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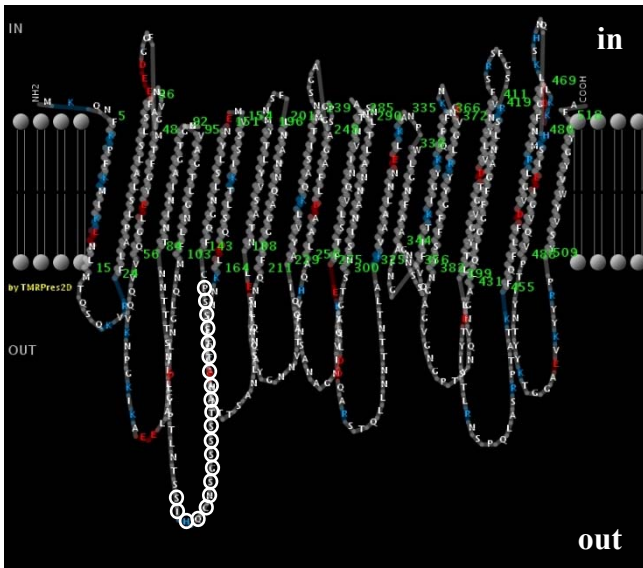
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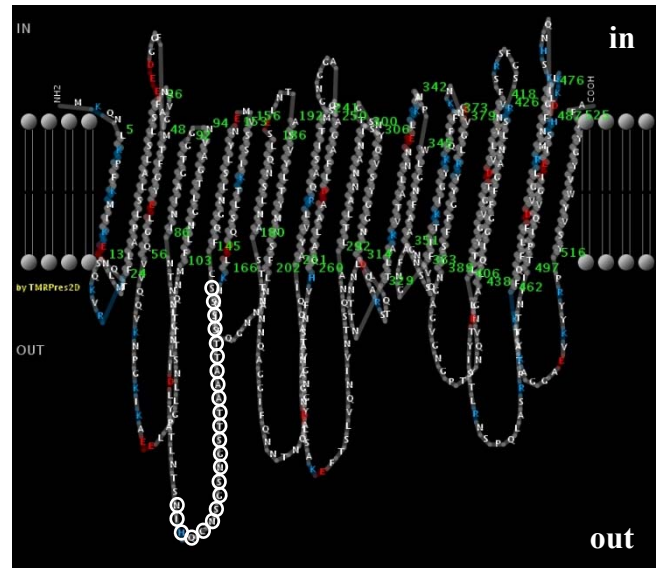
Alignment of AlpB amino acid sequences in *H. pylori* strains used in this study (1402:TK1402, 1029:TK1029, 2003:KR2003, 11638:NCTC11638). The variable region corresponding to amino acid positions 121 to 146 of AlpB is shown in underline. The replaced region for the construction of TK1402 Δ alpB/alpB₁₄₀₂V, TK1402 Δ alpB/alpB₁₁₆₃₈V, TK1402 Δ alpB/alpB₁₀₂₉V and TK1402 Δ alpB/alpB₂₀₀₃V is shown in a box.

