

TABLE S1: Sequence identity matrix of the seven ABC exporters of *E. faecalis* V583, LmrCD of *L. lactis* IL1406, PatAB of *S. pneumoniae* R6, and TM287/288 of *T. maritima* MSB8.

	Identity ^a									
	LmrCD	PatAB	TM287/288	EfrAB ^b	EfrCD ^c	EfrEF ^d	EF0942/41	EF1592/93	EF1733/32	EF2593/92
LmrCD	100.0	57.0	36.1	34.0	58.6	32.2	31.8	30.9	28.5	34.1
PatAB	57.0	100.0	37.2	35.9	57.4	31.3	32.3	33.5	27.1	33.8
TM287/288	36.1	37.2	100.0	38.2	38.8	35.4	39.5	35.9	29.9	40.4
EfrAB ^b	34.0	35.9	38.2	100.0	37.5	38.9	37.1	31.4	29.6	42.9
EfrCD ^c	58.6	57.4	38.8	37.5	100.0	32.9	33.7	31.5	29.1	35.0
EfrEF ^d	32.2	31.3	35.4	38.9	32.9	100.0	36.0	29.0	27.3	39.9
EF0942/41	31.8	32.3	39.5	37.1	33.7	36.0	100.0	29.2	29.8	41.1
EF1592/93	30.9	33.5	35.9	31.4	31.5	29.0	29.2	100.0	32.9	31.3
EF1733/32	28.5	27.1	29.9	29.6	29.1	27.3	29.8	32.9	100.0	29.4
EF2593/92	34.1	33.8	40.4	42.9	35.0	39.9	41.1	31.3	29.4	100.0

^a Sequence identity matrix was generated using ClustalW

^b EfrAB corresponds to EF2920/19

^c EfrCD corresponds to EF0789/90

^d EfrEF corresponds to EF2226/27

TABLE S2: Sequences of PCR primers for the generation of gene deletion knockouts in *E. faecalis*.

