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gi | 6322141 | ref | NP_012216.1 | -----TPSKDLKVGDLIKVHKGRIPADLVLLQSE-----PGESEFIKTDQLDGEDWKLRLVA 318
gi | 50305229 | ref | XP_452573.1 | -----TPSKDLKVGDIKLLKKGARVPADVVLQTN-----PNGESFIKTDQLDGEDWKLRLVA 321
gi | 45187794 | ref | NP_984017.1 | -----VPSKNLRVGDVLRKHKDRIPADMILLQSE-----PGESEFIKTDQLDGEDWKLRLVA 336
gi | 145607199 | ref | XP_361592.2 | RKAQLRL---SERDRLSDIIEEELAEAGDGAGKGAASHIREVLKASKDLKVGDLVRLTKGQRPVADVVLICLASEVNTASTPVASK--LAEPPELLTLDAS--GNGGASOPRDDGASDGDGSGAGAGGETFIRTDQLDGEDWKLRLVA 450
gi | 85101739 | ref | XP_961207.1 | RTGSKRLGIEQENDRLSDIIEEELTEGRGLRELPAAYLSEVSKSRDLKVGDLVRLTKGHRVADVVLICLAHEAANKETEEVPAKEEMLLDHDVDDDDVGESEKNAKTEKESNNNGAEGSSGSEFTFIRTDQLDGEDWKLRLVA 455
gi | 19114632 | ref | NP_593720.1 | -----AQNIAQADVVIKAKDRIPADMILLEITVVG-----NEAFIRTDQLDGEDWKLRLIP 234
gi | 115532300 | ref | NP_001040665.1 | -----RIEIRSAADIEVGDVVIIMHKDRRVPADVLLRTD-----SGACFIRTDQLDGEDWKLRLIP 251
gi | 17559268 | ref | NP_503858.1 | -----RVEIKSADIKVGDVIVMHKDRRVPADVLLRTSDK-----SGCFIRTDQLDGEDWKLRLIP 244
gi | 20301938 | ref | NP_609634.1 | -----YEMVPSKLVKVDVIVVEKNERVPADLILLRTSDR-----SGVVFVRTDQLDGEDWKLRLA 381
gi | 158296962 | ref | XP_317283.4 | -----PESVSSKLVKVDIIMVEKDERVPADLILLRTSDK-----SGAVFVRTDQLDGEDWKLRLA 183
gi | 73945359 | ref | XP_855968.1 | -----KVOVKSSDIQVGDVLIIEKRNORIPSDMVFLRTSEK-----AGSCFIRTDQLDGEDWKLRLVA 279
gi | 122692527 | ref | NP_001073724.1 | -----KVOVKSSDIQVGDVLIIEKRNORIPSDMVFLRTSEK-----AGSCFIRTDQLDGEDWKLRLVA 281
gi | 41327760 | ref | NP_940933.3 | -----KVOVKSSDIQVGDVLIIEKRNORIPSDMVFLRTSEK-----AGSCFIRTDQLDGEDWKLRLVA 280
gi | 114673706 | ref | XP_001143568.1 | -----KVOVKSSDIQVGDVLIIEKRNORIPSDMVFLRTSEK-----AGSCFIRTDQLDGEDWKLRLVA 241
gi | 40807502 | ref | NP_056620.2 | -----KVOVKSSDIQVGDVLIIEKRNORIPSDMVFLRTSEK-----AGSCFIRTDQLDGEDWKLRLVA 279
gi | 62664679 | ref | XP_225706.3 | -----KVOVKSSDIQVGDVLIIEKRNORIPSDMVFLRTSEK-----AGSCFIRTDQLDGEDWKLRLVA 280
gi | 113681577 | ref | NP_001038619.1 | -----KVOVKSSDIQVGDVLIIEKRNORIPADMIFLRTSEK-----AGSCFIRTDQLDGEDWKLRLVA 228
