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gi | 161076197 | ref | NP_001104452.1 | --MDIE-LPVLAELVYRGRACIKGCKSISKDKILRIAMVMSAFHDAKVPNWFHKKCFKFNQRPVSVG---DIQNIQLRFDKQKELTD---LVENIQEVI---AIGKGRSKAFNLALKDFGIEYAKSRSTCRGCEKINKDL 150
gi | 158291429 | ref | XP_312938.3 | --MDAEQLPFLAEYKSNRAMCRLCKOAIKADVLRRLAAMVQSPMHDGKVAQWYHDDCFKFKQRPATEG---DVANTEALRYEDOKKIRDAVFAKGVVAVAG---KKGKGRRTAVEAQLKDYGVEYAPSGRAMCRGCEIKILKDE 150
gi | 156523968 | ref | NP_001609.2 | MAES-SDKLYRVEYAKSGRASCKKCSSESIPKDSLRLMALMVQSPMFDGKVPWHYHFCFVKVGHSTRHPD---VEVDGFSLELRWDDQOKVKKTAE---AGGVT---GKGGDGGIGSKAEKILGDFAAEYAKSNRSTCKGCMEMKIEKGG 150
gi | 73960821 | ref | XP_863797.1 | -----MFDGKVPWHYHFCFVKVGHSTRHPD---VEVDGFSLELRWDDQOKVKKTAE---AGGVTGVAAMSDPSGKGGDGGGGKTDKTLADFAAEYAKSNRSTCKGCKLEKIEKGG 150
gi | 20806109 | ref | NP_031441.2 | MAEA-SERLYRVEYAKSGRASCKKCSSESIPKDSLRLMALMVQSPMFDGKVPWHYHFCFVKVGHSTRHPD---VEVDGFSLELRWDDQOKVKKTAE---AGGVA---GKGGDGGGGKAEKILGDFLAEYAKSNRSTCKGCKLEKIEKGG 150
gi | 6978455 | ref | NP_037195.1 | MAEA-TERLYRVEYAKSGRASCKKCSSESIPKDSLRLMALMVQSPMFDGKVPWHYHFCFVKVGHSTRHPD---VEVDGFSLELRWDDQOKVKKTAE---AGGVA---GKGGHGGGKAEKILGDFAAEYAKSNRSTCKGCKLEKIEKGG 150
gi | 27807449 | ref | NP_777176.1 | MAES-SDKLYRVEYAKSGRASCKKCSSESIPKDSLRLMALMVQSPMFDGKVPWHYHFCFVKVGHSTRHPD---VEVDGFSLELRWDDQOKVKKTAE---AGGVA---GKGGDGGGGKAEKILGDFAAEYAKSNRSTCKGCKLEKIEKGG 150
gi | 45383984 | ref | NP_990594.1 | MAET-GDKPYRAEYAKSGRASCKKCSSESIPKDSLRLMALMVQSPMFDGKVPWHYHFCFVKRARIIVSH---DIDIDGFFELRWEDQEKIKKAEI---GALQEE---KGGTRKEVGAEKILDFAAEYAKSNRSTCKGCKLEKIEKGG 150
gi | 113677594 | ref | NP_001038407.1 | MADSQDDKLYKAEYAKSGRASCKKCKDNIAKDSLRLMALMVQSPMFDGKVPWHYHFCFVWLR---AAVQSP---SDISGFDLRWDDQEKVKTAIE---SGGATG---GKGGQKGAAGKELNDFAVEYAKSNRSTCKGCKLEKIEKGG 150
gi | 30684908 | ref | NP_850165.1 | --MASPHKPRAEYAKSRSSCKTCKRSPINKNRFLGKLVSTHFDGIMPMMNHA--CILLKKTQKLSVD---DVEGLESLELRWDDQOKIRKYVEVSGAGSNTSSTS---GTSSSTANNAKLEYEIVSOISRAGCRKCEKILKDE 150
gi | 115471709 | ref | NP_001059453.1 | --MAAPPKAWKAEYAKSGRSSCKSCRSPTGKDLRLGKMWYATDFGLMPPMNHAS--CILLKKNQKLSVD---DVEGIDTLRWDDQEKIRKYVGSAP-----ATASSAAAI--SDKCTLFAEYAKSNRSTCKGCKLEKIEKGG 150
