

gi | 4506067 | ref | NP_002728.1 | -----MADVFPNDSTASQDVANRFARKGALRQKNVHEVKDHFARFFKOPTFCSHCTDFIW-----GFGKGFQCFVVKRCHEVVFPCGADKGPDIIDPRSKHKFKIHTYGSPTFCDHCGSLLYGLIHQGMK 150
gi | 6755078 | ref | NP_035231.1 | -----MADVFPNDSTASQDVANRFARKGALRQKNVHEVKDHFARFFKOPTFCSHCTDFIW-----GFGKGFQCFVVKRCHEVVFPCGADKGPDIIDPRSKHKFKIHTYGSPTFCDHCGSLLYGLIHQGMK 150
gi | 73965409 | ref | XP_548026.2 | -----MADVFPAAEPAPQDVANRFARKGALRQKNVHEVKNRFRARFFKOPTFCSHCTDFIW-----GFGKGFQCFVVKRCHEVVFPCGADKGPDIIDPRSKHKFKIHTYGSPTFCDHCGSLLYGLIHQGMK 150
gi | 27806089 | ref | NP_776860.1 | -----MADVFPAAEPAPQDVANRFARKGALRQKNVHEVKNRFRARFFKOPTFCSHCTDFIW-----GFGKGFQCFVVKRCHEVVFPCGADKGPDIIDPRSKHKFKIHTYGSPTFCDHCGSLLYGLIHQGMK 150
gi | 109489230 | ref | XP_343976.3 | -----MADVFPAAEPAPQDVANRFARKGALRQKNVHEVKNRFRARFFKOPTFCSHCTDFIW-----GFGKGFQCFVVKRCHEVVFPCGADKGPDIIDPRSKHKFKIHTYGSPTFCDHCGSLLYGLIHQGMK 150
gi | 61098322 | ref | NP_001012822.1 | -----MADVFPQSEPGAAPDAARFRARKGALRQKNVHEVKEHFKIARFFKOPTFCSHCTDFIW-----GFGKGFQCFVVKRCHEVVFPCGADKGPDIIDPRSKHKFKIHTYGSPTFCDHCGSLLYGLIHQGMK 150
gi | 292614846 | ref | XP_002662450.1 | -----MADTQSNQSS--DVANRFARKGALRQKNVHEVKEHFKIARFFKOPTFCSHCTDFIW-----GFGKGFQCFVVKRCHEVVFPCGADKGPDIIDPRSKHKFKIHTYGSPTFCDHCGSLLYGLIHQGMK 150
gi | 71986426 | ref | NP_001024517.1 | -----MSLSTNSSVDEAQRIGKAFVRRGALRQKNVHEVKEHFKIARFFKOPTFCSHCTDFIW-----GITIKQGFQCFVVKRCHEVVFPCGADKGPDIIDPRSKHKFKIHTYGSPTFCDHCGSLLYGLIHQGMK 150
gi | 24654282 | ref | NP_725626.1 | MSEGSDNNDPQQQAGEG-EAVGENKMKSRRLKRGALKKKNVFNVKDHFARFFKOPTFCSHCKDFICGYQSYAWMGFGKGFQCFVVKRCHEVVFPCGADKGDSDSPKTHQNFEPFYAGPTFCDHCGSLLYGLIHQGLK 150
gi | 158300340 | ref | XP_320290.4 | -GTGRKMADDNDTLEIIPAEENKMLNRGRGKALKKKNVFNVKDHFARFFKOPTFCSHCKDFICGFAVCHLGFQKGFQCFVVKRCHEVVFPCGADKGDSDSDTRKHFKEKWTSSPTFCDHCGSLLYGLIHQGLK 150
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150