gi | 124806112 | ref | XP_001350631.1 | EDDDEDDEDEDEDEDEEVNIPNNEKNDTQNLDDKKSVRRIFGTKNNNTSYGDDQVQNEKKKLNLDKGYLNLEEK-----DIDYAYNKKDKKEMV 537

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gi | 6322141 | ref | NP_012216.1 | CPLTQNLSENDLINRI--SITASAPKSKTHKFLGKVIYKDT-----SNPLSDVNTLWANTVLASSGFCIACVVYTGDRTRQAMNTITAKVKTGLLELEINSISKILCACVFALSILLVAFAGFHND-- 439
gi | 50305229 | ref | XP_452573.1 | CSLTQSLTENDLLNNT--TITASAPKSHSINFLGKIITYKDT-----SSPLSDVNTMVENTVLASSAACICCVIYTGRETRQALNTKSKAKTGLLELEINSLKILCACVFLLSIMLVAFAFQNNND-- 442
gi | 45187794 | ref | NP_984017.1 | PSLTQNLQDEMLTKV--HITASAPKSKTHMFTGKLIYKGS-----SAPLSVNTLWANTVLASSGTCVACVVIYTGDRTRQAMNTSKSVKTKGLLELEINSLKILCIVFTLSILLVVIIGLDDDK-- 456
gi | 145607199 | ref | XP_361592.2 | SPLSONLATEELVR-F--RVTAGKPKDKVNEFVGLLELLSPRODAMSP-----GARLPNGDELANAPLITDNTAWANTVIASRAVILAVIYVYTGDRTRQALNTSPSRKTKGLLELEINSLKILCALFLALSIIILVAFQGTNTKGN 590
gi | 85101739 | ref | XP_961207.1 | SPLSONLSTEEELVR-L--RVTAGKPKDKVNEFVGLLELLSPRODAMSP-----AAVNPREGDDVKAAPLSDNTAWANTVIASNAITLAVIYVYTGDRTRQALNTSPSRKTKGLLELEINSLKILCFLFLVLSIVLVAEGFSTAKGN 595
gi | 19114632 | ref | NP_593720.1 | CSNQHTEG-----IVHADAPLKSVHHFVGFLLNNK-----RPISDVHTLWANTVLASDG--YGVVVIYTGDRTRQALNTSPSRKTKGLLELEINSLKILCFLFLVLSIGLTFHGHKLT-- 344
gi | 115532300 | ref | NP_001040665.1 | VPHTQHLNPEADIMELNCEVYAEKPKDKIHAIFVGLKKIT-----DDNVQDGSINVENVLWANTVVASGT--AVGLVVIYTGDRTRQALNTLPEKSGVGLLDLEVNINLTKLLFCFVLVLSVVMVAMKGLDNL-- 375
gi | 17559268 | ref | NP_503858.1 | IPFTQHLNANESEIMELNCEVYAEKPKDKIHSFVGVKKIT-----ADDKIHGSLDVENVLWANTVVASGT--AIGVVIYTGDRTRQALNTLPEYKVGLLDLEINNLTLLFCFVLLASVVMMLKGFPTSL-- 368
gi | 20301938 | ref | NP_609634.1 | VPYTOKLSRDSSELHSIDASPYVEKPNNDIHSFIAMFCM-----ADGSEDTGLSDVENVLWANTVVAAGT--ATGIVVIYTGDRTRQALNTLPEYKVGLLDLEINNLTLLFCFVLLASVVMMLKGFQGP-- 503
gi | 158296962 | ref | XP_317283.4 | VPATQKLSHAGELLTIVNASLYVEKPKORDIHTIFIGIYK-----HGTTEDEGLNVENTLWANTVVASGT--AVGIVVIYTGDRTRQALNTLPEYKVGLLDLEINNLTLLFCFVLLASVVMMLKGFQGP-- 305
gi | 73945359 | ref | XP_855968.1 | VSCTQRLPALGDLFSISAYVYAKPKQLDIHSFEGFTFR-----EDCDPPIHESLSIENTLWASTIVASGT--VIGVVIYTGDRTRQALNTLPEYKVGLLDLEINNLTLLFCFVLLASVVMMLKGFQGP-- 403