gi | 17510487 | ref | NP_491072.1 | MTHSNELPVLAELVYAKSGRSNCKTCKKNLALDQLRMSMNRSTFFDGNMDSFHVYVNCVFKMIRGRDINISIRGVDLWRWDDQEKLRQETIQHFKTASPTLLE-----PLCSSTTVLSTIKTEKSLNRRGCKGCGNQFERGG 150
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

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gi | 161076197 | ref | NP_001104452.1 | VRLRKT-----VYDTEVGMKYGGQPLWHHLECFPAQLRSELGWFAS--GEDMPGFQSLADDQ---AKVKNAIPIPKSE-----ELPDKIKRAKMELE-----DTNE--EGEKKORLKDQND 300
gi | 158291429 | ref | XP_312938.3 | MRLIKKV-----AYDTEVGMKGGQPLWHHAECAFLRSELGWFEEK--AESLPGVRSRMPKEDQ---KILKGLLPAIKAE-----DVP--AKKVKKEVVK-----DEVDAADATEEKKMAEIQKA 300
gi | 156523968 | ref | NP_001609.2 | VRLSKK-----MVDPEK--POLGMIDRWYHPCFVKNRBELGFRPEYSASOLKGFSLLAEDDK--EALKKQLPVGKSEG-----KRGKDEVDGDEVAKKKS-----KKKPKDTS--KLEKALKAQNDL 300
gi | 73960821 | ref | XP_863797.1 | IRLSKK-----MLDPEK--POLGMIDRWYHPCFVKNRBELGFRPEYSASOLKGFGLLTPEDK--EALKKQLPVGKSEG-----KRGKDEVDGDEVAKKKS-----KKKPKDTS--KLEKALKAQNDL 300
gi | 20806109 | ref | NP_031441.2 | MRLSKK-----MVDPEK--POLGMIDRWYHPCFVKNRBELGFRPEYSASOLKGFSLLAEDDK--EALKKQLPVGKSEG-----KRGKDEVDGDEVAKKKS-----KKKPKDTS--KLEKALKAQNDL 300
gi | 6978455 | ref | NP_037195.1 | MRLSKK-----MLDPEK--POLGMIDRWYHPCFVKNRBELGFRPEYSASOLKGFSLLAEDDK--EALKKQLPVGKSEG-----KRGKDEVDGDEVAKKKS-----KKKPKDTS--KLEKALKAQNDL 300
gi | 27807449 | ref | NP_777176.1 | VRLSKK-----VVYDPEK--POLGMVDCWYHPCFVKNRBELGFRPEYSATHLMGFSVLLAEDQ---ETLKKQLPAIKREG-----KRGKDEVDGDEVAKKKS-----KKKPKDTS--KLEKALKAQNDL 300
gi | 45383984 | ref | NP_990594.1 | IRLSKK-----MVDPEK--POLGMIDRWYHPCFVKNRBELGFRPEYSATHLMGFSVLLAEDQ---ETLKKQLPAIKREG-----KRGKDEVDGDEVAKKKS-----KKKPKDTS--KLEKALKAQNDL 300
gi | 113677594 | ref | NP_001038407.1 | IRLSKK-----MVDPEK--POLGLIDRWYHPCFVSRRELIFKPKYAEALKGFVAVLRDQK---EELKRLPAIKREG-----KRGKDEVDG--NVVAKKS-----KEDD-----KLEONLKDQNDL 300
gi | 30684908 | ref | NP_850165.1 | VRVFSK-----PEGGPN-----KGLMWHHAKCFLEMS---SSTELESISGWRSPDSDQEALLPLVKKALPAKETAETAEARQTSNRAGTKRKNSVDNEKSKLAKSSFD---MSTSGALQPCSKKEKEMEAQTE 300
gi | 115471709 | ref | NP_001059453.1 | VRVFSK-----LEGGQ-----WYHSAKCFLEMS---PAAVENFSGWELLSHEDKRAVLDLVKKDAPSSGGTSSKSGSKRINNDQHDCKAPKIIRIS--EGTADPKGKAVVSHSANS--SDLQEKLEKESD 300
gi | 17510487 | ref | NP_491072.1 | IKAHNKGRANHFCKFLQEFDKI--EGTVEDIPGWADYEENFKIKAVGEYVEALAAKRRST--EAPPAASPTPEAEIPLVSAEGSPSSNKRPA--SEIIEIDGEGNDENDFAKRR-----MKKEARLMEVQKRMK--SD 300
