ERRATUM

Detection and characterization of an ABC transporter in *Clostridium hathewayi*

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**Erratum to: Arch Microbiol
DOI 10.1007/s00203-008-0385-3**

Unfortunately, Fig. 1 was published with errors. The correct figure is given here.

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Fig. 1 Comparison of the amino acid sequence of the ATP-binding component CmpA from *C. hathewayi* with the predicted sequences of ATP transporters from other bacteria. *A*, gi 15595087: ABC transporter, ATP-binding protein [*Borrelia burgdorferi* B31]. *B*, gi 15896201: ATPase components of ABC transporter with duplicated ATPase domains (second domain is inactivated) [*Clostridium acetobutylicum* ATCC 824]. *C*, gi 19704636: ABC transporter ATP-binding protein [*Fusobacterium nucleatum* subsp. *nucleatum* ATCC 25586]. *D*, gi 15672054: ABC transporter ATP-binding protein [*Lactococcus lactis* subsp. *lactis* Il1403]. *E*, gi 15902034: ABC transporter, ATP-binding protein [*Streptococcus pneumoniae* TIGR4]. *F*, gi 15675942 ABC transporter, ATP-binding protein [*Streptococcus pyogenes* M1GAS]

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                                     ATPbinding site              Q-loop/lid
Q   1 MIGVNNVTLRIGKKALFEDVNIKFTEGNCYGMIGANGAGKSTFLRILSGQLEPTSGDIVMTPGQRLSFLQ
A  23 LITVSNLEVAFGERVLFKDVNIKFSPGNCYGIIGANGAGKSTFLKVLGGMIEASKGEISIPKNQRVAALE
B   1 MLTVNNVSLRYGGRKLFEDVNLKFTPGNCYGIIGANGAGKSTFLKILSGEIEPNTGDVSVDSNTRISVLK
C   1 MIATASLGMRFSGRKLFEDVNLKFTPGNCYGVIGANGAGKSTFLKVLGGELEATEGEVIFDKNKRMSVLK
D   1 MLTVSDISLQFSDRKLFDEVNIKFTPGNCYGLIGANGAGKSTFLKILDGEIQPTTGHISMGPNERMSVLR
E   1 MLTVSDVSLRFSDRKLFDDVNIKFTEGNTYGLIGANGAGKSTFLKILAGDIEPTTGHISLGPDERLSVLR
F   1 MLTVSDVSLRFSDRKLFDDVNIKFTAGNTYGLIGANGAGKSTFLKILAGDIEPSTGHISLGPDERLSVLR
                                          Walker A/P-loop

      ATP binding site
Q  71 QDHFKYDEYQVLDTVIMGNARLYEIMKEKDAIYMKEEFTDEDGIKAAELEGEFASMDGWEAESDAANLLN
A  93 QDQFAYDGYKVIDTVIMGHKRLYSVQKEKDEIYSKLDFTDEDGIRAGELEAEFSELGGYEAESDAAVLLK
B  71 QDHFQYDEYEVLETVIMGNERLYSIMKEKDALYAKPDFSEEDGIKASTLEGEFAELNGWEAESEAATLLQ
C  71 QDHFQYEDEEVLNVVLMGNKKLWDIMVEKNAIYAKTDFTDEDGIRAAELEGEFAELNGWEAETEAETLLM
D  71 QNHYDYEDQTPLDVVMMGNEKLFAINQEKNAIYMNPDATDDDFMKAAELAEFGEMGGYEAEADAARLLQ
E  71 QNHFDYEDERAIDVVIMGNEKLYSIMKEKDAIYMKEDFSDEDGVRAAELEGEFAELGGWEAESEASQLLQ
F  71 QNHFDYEEERAIDVVIMGNEQLYNIMKEKDAIYMKADFSEEDGVRAAELEGIFAELGGWEAESEASQLLQ

                                            ATP binding site
Q 141 GLGIETEFHYKYMKELNGAQKVKVLLAQALFGNPDILLLLDEPTNHLDLDAIAWLEEFLINFEN-TVIVVS
A 163 GLGIDEAIHNNLMGDVEGALKVRVLLAQALFGDPDVLLLLDEPTNNLDLQSIKWLEEFLINFEN-TVIVVS
B 141 GLGISTELHSKKMSELIGGEKVKVLLAQALFGNPGILLLLDEPTNHLDIKSIAWLEEFLIDFEG-TVIVVS
C 141 GLKIGADLHHKLMKELTEPEKVKVLLAQALFGEPDVLLLLDEPTNGLDVKAISWLENFIMGLENSTVIVVS
D 141 NLGIKAEQHTDLMANLTSGEHVKVLLAKALFGKPDVLLLLDEPTNGLDIQAIAWLEEFLINFEN-TVIVVS
E 141 NLNIPEELHYQNMSELANGEKVKVLLAKALFGKPDVLLLLDEPTNGLDIQSITWLEDFLIDFDN-TVIVVS
F 141 NLNIPEDLHYQNMSELANGDKVKVLLAKALFGKPDVLLLDEPTNGLDIQSISWLEDFLIDFEN-TVIVVS
                                        WalkerB D-loop

