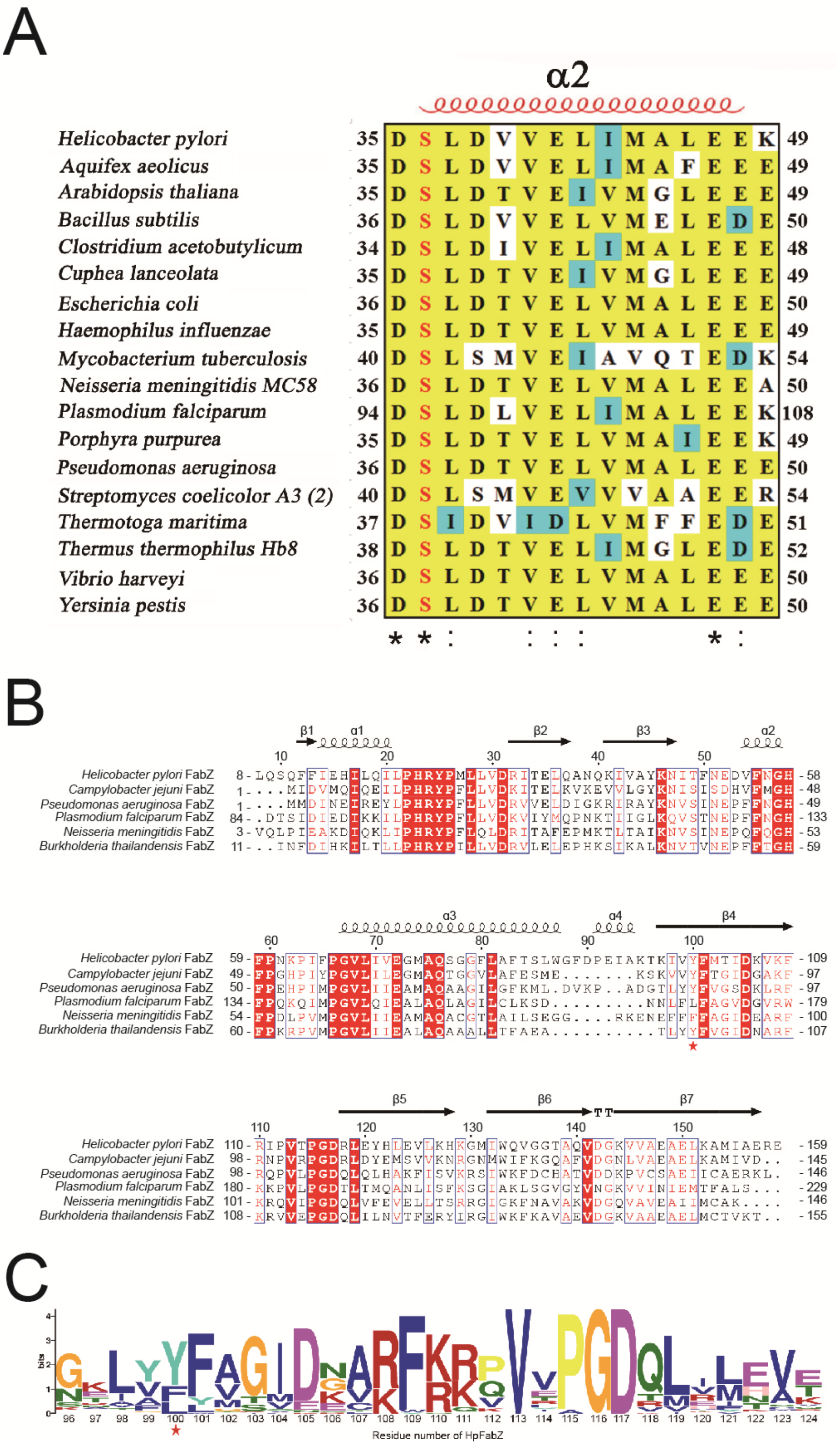
A
α2
Helicobacter pylori 35 D S L D V V E L I M A L E E K 49
Aquifex aeolicus 35 D S L D V V E L I M A F E E E 49
Arabidopsis thaliana 35 D S L D T V E I V M G L E E E 49
Bacillus subtilis 36 D S L D V V E L V M E L E D E 50
Clostridium acetobutylicum 34 D S L D I V E L I M A L E E E 48
Cuphea lanceolata 35 D S L D T V E I V M G L E E E 49
Escherichia coli 36 D S L D T V E L V M A L E E E 50
Haemophilus influenzae 35 D S L D T V E L V M A L E E E 49
Mycobacterium tuberculosis 40 D S L S M V E I A V Q T E D K 54
Neisseria meningitidis MC58 36 D S L D T V E L V M A L E E A 50
Plasmodium falciparum 94 D S L D L V E L I M A L E E K 108
Porphyra purpurea 35 D S L D T V E L V M A I E E K 49
Pseudomonas aeruginosa 36 D S L D T V E L V M A L E E E 50
Streptomyces coelicolor A3 (2) 40 D S L S M V E V V V A A E E R 54
Thermotoga maritima 37 D S I D V I D L V M F F E D E 51
Thermus thermophilus Hb8 38 D S L D T V E L I M G L E D E 52
Vibrio harveyi 36 D S L D T V E L V M A L E E E 50
Yersinia pestis 36 D S L D T V E L V M A L E E E 50
* * : : : : * :
B
β1 α1 β2 β3 α2
Helicobacter pylori FabZ
Campylobacter jejuni FabZ
Pseudomonas aeruginosa FabZ
Plasmodium falciparum FabZ
Neisseria meningitidis FabZ
Burkholderia thailandensis FabZ
α3 α4 β4
β5 β6 TT β7
C
bits
Residue number of HpFabZ

Supplementary information, Figure S3 Multiple alignment of FabZ and ACP. (A) Sequence alignment of ACP α2 helix region. Primary sequences in the helix α2 region of various bacterial ACPs are compared. Identical residues are shaded in yellow and indicated with an asterisk. Similar residues are shaded in cyan and indicated with colons. The key residue serine modified by the 4'-phosphopantetheine arm is colored in red. **(B)** Structural alignment of FabZ amino acid sequences. Primary FabZ sequences in various bacteria are aligned. Identical residues are shaded in red. The critical Tyr100 residue is marked with red star. The structural alignment was generated by Espript online server (http://espript.ibcp.fr/ESPript/ESPript/). Structures used in the alignment were obtained from Protein Data Bank (PDB) with pdb codes: 2GLL, 3D6X, 1U1Z, 1Z6B, 4I83 and 