMTDQTDYEDDFEDEMNMVYVQGLREWVMRDEVRFAIKKFKDPLLYVVKPK--NEOGFEVRLINEMVANKSLEIDYKEFIHV--HPNIAIWLADAPQVFLVMEVSEK 316
P-----DLNLSLAKTCLSVNPKDVVYDERYQQAADTCFYRFLHKSLSKDSMGLNIDBSNTELEHEEEMNSHQYIDKIKEMILNDKHTLIVSAKHLIQFH-CENLVQWIEFKPELIVLVEHCLMW 278

.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450



gi | 50311249 | ref | XP_455649.1 | AQLHYPDYTRIHSSEIHVRISDFPTLHNLRLREANLSLVRVTVGVVTRRTGVFPOLKLVKFNCLKCGALGPF--FYQDSNEEIKISFCTNCRKGGPFRINMEKILYRNYQRITLQESPGSVAPGRLPFRHREVILLWDLVDIAKPGEEV 434
gi | 45198696 | ref | NP_985725.1 | AQLHYPDYTRIHSSEIHVRISDFPTLHNLRLREANLSLVRVTVGVVTRRTGVFPOLKLVKFNCLKCGALGPF--FYQDSNEEIKISFCTNCRKGGPFRINMEKILYRNYQRITLQESPGSVAPGRLPFRHREVILLWDLVDIAKPGEEV 443
gi | 6319448 | ref | NP_009530.1 | AQLHYPDYTRIHSSEIHVRISDFPTLHNLRLREANLSLVRVTVGVVTRRTGVFPOLKLVKFNCLKCGALGPF--FYQDSNEEIKISFCTNCRKGGPFRINMEKILYRNYQRITLQESPGSVAPGRLPFRHREVILLWDLVDIAKPGEEV 424
gi | 39946004 | ref | XP_362539.1 | VVLLHYDPYERIHAEIHVRIFDLPPIHYTLRQLRQSHLCLVRVSGVVTRRTGVFPOLKLVKFNCLKCGALGPF--FQDSNVEVIVSYQCSCSRGPFVTLNSEKTVYRNYQKLTLOESPGTVAPGRLPFRHREVILLWDLVDIAKPGEEV 420
gi | 32406108 | ref | XP_323667.1 | VVLLHYDPYERIHAEIHVRIFDLPPIHYTLRQLRQSHLCLVRVSGVVTRRTGVFPOLKLVKFNCLKCGALGPF--FQDSNVEVIVSYQCSCSRGPFVTLNSEKTVYRNYQKLTLOESPGTVAPGRLPFRHREVILLWDLVDIAKPGEEV 418
gi | 19112269 | ref | NP_595477.1 | AQLHYPDYERIHAEIHVRIFDLPPIHYTLRQLRQSHLCLVRVSGVVTRRTGVFPOLKLVKFNCLKCGALGPF--FQDSNVEVIVSYQCSCSRGPFVTLNSEKTVYRNYQKLTLOESPGTVAPGRLPFRHREVILLWDLVDIAKPGEEV 417
gi | 17137132 | ref | NP_477121.1 | MVLSIFPTYERVTHIHSSEIHVRISDFPTLHNLRLREANLSLVRVTVGVVTRRTGVFPOLKLVKFNCLKCGALGPF--FVQSONTEIKPKGCPCECOSAGPFVFNMEETIYQNYQRITLQESPGKVAAGRLPFRHREVILLWDLVDIAKPGEEV 397
gi | 158291683 | ref | XP_313198.4 | MVLSTLPTYERVTHIHSSEIHVRISDFPTLHNLRLREANLSLVRVTVGVVTRRTGVFPOLKLVKFNCLKCGALGPF--FVQSONTEIKPKGCPCECOSAGPFVFNMEETIYQNYQRITLQESPGKVAAGRLPFRHREVILLWDLVDIAKPGEEV 407
gi | 33356547 | ref | NP_004517.2 | VVLLAMYPKYDRINHIHVRISHLPLVEELRSRLQHLNQLIRTSQVVTSCITGVLPQLSMVKNCKNCFVLGPF--FCOSQNEVVKPGSCPECOSAGPFVFNMEETIYQNYQRITLQESPGKVAAGRLPFRHREVILLWDLVDIAKPGEEV 412
gi | 114589012 | ref | XP_001136645.1 | VVLLAMYPKYDRINHIHVRISHLPLVEELRSRLQHLNQLIRTSQVVTSCITGVLPQLSMVKNCKNCFVLGPF--FCOSQNEVVKPGSCPECOSAGPFVFNMEETIYQNYQRITLQESPGKVAAGRLPFRHREVILLWDLVDIAKPGEEV 412
