Supplementary materials

Identification of an amylomaltase from the halophilic *archaeon Haloquadratum walsbyi* by functional metagenomics: structural and functional insights.

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Content:

Table S1. Amino acids of conserved regions in amylomaltases of *T. thermophilus* and *H. walsby*.

	T. thermophilus (O87172)	*H. walsbyi* (MZ422727)
ACTIVE SITE		
Catalytic residues	D293 E340 D395	D345 E392 D445
i) Four conserved amino acids for substrate binding	Y59 D213 R291 H394	Y61 D266 R343 H444
ii) Other conserved amino acids of the active site	F217 W258 H294 L342 N464	Y270 W310 H346 L394 N508
iii) Conserved amino acids forming part of the cleft around the active center	S57 P58 D341 G343 T393 P466	S59 P60 D393 G395 T443 P510
iv) 250s LOOP	P247 P248 D249 Y250 F251 S252 E253 T254 G255 W302	P300 P301 T302 D303 -- S304 D305 D306 G307 Y354
SUBSTRATE BINDING SITE SECONDARY	Y54 Y101 Y465	H56 R107 E509

Figure S1

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P15977_Escherichia-coli          ------------------------------------------------------------
Q6R608_Solanum-tuberosum         MVNSGLKSRKVSFRIPYYTQWGQNLLICGSDRLLGSWNVKKGLLLKPSHQGEVLVWSGSI
Q030T7_Lactococcus-lactis        ------------------------------------------------------------
A6YM39_Borrelia-burgdorferi      ------------------------------------------------------------
B5RKZ2_Borrelia-duttonii         ------------------------------------------------------------
A1QYW1_Borrelia-turicatae        ------------------------------------------------------------
O87172_Thermus-thermophilus      ------------------------------------------------------------
UBZ54001_Haloquadratum-walsbyi_MdS ----------------------------------------------------------


P15977_Escherichia-coli          ------------------------MESKRLDNAALAAGISPNYIN--AHGK---P--
Q6R608_Solanum-tuberosum         PVPPGYQSEYSYYVVDDRRNILRWEVGKKRKLLLPDGLQDGQSLELRDLWQTGSDNIPFR
Q030T7_Lactococcus-lactis        ------------------------------------------------------------
A6YM39_Borrelia-burgdorferi      ------------------------------------------------------------
B5RKZ2_Borrelia-duttonii         ------------------------------------------------------------
A1QYW1_Borrelia-turicatae        ------------------------------------------------------------
O87172_Thermus-thermophilus      ------------------------------------------------------------
UBZ54001_Haloquadratum-walsbyi_MdS ----------------------------------------------------------


P15977_Escherichia-coli          ---------QSISAETKRRLLDAMHQRTATKVAVTPVPNVMVYTSGKKMPMVVEGSGEY
Q6R608_Solanum-tuberosum         SAFKDVIFRSSWSLDGER-SLEITQNKLDQD-------GSVILQFRICCPYLEEGTSIYV
Q030T7_Lactococcus-lactis        ------------------------------------------------------------
A6YM39_Borrelia-burgdorferi      ------------------------------------------------------------
B5RKZ2_Borrelia-duttonii         ------------------------------------------------------------
A1QYW1_Borrelia-turicatae        ------------------------------------------------------------
O87172_Thermus-thermophilus      ------------------------------------------------------------
UBZ54001_Haloquadratum-walsbyi_MdS ----------------------------------------------------------


P15977_Escherichia-coli          --------SWLLTTEEGTQYKG-------HVTGGKAFNLPTKLPEGY---------HTLT
Q6R608_Solanum-tuberosum         LGSSLNLGQWKIQDGLKLVYAGDSLWQAACVMGKDDFPLKYKYCKHSKAGTSVECGASRE
Q030T7_Lactococcus-lactis        ------------------------------------------------------------
A6YM39_Borrelia-burgdorferi      ------------------------------------------------------------
B5RKZ2_Borrelia-duttonii         ------------------------------------------------------------
A1QYW1_Borrelia-turicatae        ------------------------------------------------------------
O87172_Thermus-thermophilus      ------------------------------------------------------------
UBZ54001_Haloquadratum-walsbyi_MdS ----------------------------------------------------------


                                                      β1           β2              α1
P15977_Escherichia-coli          LTQDDQRAHCRVIVAPKRCYEPQALLNKQKLWGACVQLYTLRSEKNWGIGDFG-DLKAML
Q6R608_Solanum-tuberosum         ISVDVTTGESRFVVLSDGLMREMP----WRGAGVSIPMFSVRSEADLGVGEFL-DLKLLV
Q030T7_Lactococcus-lactis        --------------MVTNTFSIEPYGEKAYHTGIAVPVFSLRTENSSGVGQFS-DLKKLA
A6YM39_Borrelia-burgdorferi      --------------MA-KYKKTRINLNLKRKSGILLNISSLPSKY--GIGDLGKGAYKFI
B5RKZ2_Borrelia-duttonii         -------------------------MKRKSGILLSISSLPSQY--GIGDLGKGAYEFI
A1QYW1_Borrelia-turicatae        -------------------------MKRKSGILLNISSLPSKY--GIGDLGRGAYKFI
O87172_Thermus-thermophilus      ---------------------MELPRAFGLLLHPTSLPGPY--GVGVLGREARDFL
UBZ54001_Haloquadratum-walsbyi_MdS ----------------------MQFDRQAGVFAHITALPGSH--GIGDLGPGARKFL
                                                     *       ::      *:*  :          :
                                      β3                                   α2
P15977_Escherichia-coli          VDVAKRGGSFIGLNPIHALYPA-NPESASPYSPSSRRWLNVIYIDVNAVEDFHLSEEAQA
Q6R608_Solanum-tuberosum         DWAVESGFHLVQLLPINDTSVNCMWWDSYPYSSLSVFALHPLYLRVEAISENIPEDIKQE
Q030T7_Lactococcus-lactis        DFTYRSGMDVIQLLPINDTTTFMDWRDSYPYRAISVFALHPLYLDIHEFWKSYTKEQQEK
A6YM39_Borrelia-burgdorferi      DFLFTSSQSYWQMFAYSPID----FTRSPPYSIFSAFAGNVYYIDLEALDKFIDS--- D
B5RKZ2_Borrelia-duttonii         DFLASSSQSYWQILLYSLPN----CSG-VPYLSYSAFAGNISYIDLNAIDRFIDV---D
A1QYW1_Borrelia-turicatae        DFLADSSQGYWQILPYSPPS----FLE-FPYSSYSAFAGNINYIDLNAIDRFIDI---D
O87172_Thermus-thermophilus      RFLKEAGGRYWQVLPLGPTG-----YGDSPYQSFSAFAGNPYLIDLRPLAERGYVRLED-
UBZ54001_Haloquadratum-walsbyi_MdS EWLETANQSVWQFCPLGPTAG---IHDDSPYQSYSAFAGNPLLISLDDLVAEGYLTSED-
                                   .    .                 **  *   :  : :  .       :
                                      β4      α3
P15977_Escherichia-coli          WWQLPTTQQTLQQARDADWVDYSTVTALKMTALRMAWKGFAQR----------------
Q6R608_Solanum-tuberosum         IRE------ARVQ-LDKKDVDYEACMATKLSIAKKIFAREKE-
Q030T7_Lactococcus-lactis        LLI------LESELNSLEKIDYERCLALKWEYAQIIYQNLAV-----------------
A6YM39_Borrelia-burgdorferi      L--------SLLKENETRYSDLKKLS-FKDKFLKEAALNFIN-----------------
B5RKZ2_Borrelia-duttonii         L--------GIFGCLEDRCIDYDKLK-TKNIILRDAALNFLH-----------------
A1QYW1_Borrelia-turicatae        L--------GTFECLEDRYVDYDKLK-AKEVILRNAALNFLH-----------------
O87172_Thermus-thermophilus      ------------PGFPQGRVDYGLLYAWKWPALKEAFRGFKE-----------------
UBZ54001_Haloquadratum-walsbyi_MdS L--------EPVPDFSPHEVVYDTVREYKHDCLQIAAERFRESIGGIAIHPHPHPDPDTT
                                                       *    :
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                                                          α4                  α5
P15977_Escherichia-coli            ------------------------------DDEQMAAFRQFVAEQGDSLFWQAAFDAL
Q6R608_Solanum-tuberosum           ------------------------------TILNSKSFQEFFSENQEWLKPYAAFCFL
Q030T7_Lactococcus-lactis          ------------------------------KYQKTKSYQQFYKQNEEWLKAYACFSYL
A6YM39_Borrelia-burgdorferi        ------------------------------RASADEVRSFEKFKKKSSYWLLDFASFVAF
B5RKZ2_Borrelia-duttonii           ------------------------------RATIDEMYAFEKFKKSAAYWLLDFSSFVAF
A1QYW1_Borrelia-turicatae          ------------------------------RATIDEIHAFEKFKKSAAYWLLDFSSFVAF
O87172_Thermus-thermophilus        ------------------------------KASPEEREAFAAFREREAWWLEDYALFMAL
UBZ54001_Haloquadratum-walsbyi_MdS VNSGVDGDTVPEVTVTLGESVNLSQDTPADSQIEKDAREFKSFYQRENHWLTDYALFMAL
                                                          .    :  *       *   : * :

                                                          α6                  α7
P15977_Escherichia-coli            HAQQVKEDEMRWGW---PAWPEMYQNVDSPEVRQFCEEHRDDVDFYLWLQWLAYSQFAAC
Q6R608_Solanum-tuberosum           RNFFETSERSQWGRF--SEFSKEKL----EKLVSKESLHYEVVSFYYYIQFHLHLQLSEA
Q030T7_Lactococcus-lactis          RDINKSANFLAWGKN--ANYDKNLF----DKLKKET----SQLDLYIFVQYLLHSQLTEA
A6YM39_Borrelia-burgdorferi        KEYYFK----ESKNAFNVLFDRGILKKNEKDLFKLRNILSKEIKVQYLQYFFFSQFQAL
B5RKZ2_Borrelia-duttonii           REYYCRF---QDPQTFNLLFSKEILKRDPKALMRLRETLNVEINIQQVLQYFFFSQFKAL
A1QYW1_Borrelia-turicatae          KEYYSKF---QSSQAFNLLFSREILKRDAKALAKLRETLEVEINIQQVLQYFFFSQFKAL
O87172_Thermus-thermophilus        KGAHGGL---PW-----NRWPLPLRKREEKALREAKSALAEEVAFHAFTQWLFFRQWGAL
UBZ54001_Haloquadratum-walsbyi_MdS RTSYDG----AW-----TDWPEPIRNRDPDALRDQYESLESDVLYHLIVQFIFDQQWQSL
                                   :              :          :           :      *:     *

                                     β5            α8              β6          β7
P15977_Escherichia-coli            WEISQGYEMPIGLYRDLAVGVAEGGAETWCDRELYCLK------ASVGAPPDILGPLGQN
Q6R608_Solanum-tuberosum           AEYAR--KKGVVLKGDLPIGVDRNSVDTWVYPNLFRMN------TSTGAPPDYFDKNGQN
Q030T7_Lactococcus-lactis          VDYCH--KLGIALKGDIAIGIAHDSVDAWTHPELFHLD------KQAGAPPDVFAVNGQN
A6YM39_Borrelia-burgdorferi        KRYAN--DKGIELIMNVPFFIAYDSADVWAYQKYFKLRFDASKDKIAGISPDYFLEQEQA
B5RKZ2_Borrelia-duttonii           KRYAS--NVGIKIISDMPIFMFYDSADVWAHQKYFKLKFDASKDKVTGMPSGNLSYKKYL
A1QYW1_Borrelia-turicatae          KKYAN--NAGIKIVSDIPIFVSYDSADVWAHQKYFKLRFDASKDKVTGVPPDCLFSKKYL
O87172_Thermus-thermophilus        KAEAE--ALGIRIIGDMPIFVAEDSAEVWAHPEWFHLDEEGRPTVVVAGVPPDYFSETGQR
UBZ54001_Haloquadratum-walsbyi_MdS QTVAA--NRGVTLVGDLPIYVALDSADVWATPEIFQLTDTNEPAVVAGVPPTD-SDDGQR
                                     .    : ::    ...:.*    : : :            .*

                                     α9          α10         β8          β9
P15977_Escherichia-coli            WGLPPMDPHIITARAYEPFIELLRANMQNCGALRIDHVMSMLRLWWIPYGETADQ-----
Q6R608_Solanum-tuberosum           WGFPTYNWEEMSKDNYGWWRARLTQMGKYFTAYRIDHILGFFRIWELPEHAMTGLCGKFR
Q030T7_Lactococcus-lactis          WGFPTYNWEKMAEDGYDWWKKRLTAMSNYFDAYRLDHILGFFRIWQMPENSVRGLLGQFS
A6YM39_Borrelia-burgdorferi        WDSAAYSWNVLKKFKYEWWAKRIGVLRKYADIIKIDHFRGFVSTWEVSAGESYAF-----
B5RKZ2_Borrelia-duttonii           WGNAAYNWKALRKDDYVWWINRIGFMHKYVDIIKFDYFRGFVSTWEISEREFSVYSS---
A1QYW1_Borrelia-turicatae          WGNAAYNWKALRKDDYVWWINRIDFLRKYVDIVRIDYFRGFVSTWEVSAEESLLF-----
O87172_Thermus-thermophilus        WGNPLYRWDVLEREGFSFWIRRLEKALEFHLVRIDHRGFEAYWEIPASCPTAV-----
UBZ54001_Haloquadratum-walsbyi_MdS WGNPVYDWAYLRNTGYNWWLDRLDRLFDLVDVTRIDHFKGFDSYYAIPIDADNPA-----
                                   *.       :     :   :       :  ::*:. .:    : :

                                                 β10                      α11
P15977_Escherichia-coli            -----------------GAY-------------VHY--PV----------------DDL
Q6R608_Solanum-tuberosum           PSIPISQEELESE-----GLWDFNRLTHPYIGQDLLQEKFGASW-TIIASTFLNEYQKGF
Q030T7_Lactococcus-lactis          PALALSAEEIENNYGIPFRQWGIERFILPFIKDWVIDEVFGRDNRDWIIQTFLDYIGDSN
A6YM39_Borrelia-burgdorferi        -----------------NGLW-------------VKS--PG----------------RDF
B5RKZ2_Borrelia-duttonii           -----------------SGQW-------------VKC--PG----------------KDF
A1QYW1_Borrelia-turicatae          -----------------GGQW-------------VKC--PG----------------KDF
O87172_Thermus-thermophilus        -----------------EGRW-------------VKA--PG----------------EKL
UBZ54001_Haloquadratum-walsbyi_MdS -----------------AGEW-------------HSV--PG----------------YDF
                                   :

                                                             β11
P15977_Escherichia-coli            LSIL----------------------AL------------------------------
Q6R608_Solanum-tuberosum           YEFKDECNTEKKIASALKSFLETSMFVESEEKLRRKLFDLLQNVALIKDPEDPRKFYPRF
Q030T7_Lactococcus-lactis          YRFKAEFNNQKAIENT----------QMENVVREGLYKLQENVIFLKDDENSEKYHPRI
A6YM39_Borrelia-burgdorferi        FNFILNEI------K-----------DLK------------------------------
B5RKZ2_Borrelia-duttonii           FRNVLSKI------N-----------DLE------------------------------
A1QYW1_Borrelia-turicatae          FKQILNEI------N-----------DLE------------------------------
O87172_Thermus-thermophilus        FQKIQEVF------G-----------EVP------------------------------
UBZ54001_Haloquadratum-walsbyi_MdS FETVREHI------G-----------SLP------------------------------

