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gi | 4503249 | ref | NP_003463.1 |      -MEAAPAAEGEGTPTQPASEKEPEMPGPRESEEEEE--EDEEEEEEKE--KSLIVEGKREKKKVERLTMQVSE--SLOREPPTIAGKGOKLCEIRIHFFLSKKKKT 103
gi | 114605909 | ref | XP_518259.2 |      -----MOVSE-----SLOREPPTIAGKGOKLCEIRIHFFLSKKKKT 36
gi | 29789160 | ref | NP_080176.1 |      MSAAAPAAEGEDAPVPPSSEKEPEMPGPRESEEEEEDEDDDEDEEEKEE--KSLIVEGKREKKKVERLTMQVSE--SLOREPPTVTGGOKLCEIRIHFFLSKKKKT 107
gi | 51948482 | ref | NP_001004255.1 |      MSAAAPAAEGEDTPTPPASEKEPEMPGPRESEEEEE--EDDDDEEEKEE--KSLIVEGKREKKKVERLTMQVSE--SLOREPPTIAGKGOKLCEIRIHFFLSKKKKT 105
gi | 153792239 | ref | NP_001093187.1 |      MSSGT-AAEGEAPAPQPASEKEPEMPGPRESEEEEE--DDDEEEEEEKEE--KSLIVEGKREKKKVERLTMQVSE--SLOREPPTIAGKGOKLCEIRIHFFLSKKKKT 103
gi | 74004120 | ref | XP_853159.1 |      -----MQELGGSDIIPPGNVESE-----EDDD--DEEEEEEEKEE--KSLIVEGKREKKKVERLTMQVSE--SLOREPPTIAGKGOKLCEIRIHFFLSKKKKT 89
gi | 60302770 | ref | NP_001012578.1 |      --MSVASSKEDTMSSEKADEQPEAENKAESEEDDE--EEEEEEEEKEE--KSLIVEGKREKKKVERLTMQVSE--SLOREPPTIFGGOKLCEIRIQFLLSKKKT 100
gi | 113674674 | ref | NP_001038741.1 |      --MEAIKTVHFLDDAEEDDE--SEESSP--KTTSKPKVKMF--ELEIVEGKREKKKVIQRLDNMSK--PKEKPKIESGGRGLDGIARINHSIGKLKA 88
gi | 42568737 | ref | NP_201160.2 |      MATELDEKTPEVNSPAKEIDVVPKEEKEVSEKEKVDSPRIGEABBEKKDEEEGEAKEGELGKEDDDVESEEEEEEEEEEGSGSKSSSEKETVTPTSERTRERRKKVERFSLSTPMRAPPSKSVSIEKGRGTPLREIPVAHKLSKRKA 150
gi | 15228428 | ref | NP_190440.1 |      MATELDEKTPTOLA--DTVAVTEKDTETKKKEVEKEDEAMEKEGEBEID--GER--VKSPVTPVSERTIRRRKTGRYVIDTPRRSSGNKLPSITGRGTRLKEIPVAHKLSKRKA 110
gi | 115441943 | ref | NP_001045251.1 |      MASDAKPDSPAGVDDPPP--KEEAKAKEGEGEEPSGQRRRKKGEAEK--ERE--VKSPVTPVSERTIRRRKTGRYVIDTPRRSSGNKLPSITGRGTRLKEIPVAHKLSKRKA 115
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

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gi | 4503249 | ref | NP_003463.1 |      DE-LRNLHKLLYNRPGVSSLKKNVGFSGFPFE--KGSVYKKKEEMLKKFRNAMLKSICEVLDLERSG--VNSELVKRILNFLMHPK--PSGKPLPKSKSSSGSKKNSSGMARKAK--RTKCPELSDESSSD--- 233
gi | 114605909 | ref | XP_518259.2 |      DE-LRNLHKLLYNRPGVSSLKKNVGFSGFPFE--KGSVYKKKEEMLKKFRNAMLKSICEVLDLERSG--VNSELVKRILNFLMHPK--PSGKPLPKSKSSSGSKKNSSGMARKAK--RTKCPELSDESSSD--- 166
gi | 29789160 | ref | NP_080176.1 |      DE-LRNLHKLLYNRPGVSSLKKNVGFSGFPFE--KGSTYKKKEEMLKKFRNAMLKSICEVLDLERSG--VNSELVKRILNFLMHPK--PSGKPLPKSKSSSGSKKNSSGMARKAK--RTKCPELSDESSSD--- 237