gi | 73984933 | ref | XP_541736.2 | VVLLAMYPKYDRINHIHVRISHLPLVEELRSRLQHLNQLIRTSQVVTSCITGVLPQLSMVKNCKNCFVLGPF--FCOSQNEVVKPGSCPECOSAGPFVFNMEETIYQNYQRITLQESPGKVAAGRLPFRHREVILLWDLVDIAKPGEEV 510
gi | 6678826 | ref | NP_032590.1 | VVLLAMYPKYDRINHIHVRISHLPLVEELRSRLQHLNQLIRTSQVVTSCITGVLPQLSMVKNCKNCFVLGPF--FCOSQNEVVKPGSCPECOSAGPFVFNMEETIYQNYQRITLQESPGKVAAGRLPFRHREVILLWDLVDIAKPGEEV 412
gi | 62647780 | ref | XP_232168.3 | VVLLAMYPKYDRINHIHVRISHLPLVEELRSRLQHLNQLIRTSQVVTSCITGVLPQLSMVKNCKNCFVLGPF--FCOSQNEVVKPGSCPECOSAGPFVFNMEETIYQNYQRITLQESPGKVAAGRLPFRHREVILLWDLVDIAKPGEEV 413
gi | 194677427 | ref | XP_869445.3 | VVLLAMYPKYDRINHIHVRISHLPLVEELRSRLQHLNQLIRTSQVVTSCITGVLPQLSMVKNCKNCFVLGPF--FCOSQNEVVKPGSCPECOSAGPFVFNMEETIYQNYQRITLQESPGKVAAGRLPFRHREVILLWDLVDIAKPGEEV 467
gi | 57524951 | ref | NP_001006139.1 | VVLLAMYPKYDRINHIHVRISHLPLVEELRSRLQHLNQLIRTSQVVTSCITGVLPQLSMVKNCKNCFVLGPF--FCOSQNEVVKPGSCPECOSAGPFVFNMEETIYQNYQRITLQESPGKVAAGRLPFRHREVILLWDLVDIAKPGEEV 399
gi | 27545265 | ref | NP_775364.1 | VVLLAMYPKYDRINHIHVRISHLPLVEELRSRLQHLNQLIRTSQVVTSCITGVLPQLSMVKNCKNCFVLGPF--FCOSQNEVVKPGSCPECOSAGPFVFNMEETIYQNYQRITLQESPGKVAAGRLPFRHREVILLWDLVDIAKPGEEV 391
gi | 71997752 | ref | NP_001022416.1 | VVMMNYPFYSRVCEIHVRISDFPTLHNLRLREANLSLVRVTVGVVTRRTGVFPOLKLVKFNCLKCGALGPF--FVQNDNEVVRTIYPCSCGKGFPTINMEETIYQNYQRITLQESPGKVAAGRLPFRHREVILLWDLVDIAKPGEEV 388
gi | 145336465 | ref | NP_175112.2 | VVFDLHFNKNIHTKIYVRIINLPLVNDLIRNTRIRLTHLTMIRIGGVVTRRTGVFPOLKLVKFNCLKCGALGPF--FFONSYSYEVKVSCECOSAGPFVFNMEETIYQNYQRITLQESPGKVAAGRLPFRHREVILLWDLVDIAKPGEEV 438
gi | 115485533 | ref | NP_001067910.1 | VVFDLHFNKNIHTKIYVRIINLPLVNDLIRNTRIRLTHLTMIRIGGVVTRRTGVFPOLKLVKFNCLKCGALGPF--FFONSYSYEVKVSCECOSAGPFVFNMEETIYQNYQRITLQESPGKVAAGRLPFRHREVILLWDLVDIAKPGEEV 463
gi | 124808572 | ref | XP_001348350.1 | EAYRISPKLYKGR-ICKVLRDWPYDGLRNLRLREANLSLVRVTVGVVTRRTGVFPOLKLVKFNCLKCGALGPF--FFONSYSYEVKVSCECOSAGPFVFNMEETIYQNYQRITLQESPGKVAAGRLPFRHREVILLWDLVDIAKPGEEV 426



gi | 50311249 | ref | XP_455649.1 | EVTGIYKNTYDGNLNAKNGPFVATVLEANSIKRREGGLHDGD--EEHGLDAFVSWDEBEREFKMSRDRGIIDKIISMAPSIYGHRIKTAIAACSLFGGVGPK 558
