CLUSTAL 2.1 multiple sequence alignment

gi|18859799|ref|NP\_572649.1| --------------------------MSSQGHHKMSGGGKKGAMEQDYTD 24

gi|158286953|ref|XP\_309029.4| --------------------------MSSQSSGMAGSQHTSSALARN--H 22

gi|27819604|ref|NP\_766206.1| ------------------------------------MSNSHPLRPFTAVG 14

gi|61556863|ref|NP\_001013091.1 ------------------------------------MSNSHPLRPFTAVG 14

gi|332823960|ref|XP\_003311323. --------------------------------------------------

gi|297290757|ref|XP\_002803769. --------------------------------------------------

gi|345778723|ref|XP\_538898.3| --------------------------------------------------

gi|151108413|ref|NP\_001092742. ------------------------------------MSNSHPLRPFTAVG 14

gi|190360739|ref|NP\_001121970. ------------------------------------MSNSHPLRPFTAVG 14

gi|56605918|ref|NP\_001008459.1 MAKNPNFQEVGHLPTGYIHCRPSESFTGYQYHHPSKMSNSHPLRPYTAVG 50

gi|50345054|ref|NP\_001002198.1 ------------------------------------MSDSHPLRPMNSAS 14

gi|17557648|ref|NP\_504839.1| --------MSDNHAFGRPIQEDGRGIVETMRTESAAISNNFNAVNSVNKS 42

gi|18859799|ref|NP\_572649.1| VVDLGDRFSADMARLCMNEQYADVEFIVEE-ERIPAHRVILAARSEYFRA 73

gi|158286953|ref|XP\_309029.4| EIELTARFSEQMAQLCMSADYSDVTFIVEG-QRIPAHRVILAARSEYFRA 71

gi|27819604|ref|NP\_766206.1| EIDHVHILSEHIGALLIGEEYGDVTFVVEK-KHFPAHRVILAARCQYFRA 63

gi|61556863|ref|NP\_001013091.1 EIDHVHILSEHIGALLIGEEYGDVTFVVEK-KRFPAHRVILAARCQYFRA 63

gi|332823960|ref|XP\_003311323. ----------------------------------------------MCRA 4

gi|297290757|ref|XP\_002803769. ----------------------------------------------MCRA 4

gi|345778723|ref|XP\_538898.3| --------------------------------------------------

