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RESEARCH ARTICLE

Functional characterization of a thermostable methionine adenosyltransferase from *Thermus thermophilus* HB27

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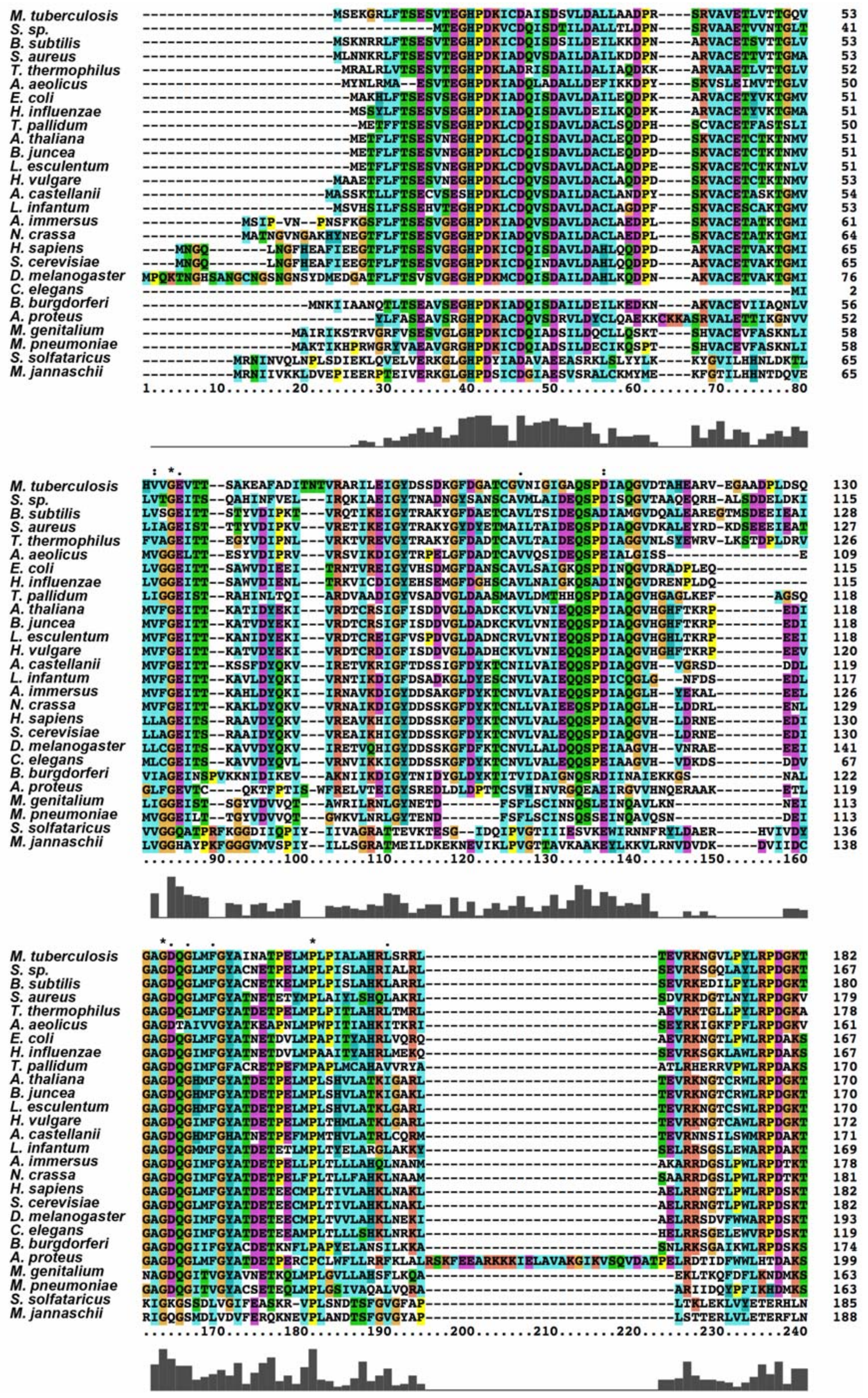
Supporting Information



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M. tuberculosis   -----------------------MSEKGRLFTSESVTEGHPDKICDAISDSVLDALLAADPR----SRVAVETLVTTGQV   53
S. sp.            -----------------------------------MTEGHPDKVCDQISDTILDALLTLDPN----SRVAAETVVNTGLT   41
B. subtilis       -----------------------MSKNRRLFTSESVTEGHPDKICDQISDSILDEILKKDPN----ARVACETSVTTGLV   53
S. aureus         -----------------------MLNNKRLFTSESVTEGHPDKIADQVSDAILDAILKDDPN----ARVACETTVTTGMA   53
T. thermophilus   ------------------------MRALRLVTSESVTEGHPDKLADRISDAILDALIAQDKK----ARVAAETLVTTGLV   52
A. aeolicus       ------------------------MYNLRMA--ESVTEGHPDKIADQLADALLDEFIKKDPY----SKVSLEIMVTTGLV   50
E. coli           -------------------------MAKHLFTSESVSEGHPDKIADQISDAVLDAILEQDPK----ARVACETYVKTGMV   51
H. influenzae     -------------------------MSSYLFTSESVSEGHPDKIADQISDAVLDEILKQDPK----ARVACETYVKTGMA   51
T. pallidum       --------------------------METFFTSESVSEGHPDKLCDQISDAVLDACLSQDPH----SCVACETFASTSLI   50
A. thaliana       -------------------------METFLFTSESVNEGHPDKLCDQISDAVLDACLEQDPD----SKVACETCTKTNMV   51
B. juncea         -------------------------METFLFTSESVNEGHPDKLCDQISDAVLDACLEQDPD----SKVACETCTKTNMV   51
L. esculentum     -------------------------METFLFTSESVNEGHPDKLCDQVSDAVLDACLAQDPE----SKVACETCTKTNLV   51
H. vulgare        -----------------------MAAETFLFTSESVNEGHPDKLCDQVSDAVLDACLAQDPD----SKVACETCTKTNMV   53
A. castellanii    ----------------------MASSKTLLFTSECVSESHPDKLCDQVSDAILDACLANDPY----SKVACETASKTGMV   54
L. infantum       -----------------------MSVHSILFSSEHVTEGHPDKLCDQVSDAVLDACLAGDPF----SKVACESCAKTGMV   53
A. immersus       ------------MSIP-VN--PNSFKGSFLFTSESVGEGHPDKIADQVSDAVLDACLAEDPL----SKVACETATKTGMI   61
N. crassa         ------------MATNGVNGAKHYNEGTFLFTSESVGEGHPDKIADQVSDAILDACLAEDPL----SKVACETATKTGMI   64
H. sapiens        ----MNGQ-------LNGFHEAFIEEGTFLFTSESVGEGHPDKICDQISDAVLDAHLQQDPD----AKVACETVAKTGMI   65
S. cerevisiae     ----MNGQ-------LNGFHEAFIEEGTFLFTSESVGEGHPDKICDQINDAVLDAHLQQDPD----AKVACETVAKTGMI   65