gi | 122692527 | ref | NP_001073724.1 | VSCTQRLPALGDLFSINAYVYAKPKQLDIHSFEGFTFR-----EDSDPPVHESLSIENTLWASTIVASGT--VIGVVIYTGDRTRQALNTLPEYKVGLLDLEINNLTLLFCFVLLASVVMMLKGFQGP-- 405
gi | 41327760 | ref | NP_940933.3 | VSCTQRLPALGDLFSISAYVYAKPKQMDIHSFEGFTFR-----EDSDPPIHESLSIENTLWASTIVASGT--VIGVVIYTGDRTRQALNTLPEYKVGLLDLEINNLTLLFCFVLLASVVMMLKGFQGP-- 404
gi | 114673706 | ref | XP_001143568.1 | VSCTQRLPALGDLFSISAYVYAKPKQMDIHSFEGFTFR-----EDSDPPIHESLSIENTLWASTIVASGT--VIGVVIYTGDRTRQALNTLPEYKVGLLDLEINNLTLLFCFVLLASVVMMLKGFQGP-- 365
gi | 40807502 | ref | NP_056620.2 | VSCTQRLPALGDLFSISAYVYAKPKQMDIHSFEGFTFR-----EDSDPPIHESLSIENTLWASTIVASGT--VIGVVIYTGDRTRQALNTLPEYKVGLLDLEINNLTLLFCFVLLASVVMMLKGFQGP-- 403
gi | 62664679 | ref | XP_225706.3 | VSCTQRLPALGDLFSISAYVYAKPKQLDIHSFEGFTFR-----EDSDPPIHESLSIENTLWASTIVASGT--VIGVVIYTGDRTRQALNTLPEYKVGLLDLEINNLTLLFCFVLLASVVMMLKGFQGP-- 404
gi | 113681577 | ref | NP_001038619.1 | VACTQRLPALGDLFSISAYVYKPKQLDIHSFEGFTFRISMKSKQTEMYKPLMLCDLCP-----EDSDPPIHESLSIENTLWASTIVASGT--VIGVVIYTGDRTRQALNTLPEYKVGLLDLEINNLTLLFCFVLLASVVMMLKGFQGP-- 374
gi | 124806112 | ref | XP_001350631.1 | FPIVDEKGNNERIINLNKKKNSVNTTGNRSSVNDGKMCNPFVNNEDNFN-----FYNVIRKKNLIDNIFLNSVITGSD--VICLVIYTGDRTRQALNTLPEYKVGLLDLEINNLTLLFCFVLLASVVMMLKGFQGP-- 669

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gi | 6322141 | ref | NP_012216.1 | *--WYIDILRYLLILFSTIIPVSLRVNLDLAKSVYARQIEHDKTIPETIVRTSTIPEDLGRIEYLLSDKGTGLTQNDMQLKKIHLG----- 521
gi | 50305229 | ref | XP_452573.1 | --WYVDIMRYLLILFSTIIPVSLRVNLDLQKSVYARQIEHDKQIEDIVRTSTIPEDLGRIEYLLSDKGTGLTQNDMQLKKIHLG----- 524
gi | 45187794 | ref | NP_984017.1 | --WYVDIMRYLLILFSTIIPVSLRVNLDLQKSVYARQIESDKSIPDIVRTSTIPEDLGRIEYLLSDKGTGLTQNDMQLKKIHLG----- 538
gi | 145607199 | ref | XP_361592.2 | WYIKIMRFLVLFSTIIPVSLRVNLDLQKSVYARQIDPDPGMPGAVVRTSMIPEDLGRIEYLLSDKGTGLTQNDMEMMKKIHLG----- 673
gi | 85101739 | ref | XP_961207.1 | IWYVKIMRFLVLFSTIIPVSLRVNLDLQKSVYARQIDPDPGMPGAVVRTSMIPEDLGRIEYLLSDKGTGLTQNDMEMMKKIHLG----- 678
gi | 19114632 | ref | NP_593720.1 | --WYISVFRYLILFSTIIPINLRNLDLAKIVHSKNSIESDNLPGVVVRSNIPPEELGRIEYVLTDKGTGLTQNDMEMMKKIHLG----- 426