      ATP binding site
Q 210 HDRYFLNKVCTQIADIDYGKIQLYAGNYDFWYESSQLMVKQMKEANRKKEEKIKELQEFIQRFSANASKS
A 232 HDRHFLNQVCTHIVDIDYGKIQVYLGNYDFWYETSQILNKQLKDAKKRSEDKIAELKTFIQRFSSNASKS
B 210 HDRHFLNKVCTMIADVDYGKITLYVGNYDFWYKSSTLALEMTKDQNKKEEKIKELKDFIARFSANASKS
C 211 HDRHFLNKVCTHITDIDYGKIKMYVGNYDFWYESNELMKTLINNKNKKLEQKRQELQEFIARFSANASKS
D 210 HDRHFLNNVCTYMADLDYGKIKLYPGNYDFWKESSELALRLQGDQNRKAEEKIAELKEFIARFSANASKS
E 210 HDRHFLNKVCTHMADLDFGKIKLYVGNYDFWKESSELAAKLLADRNAKAEEKIKQLQEFVARFSANASKS
F 210 HDRHFLNKVCTHMADLDFGKIKLFVGNYDFWKQSSELAARLQADRNAKAEEKIKELQEFVARFSANASKS

Q 280 KQATSRKRALEKIELDDIKPSSRKYPYIDFRPAREIGNEVLTVQNLSKTIDGVKVLDNISFTLNREDKVA
A 302 KQATSRKKLIEKIVEDLKPSSRKFPYVNFKSERELGKNVLTIKNLIKEFEGNLILNKFSIIVEPQQKIV
B 280 KQATSRKKMLDKLNLEDIKPSNRKYPFIGFKPEREPGNDILTVENLSKTIDGEKVLNNVSFIVSKDDKIA
C 281 KQATSRKKQLEKLQLEDMQMSNRKYPFVEFKPEREAGNNLLKVENLSKTIDGIKVLDNVSFTIETGDKVV
D 280 KQATSRKKMLDKIEVEEFVPSSRKYPFVGFEQEREIGNDLLRVENLSVAIEGEMIIENTSFILNPGDKTV
E 280 RQATSRKKMLDKIELEEIVPSSRKYPFINFKAEREIGNDLLTVENLTVKIDGETILDNISFILRPDDKTA
F 280 KQATSRKKMLDKIELEEIVPSSRKYPFINFKAEREMGNDFLTVENLSVTIDGEKIIDNISFILRPGDKAA

                                     Q-loop/lid
Q 350 LVGPNEQAKTVLFKILSGEMEPD---EGDYKWGLTTSQCYFPKDNSAEFNNDD-TIVDWLTQYSP---EK
A 372 FLG-NPMFATFLFDIITNEDRN---YKGHYEWGSTVNFSYFNKDNGKYFD-LDLNLVDWLRQYSK---EQ
B 350 LVGDNEIAQTTLFKILSGEMEPD---SGSYKWGITITNAYFPKDNSEYFNDCDLSLVDWLRQYSE---EK
C 351 FLAKNDLVKTTLLSILAGEIEAD---SGTYTWGVTTSQAYMPRDNSQYFNNTDVNLIDWLRPYSP---DE
D 350 FIGQNDIQQTTLLRALMDDVEDNWTVTGDIKWGVTSSRSYLPKDNTKDFDTSD-SILDWLRQFVLTKEED
E 350 IIGQNDIQTTALIRAIMGDIDY----EGTVKWGVTTSQSYLPKDNSADFAGGE-SILDWLRQFAS-KEED
F 350 IIGQNDIQTTALMRALADDIDY----EGTIKWGVTTSRSYLPKDNSKDFATEE-SILEWLRQFAS-KGED
          WalkerA/P-loop
                  ABC transporter signature motif          D-loop
Q 413 EATYVRGFLGRMLFAGEDGVKKVRVLSGGEKVRCMLSKLMISGANVLMLDEPTDHLDMESITALNNGLVK
A 434 DETYIRGFLGRMLFSQDEALKKASVLSGGEKVRCMLAKAMLSGANVLILDQPTNHLDLEAITSLNSGLKE
B 414 SETYIRGFLGRMLFSGEEALKKASVLSGGEKVRCMLAKTMLTNANFLMFDQPTNHLDLESITALNNGLTN
C 415 HEAFIRGFLGRMLFSGDETLKKVSVLSGGEKVRCMLSKLMSGANVLLFDNPSDHLDLESITSLNKALIK
D 419 DNTYLRGFLGRMLFKGEESLKAVNVLSGGEKVRVMLSKMMLQRANVLVLDDPTNHLDLESISALNDGLKK
E 414 DNTFLRGFLGRMLFSGDEVNKPVNVLSGGEKVRVMLSKLMLLKSNVLVLDDPTNHLDLESISSLNDGLKN
F 414 DDTFLRGFLGRMLFSGDEVKKSVNVLSGGEKVRVMLSKLMLLKSNVLILDDPTNHLDLESISSLNDGIKD
                                            WalkerB
          H-loop/switch region
Q 483 FQGVLLFSSRDHQIVETTANRIMEIVNGQLIDKI-TTYDEYLASDEMARKRQVFTLTDEQMQENE
A 504 FKGVVLFTSHDHQFIDTVANRIIEFTPNGIIDRY-MTFSEYVDDAKIRDLRNNLYGNNAGFRL
B 484 YKSNLMFTSHDHEFIQTIANRIIEITNDGIIDRK-CTYDEYLEIQ
C 485 FKGTILFGAHDHEFQTVANRIIEITPKGLVDKV-TTYDEYLEDETIQARLDEMYS
D 489 FKGSILFASHDHEFINTIANHIVVLGKSGVIDRIGETYDDFLDNAEVQEKVKALWAD
E 484 FKESIIFASHDHEFIQTLANHIIVLSKNGVIDRIDETYDEFLENAEVQAKVKELWKD
F 484 FKESVIFASHDHEFIQTIANHIVVISKNGVIDRIDETYDEFLDNPEVQARVAELWK
                  ATP binding site
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