SUPPORTING INFORMATION

Functional and structural characterization of a thermostable acetyl esterase from *Thermotoga maritima*

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Figure S1

Multiple Sequence Alignment of CE7 Members. The alignment consists of 50 amino-acid sequences in the CE7 family, including the TM0077 sequence. The conserved residues are in bold and a consensus is shown underneath the alignment. The serine, aspartate and histidine that constitute the catalytic triad are marked with a square (■). Codes: for most sequences their locus tag is given; sequences without locus tag: Tsp-JW_axe, acetyl xylan esterase 1 from *Thermoanaerobacterium* sp. 'JW/SL YS485; Gstea_estA, esterase from *Geobacillus stearothermophilus*; and Bpumi_axe, acetyl xylan esterase from *Bacillus pumilus*. All sequences can be obtained from CAZy (http://www.cazy.org/fam/CE7.html).

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TM0077     : ------------------------------------------------------------------------------------------------------------------------------------MAFFDLPL :   8
Tsp-JW_axe : ------------------------------------------------------------------------------------------------------------------------------------MGLFDMPL :   8
BH3326     : ------------------------------------------------------------------------------------------------------------------------------------MPLIDMPL :   8
Csac_2436  : -------------------------------------------------------------------------------------------------------------------------------------MVFDMPL :   7
ABC1769    : ------------------------------------------------------------------------------------------------------------------------------------MPLVDMPL :   8
Gstea_estA : --------------------------------------------------------------------------------------------------------------------------------------MFDMPL :   6
LLKF_1447  : ----------------------------------------------------------------------------------------------------------------------------------------MTKI :   4
SP_1695    : -------------------------------------------------------------------------------------------------------------------------------------MKNPALL :   7
Spr1538    : -------------------------------------------------------------------------------------------------------------------------------------MKNPALL :   7
SPCG_1668  : -------------------------------------------------------------------------------------------------------------------------------------MKNPALL :   7
SSA_0070   : -------------------------------------------------------------------------------------------------------------------------------------MKNPTLL :   7
SAK_0074   : -------------------------------------------------------------------------------------------------------------------------------------MIETMSL :   7
CPE1596    : ------------------------------------------------------------------------------------------------------------------------------------MAILDMSL :   8
DSY0351    : ------------------------------------------------------------------------------------------------------------------------------------MTIIQDAI :   8
Bpumi_axe  : ------------------------------------------------------------------------------------------------------------------------------------MQLFDLSL :   8
BPUM_0297  : ------------------------------------------------------------------------------------------------------------------------------------MQLFDLPL :   8
BSU03180   : ------------------------------------------------------------------------------------------------------------------------------------MQLFDLPL :   8
RBAM_00342 : ------------------------------------------------------------------------------------------------------------------------------------MQLYDLPL :   8
BLi00379   : -----------------------------------------------------------------------------------------------------------------------------------MQQPYDMPL :   9
