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gi|31982836|ref|NP_032747.2|      MATPVPPPSPRHLRLLRLLLSGLILGAALNGATARRPDATTCPGSLDCALKRRAKCPPGAHACGPCLQSFQEDQRGFCVPRKHLSSGEG----LPQPRLEEEIDSLAQELALKEKEAGHSRLTAQPLLEAAQKLLEPAATLGFSQWGQRL   150
gi|51948430|ref|NP_001004231.1|   MATPVPPPSPRHLRLLRLLLSGLILGAALNGATARRPDAPTCPGSLDCALKRRAKCPPGAHACGPCLQSFQEDQRGVCVPRKHQSSGEG----LPQPRLEEEIDSLARELALKEKEAGHPRLTAQPLPEASQKLLEPAATLGFSQWGQQL   150
gi|223029449|ref|NP_056207.3|     MATPLPPPSPRHLRLLRLLLSGLVLGAALRGAAAGHPDVAACPGSLDCALKRRARCPPGAHACGPCLQPFQEDQQGLCVPRMRRPPGGG----RPQPRLEDEIDFLAQELARK--ESG---HSTPPLP-KDRQRLPEPATLGFSARGQGL   150
gi|114627651|ref|XP_520386.2|     MATPLPPPSPRHLRLLRLLLSGLVLGAALRGAAAGHPDVAACPGSLDCALKRRARCPPGAHACGPCLQPFQEDQQGLCVPRMRRPPGGG----RPQPRLEDEIDFLAQELARK--ESG---HSTPPLP-KARQRLPEPATLGFSARGQGL   150
gi|73967479|ref|XP_537787.2|      MATPVPPPSPRHLRLLRLLLCGLVLGAALRGASAGRPDAAACPGSLDCALKRRARCPPGAHVCGPCLQPFQEDPQGLCVPRMRRPVGES----LPRPRLEDEIDFLAQELAHQ--EPQPPMLAAQPQPDKGQQHLEPAATLGLSERRQGP   150
gi|118099108|ref|XP_001233959.1| MVA-----AARRGALLLLLAA---LGACRPRAAR---TAEPCPRRLDCALQRRKFCPLGSSTCGPCLPNFLEDSHGHCLQEKRSPSGR-----TSVPSLEDEIDVLADVLARQ--DAT---RSHALRDGKPRTTLAPTGRQRVPSRLRQE   150
gi|292625331|ref|XP_002665965.1| -MLFSPTRSTRRARASLLLPGLLICVILAAVGAS---VPAKCPDHIECARRGRHFCKPGSSNCGPCLIPLEEDQMGHCVVRSVRYAAQSRDPVAPLSGIDEEIDFLSSVITKQQ-LSESKHSDSAPQS--PPQVQLKQKSLHKT-----T   150
gi|192447377|ref|NP_001122255.1| -MLFSPTRSTRRARASLLLPGLLICVILAAVGAS---VPAKCPDHIECARRGRHFCKPGSSNCGPCLIPLEEDQMGHCVVRSVRYAAQSRDPVAPLSGIDEEIDFLSSVITKQQ-LSESKHSDSAPQS--PPQVQLKQKSLHKT-----T   150
gi|189519069|ref|XP_684540.3|     ------MRSLSRPWASTLAEAFLITTVAVSAAMA---VVGHCPRSLDCARERRHFCQPGSLHCGPCLDPFMENKRGKCVLRRRNHPAK----VSHLPELDEEIDILSSIISKHR-ESEMKHSAPSPAASKAPENKSGSSSHYKAPPTAAT   150
                                  1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150
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gi|31982836|ref|NP_032747.2|      EPGLPSTH--GTSSPIPHTSLSSRASSGPVQMSPLEPQGRHGNGLTLVLILAFCLASSAALAVAALCWCRLQREIRLTQKADYAATAKGPTSPSTPRISPGDQRLAHSAEMYHYQHQRQQMLCLERHKEPPKELES-ASSDEENEDGDFT   300
gi|51948430|ref|NP_001004231.1|   EPGLPSTH--GTSSPTPHTSLSARASSGPVQMSPLEPQGR-GNGLALVLILAFCLASTAALAVAALCWCRLQREIRLTQKADYTATAKGPTSPTTPRISPGDERLAHSAEMYHYQHQRQQMLCLERHKDPPKELES-ASSDEENEDGDFT   300