gi|151108413|ref|NP\_001092742. EIDHVHILSEHIGALLIGEEYGDVTFVVEK-KRFPAHRVILAARCQYFRA 63

gi|190360739|ref|NP\_001121970. EIDHVHILSEHIGALLIGEEYGDVTFVVEK-KRFPAHRVILAARCQYFRA 63

gi|56605918|ref|NP\_001008459.1 EIDHVHILSEHIGALMNGEEYSDVTFIVEK-KRFPAHRVILAARCHYFRA 99

gi|50345054|ref|NP\_001002198.1 EIDHLHLLSEQLGALVPGEEYSDVTFVVEE-KRFPAHRVILAARCQYFRA 63

gi|17557648|ref|NP\_504839.1| VVQHLDELSQSFDEIFTSTDHSDVTLVLDDGTEFAAHRLILAVRSSFFRA 92

gi|18859799|ref|NP\_572649.1| LLYGGMAETT-QRQIPLEVP-LEAFKVLLRYIYSGTLLLSTLDEDSTIDV 121

gi|158286953|ref|XP\_309029.4| LLYGGLQETK-QHEITLNIP-LMAFRCLLKYIYSGSMSLMQMKEEHLLDT 119

gi|27819604|ref|NP\_766206.1| LLYGGMRESQPEAEIPLQDTTAEAFTMLLRYIYTGRATLTDEKEEVLLDF 113

gi|61556863|ref|NP\_001013091.1 LLYGGMRESQPEAEIPLQDTTAEAFTMLLRYIYTGRATLTDEKEEVLLDF 113

gi|332823960|ref|XP\_003311323. LLYGGMRESQPEAEIPLQDTTAEAFTMLLKYIYTGRATLTDEKEEVLLDF 54

gi|297290757|ref|XP\_002803769. LLYGGMRESQPEAEIPLQDTTAEAFTMLLKYIYTGRATLTDEKEEVLLDF 54

gi|345778723|ref|XP\_538898.3| -----MRESQPEAEIPLQDTTAEAFTMLLKYIYTGRATLTDEKEEVLLDF 45

gi|151108413|ref|NP\_001092742. LLYGGMRESQPEAEIPLQDTTAEAFTMLLKYIYTGRATLTDEKEEVLLDF 113

gi|190360739|ref|NP\_001121970. LLYGGMRESQPEAEIPLEDTTAEAFTMLLKYIYTGRATLTDEKEEVLLDF 113

gi|56605918|ref|NP\_001008459.1 LLYGGMRESQPEAEIPLQDTTAEAFTMLMKYIYTGRATLRDEKEEVLLDF 149

gi|50345054|ref|NP\_001002198.1 LLYGGLRESRAQAEVRLEETRAEAFSMLLRYLYTGRATLSEAREETLLDF 113

gi|17557648|ref|NP\_504839.1| MLYTGFQESH-QQLVTLQETNSVAFRAVLRYMYTSKIDFAGVELDILLEY 141

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gi|18859799|ref|NP\_572649.1| LGMANQYGFQDLEMAISNYLRQYLALDNVCMILDAARLYNLEELTEVCLM 171

gi|158286953|ref|XP\_309029.4| LGLANQYGFADLEMAISDYLRQVLSLGNVCAILDAARLFALDGLTAVCHS 169

gi|27819604|ref|NP\_766206.1| LSLAHKYGFPELEDSTSEYLCTILNIQNVCMTFDVASLYSLPKLTCMCCM 163

gi|61556863|ref|NP\_001013091.1 LSLAHKYGFPELEDSTSEYLCTILNIQNVCMTFDVASLYSLPKLTCMCCM 163

gi|332823960|ref|XP\_003311323. LSLAHKYGFPELEDSTSEYLCTILNIQNVCMTFDVASLYSLPKLTCMCCM 104

gi|297290757|ref|XP\_002803769. LSLAHKYGFPELEDSTSEYLCTILNIQNVCMTFDVASLYSLPKLTCMCCM 104

gi|345778723|ref|XP\_538898.3| LSLAHKYGFPELEDSTSEYLCTILNIQNVCMTFDVASLYSLPKLTCMCCM 95

gi|151108413|ref|NP\_001092742. LSLAHKYGFPELEDSTSEYLCTILNIQNVCMTFDVASLYSLPKLTCMCCM 163

gi|190360739|ref|NP\_001121970. LSLAHKYGFPELEDSTSEYLCTILNIQNVCMTFDVASLYSLPKLTCMCCM 163

gi|56605918|ref|NP\_001008459.1 LSLAHKYGFPELEDSTSEYLCTILNIQNVCMTFDVASLYSLPKLTCMCCM 199

gi|50345054|ref|NP\_001002198.1 LGLAHRYGLQPLEVSICEFLRTLLSTRNVCLVFDVASLYCLNGLAEACMA 163

gi|17557648|ref|NP\_504839.1| LSLAHRYDLIQLMTAISEYFKEILKNENLCSIFNAAYFFQFTDLIDYCMQ 191

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gi|18859799|ref|NP\_572649.1| FMDRNAGDLLLHNSFNTLSKESLEEVLRRDCFFAPEVQIFLAVWKWSRFN 221