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300

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gi | 161076197 | ref | NP_001104452.1 | YFRFRDDIKNMKKKIDILILKFNQDIPVTDGTE--KLFDTADLLTFAIGAESCEKNSCQFIVNKGK--YIINGNHSSEWTKCNKLLKEPTR--SACIVPEKELK--ALYNFLNTVKEI--ESTRIENFNNFPNKSTFSRSLKTKNKNNDVLV 450
gi | 158291429 | ref | XP_312938.3 | YVAIRDKLSLGVKKSLEIILSLANKQDIPENQD---PVLDRVCDLTMFGALLERCSCKG--GQYAFQKSA---YIYQGLDSAWKCNMTEKAPPR--KKIKIPBEELK--SVYSFLKRYKSVISDRVRYVPPSVNTVMKGVKKEE--ELP 450
gi | 156523968 | ref | NP_001609.2 | IWNIKDELKVKCS--ND--LKELLIFNQVPSGES-----AILDRVADGMVFGALLPCEEC--GOLVFKSDA---YYCTGDVTAWTKCMVKIQTTPNR--KEWVTPKEFR--EIS--YLKKLKVKKODRIFPPETSASVAATPPP--TASAPAAVNS 450
gi | 73960821 | ref | XP_863797.1 | IWNIKDELKVKCS--ND--LKELLIFNQVPSGES-----AILDRVADGMVFGALLPCEEC--GOLVFKSDA---YYCTGDVTAWTKCMVKIQTTPSR--KEWVTPKEFR--EIS--YLKKLKIKKODRIFPPETSAPVAAAPPP--TALAPAVNS 450
gi | 20806109 | ref | NP_031441.2 | IWNIKDELKVKCS--ND--LKELLIFNQVPSGES-----AILDRVADGMVFGALLPCEEC--GOLVFKSDA---YYCTGDVTAWTKCMVKIQTTPSR--KEWVTPKEFR--EIS--YLKKLKVKKODRIFPPESSAPALPLPLVTSAPTAVNS 450
gi | 6978455 | ref | NP_037195.1 | VWNIKDELKVKCS--ND--LKELLIFNQVPSGES-----AILDRVADGMVFGALLPCEEC--GOLVFKSDA---YYCTGDVTAWTKCMVKIQTTPSR--KEWVTPKEFR--EIS--YLKKLKIKKODRIFPPESSAPAPAPV--ITSAPTAVNS 450
gi | 27807449 | ref | NP_777176.1 | IWNVDELKVKCS--ND--LKELLIFNQVPSGES-----AILDRVADGMVFGALLPCEEC--GOLVFKSDA---YYCTGDVTAWTKCMVKIQTTPNR--KEWVTPKEFR--EIS--YFKKLKIKKODRIFPPESS--TVGAAAPPP--AASAPAVHS 450
gi | 45383984 | ref | NP_990594.1 | IWGIKDELKVKCS--ND--LKELLIFNQVPSGES-----AILDRVADGMVFGALLPCEEC--GOLVFKSDA---YYCSGDI--TAWTKCVAKIQTTPNR--KDWVTPKEFR--EIP--YLKFKKCKKODRIFPPESAAV--PNSAPP--ASAPLTETV 450
gi | 113677594 | ref | NP_001038407.1 | IWGIKDELKVKCS--ND--MKELLIANSEVPSGES-----NIVDRLESDCMVFGALLPCEEC--GOLVFKSDA---YYCTGDVTAWTKCVAKIQTTPDR--KDWVTPKEFS--EIP--FLKFKFKKODRIFPKDAPPAA--PSSG--TTSAA--TSV 450
gi | 30684908 | ref | NP_850165.1 | LWDLKDELKVKVTS--AE--LRNMLEANGD--SGPER---HLLDRCADGMFGALGCTVCFV---SFLYVHGQG---YHCSGVYSEWSKCTY--STPEFR--SKKKWKIPDEM--DNGYLK--KFKVSKAKKPERVLP--P--EKS--LCO--SQNR 450