4H4G. **(C)** MEME suite motif logos of residues around the FabZ active tunnel entrance through 72 bacterial species (http://meme-suite.org/). Each position in the motif is represented as a stack of letters, which indicates the percentage of the residue letter at that position through the total residue content of the stack. Primary FabZ sequence from *Helicobacter pylori* around the active tunnel entrance is shown, and Tyr100 is marked with red star. FabZ sequences were obtained from the following 72 bacterial species: *Acinetobacter baumannii, Acinetobacter calcoaceticus, Acetobacter pasteurianus, Achromobacter xylosoxidans, Acholeplasma brassicae, Aeromonas hydrophila, Agrobacterium fabrum, Bacillus anthracis, Bacillus cereus, Bacillus subtilis, Bacillus thuringiensis, Bordetella holmesii, Bordetella pertussis Tohama, Bradyrhizobium diazoefficiens, Burkholderia glumae, Burkholderia mallei, Burkholderia multivorans, Burkholderia pseudomallei, Burkholderia thailandensis, Burkholderia xenovorans, Campylobacter jejuni, Chloroflexus aurantiacus, Clostridium botulinum, Coxiella burnetii, Cupriavidus metallidurans, Deinococcus radiodurans, Desulfovibrio vulgaris, Enterobacter aerogenes, Enterococcus faecalis, Escherichia coli, Gloeobacter violaceus, Haemophilus influenzae, Herbaspirillum seropedicae, Ketogulonicigenium vulgare, Lactobacillus salivarius, Lactococcus lactis, Legionella pneumophila, Listeria monocytogenes, Methylomicrobium alcaliphilum, Moorella thermoacetica, Neisseria meningitidis, Phaeodactylum tricornutum, Plasmodium falciparum, Pseudomonas* *aeruginosa, Pseudomonas syringae, Ralstonia eutropha, Ralstonia pickettii, Ralstonia solanacearum, Rhodobacter sphaeroides, Rhodospirillum rubrum, Rickettsia prowazekii, Salmonella enterica, Shewanella oneidensis, Shigella dysenteriae, Shigella flexneri, Sinorhizobium fredii, Sinorhizobium medicae, Sinorhizobium meliloti, Streptococcus agalactiae, Staphylococcus epidermidis, Streptococcus mutans, Streptococcus pneumoniae, Streptococcus pyogenes, Streptococcus sanguinis, Streptococcus suis, Vibrio cholerae, Vibrio fischeri, Vibrio parahaemolyticus, Xanthomonas campestris, Yersinia enterocolitica,* and *Yersinia pestis.*