gi | 4506067 | ref | NP_002728.1 | CDTCDMNVHKQCVINVPVSLCGMDHTEKRGRIYLKAEVADEKLHVTVRDAKNLIPMDPNGLSDPVYKLLKLIIP-DPKNESKQKTKTIRSLNLPQWNSFTFKLKPDKDRRLSVEIWDWDRITRNDFMGSLSPGVSSELMKMPASGWYKLLNQ 300
gi | 6755078 | ref | NP_035231.1 | CDTCDMNVHKQCVINVPVSLCGMDHTEKRGRIYLKAEVADEKLHVTVRDAKNLIPMDPNGLSDPVYKLLKLIIP-DPKNESKQKTKTIRSLNLPQWNSFTFKLKPDKDRRLSVEIWDWDRITRNDFMGSLSPGVSSELMKMPASGWYKLLNQ 300
gi | 73965409 | ref | XP_548026.2 | CDTCDMNVHKQCVINVPVSLCGMDHTEKRGRIYLKAEVADEKLHVTVRDAKNLIPMDPNGLSDPVYKLLKLIIP-DPKNESKQKTKTIRSLNLPQWNSFTFKLKPDKDRRLSVEIWDWDRITRNDFMGSLSPGVSSELMKMPASGWYKLLNQ 300
gi | 27806089 | ref | NP_776860.1 | CDTCDMNVHKQCVINVPVSLCGMDHTEKRGRIYLKAEVADEKLHVTVRDAKNLIPMDPNGLSDPVYKLLKLIIP-DPKNESKQKTKTIRSLNLPQWNSFTFKLKPDKDRRLSVEIWDWDRITRNDFMGSLSPGVSSELMKMPASGWYKLLNQ 300
gi | 109489230 | ref | XP_343976.3 | CDTCDMNVHKQCVINVPVSLCGMDHTEKRGRIYLKAEVADEKLHVTVRDAKNLIPMDPNGLSDPVYKLLKLIIP-DPKNESKQKTKTIRSLNLPQWNSFTFKLKPDKDRRLSVEIWDWDRITRNDFMGSLSPGVSSELMKMPASGWYKLLNQ 300
gi | 61098322 | ref | NP_001012822.1 | CDTCDMNVHKQCVINVPVSLCGMDHTEKRGRIYLKAEVADEKLHVTVRDAKNLIPMDPNGLSDPVYKLLKLIIP-DPKNESKQKTKTIRSLNLPQWNSFTFKLKPDKDRRLSVEIWDWDRITRNDFMGSLSPGVSSELMKMPASGWYKLLNQ 300
gi | 292614846 | ref | XP_002662450.1 | CDTCDMNVHKQCVINVPVSLCGMDHTEKRGRIYLKAEVADEKLHVTVRDAKNLIPMDPNGLSDPVYKLLKLIIP-DPKNESKQKTKTIRSLNLPQWNSFTFKLKPDKDRRLSVEIWDWDRITRNDFMGSLSPGVSSELMKMPASGWYKLLNQ 300
gi | 71986426 | ref | NP_001024517.1 | CDTCDMNVHKQCVINVPVSLCGMDHTEKRGRIYLKAEVADEKLHVTVRDAKNLIPMDPNGLSDPVYKLLKLIIP-DPKNESKQKTKTIRSLNLPQWNSFTFKLKPDKDRRLSVEIWDWDRITRNDFMGSLSPGVSSELMKMPASGWYKLLNQ 300
gi | 24654282 | ref | NP_725626.1 | CSACDMNVHARCKENVPVSLCGDHTERRGRIYLEINVKNLLTVQIKRGNLIPMDPNGLSDPVYKLLKLIIPDDKQDS-KKTRTIRACLNPNVWNETLTYDLKPEDKDRRLSVEIWDWDRITRNDFMGSLSPGVSSELMKMPASGWYKLLNQ 300
gi | 158300340 | ref | XP_320290.4 | CTACDMNVHKRCESVSNLCCGDDHTERRGRIYLAAGLNIEVQGRNLLIPMDPNGLSDPVYKLLKLIIP-DADNV-KKTRTIRASLNPNVWNETLTYDLKPEDKDRRLSVEIWDWDRITRNDFMGSLSPGVSSELMKMPASGWYKLLNQ 300