gi | 115471709 | ref | NP_001059453.1 | LWLKDELKVKVTS--AE--LRNMLEANGD--SGPER---HLLDRCADGMFGALGCTVCFV---SFLYVHGQG---YHCSGVYSEWSKCTY--STPEFR--SKKKWKIPDEM--DNGYLK--KFKVSKAKKPERVLP--P--EKS--LCO--SQNR 450
gi | 17510487 | ref | NP_491072.1 | LWVYRQIFERMPY--TK--ISILREANGD--TPEGHDP--TAQVIERLDVNALFGCLTIC--TCSNGKIVVNS--SCRYVYVNGYALVEYKCTY--EENKPNR--TFEVS---HRLTEKHRLQDIFV-- 450
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450

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gi | 161076197 | ref | NP_001104452.1 | RP---HLPRI--SPPLYNLKFSIILGLKNQHK--ELRKRLENLGGKFEVKSSENTIAIISTELETIKKSTRMKFAEELGHIHVP--EFLDFVEAD--EGAIKYINS--CICSWGHPDKSRIP--KE--TKSLNSNSIYTKSMP-----VSRIT 600
gi | 158291429 | ref | XP_312938.3 | EP---KIKREKPPLYDMEFVILGKTATPKDQKLLKIQLGKGVVTKTASHTAAIISTPEEVLRSRMAEAKELQI--VPPEDFLEVDVGG---NAGSFTI--SRSIDWGSDDLKRIPTTEESKSRITKKSITYEKSV--AKMK 600
gi | 156523968 | ref | NP_001609.2 | S---ASADKPLSNMKIILTLGKLSRNKDEVKAMIEKLGKGLTG--HANKASLCISTKKEVEKMKMKEEVEKAEANRVSSEDFLQDVSASTKSLQELFLAHLILPFWGAEVKAEVPEVAVPAGKSGAALSKKSKGQVKEE--GINKSEKRMK 600
gi | 73960821 | ref | XP_863797.1 | S---TPPGKPLSNMKIILTLGKLSRNKDEVKAMIEKLGKGLTG--HANKASLCISTKKEVEKMKMKEEVEKAEANRVSSEDFLQDVSASTKSLQELFLAHLILPFWGAEVKAEVPEVAVPAGKSGAALSKKSKGQVKEE--GINKSEKRMK 600
gi | 20806109 | ref | NP_031441.2 | S---APADKPLSNMKIILTLGKLSRNKDEKAVKIEKLGKGLTG--HANKASLCISTKKEVEKMKMKEEVEKAEANRVSSEDFLQDVSASTKSLQELFLAHLILPFWGAEVKAEVPEVAVPAGKSGAALSKKSKGQVKEE--GINKSEKRMK 600
gi | 6978455 | ref | NP_037195.1 | S---APADKPLSNMKIILTLGKLSRNKDEKAVKIEKLGKGLTG--HANKASLCISTKKEVEKMKMKEEVEKAEANRVSSEDFLQDVSASTKSLQELFLAHLILPFWGAEVKAEVPEVAVPAGKSGAALSKKSKGQVKEE--GINKSEKRMK 600
gi | 27807449 | ref | NP_777176.1 | S---GPPDKPLSNMKIILTLGKLSRNKDEKAVKIEKLGKGLTG--HANKASLCISTKKEVEKMKMKEEVEKAEANRVSSEDFLQDVSASTKSLQELFLAHLILPFWGAEVKAEVPEVAVPAGKSGAALSKKSKGQVKEE--GINKSEKRMK 600
gi | 45383984 | ref | NP_990594.1 | S---APQDKPLSNMKIILTLGKLSRNKDEKAVKIEKLGKGLTG--HANKASLCISTKKEVEKMKMKEEVEKAEANRVSSEDFLQDVSASTKSLQELFLAHLILPFWGAEVKAEVPEVAVPAGKSGAALSKKSKGQVKEE--GINKSEKRMK 600
gi | 113677594 | ref | NP_001038407.1 | ASKNTLEAPADKPLSNMKIILTLGKLSRNKDEKAVKIEKLGKGLTG--HANKASLCISTKKEVEKMKMKEEVEKAEANRVSSEDFLQDVSASTKSLQELFLAHLILPFWGAEVKAEVPEVAVPAGKSGAALSKKSKGQVKEE--GINKSEKRMK 600