D. melanogaster   MPQKTNGHSANGCNGSNGNSYDMEDGATFLFTSVSVGEGHPDKMCDQISDAILDAHLKQDPN----AKVACETVAKTGMI   76
C. elegans        ------------------------------------------------------------------------------MI    2
B. burgdorferi    --------------------MNKIIAANQTLTSEAVSEGHPDKIADQISDAILDEILKEDKN----AKVACEVIIAQNLV   56
A. proteus        ----------------------------YLFASEAVSRGHPDKACDQVSDRVLDYCLQAEKKCKKASRVALETTIKGNVV   52
M. genitalium     ------------------MAIRIKSTRVGRFVSESVGLGHPDKICDQIADSILDQCLLQSKT----SHVACEVFASKNLI   58
M. pneumoniae     ------------------MAKTIKHPRWGRYVAEAVGRGHPDKICDQIADSILDECIKQSPT----SHVACEVFASKNLI   58
S. solfataricus   -----------MRNINVQLNPLSDIEKLQVELVERKGLGHPDYIADAVAEEASRKLSLYYLK----KYGVILHHNLDKTL   65
M. jannaschii     -----------MRNIIVKKLDVEPIEERPTEIVERKGLGHPDSICDGIAESVSRALCKMYME----KFGTILHHNTDQVE   65
                  1.......10........20........30........40........50........60........70........80

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M. tuberculosis   HVVGEVTT--SAKEAFADITNTVRARILEIGYDSSDKGFDGATCGVNIGIGAQSPDIAQGVDTAHEARV-EGAADPLDSQ  130
S. sp.            LVTGEITS--QAHINFVEL---IRQKIAEIGYTNADNGYSANSCAVMLAIDEQSPDISQGVTAAQEQRH-ALSDDELDKI  115
B. subtilis       LVSGEITT--STYVDIPKT---VRQTIKEIGYTRAKYGFDAETCAVLTSIDEQSADIAMGVDQALEAREGTMSDEEIEAI  128
S. aureus         LIAGEIST--TTYVDIPKV---VRETIKEIGYTRAKYGYDYETMAILTAIDEQSPDIAQGVDKALEYRD-KDSEEEIEAT  127
T. thermophilus   FVAGEITT--EGYVDIPNL---VRKTVREVGYTRAKYGFDADTCAVLTAIDEQSPDIAGGVNLSYEWRV-LKSTDPLDRV  126
A. aeolicus       MVGGELTT--ESYVDIPRV---VRSVIKDIGYTRPELGFDADTCAVVQSIDEQSPEIALGISS----------------E  109
E. coli           LVGGEITT--SAWVDIEEI---TRNTVREIGYVHSDMGFDANSCAVLSAIGKQSPDINQGVDRADPLEQ-----------  115
H. influenzae     LVGGEITT--SAWVDIENL---TRKVICDIGYEHSEMGFDGHSCAVLNAIGKQSADINQGVDRENPLDQ-----------  115
T. pallidum       LIGGEIST--RAHINLTQI---ARDVAADIGYVSADVGLDAASMAVLDMTHHQSPDIAQGVHGAGLKEF-------AGSQ  118
A. thaliana       MVFGEITT--KATIDYEKI---VRDTCRSIGFISDDVGLDADKCKVLVNIEQQSPDIAQGVHGHFTKRP--------EDI  118
B. juncea         MVFGEITT--KATVDYEKI---VRDTCRSIGFISDDVGLDADKCKVLVNIEQQSPDIAQGVHGHFTKRP--------EDI  118
L. esculentum     MVFGEITT--KANIDYEKI---VRDTCREIGFVSPDVGLDADNCRVLVNIEQQSPDIAQGVHGHLTKRP--------EEI  118
H. vulgare        MVFGEITT--KATVDYEKI---VRDTCRDIGFISDDVGLDADHCKVLVNIEQQSPDIAQGVHGHFTKRP--------EEV  120