Cthe_3063  : -----------------------------------------------------------------------------------------------------------------------------------MAQLYDMPL :   9
TRQ2_0870  : ------------------------------------------------------------------------------------------------------------------------------------MAFFDLPL :   8
Tpet_0847  : ------------------------------------------------------------------------------------------------------------------------------------MAFFDLPL :   8
CTN_0615   : ------------------------------------------------------------------------------------------------------------------------------------MAFFDMPL :   8
TRQ2_0504  : ------------------------------------------------------------------------------------------------------------------------------------MALFDMPL :   8
Tlet_0356  : ------------------------------------------------------------------------------------------------------------------------------------MVYFDMPL :   8
DICTH_1987 : ------------------------------------------------------------------------------------------------------------------------------------MAFFDLPL :   8
RoseRS_079 : ------------------------------------------------------------------------------------------------------------------------------------MAFFDLSF :   8
Rcas_1231  : ------------------------------------------------------------------------------------------------------------------------------------MAFFDLSF :   8
Haur_0886  : -------------------------------------------------------------------------------------------------------------------------------------MHFDMPL :   7
SGR_6428   : ------------------------------------------------------------------------------------------------------------------------------------MPSADLTL :   8
Acel_2045  : ------------------------------------------------------------------------------------------------------------------------------------MPNIDLPL :   8
Krad_3413  : ------------------------------------------------------------------------------------------------------------------------------------MPLTDLPL :   8
Arth_3303  : ------------------------------------------------------------------------------------------------------------------------------------MPLFDLPL :   8
Krad_4187  : ------------------------------------------------------------------------------------------------------------------------------------MALSDLSL :   8
Tfu_1462   : ------------------------------------------------------MFVECGRGMRPHSDRCGRQTTVVHPASRHSRGAAGDATTPYAGNRIMVRVRRGAPPNPHSTPGVPAGVSVRPSTVERTGMYVDLPL :  86
Sare_3004  : ------------------------------------------------------------------------------------------------------------------------------------MTQFDMPL :   8
SAV1457    : --------------------------------------------------------------------------------------------------------------------------------MRGAVPAFDLPP :  12
SCO7057    : ------------------------------------------------------------------------------------------------------------------------------------MALFDLPL :   8
SAML0944   : ------------------------------------------------------------------------------------------------------------------------------------MALFDLPL :   8
SAV1302    : ------------------------------------------------------------------------------------------------------------------------------------MALFDLPL :   8
CMS0795    : ----------------------------------------------------------------------------------------------------------MMIEATRPTCTRTPPTHPPAHRRTPGGSMLIEPV :  34
CMM_0227   : --------------------------------------------------------------------------------------------------------------------------------------MLIEPV :   6
Mlr6993    : ----------------------------------------------------------------------------------------------------------------------------------MPFPDLIQP- :   9
EF_1236    : -------------------------------------------------------------------------------------------------------------------------------------------- :   -
BVU_1343   : ----------------MKNRFLSMLIGAVLFVLSAAAENYPYRSDVLWVTVPDHADWLYKTGEKAKIEVQFYKYGIPQDGVEVLYELGGDMMPSDTKGTVKLKNGKAVISMGTMKEPGFRDCRLTAKLGGKTYSHHIKVG : 124