P15977_Escherichia-coli            --------------------------------------------ESKRHRCMVIGEDLG
Q6R608_Solanum-tuberosum           NVEDTTSFMDLDQHSQNVLKRLYYDYYFHRQEGLWRDNAFKTLPVLLNSSDMLACGEDLG
Q030T7_Lactococcus-lactis          GLLSTISFREFGDDYKGRLERLYNDYFYGRNYDFWKEKAYEKLPALKNATKMLACGEDLG
A6YM39_Borrelia-burgdorferi        --------------------------------------------------IWVEDFQ
B5RKZ2_Borrelia-duttonii           --------------------------------------------------IWVEDLL
A1QYW1_Borrelia-turicatae          --------------------------------------------------IWVEDLV
O87172_Thermus-thermophilus        ------------------------------------------------VLAEDLG
UBZ54001_Haloquadratum-walsbyi_MdS -------------------------------------------------FIIEDLG
                                                                                    **:
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                                       α12       β12                      α13      β13        α14
P15977_Escherichia-coli        TVPVEIVGKLRSSGVYSYKVLYFENDHEK-TFRAPKAYPEQ--SMAVAATHDLPTLRGYW
Q6R608_Solanum-tuberosum       LIPSCVHPVMQELGLVGLRIQRMPSEPDV-EFGIPSQYNYM--TVCAPSCHDCSTLRAWW
Q030T7_Lactococcus-lactis      MVPDNVPDVMYHLDILRLIIERMPADERF-VSS-LSEVPYL--SVVTTSSHDTSPLRAWW
A6YM39_Borrelia-burgdorferi    NDLEDVSRLRDFFNFPGMKIMNLAFDFDSSNQNLPHNYIKN--CIVYTGSGDNDTIREFI
B5RKZ2_Borrelia-duttonii       EDRGDAFRLRDYFNFPETRIMQFAFDFDSKNLCLPHNYIKN--CVVYTSTNESNTIRQFI
A1QYW1_Borrelia-turicatae      KDRGDTFRLRDYFGFPGTKMMQCAFDFDSANIYLPHNYIRN--CVVYTGTHESNTIRGFI
O87172_Thermus-thermophilus    VITPEVEALRDRFGLPGMKVLQFAFDDGMENPFLPHNYPAHGRVVVYTGTHDNDTTLGWY
UBZ54001_Haloquadratum-walsbyi_MdS  FIDQALHDLREYFDFPGMRVPHYADWCREGDMYQPMHYPPQ--SVAYSSTHDTDTIVGYY
                                         ..          :                  :  .  :          :
                                                   α15                                     α16
P15977_Escherichia-coli        ECGDLTLGKTLGLYPDEVVLRGLYQDRELAKQGLLDALHKYGCLPKRAGHKASLMSMTPT
Q6R608_Solanum-tuberosum       EEDEERRHRFF----------------------QAVMGSDELPPDQCTPE---------
Q030T7_Lactococcus-lactis      EENHDLTQRYY----------------------NEVMGWYGEAPNYASVE---------
A6YM39_Borrelia-burgdorferi    NSLDDLHKKYI----------------------FDYLN-------TNENF---------
B5RKZ2_Borrelia-duttonii       NSVDDEHREYI----------------------FNYFN-------TNEDF---------
A1QYW1_Borrelia-turicatae      NSVDNEHKKYI----------------------FDYFN-------TSENA---------
O87172_Thermus-thermophilus    RTATPHEKAFM----------------------ARYLADWGITF-REEEE---------
UBZ54001_Haloquadratum-walsbyi_MdS  DSLSQSQRDCL----------------------HYNLG-------VDGSE---------
                                                                          :
                                β14   α17                                              β15
P15977_Escherichia-coli        LNRGLQRYIADSNSALLGLQPEDWLDMAE----------PVNIPGTSYQYKNWRRKLSAT
Q6R608_Solanum-tuberosum       IVHFVLRQHVEAPSMWSIFPLQDLLALKEDYTTRPAVEETINDPTNPKHY--WRYRVHVT
Q030T7_Lactococcus-lactis      IIQEIIKRNLNSNAMMVILPIQDWLAMSEHFRKENAKSEQINIPADPYHY--WNYRLHCN
A6YM39_Borrelia-burgdorferi    VVWDMIRSAMGSVSDNVIVPMQDYINLGDKFS--------ANIPKSTLDN--CIFRLLES
B5RKZ2_Borrelia-duttonii       VVWDMIRGAMSSVADNVIVSMEDYLDHVVDH--------KNVSGSMLND----FRILSS
A1QYW1_Borrelia-turicatae      IVWDMIRGAMASVANSVIIPMKDYLDLVADFS-------MNISDAMLNN----FRILSG
O87172_Thermus-thermophilus    VPWALMHLGMKSVARLAVYPVQDVLALGSEAR-------MNYPGRPSGN--WAWRLLPG
UBZ54001_Haloquadratum-walsbyi_MdS  INWSIIDAVWRSDAKIGLTTLQDVLGLDSHAR--------FNEPGTASGN--WEWRCTDS
                                :    :      : :        :* :               *            :
                                          α18
P15977_Escherichia-coli        LESMFADDGVNKLLKDLDRRRRAAAKKK-----------------------------
Q6R608_Solanum-tuberosum       MESLLNDKDLTKTIKDLVRGSGRFYPQKDLESGQAKLQLGSEHPSQTQKYGLSNK
Q030T7_Lactococcus-lactis      LQALIENQEWTDFLKNFIKESKRAY-------------------------------
A6YM39_B orrelia-burgdorferi   D----LDATLSQNISFLTRLYGRALE-----------------------------
B5RKZ2_Borrelia-duttonii       D----LSTDLSKKISNITKLYGRI-------------------------------
A1QYW1_Borrelia-turicatae      D----LSDDLSKKISDITKLYGRT-------------------------------
O87172_Thermus-thermophilus    E----LSPEHGARLRAMAEATERL-------------------------------
UBZ54001_Haloquadratum-walsbyi_MdS  G----LDEDLARRLAGLTLEHVRD-------------------------------
                                      .        : :
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Figure S1. Clustal alignment of Hw-A and GH77 representative sequences. Secondary structural elements highlighted in the *T. thermophilus* sequence were according to the 3D structure described by Przylas et al. [1]. In particular, green regions refer to the (β/α)$_8$ barrel (subdomain A); the other coloured regions correspond to subdomains B2 (yellow), B1 (orange) and B3 (cyan). The three catalytic amino acids are reported in red. The non conserved amino acids in the sequences from borreliae discussed in the Introduction are shown in blue. The carbohydrate binding domains of *E. coli* [2] and potato [3] are highlighted in red.

1. Przylas, I.; Tomoo, K.; Terada, Y.; Takaha, T.; Fujii, K.; Saenger, W.; Sträter, N. Crystal Structure of Amylomaltase from Thermus Aquaticus, a Glycosyltransferase Catalysing the Production of Large Cyclic Glucans. *Journal of Molecular Biology* **2000**, *296*, 873–886, doi:10.1006/jmbi.1999.3503.
2. Mareček, F.; Møller, M.S.; Svensson, B.; Janeček, Š. A Putative Novel Starch-Binding Domain Revealed by in Silico Analysis of the N-Terminal Domain in Bacterial Amylomaltases from the Family GH77. *3 Biotech* **2021**, *11*, 229, doi:10.1007/s13205-021-02787-8.
3. Lloyd, J.R.; Blennow, A.; Burhenne, K.; Kossmann, J. Repression of a Novel Isoform of Disproportionating Enzyme (StDPE2) in Potato Leads to Inhibition of Starch Degradation in Leaves But Not Tubers Stored at Low Temperature. *Plant Physiology* **2004**, *134*, 1347–1354, doi:10.1104/pp.103.038026.

Figure S2

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AUV80673.1       ----------------------------------------------------------
QCC51341.1       ----------------------------------------------------------
QSG15659.1       ----------------------------------------------------------
QSG11910.1       ----------------------------------------------------------
QSG08987.1       ----------------------------------------------------------
QSG05483.1       ----------------------------------------------------------
QGN07616.1       MHSIGPEWREEIDDSTKTQYPAGQDRRADEQGPQRDQKRADRPLARHVDEFGRCVEETVH
QSG11921.1       ----------------------------------------------------------
QSG08998.1       ----------------------------------------------------------
QSG05496.1       ----------------------------------------------------------
CCQ33055.1       ----------------------------------------------------------
QSG02731.1       ----------------------------------------------------------
AUX09035.1       ----------------------------------------------------------
QFU81686.1       ----------------------------------------------------------
AWB27107.1       ----------------------------------------------------------
QLC34969.1       ----------------------------------------------------------
ACV11232.1       ----------------------------------------------------------
QPV62520.1       ----------------------------------------------------------
QLH84085.1       ----------------------------------------------------------
QLH79093.1       ----------------------------------------------------------
QAU11732.1       ----------------------------------------------------------
QAY20111.1       ----------------------------------------------------------
QWC20591.1       ----------------------------------------------------------
QUO46499.1       ----------------------------------------------------------
QKG93724.1       ----------------------------------------------------------
QKY17977.1       ----------------------------------------------------------
ACM57093.1       ----------------------------------------------------------
AZQ14643.1       ----------------------------------------------------------
ATW89261.1       ----------------------------------------------------------
ABQ75827.1       ----------------------------------------------------------
QZX99028.1       ----------------------------------------------------------
QZP38174.1       ----------------------------------------------------------
QZY03180.1       ----------------------------------------------------------
AUG48211.1       ----------------------------------------------------------
AEM58055.1       ----------------------------------------------------------
AHB66799.1       ----------------------------------------------------------
AJF25101.1       ----------------------------------------------------------
AAV46825.1       -----------MDTIYMFAYP------------------------------RRRVLT
QCP91534.1       ----------------------------------------------------------
QUJ72368.1       ----------------------------------------------------------
UBZ54001.1       ----------------------------------------------------------
CCC40696.1       ----------------------------------------------------------
CAJ52690.1       ----------------------------------------------------------
QCJ48434.1       ----------------------------------------------------------
AHZ21176.1       ----------------------------------------------------------
AFK19479.1       ----------------------------------------------------------
AFK19479.2       ----------------------------------------------------------
QCQ75940.1       ----------------------------------------------------------
AKU07735.1       ----------------------------------------------------------
QOS11852.1       ----------------------------------------------------------
QIB78738.1       ----------------------------------------------------------
ADE05003.1       ----------------------------------------------------------
ADE05003.2       ----------------------------------------------------------
QCC48543.1       ----------------------------------------------------------
ADQ67101.1       ----------------------------------------------------------
QIQ76396.1       ----------------------------------------------------------
QIB74651.1       ----------------------------------------------------------
AIF04697.1       ----------------------------------------------------------
AIF05955.1       ----------------------------------------------------------
QEE14682.1       ----------------------------------------------------------
ADL19304.1       ----------------------------------------------------------
AMD30778.1       ----------------------------------------------------------
AKT33963.1       ----------------------------------------------------------
ABL88479.1       ----------------------------------------------------------
ACB39188.1       ----------------------------------------------------------
AEA11843.1       ----------------------------------------------------------
ABO08194.1       ----------------------------------------------------------
ABP49821.1       ----------------------------------------------------------
AFA40300.1       ----------------------------------------------------------
AAL63326.1       ----------------------------------------------------------
NP_559144.1      ----------------------------------------------------------
AET33957.1       ----------------------------------------------------------
ABD40312.1       ----------------------------------------------------------
QXO95450.1       ----------------------------------------------------------
QVV87979.1       ----------------------------------------------------------
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CCJ37196.1      ----------------------------------------------------------GFGVL---
SAI88308.1      ---------------------------------------------------------------
CVK34217.1      ---------------------------------------------------------------
BBL68280.1      ---------------------------------------------------------------
ABN57193.1      ---------------------------------------------------------------
SAI88240.1      ---------------------------------------------------------------
CVK34142.1      ---------------------------------------------------------------
CCJ37132.1      ---------------------------------------------------------------
BBL68006.1      ---------------------------------------------------------------
ABN56987.1      ---------------------------------------------------------------


AUV80673.1      ------------------------------------------------MTLDRQSGVFC
QCC51341.1      ----------------------------MCYFQVRAAASREIRMDFDRQSGLFL
QSG15659.1      --------------------------------------------MDFDRQSGLFL
QSG11910.1      --------------------------------------------MEFDRQSGLFL
QSG08987.1      --------------------------------------------MEFDRQSGLFL
QSG05483.1      --------------------------------------------MEFDRQSGLFL
QGN07616.1      QLREKRGHATTSQPGHLD---AWPGHSRPGVSRRERDSLSRECRQPTGSMAFEKQSGVFL
QSG11921.1      --------------------------------------------MSFERQSGVFL
QSG08998.1      --------------------------------------------MSFERQSGVFL
QSG05496.1      --------------------------------------------MSFERQSGVFL
CCQ33055.1      --------------------------------------------MSFERQSGVFL
QSG02731.1      ---------------------------------------------------MFA
AUX09035.1      --------------------------------------------MTDFDRRSGVFC
QFU81686.1      --------------------------------------------MAAFDRRSGVFC
AWB27107.1      --------------------------------------------MALDRESGIFL
QLC34969.1      --------------------------------------------MNFERTSGVFC
ACV11232.1      --------------------------------------------MSFDRQSGVFL
QPV62520.1      --------------------------------------------MQQQRRSGVFL
QLH84085.1      --------------------------------------------MQQERRSGVFL
QLH79093.1      --------------------------------------------MQQERRSGVFL
QAU11732.1      --------------------------------------------MRFDRSDGVFC
QAY20111.1      --------------------------------------------MRFDRSDGVFC
QWC20591.1      --------------------------------------------MRFDRSDGVFC
QUO46499.1      --------------------------------------------MRFDRSDAVFC
QKG93724.1      --------------------------------------------MRFDRSDAVFC
QKY17977.1      --------------------------------------------MRFDRSAGVFC
ACM57093.1      --------------------------------------------MRLDRSSGVFC
AZQ14643.1      --------------------------------------------MRLDRSGGVFC
ATW89261.1      --------------------------------------------MDFDRQSGVFL
ABQ75827.1      --------------------------------------------MQFERQSGVFL
QZX99028.1      --------------------------------------------MRFDRRSGVLL
QZP38174.1      --------------------------------------------MRFDRRSGVLL
QZY03180.1      --------------------------------------------MRFDRRSGVLL
AUG48211.1      --------------------------------------------MQFERQSGVFL
AEM58055.1      ---------------------------------------------------MFL
AHB66799.1      --------------------------------------------MQFERQSGVFL
AJF25101.1      --------------------------------------------MQFERQSGVFL
AAV46825.1      RIRRRSLLTGRSSPLALPRAAHFVRAPRP-----EKPRPLKCLSGQQVRMQFERQSGVFL
QCP91534.1      --------------------------------------------MQFERQSGVFL
QUJ72368.1      --------------------------------------------MQFERQSGVFL
UBZ54001.1      --------------------------------------------MQFDRQAGVFA
CCC40696.1      --------------------------------------------MQFDRQAGVFA
CAJ52690.1      --------------------------------------------MQFDRQAGVFA
QCJ48434.1      --------------------------------------------MRFDRQSGVFL
AHZ21176.1      --------------------------------------------MRFSRQSGVFM
AFK19479.1      -----------------------------------MGLATESVSMRFSRQSGVFM
AFK19479.2      --------------------------------------------MRFSRQSGVFM
QCQ75940.1      -----------------------------------MGLATESVSMRFSRQSGVFM
AKU07735.1      --------------------------------------------MRLSRQSGVFM
QOS11852.1      --------------------------------------------MRLSRQSGVFM
QIB78738.1      --------------------------------------------MRLSRQSGVFM
ADE05003.1      -----------------------------------------MGMRLSRQSGVFM
ADE05003.2      --------------------------------------------MRLSRQSGVFM
QCC48543.1      --------------------------------------------MRFDRRSGVFL
ADQ67101.1      --------------------------------------------MRFDRQSGVFA
QIQ76396.1      --------------------------------------------MRFDRQSGVFA
QIB74651.1      --------------------------------------------MRFDRQSGVFA
AIF04697.1      ------------------------------MAVEGTSKHYGSNGRRPFMRQAGVLC
AIF05955.1      ------------------------------MAVEGTSKHYGSNGRRPFMRQAGVLC
QEE14682.1      --------------------------------------------MELPRSAGILL
ADL19304.1      -----------------------------------------------MERGSGLLL
AMD30778.1      -----------------------------------------------MERGSGILL
AKT33963.1      ------------------------------------------------MLRGFGVLL
ABL88479.1      ------------------------------------------------MLRGFGVLL
ACB39188.1      ------------------------------------------------MLRGFGVLL
AEA11843.1      ------------------------------------------------MLRGAGILL
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ABO08194.1      -------------------------------------------------MLRGAGVLL
ABP49821.1      -------------------------------------------------MLRGAGVLL
AFA40300.1      -------------------------------------------------MLRGAGVLL
AAL63326.1      -------------------------------------------------MLRGAGVLL
NP_559144.1     -------------------------------------------------MLRGAGVLL
AET33957.1      -------------------------------------------------MLRGAGILL
ABD40312.1      -----------------------------------------------MKTRGSGILL
QXO95450.1      -----------------------------------------------MKTRGCGTLL
QVV87979.1      -----------------------------------------------MKTRGCGILL
CCJ37196.1      -----------------------------------------------MNRRGSGVLL
SAI88308.1      -----------------------------------------------MNRRGSGVLL
CVK34217.1      -----------------------------------------------MNRRGSGVLL
BBL68280.1      -----------------------------------------------MNRRGSGVLL
ABN57193.1      -----------------------------------------------MNRRSSGVLL
SAI88240.1      ----------------------------------------------MIHTRGSGILL
CVK34142.1      ----------------------------------------------MIHTRGSGILL
CCJ37132.1      ----------------------------------------------MIHTRGSGILL
BBL68006.1      ----------------------------------------------MIQTRGSGILL
ABN56987.1      ----------------------------------------------MIQTRGSGILL
                                                              :