gi | 115532300 | ref | NP_001040665.1 | --WRYLMRFILLFSTIIPISLRVNLDMKALFVSWQIGRDKHIPETIVRSSTIPEELGRISFLLSDKGTGLTQNDMEMHFKKIHLG----- 457
gi | 17559268 | ref | NP_503858.1 | --WYLYARFILLFSTIIPISLRVNLDMKALFVSWQIGRDKHIPETIVRSSTIPEELGRISFLLSDKGTGLTQNDMEMHFKKIHLG----- 450
gi | 20301938 | ref | NP_609634.1 | --WRYMFRFVLLFSTIIPISLRVNLDMGKAFVSWQONDSNIQGVVRSSTIPEELGRISVYVLTDKGTGLTQNDMEMVFKKIHLG----- 585
gi | 158296962 | ref | XP_317283.4 | --WRYMFRFVLLFSTIIPISLRVNLDMGKAFVSWQONDDIEKGTIVRSSTIPEELGRMSVYVLTDKGTGLTQNDMEMIFKKIHLG----- 387
gi | 73945359 | ref | XP_855968.1 | --WYRNLFRLLLFSTIIPISLRVNLDMGKAAVGMIMKDESIPTVVRTSTIPEELGRIVYVLTDKGTGLTQNDMEMVFKRHLG----- 485
gi | 122692527 | ref | NP_001073724.1 | --WYRSLFRLLLFSTIIPISLRVNLDMGKAAVGMIMKDESIPTVVRTSTIPEELGRIVYVLTDKGTGLTQNDMEMVFKRHLG----- 487
gi | 41327760 | ref | NP_940933.3 | --WYRNLFRLLLFSTIIPISLRVNLDMGKAAVGMIMKDESIPTVVRTSTIPEELGRIVYVLTDKGTGLTQNDMEMIFKRIHLG----- 486
gi | 114673706 | ref | XP_001143568.1 | --WYRILFRLLLFSTIIPISLRVNLDMGKAVVGMIMKDESIPTVVRTSTIPEELGRIVYVLTDKGTGLTQNDMEMIFKRIHLG----- 447
gi | 40807502 | ref | NP_056620.2 | --WYRNLFRLLLFSTIIPISLRVNLDMGKAAVGMIMKDESIPTVVRTSTIPEELGRIVYVLTDKGTGLTQNDMEMVFKRHLG----- 485
gi | 62664679 | ref | XP_225706.3 | --WYRNLFRLLLFSTIIPISLRVNLDMGKAAVGMIMKDESIPTVVRTSTIPEELGRIVYVLTDKGTGLTQNDMEMVFKRHLG----- 486
gi | 113681577 | ref | NP_001038619.1 | --WYRNLFRVLLFSTIIPISLRVNLDMGKAAVGMIMKDESIPTVVRTSTIPEELGRIVYVLTDKGTGLTQNDMEMVFKRHLG----- 456
gi | 124806112 | ref | XP_001350631.1 | LWYLNFRFVLLFSTIIPISLNVNLIKIYVTLIIQRDKVESITIKNSGIIENGFVDYIFDKGTGLTQNDMEMVLMKVIHLGFDVIAHAEKNSKIQGNMMEIKQKGNVYKMKMLSYNLDMMEDVDDTSIIVLASSNYSKHDRRNKINLRG 819

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gi | 6322141 | ref | NP_012216.1 |
gi | 50305229 | ref | XP_452573.1 |
gi | 45187794 | ref | NP_984017.1 |
gi | 145607199 | ref | XP_361592.2 |
gi | 85101739 | ref | XP_961207.1 |
gi | 19114632 | ref | NP_593720.1 |
gi | 115532300 | ref | NP_001040665.1 |
gi | 17559268 | ref | NP_503858.1 |
gi | 20301938 | ref | NP_609634.1 |
gi | 158296962 | ref | XP_317283.4 |