BT_2525    : MENRMRRRMTVILNSKMNMRRFCVSAALLLTTLLAVAENNPYRSDVFWVTVPDHADWLYKTGEQANVEVQFYKYGIPGDNIAINFEIGGEMMPADTKGTVIMRKGKATIPVGTMKKPGFRDCRLTTTVDGKKYSHHVKVG : 140
Oter_2302  : ---MMRPTPAFLFVVLALLAGFSPAALAATPITPVPPGAQLRVAAVQVRVAPDHRDWTYQLGEPVKFKVAVTADNEPIDAVSVSYTIGPDMFPGEKKTAAVPLDG-LVIDAGTMQEPGFLRCIVTSEVAGKIYTGIATAA : 136
LA_1864    : ---------------------------------------------------------------------------------------------------------------------------------------MAISF :   5
Oter_0486  : ---------------------MKRFLGSARLLCATSLALLVLLTASHAAPAVLQPLKASGIYDLGEKAGWTVTMPADATLPTGGYNYTIKKNDTTTLASGPLDPSGGPVEIAVTLNEPAMLFAEVTSAAGEADRAIAGAA : 119
SGR_835    : ------------------------------------------------------------------------------------------------MHRAEIGRGRACDHLVTEQGETLSTHPLTSDGTGLHPLHHTFPF :  44
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                      *         *         *         *         *         *         *         *         *         *         *         *         *         *
TM0077     : EELKKYRP-------ERYEEKDFDEFWEETLAESE---KFPLDPVFERMES-HLKTVEAYDVTFSGY------RGQRIKGWLLVP-KLE-EEKLPCVVQYIGYNG-GRGFPHDWLFWPSMGYICFVMDTRGQGSGWLKGD : 128
Tsp-JW_axe : QKLREYTG-------TNPCPEDFDEYWNRALDEMR---SVDPKIELK-ESSFQVSFAECYDLYFTGV------RGARIHAKYIKP-K--TEGKHPALIRFHGYSS-NSGDWNDKLNYVAAGFTVVAMDVRGQGGQSQD-V : 126
BH3326     : TELKEYMG-------RNPKPDDFTEYWDRALQEMR---KVNPNVELI-PSDFQTTYAECFHLYFTGV------RGARIHAKYVRPRH--TSGTHPAVIHFHGYTM-NAGEWTGLLHYAALGYSVLAMDVRGQGGLSED-T : 127
Csac_2436  : DQLKTYMG-------TNPCPPDFDEYWQKALKEMD---DVDPQVEIVKETSIEAPYAECYNLYFTGV------KGARIRSQLIKPKK--IEKPCPAVLSFHGYAW-YSGDWSDKFALAAAGFVVAAMDVRGQNGYSED-V : 127
ABC1769    : RELLAYEG-------INPKPADFDQYWNRAKTEIE---AIDPEVTLV-ESSFQCSFANCYHFYYRSA------GNAKIHAKYVQP-K--AGEKTPAVFMFHGYGG-RSAEWSSLLNYVAAGFSVFYMDVRGQGGTSED-P : 126
Gstea_estA : AQLQKYMG-------TNPKPADFADFWSRALEELS---AQSLHYELI-PATFQTTVASCYHLYFTGV------GGARVHCQLVKPRE--QKQKGPGLVWFHGYHT-NSGDWVDKLAYAAAGFTVLAMDCRGQGGKSED-N : 125
LLKF_1447  : NNWQDYQG-------SSLKPEDFDKFWDEKINLVS---NHQFEFELI-EKNLSSKVVNFYHLWFTAI------DGAKIHAQLIVPKN--LKEKYPAILQFHGYHC-DSGDWVDKIGIVAEGNVVLALDCRGQGGLSQD-N : 123
SP_1695    : EEIKTYRG-------RDEVPEDFDDFWDGEVKNVS---TL-PSYHLE-ERDFHIPQVKCYELTFEGS------KEGKVYARIVLPK---SEEKVPLIFHFHGYMG-RGWDWADMLGFTVAGYGVVSMDVRGQSGYSQDGL : 125
Spr1538    : EEIKTYRG-------RDEVPEDFDAFWDGEVKNVS---TL-PSYHLE-ERDFHIPQVKCYELTFEGS------KEGKVYARIVLPK---SEEKVPLIFHFHGYMG-RGWDWADMLGFTVAGYGVVSMDVRGQSGYSQDGL : 125
SPCG_1668  : EEIKTYRG-------RDEVPEDFDAFWDGEVKNVS---TL-PSYHLE-ERDFRIPQVKCYELTFEGS------KEGKVYARIVLPK---SEEKVPLIFHFHGYMG-RGWDWADMLGFTVAGYGVVSMDVRGQSGYSQDGL : 125
SSA_0070   : KEMLDYRG-------RDEMPDDFDTFWDKQVVEVE---VP-QDYQLL-EKDFQIAYATCYELTFKTG------NGGQIYAKLVVPK---LSEKVPVLFHFHGYMG-QGWAWADMLAYTAAGWGVVSMDVRGQSGYSLDGN : 125
SAK_0074   : DDMREYLG-------QDQIPEDFDDFWKKQTMKYQ---GN-IEYRLD-KKDFNITFAQAYDLHFKGS------NDSIVYAKCLFPK---TNKPYPVVFYFHGYQN-QSPDWSDQLNYVAAGYGVVSMDVRGQAGQSQD-K : 124
CPE1596    : EKLYEYRG-------ISPLPEDFDEFWDSELRELA---NLDIKLELK-KADFESPIAECYDLYFNGI------NGARIYAKFMKPKE--VKRKMPALLEFHGYEE-RSNDWSNNLHYVASGMCVAVMECRGQD-YLKEDS : 127
DSY0351    : QQLETIPY-------RGVPPEDFKEFWLESLRRDA---QTKARLELE-AIAYPLSKVEVFSATVLSG------DRTKLKGYYMRPRAIDLQEALPGLVRFHGYSG-NRGQLSELLLWALQGYAVLALDVRGQCGETPDTR : 130
Bpumi_axe  : EELKKYKP-------KKTARPDFSDFWKKSLEELR---QVEAEPTLE-SYDYPVKGVKVYRLTYQSF------GHSKIEGFYAVPDQ---TGPHPALVRFHGYNASYDGGIHDIVNWALHGYATFGMLVRGQGG-SEDTS : 127
BPUM_0297  : DDLKKYKP-------KKTARPDFSDFWKASLEELN---QVEAELALE-PYDYPVKGVKVYRLTYQSF------GHSRIEGWYAVPDQ---AGLHPALVHFHGYNASYDGGIHDIVNWALHGYATFGMLVRGQGG-SEDKT : 127
BSU03180   : DQLQTYKP-------EKTAPKDFSEFWKLSLEELA---KVQAEPDLQ-PVDYPADGVKVYRLTYKSF------GNARITGWYAVPDK---EGPHPAIVKYHGYNASYDGEIHEMVNWALHGYATFGMLVRGQQS-SEDTS : 127
RBAM_00342 : DQLQTYKP-------NKTAPHDFSDFWASSLHELA---KEEAKPELK-AESYPADGVKVFRLTYRSF------GKAEIEGWYAVPDR---QGPHPAIVKYHGYNASYDGDIHDIVNWALHGYAAFGMLVRGQHS-STDTS : 127