AUV80673.1      HVASLPGPQGIGSLGAPARRFVDFLARADQSLWQFCPIGPTTVDYGNSPYSALSAVAGNP
QCC51341.1      HVASLPGPDGIGTLGEPAETFVDFLAESGQSLWQFCPLGPTIPIHDNSPYQSYSAFAGNP
QSG15659.1      HVASLPGPDGIGTLGDPAKTFVDFLADSGQSLWQFCPLGPTIPIHDNSPYQSYSAFAGNP
QSG11910.1      HIASLPGPDGIGTLGDPAETFVDFLADSGQSLWQFCPLGPTIPIHDNSPYQSYSAFAGNP
QSG08987.1      HIASLPGPDGIGTLGDPAETFVDFLADSGQSLWQFCPLGPTIPIHDNSPYQSYSAFAGNP
QSG05483.1      HIASLPGPDGIGTLGGPAETFVDFLADSGQSLWQFCPLGPTIPIHDNSPYQSYSAFAGNP
QGN07616.1      HVSSLPGPDGIGTLGAPAETFVDFLATAEQSLWQTCPIGPTDPDVGNSPYSAYSARAGNP
QSG11921.1      HVSSLSGPDGIGTLGEPAHEFVEYLETAEQSLWQTCPIGPTDPRQGNSPYSSFSARAGNP
QSG08998.1      HVSSLSGPDGIGTLGEPAHEFVEYLETAEQSLWQTCPIGPTDPRQGNSPYSSFSARAGNP
QSG05496.1      HVSSLSGPDGIGTLGEPAHEFVEYLETAEQSLWQTCPIGPTDPRQGNSPYSSFSARAGNP
CCQ33055.1      HVSSLPGPDGIGTLGQPAREFVDFLVESDQSLWQTCPIGPTDAGQGNSPYSAYSARAGNP
QSG02731.1      HPTSLPSSHGIGSIGQPSREFVDTLAEADQSLWQLCPLGPISSIHGNSPYQAYSAFAIEP
AUX09035.1      HPTALPGPGGIGTLGEPARGFLDRITEAGQSLWQLCPLGPTVGIHGNSPYQTCSAFAIDP
QFU81686.1      HPTALPGPHGIGSIGAPARSFVETIAAAGQSLWQLCPLGPTVGIHGDSPYQSSSSFALSP
AWB27107.1      HLSSLPGPHGIGDLGAT-TAVLDWLDRADQSVWQVCPINPTQGVHGHSPYASVSTFAGNP
QLC34969.1      HLTSLPGGHGIGDLGAGARDFLDLDAADQSLWQFCPLGPTTGVHGHSPYSSPSTFAGNP
ACV11232.1      HLTSLPSPHGIGDLGDGARTFLDFLERAEQSLWQFCPVTPTRGVHGHSPYASPSAFAGNP
QPV62520.1      HLTSLPGPHGVGDLGAGARTFLDFLDRADQSLWQFCPVGPTSDAYGHSPYGSSSAFAGNP
QLH84085.1      HLTSLPGPHGVGDLGAGAREFLDFLDRADQSLWQFCPVGPTSAAYGHSPYGSSSAFAGNP
QLH79093.1      HLTSLPGPHGVGDLGAGAREFLDFLDRADQSLWQFCPVGPTSAAYGHSPYGSSSAFAGNP
QAU11732.1      HVTSLPGAYGIGDLGGGAREFLSFLGDADVDHWQICPIGPTLSVAGESPYQSPSAFAGNP
QAY20111.1      HVTSLPGAYGIGDLGEGARDFLSFLGDADVDHWQICPIGPTLSVAGESPYQSPSAFAGNP
QWC20591.1      HVTSLPGAYGIGDLGQGAREFLSFLGDAGVDHWQICPIGPTLSVAGESPYQSPSAFAGNP
QUO46499.1      HVTSLPGAYGIGDLGEGAREFLSFLGDAGVDHWQICPIGPTISAAGESPYQSPSAFAGNP
QKG93724.1      HVTSLPGAYGIGDLGEGARDFLSFLGDAGVDHWQICPFGPTLSVAGESPYQSPSAFAGNP
QKY17977.1      HVTSLPGRHGIGDLGDGAAAFLSFLGDADVDYWQICPVGPTTDGAGESPYQSPSAFAGNP
ACM57093.1      HVTSLPGRHGIGDLGDGAKAFLSFLGDADIGHWQVCPLGPTMGAAGESPYQSPSAFAGNP
AZQ14643.1      HVTSLPGRHGIGDLGDGAREFLSFLGDADVGHWQICPLGPTIGAAGESPYQSPSAFAGNP
ATW89261.1      HLTSLPGPHGIGDLGDGAREFLSFLQQAEQACWQFCPLGPTSSAHGNSPYQSFSAFAGNP
ABQ75827.1      HITALPGPHGIGDLGEGAHEYIDWLASANQSVWQFCPIGPTASIHGDSPYQSYSAFAGNP
QZX99028.1      HPTALPGPYGIGDLGAGARSFLDFLDRADQSIWQVCPLGPTVGIHGHSPYQTFSGFAGNP
QZP38174.1      HPTALPGPHGIGDLGAGARSFLEFLDRADQSIWQVCPLGPTVGIHGHSPYQTFSGFAGNP
QZY03180.1      HPTALPGPHGIGDLGAGARSFLEFLDRADQSIWQVCPLGPTVGIHGHSPYQTFSGFAGNP
AUG48211.1      HLTSLPGPHGIGDLGSGARAFVDFLDRADQSLWQFCPLGPTASIHGNSPYQSSSAFAGNP
AEM58055.1      HQTSLPGPHGIGDLGAGARAFVDFLDRADQSLWQFCPLGPTASIHGNSPYQSSSAFAGNP
AHB66799.1      HQTSLPGPHGIGDLGAGARAFVDFLDRADQSLWQFCPLGPTASIHGNSPYQSSSAFAGNP
AJF25101.1      HQTSLPGPHGIGDLGAGAWAFVDFLDRADQSLWQFCPLGPTASIHGNSPYQSSSAFAGNP
AAV46825.1      HLTSLPGPHGIGDLGAGARAFVDFLDRADQSLWQFCPLGPTASIHGNSPYQSSSAFAGNP
QCP91534.1      HLTSLPGPHGIGDLGAGARAFVDFLDRADQSLWQFCPLGPTASIHGNSPYQSSSAFAGNP
QUJ72368.1      HLTSLPGPHGIGDLGAGARAFVDFLDRADQSLWQFCPLGPTASIHGNSPYQSSSAFAGNS
UBZ54001.1      HITALPGSHGIGDLGPGARKFLEWLETANQSVWQFCPLGPTAGIHDDSPYQSYSAFAGNP
CCC40696.1      HITALPGPHGIGDLGPGARNFLEWLETANQSVWQFCPLGPTAGIHDDSPYQSYSAFAGNP
CAJ52690.1      HITALPGPHGIGDLGPGARNFLEWLETANQSVWQFCPLGPTAGIHDDSPYQSYSAFAGNP
QCJ48434.1      HVSSLPGPHGIGDLGDGARAFVDFLADADQSLWQFCPLGPTSSAHGNSPYQSFSAFAGNP
AHZ21176.1      HVTSVPGPHGIGDLGDGAHAFVDFLAHAEQSMWQFCPLGPTSPVHANSPYQSASSFAGNP
AFK19479.1      HVTSVPGPHGIGDLGDGAHAFVDFLAHAEQSMWQFCPLGPTSPVHANSPYQSASSFAGNP
AFK19479.2      HVTSVPGPHGIGDLGDGAHAFVDFLAHAEQSMWQFCPLGPTSPVHANSPYQSASSFAGNP
QCQ75940.1      HVTSVPGPHGIGDLGDGAHAFVDFLAHAEQSMWQFCPLGPTSPVHANSPYQSASSFAGNP
AKU07735.1      HVTSVPGPHGIGDLGDGARAFVDFLSDAEQSMWQFCPLGPTEPAMANSPYQSTSSFAGNP
QOS11852.1      HVTSVPGPHGIGDLGDGARAFVDFLSDAEQSMWQFCPLGPTEPAMANSPYQSTSSFAGNP
QIB78738.1      HVTSVPGPHGIGDLGDGARAFVDFLADAEQSMWQFCPLGPTEPAMANSPYQSTSSFAGNP
ADE05003.1      HVTSVPGPHGIGDLGDGARAFVDFLADAEQSMWQFCPLGPTEPAMANSPYQSTSSFAGNP
ADE05003.2      HVTSVPGPHGIGDLGDGARAFVDFLADAEQSMWQFCPLGPTEPAMANSPYQSTSSFAGNP
QCC48543.1      HLTSLPGPHGIGDLGGGARAFVDWLDAAEQSYWQFCPLGPTAPVHGDSPYQAYSAFAGNP
ADQ67101.1      HVPSLPGPHGIGDLGDGARAFIDWLASAEQSLWQFCPLGPTASIHGHSPYQSYSAFAGNP
QIQ76396.1      HVPSLPGPHGIGDLGDGARAFVDWLASAEQSLWQFCPLGPTASIHGHSPYQSYSAFAGNP
QIB74651.1      HVPSLPGPHGIGDLGDGARAFVDWLASAEQSLWQFCPLGPTASIHGHSPYQSYSAFAGNP
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AIF04697.1      HLTSLPSQ----TLGEDAHRFCRLLSQIGCSVWQMLPLTPP--DEHGSPYASYSAFAVWD
AIF05955.1      HLTSLPSQ----TLGEDAHRFCRLLSQIGCSVWQMLPLTPP--DEHGSPYASYSAFAVWD
QEE14682.1      HPTSVYTRYGIGDLGPDTFQFIEFLKASSQHFMQVLPIGPT--GYADSPYQTISAFAGNP
ADL19304.1      HITSLPGSPLVGDLGPSAHEFLEILRDAGQRYWQVLPLSPTAPEHDNSPYSGLSAFAGNP
AMD30778.1      HVTSLPGSPLVGDLGPSAHEFLELLREAGQRYWQVLPLSPTAPEHDNSPYSGLSAFAGSP
AKT33963.1      PVFSLPGGCHVGDMGPEAYKFAEFLADAEATYWQVLPLGHTAPEYDDSPYSALSMLAGNP
ABL88479.1      HISSLPGGCLAGDLGPSAYKFAEFLSKAEATYWQILPLSHTLPEYDDSPYSAVSLLAGNP
ACB39188.1      HISSLPGGCLVGDLGPSAYRFADFLSEAEATYWQILPLSHTLPEYDDSPYSAASLLAGNP
AEA11843.1      PLFSLPGPHGIGDMGPAAYRFVEFLRDAGQTYWQLLPLNPVLPEYDNSPYSSTSSFAGEP
ABO08194.1      HITSLPGGCHVGDLGPEAYAFAEALAYAEQTYWQTLPINHTLPEYENSPYSAASSFAGDP
ABP49821.1      HITSLPGGCYVGDLGPEAYKFAEFLAEAEQTYWQTLPINHSVPEYENSPYSAVSSFAGDP
AFA40300.1      HITSLPGGCYVGDLGPEAYKFAEFLAEAEQTYWQTLPINHSVPEYENSPYSAVSSFAGDP
AAL63326.1      HITSLPGGCFVGDLGPEAYKFADSLAYAEQTYWQTLPINHTVPEYENSPYSAVSSYAGDP
NP_559144.1     HITSLPGGCFVGDLGPEAYKFADSLAYAEQTYWQTLPINHTVPEYENSPYSAVSSYAGDP
AET33957.1      HITSLPGGCYVGDLGPEAYKFAEGLADAGQTYWQTLPINHTLPEYENSPYNAVSSFAGDP
ABD40312.1      HITSLPGQFGIGDLGPQADRFVDFLQASGQRYWQILPVHPTDIRYDNSPYHSISAFAGNP
QXO95450.1      HITSIPTKFGIGDLGPAAYRFVEFLQKAGQRYWQVLPLHPTEHMYDNSPYHALSAFAGNP
QVV87979.1      HITSIPTQFGIGDLGPAAYRFVEFLQKAGQRYWQVLPLHPTENMYDNSPYHALSAFAGNP
CCJ37196.1      HITSLPSVYGIGDLGPAAHRFVDLLAGAGQRYWQILPLNPTCPDLGNSPYLSTSAFAGNT
SAI88308.1      HITSLPSVYGIGDLGPAAHRFVDLLAGAGQRYWQILPLNPTCPDLGNSPYQSTSAFAGNT
CVK34217.1      HITSLPSAYGIGDLGPAAHRFVDLLAGAGQRYWQILPLNPTCPDLGNSPYQSTSAFAGNT
BBL68280.1      HITSLPSVYGIGDLGPAAYRFVDLLAGAGQRYWQILPLNPTCPEFANSPYQGTSAFAGNT
ABN57193.1      HVTSLPSPYGIGDLGPAAYRFVDLLSRAGQRYWQILPLNPTCPEFANSPYQSTSAFAGNT
SAI88240.1      HITSLPSAYGIGDFGPSAYRFVEALAKARQHYWQILPLNPTRVEHASSPYYSPSAFGMNT
CVK34142.1      HITSLPSAYGIGDFGPSAYRFVEALAKARQHYWQILPLNPTRVEHASSPYYSPSAFGMNT
CCJ37132.1      HITSLPSAYGIGDFGPPAYRFVEALAKARQHYWQILPLNPTRIEHASSPYYSPSAFGMNT
BBL68006.1      HITSLPSPYGIGDFGPAAYRFVEALERARQHYWQILPLNPTEAAYAHSPYSSPSAFAANT
ABN56987.1      HITSLPSPYGVGDFGPAAYRFVDALERGRQHYWQILPLNPTETAYAHSPYSSPSAFAANI
                 ::         :*          :          *  *.        ***   *  .