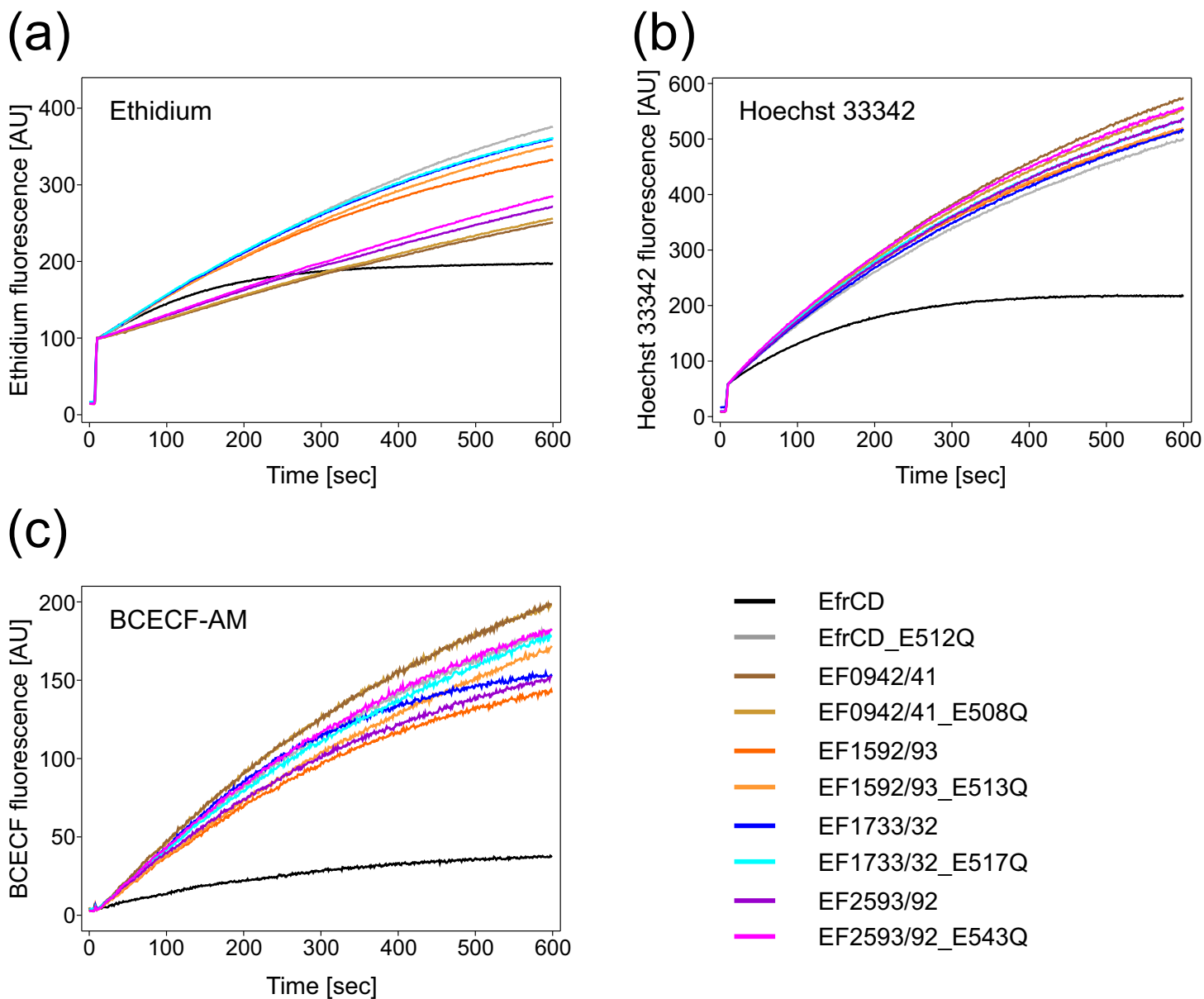
<i>efrAB</i> (<i>ef2920/19</i>)	5'-FW: atatatGCTCTTtagtCCAGGTCCGCAATCCTGCTTC 5'-RV: gtattaccgatttcGAATAAAAAGAGGTCCGGACAGAAGCG 3'-FW: cccgacctctttttattcGAAATCGGTAATACAAGCTGTCTGGCTAG 3'-RV: tatataGCTCTTCatgcGTGACCGTGGGTAATAACGAGTGC
<i>efrCD</i> (<i>ef0789/90</i>)	5'-FW: atatatGCTCTTtagtGACTGGGTGTTCTGGGATGAATGG 5'-RV: gccgtatattcctcCCTGCTTCTTCAGTGTTGGTCTGC 3'-FW: ctgaagaagcaggGAGGAATATACGGCAATTACGGCGC 3'-RV: tatataGCTCTTCatgcGAGCTAAACCGTTCGCTAAACCTGAC
<i>efrEF</i> (<i>ef2226/27</i>)	5'-FW: atatatGCTCTTtagtGCTTAGCTACATTTGCTATTGCTAGTTCCT 5'-RV: gtcggagcttGGGTTCTGCGATTTGCAAACAG 3'-FW: gcaggaaccAAGCTCCGACTCTTTACGCCAG 3'-RV: tatataGCTCTTCatgcCGTCCAACCTGGTAAATTGCACCTAGGAC
<i>ef0942/41</i>	5'-FW: atatatGCTCTTtagtCCGCAGCGACTGGAAGTCC 5'-RV: aataaccctgttcGGGCAAGACTAACTCGAAACAAGCTTC 3'-FW: gtagtcttgcccGAACAGGGTTATTATCGTGACCTTTACGAAGC 3'-RV: tatataGCTCTTCatgcCTTTAGCGACCAATATTGGCAGTGCTG