gi | 30684908 | ref | NP_850165.1 | S---SSRSERLADLVKVIAGNTRK--P--WKKRI--EAGAEFHA--NVKRG--SCLVVCGL--DIRDAEMRKRKMKVAIVREDVLYV---DCKFKQKPLPDKYKIED--SES-----LVT 600
gi | 115471709 | ref | NP_001059453.1 | S---SFLSEGLDLKLRVSVIG--SKDVVDDGKQKLDAGANFNA--VTRKDS--SCLVVCGL--DIRDAEMRKRKMKVAIVREDVLYV---DCKFKQKPLPDKYKIED--SES-----LVT 600
gi | 17510487 | ref | NP_491072.1 | S---QMSERL--IGEE--GESVVKIDKRSKGG---TRGEQFIYAAEAFDS--NNVNIKVGDLTS-----ECIRKNRVLFPDLYRVEAAL--SSRG-----TNT 600
.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600

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gi|161076197|ref|NP_001104452.1| FVKVDGLAVDPDSGLEDAHVLE--DSNNKYVSVLGLLDIQRNKNSYKVKVOLLKADKKEKYWIFRSWGRIG--TINIGNSKLEEFDFSESAKRNFKEIYADKTGNEVEQRD---NFVKTGRMYPTEIQVDDG---KLVKHESFFTSKLEI 750
gi|158291429|ref|XP_312938.3| LQVKSGLVDDPDSGLADKAHVYK--FHDVYVNCVLNKVDIQKDKNSFYKMOVLEGGDTKKKYWLFRAWGRIG--TTIGNKVNFENSSADSAMSAFEDLFLFKTGNWVRRHS---VYSKMPGAFYPIEIDYSETK--FKRLAENSIGTKSKLAP 750
gi|156523968|ref|NP_001609.2| LTLKGGAAVDPDSGLESAHVLE--KGGKVFSAITLGLVDIVKGTNSYKQLLEDDKERNYVIFRSWGRVIG--TVIGSNKLEQMPKEDAEHFMKLYEEKTGNAWHSKN---FTKYPKKFYPLEIDYGODEEAVKLLTVNPGTKSKLKP 750
gi|73960821|ref|XP_863797.1| LTLKGGAAVDPDSGLESAHVLE--KGGKVFSAITLGLVDIVKGTNSYKQLLEDDKESRYVIFRSWGRVIG--TVIGSNKLEQMPKEDAEHFMKLYEEKTGNAWHSKN---FTKYPKKFYPLEIDYGODEEAVKLLTVNPGTKSKLKP 750
gi|20806109|ref|NP_031441.2| LTLKGGAAVDPDSGLESAHVLE--KGGKVFSAITLGLVDIVKGTNSYKQLLEDDKESRYVIFRSWGRVIG--TVIGSNKLEQMPKEDAEHFMKLYEEKTGNAWHSKN---FTKYPKKFYPLEIDYGODEEAVKLLTVNPGTKSKLKP 750
gi|6978455|ref|NP_037195.1| LTLKGGAAVDPDSGLESAHVLE--KGGKVFSAITLGLVDIVKGTNSYKQLLEDDKESRYVIFRSWGRVIG--TVIGSNKLEQMPKEDAEHFMKLYEEKTGNAWHSKN---FTKYPKKFYPLEIDYGODEEAVKLLTVNPGTKSKLKP 750
gi|27807449|ref|NP_777176.1| LTLKGGAAVDPDSGLESAHVLE--KGGKVFSAITLGLVDIVKGTNSYKQLLEDDKESRYVIFRSWGRVIG--TVIGSNKLEQMPKEDAEHFMKLYEEKTGNAWHSKN---FTKYPKKFYPLEIDYGODEEAVKLLTVNPGTKSKLKP 750
gi|45383984|ref|NP_990594.1| LTLKGGAAVDPDSGLESAHVLE--KGGKVFSAITLGLVDIVKGTNSYKQLLEDDKESRYVIFRSWGRVIG--TVIGSNKLEQMPKEDAEHFMKLYEEKTGNAWHSKN---FTKYPKKFYPLEIDYGODEEAVKLLTVNPGTKSKLKP 750
gi|113677594|ref|NP_001038407.1| LTLKGGAAVDPDSGLESAHVLE--KGGKVFSAITLGLVDIVKGTNSYKQLLEDDKESRYVIFRSWGRVIG--TVIGSNKLEQMPKEDAEHFMKLYEEKTGNAWHSKN---FTKYPKKFYPLEIDYGODEEAVKLLTVNPGTKSKLKP 750
