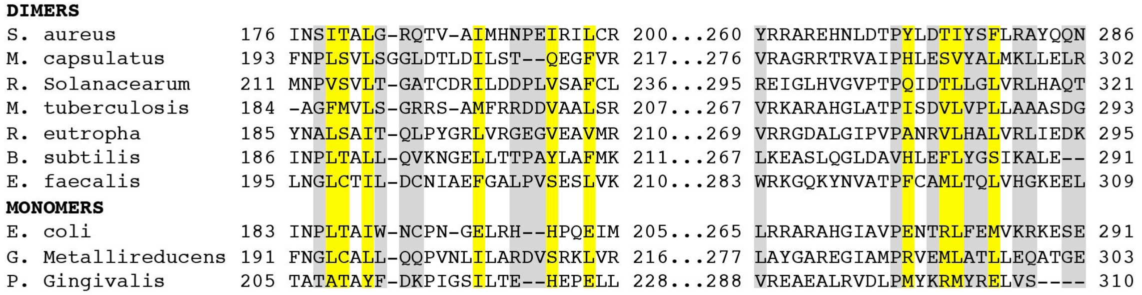
Supporting Information Figure 1. Structure-based sequence alignment showing that the dimer interface has a low level of conservation. Residues in the dimer interface are highlighted in grey. Residues that are part of the hydrophobic cluster in the interface are highlighted in yellow.



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DIMERS
S. aureus         176 INSITALG-RQTV-AIMHNPEIRILCR 200...260 YRRAREHNLDTPYLDTIYSFLRAYQQN 286
M. capsulatus     193 FNPLSVLSGGLDTLDILST--QEGFVR 217...276 VRAGRRTRVAIPHLESVYALMKLLELR 302
R. Solanacearum   211 MNPVSVLT-GATCDRILDDPLVSAFCL 236...295 REIGLHVGVPTPQIDTLLGLVRLHAQT 321
M. tuberculosis   184 -AGFMVLS-GRRS-AMFRRDDVAALSR 207...267 VRKARAHGLATPISDVLVPLLAAASDG 293
R. eutropha       185 YNALSAIT-QLPYGRLVRGEGVEAVMR 210...269 VRRGDALGIPVPANRVLHALVRLIEDK 295
B. subtilis       186 INPLTALL-QVKNGELLTTPAYLAFMK 211...267 LKEASLQGLDAVHLEFLYGSIKALE-- 291
E. faecalis       195 LNGLCTIL-DCNIAEFGALPVSESLVK 210...283 WRKGQKYNVATPFCAMLTQLVHGKEEL 309
MONOMERS
E. coli           183 INPLTAIW-NCPN-GELRH--HPQEIM 205...265 LRRARAHGIAVPENTRLFEMVKRKESE 291
G. Metallireducens 191 FNGLCALL-QQPVNLILARDVSRKLVR 216...277 LAYGAREGIAMPRVEMLATLLEQATGE 303
P. Gingivalis     205 TATATAYF-DKPIGSILTE--HEPELL 228...288 VREAEALRVDLPMYKRMYRELVS---- 310
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