gi|158286953|ref|XP\_309029.4| FMDRNAADILQHESFRHLSLDSLCSLLLRDSFFAREVEIFQAVFDWCRCN 219

gi|27819604|ref|NP\_766206.1| FMDRNAQEVLASDGFLSLSKTALLNIVLRDSFAAPEKDIFLALLNWCKHN 213

gi|61556863|ref|NP\_001013091.1 FMDRNAQEVLASDGFLSLSKTALLNIVLRDSFAAPEKDIFLALLNWCKHN 213

gi|332823960|ref|XP\_003311323. FMDRNAQEVLSSEGFLSLSKTALLNIVLRDSFAAPEKDIFLALLNWCKHN 154

gi|297290757|ref|XP\_002803769. FMDRNAQEVLSSEGFLSLSKTALLNIVLRDSFAAPEKDIFLALLNWCKHN 154

gi|345778723|ref|XP\_538898.3| FMDRNAQEVLSSEGFLSLSKTALLNIVLRDSFAAPEKDIFLALLNWCKHN 145

gi|151108413|ref|NP\_001092742. FMDRNAQEVLSSEGFLSLSKTALLNIVLRDSFAAPEKDIFLALLNWCKHN 213

gi|190360739|ref|NP\_001121970. FMDRNAQEVLSSEGFLSLSKTALLNIVLRDSFAAPEKDIFLALLNWCKHN 213

gi|56605918|ref|NP\_001008459.1 FMDRNAQEVLSSEGFLSLSKAALLSIVLRDSFAAPEKDIFQALMNWCKHN 249

gi|50345054|ref|NP\_001002198.1 YMDRNAVEVLKSDGFLTLSKSALLTVVRRDSFASSEREIFQALCHWCHHN 213

gi|17557648|ref|NP\_504839.1| YSDKHADQLLEDPSFNRLSGDSLKELLARDSFFALELKIFNAVRSWHQNN 241

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gi|18859799|ref|NP\_572649.1| SN--VDFKSVVSYVRLPLMNLEHLLQVVRPSGILDPDKILDAIDERSTSK 269

gi|158286953|ref|XP\_309029.4| ADTVPNVDVVVGKVRFELMSLEELLTVVRPSGILDPDRLLDAIGEKISSK 269

gi|27819604|ref|NP\_766206.1| AK--ENHAEIMQAVRLPLMSLTELLNVVRPSGLLSPDAILDAIKVRSESR 261

gi|61556863|ref|NP\_001013091.1 AK--ENHAEIMQAVRLPLMSLTELLNVVRPSGLLSPDAILDAIKVRSESR 261

gi|332823960|ref|XP\_003311323. SK--ENHAEIMQAVRLPLMSLTELLNVVRPSGLLSPDAILDAIKVRSESR 202

gi|297290757|ref|XP\_002803769. SK--ENHAEIMQAVRLPLMSLTELLNVVRPSGLLSPDAILDAIKVRSESR 202

gi|345778723|ref|XP\_538898.3| SK--ENHAEIMQAVRLPLMSLTELLNVVRPSGLLSPDAILDAIKVRSESR 193

gi|151108413|ref|NP\_001092742. SK--ENHAEIMQAVRLPLMSLTELLNVVRPSGLLSPDAILDAIKVRSESR 261

gi|190360739|ref|NP\_001121970. SN--ENHAEIMQAVRLPLMSLTELLNVVRPSGLLSPDAILDAIKVRSESR 261

gi|56605918|ref|NP\_001008459.1 PK--ENHAEIMQAVRLPLMSLTELLNVVRPSGLLSPDAILDAIKIRSESR 297

gi|50345054|ref|NP\_001002198.1 GDG-PEAKEVMSAVRLPLMTLSEMLNVVRPSGLLSPDDLLDAIQTRSESR 262

gi|17557648|ref|NP\_504839.1| PTMKEASKVLLELVRLPLITQTELLNCVRPTGLVSADTLLDAIEVQTQRP 291

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gi|18859799|ref|NP\_572649.1| --ALPYRAALWPEENVAAETFLSRCIQGECRDALLDGDVTTYDMENGYTR 317