<i>ef1592/93</i>	5'-FW: atatatGCTCTTtagtGGTGTTTGGGAACATAATCATCCAGCG 5'-RV: agttgatcatgagCGACAAAAATAACAGCTAGCAGTAACTTATTC 3'-FW: gctgttattttgtcgCTCATGATCAACTAATGGCAAACATGCG 3'-RV: tatataGCTCTTCatgcCCGTCAGTCATTGAGTCTGCGAC
<i>ef1733/32</i>	5'-FW: atatatGCTCTTtagtCGAAGTCTTGTGGAAAGAGCAAATCCC 5'-RV: cataaaggccaccCGCTTTTTCTCCTAGATTATCCTATTCTCCC 3'-FW: gaggaaaagagcgGGTGGCCTTTATGCGGATATGTATCAG 3'-RV: tatataGCTCTTCatgcCCTAAACTTTCAGCGACACTTTCTGCAC
<i>ef2593/92</i>	5'-FW: atatatGCTCTTtagtCGTTTCGGCGAGTCCGTCAATCC 5'-RV: cctcatcatgaattacCTCCTCCTTTTGTACTTATAAGCGCC 3'-FW: gcaaaaaggaggagGTAATTCATGATGAGGCTTCAGGAACCATAGTC 3'-RV: tatataGCTCTTCatgcGGTGGGTTTTACTTGTGCCAGTCC

TABLE S3: Sequences of PCR primers for the generation of FX-compatible knockout and complementation vectors.