AUV80673.1      LFVDLADLRERGWLERVEGE--------------------PFDDECVEYERVTDHVETH
QCC51341.1      LFVDLDRLVERGWLDELD------------RP--------DFDDGHVEYGPVREYKEAR
QSG15659.1      LFIDLDELVERGWLEDLD------------RP--------DFDDGNVEYGPVREYKEAR
QSG11910.1      LFLDLDDLVERGWLEELD------------RP--------DFNDANVEYEPVREFKEAR
QSG08987.1      LFLDLDDLVERGWLEELD------------RP--------DFDDANVEYEPVREFKEAR
QSG05483.1      LFLDLDDLVERGWLEELD------------RP--------DFDDANVEYGPVREFKEAR
QGN07616.1      LFIDLDALVDRGWLADLD------------RP--------GFDEREVEYDRVDAFKQEA
QSG11921.1      LFIELDALVEEGWLDDPD------------RP--------DFDDREVEYERVMAFKREA
QSG08998.1      LFIELDALVEEGWLDDPD------------RP--------DFDDREVEYERVMAFKREA
QSG05496.1      LFIELDALAEEGWLDDPD------------RP--------DFDDREVEYERVMAFKREA
CCQ33055.1      LFIELDPLVEAGWLDEPD------------RP--------DFDDREVEFGRVRPFKQGA
QSG02731.1      LLIDLDVLVEQELLTPQEVTPTE---------------PFPNEYVDYDAVREFKYPL
AUX09035.1      LLIDLEDLIERGLLSGNRVETER-------DDA--------RLSDDRVDYDAVRKYKRPL
QFU81686.1      LLIDLEALNERGLLTDDALEPDP-------ELDH-------ELTDDRVAYDAVRSFKTSR
AWB27107.1      LFVDLTDLVDRGWLSADALAD----------AP--------R--TDRVDYDRVVPFTEDC
QLC34969.1      LLLDLHALRDQGWLTDAELEA----------PA--------AAEPTRVDYEAVAAFKRER
ACV11232.1      LLVDLTALVERGWLDEETLEN----------PP--------G-DPRTVQYDTVTDFKRER
QPV62520.1      LLVDLTDLVDRGYLDESDLDG----------PE--------GTEPGSVNYEVVAPFVRDR
QLH84085.1      LLVDLVDLADRGYLDDSDLDG----------PE--------GAEPGSVNYEAVAPFKRQR
QLH79093.1      LLVDLVDLADRGYLDDADLDG----------PE--------GAEAGSVNYEVVAPFVRDR
QAU11732.1      LLVDLDGLVDDGWLDEGDLRP----------VP--------EFPVDRVDYDAVREYKLPL
QAY20111.1      LFVDPEGLVDDGWLDEGDLRP----------VP--------DFPTDRVDYEAVREYKLPL
QWC20591.1      LFVDPDGLVADGWLDEGDLEP----------VP--------EFPADRVDYDAVREYKLPL
QUO46499.1      LFVDPDGLVDDGWLDEDDLEP----------VP--------DFPTDRVDYDAVREYKLPL
QKG93724.1      LFVDPDGLVADGWLDEGDLTP----------VP--------DFPTDRVDYDAVREYKLPL
QKY17977.1      LLIDLDGLAADGWLDEADLEP----------AP--------EFPTDRVDYAAVREYKLPL
ACM57093.1      LLIDLDGLVDDGWLDESDLEP----------IP--------DFPEDRVDYDAVREYKQPL
AZQ14643.1      LLIDLDGLVDDGWLDESDLTP----------AP--------DFPSDRVDYEAVRGYKEPL
ATW89261.1      LLISLDRLVDDGWLTDEDLQP----------VP--------DFDEHSVDYEAVGDYKRNQ
ABQ75827.1      LLVSLDTLSEQAYFSLNDVSI----------DA--------PDARHEVEYDAVREFKTAA
QZX99028.1      LLIDLVDLAERGYLIDEEIDVDA---GGDGAGV--------DFSLHEVRYDAVESFKLDR
QZP38174.1      LLIDLVDLAERGYLDDEAAPDAG-------ESV--------DFSPHEVNYDAVESVKLDR
QZY03180.1      LLIDLVDLAERGYLEEDELAAEGDSTGEPDRDA--------DFSRHEVHYHAVESVKLDR
AUG48211.1      LLIDLRDLVDRGYLTADEVEP----------PG--------DFSQQQVNYDRVTEFTERR
AEM58055.1      LLIDLRDLVDRGYLTADEVDP----------PE--------DFSQQHVKYDRVTEFKERR
AHB66799.1      LLIDLRDLVDRGYLTADEVDP----------PE--------DFSQQHVKYDRVTEFKERR
AJF25101.1      LLIDLRDLVDRGYLTADEVDP----------PE--------DFSQQHVKYDRVTEFKERR
AAV46825.1      LLIDLRDLTDRGYLTEADTEP----------PD--------DFSGQQVNYDRVTEFKEAR
QCP91534.1      LLIDLRDLTDRGYLTEADTEP----------PD--------DFSGQQVNYDRVTEFKEAR
QUJ72368.1      LLIDLRDLTDRGYLTEADTEP----------PD--------DFSGQQVNYDRVTEFKEAR
UBZ54001.1      LLISLDDLVAEGYLTSEDLEP----------VP--------DFSPHEVVYDTVREYKHDC
CCC40696.1      LIISLDDLVADGYLTSEDLKP----------VP--------DFSPHEVAYDAVREYKHDR
CAJ52690.1      LIISLDDLVADGYLTNEDLVP----------VP--------DFSPHEVAYDAVREYKHDR
QCJ48434.1      LFVDLRDLLDRGLLTDGDLKP----------VP--------EFDPHETDYQRVSEYKRPL
AHZ21176.1      LLVDLTDLEARGWLTADDLEP----------VP--------DFDDHAVEYERVGNYKRSR
AFK19479.1      LLVDLTDLEARGWLTADDLEP----------VP--------DFDDHAVEYERVGNYKRSR
AFK19479.2      LLVDLTDLEARGWLTADDLEP----------VP--------DFDDHAVEYERVGNYKRSR
QCQ75940.1      LLVDLTDLEARGWLTADDLEP----------VP--------DFDDHAVEYERVGNYKRSR
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AKU07735.1      LLIDLTDLVERGWLTEDDLEP----------VP-------DFDPHAVDYERVGEYKRSR
QOS11852.1      LLIDLTDLVERGWLTDDDLEP----------VP-------DFDPHAVDYERVGEYKRSR
QIB78738.1      LLIDLTDLVARGWLTDADLEP----------VP-------DFDPHAVDYERVGEYKRSR
ADE05003.1      LLIDLTDLVARGWLTDADLEP----------VP-------DFDPLAVDYERVGEYKRSR
ADE05003.2      LLIDLTDLVARGWLTDADLEP----------VP-------DFDPLAVDYERVGEYKRSR
QCC48543.1      LLVSLDRLVEAGYLDAADLEP----------VP-------DFSEHEVDYRVREYKTDR
ADQ67101.1      LLVDLDQLREDGYLTDDDLEP----------VP-------AFSDHEIEYDRVAEYKREQ
QIQ76396.1      LLVDLDQLREDGYLTDDDLEP----------VP-------AFSEHEIEYDRVAEYKREQ
QIB74651.1      LLVDLDQLREDGYLTDDDLEP----------VP-------AFSEHEIEYDRVAEYKREQ
AIF04697.1      RFRDPAMHY-------------------------------RLDYE---------
AIF05955.1      RFRDPAMHY-------------------------------RLDYE---------
QEE14682.1      LLISPDGLIQMELITLEEVDQ----------CLKEIKIHDEPSKNLKVNYQNVIDLKEKI
ADL19304.1      IMVSPQLLANEGLLAADELAS----------LP-------RGEPNRVDYGLAYEHRMRL
AMD30778.1      LMVSPQLLAEEGLLTKEEVAS----------IP-------QGPRGRVDYPLAYQHRRRL
AKT33963.1      PLISLDKATRDGILTRAPPRC-------------------QPTDKADYEAAWQIKRRH
ABL88479.1      ALISLEKMAQDGLLVRSPPKC-------------------PSVERTSFAESWELKRRY
ACB39188.1      ALVSLEKMAQLGLAKRAPPSC-------------------PPAERARFAEAWELKRRY
AEA11843.1      AYISLELLAEQGVLRRSASAE-------------------FGAGRADYEAARAYKVKI
ABO08194.1      RLVSLDLMKRDGLIDQVPQC--------------------PPTPRADYQAAWEVKTKA
ABP49821.1      KLISLDLMKREGLIDQVPDC--------------------PPAERVDYAAAWEVKKKA
AFA40300.1      KLISLDLMKREGLIDQVPDC--------------------PTAERADYAAAWEVKKKA
AAL63326.1      VLISLELMKRDGLIDSVPQC--------------------PPAERADYIKAWEVKRKA
NP_559144.1     VLISLELMKRDGLIDSVPQC--------------------PPAERADYIKAWEVKRKA
AET33957.1      VLISLDLMKKDGLVDQAPQC--------------------PATERADYVKAWEVKRAV
ABD40312.1      LLISPEEMVNDGYLDPSDLQE----------GL-------EGPRDEVDYKAVIAYKERL
QXO95450.1      LLISPEMLVKDGYLDESDLEP----------LP-------DFSSDLVDFPAVIAYKNRL
QVV87979.1      LLISPEMLVKDGYLDESDLEP----------LP-------DFSSDLLDFAAVITYKNRL
CCJ37196.1      WLISPEQMVIDGLLGPEDIGD----------PP-------GFPEDRVDYRAVMDYKNNL
SAI88308.1      WLISPEQMVIDGLLAPEDIRD----------PP-------GFPEDRVDYRAVMDYKNSL
CVK34217.1      WLISPEQMVIDGLLAPEDIRD----------PP-------GFPEDRVDYRAVMDYKNSL
BBL68280.1      WLISPEQMVADGLLAPEDIAD----------PP-------GFPEDRVDYRAVLDYKNGL
ABN57193.1      WLISPEQMVADGFLAPEDIAD----------PP-------DFPADRVDYRAVLDYKNGL
SAI88240.1      LLISPDRLVRDGYLRRADLEP----------VP-------GFPEGRVAYEAATWYKDRL
CVK34142.1      LLISPDRLVRDGYLRRADLEP----------VP-------GFPEGRVAYEAVTWYKDRL
CCJ37132.1      LLISPDRLVRDGYLRRADLEP----------VP-------GFPEGRVAYEAVTWYKDRL
BBL68006.1      LLISPEMLIREGYLRKSELEP----------AP-------GFPDGRAAYEAAVWYHERL
ABN56987.1      LLISPEMLVREGYLRKSELEP----------AP-------GFPEERAAYEAAAWYRERL
                 .                                         :


AUV80673.1      LRRAHDGFEER------------------------------------------------A
QCC51341.1      LTEAFETFKAD------------------------------------------------A
QSG15659.1      LEDAFETFKTD------------------------------------------------A
QSG11910.1      LEEAFETFQEA------------------------------------------------A
QSG08987.1      LEEAFETFQEA------------------------------------------------A
QSG05483.1      LEAAFETFQEQ------------------------------------------------A
QGN07616.1      LRDAFAGFEAD------------------------------------------------A
QSG11921.1      LRDAFEGFSDV------------------------------------------------A
QSG08998.1      LRDAFEGFSDV------------------------------------------------A
QSG05496.1      LRDAFEGFSDV------------------------------------------------A
CCQ33055.1      LRNAFAGFEER------------------------------------------------A
QSG02731.1      LRTAFDRFDDD------------------------------------------------R
AUX09035.1      LREAHRNYRDR------------------------------------------------R
QFU81686.1      LRVAFETFERE------------------------------------------------Q
AWB27107.1      LEAAFEGFRDR------------------------------------------------A
QLC34969.1      LRTAFERFEQS------------------------------------------------A
ACV11232.1      LSAAFDGFEAS------------------------------------------------A
QPV62520.1      LRTAHETFAAK------------------------------------------------A
QLH84085.1      LRAAHDTFTAE------------------------------------------------A
QLH79093.1      LRTAYERFAAA------------------------------------------------A
QAU11732.1      LRTAFDRFEER------------------------------------------------A
QAY20111.1      LRTAFEQFEER------------------------------------------------A
QWC20591.1      LRTAFERFEER------------------------------------------------A
QUO46499.1      LRTAFERFEER------------------------------------------------A
QKG93724.1      LRTAFDRFEER------------------------------------------------A
QKY17977.1      LRTAFERFDEE------------------------------------------------A
ACM57093.1      LRTAFERFDEA------------------------------------------------E
AZQ14643.1      LRTAFERFDEA------------------------------------------------G
ATW89261.1      LRTAHEQFRET------------------------------------------------A
ABQ75827.1      LRTAAESFFDEFG----------------------------------------------
QZX99028.1      LRVAFERFREV------------------------------------------------A
QZP38174.1      LRTAFDRFREV------------------------------------------------A
QZY03180.1      LRTAFERFREV------------------------------------------------A
AUG48211.1      LRTAYENFDES------------------------------------------------A
AEM58055.1      LRTAYERFDES------------------------------------------------A
AHB66799.1      LRTAYERFDES------------------------------------------------A
AJF25101.1      LRTAYERFDES------------------------------------------------A
AAV46825.1      LRDAYAAFEES------------------------------------------------A
QCP91534.1      LRDAYAAFEES------------------------------------------------A
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QUJ72368.1      LRDAYAAFEES------------------------------------------------A
UBZ54001.1      LQIAAERFRESIGGIAIHPHPHPDPDTTVNSGVDGDTVPEVTVTLGESVNLSQDTPADSQ
CCC40696.1      LRIAAKRFQESVGGINIHA----DTDTTASSGVNDDIAVDVTVTLGDSVDPSQNISTHNQ
CAJ52690.1      LRIAAKRLQESVGGINIHA----DTDTTASSGVNDDIAVDVTVTLGDSVDPSQNISTHNQ
QCJ48434.1      LETAFERFESE------------------------------------------------G
AHZ21176.1      LRTAFDRFEED------------------------------------------------A
AFK19479.1      LRTAFDRFEED------------------------------------------------A
AFK19479.2      LRTAFDRFEED------------------------------------------------A
QCQ75940.1      LRTAFDRFEED------------------------------------------------A
AKU07735.1      LRTAFDRFEAE------------------------------------------------A
QOS11852.1      LRTAFDRFEAE------------------------------------------------A
QIB78738.1      LRAAFDRFEAE------------------------------------------------A
ADE05003.1      LRAAFDRFEAE------------------------------------------------A
ADE05003.2      LRAAFDRFEAE------------------------------------------------A
QCC48543.1      LRTAAERFRSADGDDGSA------------------------------------RASGSA
ADQ67101.1      LRTAHERFQSE------------------------------------------------A
QIQ76396.1      LRTAHERFQSE------------------------------------------------A
QIB74651.1      LRTAHERFQSE------------------------------------------------A
AIF04697.1      ------------------------------------------------------------
AIF05955.1      ------------------------------------------------------------
QEE14682.1      LKIAFKTFLQKQF---------------------------------------------QQ
ADL19304.1      LRLAFSRFKPS-------------------------------------------------
AMD30778.1      LELALSRFKPT-------------------------------------------------
AKT33963.1      LEEAFEKRRGW-------------------------------------------------
ABL88479.1      VEEAFETKLGW-------------------------------------------------
ACB39188.1      LEEAFEGRLGW-------------------------------------------------
AEA11843.1      I----AEAERP-------------------------------------------------
ABO08194.1      LEKAYKRHRRL-------------------------------------------------
ABP49821.1      LEKALRRGKKL-------------------------------------------------
AFA40300.1      LEKALRRGKKL-------------------------------------------------
AAL63326.1      LEKALKRAGRL-------------------------------------------------
NP_559144.1     LEKALKRAGRL-------------------------------------------------
AET33957.1      LEKALKKARAL-------------------------------------------------
ABD40312.1      FDMAYNRFAYF-------------------------------------------------
QXO95450.1      FDMAYNRFVFF-------------------------------------------------
QVV87979.1      FDMAYNRFVFF-------------------------------------------------
CCJ37196.1      FDRAFERFRER-------------------------------------------------
SAI88308.1      FDRAFERFRER-------------------------------------------------
CVK34217.1      FDRAFERFRER-------------------------------------------------
BBL68280.1      YDKAFERFKQQ-------------------------------------------------
ABN57193.1      FDTAFERFKGR-------------------------------------------------
SAI88240.1      FSIAYQRFLHS-------------------------------------------------
CVK34142.1      FSIAYQRFLHS-------------------------------------------------
CCJ37132.1      FSIAYQRFLHS-------------------------------------------------
BBL68006.1      FAAAYERFRYS-------------------------------------------------
ABN56987.1      FAAAYERFRHS-------------------------------------------------