gi | 73945359 | ref | XP_855968.1 |
gi | 122692527 | ref | NP_001073724.1 |
gi | 41327760 | ref | NP_940933.3 |
gi | 114673706 | ref | XP_001143568.1 |
gi | 40807502 | ref | NP_056620.2 |
gi | 62664679 | ref | XP_225706.3 |
gi | 113681577 | ref | NP_001038619.1 |
gi | 124806112 | ref | XP_001350631.1 |

---TVSYTSEALDIDVSDIVQS-----LVSKNDSLNNKSKVALSTTRKDMSEFRV 566
TVSYTNEIMDVIDTDFIQS-----MNSRFTNSFP-----TTTRKNISDRV 563
TVSYTMEIMDMVTDYIQT-----LTSAPNMGAAAG--VAVTGSRKEVSRV 581
TVSYANEAMDEVSSYIKQGFHVQPTLSDI-----ESTQLVTPSSFTNAAAGCTTRTRREIGARV 734
TVSYANEAMDEVATVYKQGFNLSS--SA-----ASALALTPSSITYS--AANVGATRTTRREIGSRV 736
TMGFSAEIMDVVQACIQN-----YSIP-----IPLSEDSKTLV 459
TVAFSSDAFEVQGHVRSANAG-----TVAFSSGDALBEVEQHVKSAIDS-----ALVKHFPFAKL 490
TVSHDADTFHHIGQMIQKLSGNILQQQQ-----GSLSSSSSGDSTKPMFQNRMRPEGWRE 643
TAAYGRDTPMVSAAIQSVYG-----TLTSAFADAPEDHGSEYQRLRKPDPGWRT 437
TVSYGADTMDEIQNHILRNPYSOMQS-----CAGNNTSSITLPRKAQSSAPKVRKSVSSRV 540
TVSYGADTMDEIQNHILVNAITQOC-----CAGGSSAATPPPKAPSSAPKVRKSVSSRV 542
TVSYGADTMDEIQSHVRDSYSOMQS-----CAGNNTGSTPLRKAQSSAPKVRKSVSSRI 541
TVSYGADTMDEIQSHVRDSYSOMQS-----CAGGNTGSTPLRKAQSSAPKVRKSVSSRI 502
TVSYGADTMDEIQSHVLSNVLQVHS-----QPSGHNTPSSAPLRRSQSTPKPKKSVSSRI 540
TVSYGADTMDEIQSHVLSNVLQVHS-----QTSGHNTPSSAPLRRSQSTPKPKKSVSSRI 541
TVSYGADTMDEIQSHLIQSLAQVSSA-----CNGSSASTPSPKQPPAPKVRKSVSSRI 512
ELASFSVEMENISNINNNIKLRNYTKSNHHNNISDNELYDEKNYDDQRSLSNYSDTSYGDVHLKKNYKONNMILNOMNGONRNETLTKNNNNNNNNNNNNNNNNNNNNMSLEKKKKKVKRMVDFELKYSKDPIDYVNDNIDDIYELKRHRV 969
.....910.....920.....930.....940.....950.....960.....970.....980.....990.....1000.....1010.....1020.....1030.....1040.....1050



gi | 6322141 | ref | NP_012216.1 |
gi | 50305229 | ref | XP_452573.1 |
gi | 45187794 | ref | NP_984017.1 |
gi | 145607199 | ref | XP_361592.2 |
gi | 85101739 | ref | XP_961207.1 |
gi | 19114632 | ref | NP_593720.1 |
gi | 115532300 | ref | NP_001040665.1 |
gi | 17559268 | ref | NP_503858.1 |
gi | 20301938 | ref | NP_609634.1 |
gi | 158296962 | ref | XP_317283.4 |
gi | 73945359 | ref | XP_855968.1 |
gi | 122692527 | ref | NP_001073724.1 |