gi|30684908|ref|NP_850165.1| VKVKGSRSAVHESGLDTHGILE--DGNSTVNTLLMSDLSTGTNSYIILQIIEDEKGDCCVFRKRWGRVNEKIGNKVLEEMS--KSDAVHEFKRFLFKTGNWVRRHS---VYSKMPGAFYPIEIDYSETK--FKRLAENSIGTKSKLAP 750
gi|115471709|ref|NP_001059453.1| VKVKGSRSAVHESGLDTHGILE--DGNSTVNTLLMSDLSTGTNSYIILQIIEDEKGDCCVFRKRWGRVNEKIGNKVLEEMS--KSDAVHEFKRFLFKTGNWVRRHS---VYSKMPGAFYPIEIDYSETK--FKRLAENSIGTKSKLAP 750
gi|17510487|ref|NP_491072.1| HTIKKGVVDAKFAADRCVRFVNEIDGSLVQATLSTFDLTONKNSYKQLLEDDKERNYVIFRSWGRVIG--TVIGSNKLEQMPKEDAEHFMKLYEEKTGNAWHSKN---FTKYPKKFYPLEIDYGODEEAVKLLTVNPGTKSKLAP 750
.....610.....620.....630.....640.....650.....660.....670.....680.....690.....700.....710.....720.....730.....740.....750



gi|161076197|ref|NP_001104452.1| SVONLIKLIFFIDISMKKILMEFHIDMDKMPGLKLSAHOIQSAVYRVKKEIYNVLECGSNT-----AKLIDATNRFYLIIPHNFVGLPPLTIETHQOIEDLRLQMLDSLAEIEVAYSIIKS--EDVSDAC--NPLDNHVAQIKTQIIVALDKN 900
gi|158291429|ref|XP_312938.3| AVODLVRMLFVDAMNRMVEFELDMKMPGLKLSKROLOKSAKVLSEISTLIGSGGSN-----AEFIAASNRFYSYIIPHNFGVSSVKVLDTIHQVKEKQTMLESMEIEFAYSLLNDGDHSAQDGK--NPLDAHVDLQKTSIEPMARD 900
gi|156523968|ref|NP_001609.2| PVODLIRKMFVDSMKKAMVEYEIDLOKMPGLKLSKROIQAAYSILSEVQAVSQGSSD-----SAILDLSNRFYLIIPHDFGMKPPLLNNSVQAKVEMLDNLLDIEVAYSLLRGGSDSSK---DPIDVNYEKLKTDIKVVDK 900
gi|73960821|ref|XP_863797.1| PVODLIRKMFVDSMKKAMVEYEIDLOKMPGLKLSKROIQAAYSILSEVQAVSQGSSD-----SAILDLSNRFYLIIPHDFGMKPPLLNNSVQAKVEMLDNLLDIEVAYSLLRGGSDSSK---DPIDVNYEKLKTDIKVVDK 900
gi|20806109|ref|NP_031441.2| PVQELVGMIFDVDSMKKALVEYEIDLOKMPGLKLSKROIQAAYSILSEVQAVSQGSSD-----SAILDLSNRFYLIIPHDFGMKPPLLNNSVQAKVEMLDNLLDIEVAYSLLRGGSDSSK---DPIDVNYEKLKTDIKVVDK 900
gi|6978455|ref|NP_037195.1| PVQELVGMIFDVDSMKKALVEYEIDLOKMPGLKLSKROIQAAYSILSEVQAVSQGSSD-----SAILDLSNRFYLIIPHDFGMKPPLLNNSVQAKVEMLDNLLDIEVAYSLLRGGSDSSK---DPIDVNYEKLKTDIKVVDK 900
gi|27807449|ref|NP_777176.1| PVONLIRKMFVDSMKKAMVEYEIDLOKMPGLKLSKROIQAAYSILSEVQAVSQGSSD-----SHILLDLSNRFYLIIPHDFGMKPPLLNNSVQAKVEMLDNLLDIEVAYSLLRGGSDSSK---DPIDVNYEKLKTDIKVVDK 900
gi|45383984|ref|NP_990594.1| PVODLIRKMFVDSMKKAMVEYEIDLOKMPGLKLSKROIQAAYSILSEVQAVSQGSSD-----SHILLDLSNRFYLIIPHDFGMKPPLLNNSVQAKVEMLDNLLDIEVAYSLLRGGSDSSK---DPIDVNYEKLKTDIKVVDK 900