A. castellanii    MVFGEITT--KSSFDYQKV---IRETVKRIGFTDSSIGFDYKTCNILVAIEQQSPDIAQGVH--VGRSD--------DDL  119
L. infantum       MVFGEITT--KAVLDYQKI---VRNTIKDIGFDSADKGLDYESCNVLVAIEQQSPDICQGLG---NFDS--------EDL  117
A. immersus       MVFGEITT--KAHLDYQKI---IRNAVKDIGYDDSAKGFDYKTCNVLVAIEQQSPDIAQGLH--YEKAL--------EEL  126
N. crassa         MVFGEITT--KAKLDYQKV---VRNAIKDIGYDDSSKGFDYKTCNLLVAIEEQSPDIAQGLH--LDDRL--------ENL  129
H. sapiens        LLAGEITS--RAAVDYQKV---VREAVKHIGYDDSSKGFDYKTCNVLVALEQQSPDIAQGVH--LDRNE--------EDI  130
S. cerevisiae     LLAGEITS--RAAIDYQKV---VREAIKHIGYDDSSKGFDYKTCNVLVALEQQSPDIAQGVH--LDRNE--------EDI  130
D. melanogaster   LLCGEITS--KAVVDYQKV---IRETVQHIGYDDSSKGFDFKTCNVLLALDQQSPEIAAGVH--VNRAE--------EEI  141
C. elegans        MLCGEITS--KAVVDYQVL---VRNVIKKIGYDDSSKGFDYKTCNVLVALEQQSPEIAAGVH--VDKDS--------DDV   67
B. burgdorferi    VIAGEINSPVKKNIDIKEV---AKNIIKDIGYTNIDYGLDYKTITVIDAIGNQSRDIINAIEKKGS-----------NAL  122
A. proteus        GLFGEVTC----QKTFPTIS-WFRELVTEIGYSREDLDLDPTTCSVHINVRGQEAEIRGVVHNQERAAK--------ETL  119
M. genitalium     LIGGEIST--SGYVDVVQT---AWRILRNLGYNETD-------FSFLSCINNQSLEINQAVLKN-------------NEI  113
M. pneumoniae     MVGGEILT--TGYVDVVQT---GWKVLNRLGYTEND-------FSFLSCINSQSSEINQAVQSN-------------DEI  113
S. solfataricus   VVGGQATPRFKGGDIIQPIY--IIVAGRATTEVKTESG--IDQIPVGTIIIESVKEWIRNNFRYLDAER-----HVIVDY  136
M. jannaschii     LVGGHAYPKFGGGVMVSPIY--ILLSGRATMEILDKEKNEVIKLPVGTTAVKAAKEYLKKVLRNVDVDK-----DVIIDC  138
                  ........90.......100.......110.......120.......130.......140.......150.......160

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M. tuberculosis   GAGDQGLMFGYAINATPELMPLPIALAHRLSRRL----------------------------TEVRKNGVLPYLRPDGKT  182
S. sp.            GAGDQGLMFGYACNETPELMPLPISLAHRIALRL----------------------------SEVRKSGQLAYLRPDGKT  167
B. subtilis       GAGDQGLMFGYACNETKELMPLPISLAHKLARRL----------------------------SEVRKEDILPYLRPDGKT  180
S. aureus         GAGDQGLMFGYATNETETYMPLAIYLSHQLAKRL----------------------------SDVRKDGTLNYLRPDGKV  179
T. thermophilus   GAGDQGLMFGYATDETPELMPLPITLAHRLTMRL----------------------------AEVRKTGLLPYLRPDGKA  178
A. aeolicus       GAGDTAIVVGYATKEAPNLMPWPITIAHKITKRI----------------------------SEYRKIGKFPFLRPDGKV  161
E. coli           GAGDQGLMFGYATNETDVLMPAPITYAHRLVQRQ----------------------------AEVRKNGTLPWLRPDAKS  167
H. influenzae     GAGDQGIMFGYATNETDVLMPAAITYAHRLMEKQ----------------------------SEVRKSGKLAWLRPDAKS  167