gi|158286953|ref|XP\_309029.4| --QLPYR----PEENVATPKFNSRTIHGELRSALLDGDTVSYDMEKGYTR 313

gi|27819604|ref|NP\_766206.1| DMDLNYRGMLIPEENIATMKYGAQVVKGELKSALLDGDTQNYDLDHGFSR 311

gi|61556863|ref|NP\_001013091.1 DMDLNYRGMLIPEENIATMKYGAQVVKGELKSALLDGDTQNYDLDHGFSR 311

gi|332823960|ref|XP\_003311323. DMDLNYRGMLIPEENIATMKYGAQVVKGELKSALLDGDTQNYDLDHGFSR 252

gi|297290757|ref|XP\_002803769. DMDLNYRGMLIPEENIATMKYGAQVVKGELKSALLDGDTQNYDLDHGFSR 252

gi|345778723|ref|XP\_538898.3| DMDLNYRGMLIPEENIATMKYGAQVVKGELKSALLDGDTQNYDLDHGFSR 243

gi|151108413|ref|NP\_001092742. DMDLNYRGMLIPEENIATMKYGAQVVKGELKSALLDGDTQNYDLDHGFSR 311

gi|190360739|ref|NP\_001121970. DMDLNYRGMLIPEENIATMKYGAQVVKGELKSALLDGDTQNYDLDHGFSR 311

gi|56605918|ref|NP\_001008459.1 DMDLNYRGMLIPGENIATMKYGAQVVKGELKSALLDGDTQNYDLDHGFSR 347

gi|50345054|ref|NP\_001002198.1 DMDLNYRGMLIPEENIATMKHGAVVVKGELKSALLDGDTQNYDLDHGFSR 312

gi|17557648|ref|NP\_504839.1| -HEIPFRGCKSLDTNIIPHYPHAQPLSRELSSRYTN-------------- 326

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gi|18859799|ref|NP\_572649.1| HCITDSKD-AGIVVELGTFCMINHIRMLL-WDRDSRAYSYYVEVSGD--- 362

gi|158286953|ref|XP\_309029.4| HSISETGDSSGIIVELGKLFIINHIKVLL-WDRDTRSYSYYVEVSVN--- 359

gi|27819604|ref|NP\_766206.1| HPIDDDCRSG-IEIKLGQPSIINHIRLLL-WDRDSRSYSYFIEVSMD--- 356

gi|61556863|ref|NP\_001013091.1 HPIDDDCRSG-IEIKLGQPSIINHIRLLL-WDRDSRSYSYFIEVSMD--- 356

gi|332823960|ref|XP\_003311323. HPIDDDCRSG-IEIKLGQPSIINHIRILL-WDRDSRSYSYFIEVSMD--- 297

gi|297290757|ref|XP\_002803769. HPIDDDCRSG-IEIKLGQPSIINHVRILL-WDRDSRSYSYFIEVSMD--- 297

gi|345778723|ref|XP\_538898.3| HPIDDDCRSG-IEIKLGQPSIINHIRILL-WDRDSRSYSYFIEVSMD--- 288

gi|151108413|ref|NP\_001092742. HPIDDDCRSG-IEIKLGQPSIINHIRILL-WDRDSRSYSYFIEVSMD--- 356

gi|190360739|ref|NP\_001121970. HPIDDDCRSG-IEIKLGQPSIINHIRILL-WDRDSRSYSYFIEVSMD--- 356

gi|56605918|ref|NP\_001008459.1 HPIDDDCRSG-IEIKLGQPSIINHIRILL-WDRDSRSYSYYIEVSMD--- 392

gi|50345054|ref|NP\_001002198.1 HPIEEEGRAAGIQVRLGQPSIVNHIRLLL-WDKDSRSYSYYVEVSMD--- 358

gi|17557648|ref|NP\_504839.1| -----DENISVFQIDLGKPFIINTIMMDFNWKNEVQAFTYQVHVSMDNRV 371

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gi|18859799|ref|NP\_572649.1| QQHWDRVVDYSDYHCRSWQYLYFEARPV---------------------- 390