AUV80673.1      TAVERKAFTTFRE-SNDWLDDYALFRALKRDHDSAAWTEWPRGERDRDPDALGAARGRLS
QCC51341.1      SDDEQSNFETFVEESGEWLDEYALYRALRDHYDGVSWLDWPEEAKMRDPDALAEYREELA
QSG15659.1      SDDDRADFEAFTDDAGDWLDEYALYRALRTHFDGVSWLDWPEGAKMRDPEVLAEYREELS
QSG11910.1      SDDERAAFEQFKDDAGEWLEEYALYRALRTHFDGVSWLDWPEKAKMRDPDALEQYREQLA
QSG08987.1      SDDERAAFEQFKDDAGEWLEEYALYRALRTHFDGVSWLDWPEEAKMRDPDALERYREELA
QSG05483.1      GDDERAAFEQFKDDAGEWLDEYALYRALRTHFGGVSWLDWPEEAKTRDPDALEQYREQLA
QGN07616.1      EPAAKTDFETYCGEAGDWLEEYALFRALNDHFDG-EWVEWPAEAKHRDPDALDRYREELA
QSG11921.1      DPDDLTAFESFCEENAEWLDDYALFRALDDHFDADTWLDWPDGAKFRDPDALERYREQLA
QSG08998.1      DPDDLTAFESFCEENAEWLDDYALFRALDDHFDADTWLDWPDGAKFRDPDALERYREQLA
QSG05496.1      DADDWAAFESFCEENAEWLDDYALFRALDDHFDADTWLDWPDGAKFRDPDALERYREQLA
CCQ33055.1      DEDARAAFETFRTENAEWLDDYALFRALDAHFEADTWMDWPDDAKFRDPETLDRYREELA
QSG02731.1      PDELWGAFERFRE-ETDWLHNYALFRALKREFDGESWTNWPEPVALREPDALDEYREELA
AUX09035.1      PTDLVESIEAFES-RAEWLDDYALYRALKRRFDERSWTDWPEEFRLREPDALERAREELA
QFU81686.1      PPDLVDGLEQFRA-ESTWLEEYAHFAALKADFDRQAWLDWPEPIRLRDPDALERSCEQRA
AWB27107.1      TDEERATFEAFREREAGWLADYSLFVTLRERFDGQPWADWPAEFASRDPDAIETIRTERA
QLC34969.1      DAGESDAFAAFRERERDWLADYALYRALKRVHGGESWTEWPRELRERDPDALAAAREEHA
ACV11232.1      EADDRAAFEAFREREATWLRDYTLFTALKAAYDGVPWPEWPADLAGRDPPALEAARETHA
QPV62520.1      SGEERAAFESFRERESAWLEDYALYAALKGAHGDAAWTDWPADLVRREADALSAARETHA
QLH84085.1      SEEERAAFEAFREREAAWLADYALYAALKDAHGDAAWTDWPADLARRDADALAAARETHA
QLH79093.1      SEDERADFAAFRERESAWLADYALYAALSEAHGGAAWTDWPVDLARRDADALAAARENHA
QAU11732.1      TEEDRAALDAFVDDE-PWLADYALFRAVSDARPEDVWTEWPAPLRTRDPEALSGAREDHA
QAY20111.1      TKEDRAALGAFRERE-PWLADYALFRALSDARPEDVWTEWPAPLRTRDPDALAEAREEHA
QWC20591.1      TDADRAAVDEFRERE-PWLPDYALFRALSDARPEDVWTEWPEPLRTRDPEALASAREEHA
QUO46499.1      SEDDRAAVAEFREHE-PWLADYALFRALSDARPEDVWTDWPAPLRTRDPEALADAREEHA
QKG93724.1      TEADRAALDEFRERE-PWLADYALFRALSDARPEDVWTDWPAPLRTRDPEALAEARDEHA
QKY17977.1      GEEAEADLDAFRERE-PWLADYALFRALSEARDEDTWVEWPEPLRTRDPEALAEARERHA
ACM57093.1      AGKAHSEFDAFRERE-PWLDDYALFRAMSGERDDDTWVEWPDPLRTREPEALDEARERHA
AZQ14643.1      AGDAAPDFDAFCERE-SWLDDYALFRALSAERDEATWVDWPDPLRTREPDALADARERHA
ATW89261.1      TDDDYAALDEFRD-EESWVDDYALFRALKQKHDGVAWVDWPEPIRTRDPDALSEAREELS
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QZX99028.1      SDDDRASFAEFRDREADWLADYALFRALKAEFDETLWTEWPEPARTRDPDALAAYREDLA
QZP38174.1      SDDERETFAAFREREADWLADYALFRALKREFDGTLWTEWPEPVRTRDPDALADYRDELA
QZY03180.1      SDGEREAFAAFREREGDWLADYALFRALKREFDGTLWTEWPEPVRTRDPDALADYRDELA
AUG48211.1      AEADRNAFAEFCEREAGWVDDYALFTALKTEFDDAGWMDWPDDIRTREPAAMERYQEELA
AEM58055.1      SDADQQSFAEFCEREAGWLDDYALFTALKAEFDDAGWMDWPDDIRTREPAAVERYRDELA
AHB66799.1      SDADQQSFAEFCEREAGWLDDYALFTALKAEFDDAGWMDWPDDIRTREPAAVERYRDELA
AJF25101.1      SDADQQSFAEFCEREAGWLDDYALFTALKAEFDDAGWMDWPDDIRTREPAAVERYRDELA
AAV46825.1      SDADQQSFTKFCEREAGWLDDYALFTALKAEFDDAGWMDWPDDIRTREPAAMERYQDDLA
QCP91534.1      SDADQQSFTKFCEREAGWLDDYALFTALKAEFDDAGWMDWPDDIRTREPAAMERYQDDLA
QUJ72368.1      SDADQQSFTEFCEREAGWLDDYALFTALKAEFDDAGWMDWSDDIRTREPAAMERYQDDLA
UBZ54001.1      IEKDAREFKSFYQRENHWLTDYALFMALRTSYD-GAWTDWPEPIRNRDPDALRDQYESLE
CCC40696.1      TSIDATAFKPFYHRESHWLTDYALFMALRTSYD-GAWTDWPESIRHRDPDALSDQYESLD
CAJ52690.1      TSIDATAFKSFYRRESHWLTDYALFMALRTSYD-GAWTDWPESIQHRDPDALSDQYESLD
QCJ48434.1      SDDEREAFEAFRERESSWLDDYTLFISLKEAHDHVAWTDWPEGLKTREPDALEQARDDLE
AHZ21176.1      SEDDRDAFEAFREREAHWLEDYALFASLKDEFE-GAWIDWPTELKTRDPDALARARDEHE
AFK19479.1      SEDDRDAFEAFREREAHWLEDYALFASLKDEFE-GAWIDWPTELKTRDPDALARARDEHE
AFK19479.2      SEDDRDAFEAFREREAHWLEDYALFASLKDEFE-GAWIDWPTELKTRDPDALARARDEHE
QCQ75940.1      SEDDRDAFEAFREREAHWLEDYALFASLKDEFE-GAWIDWPTELKTRDPDALARARDEHE
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QOS11852.1      AEDDRAALDAFREREAGWLEDYALFAALKDEFR-RAWIDWPTELKTRDPDALADAREEYA
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ADE05003.1      TEDDRAALDAFREREAGWLEDYALFAALKDEFR-RAWIDWPTELKTRDPDALADARAEYA
ADE05003.2      TEDDRAALDAFREREAGWLEDYALFAALKDEFR-RAWIDWPTELKTRDPDALADARAEYA
QCC48543.1      TEADREAFEAFRERESGWLDDYALFMALRTRYD-GAWTSWPEPIRARDPDALDAHREELA
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QIQ76396.1      TTEDREAFDAFCERESSWLDGYALFMALRTRYD-GAWTTWPQEIRTHDEAAINRHREELA
QIB74651.1      TTEDREAFDAFCERESSWLDGYALFMALRTRYD-GAWTTWPQEIRTHDEAAINRHREELA
AIF04697.1      ------SVEKWIEKNLHWLEDYALFAVLKYQLDGLPWTQWPAPLRDRDPEAIKEVIDELY
AIF05955.1      ------SVEKWIEKNLHWLEDYALFAVLKYQLDGLPWTQWPAPLRDRDPEAIKEVIDELY
QEE14682.1      NSKLNDSFVKFCEEQAYWLDDFVLFYSLKVANNLQSWITWPKNFALRHKNALKVWIAGHS
ADL19304.1      --G---DYDRFLDRNSWWLEDYALYVSLREHFKGSDWSSWPEGLRRRDRGEMQAWREKLK
AMD30778.1      --G---DYDRFVDSNSWWLSDYALYASLREHFNGSDWGSWPEGLRRRDRKELEAWGQKLK
AKT33963.1      --G---EFEEFAARNSWWLEPYGVYMALREAY-SAPWTRWPKEL-REGV----DLPEELR
ABL88479.1      --R---DYEEFIAENSWWLESYGRYMALRETF-RVPWIQWPEWARRLNT----PLPPKLA
ACB39188.1      --R---DYEEFAARNSWWLEPYGRYMALREAF-GGPWTAWPAWARRPNA----DLPPRLE
AEA11843.1      --K---DLDEFVG-RNEWLEDYALYSALREYF-GRPWVEWPRELRDRDPAALRQWREKLR
ABO08194.1      --K---DFTAFMEEEWEWLGEYATYMALRERH-G-PHP--PRGNAP------------R
ABP49821.1      --S---DYKNFVE-STPWLEDYAYYMAMRDLY-G-PWPKWPRRDPP------------G
AFA40300.1      --S---DYKNFAE-STPWLEDYAYYMAMRDLY-G-PWPKWPRKEPP------------G
AAL63326.1      --S---DYRHFKD-VTPWLDDYAYYMAMRERF-G-PWPVWPKEEPP------------P
NP_559144.1     --S---DYRHFKD-VTPWLDDYAYYMAMRERF-G-PWPVWPKEEPP------------P
AET33957.1      --S---DYRNFVD-KTPWLEDYAYYMAMRERH-G-PWGRWPDEAPP------------R
ABD40312.1      --GSDPRFIDFCSEQAWWLDDYALFTAIRKYYAPAVWSDWPHPLKERDPQALHEFQEKNN
QXO95450.1      --GTDPAFLTFCEEQAWWLDDYALFAIKKHYPDILWSDWPSGLRNHNENELHEFKKLYH
QVV87979.1      --GTDPAFLTFCEEQAWWLDDYALFSAIKKHYPDILWSDWPSGLRNHNENELHEFKKLYH
CCJ37196.1      --GPDFRYKEFAAGNVSWLDDYAIFVALRERFEGKVWGDWPPDIRDRHQDALHAYGTELA
SAI88308.1      --GPDFRYKEFAAGNVSWLDDYAIFVALRERFEGKVWGDWPPNIRDRHQDALHAYGTELE
CVK34217.1      --GPDFRYKEFAAGNVSWLDDYAIFVALRERFEGKVWGDWPPNIRDRHQDALHAYGTELE
BBL68280.1      --GCDFRYEDFAAGNTSWLNDYAIFVALKGEFPGKAWSDWPTGIRDRREEALRKRGTELA
ABN57193.1      --DSDFRYEDFAADNTSWLNDYAIFMALRERFSGKVWGDWPAGIRDRHDEALRKYGTELA
SAI88240.1      --GPERGYEEFCDENAWWLEDHALFVALKDHFHRQEWSRWPEEVRARQSEALDDLQRRLA
CVK34142.1      --GPERGYEEFCDRNAWWLEDHALFVALKDHFGLEWSRWPEEVRARQSEALDDLQRRLA
CCJ37132.1      --GPERGYEEFCDENAWWLEDHALFVALKDHFHGQEWSRWPEEVRARQSEALDDLQRRLA
BBL68006.1      --GPDRRFEAFCDGAGWWLDDHALFVALKDHFRGQAWTRWPDEIRAREPEALKEMRELLD
ABN56987.1      --GPDRRFETFCDGTGWWLDDHALFVALKGHFRGQAWNRWPEDIRARETGALKEMRELLD
                      :        *:   .  :    :

