



Figure S1 Sequence alignment of TAG from different organisms (*S. aureus* MSSA476; *S. aureus* MRSA252; *S. typhi*; *E. coli*; gi|152977981, *Actinobacillus succinogenes*; gi|152997561, *Marinomonas* sp. MWYL1; gi|343518949, *Haemophilus pittmaniae*; gi|145637785, *Haemophilus influenzae*; gi|333924919, *Serratia* sp. AS12; gi|237728860, *Citrobacter* sp. 30\_2; gi|251793702, *Aggregatibacter aphrophilus*; gi|82545914, *Shigella boydii*; gi|238750270, *Yersinia rohdei*; gi|345429072, *Haemophilus parainfluenzae*; gi|15603466, *Pasteurella multocida*)

Table S1 Thermodynamic parameters for wild type TAG toward 3-MeA interactions at pH7.8 and pH5.8 obtained by isothermal titration calorimetry

	<b>pH7.8</b>	<b>pH5.8</b>
N (stoichiometry)	Fixed to 1	Fixed to 1
K ( $M^{-1}$ )	4550	2120
$K_d$ ( $\mu M$ )	220	471
$\Delta H$ (cal/mol)	-12300	-6700
$\Delta S$ (cal/mol)	-25.9	-7.9