gi | 45198696 | ref | NP_985725.1 | EVTGIYKNTYDGNLNAKNGPFVATVLEANSIKRREGGLHDGD--EEHGLDAFVSWDEBEREFKMSRDRGIIDKIISMAPSIYGHRIKTAIAACSLFGGVGPK 569
gi | 6319448 | ref | NP_009530.1 | EVTGIYKNTYDGNLNAKNGPFVATVLEANSIKRREGGLHDGD--EEHGLDAFVSWDEBEREFKMSRDRGIIDKIISMAPSIYGHRIKTAIAACSLFGGVGPK 547
gi | 39946004 | ref | XP_362539.1 | EVTGIYKNTYDGNLNAKNGPFVATVLEANSIKRREGGLHDGD--EEHGLDAFVSWDEBEREFKMSRDRGIIDKIISMAPSIYGHRIKTAIAACSLFGGVGPK 535
gi | 32406108 | ref | XP_323667.1 | EVTGIYKNTYDGNLNAKNGPFVATVLEANSIKRREGGLHDGD--EEHGLDAFVSWDEBEREFKMSRDRGIIDKIISMAPSIYGHRIKTAIAACSLFGGVGPK 542
gi | 19112269 | ref | NP_595477.1 | DVTGIYRNNFDASLNTKNGPFVATVLEANSIKRREGGLHDGD--TDDEFSLSRLDDEEERTRALAKSPDIHNRITIASMAPSIYGHRSIKTAIAAALFGGVGPK 538
gi | 17137132 | ref | NP_477121.1 | EVTGIYKNTYDGNLNAKNGPFVATVLEANSIKRREGGLHDGD--EEHGLDAFVSWDEBEREFKMSRDRGIIDKIISMAPSIYGHRIKTAIAACSLFGGVGPK 512
gi | 158291683 | ref | XP_313198.4 | EVTGIYKNTYDGNLNAKNGPFVATVLEANSIKRREGGLHDGD--EEHGLDAFVSWDEBEREFKMSRDRGIIDKIISMAPSIYGHRIKTAIAACSLFGGVGPK 522
gi | 33356547 | ref | NP_004517.2 | ELTGIYHNNYDGSNLNTANGPPVFATVILANHVAKKDN--KQVAVGELDDEDVDMITSLSKDQIQEIKIFASTAPSIYGHEDIKRGALALFGGEPK 527
gi | 114589012 | ref | XP_001136645.1 | ELTGIYHNNYDGSNLNTANGPPVFATVILANHVAKKDN--KQVAVGELDDEDVDMITSLSKDQIQEIKIFASTAPSIYGHEDIKRGALALFGGEPK 527
gi | 73984933 | ref | XP_541736.2 | ELTGIYHNNYDGSNLNTANGPPVFATVILANHVAKKDN--KQVAVGELDDEDVDMITSLSKDQIQEIKIFASTAPSIYGHEDIKRGALALFGGEPK 625
gi | 6678826 | ref | NP_032590.1 | ELTGIYHNNYDGSNLNTANGPPVFATVILANHVAKKDN--KQVAVGELDDEDVDMITSLSKDQIQEIKIFASTAPSIYGHEDIKRGALALFGGEPK 527
gi | 62647780 | ref | XP_232168.3 | ELTGIYHNNYDGSNLNTANGPPVFATVILANHVAKKDN--KQVAVGELDDEDVDMITSLSKDQIQEIKIFASTAPSIYGHEDIKRGALALFGGEPK 528
gi | 194677427 | ref | XP_869445.3 | ELTGIYHNNYDGSNLNTANGPPVFATVILANHVAKKDN--KQVAVGELDDEDVDMITSLSKDQIQEIKIFASTAPSIYGHEDIKRGALALFGGEPK 582
gi | 57524951 | ref | NP_001006139.1 | ELTGIYHNNYDGSNLNTANGPPVFATVILANHVAKKDN--KQVAVGELDDEDVDMITSLSKDQIQEIKIFASTAPSIYGHEDIKRGALALFGGEPK 514
gi | 27545265 | ref | NP_775364.1 | ELTGIYHNNYDGSNLNTANGPPVFATVILANHVAKKDN--KQVAVGELDDEDVDMITSLSKDQIQEIKIFASTAPSIYGHEDIKRGALALFGGEPK 506
gi | 71997752 | ref | NP_001022416.1 | EVTGVYTNDFDGLSNTKNGPFVATVLEANSIKRREGGLHDGD--EEHGLDAFVSWDEBEREFKMSRDRGIIDKIISMAPSIYGHRIKTAIAACSLFGGVGPK 502