gi | 41327760 | ref | NP_940933.3 |
gi | 114673706 | ref | XP_001143568.1 |
gi | 40807502 | ref | NP_056620.2 |
gi | 62664679 | ref | XP_225706.3 |
gi | 113681577 | ref | NP_001038619.1 |
gi | 124806112 | ref | XP_001350631.1 |

RDMLLTLAICHNVTPFPED-----DELTYQAAAPDEIAIVKFTESVGLSLFKRDRHSITSLLHEHSGKT- 629
IDLVTTLAICHNVTPFPED-----GELTYQAAAPDEIAIVKFTESVGLSLFKRDRHSITSLFDHDSGMK- 626
RDLVLLALACHNVTPFPED-----NELAYQAAAPDEIAIVKFTESVGLSLFKRDRHSITSLFHEYSQVN- 644
RDVLLALALACHNVTPFDE-ED-----GKTVTSYQAAAPDEIAIVKFTESVGLSLFKRDRHSITSLFSETGK- 800
RDVLLALALACHNVTPFSEEDEN-----GHTVNSYQAAAPDEIAIVKFTESVGLSLFKRDRHSITSLFSAETGRPV- 805
RNLVLLALALACHNVTPFKGH-----DGVVSYQAAAPDEIAIVKFTESVGLSLFKRDRHSITSLFSAETGRPV- 518
QNAVEIALACHNVTPFENGEE-----ISYQAAAPDEIAIVKFTESVGLSLFKRDRHSITSLFSAETGRPV- 556
KNAVESLALACHNVTPFLENGE-----LSYQAAAPDEIAIVKFTESVGLSLFKRDRHSITSLFSAETGRPV- 549
WEAVRALALACHNVTPVSDDED--NRVSTASTVGGNN--PTK--SVINTEAPG--STDEHQYQAAAPDEIAIVKFTESVGLSLFKRDRHSITSLFSAETGRPV- 743
WESVKALALACHNVTPVYESNNGGSGSISSTSDRRQ--PAR--SISVESQAGEPSTK--PATTEKTYQAAAPDEIAIVKFTESVGLSLFKRDRHSITSLFSAETGRPV- 553
HEAVKAIALACHNVTPVVEPRAG--MTGEAEYTEADDF--DGNRTYQAAAPDEIAIVKFTESVGLSLFKRDRHSITSLFSAETGRPV- 621
HEAVKAVALACHNVTPVVEARAG--AAGETEFAEADDF--DDNRTYQAAAPDEIAIVKFTESVGLSLFKRDRHSITSLFSAETGRPV- 622
HEAVKAIVLACHNVTPVYESRAG--VTEETFEAEDDF--DENRTYQAAAPDEIAIVKFTESVGLSLFKRDRHSITSLFSAETGRPV- 622
HEAVKAIVLACHNVTPVYESRAG--VTEETFEAEDDF--DENRTYQAAAPDEIAIVKFTESVGLSLFKRDRHSITSLFSAETGRPV- 583
HEAVKAIALACHNVTPVVEARAG--ITISRDLEAEMQKTF--DENRTYQAAAPDEIAIVKFTESVGLSLFKRDRHSITSLFSAETGRPV- 621
HEAVKAIALACHNVTPVVEARAG--ITISRDLEAEMQKTF--DENRTYQAAAPDEIAIVKFTESVGLSLFKRDRHSITSLFSAETGRPV- 622
HEAVKAIALACHNVTPVVEARAG--ITISRDLEAEMQKTF--DENRTYQAAAPDEIAIVKFTESVGLSLFKRDRHSITSLFSAETGRPV- 594
FOTLFLSFLICNNIRTLKESSNKEKEKTKKKKERKEDFQKNLYYLILKVNRRKKDVKRKKKENNSDNYKSTONKPKKHP--SNSSESE--FSSHSDVSYQAAAPDEIAIVKFTESVGLSLFKRDRHSITSLFSAETGRPV- 1104
.....1060.....1070.....1080.....1090.....1100.....1110.....1120.....1130.....1140.....1150.....1160.....1170.....1180.....1190.....1200



gi | 6322141 | ref | NP_012216.1 |
gi | 50305229 | ref | XP_452573.1 |