gi | 51948482 | ref | NP_001004255.1 |      DE-LRNLHKLLYNRPGVSSLKKNVGFSGFPFE--KGSTYKKKEEMLKKFRNAMLKSICEVLDLERSG--VNSELVKRILNFLMHPK--PSGKPLPKSKSSSGSKKNSSGMARKAK--RTKCPELSDESSSD--- 235
gi | 153792239 | ref | NP_001093187.1 |      DE-LRNLHKLLYNRPGVSSLKKNVGFSGFPFE--KGSIYKKKEEMLKKFRNAMLKSICEVLDLERSG--VNSELVKRILNFLMHPK--PSGKPLPKSKSSSGSKKNSSGMARKAK--RTKCPELSDESSSD--- 233
gi | 74004120 | ref | XP_853159.1 |      DE-LRNLHKLLYNRPGVSSLKKNVGFSGFPFE--KGSAYKKKEEMLKKFRNAMLKSICEVLDLERSG--VNSELVKRILNFLMHPK--PSGKPLPKSKSSSGSKKNSSGMARKAK--RTKCPELSDESSSD--- 219
gi | 60302770 | ref | NP_001012578.1 |      DE-LRNLHKLLYNRPGVSSLKKNVGFSGFPFE--KGSDYKKKEEMLKKFRNAMLKSICEVLDLERSG--VNSELVKRILNFLMHPK--PSGKPLPKSKSSSGSKKNSSGMARKAK--RTKCPELSDESSSD--- 230
gi | 113674674 | ref | NP_001038741.1 |      PL-LKPLHKLLYDRPAASTLRNLRLFNGFPFK--EDSDLYNKKMEKVKRLPKLLKITQTLDLERSG--QVVLSERIMKFLAQPT--NSGKPLPKSKSSSGSKKNSSGMARKAK--RTKCPELSDESSSD--- 224
gi | 42568737 | ref | NP_201160.2 |      DNLMLLHTILFGKAKAQMVKRNIGFSGFAWSEKEEEKQRAIKEKIKDKCVKELIVFCVLDIPTSRNVKEELAVKVEFLESPKETRDVIIADQEK--AKRRKSTPKRKSGSESSDTPAKRRKTTKK--RDLPSDTEBGKEGDA 297
gi | 15228428 | ref | NP_190440.1 |      DNLFLLHTILYGKAKAQMVKRNIGFSGFAWSEKEEEKQRAIKEKIKDKCVKELIVFCVLDIPTSRNVKEELAVKVEFLESPKETRDVIIADQEK--AKRRKSTPKRKSGSESSDTPAKRRKTTKK--RDLPSDTEBGKEGDA 258
gi | 115441943 | ref | NP_001045251.1 |      DNLSSLHVLMYGRKSNVHFLKRNISGFSVWTDNQ--KRTRIEKELDKFNKELLDFCEILDIHVSRAAIKKEEVSAKLLEFLESPCITRDVVLDDKKGKRRGRRSKGNGQATEAGADDKKRRKSQQTEAAKNDDEDDEGDA 264
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300

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gi | 4503249 | ref | NP_003463.1 |      -----EDEKKNK-----ESSDDEDDKES-----EEE--PPKTAKR-----EKPKQKATSKSKKSVKSAN--VKKADSSTTKKQNSSKKESESE 304
gi | 114605909 | ref | XP_518259.2 |      -----EDEKKNK-----ESSDDEDDKES-----EEE--PPKTAKR-----EKPKQKATSKSKKSVKSAN--VKKADSSTTKKQNSSKKESESE 237
gi | 29789160 | ref | NP_080176.1 |      -----EDEKKNK-----ESSDEEDEKES-----EEEQPPKTAKR-----EKAKQKATAKSKKSVKSAN--VKKADSSTTKKQNSSKKESESE 309
gi | 51948482 | ref | NP_001004255.1 |      -----EDEKKNK-----ESSDEEDEKES-----EEEQPPKTAKR-----EKAKQKATAKSKKSVKSAN--VKKADSSTTKKQNSSKKESESE 307
gi | 153792239 | ref | NP_001093187.1 |      -----EDEKKNK-----ESSDEEDDKES-----EEE--PPKTSKR-----EKPKQKATPKSKKSVKSAN--VKKADSSTTKKQNSSKKESESE 304
gi | 74004120 | ref | XP_853159.1 |      -----EDEKKNK-----ESSDDEDDKES-----EEE--PPKTSKR-----EKPKQKATSKSKKSVKSAN--VKKADSSTTKKQNSSKKESESE 290
gi | 60302770 | ref | NP_001012578.1 |      -----EDEKKEK-----DDSS--EKES-----EEE--PPRRASKR-----EKSK--KVTSKPKKTVKGAN--VKKADSSTTKKQNSSSKRESESE 298