pCJK245_FX	
<i>ccdB</i> from pINIT_cat	<i>ccdB</i> _XbaI_FW: atatatctagaGGCCGCTCTTCTAGTCGACCTG <i>ccdB</i> _NcoI_RV: atatatccatggCGGTGGCCGCTCTTCATGC
pMSP3535_FX_em and pMSP3535_FX_cat	
pMSP3535_FX_em	pMSP3535_FX_FW: CGCTCTTCCGCaTaaTCGCTCACTGAC pMSP3535_FX_RV: atatatgctcttcTACTCATTGAGTGCCTCCTTATAAATTTATTTGTAG
pMSP3535_FX_cat	pMSP3535_FX_cat_FW: CGAACACGAACCGTCTTATCTCCCATTATATC pMSP3535_FX_cat_RV: GGAGAACTTGGAAGTAGCATTAGAGAAAGC
<i>cat</i> from pCJK245	<i>cat</i> _FW: GCGAACGAAAAACAATTGCAAAAGCAGATTG <i>cat</i> _RV: GCACACGAAAAACAAGTTAAGGGATGC

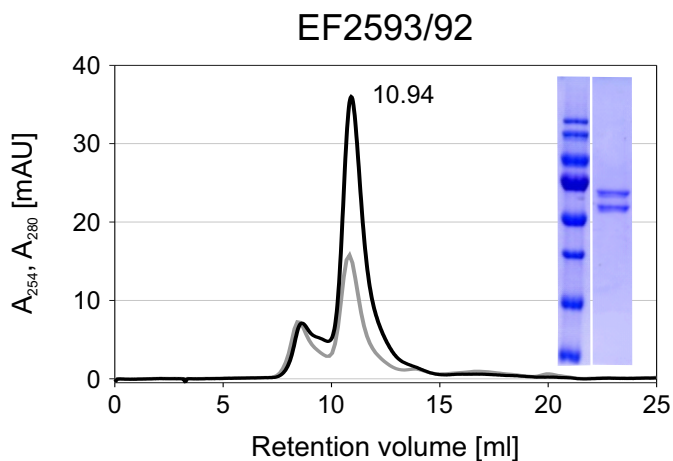
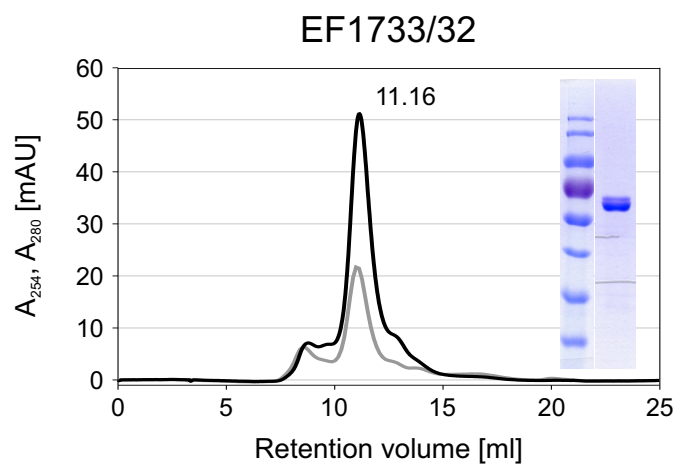
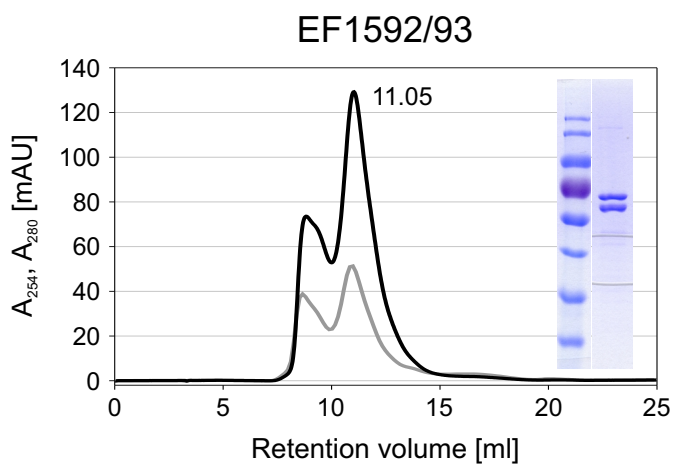
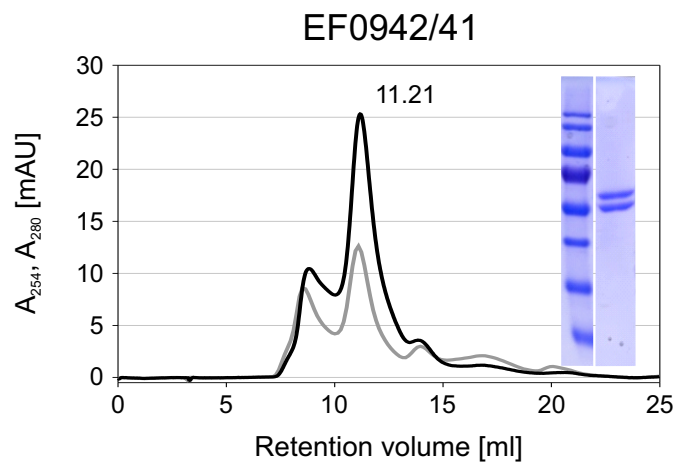
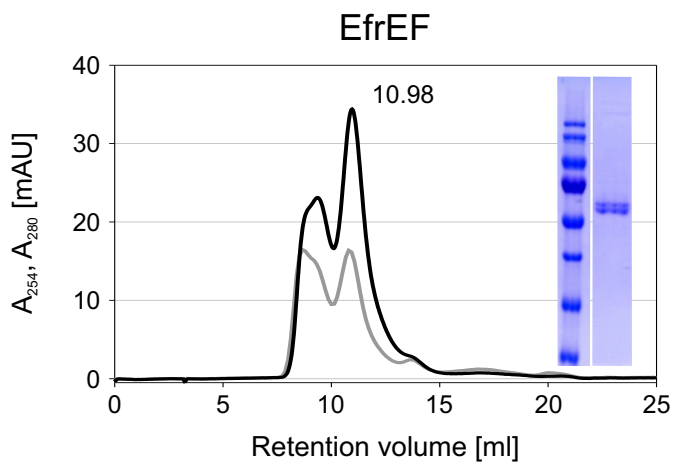
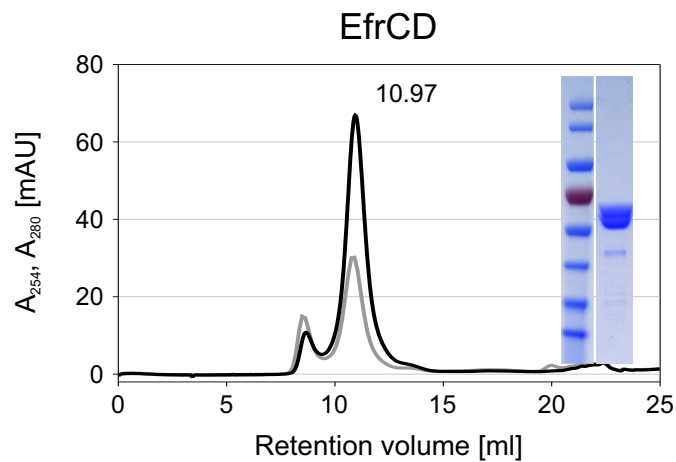
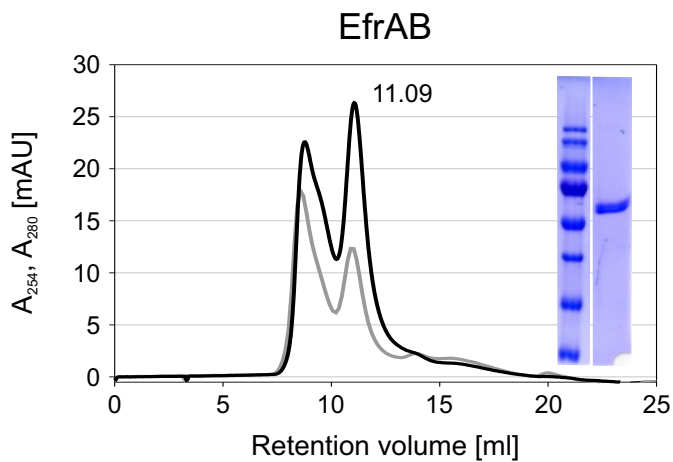
TABLE S4: Sequences of PCR primers for amplification of the open reading frames from genomic DNA of *E. faecalis* V583 and for the generation of the inactive E to Q mutant by mutating the conserved Walker B glutamate of the consensus site to a glutamine using QuikChange site-directed mutagenesis.