BLi00379   : EQLYQYKP-------ERTAPADFKEFWKGSLEELA---NEKAGPQLE-PHEYPADGVKVYWLTYRSI------GGARIKGWYAVPDR---QGPHPAIVKYHGYNASYDGDIHDIVNWALHGYAAFGMLVRGQNS-SEDTE : 128
Cthe_3063  : EELKKYKP-------ALTKQKDFDEFWEKSLKELA---EIPLKYQLI-PYDFPARRVKVFRVEYLGF------KGANIEGWLAVPEG---EGLYPGLVQFHGYNWAMDGCVPDVVNWALNGYAAFLMLVRGQQGRSVDNI : 129
TRQ2_0870  : EELKKYRP-------ERYEEKDFDEFWKETLAESE---KFPLDPVFERMES-HLKTVEVYDVTFSGY------RGQRIKGWLLVP-KLE-EEKLPCVVQYIGYNG-GRGFPHDWLFWPSMGYICFVMDTRGQGSGWLKGD : 128
Tpet_0847  : EELKKYRP-------ERYEEKDFDEFWEGTLAENE---KFPLDPVFERMES-HLKTVEAYDVTFSGY------MGQRIKGWLLVP-KLE-EEKLPCVVQYIGYNG-GRGFPHDWLFWPSMGYICFVMDTRGQGSGWMKGD : 128
CTN_0615   : EELKKYRP-------ERYEEKDFDEFWRETLKESE---GFPLDPVFEKVDF-HLKTVETYDVTFSGY------RGQRIKGWLLVP-KLA-EEKLPCVVQYIGYNG-GRGFPHDWLFWPSMGYICFVMDTRGQGSGWMKGD : 128
TRQ2_0504  : EKLRSYLP-------DRYEEEDFDLFWKETLEESR---KFPLDPIFERVDY-LLENVEVYDVTFSGY------RGQRIKAWLILP-VVKKEERLPCIVEFIGYRG-GRGFPFDWLFWSSAGYAHFVMDTRGQGTSRVKGD : 129
Tlet_0356  : EDLRKYLP-------QRYEEKDFDDFWKQTIHETR---GYFQEPILKKVDF-YLQNVETFDVTFSGY------RGQKIKGWLILP-KFR-NGKLPCVVEFVGYGG-GRGFPYDWLLWSAAGYAHFIMDTRGQGSNWMKGD : 128
DICTH_1987 : SELWKYLP-------EREEPEDFDSFWKETLEESK---KYPLNPIFEKVDF-GLELVDTYDVTFSGY------KGQRIKGWLIAP-KNR-SGKLPGIVEYIGYGG-GRSFAYDFLLWANMGFIHLIMDTRGQGSSWSPGN : 128
RoseRS_079 : DELQRYLP-------PREEPPDFDAFWQATLEEAR---MYPLDVRFEPYDA-GLTTVETFDVTFRGY------GGQPIKGWLLLP-RHA-SHPLPAVVEYIGYGG-GRGFPTDWLLWSAAGYAHLVMDTRGQGSAWLKGD : 128
Rcas_1231  : DELQQYRP-------PREEPPDFDAFWRMTLDEAR---AYPLDARFEPCDA-GLATVETFDVTFRGY------GGQPIKGWLLLP-RHR-SGPLPCVVEYIGYGG-GRGFPTDWLLWSAAGYAHLVMDTRGQGSAWLKGD : 128
Haur_0886  : EQLREYRP-------DRNEPADFDQFWQTTLADAR---QYPLNANFEPYDM-GLPLIEAYDVTFNGY------GGQPIKGWFLLP-RNT-TKPIPCVVEYIGYGG-GRGLAIDWLLWPTAGYAVFAMDNRGQGSNWRTGD : 127
SGR_6428   : AECRAYRP-------ELPLPDGFDAFWSDTLDERAPGGAPDRRPRFDEVDS-GLVQVRAYDVSVPGH------DGRPVRGWLRMPAGATG--PLGCVVEFLGYGR-GRGLAHEQLMWACAGYAHLVMDTRGQGWSSATGD : 131
Acel_2045  : DQLTTYAP-------ALPQPADLDQFWSATLAE-----APDPEPTFTPVDT-GLRCVESYDVTFCGY------GGQPIRAWLHLPPAALRHEPLSGVVQFQGYNG-GRGLAHEHVFWALAGYAHLVMDTRGQGSGWTTGD : 128
Krad_3413  : EELRAYRG-------DVAEPADFDAFWADSLALAR---EHDLAVTLSPHTGPALPALRVEDVRFAGW------AGDPIAAWLIRPAHLPG--PLPVVVEFIGYSG-GRGLPVDRTTWAAAGFAHLVVDTRGMG-----QD : 124
Arth_3303  : EQLRNYTS-------GVTAPADLDAFWDRTISEAR---EYPLDAVFEPVDN-YLTVIDTFDVTFAGF------GGSPVKGWLHLPSNRPADEPLPVVVQYVGYSG-GRGLSNQDTKWAQAGYAHFIMDNRGQGYGGLLGH : 130
Krad_4187  : EDLEKLDL-------TLHEPAGLDEFWARTLSAAD---AHPLDVHREPVVT-HLTTLRHEDLSFAGY------DGHRINAWLVLPAGAEG--PLPAVVEFVGYGG-GRGLPQDRLTWASAGYAHLVVDTRGQG-AAWGSG : 127
Tfu_1462   : DRLREYRA-------EREAPADFAEFWEQSLAEAR---THPLGLQVTAVDT-PIRTLDTYDVVFHGY------DGHPIRAWLKTPKDATG--PLPVVVEFPGYGN-GRGDVVESLEWASAGFAHLSMDARGQG-AAGSRA : 205
Sare_3004  : DQLRAFRY-------DETEPADFDVFWAKTLGEVR---HHELDVVQCPVDT-RLRTVTVDDVAFNGF------GGDRVRAWLVRPAGLAG--PLPAVVEFIGYGG-GRGLPHEKLLWASAGFAHLVVDTRGQG-GLWS-V : 126
SAV1457    : AELENHRP-------APHEPADFDAFWQATLKESG---QAEPVLSVRPFDS-GLRLVETWDVTFRGF------AGDPVRAWYTRPAEAPR--PLPAVVEYAGYGR-GRGLPHERLTWAAAGYAHLLMDNRGQG-DQYGCG : 131
SCO7057    : DELHTYRS-------ASAEPEDFDAFWSKTLAEAR---EHDLDARFEPVDT-GLSTVRVYDVTFAGF------GGHPVKAWLTLPAAAAE--PLPLVVEFVGYGG-GRGLPHEHLLWASTGRAHFVMDTRGQG-SAWGGG : 127
SAML0944   : DELRHCRS-------ESAEPEDFDAFWGKTLEEAR---EYDLDARFEPVDT-GLSTVRVHDVTFAGF------GGHPVKGWLILPAAAAE--PLPLVVEFVGYGG-GRGLPHEHLLWASTGRAHFVMDTRGQG-SAWGGG : 127
SAV1302    : DQLRGYRS-------ASAEPEDFDAFWAKTLQEAR---QYDLGPRFEPVET-HLETVEVYDVTFAGF------DGHPVKGWLTLPARANA--PLPTVVEFIGYGG-GRGLPHTHLLWASAGFAHFVMDTRGQG-SAWGGG : 127
CMS0795    : DAARAHVS-------SHVDPEDFDAFWADTLAEAA---QHDLDVRLAPVQT-DLALVDVQDVTFAGS------GGTDVRAWLRTPRGATG--PLPTVVSYVGYGG-GRGRAEETLIYAAAGFAHLQMDTRGQG-SYWSAG : 153
CMM_0227   : DAARAHVS-------SHVDPDDFDAFWADTLAEAA---RHDLDVRLAPVET-DLALVDVQDVTFAGS------GGTDVRAWLRTPAGATG--PLPTVVSYVGYGG-GRGRAEETLIYAAAGFAHLQMDTRGQG-SYWSAG : 125
Mlr6993    : -ELGAYVS-------SVGMPDDFAQFWTSTIAEAR---QAGGEVSIVQAQT-TLKAVQSFDVTFPGY------GGHPIKGWLILPTHHKG--RLPLVVQYIGYGG-GRGLAHEQLHWAASGFAYFRMDTRGQG-SDWSVG : 127
EF_1236    : ------------------MNEYFEEFWQKTKEELQ---KIPLDIHRR-VIDYPLENVQVEQVDFLSF------LGERIFGYLLLPKT---AGKQPIVIDCLGYMN-HIQEPWQFAHWTQIGCACFVIDNRGQG-GLTKDR : 106
