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gi|47086565|ref|NP_997905.1|      YKPDLIWSDGDWEAPDITYWNSTEFLLAWLYNDSPVKDI VVVNDRWNGG-----CYCKHGGYYNCADKFNPKLLNHKWEKCSVDKISWGYRRNMKLSBELMDLPELVQDLVYIVALGGNYLLS[GP]ADGVIAPVFERLRGIGAW 349
gi|57525882|ref|NP_001003559.1|  YKPDLIWSDGDWEAPDITYWNSTEFLLAWLYNDSPVKDI VVVNDRWNGG-----CYCKHGGYYNCADKFSPELPPKHWEKCSVDTI SWGYRRNMKLSBELMDLPA LIKDLVYIVALGGNYLLNVP[ADGVIAPVFERLRGIGAW] 349
gi|31541781|ref|NP_077205.2|     YKPDLIWSDGEWECPTDYWNSTEFLLAWLYNDSPVKDEIVVNDRWGON-----CSCHGGYYNCQDKYKPSLPPDHKWEKCSMDRASWGYRKDMTMTSTIAKENIIEELVQIVSLGGNYLLNIGPTKDG LIVPIFQERLLAVGKW 347
gi|6978861|ref|NP_036694.1|     YKPDLIWSDGEWECPTDYWNSTEFLLAWLYNDSPVKDQVVVNDRWGON-----CSCHGGYYNCEDKYPHSLPPDHKWEKCSVDKASWGYRRDMSMTSTVDENEIIEELVQIVSLGGNYLLNIGPNKDGVIIVPIFQERLLAVGKW 357
gi|119360348|ref|NP_000138.2|    YKPDLIWSDGEWECPTDYWNSTNFLSWLYNDSPVKDEVVVNDRWGON-----CSCHGGYYNCEDKFKPQSLPPDHKWEKCSIDKFSWGYRRDMALS DVTEESEIIEELVQIVSLGGNYLLNIGPTKDG LIVPIFQERLLAVGKW 361
gi|114554669|ref|XP_524607.2|    YKPDLIWSDGEWECPTDYWNSTNFLSWLYNDSPVKDEVVVNDRWGON-----SIDKFSWGYRRDMAMSDVTEESEIIEELVQIVSLGGNYLLNIGPTKDG LIVPIFQERLLAVGKW 422
gi|114051279|ref|NP_001039500.1| YKPDLIWSDGEWECPTDYWNSTDFLLAWLYNDSPVKDEVVVNDRWGON-----CSCHGGYYNCCKDKFQPEITLPPDHKWEKCSIDQSWGYRRDMEMADITNESTIIEELVQIVSLGGNYLLNIGPTKDG LIVPIFQERLLAVGKW 364
gi|50979046|ref|NP_001003250.1| YKPDLIWSDGEWECPTDYWNSTDFLLAWLYNDSPVKDHHVVVNDRWGON-----CSCHGGYYNCQDKYKPSLPPDHKWEKCSIDKFSWGYRRNMVMSDVASICEIIEELVQIVSLGGNYLLNIGPTKDG LIVPIFQERLLAVGKW 362
gi|118101754|ref|XP_417835.2|    YKPDLIWSDGDWEAPDITYWNSTEFLLAWLYNDSPVKDITVVVNDRWGON-----CSCHGGYYNCADKFKPGLTLLAHKWEKCSIDKISWGYRSNMHIDELMDVASIIEELVQIVSFGGNYLLNIGPTKEGVIIVPIFQERLLAVGKW 346
gi|39975075|ref|XP_368928.1|    YISDLQVPMETLAV--KYGTDIMWCDCGASNGTAEFAARWNNEARQKQNRVAINSRCGTAAHAADFTEPEYQTFSSAQDFKWSNRGMDPYSYGNRAIQDEEYMNATTIVHTLVDMVSKHGNFLLNIGPKPDGTTAPIMADNLR IAGRW 681
gi|145611908|ref|XP_369202.2|    FVVDLQLPQMNIIAYDDRYEIEELMWCIDIGNANNSLTFASAWINWARDRGROVTFNDRCC--IPGDFAPPEYFTHDGLVVPKWESSRGMDPFSYGNRPTPDAAYLTGLDIVKSLVDIVKNGNLLLDVGPRA DGIPEVMRRGLRDAAGW 595