gi|113677594|ref|NP_001038407.1| PVODLIRKMFVDSMKKAMVEYEIDLOKMPGLKLSKROIQAAYSILSEVQAVSQGSSD-----SHILLDLSNRFYLIIPHDFGMKPPLLNNSVQAKVEMLDNLLDIEVAYSLLRGGSDSSK---DPIDVNYEKLKTDIKVVDK 900
gi|30684908|ref|NP_850165.1| SLIEMLKMLFDVETYSAMMEFEINMSEMPGLKLSKHNKIQGFALTEIQRLTSEDDP--PIMKESLLVDASNRFFTMIPSS---IHPHIIREDDEDFKSKVQMLLEALQDIEIASRVLGVDFDVSDES---LDDKVKKLCIDISPLPH 900
gi|115471709|ref|NP_001059453.1| QLLELMNMLFNIETRAAMLKFNSEMPGLKLSKHNKIQGFALTEIQRLTSEDDP--PIMKESLLVDASNRFFTMIPSS---IHPHIIREDDEDFKSKVQMLLEALQDIEIASRVLGVDFDVSDES---LDDKVKKLCIDISPLPH 900
gi|17510487|ref|NP_491072.1| SVKEVVMGIFDVENMKSALKSFEMDNKMLGRLSHNINLAFVFLNIDSLVVKLPID-----ASRLIDFSNRFYLIIPHDFGMKPPLLNNSVQAKVEMLDNLLDIEVAYSLLRGGSDSSK---DPIDVNYEKLKTDIKVVDK 900
.....760.....770.....780.....790.....800.....810.....820.....830.....840.....850.....860.....870.....880.....890.....900



gi|161076197|ref|NP_001104452.1| SEEFILSQVYKNTAETHRSYDLKLVDFVKVSRQGEARRFKPFK--KLNHRLLWEGSRITNFVGIILNGLRIAPPEAPVTGYMFGKGIYFADMVSKSANYCCHSQNSIGLMLLSEVALGDMMEGTSAKYIN--KLSNKNKSCFGRGR 1050
gi|158291429|ref|XP_312938.3| SEEFALLQYVYRNTAETHRTYELKVEVAEIFKRRGDEDRRYQPFK--KLNHRLLWEGSRITNFVGIILNGLRIAPPEAPVTGYMFGKGIYFADMVSKSANYCCHSQNSIGLMLLSEVALGDMMEGTSAKYIN--KLSNKNKSCFGRGR 1050
gi|156523968|ref|NP_001609.2| SEEAETIRKVKNTAETHNAYDLEVIDIFKIEREGESQRYKPFK--QLNHRLLWEGSRITNFVGIILNGLRIAPPEAPVTGYMFGKGIYFADMVSKSANYCCHSQNSIGLMLLSEVALGDMMEGTSAKYIN--KLSNKNKSCFGRGR 1050
gi|73960821|ref|XP_863797.1| SEEAETIRKVKNTAETHNAYDLEVIDIFKIEREGESQRYKPFK--QLNHRLLWEGSRITNFVGIILNGLRIAPPEAPVTGYMFGKGIYFADMVSKSANYCCHSQNSIGLMLLSEVALGDMMEGTSAKYIN--KLSNKNKSCFGRGR 1050
gi|20806109|ref|NP_031441.2| SEEAETIRKVKNTAETHNAYDLEVIDIFKIEREGESQRYKPFK--QLNHRLLWEGSRITNFVGIILNGLRIAPPEAPVTGYMFGKGIYFADMVSKSANYCCHSQNSIGLMLLSEVALGDMMEGTSAKYIN--KLSNKNKSCFGRGR 1050
gi|6978455|ref|NP_037195.1| SEEAETIRKVKNTAETHNAYDLEVIDIFKIEREGESQRYKPFK--QLNHRLLWEGSRITNFVGIILNGLRIAPPEAPVTGYMFGKGIYFADMVSKSANYCCHSQNSIGLMLLSEVALGDMMEGTSAKYIN--KLSNKNKSCFGRGR 1050
gi|27807449|ref|NP_777176.1| SEEAETIRKVKNTAETHNAYDLEVIDIFKIEREGESQRYKPFK--QLNHRLLWEGSRITNFVGIILNGLRIAPPEAPVTGYMFGKGIYFADMVSKSANYCCHSQNSIGLMLLSEVALGDMMEGTSAKYIN--KLSNKNKSCFGRGR 1050
gi|45383984|ref|NP_990594.1| SEEAETIRKVKNTAETHNAYDLEVIDIFKIEREGESQRYKPFK--QLNHRLLWEGSRITNFVGIILNGLRIAPPEAPVTGYMFGKGIYFADMVSKSANYCCHSQNSIGLMLLSEVALGDMMEGTSAKYIN--KLSNKNKSCFGRGR 1050