T. pallidum       GAGDQGIMFGFACRETPEFMPAPLMCAHAVVRYA----------------------------ATLRHERRVPWLRPDAKS  170
A. thaliana       GAGDQGHMFGYATDETPELMPLSHVLATKIGARL----------------------------TEVRKNGTCRWLRPDGKT  170
B. juncea         GAGDQGHMFGYATDETPELMPLSHVLATKIGAKL----------------------------TEVRKNGTCRWLRPDGKT  170
L. esculentum     GAGDQGHMFGYATDETPELMPLSHVLATKLGARL----------------------------TEVRKNGTCSWLRPDGKT  170
H. vulgare        GAGDQGIMFGYATDETPELMPLTHMLATKLGARL----------------------------TEVRKNGTCAWLRPDGKT  172
A. castellanii    GAGDQGHMFGHATNETPEFMPMTHVLATRLCQRM----------------------------TEVRNNSILSWMRPDAKT  171
L. infantum       GAGDQGMMFGYATDETETLMPLTYELARGLAKKY----------------------------SELRRSGSLEWARPDAKT  169
A. immersus       GAGDQGIMFGYATDETPELLPLTLLLAHQLNANM----------------------------AKARRDGSLPWLRPDTKT  178
N. crassa         GAGDQGIMFGYATDETPELFPLTLLFAHKLNAAM----------------------------SAARRDGSLPWLRPDTKT  181
H. sapiens        GAGDQGLMFGYATDETEECMPLTIVLAHKLNAKL----------------------------AELRRNGTLPWLRPDSKT  182
S. cerevisiae     GAGDQGLMFGYATDETEECMPLTIVLAHKLNAKL----------------------------AELRRNGTLPWLRPDSKT  182
D. melanogaster   GAGDQGIMFGYATDETEECMPLTVVLAHKLNEKI----------------------------AELRRSDVFWWARPDSKT  193
C. elegans        GAGDQGIMFGYATDETEEAMPLTLLLSHKLNRKL----------------------------HELRRSGELEWVRPDSKT  119
B. burgdorferi    GAGDQGIIFGYACDETKNFLPAPYELANSILKKA----------------------------SNLRKSGAIKWLRPDSKS  174
A. proteus        GAGDQGLMFGYATDETPERCPCLWFLLRRFKLALRSKFEEARKKKIELAVAKGIKVSQVDATPELRDTIDFWWLHTDAKS  199
M. genitalium     NAGDQGITVGYAVNETKQLMPLGVLLAHSFLKQA------------------------------EKLTKQFDFLKNDMKS  163
M. pneumoniae     GAGDQGITVGYACSETEQLMPLGSIVAQALVQRA------------------------------ARIIDQYPFIKHDMKS  163
S. solfataricus   KIGKGSSDLVGIFEASKR-VPLSNDTSFGVGFAP------------------------------LTKLEKLVYETERHLN  185
M. jannaschii     RIGQGSMDLVDVFERQKNEVPLANDTSFGVGYAP------------------------------LSTTERLVLETERFLN  188
                  .......170.......180.......190.......200.......210.......220.......230.......240
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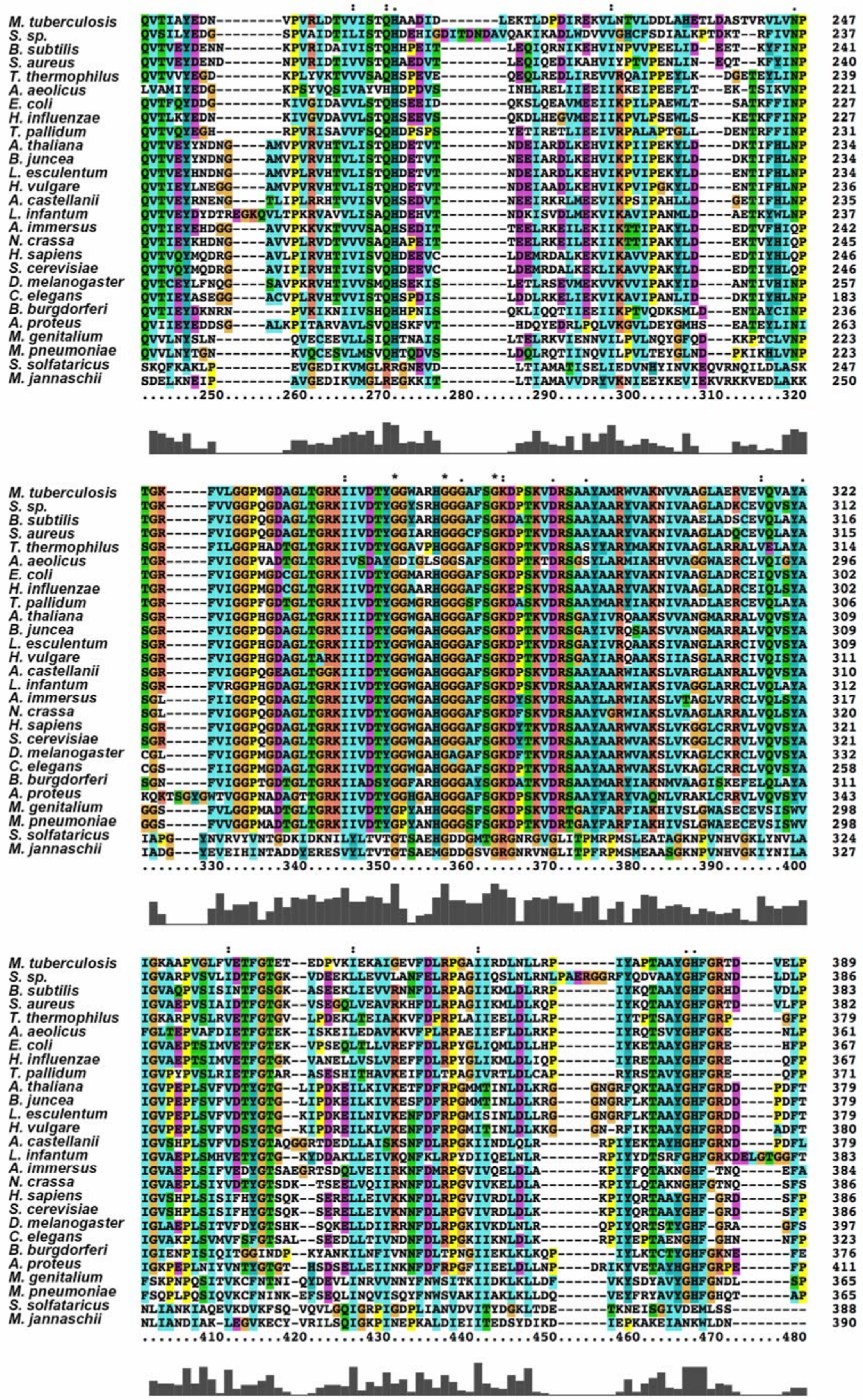

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                                          :   :.                         :                     .