BVU_1343   : FSPEKLQP-------YTQLPSDFNEFWNKTKAEAA---RFPLTYTKEYVEKYSTDKIDCYLIRLQLN-----KQSQCIYGYLFYPKA---EGKYPVVLCPPGAGIKTIKGPMRHKYYAEEGCIRFEIEIHGLNPELDEDT : 246
BT_2525    : FSPEKLRP-------YTTMPADFQQFWENQKAELA---KFPLTYTKEHVKKYSTDQIDCYLIKLQVN-----QRGQSIYGYLFYPKK---EGKYPVVLCPPGAGIKTIKEPLRHKYYAEQGCIRFEIEIHGLNPEMSEEE : 262
Oter_2302  : FAPEKIKP-------YQTEPEDFEAFWKTQLEELA---QAPVEPILTLLPDQCTDKVNVYHVSFRTVGPSWMKVPARIYGMLCEPKA---PGKYPAVLKVPGAGVRPYPG---DKGLAARGVITLEIGIHGIPVNLPESF : 260
LA_1864    : DECFQTYP-------ELHSPSDLEEFWSEAIRDLK---NFPIKKQSKALLKGSIIKETIYDISFQSW------ENAILTGTLVIPRK---RGDLPVVVYFHDYGK---DRPGIIKGLTETGVAQLILDLRGHGSQLIRPL : 123
Oter_0486  : VAPTQLQP-------VVARPADFDAFWTWMIQVLH---RIPVEPALKNGES-GRDGVEYATIRMNNI------DGSHVYGQLAKPAR---EGKFPALLMLQWAGGPYPLQKPWVVDHAAEGWLALNIEPHDVPGDMPKEF : 239
SGR_835    : DPTHGHDLPRLLTVEAPPGPEDFADFWRERHARAL---RVDPAPRIEGPWT-TVDGVRVADISYTSV------DGVRIGGWLTVPADG---HVTRGCVSTHGYGG----RAAPDPRQAPPGTATIWPCLRGLG---TRSL : 164
                                      fW                                                         P                gy                 G        rgq
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TM0077     : TPDYPEGPVDPQYPG-FMTRGILDPRTYYYRRVFTDAVRAVEAAASFPQVD----QERIVIAGGSQGGGIALAVSALSKKA----------KALLCDVPFLCHFRRAVQLVDTH-PYAEITNFLKTHR-DKEEI--VFRT : 249
Tsp-JW_axe : GGVTGNTLNGHIIRG----LDD-DADNMLFRHIFLDTAQLAGIVMNMPEVD----EDRVGVMGPSQGGGLSLACAALEP----------RVRKVVSEYPFLSDYKRVWDLDLAKNAYQEITDYFRLFDPRHERENEVFTK : 247
BH3326     : GGVKGNTHSGHIIRG----LDD-NADQLLFRHVFLDTAQLANIVMNLPEVD----EERVAVTGWSQGGALAIACAALEP----------KIKKVAPVYPFLSDYQRVWEMDLAEKAYDELQTYFRRFDPQHRREAEIFTK : 248
Csac_2436  : GGVKGNTVHGHIIRG----LDG-DKEDLLYRQIFLDTAELAKIIANMPDVD----SSKIAAMGFSQGGGLALACGALSP----------YVSRVISVYPFLCDYKRVWEMDLAKDAYEEIRTYFRFRDPLHEREDEIFTK : 248
ABC1769    : GGVRGNTYRGHIIRG----LDA-GPDALFYRSVFLDTVQLVRAAKTLPHID----KTRIMATGWSQGGALTLACAALVP----------EIKRLAPVYPFLSDYKRVWQMDLAVRSYKELADYFRSYDPQHKRHGEIFER : 247
Gstea_estA : LQVKGPTLKGHIIRG----IEDPNPHHLYYRNVFLDTVQAVRILCSMDHID----RERIGVYGASQGGALALACAALEPS---------VVKKAVVLYPFLSDYKRAQELDMKNTAYEEIHYYFRFLDPTHEREEEVFYK : 248
LLKF_1447  : IQTMGMTMKGLIVRG----IDE-GYENLYYVRQFMDLITATKILSEFDFVD----ETNISAQGASQGGALAVACAALSP----------LIKKVTATYPFLSDYRKAYELGAEESAFEELPYWFQFKDPLHLREDWFFNQ : 244
SP_1695    : RSPLGNTVKGHIIRG----AVE-GRDHLFYKDVYLDIYQLVEIVASLSQVD----EKRLSSYGASQGGALALVAAALNP----------RIQKTVAIYPFLSDFRRVIEIGNTSEAYDELFRYFKFHDPFHETEEEIMAT : 246
Spr1538    : RSPLGNTVKGHIIRG----AVE-GRDHLFYKDVYLDIYQLVEIVASLSQVD----EKRLSSYGASQGGALALVAAALNP----------RIQKTVAIYPFLSDFRRVIEIGNTSEAYDELFRYFKFYDPFHETEEEIMAT : 246
SPCG_1668  : RSPLGNTVKGHIIRG----AME-GRDHLFYKDVYLDIYQLVEIVASLSQVD----EKRLSSYGASQGGALALVAAALNP----------RIQKTVAIYPFLSDFRRVIEIGNTSEAYDELFRYFKFHDPFHETEEEIMAT : 246
SSA_0070   : REVRGNTVKGHIIRG----ALD-GPDQLFFKDVYLDVYTLVELVAGLDFVD----ENRLSSFGGSQGGALALVAAALNS----------RIKQTVAIYPFLADFRRVLEIGNTSEAYDELFRYFKFHDPFHETEEQLLRT : 246
SAK_0074   : GHFDGITVKGQIVRG----MIS-GPNHLFYKDIYLDVFQLIDIVATLESVD----SNQLYSYGWSQGGALALIAAALNP----------KIVKTVAVYPFLSDFRRVLDLGNVSEPYDELFRYFKYSDPFHKTENNVLKT : 245
CPE1596    : CKFKSFKSKGHIVRG----LVE-GREKLLFKNIFLDTAILARIVMNMEWVD----EERVFATGGSQGGALALACAALEN----------RIKGVYAYYPFLCDYKRIWVMDLGGDSYDELIRYFKFIDPNHENEEYVFNT : 248
DSY0351    : VYPSG-AFSGWLTLG----LES--PHTHYLRQVYLDGVRAVEALANQPEVD----EKRIGCMGKSQGGGLAVIAGGVINALGQEVNLKGGVKAVSAAMPFLADFRSSYQLQKGG-PLEELAWYFQLHDPEHQREEGIFTT : 258
Bpumi_axe  : VTPGG-HALGWMTKG----ILS--KDTYYYRGVYLDAVRALEVIQSFPEVD----EHRIGVIGGSQGGALAIAAAALSD----------IPKVVVADYPYLSNFERAVDVALEQ-PYLEINSYFRRNS-DPKVEEKAFET : 244
BPUM_0297  : VTPGG-QALGWMTKG----ILS--KETYYYRGVYLDAVRALDVIQSFPEVD----EHRIGVVGGSQGGALAVAAAALSD----------IPKVVVADYPYLSNFERAVDVALEQ-PYLEINSYFRRNS-DPAVEEKAFET : 244
BSU03180   : ISPHG-HALGWMTKG----ILD--KDTYYYRGVYLDAVRALEVISSFDEVD----ETRIGVTGGSQGGGLTIAAAALSD----------IPKAAVADYPYLSNFERAIDVALEQ-PYLEINSFFRRNG-SPETEVQAMKT : 244
RBAM_00342 : VSPHG-HVPGWMTKG----ILD--KDTYYYRGVYLDAVRALEVISGFDEVD----ETRIAVIGGSQGGGLSIAAAALSD----------IPRAVAADYPYLSNFERAIDVALDE-PYLEINSFFRKNG-SPETEKAAMNT : 244
