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gi |22122667|ref|NP_666260.1|  ---MFVVAFVGLSLVAWHP-----GVTAEKVNQVRVRAV---PQAVSCLQSDWYKWTDCFPCKDKKYRYSLLQPSKFGGITCSGDIWDEASCDSPICLRQAACCGDFOCRETRCLKRHLVNCNGDNCCLDGSDESDDCEDV 133
gi |109475204|ref|XP_233251.4|  ---MFVVAFVGLSLMAWHS-----GVTAEKVNQVRVRAV---PQAVSCLQSDWSEWDCFPCKNEKYRYSLLQPSKFGGITCSGDIWDKANCDSPICLRQAACCGDFOCRETRCLKRHLVNCNGDQCCLDGSDEDNCDDA 133
gi |4557389|ref|NP_000553.1|  ---MFVVAFVGLSLMLTQCP-----GVTAEKVNQVRVRAA---PAAVTCOLSNWSEWDCFPCKDKKYRHSLLQPNKFGGITCSGDIWDAQSCSSSTTCVROAACCGDFOCCKETGRCLKRHLVNCNGDQCCLDGSDEDDCEDV 133
gi |114556800|ref|XP_513435.2|  ---MFVVAFVGLSLMLTQCP-----GVTAEKVNQVRVRAA---PAAVTCOLSNWSEWDCFPCKDKKYRHSLLQPNKFGGITCSGDIWDAQSCSSSTTCVROAACCGDFOCCKETDRCLKRHLVNCNGDQCCLDGSDEDDCEDV 133
gi |73956396|ref|XP_536695.2|  ---MFAAAFVGLSLMLTQCP-----GVTIQEKNVRRVSRVAVSAPITAVPQOLSNWSEWDCFPCKDKKYRYSLLQPNKFGGITCSGDIWDAQSCHSPITACLHQAACCGDFOCCKETGRCLKRHLVNCNGDKDCLDGSDEDDCEDV 136
gi |114053319|ref|NP_001039750.1|  ---MFAAAFVGLSLMLTQCP-----GVTIQEKNVRRVSRVAVSAPITAVPQOLSNWSEWDCFPCKDKKYRYSLLQPNKFGGITCSGDIWDAQSCHSPITACLHQAACCGDFOCCKETGRCLKRHLVNCNGDKDCLDGSDEDDCEDV 136
gi |118094713|ref|XP_426667.2|  MWSLQCVSPLLILICLSLSTARWAAAGCGEPAAPVQARRSSRDISS---PPPVDQLQVQSEWDCFPCKGRKRRHRTLLQPMAMFGGQRCRGLPWLWDSQSCASWESCARAFSCGNDFOCCKESGRCKIKHQLVNCNTDRCRGSDEDDCEDV 148
gi |51011083|ref|NP_001003496.1|  -----MFACGPKRCRIGKSLRNCNGEPCCLNKDDEADCEAF 35
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