gi|223029449|ref|NP_056207.3|     ELGLPSTP--GTPTPTPHTSLGSPVSSDPVHMSPLEPRGGQGDGLALVLILAFCVAGAAALSVASLCWCRLQREIRLTQKADYATAKA-PGSPAAPRISPGDQRLAQSAEMYHYQHQRQQMLCLERHKEPPKELDT-ASSDEENEDGDFT   300
gi|114627651|ref|XP_520386.2|     ELGLPSTP--GTPTPTPHTSLGSPVSSDPVHMSPLEPRGGQGDGLALG----------------RSWSGVGRGSR-----------------------------------------------------------------------   300
gi|73967479|ref|XP_537787.2|      NLGTSSTG--GTPAPTPHTSLGPPVSSVPVHISPLEPRGGRGDGLVLVLIVASSVAGAAAVAVAALCWCRLQRDIRLTQKADYAAPQA-PGSP-------------------------------------------------   300
gi|118099108|ref|XP_001233959.1| LLQRGPAG--SKAAATLPTSTTATAPKYPVEAAPVP----SNDDVVLGLIVVCTLAGISALIVAAVCWCRLQKEVRLAQKADYSAQRVASPLP-YDKISPGDKTLAQSAQMYHYQHQKQQMLSMEKHKEEPKVPDS-ASSDEENEDGDFT   300
gi|292625331|ref|XP_002665965.1| TVEPMTT---SPTAPTHTT--NSSNRHGPVIS-PNP----SRDSLLVLMISLCIIVGAMALILVTVCWVRLQRETRLAQKVDYPAFQEAANRN-NTS--SGDKTLAHSAQMYHYQHQKQQMLSMEKHKAEPKVSESGGHSDEETEEGDFT   300
gi|192447377|ref|NP_001122255.1| TVEPMTT---SPTAPTHTT--NSSNRHGPVIS-PNP----SRDSLLVLMISLCIIVGAMALILVTVCWVRLQRETRLAQKVDYPAFQEAANRN-NTS--SGDKTLAHSAQMYHYQHQKQQMLSMEKHKAEPKVSESGGHSDEETEEGDFT   300
gi|189519069|ref|XP_684540.3|     SIQPPTRGLISSTSPTSNTPFISAVHSAPFII-PYP----SEDHSFIIFLGVFLMVGSVAMVLTGVCWVRMQRGCRLAQKVDYPAFGLIGPNS-YDSGMSGDKKLAQSAQMYHFQLQKQQMMSLK-QRSDSKIPDSGATSDEENEDGDFT   300
                                  .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300
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                                           .*    : * . :
gi|31982836|ref|NP_032747.2|      VYECPGLAPTGEMEVRNPLFDHSTLSAPVPGPHSLPPLQ-   340
gi|51948430|ref|NP_001004231.1|   VYECPGLAPTGEMEVRNPLFDHSTLSAPVPGPHSSPPLQ-   340
gi|223029449|ref|NP_056207.3|     VYECPGLAPTGEMEVRNPLFDHAALSAPLPAPSSPPALP-   340
gi|114627651|ref|XP_520386.2|     ---------TGEMEVRNPLFDHAALSAPLPAPSSPPALP-   340
gi|73967479|ref|XP_537787.2|      -------ATPGISPGDQRLAHSAEMYHYQHQRQQMRCLER   340
gi|118099108|ref|XP_001233959.1| VYECPGLAPTGEMEVRNPLFDDSSLHPPNPKVHP------   340
gi|292625331|ref|XP_002665965.1| VYECPGLAPTGEMEVKNPLFDDST--LHSQKNHK------   340
gi|192447377|ref|NP_001122255.1| VYECPGLAPTGEMEVKNPLFDDST--LHSQKNHK------   340
gi|189519069|ref|XP_684540.3|     VYECPGLAPTGEMEVKNPLFDDSTFHLHLQRSYN------   340
                                  .......310.......320.......330.......340
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