M. tuberculosis  QVTIAYEDN--------VPVRLDTVVISTQHAADID-------LEKTLDPDIREKVLNTVLDDLAHETLDASTVRVLVNP  247
S. sp.           QVSILYEDG--------SPVAIDTILISTQHDEHIGDITDNDAVQAKIKADLWDVVVGHCFSDIALKPTDKT--RFIVNP  237
B. subtilis      QVTVEYDENN-------KPVRIDAIVISTQHHPEIT--------LEQIQRNIKEHVINPVVPEELID--EET--KYFINP  241
S. aureus        QVTVEYDEND-------NPVRIDTIVVSTQHAEDVT--------LEQIQEDIKAHVIYPTVPENLIN--EQT--KFYINP  240
T. thermophilus  QVTVVYEGD--------KPLYVKTVVVSAQHSPEVE--------QEQLREDLIREVVRQAIPPEYLK---DGETEYLINP  239
A. aeolicus      LVAMIYEDG--------KPSYVQSIVAYVHHDPDVS--------INHLRELIIEEIIKKEIPEEFLT---EK-TSIKVNP  221
E. coli          QVTFQYDDG--------KIVGIDAVVLSTQHSEEID--------QKSLQEAVMEEIIKPILPAEWLT----SATKFFINP  227
H. influenzae    QVTLKYEDN--------KIVGVDAVVLSTQHSEEVS--------QKDLHEGVMEEIIKPVLPSEWLS----KETKFFINP  227
T. pallidum      QVTVQYEGH--------RPVRISAVVFSQQHDPSPS--------YETIRETLIEEIVRPALAPTGLL---DENTRFFINP  231
A. thaliana      QVTVEYYNDNG----AMVPVRVHTVLISTQHDETVT--------NDEIARDLKEHVIKPIIPEKYLD----DKTIFHLNP  234
B. juncea        QVTVEYYNDNG----AMVPVRVHTVLISTQHDETVT--------NEEIARDLKEHVIKPIIPEKYLD----DKTIFHLNP  234
L. esculentum    QVTVEYHNDNG----AMVPLRVHTVLISTQHDETVT--------NDEIARDLKEHVIKPVIPEKYLD----ENTIFHLNP  234
H. vulgare       QVTIEYLNEGG----AMVPVRVHTVLISTQHDETVT--------NDEIAADLKEHVIKPVIPGKYLD----ENTIFHLNP  236
A. castellanii   QVTVEYRNENG----TLIPLRRHTVVISVQHSEDVT--------NEEIRKRLMEEVIKPSIPAHLLD----GETIFHLNP  235
L. infantum      QVTVEYDYDTREGKQVLTPKRVAVVLISAQHDEHVT--------NDKISVDLMEKVIKAVIPANMLD----AETKYWLNP  237
A. immersus      QVTIEYEHDGG----AVVPKKVKTVVVSAQHSEDIT--------TEELRKEILEKIIKTTIPAKYLD----EDTVFHIQP  242
N. crassa        QVTIEYKHDNG----AVVPLRVDTVVVSAQHAPEIT--------TEELRKEILEKIIKTTIPAKYLD----EKTVYHIQP  245
H. sapiens       QVTVQYMQDRG----AVLPIRVHTIVISVQHDEEVC--------LDEMRDALKEKVIKAVVPAKYLD----EDTIYHLQP  246
S. cerevisiae    QVTVQYMQDRG----AVIPIRVHTIVISVQHDEEVC--------LDEMRDALKEKLIKAVVPAKYLD----EDTIYHLQP  246
D. melanogaster  QVTCEYLFNQG----SAVPKRVHTIVVSMQHSEKIS--------LETLRSEVMEKVVKVVIPAKYID----ANTIVHINP  257
C. elegans       QVTIEYASEGG----ACVPLRVHTVVISTQHSPDIS--------LDDLRKELIEKVIKAVIPANLID----DKTIYHLNP  183
B. burgdorferi   QVTIEYDKNRN-------PVKIKNIIVSHQHHPNIS--------QKLIQQTIIEEIIKPTVQDKSMLD---ENTAYCINP  236
A. proteus       QVIIEYEDDSG----ALKPITARVAVLSVQHSKFVT---------HDQYEDRLPQLVKGVLDEYGMHS---EATEYLINI  263
M. genitalium    QVVLNYSLN---------QVECEEVLLSIQHTNAIS--------LTELRKVIENNVILPVLNQYGFQD---KKPTCLVNP  223
M. pneumoniae    QVVLNYTGN---------KVQCESVLMSVQHTQDVS--------LDQLRQTIINQVILPVLTEYGLND---PKIKHLVNP  223
S. solfataricus  SKQFKAKLP---------EVGEDIKVMGLRRGNEVD---------LTIAMATISELIEDVNHYINVKEQVRNQILDLASK  247
M. jannaschii    SDELKNEIP---------AVGEDIKVMGLREGKKIT---------LTIAMAVVDRYVKNIEEYKEVIEKVRKKVEDLAKK  250
                 .......250.......260.......270.......280.......290.......300.......310.......320

                                         :     *     * .   *:     .   .                    :    .
