

# 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. coliO8         -----MSYIRVNVVNGKAYRQYHSKTGRLEIWLSPLNTRHNLKWLSDINFEVAPGE 52
E. coliO9a       -----MSIKVQHVGKAYKYYPKWNRVIEKLLPGDKPRHSSKWWLKDINFSIEPGE 51
K. pneumoniaeO1  ---MHPVINFSHVTKKEYPLYHHIGSGIKDLIFHPKRAFQLLKGKRYLAIEDVSFTVGKGE 57
K. pneumoniaeO8  ---MEPVINFSNVTKKEYPLYHHIGSGIKDLVFPKRAFQLLKGKRYLAIEDISFTVAKGE 57
A. salmonicida   -----MSEPVLAVSGVKNKSFPIYRSPWQALWHALNPKADVQVQALRDIETVYRGE 52
Y. enterocoliticaO_3  MTSLIFKNVTMSYPIYNAHSQSLRNQLVVRVSTGGRIGGSRGEVVTVTALDNISFELNSGD 60
E. coliK1        -----MIKIENLTKSYRTPPTGRHYVFKNLNIIIFPKGY 32
E. coliK5        -----MIKIENLTKSYRTPPTGRHYVFKDLNIEIPSGK 32
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### Walker A

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P. aeruginosa      AVGIIVGVNGAGKSTLLKMIAGTTQPTCGEIRVAGRVAALLELGMGFHPDFTGRQNVFMAG 112
E. coliO8         AVGIIVGVNGAGKSTLLKLTGTSTRPPTGEIEISGRVAALLELGMGFHSDFTGRQNVYMSG 112
E. coliO9a       AVGIIVGVNGAGKSTLLKLLTGTTPQTKGSIEIQGRVAALLELGMGFHPDFTGRQNVYMSG 111
K. pneumoniaeO1  AVALIGRNGAGKSTSLGLVAGVIKPTKGTVTTEGRVASMELGGGFHPPELTGRENIYLNA 117
K. pneumoniaeO8  AVALIGRNGAGKSTSLGLVAGVIKPTKGSVTTTHGRVASMELGGGFHPPELTGRENIYLNA 117
A. salmonicida   TIGIVGHNGAGKSTLLQLITGVMQPDGQITRTGRVVGLELGGGFNPEFTGRENIFFNG 112
Y. enterocoliticaO_3  SVGLIGHNGAGKSTLLRMTMAGIYPASSGEIIREGSVATVFELGAGMDPELGSYENIMRML 120
E. coliK1        NIALIGQNGAGKSTLLRIIGGIDRDPDSGNIITEHKISWPVGLAGGFQGSALTGRENVKFVA 92
E. coliK5        SVAFIGRNGAGKSTLLRMIGGIDRDPDSGKIITNKTISWPVGLAGGFQGSALTGRENVKFVA 92
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### Signature