gi | 145336465 | ref | NP_175112.2 | EVTGIYKNTYDGNLNAKNGPFVATVLEANSIKRREGGLHDGD--EEHGLDAFVSWDEBEREFKMSRDRGIIDKIISMAPSIYGHRIKTAIAACSLFGGVGPK 553
gi | 115485533 | ref | NP_001067910.1 | EVTGIYKNTYDGNLNAKNGPFVATVLEANSIKRREGGLHDGD--EEHGLDAFVSWDEBEREFKMSRDRGIIDKIISMAPSIYGHRIKTAIAACSLFGGVGPK 578
gi | 124808572 | ref | XP_001348350.1 | EVLGIYKTKYDIGNIKYGFPIQLQTEIENNIKERED--IQLSELDEIDKILKLDKDPNTRIRIITSLAPAIWGHKDIKTSIAYALFGGVGKGGDKSFKNNETNNFGVQNRDILNNGGHTIRGDNVLLLDGPGI 564



gi | 50311249 | ref | XP_455649.1 | AKSQILKVEKTAHRAVFAFGGASAVGLTASVRRKDIINKEWTLEGGALVLDKGVCLIDEFDKMDQDRSIEHEAMEQOISISKAGIVTSLQARCVIAAANPIGGRYNSLPLSQNVNLTPEILSRFDILLCVVRDLVDEESDNLRLAS 708
gi | 45198696 | ref | NP_985725.1 | AKSQILKVEKTAHRAVFAFGGASAVGLTASVRRKDIINKEWTLEGGALVLDKGVCLIDEFDKMDQDRSIEHEAMEQOISISKAGIVTSLQARCVIAAANPIGGRYNSLPLSQNVNLTPEILSRFDILLCVVRDLVDEESDNLRLAS 719
gi | 6319448 | ref | NP_009530.1 | AKSQILKVEKTAHRAVFAFGGASAVGLTASVRRKDIINKEWTLEGGALVLDKGVCLIDEFDKMDQDRSIEHEAMEQOISISKAGIVTSLQARCVIAAANPIGGRYNSLPLSQNVNLTPEILSRFDILLCVVRDLVDEESDNLRLAS 697
gi | 39946004 | ref | XP_362539.1 | AKSQVLYKAEKTAHRAVFAFGGASAVGLTASVRRKDIINKEWTLEGGALVLDKGVCLIDEFDKMDQDRSIEHEAMEQOISISKAGIVTSLQARCVIAAANPIGGRYNSLPLSQNVNLTPEILSRFDILLCVVRDLVDEESDNLRLAS 685
gi | 32406108 | ref | XP_323667.1 | AKSQVLYKAEKTAHRAVFAFGGASAVGLTASVRRKDIINKEWTLEGGALVLDKGVCLIDEFDKMDQDRSIEHEAMEQOISISKAGIVTSLQARCVIAAANPIGGRYNSLPLSQNVNLTPEILSRFDILLCVVRDLVDEESDNLRLAS 685
gi | 19112269 | ref | NP_595477.1 | AKSQFLKYKVEKTAHRAVFAFGGASAVGLTASVRRKDIINKEWTLEGGALVLDKGVCLIDEFDKMDQDRSIEHEAMEQOISISKAGIVTSLQARCVIAAANPIGGRYNSLPLSQNVNLTPEILSRFDILLCVVRDLVDEESDNLRLAS 688
gi | 17137132 | ref | NP_477121.1 | AKSQFLKYKVEKTAHRAVFAFGGASAVGLTASVRRKDIINKEWTLEGGALVLDKGVCLIDEFDKMDQDRSIEHEAMEQOISISKAGIVTSLQARCVIAAANPIGGRYNSLPLSQNVNLTPEILSRFDILLCVVRDLVDEESDNLRLAS 662
gi | 158291683 | ref | XP_313198.4 | AKSQFLKYKVEKTAHRAVFAFGGASAVGLTASVRRKDIINKEWTLEGGALVLDKGVCLIDEFDKMDQDRSIEHEAMEQOISISKAGIVTSLQARCVIAAANPIGGRYNSLPLSQNVNLTPEILSRFDILLCVVRDLVDEESDNLRLAS 672
gi | 33356547 | ref | NP_004517.2 | AKSQFLKYKVEKTAHRAVFAFGGASAVGLTASVRRKDIINKEWTLEGGALVLDKGVCLIDEFDKMDQDRSIEHEAMEQOISISKAGIVTSLQARCVIAAANPIGGRYNSLPLSQNVNLTPEILSRFDILLCVVRDLVDEESDNLRLAS 677