BLi00379   : ISHHG-HVPGWMTKG----ILD--PKTYYYRGVYLDAVRAVEVVSGFAEVD----EKRIGVIGASQGGGLAVAVSALSD----------IPKAAVSEYPYLSNFQRAIDTAIDQ-PYLEINSFFRRNT-SPDIEQAAMHT : 245
Cthe_3063  : VPGSG-HALGWMSKG----ILS--PEEYYYRGVYMDAVRAVEILASLPCVD----ESRIGVTGGSQGGGLALAVAALSG----------IPKVAAVHYPFLAHFERAIDVAPDG-PYLEINEYLRRNS-GEEIERQVKKT : 246
TRQ2_0870  : TPDYPEDPVDPQYPG-FMTRGILDPRTYYYRRVFTDAVRAVEAAASFPRVD----HERIVIAGGSQGGGIALAVSALSKKA----------KALLCDVPFLCHFRRAVQLVDTH-PYAEITNFLKTHR-DKEEI--VFRT : 249
Tpet_0847  : TPDYPEDPVDPQYPG-FMTRGILDPRTYYYRRVFTDAVRAVEAAASFPRVD----HERIVIAGGSQGGGIALAVSALSKKA----------KALLCDVPFLCHFRRAVQLVDTH-PYAEITNFLKTHR-DKEEI--VFRT : 249
CTN_0615   : TPDYPEGPVDPQYPG-FMTRGILDPGTYYYRRVFVDAVRAVEAAISFPRVD----SRKVVVAGGSQGGGIALAVSALSNRV----------KALLCDVPFLCHFRRAVQLVDTH-PYVEITNFLKTHR-DKEEI--VFRT : 249
TRQ2_0504  : TPDYCDEPINPQFPG-FMTRGILDPRTYYYRRVFTDAVRAVETASSFPGID----PERIAVVGTSQGGGIALAVAALSEIP----------KALVSNVPFLCHFRRAVQITDNA-PYSEIVNYLKVHR-DKEEI--VFRT : 250
Tlet_0356  : TPDYEDNPSDPQYPG-FLTKGVLNPETYYYRRVFMDAFMAVETISQLEQID----SQTIILSGASQGGGIALAVSALSSKV----------MALLCDVPFLCHYKRAVQITDSM-PYAEITRYCKTHI-DKIQT--VFRT : 249
DICTH_1987 : TPDYDDEPFDPQYSG-FMTRGILHPKKYYYRRVFTDAVRAVETLMAFPDVD----RERIGITGGSQGGGITIAVAGLAPYVG------IDIKIAMPDVPFLCHYRRAVEITDGY-PYQEIVQYLKTHR-DHVDK--VFKT : 253
RoseRS_079 : TPDPEPEGSNPHHPG-FMTRGITSPYTYYYRRVFTDAVRAIEAARAHPAID----AGRIAVTGGSQGGGIALAVAGLVHDI----------RATMPDVPFLCHYRRATEITDAN-PYYEIARYCKVHR-DRVEA--VFQT : 249
Rcas_1231  : TPDPEPEGSNPHHPG-FMTRGIASPFTYYYRRVFTDAVRAVEAARAHPAVD----ARRVAVTGGSQGGGIAIAVAGLMHDI----------RATMPDVPFLCHYRRATEISDSN-PYFEIARYCKVHR-DRVEA--VFQT : 249
Haur_0886  : TPDTEIEGGNPQIPG-FMTRGVLNPQNYYYRRLFTDAVRAIEAARSHPLVD----AGKVALAGGSQGGGISLAAAGLQPDV----------AAVLPDVPFLCHYRRATTMVDTY-PYAEVAQYCARHR-TKIEQ--VFNT : 248
SGR_6428   : TPDTDPGSAG-SVPG-FLTRGVESPATHYYRRVFTDAVRCVRAMREHPEVD----PARIVVTGVSQGGGIALAVAGLVP----------GLAGVMPDVPFLCNIPRAARIAATP-PYTEIAAYLRLHR-DRVEP--VFHT : 251
Acel_2045  : TIDAAEAPP--AQPG-FMTRGILDPSTYYYRRVYVDAVQAVRTLRAHPLVD----AARVAVTGVSQGGGLSLAAAALVP----------DVAAVMPDVPFLCHFRRACEISPAD-PYGEIVRYLKAHR-DQVEQ--VFAT : 247
Krad_3413  : TPDPDPTAPGGQWVGGFMTKGVGDPSTYFYRRAYVDCARAVEVAHALPALGVDVDPARVVVRGGSQGGAFTLAAAGLSG---------DRVAAALVDVPFLCHLRRAVDTASEG-PYPEVVTYLRRHSPEAVEQ--TFRT : 252
Arth_3303  : TADPHPSAGDVAHAG-LMTRGVGSREDYYYRRVYVDAFRAVEAAQAHPAV----DASRVVVAGVSQGGGISVAVAGLAAGRL------DGVIAALPDVPFLQDFPRAIDITPRG-PYPEIAAFLARHR-DRYES--ILAV : 255
Krad_4187  : GATADPVGYDVSTPG-FMTRGILDKDTYYYRRVFTDAVRAVRAARSLPEVR----ADAVCVAGASQGGAIALAAASLSP----------DVRAVMADVPFLSWFRRALQITAVE-PYTEVVRYLSVHR-DHVER--VLDT : 248
Tfu_1462   : GATPDPVGSAPSHPG-FMTRGIEDPATYYYRRVIVDAVRAVEAARALDIAD----PERVAVVGGSQGGGLALAAAGLVD----------GLAGVVSCVPFLCHIDRAITITDAH-PYAEITKYLSIHR-TKAPA--VLRT : 326
Sare_3004  : SDTPDPYGTGSSAPG-FLTRGISSPEDYYYRRVFSDGVRAVEAVRTLPVVD----ASRVIVTGSSQGGAIALAVSGLVP----------DIAGVAARSPFLCAIRRAVAVTDSD-PYAELRRFLGIHR-HEITH--AFGV : 247
SAV1457    : GDTPDPHATAPSGPG-PAVRGLLDPRDYHYRRLITDAVRAVAALRALPGVD----GSRVAAVGNSQGGGLALAVAGLVP----------DLAAVLVSAPFLCGIRRALELTDAA-PYGEITAYLAVHR-GAEAA--AYRT : 252
SCO7057    : GGTADPVGGTPAYPG-FMTRGLDAPENYYYRRVFTDAVRAVEAARSHPLTD----PSRTVALGASQGGGITIAVGGLVR----------DLAAVAPDVPFLCDFPRATTLTDRH-PYREVGLYLKTHR-GRSGD--ALRT : 248
SAML0944   : GGTADPVGGTPAYPG-FMTRGLDAPENYYYRRVFTDAVRAVEAARSHPLTD----PARTVALGGSQGGGITIAVGGLVP----------DLTAVAPDVPFLCDFPRATRLTDRH-PYREIGLYLKTHR-GRTED--ALRT : 248
SAV1302    : D-TPDPVGSGPAFPG-FMTRGVEDPESYYYRRLFTDGVRAVEAARAHPLTD----SARVAAVGTSQGGGITIAVGGLVP----------DLAAVAPDVPFLCDFPRATTLTDRD-PYREIGRYLKTNR-GRTEQ--VQRT : 247
CMS0795    : D-TADHGEAGPAIPG-FMTRGIASRETYYYRRLFTDAVRAVDVARSLDVVD----PARIAVQGGSQGGGMALAVAGLRD----------DLAAVSAYVPFLSDIERATHITDAY-PYHEVVDYLKTHR-GRGED--VHAV : 273
CMM_0227   : D-TADHGEAGPAIPG-FMTRGIASRDTYYYRRLFTDAVRAVDVARSLDVVD----PARIAVQGGSQGGGMALAVAGLRD----------DVAAVSAYVPFLCDIERATHITDAY-PYHEVVDYLKTHR-GRGED--VHAV : 245
Mlr6993    : E-TADPVGSTSSIPG-FMTRGVLDKNDYYYRRLFTDAVRAIDALLGLDFVD----PERIAVCGDSQGGGISLAVGGIDP----------RVKAVMPDVPFLCDFPRAVQTAVRD-PYLEIVRFLAQHR-EKKAA--VFET : 247