gi|158286953|ref|XP\_309029.4| QRNWERIVDHTKYYCRSWQYLYFPAQAV---------------------- 387

gi|27819604|ref|NP\_766206.1| ELDWIRVIDHSHYLCRSWQKLYFPARVC---------------------- 384

gi|61556863|ref|NP\_001013091.1 ELDWIRVIDHSHYLCRSWQKLYFPARVC---------------------- 384

gi|332823960|ref|XP\_003311323. ELDWVRVIDHSQYLCRSWQKLYFPARVCSGDGVSLWCPLWSRTPELKQSS 347

gi|297290757|ref|XP\_002803769. ELDWVRVIDHSQYLCRSWQKLYFPARVCSGDRVSRWCPLWSRTPELKQSS 347

gi|345778723|ref|XP\_538898.3| ELDWIRVIDHSQYLCRSWQKLYFPARVC---------------------- 316

gi|151108413|ref|NP\_001092742. ELDWVRVIDHSQYLCRSWQKLYFPARVC---------------------- 384

gi|190360739|ref|NP\_001121970. ELDWIRVIDHSQYLCRSWQKLYFPARVC---------------------- 384

gi|56605918|ref|NP\_001008459.1 ELDWIRVIDHSKYLCRSWQNLYFPARVC---------------------- 420

gi|50345054|ref|NP\_001002198.1 ELDWVRVVDHSKFLCRSWQQLYFPARVC---------------------- 386

gi|17557648|ref|NP\_504839.1| DAHWNLVADYSEYDCRGTQRLFFTDSVV---------------------- 399

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gi|18859799|ref|NP\_572649.1| -------RFIRLVGTQNTVNRVFHVVGLEAMHTAKVPRLV--NHFVAPKT 431

gi|158286953|ref|XP\_309029.4| -------RYIRLVGTHNTVNKVFHVVALEAMFTESTTPVV--DGILQPAY 428

gi|27819604|ref|NP\_766206.1| -------RYIRIVGTHNTVNKIFHIVAFECMFTNKAFTLE--KGLIVPLE 425

gi|61556863|ref|NP\_001013091.1 -------RYIRIVGTHNTVNKIFHIVAFECMFTNKAFTLE--KGLIAPME 425

gi|332823960|ref|XP\_003311323. LLGLPKCRYIRIVGTHNTVNKIFHIVAFECMFTNKTFTLE--KGLIVPME 395

gi|297290757|ref|XP\_002803769. LFGLPKCRYIRIVGTHNTVNKIFHIVAFECMFTNKTFTLE--KGLIVPME 395

gi|345778723|ref|XP\_538898.3| -------RYIRIVGTHNTVNKIFHIVAFECMFTNKTFTLE--KGLIVPME 357

gi|151108413|ref|NP\_001092742. -------RYIRIVGTHNTVNKIFHIVAFECMFTNKTFTLE--KGLIVPME 425

gi|190360739|ref|NP\_001121970. -------RYIRIVGTHNTVNKIFHIVAFECMFTNKTFTLE--KGLIVPME 425

gi|56605918|ref|NP\_001008459.1 -------RYIRIVGTHNTVNKVFHIVAFECMFTNKTFALE--KGLIVPTE 461

gi|50345054|ref|NP\_001002198.1 -------RFIRVVGTHNTVNKVFHLVALECMYTLRPFTLE--KGLLVPTE 427

gi|17557648|ref|NP\_504839.1| -------RHILIR-VNNSMSCKLEGSRIEAMFSTETMPVEPVHKVIVPHR 441

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gi|18859799|ref|NP\_572649.1| NVATVEMSAIVTDGVSRTRNALINGDYVRYDWDSGYTCHQLGSGEIVVRL 481