gi | 113674674 | ref | NP_001038741.1 |      DDDD--DDGDEETTKGSKGTEKSAKASQKHDDSEDKSIEEDESSDDVDDDDSKEDSKEETSPPQKSSTGKSTKSDKMSDQSPSDETDDSDYCEDKDAKTTKKKPAAKRPAKVPPKKAADSSNRKKTTASSKRRDESE 371
gi | 42568737 | ref | NP_201160.2 |      DSE--GTNDPHEE--DAAPEEESD--HEKTDDEKD--EVVEKEPKSKKSSS--SKKVESSSGKGDKQPSAKGSARSGEKSSKIAKSSSPAKKQVDHVESKEKSSKQPSKPA 408
gi | 15228428 | ref | NP_190440.1 |      GSE--GTNDSNGE--DDVAPEEENNK--SEDETDEDKKAEKTKSTDKRL--SKRTKEKEPAAE--EKSIKGAKSSRFVDKSTSSSSKQVDKDDSSKERGKTQTSKPA 368
gi | 115441943 | ref | NP_001045251.1 |      DSEADAMGEEDDESEAK--DNAGSDERPEPPAKKATDDKTKKAKEDTAAKKASTRPAGVSKPSQTEDDDEPEVELESKVKVYSSKSESSDVTVDKTTKKASKSKDEGDKDNNSGALNKARK 396
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450

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gi | 4503249 | ref | NP_003463.1 |      D-----SSDDEPLIKLKKKPPTDEELKEIIKLLASANLEEVTMKQICCKVYENYPTYDLTKRDFIKTTVKELIS----- 375
gi | 114605909 | ref | XP_518259.2 |      D-----SSDDEPLIKLKKKPPTDEELKEIIKLLASANLEEVTMKQICCKVYENYPTYDLTKRDFIKTTVKELIS----- 308
gi | 29789160 | ref | NP_080176.1 |      D-----SSDDEPLIKLKKKPPTDEELKEIIKLLADANLEEVTMKQICCKVYENYPACDLTKRDFIKTTVKELIS----- 380
gi | 51948482 | ref | NP_001004255.1 |      D-----SSDDEPLIKLKKKPPTDEELKEIIKLLADANLEEVTMKQICCKVYENYPAYDLTKRDFIKTTVKELIS----- 378
gi | 153792239 | ref | NP_001093187.1 |      D-----SSDDEPLIKLKKKPPTDEELKEIIKLLASANLEEVTMKQICCKVYENYPAYDLTKREFIKTTVKELIS----- 375
gi | 74004120 | ref | XP_853159.1 |      D-----SSDDEPLIKLKKKPPTDEELKEIIKLLASANLEEVTMKQICCKVYENYPAYDLTKRDFIKTTVKELIS----- 361
gi | 60302770 | ref | NP_001012578.1 |      D-----SSDNEPLIKLKKKPPTDEELKEIIKLLANANLEEVTMKQICCKVYENYPSYDLDRKDFIKTTVKELIS----- 369
gi | 113674674 | ref | NP_001038741.1 |      S-----SDDDPLIKMIKKPPTDEELKEIIKENVKDLLKANLEEVTMKQITTRVYDKYPDFDLSSRKEFIRETVKNMIS----- 442
gi | 42568737 | ref | NP_201160.2 |      K-----GSKEGKATKKGKAEPTRKEMLVVSKILVEVDFNTATLSDILQRLSDHFG--VELSHRKEVEKVDVITEAINAMDDDEEEDEEEEAAGSDKEKEVEVKEGEEEEKAAESEDKEKEKEPKD 530
gi | 15228428 | ref | NP_190440.1 |      K-----GSKDQGSRRKG--KEEPTRKELHVVVTKILKEVDFNTATLSDILQRLSDHFG--IDLMHRKAEVKDITTDAINEMSDDDEKEEDTEEDEGEKEGKD----- 462
gi | 115441943 | ref | NP_001045251.1 |      KDAAKTTKNKGKGSTEGAAPTTELHAVVSDILKEVDFNTATLSDILQRLSDHFG--MDLMDRKESEVKHIEVINSMSDDEEGEEDNAEDDKNAKEENSKEDADGDEK----- 509
.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....

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