### Walker B

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P. aeruginosa      QLLGMQVEEIQALMPDIEAFAEIGEAEIEQPVRTYSSGMQMLAFSVATARRPDILIVDEA 172
E. coliO8         QLLGLSSEKITELMPQIEEFAEIGDYIDQPVRYSSGMQVRLAFSVATAIRPDVLIIDEA 172
E. coliO9a       LMMGLGREEIERLMPDIEAFAEIDIGDYIEFPVRIYSSGMQMLAFAVATASRPDILIVDEA 171
K. pneumoniaeO1  TLLGLRRKEVQQRMERIEEFSELGEFIDEPIRVYSSGMLAKLGFVSIQVPEPDLIIDEV 177
K. pneumoniaeO8  TLLGLRRKEVQQRMERIEEFSELGEFIDEPIRVYSSGMLAKLGFVSIQVPEPDLIIDEV 177
A. salmonicida   AILGMSQREMDRLERILSFAAIGDFIDQPVKNYSSGMMVRLAFSVIINTDPDVLIIIDEA 172
Y. enterocoliticaO_3  LLLGNSVASAKSKIPEIEEFCELGDFLVLPVRTYSSGMTMLMFVAVATSMRPEILLIDEM 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	LSVGDAYFQHKSFERIRSRFRKAGTTLTLLIVSHDRSAIQSICDSAILLEQGRMAMRGRPEEV		232
E. coliO8	LSVGDAYFQHKSFERIRKFRQEGTTLTLLVSHDKQAIQSI CDRAILLNKGQIEMEGEPEAV		232
E. coliO9a	LSVGDSTRFQAKCYARIADFKEQGTTLTLLVSHSAGDIVKHCDRAIFLNKNGDICMDGTARDV		231
K. pneumoniaeO1	LAVGDIAFQAKCIQTIRDFKRRGVTILFVSHNMSDVEKICDRVIWIENHRLREVGSAERI		237
K. pneumoniaeO8	LAVGDISFQAKCIKTIREFKKGGVTILFVSHNMSDVERICDRVWVIENHRLREIGSAERI		237
A. salmonicida	LAVGDDAFQQRKCYARLKLQSQGVTTILLVSHAAGSVIELCDRAVLLDRGEVLLQGEPKAV		232
Y. enterocoliticaO_3	FGTGDAAFQEKAEKMRDWIAGSDIFVFASHDRSLIKKLCNRIFRLEHGLIYEESMDIL-		239
E. coliK1	TAVGDAKFKKCSDFDKIREKSHLIMVSHSERALKEYCDVAIYLNKEGQGFYKNVTEA		211
E. coliK5	TAVGDARFKEKCAQLFKERHKESFLMVSHSLNSLKEFCDVVAIVFKNSYIIGYYENVQSG		211
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P. aeruginosa	MDYYNALLAEREGQTVRQEMLADGQVRTISGTGEAAILDVRMVDQRQRALEVVVEVQAVT		292
E. coliO8	MDYYNALLADKQNSIKQVEHNG-KTQTVSGTGEVTTISEVHLLDEQGNVTEFVSVGHRVS		291
E. coliO9a	TNRYLDELFGKPKDSATKSATAISSAGSESQMSLDEIEDVYHTRPGYRPEEYRWGQGA		291
K. pneumoniaeO1	IELYKQAMA-----		246
K. pneumoniaeO8	IELYKQAMA-----		246
A. salmonicida	VHNYHKLHMEGDERARFRYHLRQTGRGDSYISDESTSEPKIKSAPGILSVDLQFQSTVW		292
Y. enterocoliticaO_3	-----		
E. coliK1	IADYKKDL-----		219
E. coliK5	IDEYKMYQDLIDIE-----		224
P. aeruginosa	LEVEVEVRQDIERLILGFMIKDRLGQPMYGINTHRLDKALTDLKAGERITYRFAFDMRLG		352
E. coliO8	LQVNVVEVKDDIPELVVGYMIKDRLGQPIFGTNTYHLNQTTLTSLKKGKRSFLFSFDARLG		351
E. coliO9a	KIIDYHIQSAGVDFPPLSTGNQQTDFLMKVVFEYDFDCVVPGILIKTLDLGLFLYGTNSFL		351
K. pneumoniaeO1	-----		
K. pneumoniaeO8	-----		
A. salmonicida	YESKGAVLSDVHIESF-----		308
Y. enterocoliticaO_3	-----		
E. coliK1	-----		
E. coliK5	-----		
P. aeruginosa	KGHYSVALSLRSLDRLDRNFWEWRDYGLVFHVINNRQEDFVGCSSLGAETHISRSGEAL		412
E. coliO8	VGSYSVAVALHTSSTHLGKNYEWDRDLAVVFNVNTEQQEFVGVSWLPPELEIS-----		404
E. coliO9a	ASEGRENISVSRGDVVRVFKFSLPVDLNSGDYLLSFGISAGNPQTDMTPLDRRYDSIILHV		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.