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gi |22122667|ref|NP_666260.1|  RVIEDDCHQVEPIPGSERAALGYNILTQEEAQSVDYAKYGGCETVYNGDWRKRLQYDPFCERLYYGEDEKYFRKPYNFKLYHFEALADTISSEFYDDANDLFFHIKNGKSHAGVTVGVAPEKVPVIEVTGSGKASSFLNKLNKYN 283
gi |109475204|ref|XP_233251.4|  RVIEDDCHQVEPIPGSERAALGYNILTQEEGQSVVDYAKYGGCETVYNGDWRKRLQYDPFCERLYYGEDEKYFRKPYNFKLYHFEALADTISSEFYDDANDLFFSKIQRDKSQNSVTFGSPAKSPIITLDASVSWDESSFMKELSKYN 283
gi |4557389|ref|NP_000553.1|  RAIDEDCSQVEPIPGSQKAALGYNILTQEDAQSVDYAKYGGCETVYNGEWRELRYDSTCERLYYGEDEKYFRKPYNFKLYHFEALADTISSEFYDANADLLSKVKKDKSDSFGVTIGIGPAGSPILLVGVGVSHSDTSLNKLNKYN 283
gi |114556800|ref|XP_513435.2|  RAIDEDCSQVEPIPGSQKAALGYNILTQEDAQSVDYAKYGGCETVYNGEWRELRYDSTCERLYYGEDEKYFRKPYNFKLYHFEALADTISSEFYDANADLLSKVKKDKSDSFGVTIGIGPAGSPILLVGVGVSHSDTSLNKLNKYN 283
gi |73956396|ref|XP_536695.2|  RVAENDCSQVEPIPGSESAALGYNILTQKEAHQVVDPRRYGGCETVYNGEWREIRYDPTCERLYYGEDEKYFRKPYNFKLYHFEALADTRFSSSELYDDADHLLSKVKNNFVSTGVTVGVVSTGSSVTVVGVSSQNSLDELKKNY 286
gi |114053319|ref|NP_001039750.1|  RILENDCSQVDPIPGSEKAALGYNILTQEEAHQVVDARYGGCETVYNGEWRELRYDPAERLYYGDDEKYFRKPYNFKLYHFEAQADTKISSEIYNADNADLLSKVKNDKVSVSGLTIGVGIIRVPTVITAGVMSQDAAFKLLSKYH 286
gi |118094713|ref|XP_426667.2|  -EIEHPDNLFPPIPGSEKAARGYNILTQAKRYIYDPKFLGSHCESVYNGEWRELRYDAAERLYYGEDEKYLLKPYVQFLAHADSGFSEFYDSDKLDLADLKSSEGGGFTIGIGPKFIIDFKLNLGFLRGRKSLKNFTHT 297
gi |51011083|ref|NP_001003496.1|  NRGENKCEGMLIIPGADKATLGYNALTGSFVSRVLDENYVGGVCEYLYNGEWKRLTFDFPCEHLSVDDAEKYRKPYNFLSFDQIMQAQSHSESSDYEDAVSFLRAKHSNSFNFGIKPQIG-----FVEFGVEFAEFMFLNISKYT 179
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300

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gi |22122667|ref|NP_666260.1|  *KRYGFMRVSTKIQTAQFKMRRNNIVLDEGMLQSLMELPEQFNQYGMVAKFINDYGTHYITSGTMGGIYEVYVVLVDKEMKREGTIVDEYQKCIIGGGIGIKIDS--IIEGVGISGEFCEN---SGDQDRDIRKKILGVEDIIISRVGGG 427
gi |109475204|ref|XP_233251.4|  *KRYGFMRVSTKIQTAQFKMRRNNIVLDEGMMESLMELPEQFNQYGMVSKFINDYGTHYITSGTMGGIYEVYVVLVDKEMKREGTIVDEYQKCIIGGGVGLQFGEK--IIEGDLISGESVYM---TGDNQDKRKKDLAVEDIISRVGGG 427
gi |4557389|ref|NP_000553.1|  *KRFIFTRIFTKVTAHFQKMRKDDIMLDEGMLQSLMELPDQYNYGMVAKFINDYGTHYITSGSMGGIYEVYVVLVDKAKMESLGITSRDITTCFGLSGLQIYEDK--INVGGLSGDHCKK---FGGGKTERAKAMAVEDIISRVGGG 427
gi |114556800|ref|XP_513435.2|  *KRFIFTRIFTKVTAHFQKMRKDDIMLDEGMLQSLMELPDQYNYGMVAKFINDYGTHYITSGSMGGIYEVYVVLVDKAKMESLGITSRDITTCFGLSGLQIYEDK--INVGGLSGDHCKK---FGGGKTERAKAMAVEDIISRVGGG 427
gi |73956396|ref|XP_536695.2|  *KKYSFRLRVFTKVTAHFQKMRRENIVLDEGMLQSLMELPEQYNYGMVAKFINDYGTHYITSGSMGGIYEVYVVLVDKAKMESLQRTISRDITTEKFCGTSVGIYDYANWMIKGSIGGGKGCEN---IGGGDKGHRLLTAVEDIISRVGGG 432
gi |114053319|ref|NP_001039750.1|  *KRYGFMRVSTKIQTAHFQKMRRENIVLDEGMLQSLMELPERYHYGMVAKFINDYGTHYITSGSMGGIYEVYVVLVDKAKMETAGVTSAETQKCFGVSLGIEVEYSEATQIKGSSSLGPKCK---SGDGKLTENEKAMGVEDFISRVGGD 432
gi |118094713|ref|XP_426667.2|  *AKNLGFIIRIAIKVTAHFQKMRRENIVLDEDMILISRELDPDYNYGMVAKFINDYGTHYITSGTMGGILEYVLLVNDKEMRRKDIYBVTTCFGLSGLVSAKLL-MLHWEASVLSVCAEKLNLNAVDFSDAGSNSVMVEDIISRVKGGD 446
gi |51011083|ref|NP_001003496.1|  *KREMGFVQLMSKIQTSQFKMRSKDLVLDDEMLWALSDLPDHYHFGAYSQFFNEYGTHYVTEGTMGLMDYVAVVNNINEMENQMTQMIGSCIGGSGFLVFMK---IKATVKGKSCGK---FTSNEKTSDESHSAIKDVFQVKGKN 321
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450