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300



gi | 4506067 | ref | NP_002728.1 | EGEYYNVPVPEGDEEGNMLRQKFEK--AKLGPAGNKVIPSSEDRKQ--PSNNLDRVKLTDNFNLMVLGKGSFGKVMADRKGTBELYAIKILKRDVVIQDDVVECTMVEKRVLALLDKPPFLTQLHSCFQIVDRLYFVMEYVNGGD 450
gi | 6755078 | ref | NP_035231.1 | EGEYYNVPVPEGDEEGNMLRQKFEK--AKLGPVGNKVIPSSEDRKQ--PSNNLDRVKLTDNFNLMVLGKGSFGKVMADRKGTBELYAIKILKRDVVIQDDVVECTMVEKRVLALLDKPPFLTQLHSCFQIVDRLYFVMEYVNGGD 450
gi | 73965409 | ref | XP_548026.2 | EGEYYNVPVPEGDEEGNMLRQKFEK--AKLGPAGNKVIPSSEDRKQ--PSNNLDRVKLTDNFNLMVLGKGSFGKVMADRKGTBELYAIKILKRDVVIQDDVVECTMVEKRVLALLDKPPFLTQLHSCFQIVDRLYFVMEYVNGGD 450
gi | 27806089 | ref | NP_776860.1 | EGEYYNVPVPEGDEEGNMLRQKFEK--AKLGPAGNKVIPSSEDRKQ--PSNNLDRVKLTDNFNLMVLGKGSFGKVMADRKGTBELYAIKILKRDVVIQDDVVECTMVEKRVLALLDKPPFLTQLHSCFQIVDRLYFVMEYVNGGD 450
gi | 109489230 | ref | XP_343976.3 | EGEYYNVPVPEGDEEGNMLRQKFEK--AKLGPAGNKVIPSSEDRKQ--PSNNLDRVKLTDNFNLMVLGKGSFGKVMADRKGTBELYAIKILKRDVVIQDDVVECTMVEKRVLALLDKPPFLTQLHSCFQIVDRLYFVMEYVNGGD 450
gi | 61098322 | ref | NP_001012822.1 | EGEYYNVPVPEGDEEGNMLRQKFEK--AKLGPAGNKVIPSSEDRKQ--PSNNLDRVKLTDNFNLMVLGKGSFGKVMADRKGTBELYAIKILKRDVVIQDDVVECTMVEKRVLALLDKPPFLTQLHSCFQIVDRLYFVMEYVNGGD 450
gi | 292614846 | ref | XP_002662450.1 | EGEYYNVPVPEGDEEGNMLRQKFEK--AKLGPAGNKVIPSSEDRKQ--PSNNLDRVKLTDNFNLMVLGKGSFGKVMADRKGTBELYAIKILKRDVVIQDDVVECTMVEKRVLALLDKPPFLTQLHSCFQIVDRLYFVMEYVNGGD 450
gi | 71986426 | ref | NP_001024517.1 | EGEYYNVPVPEGDEEGNMLRQKFEK--AKLGPAGNKVIPSSEDRKQ--PSNNLDRVKLTDNFNLMVLGKGSFGKVMADRKGTBELYAIKILKRDVVIQDDVVECTMVEKRVLALLDKPPFLTQLHSCFQIVDRLYFVMEYVNGGD 450
gi | 24654282 | ref | NP_725626.1 | DEGEYYNVPVCA-DDEQDLKLRKQKPSQ--KIPMVMRSDDTNT--HTSKKDMIRATDFNFKVGLKGSFGKVLAEERKGSBELYAIKILKRDVVIQDDVVECTMVEKRVLALLDKPPFLTQLHSCFQIVDRLYFVMEYVNGGD 450
gi | 158300340 | ref | XP_320290.4 | EGEYYNVPVPEGADLVQLKS-QMR--KIPMVMRSDDTNT--HTSKKDMIRATDFNFKVGLKGSFGKVLAEERKGSBELYAIKILKRDVVIQDDVVECTMVEKRVLALLDKPPFLTQLHSCFQIVDRLYFVMEYVNGGD 450