gi|113677594|ref|NP_001038407.1| SEEAETIRKVKNTAETHNAYDLEVIDIFKIEREGESQRYKPFK--QLNHRLLWEGSRITNFVGIILNGLRIAPPEAPVTGYMFGKGIYFADMVSKSANYCCHSQNSIGLMLLSEVALGDMMEGTSAKYIN--KLSNKNKSCFGRGR 1050
gi|30684908|ref|NP_850165.1| SEDYRLIEKYLNTAETHNAYDLEVIDIFKIEREGESQRYKPFK--QLNHRLLWEGSRITNFVGIILNGLRIAPPEAPVTGYMFGKGIYFADMVSKSANYCCHSQNSIGLMLLSEVALGDMMEGTSAKYIN--KLSNKNKSCFGRGR 1050
gi|115471709|ref|NP_001059453.1| CEDYRLIEKYLNTAETHNAYDLEVIDIFKIEREGESQRYKPFK--QLNHRLLWEGSRITNFVGIILNGLRIAPPEAPVTGYMFGKGIYFADMVSKSANYCCHSQNSIGLMLLSEVALGDMMEGTSAKYIN--KLSNKNKSCFGRGR 1050
gi|17510487|ref|NP_491072.1| CDDWNMHHQYLKNTAETHNAYDLEVIDIFKIEREGESQRYKPFK--QLNHRLLWEGSRITNFVGIILNGLRIAPPEAPVTGYMFGKGIYFADMVSKSANYCCHSQNSIGLMLLSEVALGDMMEGTSAKYIN--KLSNKNKSCFGRGR 1050
.....910.....920.....930.....940.....950.....960.....970.....980.....990.....1000.....1010.....1020.....1030.....1040.....1050



gi|161076197|ref|NP_001104452.1| MPDPKSYIRSQVEIPIYGETIIDEH---LKSLLLYNEYIVYDVAQVNIQYLFMRFEKYSY--- 1115
gi|158291429|ref|XP_312938.3| QPDPKSHVRPDGVEIPMGKGVNEK---LKSLLLYNEYIVYDVAQVNIQYLFMRFEKYSY--- 1115
gi|156523968|ref|NP_001609.2| TPDPK-ASITLDGVEVPLGTGIPSGV---NDTCLLYNEYIVYDIAQVNLKYLKLLKFNFKTSLW 1115
gi|73960821|ref|XP_863797.1| TPDPK-ASITLDGVEVPLGTGIPSGV---NDTCLLYNEYIVYDIAQVNLKYLKLLKFNFKTSLW 1115
gi|20806109|ref|NP_031441.2| TPDPK-ASITLDGVEVPLGTGIPSGV---NDTCLLYNEYIVYDIAQVNLKYLKLLKFNFKTSLW 1115
gi|6978455|ref|NP_037195.1| APDPK-ASITLDGVEVPLGTGIPSGV---NDTCLLYNEYIVYDIAQVNLKYLKLLKFNFKTSLW 1115
gi|27807449|ref|NP_777176.1| TPDPK-ASITLDGVEVPLGTGIPSGV---NDTCLLYNEYIVYDIAQVNLKYLKLLKFNFKTSLW 1115
gi|45383984|ref|NP_990594.1| APDPK-ASITLDGVEVPLGTGIPSGV---NDTCLLYNEYIVYDIAQVNLKYLKLLKFNFKTSLW 1115
gi|113677594|ref|NP_001038407.1| APDPK-ASITLDGVEVPLGTGIPSGV---NDTCLLYNEYIVYDIAQVNLKYLKLLKFNFKTSLW 1115
gi|30684908|ref|NP_850165.1| VPQDEFAKWRDVTVPCKGVPVSKV---KASELMYNEYIVYDIAQVNLKYLKLLKFNFKTSLW 1115
gi|115471709|ref|NP_001059453.1| VPLESEFAKWRDVTVPCKGVPVSKV---KASELMYNEYIVYDIAQVNLKYLKLLKFNFKTSLW 1115
gi|17510487|ref|NP_491072.1| CPREIGSYNHPDGTIPLGLTVMQLQCKQDVYHLLYNEFIVYDVAQVNIQYLFMRFEKYSY--- 1115
.....1060.....1070.....1080.....1090.....1100.....1110.....

