

# Determination of the Quaternary Structure of a Bacterial ATP-Binding Cassette (ABC) Transporter in Living Cells

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## SUPPLEMENTAL INFORMATION

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P. aeruginosa -----MGQIRVSGLGKAYKQYPNRWSRLFEWLVFPSPRRHHLHWILREVEFTIEPGE 52
E. coli08 -----MSYIRVNVVNGKAYRQYHSKTGRLIEWLSPLNTRHNLKWLSDINFEVAPGE 52
E. coli09a -----MSIKVQHVHGKAYKYYPKWNRVIEKLLPGDKPRHSKWKVLDKDNFVSIEPGE 51
K. pneumoniae01 ---MHPVINFSHVTKKEYPLYHHIGSGIKDLIFHPKRAFQLLKGKRYLAIEDVSFTVGKGE 57
K. pneumoniae08 ---MEPVINFSNVTKKEYPLYHHIGSGIKDLVFPKRAFQLLKGKRYLAIEDISFTVAKGE 57
A. salmonicida -----MSEPVLAVSGVNKSFPIYRSWPQALWHALNPKADVQVQALRDIELTVYRGE 52
Y. enterocolitica0_3 MTSLIFKNVMTSYPYIYNAHSQSLRNQLVVRVSTGGRIGGSRGEVVTVTALDNISFELNSGD 60
E. coliK1 -----MIKIENLTKSYRTPPTGRHYVFKNLNIIFPKGY 32
E. coliK5 -----MIKIENLTKSYRTPPTGRHYVFKDLNIEIPSGK 32
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### Walker A

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P. aeruginosa AVGIIVGVNGAGKSTLLKMIAGTTQPTCGEIRVAGRVAALLELGMGFHPDFTGRQNVFMAG 112
E. coli08 AVGIIVGVNGAGKSTLLKLTGTSTRPTTGEIEISGRVAALLELGMGFHSDFTGRQNVYMSG 112
E. coli09a AVGIIVGVNGAGKSTLLKLTGTQPTKGSIEIQGRVAALLELGMGFHPDFTGRQNVYMSG 111
K. pneumoniae01 AVALIGRNGAGKSTSLGLVAGVIKPTKGTVTTEGRVASMELGGGFHPDLTGRENIYLNA 117
K. pneumoniae08 AVALIGRNGAGKSTSLGLVAGVIKPTKGSVTTTHGRVASMELGGGFHPDLTGRENIYLNA 117
A. salmonicida TIGIVGHNGAGKSTLLQLITGVMQPDGQITRTGRVVGLELGGGFNPEFTGRENIFFNG 112
Y. enterocolitica0_3 SVGLIGHNGAGKSTLLRMTMAGIYPASSGEIIREGSAVTVFELGAGMDPELGSYENIMRML 120
E. coliK1 NIALIGQNGAGKSTLLRIIGGIDRPSGNIITEHKISWPVGLAGGFQGSALTGRENVKFVA 92
E. coliK5 SVAFIGRNGAGKSTLLRMIGGIDRPSGKIITNKTISWPVGLAGGFQGSALTGRENVKFVA 92
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### Signature