EF_1236    : VPYQTIWHEAPMGRG------FLDKEDWYQRRLFADHLRSVEVVRTFTEIN----QDQIILRGGSQGGGVVLMVNSLVDFP---------ILATFADVPSHSCLENRVAEGTGS--YQIIHQYLQEHP---QAHEKIAAV : 222
BVU_1343   : FGEISRAFSSRENGY--LVNGLDSRENYMKRVYLACVRSIDLLTSLPEWD----GKNVIVQGGSQGGALALITAGLDKR----------VTACVANHPALSDMAGYKAGRAGG--YPHLFKNTVD-----MDTPAKMKT : 363
BT_2525    : FKEISAAFNGRENGY--LSNGLDSRDNYMKRVYLACVRSIDLLTSLPEWD----GKNVVVQGGSQGGALALVTAGLDQR----------VTACVANHPALSDMAGYKAGRAGG--YPHFFRNTVD-----MDTPEKIRT : 379
Oter_2302  : YDVL---YAGALTGY--WTFNSDNRETYYYRRVYLSCVRANDFLTARENWD----GKNLVVMGASQGGQLSLVTAALDLR----------VSGLAVTHPAGCDWAAPLHGRAGG--WPHPFMPGADGKPSANATPARMAA : 379
LA_1864    : LKEGELPDPDWTPGY--FTKGLDGKDSFYMKGLYLDVIRAVEFLRLTDGID----GDKIILAGKSMGASLAAFGAAFTN----------RIKGLILETPNFCHIDDNQLKLDKS-WMKEIDTQLNSFK---TKKTAMKKS : 243
Oter_0486  : YDALPAMIKSYNTIY------NDSRDRNYFLRMYLGAYRAVDYLAGRPDWD----GRTLLVTGTSMGGQQSLAVAGLHP----------QITHVIVHVPAGADANAALHGRSEG--------YPNWDR----TNPKVMET : 347
SGR_835    : LPGVAPRSAGHVLHG------IEARESYVIGGCVADVWCAATALSSLVPET----SGRLTYLGTSFGGGIGALALPWDDR----------FRAAGLTVPTFGNHPLRVTLPCTG-SGESVRARLAEDP-------SVLDV : 276
                                                                            G SqGg                              P
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TM0077     : LSYFDGVNFAARA--KIPALFSVGLMDNICPPSTVFAAYNYYAGP--------------KEIRIYPYNNHEG-----GGSFQAVEQVKFLKKLFEKG----------------- : 325
Tsp-JW_axe : LGYIDVKNLAKRI--KGDVLMCVGLMDQVCPPSTVFAAYNNIQSK--------------KDIKVYPDYGHEP-----MRG-FGDLAMQFMLELYS------------------- : 320
BH3326     : LGYIDIQHLAPLV--KGEVLLAVGLMDTVCPPSTQFAMYNKLTTT--------------KSIELYPDFAHED-----LPG-HRDRIFQFLSDL--------------------- : 319
Csac_2436  : LGYIDVQHLAKWI--KAEVLMVTGLMDTICPPSTQFAAYNKIQSK--------------KQMLIYPDFGHEQ-----IFY-LNDRIFMYLMEMLE------------------- : 321
ABC1769    : LGYIDVQHLADRI--QGDVLMGVGLMDTECPPSTQFAAYNKIKAK--------------KSYELYPDFGHEH-----LPG-MNDHIFRFFTS---------------------- : 317
Gstea_estA : LGYIDIQLLADRI--CADVLWAVALEDHICPPSTQFAVYNKIKSK--------------KDMVLFYEYGHEY-----LPT-MGDRAYLFFCPIFFPIQKRNVK----------- : 329
LLKF_1447  : LEYIDIQNLAPRI--KAEVIWILGGKDTVVPPITQMAAYNKIQSK--------------KSLYVLPEYGHEY-----LPK-ISDWLRENQ------------------------ : 312
SP_1695    : LAYIDVKNLAHRI--QGEVKMITGLDDDVCYPITQFAIYNRLTCD--------------KTYRIMPEYAHEA-----MNVFVNDQVYNWLCGSEIP-------FKYLK------ : 326
Spr1538    : LAYIDVKNLAHRI--QGEVKMITGLDDDVCYPITQFAIYNRLTCD--------------KTYRIMPEYAHEA-----MNVFVNDQVYNWLCGSEIP-------FKYLK------ : 326
SPCG_1668  : LAYIDVKNLAHRI--QGEVKMITGLDDDVCYPITQFAIYNRLTCD--------------KTYRIMPEYAHEA-----MNVFVNDQVYNWLCGSEIP-------FKYLK------ : 326
SSA_0070   : LAYIDVKNLAHRI--SCPVQMIIGLEDDVCYPITQFAIYNRLAGE--------------KEYHLLPEYGHEA-----MNVRVSDTVFNWLCGTKIKRLSLISDFKSER------ : 333
SAK_0074   : LAYIDVKNFAHRI--SCPVVLLTALKDDICPPSTQFAIFNRLTST--------------KKHLLLPDYGHDP-----MTVQVKDYIFDQLTGSQFT-------KQKIE------ : 325
CPE1596    : LGYIDIKNMAHRI--KGKVNMAIGLRDDICPPSIQFAAYNNILCE--------------K-ELVLYDGGQKP-----YLLNLKDKIYKWAINL--------------------- : 319
DSY0351    : LDYFDGVHFAPWLGKKTACLVSMGLKDTVCPPATVYWLYKGICGE--------------KKLLIYPEYEHES-----PDGFVDRQIEFFAKELL-------------------- : 333
Bpumi_axe  : LSYFDLINLAGWV--KQPTLMAIGLIDKITPPSTVFAAYNHLETD--------------KDLKVYRYFGHEF-----IPAFQTEKLSFLQKHLLLST----------------- : 320
BPUM_0297  : LSYFDLINLAGWV--NQPTLMAIGLIDQITPPSTVFAVYNHLETD--------------KDLKVYRYFGHEY-----ISAFQTEKLAFLQKHLTN------------------- : 318
BSU03180   : LSYFDIMNLADRV--KVPVLMSIGLIDKVTPPSTVFAAYNHLETK--------------KELKVYRYFGHEY-----IPAFQTEKLAFFKQHLKG------------------- : 318
RBAM_00342 : LAYFDIMNLADRV--KVPVLMSIGLIDRVTPPSTVFAAYNHLETE--------------KELKVYRYFGHEY-----IPSFHTEKLAFLKAHLKG------------------- : 318
BLi00379   : LSYFDVMNLAQLV--KATVLMSIGLVDTITPPSTVFAAYNHLETD--------------KEIKVYRYFGHEY-----IPPFQTEKLAFLRKHLK-------------------- : 318
Cthe_3063  : LSYFDIMNLAPRI--KCRTWICTGLVDEITPPSTVFAVYNHLKCP--------------KEISVFRYFGHEH-----MPGSVEIKLRILMDELNP------------------- : 320