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450



gi | 4506067 | ref | NP_002728.1 | LMYHIQVQVGFKEPQAVFYA--AEISIGLFFLHK--RGIIYRDLK-LDNVMLDSEG--HIKIADFQGMCKEHHMDGVTTRFCGTPDYIAPETIAYQPYGKSVDDWYAGVLLYEMLAGPPDFGDEDELFQSIEMHNVSYPKSLSKEAV 600
gi | 6755078 | ref | NP_035231.1 | LMYHIQVQVGFKEPQAVFYA--AEISIGLFFLHK--RGIIYRDLK-LDNVMLDSEG--HIKIADFQGMCKEHHMDGVTTRFCGTPDYIAPETIAYQPYGKSVDDWYAGVLLYEMLAGPPDFGDEDELFQSIEMHNVSYPKSLSKEAV 600
gi | 73965409 | ref | XP_548026.2 | LMYHIQVQVGFKEPQAVFYA--AEISIGLFFLHK--RGIIYRDLK-LDNVMLDSEG--HIKIADFQGMCKEHHMDGVTTRFCGTPDYIAPETIAYQPYGKSVDDWYAGVLLYEMLAGPPDFGDEDELFQSIEMHNVSYPKSLSKEAV 600
gi | 27806089 | ref | NP_776860.1 | LMYHIQVQVGFKEPQAVFYA--AEISIGLFFLHK--RGIIYRDLK-LDNVMLDSEG--HIKIADFQGMCKEHHMDGVTTRFCGTPDYIAPETIAYQPYGKSVDDWYAGVLLYEMLAGPPDFGDEDELFQSIEMHNVSYPKSLSKEAV 600
gi | 109489230 | ref | XP_343976.3 | LMYHIQVQVGFKEPQAVFYA--AEISIGLFFLHK--RGIIYRDLK-LDNVMLDSEG--HIKIADFQGMCKEHHMDGVTTRFCGTPDYIAPETIAYQPYGKSVDDWYAGVLLYEMLAGPPDFGDEDELFQSIEMHNVSYPKSLSKEAV 600
gi | 61098322 | ref | NP_001012822.1 | LMYHIQVQVGFKEPQAVFYA--AEISIGLFFLHK--RGIIYRDLK-LDNVMLDSEG--HIKIADFQGMCKEHHMDGVTTRFCGTPDYIAPETIAYQPYGKSVDDWYAGVLLYEMLAGPPDFGDEDELFQSIEMHNVSYPKSLSKEAV 600
gi | 292614846 | ref | XP_002662450.1 | LMYHIQVQVGFKEPQAVFYA--AEISIGLFFLHK--RGIIYRDLK-LDNVMLDSEG--HIKIADFQGMCKEHHMDGVTTRFCGTPDYIAPETIAYQPYGKSVDDWYAGVLLYEMLAGPPDFGDEDELFQSIEMHNVSYPKSLSKEAV 600
gi | 71986426 | ref | NP_001024517.1 | LMYHIQVQVGFKEPQAVFYA--AEISIGLFFLHK--RGIIYRDLK-LDNVMLDSEG--HIKIADFQGMCKEHHMDGVTTRFCGTPDYIAPETIAYQPYGKSVDDWYAGVLLYEMLAGPPDFGDEDELFQSIEMHNVSYPKSLSKEAV 600
gi | 24654282 | ref | NP_725626.1 | LMFQIQVQVGFKEPQAVFYA--AEISIGLFFLHK--RGIIYRDLK-LDNVMLDSEG--HIKIADFQGMCKEHHMDGVTTRFCGTPDYIAPETIAYQPYGKSVDDWYAGVLLYEMLAGPPDFGDEDELFQSIEMHNVSYPKSLSKEAV 600
