

Legends for Supplementary Tables and Figures

Table S1 Interactions of metal ion (Mg^{2+}) with *A. baumannii* AIIMS 7 PMM residues

Fig. S1 Amplification of *algC* from genome of *A. baumannii* AIIMS 7

Lane M: Molecular weight marker (in kb); lane 1: *algC* gene (1781 bp) amplified from genomic DNA; Lane 2: Negative PCR control (DNase, RNase free water)

Fig.S2 Amplification of internal coding regions of cDNA of *algC* by RT-PCR assay

Lane M: Molecular weight marker (in kb), lane 1: coding region 1 (463 bp); lane2: coding region 2 (1360 bp) amplified from cDNA; Lane 3: Negative PCR control (total RNA used as template for direct PCR)

Fig. S3 Promoter region of *algC* gene

algC transcription initiation site and the direction of transcription are indicated by the large, bold type and the black curved arrow, respectively. The predicted matching -10 (GATAGA) and -35 (TTGAATA) promoter regions and a putative RBS (highlighted in grey) are also shown. The black horizontal arrow identifies the *algC* initiation codon.

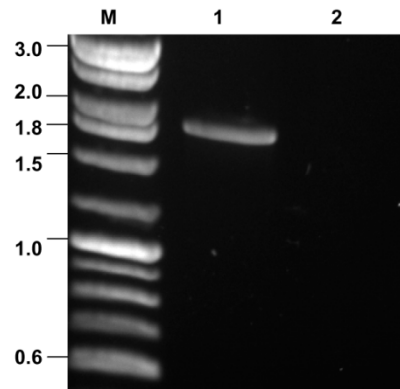
Fig. S4 CLUSTALW alignment of target and template sequences used for 3-D model building

Alignment of target PMM/PGM sequence(AEC46864) from *A. baumannii* AIIMS 7 with template sequence (1K2Y) from *P. aeruginosa* PMM/PGM S108A mutant. Respective colored regions show: metal binding residues, Ser104(domain 1, Green), Asp244, Asp246, Asp248 (domain 2, Pink);sugar binding residues, Glu327, Ala329, His331 (domain 3, Yellow); phosphate binding residues: Lys287 (domain 3, yellow), Arg 427, Arg 438 (domain 4, Blue)

SUPPLEMENTARY TABLES & FIGURES

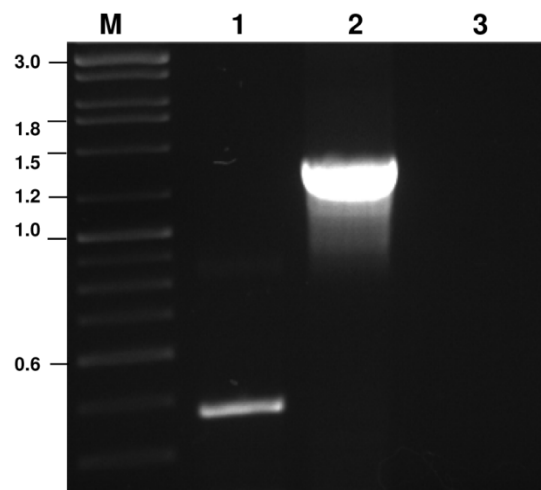
Suppl. Table S1 Interactions of metal ion (Mg^{2+}) with *A. baumannii* AIIMS 7 PMM residues

S.No	Residues	Distance in Å
1	SER 104 OG ---- Mg	2.006
2	ASP 244 OD2 ----Mg	2.214
3	ASP 244 OD1 ----Mg	2.032
4	ASP 248 OD1 ----Mg	2.060
5	ASP 248 OD2 ----Mg	2.138
6	ASP 246 OD2 ----Mg	2.057
7	ASP 246 OD1 ----Mg	2.051



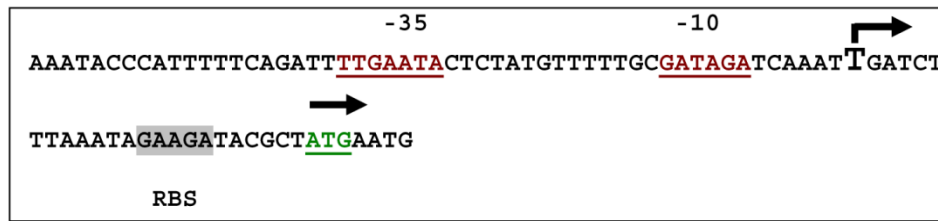
Suppl. Fig. S1 Amplification of *algC* from genome of *A. baumannii* AIIMS 7