.....610.....620.....630.....640.....650.....660.....670.....680.....690.....700.....710.....720.....730.....740.....750

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gi|47086565|ref|NP_997905.1|      LQINGEAIYGSFWR-----VQENAVTPVWYTKAKKSTVYAIFTTNP--MQNIFQLSAPNTTDSVTVVTLGSPK---PLKWAFLQS---SGLMVVLPPELP---FSPA YAWTLKMEGVA 451
gi|57525882|ref|NP_001003559.1|  LQINGEAIYATSSWR-----VQAEAVTPVWYTSKNSTVYAIFTSSP--NQNTFELSAPKTSNDTVVTLGNPK---PLKWAFLHS---SGLLILLPDLF---FSPA QAWTLKLEGVA 451
gi|31541781|ref|NP_077205.2|     LQINGEAIYASKPWR-----VQSEKNKIVVWYTTKNTTVYAIFFLYWP--ENGIVNLKSPKMTSAKIKITMLGEG---DLSWIQDPL---EGLVITLPLPPTVLPVFAWTLK LKAKVN 452
gi|6978861|ref|NP_036694.1|     LQINGEAIYASKPWR-----VQSERNKIVVWYTTKDSAVYAIFFLHWP--EDGVVNLQSPKMTSAKIKITMLGMEG---ELHWIQDPL---EGLVITLPLPPTVLPVFAWTLK LKAKVN 462
gi|119360348|ref|NP_000138.2|    LSINGEAIYASKPWR-----VQWEKNTTSVWYTSKGS AVYAIFFLHWP--ENGVLNLESPITTTSTIKITMLGIQG---DLKWTDPD---KGLFISLPLPSPS AVPAEFAWTIK LKGVK 466
gi|114554669|ref|XP_524607.2|    LSINGEAIYASKPWR-----VQWEKNTTSVWYTSKGS AVYAIFFLHWP--ENGVLNLESPITTTSTIKITMLGIQG---DLKWTDPD---KGLLISLPLPSPS AVPAEFAWTIK LKGVK 527
gi|114051279|ref|NP_001039500.1|  LSINGEAIYASKPWR-----VQSEKN--SVWYTSKGLAVYAILLHWP--EYGLSLISPIATSTIKITMLGIQK---DLKWLNPSC---KGLLVFLPLPSPAALPTEFAWTIK LKGVK 468
gi|50979046|ref|NP_001003250.1|  LSINGEAIYASKPWR-----VQLEKNTTSVWYTSRGMIVYAIFFLWNP--ENGVLNLESPITTTSTIKITMLGIQK---DLKWTDPD---GLLIYLPQLSLFTELPVFAWTIK LKGVK 466
gi|118101754|ref|XP_417835.2|    LDINGEAIYASKPWR-----VQMNSTDTVWYTSKGS AVYAIFFLWNP--NSVLQLSVPTTSPAPQVITMLGFAG---TLQWQQPPG---EGLLVTLPDAPPSPVRSQPGWAVRLEGV K 451
gi|39975075|ref|XP_368928.1|    IKRHEASLYNTVWFLSQVGSQDGAIPDVRFTRAKDAFYSLFLEKPKIGGDGYVITIPAAVPLEGDEVSLLVGGGKLAFAKIVGSPGGQGGDKSLKIKVDQKLLDNEEICWVFKIYVA 803
gi|145611908|ref|XP_369202.2|    IRSHAEAVFDTRFWC-----HGPGRDP--FRYTVTDDAFYIHVNARF--AGGGAVLVVDPDRVFLDGKVVVVG---ALAGIEVPAALNADGTVGLSLSDDEVVAADDYV VFKIQYNL 702
.....760.....770.....780.....790.....800.....810.....820.....830.....840.....850.....860.....870..

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