### Walker B

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P. aeruginosa QLLGMQVEEIQALMPDIEAFIEAIEGAEIEQPVRTYSSGMQMLAFSVATARRPDILIVDEA 172
E. coli08 QLLGLSSEKITELMPQIEEFAEIGDYIDQPVRYSSGMQVRLAFSVATAIRPDVLIIDEA 172
E. coli09a LMMGLGREEIERLMPDIEAFADIGDYIEFPVRIYSSGMQMLAFAVATASRPDILIVDEA 171
K. pneumoniae01 TLLGLRRKEVQQRMERIEEFSELGEFIDEPIRVYSSGMLAKLGFSVISQVEPDILIIIDEV 177
K. pneumoniae08 TLLGLRRKEVQQRMERIEEFSELGEFIDEPIRVYSSGMLAKLGFSVISQVEPDILIIIDEV 177
A. salmonicida AILGMSQREMDRLERILSFAAIGDFIDQPVKNYSSGMMVRLAFSVIINTDPDVLIIDEA 172
Y. enterocolitica0_3 LLLGNSVASAKSKIPEIEEFCELGDFLVLPVRYSSGTMRLMFAVATSMRPEILLIDEM 180
E. coliK1 RLYAK-RDELNERVDFVEESELGKYFDMPIKTYSSGMRSRLAFGLSMAFKFDYYLIDEI 151
E. coliK5 RLYAK-QEELKEKIEFVEEFAELGKYFDMPIKTYSSGMRSRLGFLSMAFKFDYYIVDEV 151
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	<u>D-loop</u>	<u>H-loop</u>	
P. aeruginosa	LSVGDAYFQHKSFERIRSRFRKAGTTLTLLVSHDRSAIQSICDSAILLEQGRMAMRGRPEEV		232
E. coliO8	LSVGDAYFQHKSFERIRKFRQEGTTLTLLVSHDKQAIQSI CDRAILLNKGQIEMEGEPEAV		232
E. coliO9a	LSVGDSTRFQAKCYARIADFKEQGTTLTLLVSHSAGDIVKHCDRAIFLNKNGDICMDGTARDV		231
K. pneumoniaeO1	LAVGDIAFQAKCIQTIRDFKRRGVTILFVSHNMSDVEKICDRVIWIENHRLREVGSAERI		237
K. pneumoniaeO8	LAVGDISFQAKCIKTIREFKKGVITILFVSHNMSDVERICDRVVWIENHRLREIGSAERI		237
A. salmonicida	LAVGDDAFQQRKCYARLKLQSQGVITILLVSHAAGSVIELCDRAVLLDRGEVLLQGEPKAV		232
Y. enterocoliticaO_3	FGTGDAAFQEKAEKMRDWIAGSDIFVFASHDRSLIKKLCNRIFRLEHGLIYEESMDIL-		239
E. coliK1	TAVGDAKFKKCSDFDKIREKSHLIMVSHSERALKEYCDVAIYLNKEGQGFYKNVTEA		211
E. coliK5	TAVGDARFKEKCAQLFKERHKESFLMVSHSLNSLKEFCDVAIIVFKNSYIIGYYENVQSG		211
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P. aeruginosa	MDYYNALLAEREGQTVRQEMLADGQVRTISGTGEAAILDVRMVDQRQRALEVVVEVQAVT		292
E. coliO8	MDYYNALLADKQNSIKQVEHNG-KTQTVSGTGEVITISEVHLLDEQGNVTEFVSVGHRVS		291
E. coliO9a	TNRYLDELFGKPKDSATKSATAISSAGSESQMSLDEIEDVYHTRPGYRPEEYRWGQGA		291
K. pneumoniaeO1	IELYKQAMA-----		246
K. pneumoniaeO8	IELYKQAMA-----		246
A. salmonicida	VHNYHKLHMEGDERARFRYHLRQTGRGDSYISDESTSEPKIKSAPGILSVDLQPQSTVW		292
Y. enterocoliticaO_3	-----		
E. coliK1	IADYKKDL-----		219
E. coliK5	IDEYKMYQDLIDIE-----		224
P. aeruginosa	LEVEVEVRQDIERLILGFMIKDRLGQPMYGINTHRLDKALTDLKAGERITYRFAFDMRLG		352
E. coliO8	LQVNVVEVKDDIPELVVGYMIKDRLGQPIFGTNTYHLNQTTLTSLKKGKRSFLFSFDARLG		351
E. coliO9a	KIIDYHIQSAGVDFPPLSTGNQQTDFLMKVVFEYDFDCVVPGLIKTLDLGLFLYGTNSFL		351
K. pneumoniaeO1	-----		
K. pneumoniaeO8	-----		
A. salmonicida	YESKGAVLSDVHIESF-----		308
Y. enterocoliticaO_3	-----		
E. coliK1	-----		
E. coliK5	-----		
P. aeruginosa	KGHYSVALSLRDLSDHLDNRNFEWRDYGLVFHVINNRQEDFVGCSSLGAETHISRSGEAL		412
E. coliO8	VGSYSVAVALHTSSTHLGKNYEWDRDLAVVFNVVNTEQQEFGVSVLWLPPELEIS-----		404
E. coliO9a	ASEGRENISVSRGDVRFKFLSPVLDLNSGDYLLSFGISAGNPQTDMTPLDRRYDSIILHV		411
K. pneumoniaeO1	-----		
K. pneumoniaeO8	-----		
A. salmonicida	-----		
Y. enterocoliticaO_3	-----		
E. coliK1	-----		
E. coliK5	-----		
P. aeruginosa	DPTSAESTP-----		421
E. coliO8	-----		
E. coliO9a	TKSMDFWGVIDLKSSFTSYQ		431
K. pneumoniaeO1	-----		
K. pneumoniaeO8	-----		
A. salmonicida	-----		
Y. enterocoliticaO_3	-----		
E. coliK1	-----		
E. coliK5	-----		

**FIGURE S1.** Amino acid alignment of Wzt of *Pseudomonas aeruginosa* with other bacterial ATP-binding proteins involved in PS export. Asterisks represent identical amino acids and periods represent similar amino acids. As seen, *Pseudomonas aeruginosa* Wzt N terminus contains the highly conserved ATP-binding motif consisting of sites Walker A and Walker B, and other motifs, while the C terminus shows significant sequence diversity of the PS binding domain. Alignments were performed by using the CLUSTAL program.<sup>1</sup>

## REFERENCES

1. M. A. Larkin, *et al.*, Clustal W and Clustal X version 2.0, *Bioinformatics*, 2007, **23**, 2947-2948.