M. tuberculosis  TGK-----FVLGGPMGDAGLTGRKIIVDTYGGWARHGGGAFSGKDPSKVDRSAAYAMRWVAKNVVAAGLAERVEVQVAYA  322
S. sp.           TGK-----FVVGGPQGDAGLTGRKIIVDTYGGYSRHGGGAFSGKDPTKVDRSAAYAARYVAKNIVAAGLADKCEVQVSYA  312
B. subtilis      TGR-----FVIGGPQGDAGLTGRKIIVDTYGGYARHGGGAFSGKDATKVDRSAAYAARYVAKNIVAAELADSCEVQLAYA  316
S. aureus        TGR-----FVIGGPQGDAGLTGRKIIVDTYGGIARHGGGCFSGKDPTKVDRSAAYAARYVAKNIVAAGLADQCEVQLAYA  315
T. thermophilus  SGR-----FILGGPHADTGLTGRKIIVDTYGGAVPHGGGAFSGKDPTKVDRSASYYARYMAKNIVAAGLARRALVELAYA  314
A. aeolicus      TGR-----FVIGGPVADTGLTGRKIVSDAYGDIGLSGGSAFSGKDPTKTDRSGSYLARMIAKHVVAGGWAERCLVQIGYA  296
E. coli          TGR-----FVIGGPMGDCGLTGRKIIVDTYGGMARHGGGAFSGKDPSKVDRSAAYAARYVAKNIVAAGLADRCEIQVSYA  302
H. influenzae    TGR-----FVIGGPMGDCGLTGRKIIVDTYGGAARHGGGAFSGKEPSKVDRSAAYAARYVAKNIVAAGLADRCEIQLSYA  302
T. pallidum      TGR-----FVIGGPFGDTGLTGRKIIVDTYGGMGRHGGGSFSGKDASKVDRSAAYMARYIAKNIVAADLAERCEVQLAYA  306
A. thaliana      SGR-----FVIGGPHGDAGLTGRKIIIDTYGGWGAHGGGAFSGKDPTKVDRSGAYIVRQAAKSVVANGMARRALVQVSYA  309
B. juncea        SGR-----FVIGGPDGDAGLTGRKIIIDTYGGWGAHGGGAFSGKDPTKVDRSGAYIVRQSAKSVVANGMARRALVQVSYA  309
L. esculentum    SGR-----FVIGGPHGDAGLTGRKIIIDTYGGWGAHGGGAFSGKDPTKVDRSGAYIVRQAAKSIVANGLARRCIVQVSYA  309
H. vulgare       SGR-----FVIGGPHGDAGLTARKIIIDTYGGWGAHGGGAFSGKDPTKVDRSGAYIARQAAKSIIASGLARRCIVQISYA  311
A. castellanii   SGR-----FVIGGPQGEAGLTGGKIIIDTYGGWGAHGGGAFSGKDPSKVDRSAAYAARWIAKSLVARGLANRALVQVSYA  310
L. infantum      SGR-----FVRGGPHGDAGLTGRKIIVDTYGGWGAHGGGAFSGKDPSKVDRSAAYAARWIAKSIVAGGLARRCLVQLAYA  312
A. immersus      SGL-----FIIGGPQGDAGLTGRKIIVDTYGGWGAHGGGAFSGKDYSKVDRSAAYLARWIAKSLVTAGLVRRCLVQLSYA  317
N. crassa        SGL-----FVIGGPQGDAGLTGRKIIVDTYGGWGAHGGGAFSGKDFSKVDRSAAYVGRWIAKSLVAAGLARRALVQLSYA  320
H. sapiens       SGR-----FVIGGPQGDAGLTGRKIIVDTYGGWGAHGGGAFSGKDYTKVDRSAAYAARWVAKSLVKGGLCRRVLVQVSYA  321
S. cerevisiae    SGR-----FVIGGPQGDAGLTGRKIIVDTYGGWGAHGGGAFSGKDYTKVDRSAAYAARWVAKSLVKGGLCRRVLVQVSYA  321
D. melanogaster  CGL-----FVIGGPMGDAGLTGRKIIVDTYGGWGAHGAGAFSGKDFTKVDRSAAYAARWVAKSLVKAGLCKRCLVQVSYA  332
C. elegans       CGS-----FIIGGPMGDAGLTGRKIIVDTYGGWGAHGGGAFSGKDPTKVDRSAAYAARWVAKSLVKAGLCRRCLVQVSYA  258
B. burgdorferi   SGN-----FVIGGPTGDTGLTGRKIIADSYGGFARHGGGAYSGKDATKVDRSAAYMARYIAKNMVAAGISKEFELQLAYA  311
A. proteus       KQKTSGYGWTVGGPNADAGTTGRKIIVDTYGGHGAHGGGAFSGKDPSKVDRSAAYYARYVAQNLVRAKLCRRVLVQVSYV  343
M. genitalium    GGS-----FVLGGPMADTGLTGRKIIVDTYGPYAHHGGGSFSGKDPSKVDRTGAYFARFIAKHIVSLGWASECEVSISWV  298
M. pneumoniae    GGS-----FVVGGPMADTGLTGRKIIVDTYGPYANHGGGSFSGKDPTKVDRTGAYFARFIAKHIVSLGWAEECEVSISWV  298
S. solfataricus  IAPG---YNVRVYVNTGDKIDKNILYLTVTGTSAEHGDDGMTGRGNRGVGLITPMRPMSLEATAGKNPVNHVGKLYNVLA  324
M. jannaschii    IADG---YEVEIHINTADDYERESVYLTVTGTSAEMGDDGSVGRGNRVNGLITPFRPMSMEAASGKNPVNHVGKIYNILA  327
                 .......330.......340.......350.......360.......370.......380.......390.......400

                           :              :              :                        ..