gi | 114589012 | ref | XP_001136645.1 | AKSQFLKYKVEKTAHRAVFAFGGASAVGLTASVRRKDIINKEWTLEGGALVLDKGVCLIDEFDKMDQDRSIEHEAMEQOISISKAGIVTSLQARCVIAAANPIGGRYNSLPLSQNVNLTPEILSRFDILLCVVRDLVDEESDNLRLAS 677
gi | 73984933 | ref | XP_541736.2 | AKSQFLKYKVEKTAHRAVFAFGGASAVGLTASVRRKDIINKEWTLEGGALVLDKGVCLIDEFDKMDQDRSIEHEAMEQOISISKAGIVTSLQARCVIAAANPIGGRYNSLPLSQNVNLTPEILSRFDILLCVVRDLVDEESDNLRLAS 775
gi | 6678826 | ref | NP_032590.1 | AKSQFLKYKVEKTAHRAVFAFGGASAVGLTASVRRKDIINKEWTLEGGALVLDKGVCLIDEFDKMDQDRSIEHEAMEQOISISKAGIVTSLQARCVIAAANPIGGRYNSLPLSQNVNLTPEILSRFDILLCVVRDLVDEESDNLRLAS 677
gi | 62647780 | ref | XP_232168.3 | AKSQFLKYKVEKTAHRAVFAFGGASAVGLTASVRRKDIINKEWTLEGGALVLDKGVCLIDEFDKMDQDRSIEHEAMEQOISISKAGIVTSLQARCVIAAANPIGGRYNSLPLSQNVNLTPEILSRFDILLCVVRDLVDEESDNLRLAS 678
gi | 194677427 | ref | XP_869445.3 | AKSQFLKYKVEKTAHRAVFAFGGASAVGLTASVRRKDIINKEWTLEGGALVLDKGVCLIDEFDKMDQDRSIEHEAMEQOISISKAGIVTSLQARCVIAAANPIGGRYNSLPLSQNVNLTPEILSRFDILLCVVRDLVDEESDNLRLAS 732
gi | 57524951 | ref | NP_001006139.1 | AKSQFLKYKVEKTAHRAVFAFGGASAVGLTASVRRKDIINKEWTLEGGALVLDKGVCLIDEFDKMDQDRSIEHEAMEQOISISKAGIVTSLQARCVIAAANPIGGRYNSLPLSQNVNLTPEILSRFDILLCVVRDLVDEESDNLRLAS 664
gi | 27545265 | ref | NP_775364.1 | AKSQFLKYKVEKTAHRAVFAFGGASAVGLTASVRRKDIINKEWTLEGGALVLDKGVCLIDEFDKMDQDRSIEHEAMEQOISISKAGIVTSLQARCVIAAANPIGGRYNSLPLSQNVNLTPEILSRFDILLCVVRDLVDEESDNLRLAS 656
gi | 71997752 | ref | NP_001022416.1 | AKSQFLRYAAHIAQRVSLTITGKASAVGLTASVRRKDIINKEWTLEGGALVLDKGVCLIDEFDKMDQDRSIEHEAMEQOISISKAGIVTSLQARCVIAAANPIGGRYNSLPLSQNVNLTPEILSRFDILLCVVRDLVDEESDNLRLAS 652
gi | 145336465 | ref | NP_175112.2 | AKSQFLKYKVEKTAHRAVFAFGGASAVGLTASVRRKDIINKEWTLEGGALVLDKGVCLIDEFDKMDQDRSIEHEAMEQOISISKAGIVTSLQARCVIAAANPIGGRYNSLPLSQNVNLTPEILSRFDILLCVVRDLVDEESDNLRLAS 703
gi | 115485533 | ref | NP_001067910.1 | AKSQFLKYKVEKTAHRAVFAFGGASAVGLTASVRRKDIINKEWTLEGGALVLDKGVCLIDEFDKMDQDRSIEHEAMEQOISISKAGIVTSLQARCVIAAANPIGGRYNSLPLSQNVNLTPEILSRFDILLCVVRDLVDEESDNLRLAS 728
gi | 124808572 | ref | XP_001348350.1 | GKSQVLYKVEKTAHRAVFAFGGASAVGLTASVRRKDIINKEWTLEGGALVLDKGVCLIDEFDKMDQDRSIEHEAMEQOISISKAGIVTSLQARCVIAAANPIGGRYNSLPLSQNVNLTPEILSRFDILLCVVRDLVDEESDNLRLAS 714