	Amplification of ORF from gDNA	QuikChange of E to Q mutant
<i>efrAB</i> (<i>ef2920/19</i>)	FW: atatatGCTCTTctagtAAGTTAATGTGGCGTTACACAATGCG RV: tatataGCTCTTCatgcTTCCTCATAGTCGCCTTCTTCAGC	FW: TTGATTTTAGATcAGGCGACTAGTTCAGTCG RV: CGACTGAACTAGTCGCCTgATCTAAAATCAA
<i>efrCD</i> (<i>ef0789/90</i>)	FW: atatatGCTCTTctagtGGTTCGGCGGCGGTGGCGTTCTGACCTTATTATTCAACACGCC RV: tatataGCTCTTCatgcTTCAAAAACAAATTGATTTTTATAAAGTCCGC	FW: GAATTATTAATTTTGGATcAAGCAACAAG RV: CTTGTTGCTTgATCCAAAATTAATAATTC
<i>efrCD</i> (<i>ef0789/90</i>) with its native promoter	FW: atatatGCTCTTctagtCACTTTATGATAGGAAAACTTGTGAAAAATTAAGTGTTCG RV: tatataGCTCTTCatgcTTCAAAAACAAATTGATTTTTATAAAGTCCGC	FW: GAATTATTAATTTTGGATcAAGCAACAAG RV: CTTGTTGCTTgATCCAAAATTAATAATTC
<i>efrEF</i> (<i>ef2226/27</i>)	FW: atatatGCTCTTctagtAAATTAATGAAAGAGTTTATTAAAGAAAATAAATGGATTGTTCTTGCG RV: tatataGCTCTTCatgcAGTGGTTTGAAATTGACTATTATATAAGCTGGCG	FW: CTCGATcAAGCAACTTCGAGTGTGGAC RV: CGAAGTTGCTTgATCGAGAATAACAACGGG
<i>ef0942/41</i>	FW: atatatGCTCTTctagtTTTGGTTTATTGAAATACGCAAAAAATTATCGAAAAACAA RV: tatataGCTCTTCatgcTTGTGCTTTTTGATTAAACTGTGCTTCGTAAAG	FW: GATGCTTATTTTAGATcAAGCGACCAGTTCAG RV: CTGAACTGGTCGCTTgATCTAAAATAAGCATC
<i>ef1592/93</i>	FW: atatatGCTCTTctagtAATAGTTTTGAATGGATTGGCAATATGCTAAAA RV: tatataGCTCTTCatgcGCTCTTAATAAGTCGTATTGCGATTGATATAAATG	FW: ATTTTAATTTTAGACcAAGCAACCTCCAGTAT RV: ATACTGGAGGTTGCTTgGTCTAAAATTAATAAT
<i>ef1733/32</i>	FW: atatatGCTCTTctagtTCCATATTCAAAAAATTAGGCTGGTTTTTTAAGC RV: tatataGCTCTTCatgcAACTCCGTACTTTGTAAGTACTGATACATATCCGC	FW: CCAAAATTTTAGTTTTAGATcAAGCAACCGCTAATATT RV: ATATTAGCGGTTGCTTgATCTAAAATAAATTTGG
<i>ef2593/92</i>	FW: atatatGCTCTTctagtATTAAGTACTGCAACGGATGTCATTATGGTCGG RV: tatataGCTCTTCatgcGGCTACTTCTTCTGAAAAGTACTGTTATATAAGTCAG	FW: CGTTTTAATTTTGGATcAAGCCACCTCAAGTG RV: CACTTGAGGTGGCTTgATCCAAAATTAATAACG



Supplementary Figure 1

Fluorescent dye transport mediated by EF0942/41, EF1592/93, EF1733/32 and EF2593/92. Ethidium (a), Hoechst 33342 (b) and BCECF-AM (c) transport was measured as shown in Figure 1. *L. lactis* NZ9000 $\Delta lmrA\Delta lmrCD$ cells expressing wildtype or inactive E to Q mutant transporters of EF0942/41, EF1592/93, EF1733/32 and EF2593/92 were supplemented with ethidium, Hoechst 33342, or BCECF-AM and fluorescence was measured. The traces for EfrCD shown in Figure 1 are plotted for reference.



[μ g of protein/ liter of expression culture]	
EfrAB	11
EfrCD	60
EfrEF	16
EF0942/41	11
EF1592/93	64
EF1733/32	24
EF2593/92	16

Supplementary Figure 2

SEC profiles of purified enterococcal ABC exporters. The proteins were expressed in and purified from *L. lactis*. Size-exclusion chromatography using a Superdex 200 increase 10/300 GL column was performed in 20 mM Tris/HCl pH 7.4, 150 mM NaCl and 0.03% β -DDM. The peak eluting at around 11 ml retention volume corresponds to the size of typical heterodimeric ABC exporters. A_{280} is shown in black and A_{254} in gray. Peak fractions used for ATPase activity measurements were analyzed by SDS-PAGE and shown as insets. The protein yields contained in the respective 11 ml peak fractions (0.5 ml) were normalized to $\mu\text{g/liter}$ of expression culture and listed in the table.