AUV80673.1      GEIAFREFCQFCFDQQWSALRSYATQHDVSLVGDVPIYVAGDSADVWANRDVFQLDEEGQ
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QZX99028.1      SDDDRASFAEFRDREADWLADYALFRALKAEFDETLWTEWPEPARTRDPDALAAYREDLA
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QZY03180.1      SDGEREAFAAFREREGDWLADYALFRALKREFDGTLWTEWPEPVRTRDPDALADYRDELA
AUG48211.1      AEADRNAFAEFCEREAGWVDDYALFTALKTEFDDAGWMDWPDDIRTREPAAMERYQEELA
AEM58055.1      SDADQQSFAEFCEREAGWLDDYALFTALKAEFDDAGWMDWPDDIRTREPAAVERYRDELA
AHB66799.1      SDADQQSFAEFCEREAGWLDDYALFTALKAEFDDAGWMDWPDDIRTREPAAVERYRDELA
AJF25101.1      SDADQQSFAEFCEREAGWLDDYALFTALKAEFDDAGWMDWPDDIRTREPAAVERYRDELA
AAV46825.1      SDADQQSFTKFCEREAGWLDDYALFTALKAEFDDAGWMDWPDDIRTREPAAMERYQDDLA
QCP91534.1      SDADQQSFTKFCEREAGWLDDYALFTALKAEFDDAGWMDWPDDIRTREPAAMERYQDDLA
QUJ72368.1      SDADQQSFTEFCEREAGWLDDYALFTALKAEFDDAGWMDWSDDIRTREPAAMERYQDDLA
UBZ54001.1      IEKDAREFKSFYQRENHWLTDYALFMALRTSYD-GAWTDWPEPIRNRDPDALRDQYESLE
CCC40696.1      TSIDATAFKPFYHRESHWLTDYALFMALRTSYD-GAWTDWPESIRHRDPDALSDQYESLD
CAJ52690.1      TSIDATAFKSFYRRESHWLTDYALFMALRTSYD-GAWTDWPESIQHRDPDALSDQYESLD
QCJ48434.1      SDDEREAFEAFRERESSWLDDYTLFISLKEAHDHVAWTDWPEGLKTREPDALEQARDDLE
AHZ21176.1      SEDDRDAFEAFREREAHWLEDYALFASLKDEFE-GAWIDWPTELKTRDPDALARARDEHE
AFK19479.1      SEDDRDAFEAFREREAHWLEDYALFASLKDEFE-GAWIDWPTELKTRDPDALARARDEHE
AFK19479.2      SEDDRDAFEAFREREAHWLEDYALFASLKDEFE-GAWIDWPTELKTRDPDALARARDEHE
QCQ75940.1      SEDDRDAFEAFREREAHWLEDYALFASLKDEFE-GAWIDWPTELKTRDPDALARARDEHE
AKU07735.1      AEDDRAALDAFREREAGWLEDYALFAALKDEFR-RAWIDWPTELKTRDPDALADAREEYA
QOS11852.1      AEDDRAALDAFREREAGWLEDYALFAALKDEFR-RAWIDWPTELKTRDPDALADAREEYA
QIB78738.1      TEDARAALDAFREREAGWLDDYALFAALKDEFR-RAWIDWPTELKTRDPDALADARAEYA
ADE05003.1      TEDDRAALDAFREREAGWLEDYALFAALKDEFR-RAWIDWPTELKTRDPDALADARAEYA
ADE05003.2      TEDDRAALDAFREREAGWLEDYALFAALKDEFR-RAWIDWPTELKTRDPDALADARAEYA
QCC48543.1      TEADREAFEAFRERESGWLDDYALFMALRTRYD-GAWTSWPEPIRARDPDALDAHREELA
ADQ67101.1      TTEDREAFDAFREHESSWLDGYALFMALRTRYD-GAWTTWPQEIRTHDEAAINRHREELA
QIQ76396.1      TTEDREAFDAFCERESSWLDGYALFMALRTRYD-GAWTTWPQEIRTHDEAAINRHREELA
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AIF05955.1      ------SVEKWIEKNLHWLEDYALFAVLKYQLDGLPWTQWPAPLRDRDPEAIKEVIDELY
QEE14682.1      NSKLNDSFVKFCEEQAYWLDDFVLFYSLKVANNLQSWITWPKNFALRHKNALKVWIAGHS
ADL19304.1      --G---DYDRFLDRNSWWLEDYALYVSLREHFKGSDWSSWPEGLRRRDRGEMQAWREKLK
AMD30778.1      --G---DYDRFVDSNSWWLSDYALYASLREHFNGSDWGSWPEGLRRRDRKELEAWGQKLK
AKT33963.1      --G---EFEEFAARNSWWLEPYGVYMALREAY-SAPWTRWPKEL-REGV----DLPEELR
ABL88479.1      --R---DYEEFIAENSWWLESYGRYMALRETF-RVPWIQWPEWARRLNT----PLPPKLA
ACB39188.1      --R---DYEEFAARNSWWLEPYGRYMALREAF-GGPWTAWPAWARRPNA----DLPPRLE
AEA11843.1      --K---DLDEFVG-RNEWLEDYALYSALREYF-GRPWVEWPRELRDRDPAALRQWREKLR
ABO08194.1      --K---DFTAFMEEEWEWLGEYATYMALRERH-G-PHP--PRGNAP------------R
ABP49821.1      --S---DYKNFVE-STPWLEDYAYYMAMRDLY-G-PWPKWPRRDPP------------G
AFA40300.1      --S---DYKNFAE-STPWLEDYAYYMAMRDLY-G-PWPKWPRKEPP------------G
AAL63326.1      --S---DYRHFKD-VTPWLDDYAYYMAMRERF-G-PWPVWPKEEPP------------P
NP_559144.1     --S---DYRHFKD-VTPWLDDYAYYMAMRERF-G-PWPVWPKEEPP------------P
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QVV87979.1      --GTDPAFLTFCEEQAWWLDDYALFSAIKKHYPDILWSDWPSGLRNHNENELHEFKKLYH
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SAI88308.1      --GPDFRYKEFAAGNVSWLDDYAIFVALRERFEGKVWGDWPPNIRDRHQDALHAYGTELE
CVK34217.1      --GPDFRYKEFAAGNVSWLDDYAIFVALRERFEGKVWGDWPPNIRDRHQDALHAYGTELE
BBL68280.1      --GCDFRYEDFAAGNTSWLNDYAIFVALKGEFPGKAWSDWPTGIRDRREEALRKRGTELA
ABN57193.1      --DSDFRYEDFAADNTSWLNDYAIFMALRERFSGKVWGDWPAGIRDRHDEALRKYGTELA
SAI88240.1      --GPERGYEEFCDENAWWLEDHALFVALKDHFHRQEWSRWPEEVRARQSEALDDLQRRLA
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CCJ37132.1      --GPERGYEEFCDENAWWLEDHALFVALKDHFHGQEWSRWPEEVRARQSEALDDLQRRLA
BBL68006.1      --GPDRRFEAFCDGAGWWLDDHALFVALKDHFRGQAWTRWPDEIRAREPEALKEMRELLD
ABN56987.1      --GPDRRFETFCDGTGWWLDDHALFVALKGHFRGQAWNRWPEDIRARETGALKEMRELLD
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AUV80673.1      GEIAFREFCQFCFDQQWSALRSYATQHDVSLVGDVPIYVAGDSADVWANRDVFQLDEEGQ
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QSG15659.1      ETIEYRKFLQWLFDEQWSELKAYANERGVDLVGDMPIYVDLDSADVWANPEIFKLDEQRE
QSG11910.1      ETIEYRQFLQWLFDQQWSALKEYANERGVKLVGDVPIYVDLDSADVWANPEIFKLDEQRE
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QSG05483.1      ETVEYRQFLQWLFDQQWSALKDYANERGVKLVGDVPIYVDLDSADVWANPEIFKLDEQRE
QGN07616.1      EEIRFRKFLQWVFETQWQALRSYADDRGVSLVGDMPIYVGTNSADVWANPELFKLDEDLE
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QSG08998.1      RDVRFRQFLQWVFDRQWAELREHAHEHGIELVGDMAIYVGTNSADVWANPEIFKLDEERE
QSG05496.1      RDVRFRQFLQWVFDRQWAELREHAHEHGVELVGDMAIYVGTNSADVWANPEIFKLDEERE
CCQ33055.1      EDVRFRQFCQWRFERQWADLRAYAHERGIDLVGDMPIYVGANSVDVWANPEIFKLDDDRE
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AUX09035.1      NEISYRVFLQAVAHDQWYRLHEYATDRGIDVVGDVPIYVALDSADVWANRELFELDADGE
QFU81686.1      SDIRYHAFVQYLAAEQWTELRDHAAAHGVEIVGDLPIYVALDSADVWANPDIFELEDHGT
AWB27107.1      DRIAYHAFVQWIFDEQWQRFRAAAADRGIDLIGDLPIYVAWDSADVWAHREAFDLRADGH
QLC34969.1      DEVRYHAFVQWRFDEQWRALREASERDIRLLGDVPMYAALDSADVWANREAFAVDTAGN
ACV11232.1      EAIRYHAFVQWLFDEQWRALRAAADERGISLVGDLPIYVAWDSADVWANPEAFELDDEGG
QPV62520.1      EAVDYHAFVQWVFDTQWRELRAAAAERGIELVGDLPIYVALDSADVWANQEAFRLDDDGR
QLH84085.1      EAVDYHAFVQWVFDAQWRELRAEAAERGVELVGDLPIYVALDSADVWADQDAFQLDEGGD
QLH79093.1      EAVEYHAFVQWVFDAQWRELRAAAADRGVELVGDLPIYVALDSADVWADQDAFQLDDDGR
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QAY20111.1      AEVRFRAFVQWTFDRQWHELRAVAADEGVSIVGDVPIYVALDSADVWASPEAFRLDEGNR
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QUO46499.1      REVRFREFVQWTFDRQWRDLRAVAAEEGVSIVGDVPIYVALDSADVWASPEAFRLDEGNR
QKG93724.1      REIRFREFVQWTFDRQWRDLRAVAAEEGVSIVGDVPIYVALDSADVWASPEAFRLDEGNR
QKY17977.1      TEVRFREFVQWTFDRQWRDMRAVAAEEGVSIVGDVPIYVALDSADVWANPEAFRLDESNR
ACM57093.1      TEVRFGEFLQWMFDRQWRDLRAVAADEGVSIVGDVPIYVALDSADVWANPEAFRLDEGNR
AZQ14643.1      GEIRFREFVQWVFDRQWRELRSVADDEGVSIVGDVPIYVALDSADVWANPEAFRLDEGNR
ATW89261.1      EEIEYQTLIQYWFDKQWQAFKADAEEKGIKLVGDVPIYVGLDSADVWSSPEAFQLDDQNR
ABQ75827.1      SDIAYRKFVQFVFDRQWRELHQKATDAGVTLVGDLPIYVALDSADVWADPEAFELNDAHQ
QZX99028.1      DEIEFRAFCQWTFDRQWRDLRAAAADRGIEILGDLPIYVALDSADVWAAPAAFDLTDDGR
QZP38174.1      DEVDFRAFCQWTFDRQWRDLRADAADRGVEILGDLPIYVALDSADVWAAPEAFDLDDDGR
QZY03180.1      DAVDFRAFCQWTFDRQWRDLRADAADRGVEILGDLPIYVALDSADVWAAPEAFDLDDDGR
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AEM58055.1      DDIRYHKFVQWCFDSQWQALAEYAAERDIGLVGDLPIYVGLDSADVWAYPEVFRLDDDHH
AHB66799.1      DDIRYHKFVQWCFDSQWQALAEYAAERDIGLVGDLPIYVGLDSADVWAYPEVFRLDDDHH
AJF25101.1      DDIRYHKFVQWCFDSQWQALAEYAAERDIGLVGDLPIYVGLDSADVWAYPEVFRLDDDHH
AAV46825.1      DDIRYHKFVQWCFDSQWQALADYAAERDIGLVGDLPIYVGLDSADVWAYPEVFRLDDDHH
QCP91534.1      DDIRYHKFVQWCFDSQWQALADYAAERDIGLVGDLPIYVGLDSADVWAYPEVFRLDDDHH
QUJ72368.1      DDIRYHKFVQWCFDSQWQALADYAAERDIGLVGDLPIYVGLDSADVWAYPEVFRLDDDHH
UBZ54001.1      SDVLYHLIVQFIFDQQWQSLQTVAANRGVTLVGDLPIYVALDSADVWATPEIFQLTDTNE
CCC40696.1      SEVIYHLIIQFIFDQQWQSLQAAATDRDITLVGDLPIYVALDSADVWATPDVFQLTKDNE
CAJ52690.1      SEVIYHLIIQFIFDQQWQSLQAAATDRDITLVGDLPIYVALDSADVWATPDVFQLTKDNE
QCJ48434.1      AERRYHAFCQYLFDEQWRDLKSYASDRGISLVGDLPIYVALDSADVWASPEAFDLDENNE
AHZ21176.1      DEIRYREFVQFCFDEQWRDLAAYADEKSVTLVGDLPIYVALDSADVWAAPEAFDLTESHE
AFK19479.1      DEIRYREFVQFCFDEQWRDLAAYADEKSVTLVGDLPIYVALDSADVWAAPEAFDLTESHE
AFK19479.2      DEIRYREFVQFCFDEQWRDLAAYADEKSVTLVGDLPIYVALDSADVWAAPEAFDLTESHE
QCQ75940.1      DEIRYREFVQFCFDEQWRDLAAYADEKSVTLVGDLPIYVALDSADVWAAPEAFDLTESHE
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ADE05003.2      DEIRYREFVQFCFDEQWRALADYADEKGITLVGDLPIYVALDSADVWAAPEAFDLTESNE
QCC48543.1      PEVHYREFVQFVFDRQWRDLREYAHERGVDLVGDLPIYVALDSADVWASPEAFDLTPDRE
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QIQ76396.1      DEVSYRKFAQFVFDTQWRELKAYANDHGVKLVGDLPIYVALDSADVWAAPEAFDLTEENE
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AIF04697.1      GSMGKWMEEQFIIKIDWSQLRNTAEECGVSLFGDLPFFVAHDSADVWANQHLFKLEASGA
AIF05955.1      GSMGKWMEEQFIIKIDWSQLRNTAEECGVSLFGDLPFFVAHDSADVWANQHLFKLEASGA
QEE14682.1      RELKLYKFIQWIFSIQWTNLRDFAHKNNVEIIGDMPIFVAHDSVDVWANSDLFTLNPDGT
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AMD30778.1      SRVELELFTQYEFFSQWSRLRAHARRLGIRIIGDIPIYVSYDSADAWANPRIFKLNRDLR
AKT33963.1      RRAQFYQYVQYVFWSQWLELRRHVNNLGIFIIGDLPIYPAHDSADVWDGRRYFKLAPDGA
ABL88479.1      KLAEFYKYVQYVFWRQWDDLKRYVNSLGIFIIGDLPIYPALDSADVWEGRRYFKLAPDGT
ACB39188.1      RRADFYRYVQFHFWLQWEELKRYVNSLGIFIIGDLPIYPALDSADVWEGQRYFKLAPDGA
AEA11843.1      RRIELEYLLQYFFWTQWRELKRHANSLGIFLIGDLPIYLSLDSADVWAHRELFKLDAEGR
ABO08194.1      DRVEFYAFAQFVFWTQWRRLKEYVNSLGIFLIGDLPYYPGPDSADVWAHPRLFKVGQDGR
ABP49821.1      ELVELYKFAQFVFWRQWRELKQYVNSLGIFLIGDLPIYPSLDSADVWRHRRYFKITEDGA
AFA40300.1      ELVELYKFAQFVFWRQWRELKQYVNSLGIFLIGDLPIYPSLDSADVWRHRRYFKITEDGA
AAL63326.1      ASLELYKFAQFVFWTQWERFKEYVNSLGIFLIGDLPFYPSLDSVDVWRNKKYFKVGEDGR
NP_559144.1     ASLELYKFAQFVFWTQWERFKEYVNSLGIFLIGDLPFYPSLDSVDVWRNKKYFKVGEDGR
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QXO95450.1      SVIEREQFLQFIFFHQWAALRKRSHELGIWLIGDIPIYVDYDSSDAWTHQHLFQLNEDKK
QVV87979.1      SVIEREQFLQFIFFHQWAALRKRSHELGIWLIGDIPIYVDYDSSDAWTHQHLFQLNEDKK
CCJ37196.1      DRILREKFLQYVFDRQWKTLKNHCRSRHLQVIGDLPVYLTYDSVDLWANPDLFKLDEQKK
SAI88308.1      DRILREKFLQYVFDRQWKTLKNHCRSRHLQVIGDLPVYLTYDSVDIWANPDLFKLDEQKK
CVK34217.1      DRILREKFLQYVFDRQWKTLKNHCRSRHLQVIGDLPVYLTYDSVDIWANPDLFKLDEQKK
BBL68280.1      DRILREKFLQYVFDRQWQALKVHCRARHLQIIGDVPIYVTYDSVDLWANPGLFKLDEQKK
ABN57193.1      DRIFREKFLQYVFDRQWETLKKHCRMRHLQVIGDIPFYLTYDSVDLWANPRLFKLDEQKK
SAI88240.1      DGVRKEKFLQYLAARQWSALHRHCTDLGIQVIGDIPIYVAYDSVDVWQNPGIFKLDEDLR
CVK34142.1      DVVRKEKFLQYLAARQWSALHRHCTDLGVQVIGDIPIYVAYDSVDVWQNPGIFKLDEDLR
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ABN56987.1      DRIRKEKFLQYIAARQWSALRRYCTERGIQVIGDIPIYVAYDSVDVWAHPGIFKLDEDLR
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AUV80673.1      PTAVAGVPDAPDEVFSAQRWGMPLFDWEALERTGFAWWRSRLERLFAQCDIVRIDHFRGL
QCC51341.1      PKYVSGVPPDE-FSDDGQMWGTPVYDWDALDERDYGWWVKRFERLLQRVDIFRIDHFKGF
QSG15659.1      PKYVSGVPPDE-FSDDGQMWGTPVYDWAALAERDYGWWVSRFERLLQRVDIFRIDHFKGF
QSG11910.1      PEYVSGVPPDE-FSDDGQMWGTPVYDWAALAERDYGWWVSRFERLLQRVDIFRIDHFKAF
QSG08987.1      PEYVSGVPPDE-FSDDGQMWGTPVYDWAALAERDYGWWVSRFERLLQRVDIFRIDHFKAF
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QGN07616.1      PAYVAGVPPDE-FSETGQLWGMPVYDWAAHAEDEYEWWLQRFEGLLDRFDVFRIDHFKGF
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AUX09035.1      PAVVAGVPPGD--DDDGQKWGNPVYDWDALAATGYEWWVDRMAWTLDLVDLVRLDHFRGF
QFU81686.1      PAVVSGVPPGGGGETDGQKWGNPVYDWDRLAETSYEWWVDRFERLFELVDIARLDHFLAF
AWB27107.1      PAAVAGVPPNP--GDDGQRWGMPVYDWDALA-PEYDWWVARLDRLLALVDRVRIDHFKAF
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QPV62520.1      PTAVAGVPPNP--GDDGQRWGNPVYDWGRLRETDYEWWRDRLSRLLDLVDLARIDHFKAF
QLH84085.1      PTAVAGVPPNP--GDDGQRWGNPVYDWDRLRETDYEWWRRRLSRLLDLVDLARIDHFKAF
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QIB74651.1      PVAVAGVPPNP--NDDGQRWGNPLYDWDYLRENDYDWWMDRLARLFELVDVTRIDHFKGF
AIF04697.1      PSVVAGVPPDY-FSEDGQKWGTVLYNWDAHRDEDFAWWKARTARMFEMFDLVRIDHFRAL
AIF05955.1      PSVVAGVPPDY-FSEDGQKWGTVLYNWDAHRDEDFAWWKARTARMFEMFDLVRIDHFRAL
QEE14682.1      LEYQAGVPPDY-FSKTGQLWGNPLYKWEILQERNFKWFIQRFKRQIELFDWIRVDHFRGF
ADL19304.1      PTYVSGVPPDY-FSRTGQLWNTPVYDWESLRRERYSWWIRRFAHASELFDAVRLDHFRGF
AMD30778.1      PAFVSGVPPDY-FSRTGQLWNTPVYDWEELRRERYSWWVKRMAHASRLFDAVRLDHFRGF
AKT33963.1      PLYVSGVPPDY-FSPTGQLWGTPVYDWDAVRRDRYAWWARRLRRMLEAFDYIRLDHFRGY
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AET33957.1      PLYVAGVPPDY-YSATGQLWGNPVYNWEALERDGYRWWVERLRHMLEVFDYVRLDHFRGY
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QVV87979.1      PLYVAGVPPDY-FSATGQVWNNPIYDWDEMKKTGFSWWVKRMEHELKFVDYVRIDHFRGL
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                 .***         .* *.  ::.*          : *:  *         *  *:*** .


AUV80673.1      ERYWAIPADESDPNVGEWRDVPSEAFFDALSRE----FGDLSARAFAEDIGHPTDAVDDL
QCC51341.1      ESYWEIPADAETAREGEWVEGPHEDVFYAIRDE----LGDLP--IVVEDLGEITPKMEEI
QSG15659.1      ESYWEIPADADTAREGEWVDGPHEDIFYAVRDE----LGELP--IVVEDLGEITDEMDRI
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AUX09035.1      ESFWAVPVDAPA-REGEWRPGPGRDLFETIERAVETVSEGLP--AIAENLGHVTDEVETL
QFU81686.1      DRYWAIPADAPA-HEGEWRDGPGRELFETVADG----CDELP--LIAEDLGHLTDGVERL
AWB27107.1      ESFWAIPAEKSDPAAGEWRAGPGAAFFERVRAE----HGALP--FIVEDLGFLDDALATL
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AHZ21176.1      DEYWAIDASSDNPEDGEWRDAPGHDFFETVERE----LGELP--FIVEDLGFLDASLVDL
AFK19479.1      DEYWAIDASSDNPEDGEWRDAPGHDFFETVERE----LGELP--FIVEDLGFLDASLVDL
AFK19479.2      DEYWAIDASSDNPEDGEWRDAPGHDFFETVERE----LGELP--FIVEDLGFLDASLVDL
QCQ75940.1      DEYWAIDASSDNPEDGEWRDAPGHDFFETVERE----LGELP--FIVEDLGFLDASLVDL
AKU07735.1      DEFWAIDADSDDPGNGEWRDAPGHDFFETVERE----LGDLP--FIVEDLGFLDASLVDL
QOS11852.1      DEFWAIDADSDDPGNGEWRDAPGHDFFETVERE----LGDLP--FIVEDLGFLDASLVDL
QIB78738.1      DEFWAIDADSDDPGDGEWRDAPGHDFFETVERE----LGDLP--FIVEDLGFLDASLVDL
ADE05003.1      DEFWAIDADSDDPGDGEWRDAPGHDFFETVERE----LDDLP--FVVEDLGFLDASLVDL
ADE05003.2      DEFWAIDADSDDPGDGEWRDAPGHDFFETVERE----LDDLP--FVVEDLGFLDASLVDL
QCC48543.1      DEFWAIPADSDSPADGEWRDAPGADFFETVGER----LGELP--FVVEDLGFLDQSLVDL
ADQ67101.1      DEYWAIPADAHSPAAGEWRDAPGHDFFETVEDQ----FGDLP--FIVEDLGFLDQRMTDL
QIQ76396.1      DEYWAIPADAHSPAAGEWRDAPGHDFFETVEDQ----FGDLP--FIVEDLGFLDQRMTDL
QIB74651.1      DEYWAIPADAHSPAAGEWRDAPGHDFFETVEDQ----FGDLP--FIVEDLGFLDQRMTDL
AIF04697.1      DSAWEIPAHHPTAKNGQWVQGPKAELLEAILEV----APAGK--IVAEDLGIIPPSVVEL
AIF05955.1      DSAWEIPAHHPTAKNGQWVQGPKAELLEAILEV----APAGK--IVAEDLGIIPPSVVEL
QEE14682.1      QAFWRISGTAKDAIDGKWIKAPGEDLFIEVQKQ----LGILP--IIAEDLGVITSEVEAL
ADL19304.1      AAYWEVPAGEKTAVNGRWARGPGEDLFRRVMRE----VPRLQ--LIAEDLGFITPDVVQL
AMD30778.1      AAYWEVPAGERTAVRGRWAQGPGDLFRAIMAA----APRLQ--LIAEDLGLITPDVVRL
AKT33963.1      VAYWEVPHGEETAVRGRWAPGPGEELFKAVEDA------LQR--LIAEDLGLITPDVVEL
ABL88479.1      VSYWEVPYGEPTAVRGRWAPGPGEELFKAVEET------LPR--LIAEDLGFITPDVVEL
ACB39188.1      AAYWEVPYGEPTAVRGRWAPGPGEELFRAAEDA------LPR--LIAEDLGFITPDVVEL
AEA11843.1      AAYWEVPAGEKTAVNGRWVPAPGGELLERARDE----LGGLK--IIAEDLGYITPDVVEL
ABO08194.1      AAYWEVPAGEPTAAGGRWVPGPGKRLFDAAAAE----VDLGR--LVAEDLGYITPDVEEL
ABP49821.1      VAYWEVPAGEKTAVNGRWVPAPGAELLEKARSE----LGELR--LIAEDLGYITPDVVEL
AFA40300.1      AAYWEVPAGEKTAVRGRWVPAPGAELLEKARAE----LGELR--LIAEDLGYITPDVVEL
AAL63326.1      VAYWEVPGGETTAVRGRWAPSPGRRLFEAAAAA----VDLGR--LIAEDLGYITPEVEAL
NP_559144.1     VAYWEVPGGETTAVRGRWAPSPGRRLFEAAAAA----VDLGR--LIAEDLGYITPEVEAL
AET33957.1      LAYWEIPGGETTAARGRWAPSPGKRLFDAASAA----VELGR--LIAEDLGYITPDVEAL
ABD40312.1      VGFWEIRAGSDTAIEGRWIEAPAWDFIRTLVKE----FPCLP--IIAEDLGIITSDVREI
QXO95450.1      VGYWEIKAGSDTAIDGRWISAPVWDLLRTWTKK----FPCFP--VIAEDLGIITPDVREV
QVV87979.1      VGYWEIKAGSDTAIDGRWISAPVWDLLRTWTKK----FPCFP--VIAEDLGIITPDVREV
CCJ37196.1      VQYWEVPVDEMTAENGRWVDAPGRDLFTLLARS----RSCLP--IIAEDLGYITSDVHEM
SAI88308.1      VQYWEVPAGETTAENGRWVDAPGRDFFTLLARS----RSCLP--IIAEDLGYITSDVHEM
CVK34217.1      VQYWEVPAGETTAENGRWVDAPGRDFFTLLARS----RSCLP--IIAEDLGYITSDVHEM
BBL68280.1      VQYWEVPAGDETARNGRWVDAPGRDLFTLLARS----RPCLP--IIAEDLGYITPDVHEM
ABN57193.1      VQFWEVPAGEETARNGHWVDAPGRDLFTLLARS----RSCLP--IIAEDLGHITPDVHEM
SAI88240.1      ADYYEVPAGDATAEHGTWVDGPGPGFFGVLARQ----FPCFA--IVAEDLGANTPAVQGL
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CVK34142.1      ADYYEVPAGDATAEHGTWVDGPGPGFFGVLARQ----FPCFA--IVAEDLGANTPAVQGL
CCJ37132.1      ADYYEVPAGDATAEHGAWVDGPGPEFFEVLARQ----FPCFA--IVAEDLGANTPAVQGL
BBL68006.1      ADYYEIPAGDPTAEHGTWVDGPGAGFFEALVRK----HPCFA--IVAEDLGANTPAVQAL
ABN56987.1      ADYYEVPAGDATAERGTWVDGPGEDFFEALARK----HPCFP--IVAEDLGANTPAVQAL
                 : :        * *   *    .:               . *::*           .