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gi | 50311249 | ref | XP_455649.1 | FVVD SHIRSHPDKLLDDFFD---GNVPTENPGEQDEETPLSAKORRLONLKREKEEISPISEHMLMKYIHYARTKVPKLGHMD---MDKVSRYADLRRESVITGSFPIIVRHLESILRIAESFAKMRLESFVSSWDLDRAIKVVTD 851
gi | 45198696 | ref | NP_985725.1 | FVVD SHIRSHPESDIHEPA---DEDMEEADAG---AALSNRQKLRHRDKKEEISPISEVLMKYIHYARTKVPKLGHMD---MGKVSRYADLRRESIITGSFPIIVRHLESILRIAESFAKMRLESFVSSWDLDRAIKVVTD 858
gi | 6319448 | ref | NP_009530.1 | FVVD SHVRSHPENDEDEGEELKNNGESAIQCEBINEQLNARORLQRQKKEEISPISEBLLMKYIHYARTKVPKLGHMD---MDKVSRYADLRRESISITGSFPIIVRHLESILRIAESFAKMRLESFVSSYDLDRAIKVVVD 843
gi | 39946004 | ref | XP_362539.1 | FIVGSHSRSHPTTMAQQTADG--SMEVEHD---SEQ-ADTQGS---ERKKEGEIP---ODLLRKYIHYAREKCSPKLYHMD---EDKVARLFADMRRRESLATGAVPIIVRHLEAIIRISEAFCRMRLSEYCTAQDIDRAIAVTV 816
gi | 32406108 | ref | XP_323667.1 | FIVGSHSRSHPLMNNNTQDASGGDSMEVEHD---TQAAAETQTEGHEGRKKEGEIP---OBLLRKYIHYAREKCSPKLYHMD---EDKVARLFADMRRRESLATGAVPIIVRHLEAIIRISEAFCRMRLSEYCTAQDIDRAIAVTV 829
gi | 19112269 | ref | NP_595477.1 | FVVS SHIRSHPAFDPN---MDVLKKVPTETGIDAKPIIP---ODLLRKYIHYAREKCSPKLYHMD---EDKVARLFADMRRRESLATGAVPIIVRHLEAIIRISEAFCRMRLSEYCTAQDIDRAIAVTV 807
gi | 17137132 | ref | NP_477121.1 | FVVHSHMKHHPSEEQ---PLEEE---PQLKTVDEIPDOLLRKYIHYAREKCSPKLYHMD---EDKVARLFADMRRRESLATGAVPIIVRHLEAIIRISEAFCRMRLSEYCTAQDIDRAIAVTV 777
gi | 158291683 | ref | XP_313198.4 | FVVA SHIKHHPKSE---AEEED---TQEDTQIPIODLLRKYIHYAREKCSPKLYHMD---EDKVARLFADMRRRESLATGAVPIIVRHLEAIIRISEAFCRMRLSEYCTAQDIDRAIAVTV 785
gi | 33356547 | ref | NP_004517.2 | FVVGSHVRRHPSNKEEGLANGSAAEPAM---PNTYGVPELPOEVLKYYIYAKERVHPKLNOMD---ODKVARMYDLRKESSMAGSIPITVRHIESMIRMAEAHARIMHLRDYVIEDDVMMAIRVMLE 800
gi | 114589012 | ref | XP_001136645.1 | FVVGSHVRRHPSNKEEGLANGSAAEPAM---PNTYGVPELPOEVLKYYIYAKERVHPKLNOMD---ODKVARMYDLRKESSMAGSIPITVRHIESMIRMAEAHARIMHLRDYVIEDDVMMAIRVMLE 800
gi | 73984933 | ref | XP_541736.2 | FVVGSHIRHHPNKEEGLGSSQTQEPAM---PNTYGVPELPOEVLKYYIYAKERVHPKLNOMD---ODKVARMYDLRKESSMAGSIPITVRHIESMIRMAEAHARIMHLRDYVIEDDVMMAIRVMLE 897
gi | 6678826 | ref | NP_032590.1 | FVVGSHVRRHPSNKKDEGLTNGGTTLEPAM---PNTYGVPELPOEVLKYYIYAKERVHPKLNOMD---ODKVARMYDLRKESSMAGSIPITVRHIESMIRMAEAHARIMHLRDYVIEDDVMMAIRVMLE 800