gi | 45187794 | ref | NP_984017.1 |
gi | 145607199 | ref | XP_361592.2 |
gi | 85101739 | ref | XP_961207.1 |
gi | 19114632 | ref | NP_593720.1 |
gi | 115532300 | ref | NP_001040665.1 |
gi | 17559268 | ref | NP_503858.1 |
gi | 20301938 | ref | NP_609634.1 |
gi | 158296962 | ref | XP_317283.4 |
gi | 73945359 | ref | XP_855968.1 |
gi | 122692527 | ref | NP_001073724.1 |
gi | 41327760 | ref | NP_940933.3 |
gi | 114673706 | ref | XP_001143568.1 |
gi | 40807502 | ref | NP_056620.2 |
gi | 62664679 | ref | XP_225706.3 |
gi | 113681577 | ref | NP_001038619.1 |
gi | 124806112 | ref | XP_001350631.1 |

LNVEILQVFPFNSDKRMGLIIVR-----DEQLDEYWFQKQADTVMSK--IVESNDWLEBETGNMAREGLRLTVIGRKKLNKKIYEQFOKEYNDASLSMLN--RDQMSQVITKYLEHDLLELLGLTGVEDKLDKDKVKS--SIELLRNA 766
LEYDIKILFFPNSDKRMGLIIVR-----DKLKQYWFQKQADTVMSK--IVVRNDWLEBETGNMAREGLRLTVIGRKKLNKKIYEQFOKEYNDASLSMLN--RDQMSQVITKYLEHDLLELLGLTGVEDKLDKDKVKS--SIELLRNA 763
LQYDILHVFPPFNSDKRMGLIIVR-----DRTKNEIWFQKQADTVMSK--IVQSNWLEBEEVSNMAREGLRLTVIARKKLSTRLYEQFOKEYNDASLSMLN--RDEAMNEVVKRHLNLELLGLTGVEDKLDKDKVKS--SIELLRNA 781
LQYDILHVFPPFNSDKRMGLIIVR-----EIGSGEITWFYKQADTVMSK--IVAANDWLEBETGNMAREGLRLTVVGRKKLSAEQYREFSSRYQASLAISNG--RDAGMQKVVSHYLERDLELLGLTGVEDKLDKDKVKS--SIELLRNA 924
VKVRLLDIFPNSDKRMGLIIVR-----VVKKILNIFPFKSETKRMGLIIVR-----SPDEKIFLYLKQADTVMSK--MVOYNDWLEBEEVSNMAREGLRLTVVAKRKLAEYSAFSAHSDASLSFNSR--RDKKMEIIVSRLENMDLLGLTGVEDKLDKDKVKS--SIELLRNA 654
KQFQILHVFPPFNSDKRMGLIIVR-----DETDDEVLLMKQADTVMSK--MVOYNDWLEBEEVSNMAREGLRLTVVAKRKLAEYSAFSAHSDASLSFNSR--RDKKMEIIVSRLENMDLLGLTGVEDKLDKDKVKS--SIELLRNA 693
IQFQILHVFPPFNSDKRMGLIIVR-----BETSGEVLLYKQADTVMSK--MVOYNDWLEBEEVSNMAREGLRLTVVAKRKLAEYSAFSAHSDASLSFNSR--RDKKMEIIVSRLENMDLLGLTGVEDKLDKDKVKS--SIELLRNA 686
LHVQILQVFPFNSDKRMGLIIVR-----ESKTGQIFLYLKQADTVMSK--MVOYNDWLEBEEVSNMAREGLRLTVVAKRKLAEYSAFSAHSDASLSFNSR--RDKKMEIIVSRLENMDLLGLTGVEDKLDKDKVKS--SIELLRNA 879
LTVQILQVFPFNSDKRMGLIIVR-----ELNGGEIIFLYLKQADTVMSK--MVOYNDWLEBEEVSNMAREGLRLTVVAKRKLAEYSAFSAHSDASLSFNSR--RDKKMEIIVSRLENMDLLGLTGVEDKLDKDKVKS--SIELLRNA 689