M. tuberculosis  IGKAAPVGLFVETFGTET--EDPVKIEKAIGEVFDLRPGAIIRDLNLLRP-------IYAPTAAYGHFGRTD----VELP  389
S. sp.           IGVARPVSVLIDTFGTGK--VDEEKLLEVVLANFELRPAGIIQSLNLRNLPAERGGRFYQDVAAYGHFGRND----LDLP  386
B. subtilis      IGVAQPVSISINTFGSGK--ASEEKLIEVVRNNFDLRPAGIIKMLDLRRP-------IYKQTAAYGHFGRHD----VDLP  383
S. aureus        IGVAEPVSIAIDTFGTGK--VSEGQLVEAVRKHFDLRPAGIIKMLDLKQP-------IYKQTAAYGHFGRTD----VLFP  382
T. thermophilus  IGKARPVSLRVETFGTGV--LPDEKLTEIAKKVFDPRPLAIIEELDLLRP-------IYTPTSAYGHFGRP------GFP  379
A. aeolicus      FGLTEPVAFDIETFGTEK--ISKEILEDAVKKVFPLRPAEIIEFLDLRKP-------IYRQTSVYGHFGKE------NLP  361
E. coli          IGVAEPTSIMVETFGTEK--VPSEQLTLLVREFFDLRPYGLIQMLDLLHP-------IYKETAAYGHFGRE------HFP  367
H. influenzae    IGVAEPTSIMVETFGTGK--VANELLVSLVREFFDLRPYGLIKMLDLIQP-------IYRETAAYGHFGRE------QFP  367
T. pallidum      IGVPYPVSLRIETFGTAR--ASESHITHAVKEIFDLTPAGIVRTLDLCAP-------RYRSTAVYGHFGRE------QFP  371
A. thaliana      IGVPEPLSVFVDTYGTG--LIPDKEILKIVKETFDFRPGMMTINLDLKRG----GNGRFQKTAAYGHFGRDD----PDFT  379
B. juncea        IGVPEPFSVFVDTYGTG--LIPDKEILKIVKESFDFRPGMMTINLDLKRG----GNGRFLKTAAYGHFGRDD----PDFT  379
L. esculentum    IGVPEPLSVFVDTYGTG--KIPDKEILNIVKENFDFRPGMISINLDLLRG----GNGRFLKTAAYGHFGRDD----PDFT  379
H. vulgare       IGVPEPLSVFVDSYGTG--KIPDREILKLVKENFDFRPGMITINLDLKKG----GN-RFIKTAAYGHFGRDD----ADFT  380
A. castellanii   IGVSHPLSVFVDSYGTAQGGRTDEDLLAISKSNFDLRPGKIINDLQLR-------RPIYEKTAYHGHFGRND----PDFL  379
L. infantum      IGVAEPLSMHVETYGTG--KYDDAKLLEIVKQNFKLRPYDIIQELNLR-------RPIYYDTSRFGHFGRKDELGTGGFT  383
A. immersus      IGVAEPLSIFVEDYGTSAEGRTSDQLVEIIRKNFDMRPGVIVQELDLA-------KPIYFQTAKNGHF-TNQ-----EFA  384
N. crassa        IGVAEPLSIYVDTYGTSDK--TSEELVQIIRNNFDLRPGVIVKELDLA-------KPIYLQTAKNGHFGTNQ-----SFS  386
H. sapiens       IGVSHPLSISIFHYGTSQK--SERELLEIVKKNFDLRPGVIVRDLDLK-------KPIYQRTAAYGHF-GRD-----SFP  386
S. cerevisiae    IGVSHPLSISIFHYGTSQK--SERELLEIVKNNFDLRPGVIVRDLDLK-------KPIYQRTAAYGHF-GRD-----SFP  386
D. melanogaster  IGLAEPLSITVFDYGTSHK--SQKELLDIIRRNFDLRPGKIVKDLNLR-------QPIYQRTSTYGHF-GRA-----GFS  397
C. elegans       IGVAKPLSVMVFSFGTSAL--SEEDLLTIVNDNFDLRPGKIIKNLDLK-------RPIYEPTAENGHF-GHN-----NFP  323
B. burgdorferi   IGIENPISIQITGGINDP--KYANKILNFIVNNFDLTPNGIIEKLKLKQP-------IYLKTCTYGHFGKNE------FE  376
A. proteus       IGKPEPLNIYVNTYGTGT--HSDSELLEIINKNFDFRPGFIIEELDLLNP----DRIKYVETAYHGHFGRPE------FP  411
M. genitalium    FSKPNPQSITVKCFNTNI-QYDEVLINRVVNNYFNWSITKIIDKLKLLDF------VKYSDYAVYGHFGNDL------SP  365
M. pneumoniae    FSQPLPQSIQVKCFNINK-EFSEQLINQVISQYFNWSVAKIIAKLKLLDQ------VEYFRYAVYGHFGHQT------AP  365
S. solfataricus  NLIANKIAQEVKDVKFSQ-VQVLGQIGRPIGDPLIANVDVITYDGKLTDE------TKNEISGIVDEMLSS---------  388
M. jannaschii    NLIANDIAK-LEGVKECY-VRILSQIGKPINEPKALDIEIITEDSYDIKD------IEPKAKEIANKWLDN---------  390
                 .......410.......420.......430.......440.......450.......460.......470.......480
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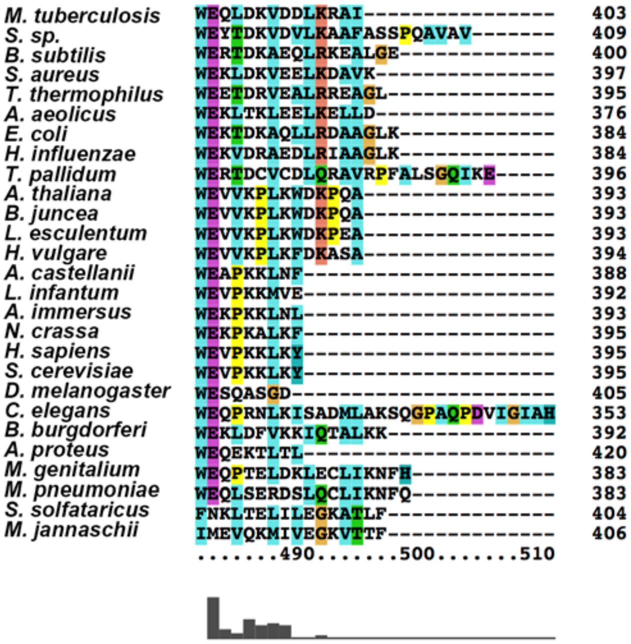

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M. tuberculosis    WEQLDKVDDLKRAI----------------   403