AUV80673.1      RTRYGLASLKLLPFVDWC-EEDHPHKPHRYTADTVAYTSTHDSETARGAYES-LSDEQRA
QCC51341.1      RDTLGYPGMVVAAFADWC-DGDSRYHPANYDANSVAYTSTHDTDTVVGWYDA-LDEQDRE
QSG15659.1      REDLGYPGMNVAAFTDWC-DGDSRYHPSSYDENSVAYTSTHDTDTVAGWYAD-LDEQQKD
QSG11910.1      RDDLGYPGMNVAAFADWC-DGDSRYHPVTYDENSVAYTSTHDTDTLVGWYED-LDDRQLD
QSG08987.1      RDDLGYPGMNVAAFADWC-DGDSRYHPVTYDENSVAYTSTHDTDTLVGWYED-LDDRQLD
QSG05483.1      RDDLGYPGMNVAAFADWC-DGDSRYHPVTYDENSVAYTSTHDTDTLVGWYED-LDDRQLD
QGN07616.1      RDAFEFPGMSVAAMADWC-DPSQGHHPASYTENTVAYASTHDTDTVPGWYAS-LSDAQRE
QSG11921.1      RDAFGFPGMRVAGMADWC-DDDHTHHPANYDDDSVAYASTHDTSTTPGWYED-LSETQKQ
QSG08998.1      RDAFGFPGMRVAGMADWC-DDDHTHHPANYDDDSVAYASTHDTSTTPGWYED-LSETQKQ
QSG05496.1      RDAFGFPGMRVAGMADWC-DDDHTHHPANYDDDSVAYASTHDTSTTPGWYED-LSETQKQ
CCQ33055.1      RDAFGFPGMRVAGMADWC-DAESTHHPASYDEPSVAYTSTHDTSTTVGWVKD-LSKKQRE
QSG02731.1      RRDIDAPGMKVMQYADWC-SEDHIYLPHTYEEDTVAYPGTHDTNTVRGWYEA-LEDEQVD
AUX09035.1      RRELGAPGMNVMQYADWC-TEDHGYQPHTYAADSVAYPSTHDTDTVCGYYEA-LGEDQRD
QFU81686.1      RQSIGAPGMRVLQYADWC-TEDHRYQPHVYPEDSVAYPATHDTNTVVGWYES-VDGEQRD
AWB27107.1      RDRFEFPGMRVPHYADWC-AERHRHKPAGYPERSVAYTSTHDTNTARGYVES-LDDRQRS
QLC34969.1      RDHLGFPGMRVPEYADWC-AEHHRYKPSDYPRDCVAYTSTHDTDTAVGYYES-LGERQRD
ACV11232.1      RDRFEFPGMRVPQYADWC-REGHRYKPTVYPDHCVGYTSTHDTDTAVGFYEK-LSAEQRD
QPV62520.1      RDRFEFPGMRVPHYADWC-AETDRYKPATYPRQSVGYTSTHDTDTAVGWYES-LSEEQRD
QLH84085.1      RDRFEFPGMRVPHYADWC-AETDRYKPATYPRQSVGYTSTHDTDTAVGWYES-LSAEQRD
QLH79093.1      RDRLEFPGMRVPHYADWC-AETDRYKPATYPRQSVGYTSTHDTDTAVGWYES-LSAEQRD
QAU11732.1      MAEFGFPGMRVPQYADWC-AEGNEYQPMHYSEGVVGYTSTHDTDTWAGYFDD-LPAEQRD
QAY20111.1      MAEFGFPGMRVPQYADWC-AEGNEYQPMHYGEGVVGYTSTHDTDTWAGYFED-LPAEQRD
QWC20591.1      MAEFGFPGMRVPQYADWC-AEGNEYQPMHYGEDVVGYTSTHDTDTWVGYFGD-LPAEQRD
QU046499.1      MAEFGFPGMRVPQYADWC-AEGNEYQPIHYGEGVVGYTSTHDTDTWAGYFED-LPAAQRD
QKG93724.1      MAEFGFPGMRVPQYADWC-AEGNQYQPMHYGEGVVGYTSTHDTDTWVGYFED-LPPEQRD
QKY17977.1      MAEFGFPGMRVPQYADWC-QEGNPYQPMHYPEGVVGYTSTHDTDTWVGYFED-LPERQRD
ACM57093.1      MVEFGFPGMRVPQYADWC-AEGNQYQPMHYPEGVVGYTSTHDTDTWVGYFEG-LPERQRD
AZQ14643.1      MAEFGFPGMRVPQYADWC-AEGDQYQPMHYPEGVVGYTATHDTNTWVGYFES-LPERQRD
ATW89261.1      MDRFDFPGMRVPQYADWC-QGGNEHQPMNYPKNSVGYTSTHDTDTFDGYYQT-LSERQRD
ABQ75827.1      RESLNFPGMRVPQYADWC-QEGDMYQPMHYPRQCVAYTATHDTNTTVGYYNS-LSARQRD
QZX99028.1      REAFDLPGMRVPQYADWC-QQGHMYQPMHYPEDCVAYTSTHDTDTAVGYYES-LDDRQRD
QZP38174.1      REAFDLPGMRVPQYADWC-QQGHMYQPMHYPEDCVAYTSTHDTDTAVGYYES-LGDRQRD
QZY03180.1      REAFDLPGMRVPQYADWC-QQGHMYQPMHYPEDCVAYTSTHDTDTAVGYYES-LGDRQRD
AUG48211.1      RDQFGFPGMRVPQYADWC-EEGHMYQPMHYPESAVGYTSTHDTDTIVGYYRG-LSDRQRD
AEM58055.1      RDRFGFPGMRVPQYADWC-EEGHMYQPMHYPESAVGYTSTHDTDTIVGYYRD-LADRQRD
AHB66799.1      RDRFGFPGMRVPQYADWC-EEGHMYQPMHYPESAVGYTSTHDTDTIVGYYRD-LADRQRD
AJF25101.1      RDRFGFPGMRVPQYADWC-EEGHMYQPMHYPESAVGYTSTHDTDTIVGYYRD-LADRQRD
AAV46825.1      RDEFGFPGMRVPQYADWC-EEGHMYQPMHYPESAVGYTSTHDTDTIVGYYRD-LADRQRD
QCP91534.1      RDEFGFPGMRVPQYADWC-EEGHMYQPMHYPESAVGYTSTHDTDTIVGYYRD-LADRQRD
QUJ72368.1      RDEFGFPGMRVPQYADWC-EEGHMYQPMHYPESAVGYTSTHDTDTIVGYYRD-LADRQRD
UBZ54001.1      REYFDFPGMRVPHYADWC-REGDMYQPMHYPPQSVAYSSTHDTDTIVGYYDS-LSQSQRD
CCC40696.1      REHFNFPGMRVPHYADWC-HEGNMYQPMHYPAQSVAYSSTHDTNTIVGYYDS-LSHSQRD
CAJ52690.1      REHFNFPGMRVPHYADWC-HEGNMYQPMHYPAQSVAYSSTHDTNTIVGYYGS-LSHSQRD
QCJ48434.1      RDHFEFPGMRVPHYADWC-REGDMNQPMHYPHGSIGYTATHDTDTTVGYYRS-LPDDQTD
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AFK19479.1      RDRFAFPGMRVPQYADWC-REGDMYQPMHYPENSVAYTSTHDTDTFVGYYQS-LDDHTRD
AFK19479.2      RDRFAFPGMRVPQYADWC-REGDMYQPMHYPENSVAYTSTHDTDTFVGYYQS-LDDHTRD
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ADE05003.2      RDRFAFPGMRVPQYADWC-REGDMYQPMHYPESSVAYTSTHDTDTFVGYYRD-LDDRTRD
QCC48543.1      RERFGFPSMRVPHYADWC-QEGDMYQPMHYPENSVAYSSTHDTNTLVGYCEN-LSDRQRS
ADQ67101.1      RDRFGFPGMRVPQYANWC-QEGDMYQPMFPENSVGYTSTHDTNTFVGYYRD-LPADQKD
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AIF04697.1      RKQNGIPGMAVLHFSND--DVDNPHNPENHSEDTVVYTGTHDNDTTVGWGGKP-------
AIF05955.1      RKQNGIPGMAVLHFSND--DVDNPHNPENHSEDTVVYTGTHDNDTTVGWGGKP-------
QEE14682.1      RDKFNFPGMKILQFAFGS-DEENYLPHNFVHNCISYTGTHDNNTTLGWWQNDATKTEKK
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AMD30778.1      RERLGIPGLKVLQFAWDG-SPNNPYLPHNYARNFIVYTGTHDNNTIVGWFFHEASPRARA
AKT33963.1      RRRLGIPGMRVLQFAWDG-NPANEHKPHNYERNLVAYTGTHDNNTVVGWWRDEAPPRARR
ABL88479.1      RRRLGIPGMRVLQFAWDG-NPANEHKPHNYERNLVAYTGTHDNNTIVGWWREETTPRSRR
ACB39188.1      RYRLGIPGMRVLQFAWDG-NPANEHKPHNYERNLVAYTGTHDNNTTLGWWREETTPRSRR
AEA11843.1      RDRFGLPGMRVLQFAWDG-NPANEHKPHNHVKNSVVYTGTHDNNTIVGWFFREASPKARR
ABO08194.1      RDSLGLPGMRVLQFAWDG-NPANLHKPHNHVKNSLVYTGTHDNNTAVGWFTEEATPAVRR
ABP49821.1      RDRLGFPGMRVLQFAWDG-NPANEHKPHNHVKNSVVYTGTHDNNTAVGWYLEEATPRARR
AFA40300.1      RDRFGLPGMRVLQFAWDG-NPANEHKPHNHVKNSVVYTGTHDNNMAVGWYQEEATPRARR
AAL63326.1      REELGLPGMRVLQFAWDG-NPANPHKPHNHVKNAVVYTGTHDNNTAVGWYKEEATARARR
NP_559144.1     REELGLPGMRVLQFAWDG-NPANPHKPHNHVKNAVVYTGTHDNNTAVGWYKEEATARARR
AET33957.1      RDELGLPGMRVLQFAWDG-NPANPHKPHNHVKNSVVYTGTHDNNTAVGWYLQEASPRARR
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ABD40312.1      MREFMIPGMKVLVFAFSSPTGDNPYILHNIPKDSVVYTGTHDNTPVRGWYELDATHEEKQ
QXO95450.1      MREFDIPGMKVLIFAFSSETGDNPYILHNIPPNTVVYTGTHDNTPVLGWFLHEATPEEKQ
QVV87979.1      MREFDIPGMKVLIFAFSSETGDNPYILHNIPPNTVVYTGTHDNTPVLGWFLHEATPEEKQ
CCJ37196.1      MAHFGFPGMKVLIFGFSGDVARNPHAPHNITGGCIAYTGTHDNNTVRGWFEHEVSGDQRD
SAI88308.1      MAHFGFPGMKVLIFGFSGDVARNPHAPHNITGGCIAYTGTHDNNTVRGWFEHEVSGEQRD
CVK34217.1      MAHFGFPGMKVLIFGFSGDVARNPHAPHNITGGCIAYTGTHDNNTVRGWFEHEVSGEQRD
BBL68280.1      MAYFGFPGMKILIFGFSGDVAQNPHAPHNFAKGYVAYTGTHDNNTVRGWFEHETSEEQKN
ABN57193.1      MAYFGFPGMKILTFGFSGDVAQNPHAPHNITEGSVAYTGTHDNNTVRGWFGREVPDDQKN
SAI88240.1      LDRFGFPGMKILLFAFGEGLPESAHIPHNYVPNLICYTGTHDNNTARGWFEEEASEEDKQ
CVK34142.1      LDRFGFPGMKILLFAFGEGLPESAHIPHNYVPNLICYTGTHDNNTARGWFEEEASEEDKQ
CCJ37132.1      LDRFGFPGMKILLFAFGEGLPGSAHIPHNYVPNLICYTGTHDNNTARGWFEEEASEEDKQ
BBL68006.1      LDRFDFPGMKILLFAFGEGIAGSAHIPHNYVHNLICYTGTHDNNTARGWFEEEATDEDKE
ABN56987.1      LDRFDFPGMKILLFAFGEGIARTPHIPHNYVHNLICYTGTHDNNTARGWFEEEASEEDKE
                .: :                      : * .***.     *