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gi |22122667|ref|NP_666260.1|  :VWGSVLHNSSAITYQSWGRSLKYNPVVIDFEMQPIYQLLRH--TNLGPLETKRNLRRALDQYLMEFNACRCGPCFNNGVPILEGTSCKCCQCSMGRQGLACERVIIEGLKDFKAAGHWCWSSWSECRGGSQERRRCNNPPPKNGGTF 576
gi |109475204|ref|XP_233251.4|  :SRWSTGLAHNSSAITYRSWGRSLKYNPVVIDFEMQPIYQLLRH--TNLGPLETKRNLRRALDQYLMEFNACRCGPCFNNGVPILEGTSCKCCQCSMGRQGLACERVIIEGLKDFKAAGHWCWSSWSECRGGSQERRRCNNPPPKNGGTF 576
gi |4557389|ref|NP_000553.1|  :SGWSGGLAQRNSTITYRSWGRSLKYNPVVIDFEMQPIHEVLRH--TSLGPLEAKRNLRRALDQYLMEFNACRCGPCFNNGVPILEGTSCKCCQCRGLGSLGAAACEOTETE--GAKADGWSWCWSSWSECRAGIQERRRECDNPAPONGGAF 573
gi |114556800|ref|XP_513435.2|  :SGWSGGLAQRNSTITYRSWGRSLKYNPVVIDFEMQPIHEVLRH--TSLGPLEAKRNLRRALDQYLMEFNACRCGPCFNNGVPILEGTSCKCCQCRGLGSLGAAACEOTETE--GAKADGWSWCWSSWSECRAGIQERRRECDNPAPONGGAF 573
gi |73956396|ref|XP_536695.2|  :SGWGAGLAEKRSITYRSWGRSLKYNPVVIDFEMQPIHEVLRH--TTLGPLETKRNLRRALDQYLMEFNACRCGPCFNNGKPILEGTSCKCCQCPFLGRRLGSLDCEMEQK---GAKADGWSWCWSSWSECRAGIQERRRECDNPAPONGGAS 578
gi |114053319|ref|NP_001039750.1|  :SGWGSLTQDSSSLITYRSWGRSLKYNPAVIDFEMQPIHEILLQH--TNLGSLTKRNLRRALDQYLMEFNACRCGPCFNNGVPILEGTSCKCCQCPVGHGGLACEQMOSE---GAKADGWSWCWSSWSECRAGIQERRRECDNPAPONGGAS 578
gi |118094713|ref|XP_426667.2|  :TSYARPISWSDNTYRRWGRSLKYNPAIIDFELQPIHEILLPR--SDAGNMETKROHLKQALDEYLLFNAACRCGPCFNNGVPILEGTSCKCCQCPVGHGGLACEQMOSE---GAEVDGRWSCWSSWSECRAGIQERRRECDNPAPONGGAF 592
gi |51011083|ref|NP_001003496.1|  :TASSAGSLGKIDAKSYKDWGKSLKYNPALIEFELPIYELLRLSTAAEQLSKLPVHKMAWEEYMQFNPCRCAPCLNNGVPLVSLGAGSCLCKNGYTGAAACEETERK---GPIIDGVWSCWSTWSSCLFKKTRSRDCNNPSPKDGGLP 467
.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600

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gi |22122667|ref|NP_666260.1|  * * *..*  CLGRNLQTAQC 587
gi |109475204|ref|XP_233251.4|  CLGKSLQTAQC 587
gi |4557389|ref|NP_000553.1|  *CPGRKQVTAQC 584
gi |114556800|ref|XP_513435.2|  *CPGRKQVTAQC 584
gi |73956396|ref|XP_536695.2|  *CPGWKAQTAQC 589
gi |114053319|ref|NP_001039750.1|  *CPGHRVQTAQC 589
gi |118094713|ref|XP_426667.2|  *CMGRDVQSSC 603
gi |51011083|ref|NP_001003496.1|  *CLGKSLQKKS 478
.....610.

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