Supplementary Figure 3

Alignment of TMDs for homology model of EfrCD. Transmembrane domains (TMDs) of bacterial ABC exporters were aligned using MAFFT for model building.

EF0789 VEFDHVSFRYP-GDEEDTLKDISFSISIQPGEMIGIVGATGAGKSTLAQLIPRLFDPEEGKIEVGGVDLREVNHSRLKTVSVFLQKAILFSGTIAQNLRHGKR-DASEADMERASGGIAQAKFEIEKL
PatA LSFENVLFTYP-MDKPEMLKDVSTFTEPGQMVGVGATGAGKSTLAQLIPRLFDPEQGAIKIGGKDIRVSEGLTRKTVSVIVLQRAILFSGTIADNLRQGGK-NATLFEMERAANIAQASEFIHRM
LmrC VKFDHVSFSYP-NDEEPTLKDISEFEVAGOMVGVGATGAGKSTLAQLIPRLFDPEEGTVSVGGKDLTRVSRGTLKRNISIVLQKAILFSGTIAGNIKQGGK-DATDEEMTRAQIQAAEFITTK
EF0942 ITFDHVDFRYE-DEAGLALENINFTIPEKGSILGIIPTGSGKSTLIQLIPRFYDVSAGNLFINGVNRDWFLLTLRQQVASVPCAVLFTGTIRENLQWGF-NATDEDCWEALAIACKEFVQQL
EF2593 LAFEHVNRYRQ-HAENLALEDIDFSAKSGETVAIIGGTGSGKSTLMLNLPRLIDPERGRVEYDELDRVTVKLKLDRGHISAVPQETVLFSGTIKENLKWGRE-DATDEEIVAAKIAQHDFIISL
EF2920 LEFKNVTFAYPGHAESEPVLRNVSFKASPGETVAFIGSTGSGKSTLIQLIPRFYDVSSEGEILLDGVNVVEYKLSALRNKIYIPIKALLFTGTIADNRYGKE-DATLEEMERADIAQATEFVQSK
TM_0287 VSFENVEFRYF-ENTDPVLSGVNFSVKGSLVAVLGETGSGKSTLMLNLPRLIDPERGRVEYDELDRVTVKLKLDRGHISAVPQETVLFSGTIKENLKWGRE-DATDEEIVAAKIAQHDFIISL
EF2226 ICFDHVTFQYT-ETADPVLBNVSFVIEPKGKTAIVGATGAGKSTLVLKLLRINEVTAQTISMSGDIRSLSQQTIRQVISVVPKAFILFSGTILSNLLMGNA-KATTEEIRTALETQSSSEFDDSL
EF1592 VTFDHVSFHFSDDEPETPILSDVSFSAPKGETIIGLGETGSGKSTLMLNLPRLIDPERGRVEYDELDRVTVKLKLDRGHISAVPQETVLFSGTIKENLKWGRE-DATLEEIVAAKIAQHDFIISL
EF0790 VALNHVVFQYN--PETPVLKDVSIHVDKEMVALVGPVSGKSTLMLNLPRLIDPERGRVEYDELDRVTVKLKLDRGHISAVPQETVLFSGTIKENLKWGRE-DATLEEIVAAKIAQHDFIISL
LmrD IQENLDFEYL--PGKPVLLKKNVDVKKQOMVALVGPVSGKSTLMLNLPRLIDPERGRVEYDELDRVTVKLKLDRGHISAVPQETVLFSGTIKENLKWGRE-DATLEEIVAAKIAQHDFIISL
PatB VEISHIDFSYL--PDKPILKDVSIASAEKGMVAUVGPTGSGKSTLMLNLPRLIDPERGRVEYDELDRVTVKLKLDRGHISAVPQETVLFSGTIKENLKWGRE-DATLEEIVAAKIAQHDFIISL
EF0941 VEFKVDVFSYT--PTRPLIENFNLIAEPGETIAIVGRGAGKSTLMLNLPRLIDPERGRVEYDELDRVTVKLKLDRGHISAVPQETVLFSGTIKENLKWGRE-DATLEEIVAAKIAQHDFIISL
EF2227 IEFKNVQFGYT--PEKILMKNVDFSVQPKKTVAVIGPTGAGKSTLMLNLPRLIDPERGRVEYDELDRVTVKLKLDRGHISAVPQETVLFSGTIKENLKWGRE-DATLEEIVAAKIAQHDFIISL
EF2592 VSEFHVAFGYS--PEKLLMKDFNLNVKPGEMVAIVGPTGAGKSTLMLNLPRLIDPERGRVEYDELDRVTVKLKLDRGHISAVPQETVLFSGTIKENLKWGRE-DATLEEIVAAKIAQHDFIISL
EF2919 VEFENVVFSYD--PEKPLIRNLFKVDAGOMVAIVGPTGAGKSTLMLNLPRLIDPERGRVEYDELDRVTVKLKLDRGHISAVPQETVLFSGTIKENLKWGRE-DATLEEIVAAKIAQHDFIISL
TM_0288 IEFKNVWFSYD--KKKPVLLKKNVDVKKQOMVALVGPVSGKSTLMLNLPRLIDPERGRVEYDELDRVTVKLKLDRGHISAVPQETVLFSGTIKENLKWGRE-DATLEEIVAAKIAQHDFIISL
EF1593 VDFQHVYFRYE--EGKNILTDVSFHTPEQOTIALVGPVSGKSTLMLNLPRLIDPERGRVEYDELDRVTVKLKLDRGHISAVPQETVLFSGTIKENLKWGRE-DATLEEIVAAKIAQHDFIISL
SAV1866 IDIDHVSFQYN-DNEAPILKKNVDVKKQOMVALVGPVSGKSTLMLNLPRLIDPERGRVEYDELDRVTVKLKLDRGHISAVPQETVLFSGTIKENLKWGRE-DATLEEIVAAKIAQHDFIISL
VC_MsbA IEFKRVVFSYD--GKNEVLKKNISFVANEGETVALVGPVSGKSTLMLNLPRLIDPERGRVEYDELDRVTVKLKLDRGHISAVPQETVLFSGTIKENLKWGRE-DATLEEIVAAKIAQHDFIISL
EC_MsbA VDFKVDVFTYQ-GKEKPALSHVSFSTPQKGTVALVGRSGSGKSTLMLNLPRLIDPERGRVEYDELDRVTVKLKLDRGHISAVPQETVLFSGTIKENLKWGRE-DATLEEIVAAKIAQHDFIISL
ST_MsbA VEFKRVVFSYD--GKNEVLKKNISFVANEGETVALVGPVSGKSTLMLNLPRLIDPERGRVEYDELDRVTVKLKLDRGHISAVPQETVLFSGTIKENLKWGRE-DATLEEIVAAKIAQHDFIISL
EF1733 ISMKIDVFSYP-KEETVALENQFSLQGETIIGVIGKTGAGKSTLMLNLPRLIDPERGRVEYDELDRVTVKLKLDRGHISAVPQETVLFSGTIKENLKWGRE-DATLEEIVAAKIAQHDFIISL