AUV80673.1      CFEAYFDGPVAAETVHETCIEAVWGSEANLALAQIQDVLGRGNEARFNVPGTTAGNWAWR
QCC51341.1      CLHYAV-DHEGGD-VHWDILDTVWNSDSVIALAQVQDPLGYGSEARFNVPGTVEGNWAWR
QSG15659.1      CLHYAV-DYEGGD-VHWDILDTIWGSDSVITLAQVQDPLGYGSDARFNVPGTEEDNWAWR
QSG11910.1      CLHYAV-DYEGGD-VHWDILDTVWGSDSAITLAQVQDPLGYGSEARFNVPGTEEGNWSWR
QSG08987.1      CLHYAV-DYEGGD-VHWDILDTVWGSDSAITLAQVQDPLGYGSEARFNVPGTEEGNWSWR
QSG05483.1      CLHYAV-DYEGGD-VHWDILDTVWGSDSVITLAQVQDPLGYGSEARFNVPGTEKGNWSWR
QGN07616.1      CLHDVV-DGNSDD-PHWNIVETIWASEAVLTLVQCQDLLGLGTAHRFNFPGTAEGNWAWR
QSG11921.1      CLHSVV-DHEGDE-VHWDIIEAVWASPAIITLAQFQDFLGLGDEHRFNLPGTATGNWKWR
QSG08998.1      CLHSVV-DHEGDE-VHWDIIEAVWASPAIITLAQFQDFLGLGDEHRFNLPGTATGNWKWR
QSG05496.1      CLHSVV-DHEGGE-VHWDIIEAVWASPAIITIAQFQDFLGLGDEHRFNLPGTATGNWKWR
CCQ33055.1      CLYFAV-DHEGGP-INWDVIETVWETPAVITFAQFQDFHGLGDEHRFNLPGTATGNWKWR
QSG02731.1      CLHYYL-GSDGSE-IHWDMIERAWHTASSLAVVPLQDLYGLGAEARFNTPGTESGNWDWR
AUX09035.1      CLHYYM-GTDGSE-IHWEFIEAAWGSDSVFAVAPLPDLFGLGSEARFNTPGTADGNWEWR
QFU81686.1      CLHYYL-STDGHE-IHWEFLEAAWESDAVFAITPLPDLYGLGDEARFNTPGTADGNWEWR
AWB27107.1      CLEYAL-ATDAE-RAVWDLLEAVWQSDAALAIAPVQDLLDLGSESRLNDPAGG-DDWTWR
QLC34969.1      CFDYAL-DFDGDESPAWALLDAVWDSPAVVAMTTLPDLLTLGSDARLNTPGTGTGNWAWR
ACV11232.1      CLEYAL-ATDGD-SIAWDLLIEAVWHSDAALAMTTVPDLLERGSDARLNQPGTGEGNWTWR
QPV62520.1      CLHYAL-ATDGE-RVAWDLIEAVWDSDAALALTTVPDLLELGSEARFNVPGTAEGNWRWR
QLH84085.1      CLHYAL-ATDGE-RIAWDLIEAVWDSDAALALTTVPDLLELGSEARFNVPGTAENNWRWR
QLH79093.1      CLHYAL-ATDGE-RIAWDLIEAVWDSDAALALTTVPDLLELGSEARFNVPGTAEGNWRWR
QAU11732.1      CFRYNV-GAGPDEPVEWAIVDEVWASDAILAVTTLQDLLGLGSEARFNEPGTLAGNWEWR
QAY20111.1      CFRYNV-GSDPDEPPEWAIIDEVWSSDAILAVATIQDLLGLGSESRFNEPGTLDGNWEWR
QWC20591.1      CFRYNV-GSDPDEPTEWAIIDEVWSSDAILAVTTVQDLFGLGSEARFNEPGTLAGNWEWR
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QKG93724.1      CFRYNV-GSDPEEPPEWAIIDAVWGSDAILAVTTLQDLLGLGSDARFNEPGTLAGNWEWR
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CAJ52690.1      CLHYNL-GVDGSE-INWSIIDAVWRSDAQIGFTTLQDILGLDSHARFNEPGTASGNWQWR
QCJ48434.1      CLHYNL-GVDGSD-INWSLIEAVWNSEAVLAMTTVPDLLGLGSDTRFNTPGTAEGNWSWR
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QCQ75940.1      CLHYNI-GADGSE-IHWSIIDAVWNSASVLAFTTVQDLLGLDSRARFNTPGTQNGNWEWR
AKU07735.1      CLHYNI-GADGSE-IHWSIIDAVWNSASVLAFTTTQDLLGLGSDARFNTPGTQTGNWEWR
QOS11852.1      CLHYNI-GADGSE-IHWSIIDAVWNSASVLAFTTTQDLLGLGSDARFNTPGTQTGNWEWR
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QIB74651.1      CLHYNI-GADGSE-IHWSIIDAVWRSNAVIAFTTIQDILGLGAEARFNVPGTTDGNWRWR
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AIF05955.1      ---------------VQDLIQDALNSPANLAIIPLQDVMGLDSQARMNTPGTLDGNWEWR
QEE14682.1      NLREYLNTKSENKSVVDDLIRILYRSIAKVAIIPIQDLLGQGEEARMNTPSVEGGNWQYQ
ADL19304.1      EAMNYMGLR-DAREINWAFIRLAMMSVADVSIFPVQDVLGLGPEARMNTPGTVGNNWRWR
AMD30778.1      QALRYMGLN-SARDINWAFIRLAMMSVADVSIFPAQDVLGLGPEARMNTPGTVSNNWLWR
AKT33963.1      EALAYMGGC-R-GAVNWCFIRLLFSTVADVAVVPIQDVLGLGAEARINKPATSRGNWKWR
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ABL88479.1      EALAYIGGC-G-REINWCFIRLLFSTVADVAVVPIQDVLGLGSEARINKPGTLRGNWKWR
ACB39188.1      EALAYMGGC-R-GGVSWCFIRLLFSTVADVAVVPMQDALGLGSEARMNKPGTARGNWKWR
AEA11843.1      EALEYMGRR-SAKDIHWAFIRLAYFSVADVAVVPMQDFMGLGPEARINRPGTRGGNWVWR
ABO08194.1      EVLKYGNCR-P-REINWCLIRLAHMSVADVAIVPMQDVLGLGSEARMNKPGTVGGNWRWR
ABP49821.1      EFCQYAKCS-AAEGVHWCFIRLAYMSVANVAIVPIQDVLGLGSEARMNKPGTVGGNWRWR
AFA40300.1      EFREYAKCA-SGEGVNWCFIRLAHMSVADVAIVPMQDVLGLGSEARMNKPGTMGGNWRWR
AAL63326.1      EFKKYSNCA---GEVHWCFIKLAHMSVANVAIVPVQDLLGLGSEARMNRPGTVGGNWKWR
NP_559144.1     EFKKYSNCA---GEVHWCFIKLAHMSVANVAIVPMQDLLGLGSEARMNRPGTVGGNWKWR
AET33957.1      EFRQYSNCR---EAVNWCFIKLAYMSVADVAVVPMQDVLGLGPEARMNRPGTVGGNWRWR
ABD40312.1      RLIAYLGREPEIHEISDIFIRLAMMSSANTAIIPIQDILGLDSSARMNKPGTEHGNWRWR
QXO95450.1      RFVSYIGYEVSSEKVSDVFVRLAMMSSANTAIISMQDVLGLDISARMNRPGSEKGNWRWM
QVV87979.1      RFVSYIGYEVSSEKVSDVFVRLAMMSSANTAIISMQDVLGLDISARMNRPGSEKGNWRWM
CCJ37196.1      LLFRYIGGTFGADHAHRILIRLAMLSPAETVIVPMQDILGLGEEARMNRPGTAEGNWEWR
SAI88308.1      LLFRYIGGSFGAEHVHRILIRLAMLSPAETVIVPMQDILGLGEEARMNRPGTAEGNWEWR
CVK34217.1      LLFRYIGGSFGAEHVHRILIRLAMLSPAETVIVPMQDILGLGEEARMNRPGTAEGNWEWR
BBL68280.1      LLFRYIGGSVSGDQVHRILIRLAMLSPADTVIVPMQDILGLGEEARMNRPGTTEANWEWR
ABN57193.1      LLFRYIGGPVSGDEIHRILIRLAMLSPADTVIVPMQDILGLGEEARMNRPGTTEGNWEWR
SAI88240.1      RFFAYIGREVTAEEVPRELIRLAMTSVARTSIIPMQDILGLGAAARMNYPSTSDGNWEWR
CVK34142.1      RFFAYIGREVTAEEVPRELIRLAMTSVARTSIIPMQDILGLGAEARMNYPSTSDGNWEWR
CCJ37132.1      RFFAYIGREVAADEVPRELIRLAMTSVARASIIPMQDILGLGAEARMNYPSTSDGNWEWR
BBL68006.1      RFFAYAGREVRADSVHREFVRLGMTSVARACIVPMQDVLGLGAAARMNYPSTTGNWEWR
ABN56987.1      RFFTYIGREVAADEVHRELVRLAMTSVARACIVPMQDVLGLGAAARMNYPSTTGNWVWR
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AUV80673.1      VREEQLTD-AAAGWLAEATRDANR------
QCC51341.1      VSEDALSG-DVVQNLYDITEESDRLAE----
QSG15659.1      VSEDALSA-DVAERLYEITESSGRLTD----
QSG11910.1      VSEDALTD-EVAQRLYDITEATGRLTD----
QSG08987.1      VSEDALTD-EVAQRLYDITEATGRLTD----
QSG05483.1      VGEDALTD-EVAQRLYDITEATGRLTD----
QGN07616.1      VLPSELTD-DVAERLAAVSRRTDRA------
QSG11921.1      MRRSELDP-AVAERLADVTRRTDRR------
QSG08998.1      MRRSELDP-AVAERLADVTRRTDRR------
QSG05496.1      MRRSELDP-AVAERLADVTRRTDRR------
CCQ33055.1      MLDSELDS-AVADRLADVTRKADRT------
QSG02731.1      CTDELL-ESFPTDRLRTITDEADR-------
AUX09035.1      CPAALITAEFPTERLRAVTDGTDRVTLN---
QFU81686.1      LSTDRL-ESFPTARLRELTARTDRLDETTSH
AWB27107.1      LPAGALDD-ALADRLRATTDAALR-------
QLC34969.1      VDEGALAD-DLAARLADVTANARR-------
ACV11232.1      VTADELDA-DTADRLAAVTRASLR-------
QPV62520.1      VTADQLDP-DVADELAGVTAATLR-------
QLH84085.1      VTADQLDP-AVAGELAGVTAATLR-------
QLH79093.1      VTADRLDP-AVADELAGVTAATLR-------
QAU11732.1      VTREALDD-AIADRLWELAGDHVR-------
QAY20111.1      VARDDLDD-AIADRLWELAGKHVR-------
QWC20591.1      VSRDALDD-AIADRLWELGGTHVR-------
QUO46499.1      VARDALDD-EIADRLWELSGKHVR-------
QKG93724.1      VARDALDD-EIADRLWELGGRHVR-------
QKY17977.1      VTRDALDD-AVADRLWDLAGRHVR-------
ACM57093.1      VRRDALDD-AIADRLWDLAGHHVR-------
AZQ14643.1      VRREALDD-DIADRLFELAGRHVR-------
ATW89261.1      VTSEGLDE-RIAKKLGTMTAIEIR-------
ABQ75827.1      CTSEGLSD-ALAGRLAALSAEHIRD------
QZX99028.1      VTEAGLDG-AVADRLARITDATVR-------
QZP38174.1      VTEDGLND-AVAERLARITDATVR-------
QZY03180.1      VTEDGLND-AVAERLARITDATVR-------
AUG48211.1      VTDAALDA-DVAERLRRVTDRTIR-------
AEM58055.1      VTEDAIND-EVAERLRQVTDRTIR-------
AHB66799.1      VTEDAIND-EVAERLRQVTDRTIR-------
AJF25101.1      VTEDAIND-EVAERLRQVTDRTIR-------
AAV46825.1      VTDTALDA-DIAERLRRVTDRTIR-------
QCP91534.1      VTDTALDA-DIAERLRRVTDRTIR-------
QUJ72368.1      VTEDALDT-DVAERLRQVTDRTIR-------
UBZ54001.1      CTDSGLDE-DLARRLAGLTLEHVRD------
CCC40696.1      CTDSGLDD-DLARRLAGLTIEHVRD------
CAJ52690.1      CTDSGLDD-DLARRLAGLTIEHVRD------
QCJ48434.1      CTYEGLDE-SVAERLRDVTDFTIR-------
AHZ21176.1      VTREGLDD-DVSARLAELTDLHIRN------
AFK19479.1      VTREGLDD-DVSARLAELTDLHIRN------
AFK19479.2      VTREGLDD-DVSARLAELTDLHIRN------
QCQ75940.1      VTREGLDD-DVSARLAELTDLHIRN------
AKU07735.1      VTREGLDD-GVADRLANLTDLHIRN------
QOS11852.1      VTREGLDD-GVADRLANLTDLHIRN------
QIB78738.1      VTREGLDD-GVADRLASLTDLHIRN------
ADE05003.1      VTREGLDD-GVADRLASLTDLHIRN------
ADE05003.2      VTREGLDD-GVADRLASLTDLHIRN------
QCC48543.1      CTVEAFSE-ALADRLARLTDEHIRN------
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ADQ67101.1        CTEEGFDE-ELASRLARLTDEHIR-------
QIQ76396.1        CTEEGFDE-ELASRLARLTDEHIR-------
QIB74651.1        CTEEGFDE-ELASRLARLTDEHIR-------
AIF04697.1        FDWDELTN-DSLNWFGQQVYRSGRGN-----
AIF05955.1        FDWDELTN-DSLNWFGQQVYRSGRGN-----
QEE14682.1        VKIDNDVK-NRAKFLKKITKLYGRKVII---
ADL19304.1        LESFDGLR-RAARRLRDMTRAYGR-------
AMD30778.1        LDSLEGLW-RTASRLRDMTRSYGR-------
AKT33963.1        LHAQPP-P-TYARRLRRLAKLYGR-------
ABL88479.1        LAKDPP-I-NFAVRLRRLAKLYGR-------
ACB39188.1        MAGDPP-R-AVAARLRRLARIYGR-------
AEA11843.1        MTELPG-R-ALARRIRRLARLYGR-------
ABO08194.1        LAEQPP-R-ALLRKLREVTRLYGR-------
ABP49821.1        LAKMPN-A-AVRRRLRKLTRIYGR-------
AFA40300.1        LAKMPD-A-AVLRRLRKLTRTYGR-------
AAL63326.1        LGAQPE-P-RVWKRLRDVTRTYGR-------
NP_559144.1       LGAQPE-P-RVWKRLRDVTRTYGR-------
AET33957.1        MAKQPE-P-RQWRRLRSLARLYGR-------
ABD40312.1        LQERMISE-ELSRRLSELVKIYGR-------
QXO95450.1        MQERMITE-DLAYYIRTLTTTYGRL------
QVV87979.1        MQERMITE-DLAYYIRTLTTTYGRL------
CCJ37196.1        LRREQMRE-QAMQEFSEVTGLYGRK------
SAI88308.1        LRREQMRE-QAMQEFSEVTGLYGRK------
CVK34217.1        LRREQMRE-QAMQEFSEVTGLYGRK------
BBL68280.1        LRPDQIGE-ESMRELAEVTGIYGRG------
ABN57193.1        LRPDQAGE-ESMREFAEVTGIYGRG------
SAI88240.1        MTPAEFAG-APFDRLRRLTELCGRA------
CVK34142.1        MTPAEFAG-APFDRLRRLTELCGRA------
CCJ37132.1        MTPREFAD-APFDRLGRFTELCGRA------
BBL68006.1        MTPEEFAG-APFEWLRELTELTGRG------
ABN56987.1        MTPEEFAG-APFEWLRGLTELTGRG------
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Figure S2. Clustal alignment of Hw-A and 83 archaeal amylomaltases present in the CAZy GH77 family. Hw-A is reported in red.
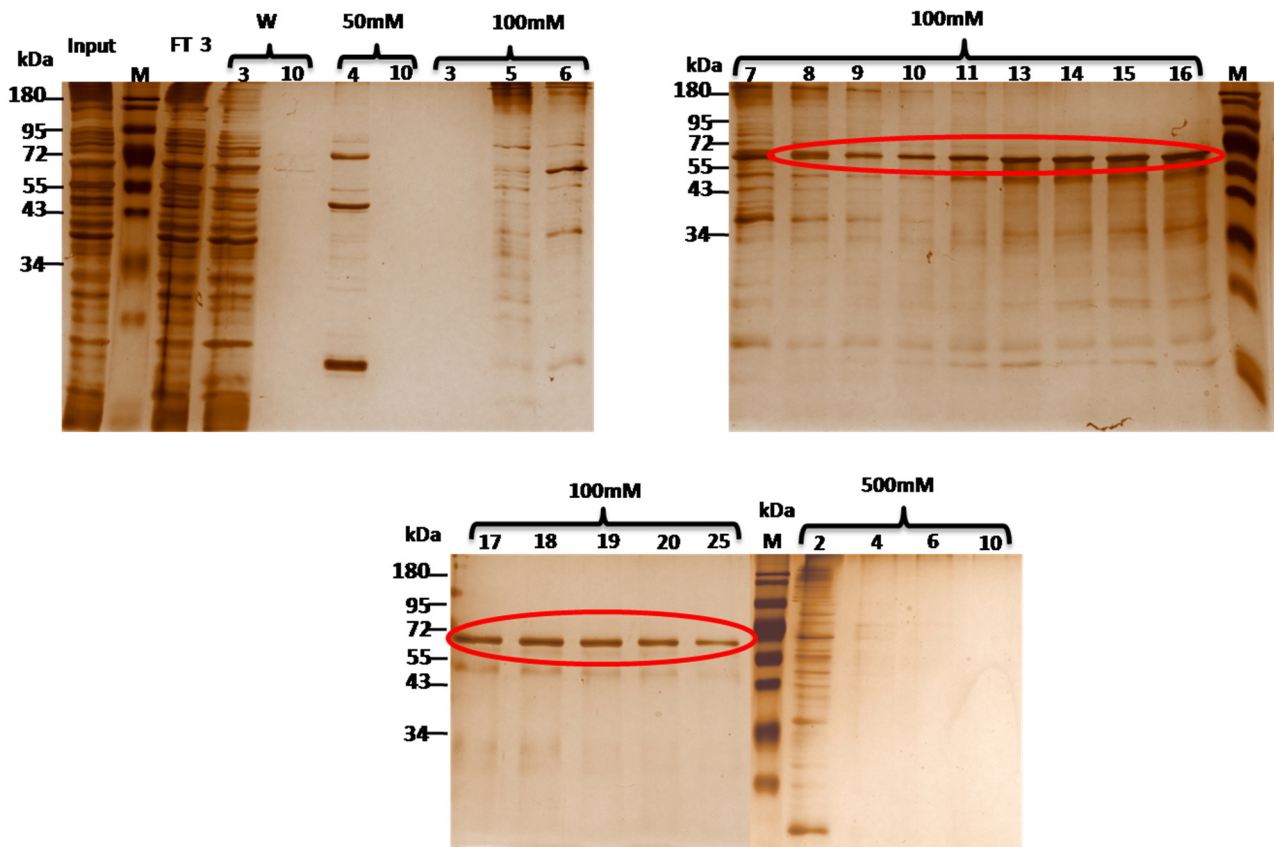
Figure S3

Figure S3.SDS-PAGE on 15% polyacrylamide gel of the fractions obtained from IMAC chromatography. Input: Soluble fraction of sonicated induced expression cells;M: Marker Thermo Scientific Page Ruler Prestained Protein Ladder; FT: flow-through; W: wash buffer; 50mM: fraction eluted with 50mM imidazole elution buffer; 100mM: fraction eluted with 100mM imidazole elution buffer; 500mM: fraction eluted with 500mM imidazole elution buffer.The recombinant protein was circled in red. Protein electrophoretic bands were revealed by silver staining.