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CLUSTAL 2.0.11 multiple sequence alignment

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gi|330858329|gb|AEC46864.1|  --MNVRSFSPKNIFRAYDIRGKLS-YLTTDVVRSIAYGLAQYKQAEQTQ 47
1K2Y_X|PDBID|CHAIN|SEQUENCE MSTAKAPTLPASIFRAYDIRGVGDTLTAETAYWIGRAIGSES LARGEPC 50
                               ::* .***** :. **:.. *. :... :.

gi|330858329|gb|AEC46864.1|  LIIGYDARLTSPAYAHLEIEILVEQGLNVTNIGCCSTPMYYIAREFGG- 96
1K2Y_X|PDBID|CHAIN|SEQUENCE VAVGRDGRLSGPVLVKLIQGLVDCGCQVSDVGMVPTPVLYYAANVLEGG 100
                               ::* .**.*. :. : : **: * :*::** .**::** * . : *

gi|330858329|gb|AEC46864.1|  NGIMVTAHNPKSDNGIKWILRGEPPSPEMIQQVGEFAQTYVPHTHTISLL 146
1K2Y_X|PDBID|CHAIN|SEQUENCE SGVMLTGAHNPPDYNGFKIVVAGETLANEQIQLRERIEKNDLASGVGSV 150
                               .**::**.*. :*:* :. **: : * ** : * :. : : :

gi|330858329|gb|AEC46864.1|  ELSTPQFNSEFCKKYQQAIFNDIQLKRPLKVVL DGLHGSAGHCSKLVLEK 196
1K2Y_X|PDBID|CHAIN|SEQUENCE EQ-----VDILPRYFKQIRDDIAMAKPMKVVD CGNGVAGVIA PQLIEA 194
                               * :. : * : * ** : :*:**.* : * ** : :.*

gi|330858329|gb|AEC46864.1|  MGCEVIALRTTPNGEFPDHAPDP SHAHLKELRKTIIEQGADIGIALDGD 246
1K2Y_X|PDBID|CHAIN|SEQUENCE LGCSVIPLYCEVDGNFPNHPDPGKPENLKDLIAKVKAENADLGLAFDGD 244
                               :**.*.* :*:*.* ***. :. :*:** :. : .**.*:***

gi|330858329|gb|AEC46864.1|  GDRVVLLDEKANILTADRLLSLFAQMCLEQQPDKEIVFDVKCSLMVQRTV 296
1K2Y_X|PDBID|CHAIN|SEQUENCE GDRVGVVTNTGTIIYPDRLLMLFAKD VVSRNPGADII FDVKCTRRLIALI 294
                               **** :. :...* .***** ***: :...* .:*****: : :

gi|330858329|gb|AEC46864.1|  ERLGKPKMIRTGSSFLRAYLSQSNGNAIFGGEYAGHYVFN DGRGFGYDD 346
1K2Y_X|PDBID|CHAIN|SEQUENCE SGYGRPVVMWKTGHS LIKKMKETG--ALLAGEMSGHVFFKER-WFGFDD 341
                               . **:* * :** *:: :...* :...** :** .*: : **:*

gi|330858329|gb|AEC46864.1|  GLYAALRVMEYFTESSATTISDLFSNPERCCTEDTYIGTHQSDPKHVLQ 396
1K2Y_X|PDBID|CHAIN|SEQUENCE GIYSAARLLEILSQDQDSE-HVFSAFP SDISTPEINITVTEDSKFAIIE 390
                               *:*.* **:* :...* :. :**.*. . * . * . : :

gi|330858329|gb|AEC46864.1|  DIEILSHRLGARISKIDGVRLDFDDGFGIIRASNTGEYFTVRF DADNPLR 446
1K2Y_X|PDBID|CHAIN|SEQUENCE ALQRDAQWGE GNITLDGVRVDYPKGWGLVRASNTTPVLVLRFEADTEEE 440
                               :. :. :*::*****.* :*::***** :*::**.*.

gi|330858329|gb|AEC46864.1|  LKEIQQKFIDMLQERYPQIAQELMSL 472
1K2Y_X|PDBID|CHAIN|SEQUENCE LERIKTVFRNQLKAVDSSLVPVF-- 463
                               *:.*: * : * : :... :

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