Fig. S1

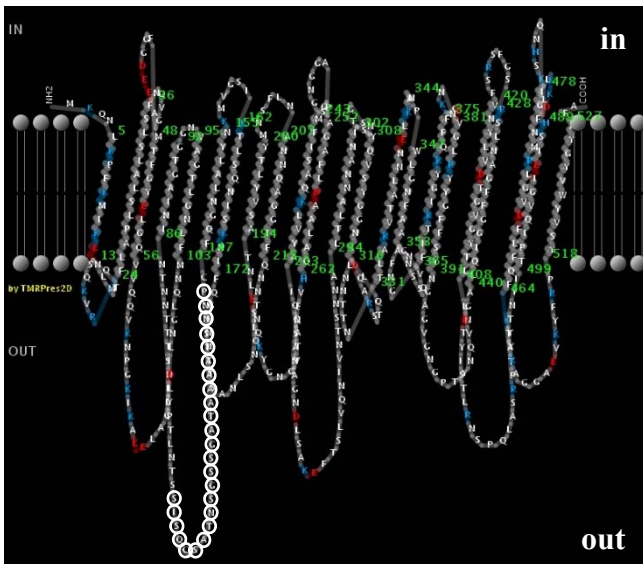
(A) TK1029



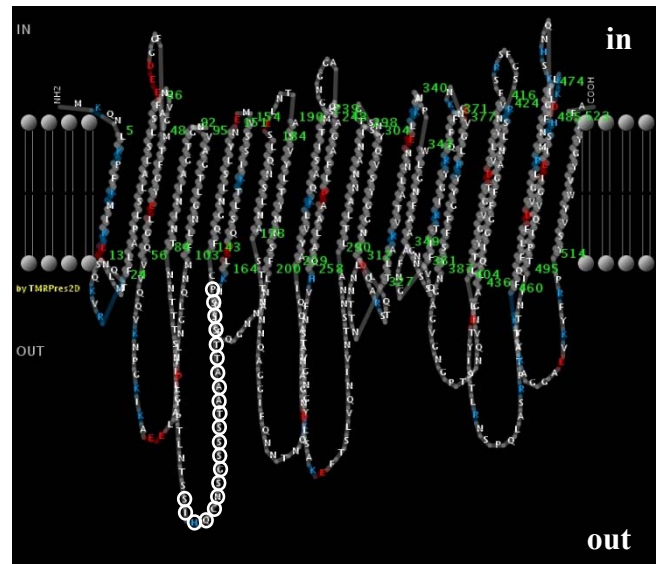
(B) KR2003



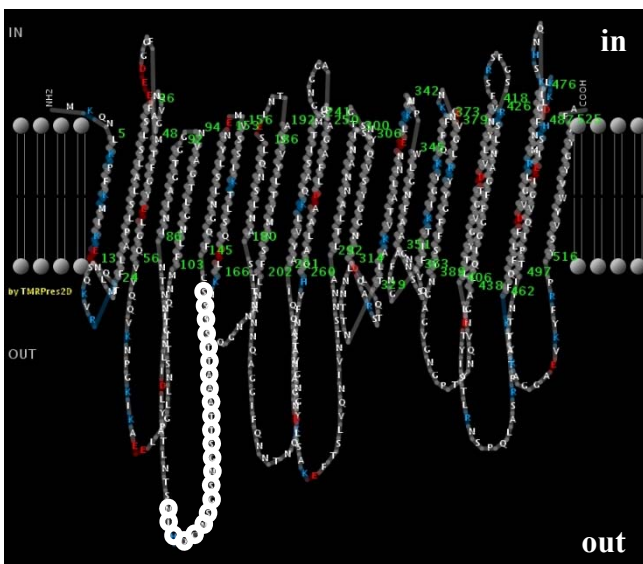
(C) TK1402 Δ *alpB*/*alpB*₁₁₆₃₈



(D) TK1402 Δ *alpB*/*alpB*₁₀₂₉



(E) TK1402 Δ *alpB*/*alpB*₂₀₀₃



Two-dimensional structure of AlpB from strains TK1029 (A), KR2003 (B), TK1402 Δ *alpB*/*alpB*₁₁₆₃₈ (C), TK1402 Δ *alpB*/*alpB*₁₀₂₉ (D), and TK1402 Δ *alpB*/*alpB*₂₀₀₃ (E), based on the prediction by PRED-TM3B. The amino acids of the variable region are shown by white circles. Strains TK1402 Δ *alpB*/*alpB*₁₁₆₃₈, TK1402 Δ *alpB*/*alpB*₁₀₂₉ and TK1402 Δ *alpB*/*alpB*₂₀₀₃ were restored strains derived from the TK1402 *alpB* mutant restored with NCTC11638, TK1029 or KR2003 *alpB*, respectively.

Fig. S2