gi | 62647780 | ref | XP_232168.3 | FVVGSHVRRHPSNKKDEGLTNGGTTLEPAM---PNTYGVPELPOEVLKYYIYAKERVHPKLNOMD---ODKVARMYDLRKESSMAGSIPITVRHIESMIRMAEAHARIMHLRDYVIEDDVMMAIRVMLE 801
gi | 194677427 | ref | XP_869445.3 | FVVGSHVRRHPSNKKDEGLTNGGTTLEPAM---PNTYGVPELPOEVLKYYIYAKERVHPKLNOMD---ODKVARMYDLRKESSMAGSIPITVRHIESMIRMAEAHARIMHLRDYVIEDDVMMAIRVMLE 853
gi | 57524951 | ref | NP_001006139.1 | FVVS SHVKKHHPGSKA---VNGDADPEVIL---PNTYGVPELPOEVLKYYIYAKERVHPKLNOMD---ODKVARMYDLRKESSMAGSIPITVRHIESMIRMAEAHARIMHLRDYVIEDDVMMAIRVMLE 784
gi | 27545265 | ref | NP_775364.1 | FVVGSHIKHHPNKE---GVAGLEEVVL---PNTYGVPELPOEVLKYYIYAKERVHPKLNOMD---ODKVARMYDLRKESSMAGSIPITVRHIESMIRMAEAHARIMHLRDYVIEDDVMMAIRVMLE 776
gi | 71997752 | ref | NP_001022416.1 | FVVGSHVRRHPSNKEEGLANGSAAEPAM---PNTYGVPELPOEVLKYYIYAKERVHPKLNOMD---ODKVARMYDLRKESSMAGSIPITVRHIESMIRMAEAHARIMHLRDYVIEDDVMMAIRVMLE 774
gi | 145336465 | ref | NP_175112.2 | FVVS SHFKSQPKGKMGED---SDPEDEIGGS---SGS TDPVLPONLLRKYIYAKERVHPKLGELD---AKKLETVYANLRRESMNGQVSIATRHLSESMIRMAEAHARIMHLRDYVIEDDVMMAIRVMLE 825
gi | 115485533 | ref | NP_001067910.1 | FVVD SHARSQPKGANLSDRVPTDVEDDPLAA---ARQADPDILSODMLKYYIYAKERVHPKLNOMD---LDKISHVYAE LRRES SHGQGVPIAVRHIESIIRMSAEHARIMHLRSVSGEDVDMAIRVLLD 853
gi | 124808572 | ref | XP_001348350.1 | FVVVTHQLSHPKLENTQNYKRITENLNKVIIVS---SAVEPIPLDOLLRKYIHYARTKVPKLSQVPAEISAKLSNFYRVRQKASAGCGVPLLRHIESIIRIAEANAKMRLSHQIYSKDVVYAIATLLE 842
.....910.....920.....930.....940.....950.....960.....970.....980.....990.....1000.....1010.....1020.....1030.....1040.....1050

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gi | 50311249 | ref | XP_455649.1 | SFVGAOKISVRRQLOR--SFAYVITMGTM----- 877
gi | 45198696 | ref | NP_985725.1 | SFVGAOKISVRRQLOR--SFAYITMSRGD----- 885
gi | 6319448 | ref | NP_009530.1 | SFVDAOKVSVRRQLRR--SFAYITLGH----- 868
gi | 39946004 | ref | XP_362539.1 | SFVGSQKVSCKKALAR--AFAKYILARPAGAGRRLAGT--GRGGRAFAAASA 865
gi | 32406108 | ref | XP_323667.1 | SFVGSQKVSCKKALAR--AFAKYILNRPQTGNNGSCSGTISQRRRGARRGVSAAA 882
gi | 19112269 | ref | NP_595477.1 | SFVNAOKMSVRRSLR--TFAKYILI----- 830
gi | 17137132 | ref | NP_477121.1 | SFIEAOKFVSMKKMRS--TFQKYLSPQKDHSELLFFILROLDLQLAIRCKDG---PGATHVEIMERDLIERAKQLDIVNLKPFYSEDLFRTNGFSYDPKRRITLQIVVDGNTA 887