gi | 158300340 | ref | XP_320290.4 | LMFQIQVQVGFKEPQAVFYA--AEISIGLFFLHK--RGIIYRDLK-LDNVMLDSEG--HIKIADFQGMCKEHHMDGVTTRFCGTPDYIAPETIAYQPYGKSVDDWYAGVLLYEMLAGPPDFGDEDELFQSIEMHNVSYPKSLSKEAV 600
.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600



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gi |4506067|ref|NP_002728.1|  SICKGLMTKHPAKRLGCGPEGE---RDVREHAFFRRIDWEKLENREIQPPFKPKVCG-KGAENFDKFFTRGQPVLTTPDQLVIANIDQSDFEFGFSYVNPQFVHPILQSAV  710
gi |6755078|ref|NP_035231.1|  SICKGLMTKHPAKRLGCGPEGE---RDVREHAFFRRIDWEKLENREIQPPFKPKVCG-KGAENFDKFFTRGQPVLTTPDQLVIANIDQSDFEFGFSYVNPQFVHPILQSAV  710
gi |73965409|ref|XP_548026.2|  SICKGLMTKHPGKRLGCGPEGE---RDVREHAFFRRIDWEKLENREIQPPFKPKVCG-KGAENFDKFFTRGQPVLTTPDQLVIANIDQSDFEFGFSYVNPQFVHPILQSAV  710
gi |27806089|ref|NP_776860.1|  SICKGLMTKHPGKRLGCGPEGE---RDVREHAFFRRIDWEKLENREIQPPFKPKVCG-KGAENFDKFFTRGQPVLTTPDQLVIANIDQSDFEFGFSYVNPQFVHPILQSAV  710
gi |109489230|ref|XP_343976.3|  SICKGLMTKHPAKRLGCGPEGE---RDVREHAFFRRIDWEKLENREIQPPFKPKVCG-KGAENFDKFFTRGQPVLTTPDQLVIANIDQSDFEFGFSYVNPQFVHPILQSAV  710
gi |61098322|ref|NP_001012822.1|  SICKGLMTKHPAKRLGCGLEGE---RDIREHAFFRRIDWEKLENREIQPPFKPKVCG-KGAENFDKFFTRGQPVLTTPDQLVIANIDQSDFEFGFSYVNPQFVHPLENVA  710
gi |292614846|ref|XP_002662450.1|  SICKGLMTKHPGKRLGCGQEGE---RDIREHAFFRRIDWDLANREIQPPFKPKVCG-KGAENFDKFFTRGQPVLTTPDQLVIANIDQADFDGFIQVNPQFVHPILVNTIE  710
gi |71986426|ref|NP_001024517.1|  SLCKALLIKNPSKRLGCTGDDEEASRDIKEHPFFRRIDWFKIETRCIQPPFKPKLKTDRSLENFDHSFLKLPKMTKPPDWEVLENLKGDEFSNFFVNPFFVVKDVEE---  710
gi |24654282|ref|NP_725626.1|  EACKGFLTKQPNKRLGCGSSGE---EDVRLHPPFFRRIDWEKLENREIQPPFKPKIKHRKDVSNFDKQFTSEKTDLTPDKVFMMLDQSEFVGFSYMNPQVVFSE-----  710
gi |158300340|ref|XP_320290.4|  DVCKGLLTKNPKRLGCGARGE---EDVRAHAFFRRIDWEKLENREIQPPFKPKIKHRKDVSNFDKQFTSEKTDLTPDKLFMMMLDQTEFNGFSYLNQPEFVQV-----  710
.....610.....620.....630.....640.....650.....660.....670.....680.....690.....700.....710

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