EF0789 AEGYDAPVEERNNSFGGQKORLSITRGVIGEPKILILDDSTSDALDARERLVREALDKELKETTIVIAQKISSVVHADRIILVLDNGRLVGGEGTHEELAAT-NEVVOEIVETQKCKEEA-----
PatA EKTTFEAPVEERGNTNFGGQKORMSIAIRGIVSNRILIFDDSTSDALDAKSERLVREALNKDLKGTITIIIAQKISSVVHADRIILVLDNGRLVGGEGTHADLVAN-NAVYREIVETQK-----
LmrC DGQYSEVEVEERNNSFGGQKORLSITRGVVKNEPVLILDDSTSDALDAKSEKLVREALNKELKETTIIIAQKISSVVHADRIILVLDNGRLVGGEGTHQELVAE-NKIVQEIYDQKQED-----
EF0942 DQGLDTPVNEGGKNSFGGQKORLTIARALIRKPHLLILDDSTSDALDYQDLNLRALQKERAETVILISQVSSSIATANQILVLDGKAVAGLTHEELLTS-SKEQOEIVASQEEETHAN----
EF2593 AEGLDSHVEGGGNSFGGQKORLTIARALVKEADVVVFDSSFDALDFKIDANLRKALKEQMTDAIVVLAQEVSTVMEASTILVLDGKLVGKCTHEELLAN-NQTYQEIIVHSQLEEDLA----
EF2920 PQGYDEPLSGGNTNFGGQKORLTIARAIIRNPEIYIFDSSFDALDYQDLNLRARLKKETTESVILVIAQVSGTIMHADRIIVLNEGDDVVGIGTHRELLLET-CEIYDIASQLESEELA----
TM_0287 PEGYDVRVERGGRNFGGQKORLSIARALVKKPKVILDDSTSDVDEITEKRILDLGKRYTKGCTTIIIAQKISSVVHADRIILVLDGKAVAGLTHEELLTS-SKEQOEIVASQEEETHAN----
EF1592 PQGIESFVAQGGNSYSGGQKORMCTARALIKADVYIFDSSFDALDYKIDALRAALHAQMSDKTLLVIAQRLSTIMNADNIVLDEGRIVDQGTADLLTT-NSYVQDFAKSQGILEK-----
EF0790 PEGYAIIVGERGVGLSGGQKORLSIARALTKDPAILILDDTTSVDMETESKIQKELGRLTEKKTTFIIAHRISVREANLILMMEKGRVVEGTHSELVEQ-KGKVFVYQKGLGTLKEGESRG
EF2227 EQGYDEITTEENNLFTGOKQLVSIARTIITNPELILDEATSNVDITVEAKIQKAMDEAIKGRTSFVIAHRLKTIILNADRIIVLRDGEVIEEGNHHELVEQ-DGFVYAEVYKNOVFVE-----
LmrD PDKYETHVSDDESFSVGGQKQISARTIITNPELILDEATSNVDITVEEQIQWAMEAAIAGRTSFVIAHRLKTIILNADKIVLVLDGKAVAGLTHEELLTS-SKEQOEIVASQEEETHAN----
PatB PDKYDILDDQDQISFAGQKQLSIARTIMISNPPMILDEATSNVDITVEEQIQWAMEAAIAGRTSFVIAHRLKTIILNADQITVLKDGVEIERNHHELLKL-GGFVYSELVHNOVFVE-----
EF0941 PQGLDTEIGSQVKISGQORQMTIARTIMISNPPMILDEATSNVDITVEEQIQWAMEAAIAGRTSFVIAHRLKTIILNADQITVLKDGVEIERNHHELLKL-GGFVYSELVHNOVFVE-----
EF2227 PQGYDITISENGALSGGQOQLTIARTIILANPPVILDEATSNVDITVEEQIQWAMEAAIAGRTSFVIAHRLSTIENADLILVMKNGDIEKGTQHELLQA-PTLVASLNSQFQTT-----
EF2592 PEGYQITLNEASNISQGORLTIARAFLANPDLILDEATSNVDITVEEQIQWAMEAAIAGRTSFVIAHRLSTIENADLILVMKNGDIEKGTQHELLQA-PTLVASLNSQFQTT-----
EF2919 PDGYEMEINSEGDVNSLQKOLLTIARAVISDEKILILDEATSNVDITVEEQIQWAMEAAIAGRTSFVIAHRLSTIENADLILVMKNGDIEKGTQHELLQA-PTLVASLNSQFQTT-----
TM_0288 PEGYEVLTLDNGEDLSQGOROLLTIARAFLANPKILILDEATSNVDITVEEQIQWAMEAAIAGRTSFVIAHRLSTIENADLILVMKNGDIEKGTQHELLQA-PTLVASLNSQFQTT-----
EF1593 KDGYEIVVEERGSTLSAGORQLISFARALLADEKILILDEATSNVDITVEEQIQWAMEAAIAGRTSFVIAHRLSTIENADLILVMKNGDIEKGTQHELLQA-PTLVASLNSQFQTT-----
SAV1866 PQGYDEVEGERGVKLSGGQKORLSIARTIPLNPELILDEATSDLDSESIICEALDVLSKDRITLIVAHRLSTIENADLILVMKNGDIEKGTQHELLQA-PTLVASLNSQFQTT-----
EF1733 PNTHAKVIERGASYSQGORQLISPARTIVTPKILVLDDEANIDTEPEGLICEGLAKMRCRTIITIAHRLSTIENADLILVMKNGDIEKGTQHELLQA-PTLVASLNSQFQTT-----
VC_MsbA PQGLDTEVIGENGTSLSGGQKORLTIARALLRDPVILILDEATSDLDSESERAIQALDELQKNRTSLVIAHRLSTIEQADEIVVVEDEGIIERGRHADLLAQ-DGAVACLHRIQFGE-----
EC_MsbA DNGLDTEVIGENGVLLSGGQKORLTIARALLRDPVILILDEATSDLDSESERAIQALDELQKNRTSLVIAHRLSTIEQADEIVVVEDEGIIERGRHADLLAQ-DGAVACLHRIQFGE-----
ST_MsbA DNGLDTEVIGENGVLLSGGQKORLTIARALLRDPVILILDEATSDLDSESERAIQALDELQKNRTSLVIAHRLSTIEQADEIVVVEDEGIIERGRHADLLAQ-DGAVACLHRIQFGE-----
EF1733 PEGYDVMVERGVLSGGQKORLSIARALIVEEELLILDDALSADAKTEEAILSNLKEITRQEKTTIIAHLSSVMHAKELVLVDEGKIITERGTHPELLAQ-KGVYQRMVEKQLEAKIEGSES

Supplementary Figure 4

Alignment of NBDs for homology model of EfrCD. Nucleotide binding domains (NBDs) of bacterial ABC exporters were aligned using MAFFT for model building.