

E206

315

Staphylococcus aureus Lys-PG-MprF
 Listeria monocytogenes Lys-PG-MprF
 Clostridium perfringens Lys-PG-MprF
 Bacillus anthracis Lys-PG-MprF
 Agrobacterium tumefaciens Lys-PG-MprF
 Rhizobium tropici Lys-PG-MprF
 Bacillus subtilis Lys+Ala-PG-MprF
 Enterococcus faecalis Lys+Ala-PG MprF2
 Enterococcus faecalis MprF1
 Methanoscincula Barkeri Ala-PG-MprF
 Paenibacillus polymyxa Ala-PG-MprF
 Kineococcus radiotolerans Ala-PG-MprF
 Pseudomonas aeruginosa Ala-PG-MprF
 Pseudomonas putida Ala-PG-MprF
 Burkholderia phymatum Ala-PG-MprF

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385
 Staphylococcus aureus Lys-PG-MprF
 Listeria monocytogenes Lys-PG-MprF
 Clostridium perfringens Lys-PG-MprF
 Bacillus anthracis Lys-PG-MprF
 Agrobacterium tumefaciens Lys-PG-MprF
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 Paenibacillus polymyxa Ala-PG-MprF
 Kineococcus radiotolerans Ala-PG-MprF
 Pseudomonas aeruginosa Ala-PG-MprF
 Pseudomonas putida Ala-PG-MprF
 Burkholderia phymatum Ala-PG-MprF

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490

Staphylococcus aureus Lys-PG-MprF
 Listeria monocytogenes Lys-PG-MprF
 Clostridium perfringens Lys-PG-MprF
 Bacillus anthracis Lys-PG-MprF
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 Pseudomonas aeruginosa Ala-PG-MprF
 Pseudomonas putida Ala-PG-MprF
 Burkholderia phymatum Ala-PG-MprF

525

560

YFIP-A-KDV-T-SFLM-SYQKDIIAKIP--S--LS--L-A-I--L--V--FFTSMI-F-FVNN
 -FL-EGLP-L-L-F-L-L-Q-K-V-A-H--R-F--L-V-I--F--V-YSGGLL-L-ILSS
 -KF-N-G-LP-Y-E-IV-S-K-V-A-Y-K-I-V-V-S-S-L-V-FISGAI-I-VLSN
 -FI-A-A-P-A-L-E-T-T-GV-IWT-LQ--R DFLGK-L-GSWASAAL-T-V-FA-GLM-V-ILST
 -I-S-Q-L-A-V-R-L-A-P-P-P-L-L-S-T-F-A-I-IL-GTM-L-IFSS
 -I-T-RWL-R-ACAASA-R-L-M-P-Q-L-L-S-A-F-A-L-LL-GMM-L-VFSS
 -RI-A-P-A-I-E-T-T-NV-LLV-VQ--R AVLVRILQGS-LS-L-I-V-FVAGLI-V-LASV
 -Y-R-Q-L-L-K-QI-TLE-I-A-H-K-L-E-V-V-L-L-YFSGIM-M-VLLA
 -FF-D-N-L-P-R-LF-S-QK-V-A-H-F-I-L-V-A-A-L-YFAGIM-MVLLST
 -I-E-K-A-TYS-SL-S-E-L-T-P-R-I-F-S-I-L-V-FL-GGVS-L-LFSG
 -L-A-E-TGWDYS-LN-AWQK-WVG-WPGQFR-FLAD-L-G-VWA-LGKLW-LISGVV-L-LLSA
 -LGAA-R-T-A-A-G-TPG-P-A-A-G-S-P-V-R-VPSVLTSPV-L-ALS-
 -AI-R-V-A-S-G-F-A-AP-I-L-A-I-L-V-FLSGVV-L-LFSG
 -AI-K-A-A-S-G-L-A-AP-I-L-S-I-L-V-FLSGVV-L-LFSG
 -L-H-H-A-A-TV-S-Q-L-A-P-LF-L-S-L-T-FVVGGM-L-VISS

595

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Pseudomonas aeruginosa Ala-PG-MprF
Pseudomonas putida Ala-PG-MprF
Burkholderia phymatum Ala-PG-MprF

665 R437 700

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Enterococcus faecalis MprF1
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Burkholderia phymatum Ala-PG-MprF

735 770

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805 840

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Pseudomonas putida Ala-PG-MprF
Burkholderia phymatum Ala-PG-MprF

Supplemental Figure 1: Amino acid sequence alignment of the hydrophobic N-terminal parts of MprF proteins of various bacterial species, known to synthesize Lys-PG, Ala-PG, or both. Conserved charged amino acid and proline positions are indicated. *Staphylococcus aureus* (Q2G2M2), *Listeria monocytogenes* (Q71YX2), *Clostridium perfringens* MprF2 (Q0STHJ7), *Bacillus anthracis* (B0AWU), *Agrobacterium tumefaciens* (A9CHP8), *Rhizobium tropici* (Q8GQE5), *Bacillus subtilis* (C0H3X7), *Enterococcus faecalis* MprF2 (S0L1V5), *Enterococcus faecalis* MprF1 (Q839W9), *Methanosaarcina barkeri* (Q469T9), *Paenibacillus polymyxa* (E0RDN6), *Kineococcus radiotolerans* (A6W5P4), *Pseudomonas aeruginosa* (A6VA53), *Pseudomonas putida* (Q88NK5), *Burkholderia phymatum* (B2JPD9).