LTVQILQVFPFNSDKRMGLIIVR-----DESTAEIIFMYKQADTVMSK--MVOYNDWLEBEEVSNMAREGLRLTVVAKRKLAEYSAFSAHSDASLSFNSR--RDKKMEIIVSRLENMDLLGLTGVEDKLDKDKVKS--SIELLRNA 757
LTVQILQVFPFNSDKRMGLIIVR-----DESTAEIIFMYKQADTVMSK--MVOYNDWLEBEEVSNMAREGLRLTVVAKRKLAEYSAFSAHSDASLSFNSR--RDKKMEIIVSRLENMDLLGLTGVEDKLDKDKVKS--SIELLRNA 758
LTVQILQVFPFNSDKRMGLIIVR-----DESTAEIIFMYKQADTVMSK--MVOYNDWLEBEEVSNMAREGLRLTVVAKRKLAEYSAFSAHSDASLSFNSR--RDKKMEIIVSRLENMDLLGLTGVEDKLDKDKVKS--SIELLRNA 758
LTVQILQVFPFNSDKRMGLIIVR-----DESTAEIIFMYKQADTVMSK--MVOYNDWLEBEEVSNMAREGLRLTVVAKRKLAEYSAFSAHSDASLSFNSR--RDKKMEIIVSRLENMDLLGLTGVEDKLDKDKVKS--SIELLRNA 719
LTVQILQVFPFNSDKRMGLIIVR-----DESTAEIIFMYKQADTVMSK--MVOYNDWLEBEEVSNMAREGLRLTVVAKRKLAEYSAFSAHSDASLSFNSR--RDKKMEIIVSRLENMDLLGLTGVEDKLDKDKVKS--SIELLRNA 757
LTVQILQVFPFNSDKRMGLIIVR-----DESTAEIIFMYKQADTVMSK--MVOYNDWLEBEEVSNMAREGLRLTVVAKRKLAEYSAFSAHSDASLSFNSR--RDKKMEIIVSRLENMDLLGLTGVEDKLDKDKVKS--SIELLRNA 758
LTVQILQVFPFNSDKRMGLIIVR-----DESTAEIIFMYKQADTVMSK--MVOYNDWLEBEEVSNMAREGLRLTVVAKRKLAEYSAFSAHSDASLSFNSR--RDKKMEIIVSRLENMDLLGLTGVEDKLDKDKVKS--SIELLRNA 730
LTVQILQVFPFNSDKRMGLIIVR-----DESTAEIIFMYKQADTVMSK--MVOYNDWLEBEEVSNMAREGLRLTVVAKRKLAEYSAFSAHSDASLSFNSR--RDKKMEIIVSRLENMDLLGLTGVEDKLDKDKVKS--SIELLRNA 1238
.....1210.....1220.....1230.....1240.....1250.....1260.....1270.....1280.....1290.....1300.....1310.....1320.....1330.....1340.....1350



gi	6322141	ref	NP_012216.1	-----	1151
gi	50305229	ref	XP_452573.1	-----	1148
gi	45187794	ref	NP_984017.1	-----	1166
gi	145607199	ref	XP_361592.2	-----	1364
gi	85101739	ref	XP_961207.1	-----	1331
gi	19114632	ref	NP_593720.1	-----	1033
gi	115532300	ref	NP_001040665.1	-----	1071
gi	17559268	ref	NP_503858.1	-----	1064
gi	20301938	ref	NP_609634.1	-----	1256
gi	158296962	ref	XP_317283.4	-----	1066
gi	73945359	ref	XP_855968.1	-----	1147
gi	122692527	ref	NP_001073724.1	-----	1136
gi	41327760	ref	NP_940933.3	-----	1147
gi	114673706	ref	XP_001143568.1	-----	1108
gi	40807502	ref	NP_056620.2	-----	1135
gi	62664679	ref	XP_225706.3	-----	1147
gi	113681577	ref	NP_001038619.1	-----	1108
gi	124806112	ref	XP_001350631.1	-----	1618

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