gi | 158291683 | ref | XP_313198.4 | SFIEAOKFVSMKKMRA--TFQKYLSPQKDHSELLFFILROLDLQLAIRCKEAGRRGKABEGDRPRTTVVEVMERDLSERAKAIDIFNLKPFLESELFRQNGFTYDAKRVIVQVPEAAEP 906
gi | 33356547 | ref | NP_004517.2 | SFIDTQKFSVMRSMRK--TFARYLSFRRDNNELELLFILKQLVAEQVTYQRNRFQ---AQODTIEVPEKDLVDKARQINIHNLSAFYDSELFRMKNKFSHDLKRRKMILQOF 904
gi | 114589012 | ref | XP_001136645.1 | SFIDTQKFSVMRSMRK--TFARYLSFRRDNNELELLFILKQLVAEQVTYQRNRFQ---AQODTIEVPEKDLVDKARQINIHNLSAFYDSELFRMKNKFSHDLKRRKMILQOF 905
gi | 73984933 | ref | XP_541736.2 | SFIDTQKFSVMRSMRK--TFARYLSFRRDNNELELLFILKQLVAEQVTYQRNRFQ---AQODTIEVPEKDLVDKARQINIHNLSAFYDSELFRMKNKFSHDLKRRKMILQOF 1001
gi | 6678826 | ref | NP_032590.1 | SFIDTQKFSVMRSMRK--TFARYLSFRRDNNDLLELLFILKQLVAEQVTYQRNRFQ---AQODTIEVPEKDLMDKARQINIHNLSAFYDSDLFKFKNKFSDRLKRLKILQOF 904
gi | 62647780 | ref | XP_232168.3 | SFIDTQKFSVMRSMRK--TFARYLSFRRDNNDLLELLFILKQLVAEQVTYQRNRFQ---AQODTIEVPEKDLMDKARQINIHNLSAFYDSDLFKFKNKFSDRLKRLKILQOF 905
gi | 194677427 | ref | XP_869445.3 | SFVDTQKFSVMRMRK--TFARYLSFRRDNNELELLFILKQLVAEQVTYQRNRFQ---AQODTIEVPEKDLVDKARQINIHNLSAFYDSELFRMKNKFSHDLKRRKILQOF 957
gi | 57524951 | ref | NP_001006139.1 | SFIDTQKFSVMRSMRK--TFARYLSFRRDNNELELLFILKQLVAEQVTYQRNRFQ---AQODTIEVPEKDLVDKARQINIHNLSAFYDSELFRMKNKFSHDLKRRKILQOF 888
gi | 27545265 | ref | NP_775364.1 | SFIDTQKFSVMRSMRK--TFARYLAFRRDNNELELLFILKQLVSEQVSYQRNRYG---AQODTIEVPEKDLVDKARQINIHNLSAFYDSDLFRSNKFSHDLKRRKILQOF 880
gi | 71997752 | ref | NP_001022416.1 | SFVNTQKASIMRMMKK--TFSRHLTENRSANELLELLFILKQLRQOMHATARAAG---HILQSVTIPSEPIEKAQOLRTENVKPFVYSEIFASNFVYDPSKKTIVQEIF 881
gi | 145336465 | ref | NP_175112.2 | SFISTQKFGVQRTLRE--SFKRYITVKKDFNSLLLVLLKELVKNALKFEIISGSN---SGLPTIEVKVIEELQTKAKEYDADLRPFPS--TDFSKAHFELDHGRGMKCPKRLITW 936
gi | 115485533 | ref | NP_001067910.1 | SFISTQKFGVQKALOK--NFRKYMVYKKDYNELLLLLLRTLVKDVLFHFEEIVSGPT---RLRTHIEVKVIEDLKNKAEYIYDLRPFPS--AHFRDNFVLDGGRGILRHPLAA 961
gi | 124808572 | ref | XP_001348350.1 | SVVSCRFQFAVAKQLSK--EFARYRALFRGGYVLRRELLRRTVQMTIQEONLNKASAKDFDNDSGEGTSEAEILNPNVNFPLHFMKTAQMKFSEYQVNWMMKSKVFNEHYAVIKRDGVEGLIKKPKV 971
.....1060.....1070.....1080.....1090.....1100.....1110.....1120.....1130.....1140.....1150.....1160.....1170.....1180

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