S. sp.             WEYTDKVDVLKAAFASSPQAVAV-------   409
B. subtilis        WERTDKAEQLRKEALGE-------------   400
S. aureus          WEKLDKVEELKDAVK---------------   397
T. thermophilus    WEETDRVEALRREAGL--------------   395
A. aeolicus        WEKLTKLEELKELLD---------------   376
E. coli            WEKTDKAQLLRDAAGLK-------------   384
H. influenzae      WEKVDRAEDLRIAAGLK-------------   384
T. pallidum        WERTDCVCDLQRAVRPFALSGQIKE-----   396
A. thaliana        WEVVKPLKWDKPQA----------------   393
B. juncea          WEVVKPLKWDKPQA----------------   393
L. esculentum      WEVVKPLKWDKPEA----------------   393
H. vulgare         WEVVKPLKFDKASA----------------   394
A. castellanii     WEAPKKLNF---------------------   388
L. infantum        WEVPKKMVE---------------------   392
A. immersus        WEKPKKLNL---------------------   393
N. crassa          WEKPKALKF---------------------   395
H. sapiens         WEVPKKLKY---------------------   395
S. cerevisiae      WEVPKKLKY---------------------   395
D. melanogaster    WESQASGD----------------------   405
C. elegans         WEQPRNLKISADMLAKSQGPAQPDVIGIAH   353
B. burgdorferi     WEKLDFVKKIQTALKK--------------   392
A. proteus         WEQEKTLTL---------------------   420
M. genitalium      WEQPTELDKLECLIKNFH------------   383
M. pneumoniae      WEQLSERDSLQCLIKNFQ------------   383
S. solfataricus    FNKLTELILEGKATLF--------------   404
M. jannaschii      IMEVQKMIVEGKVTTF--------------   406
                   .......490.......500.......510
```

Fig. S1 The sequence alignment was created using the Clustal X software. This histogram under the sequences indicates the similarity of each position. The organisms for other MATs sequences and their respective GenBank accession numbers were as follows: *Acanthamoeba castellanii*, Q95032; *Amoeba proteus*, O09486; *Arabidopsis thaliana*, NP_192094; *Ascobolus immersus*, P50304; *Aquifex aeolicus*, NP_213786; *Bacillus subtilis*, NP_390933; *Borrelia burgdorferi*, NP_212510; *Brassica juncea*, P49611; *Caenorhabditis elegans*, NP_872086; *Drosophila melanogaster*, CAA54567; *Escherichia coli*, NP_289514; *Haemophilus influenzae*, NP_439330; *Homo sapiens*, NP_005902; *Hordeum vulgare*, P50299; *Leishmania infantum*, O43938; *Lycopersicum esculentum*, XP_004252944; *Mycobacterium tuberculosis*, NP_215908; *Mycoplasma genitalium*, NP_072707; *Mycoplasma pneumoniae*, NP_109748; *Neurospora crassa*, XP_965430; *Rattus norvegicus*, NP_599178; *Staphylococcus aureus*, P50307; *Sulfolobus solfataricus* YP_005643019; *Synechocystis* sp., YP_007450090; *Thermus thermophilus* YP_144908; *Treponema pallidum*, NP_219231: *Methanocaldococcus jannaschii* Q58605

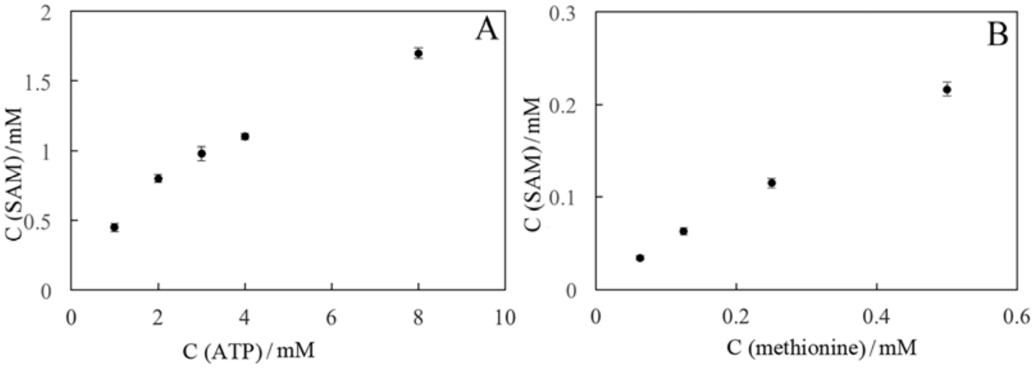

Fig. S2 To determine the kinetic parameters, accumulation of produced SAM vs. different substrates ATP or methionine concentration were measured by HPLC. The velocities of the production of SAM were used to draw Lineweaver-Burk plot (Fig. 3) and to estimate K_M and *V*max