gi|158286953|ref|XP\_309029.4| NVATVERSANVMEGVSRTRNVLLNGDVKNYDWDSGYTCHQIGTGVILIQL 478

gi|27819604|ref|NP\_766206.1| NVATIADCASVIEGVSRSRNALLNGDTKNYDWDSGYTCHQLGSGAIVVQL 475

gi|61556863|ref|NP\_001013091.1 NVATIADCASVIEGVSRSRNALLNGDTKNYDWDSGYTCHQLGSGAIVVQL 475

gi|332823960|ref|XP\_003311323. NVATIADCASVIEGVSRSRNALLNGDTKNYDWDSGYTCHQLGSGAIVVQL 445

gi|297290757|ref|XP\_002803769. NVATIADCASVIEGVSRSRNALLNGDTKNYDWDSGYTCHQLGSGAIVVQL 445

gi|345778723|ref|XP\_538898.3| NVATIADCASVIEGVSRSRNALLNGDTKNYDWDSGYTCHQLGSGAIVVQL 407

gi|151108413|ref|NP\_001092742. NVATIADCASVIEGVSRSRNALLNGDTKNYDWDSGYTCHQLGSGAIVVQL 475

gi|190360739|ref|NP\_001121970. NVATIADCASVIEGVSRSRNALLNGDTKNYDWDSSYTCHQLGSGAIVVQL 475

gi|56605918|ref|NP\_001008459.1 NVATIADCASVIEGVSRSRNALLNGDTKNYDWDSGYTCHQLGSGAIVVQL 511

gi|50345054|ref|NP\_001002198.1 NVATVQACASVVEGVSRSRNALLNGDTSHYDWDSGYTCHQLGSGAIVIQL 477

gi|17557648|ref|NP\_504839.1| NITTIENHARVVEGVSRCRNALINGDSSSYDWDTGYTCHQIGSGLIMIQL 491

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gi|18859799|ref|NP\_572649.1| GQPYYLGSMRLLLWDCDDRTYSFYIEISTNRKEWQMVVDRRNDRTRSWQN 531

gi|158286953|ref|XP\_309029.4| GQPYWIDSLRLLLWDCDNRSYSFYIEVSANMTDWEVVVDKQSDHLKSWQH 528

gi|27819604|ref|NP\_766206.1| AQPYIIGSIRLLLWDCDDRSYSYYVEVSTNQQQWTMVADRTKVSCKSWQS 525

gi|61556863|ref|NP\_001013091.1 AQPYMIGSIRLLLWDCDDRSYSYYVEVSTNQQQWTMVADRTKVSCKSWQS 525

gi|332823960|ref|XP\_003311323. AQPYMIGSIRLLLWDCDDRSYSYYVEVSTNQQQWTMVADRTKVSCKSWQS 495

gi|297290757|ref|XP\_002803769. AQPYMIGSIRLLLWDCDDRSYSYYVEVSTNQQQWTMVADRTKVSCKSWQS 495

gi|345778723|ref|XP\_538898.3| AQPYMIGSIRLLLWDCDDRSYSYYVEVSTNQQQWTMVADRTKVSCKSWQS 457

gi|151108413|ref|NP\_001092742. AQPYMIGSIRLLLWDCDDRSYSYYVEVSTNQQQWTMVADRTKVSCKSWQS 525

gi|190360739|ref|NP\_001121970. AQPYMIGSIRLLLWDCDDRSYSYYVEVSTNQQQWTMVADRTKVSCKSWQS 525

gi|56605918|ref|NP\_001008459.1 AQPYMIGSIRLLLWDCDDRSYSYYIEVSTNQQQWTMVADRTKVSCKSWQT 561

gi|50345054|ref|NP\_001002198.1 AQPYMLGSMRLLLWDCDERSYSYYVELSTNQQNWVKIVDRTKDECRSWQT 527

gi|17557648|ref|NP\_504839.1| AQPYIISSMRILLWNCDDRFYSYYVAVSKNQDEWVTIVDRTNEECHGWQE 541

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gi|18859799|ref|NP\_572649.1| FHFTPRPVVYIRIVGTRNTANEIFHCVHLECPTQDKNYLKKIADMEKERE 581

gi|158286953|ref|XP\_309029.4| FAFQPKVVVYIRIVGTHNTANEMFHCVHFECPSQEPEFLRRERAIPIEAS 578

gi|27819604|ref|NP\_766206.1| VTFERQPASFIRIVGTHNTANEVFHCVHFECPEQQSNQKEDSSEEPGTGD 575

gi|61556863|ref|NP\_001013091.1 VTFERQPASFIRIVGTHNTANEVFHCVHFECPEQQSTQKEDSSEEPGTGD 575

gi|332823960|ref|XP\_003311323. VTFERQPASFIRIVGTHNTANEVFHCVHFECPEQQSSQKEENSEESGTGD 545

gi|297290757|ref|XP\_002803769. VSFERQPASFIRIVGTHNTANEVFHCVHFECPEQQSSQKEENSEESGTGD 545

gi|345778723|ref|XP\_538898.3| VTFERQPASFIRIVGTHNTANEVFHCVHFECPEQQSSHKEDSSEESGPGE 507

gi|151108413|ref|NP\_001092742. VTFERQPASFIRIVGTHNTANEVFHCVHFECPEQQSSQKEENSEESGTGD 575

gi|190360739|ref|NP\_001121970. VTFERRPASFIRIVGTHNTANEVFHCVHFECPEQQSAQK-DSSDEPGTGG 574

gi|56605918|ref|NP\_001008459.1 ITFDKQPASFIRIVGTQNTANEVFHCVHFECPAQSGTHKDEGCKEVATTE 611

gi|50345054|ref|NP\_001002198.1 LTFDRQPASFIRIVGTHNTANEVFHCVHFECPAQMDTVVKEGSPGPDQPK 577

gi|17557648|ref|NP\_504839.1| LIFDPLPVVYIRLVGTRNSINEVFHVVHLEAPSNVPIAIK---------- 581

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gi|18859799|ref|NP\_572649.1| KREKEKKTAKTDDDNIASTSGSSLASGHAESPSTSSSSSQSVLRSIHWPP 631