TRQ2_0870  : LSYFDGVNFAVRA--KIPALFSVGLMDNICPPSTVFAAYNHYAGP--------------KEIRIYPYNNHEG-----GGSFQAIEQVKFLKRLFEKG----------------- : 325
Tpet_0847  : LSYFDGVNFAVRA--KIPALFSVGLMDNICPPSTVFAAYNHYAGP--------------KEIRIYPYNNHEG-----GGSFQAIEQVKFLKRLFEKG----------------- : 325
CTN_0615   : LSYFDGVNFAARA--KVPALFSVGLMDTICPPSTVFAAYNHYAGP--------------KEIRIYPYNNHEG-----GGSFQAIEQVKFLKRLFEEG----------------- : 325
TRQ2_0504  : LSYFDGVNFAARA--KIPALFSVALMDKTCPPSTVFAAYNHYAGP--------------KEIKVYPFNEHEG-----GESFQRMEELRFMKRILKGEFKA-------------- : 329
Tlet_0356  : LSYFDGVNFAARA--KCPALFSVGLMDDICPPSTVFAAYNYYAGE--------------KDIRIYPYNNHEG-----GGSFHTLEKLKFVKKTISMRE---------------- : 326
DICTH_1987 : LSYFDGVNFAVRA--KAKALFSVALMDNICPPSTVFAAYNYYGGE--------------KEIKVYPFNGHEG-----GGTFHTYEKMKFAKRNLKD------------------ : 328
RoseRS_079 : LSYFDGVNFAARA--QAPALFSVGLMDDVCPPSTVYAAYNHYDGP--------------KQIRVYRYNQHEG-----GGTFQNQEKIRFLRTVLGG------------------ : 324
Rcas_1231  : LSYFDGINFAARA--QAPALFSVGLMDDVCPPSTVYAAYNYYAGR--------------KEIRVYRYNQHEG-----GGTFQNQEKIRFLREAVEV------------------ : 324
Haur_0886  : LDYFDGMQFAARA--TCPTLFSVGLMDDVCPPSTVFAAYNHYAGP--------------KEITVWQFNRHEG-----GENFQTLEKLKFLTKLWGNEERTA------------- : 328
SGR_6428   : LSYFDGAHHATRA--TAPALFSIAMADDICPPSTCFTAYNRYAGP--------------KDVRVYEFNGHEG-----GAEHHRAEQLAWVRALFAGLPADRTDRA--------- : 335
Acel_2045  : LAYFDGAVLATRA--TAPALFSVAVMDQICPPSTVFAAFHAYRGP-------------KEIVVYPFNDHEG-----GGPFQAGRQLRWLAAVLEK------------------ : 322
Krad_3413  : LSYVDGANFARRA--AAPALFSVALMDPVCPPSTVFAAYNRYGER---------AGSPRKDIDVWEFGDHGG-----GLGFQVQRQLRFLDGLGLR------------------ : 332
Arth_3303  : LNYFDGVNLGRAA--TAPALFSAAQADDICPPSTVFASFNAYGTKPATADPASGRGAPAKDIEVYRFNNHEG-----GQEHQWNRQLEYLRKMLG------------------- : 343
Krad_4187  : LDHFDVAHLVPRA--TAPALISLALMDRVCPPSTVWAAYRRYGGP--------------AELSVHPFNDHEG-----GQTHQWRRQLEWLSALLTAPGASA------------- : 328
Tfu_1462   : LSYIDGVHFAARA--TAPALLTVGLMDPVCPPSTVFAAYNAYAGPK--------------DLLVWPYNAHEG-----GGVEDLRASMAFLAPLLDGRPVAAHNTVTIHDQAATG : 419
Sare_3004  : LGYFDGVFMARRA--RRPGWFSAGLMDDVCPPSSVFAAANEFAGPV--------------HVEVWPYNGHEG-----GGVDDDRLLLDWGANLVAGP-----------DE---- : 325
SAV1457    : LSYVEGVSFARRA--TAPAHFGIGLRDTVCPPSGAYAAYNRYAELTG--------HDPLKEIHPYPFNQHEG-----GDAVHVRRQLTWLDGILGG------------------ : 333
SCO7057    : LSYFDGVHFAARG--RAPALFSAALEDQTCPPSTVFAAFNAWTHED-------------KTIEVYDFNDHEG-----GGPYQEAAKLRWLSRHA-------------------- : 322
SAML0944   : LSYFDGVHFAARG--RAPALFSAALEDQTCPPSTVFAAFNAWAHED-------------KAIEVYDFNDHEG-----GGPFQEAAKLRWLRSYV-------------------- : 322
SAV1302    : LSYFDGVHFAARG--SAPALFSAALEDQTCPPSTVFAAFNAWAHAD-------------KAIEVYDFNDHEG-----GGPYQEAAQLRWLPDRLR------------------- : 322
CMS0795    : LRHFDGVAFSRRA--TAPARFSVGLMDATCPPSTVYGAFNAYAGE--------------KEIVEWEYNGHDG-----GGIDDELGTLAFLKRRMG------------------- : 347
CMM_0227   : LRYFDGVAFSRRA--TAPARFSVGLMDATCPPSTVYGAFNSYAGE--------------KEIVEWEYNGHDG-----GGIDDELGTLAFLWRRMG------------------- : 319
Mlr6993    : LNYFDCVNFARRS--KAPALFSVALMDEVCPPSTVYGAFNAYAGE--------------KTITEYEFNNHEG-----GQGYQERQQMTWLSRLFGVG----------------- : 323
EF_1236    : LPYFDSRHFVSQI--KNPVFASVGSHDPICPMKDFFPSYHQIKAR--------------KAVRVYWKKGHGG-----GETTQIRREMRQIQQLLQEVKNENSYV---------- : 305
BVU_1343   : LAYYDVVNFAKQI--TVPVYMTWGFNDNTCPPTTSYIVYNVLNCP--------------KEALITPVNEHWT-----SEDTEYGHLLWIKKHLK-------------------- : 436
BT_2525    : MAYYDVVNFAQLI--RADTYMTWGFNDNVCPPTTSYIVYNVLNCP--------------KEALITPINEHWT-----SSDTEYGHLLWIKKHLK-------------------- : 452
Oter_2302  : LAYYDAVNFAKRI--KVPGYYNWGYNDVVTPPTSTYAAYNVITAP--------------KTLGLTLEMGHQY-----NEEQWKAIDNWVTQAIGVK------------------ : 454
LA_1864    : LAYYDSINFSKKI--KVPTLVSVGMEDRISHPKSIFAFFNHLNCD--------------KRMQVYPTEGNEAG---FKDEKQNGANLEFVREIFFPE----------------- : 321
Oter_0486  : ARYFDTVNFAPHI--KARSLVSLGFLDRVCPPAGIWTAFNLIAGP--------------KEVVPLVEAAHNHQSTPEQQRAYYDRSKAWMDALVKGQEP--------------- : 430
SGR_835    : LAYFDAATAARHL--RIPVHVGAALFDPSVPPPGQFAVHNALAGP--------------RELVVLRAGHFDHP----GERAETAALEEAQRQFLSLRT---------------- : 354
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