gi|158286953|ref|XP\_309029.4| GEE---------------------------------SAEESVVD------ 589

gi|27819604|ref|NP\_766206.1| PST---------------------------------PNQQLDPHAPR--- 589

gi|61556863|ref|NP\_001013091.1 LST---------------------------------PSQQLDPHAPR--- 589

gi|332823960|ref|XP\_003311323. TSL---------------------------------AGQQLDSHALR--- 559

gi|297290757|ref|XP\_002803769. TSL---------------------------------AGQQLDSHALR--- 559

gi|345778723|ref|XP\_538898.3| PG----------------------------------PGPQLDPHALQ--- 520

gi|151108413|ref|NP\_001092742. TSL---------------------------------AGQQLDSHALR--- 589

gi|190360739|ref|NP\_001121970. ASA---------------------------------AGQQLDPHALQ--- 588

gi|56605918|ref|NP\_001008459.1 VGT---------------------------------GEQQLVSRPVR--- 625

gi|50345054|ref|NP\_001002198.1 PET---------------------------------SSQNSYSQSLM--- 591

gi|17557648|ref|NP\_504839.1| --------------------------------------------------

gi|18859799|ref|NP\_572649.1| QTREVAVAPLTPPALSPPGTPALPAPLTPATSSPHNNHEQNQPSNISADA 681

gi|158286953|ref|XP\_309029.4| ------EAPLRQESVTD--------------------------------- 600

gi|27819604|ref|NP\_766206.1| -------APSASSLPPSPGP---------NSRSPNQQNQ----------- 612

gi|61556863|ref|NP\_001013091.1 -------APSASSLPPSPGP---------NLHSPNQQNQ----------- 612

gi|332823960|ref|XP\_003311323. -------APSGSSLPSSPGS---------NSRSPNRQHQ----------- 582

gi|297290757|ref|XP\_002803769. -------APSGSSLPSSPGS---------NSRSPNRQHQ----------- 582

gi|345778723|ref|XP\_538898.3| -------APSGSSLPSSPGS---------ASRSPNRQHQ----------- 543

gi|151108413|ref|NP\_001092742. -------APSGSSLPSSPGS---------NSRSPNRQHQ----------- 612

gi|190360739|ref|NP\_001121970. -------APSGSSLPSSPGS---------NSRSPNRQHQ----------- 611

gi|56605918|ref|NP\_001008459.1 -------AASTSSLHSPPGS---------TLRSHAHQP------------ 647

gi|50345054|ref|NP\_001002198.1 -------AQKPSSSSSHT-------------------------------- 602

gi|17557648|ref|NP\_504839.1| --------------------------------------------------

gi|18859799|ref|NP\_572649.1| SHHTSPSSRSNPSPSLSRSRSQSAELEPVPPLVELDTRETL 722

gi|158286953|ref|XP\_309029.4| -----------------------------------------

gi|27819604|ref|NP\_766206.1| -----------------------------------------

gi|61556863|ref|NP\_001013091.1 -----------------------------------------

gi|332823960|ref|XP\_003311323. -----------------------------------------

gi|297290757|ref|XP\_002803769. -----------------------------------------

gi|345778723|ref|XP\_538898.3| -----------------------------------------

gi|151108413|ref|NP\_001092742. -----------------------------------------

gi|190360739|ref|NP\_001121970. -----------------------------------------

gi|56605918|ref|NP\_001008459.1 -----------------------------------------

gi|50345054|ref|NP\_001002198.1 -----------------------------------------

gi|17557648|ref|NP\_504839.1| -----------------------------------------