

Supplementary Materials

Figure S1. Sequence alignment of NAGS from *N. gonorrhoeae*, *E. coli*, *S. typhimurium* and *P. aeruginosa*. The secondary structural elements are indicated by boxes in yellow-green (β -strand) and red (α -helix) above the sequence. Residues involved in AcCoA and NAG binding are indicated in green and blue, respectively. The residues which are proposed to be involved in arginine binding are shown in yellow-green.

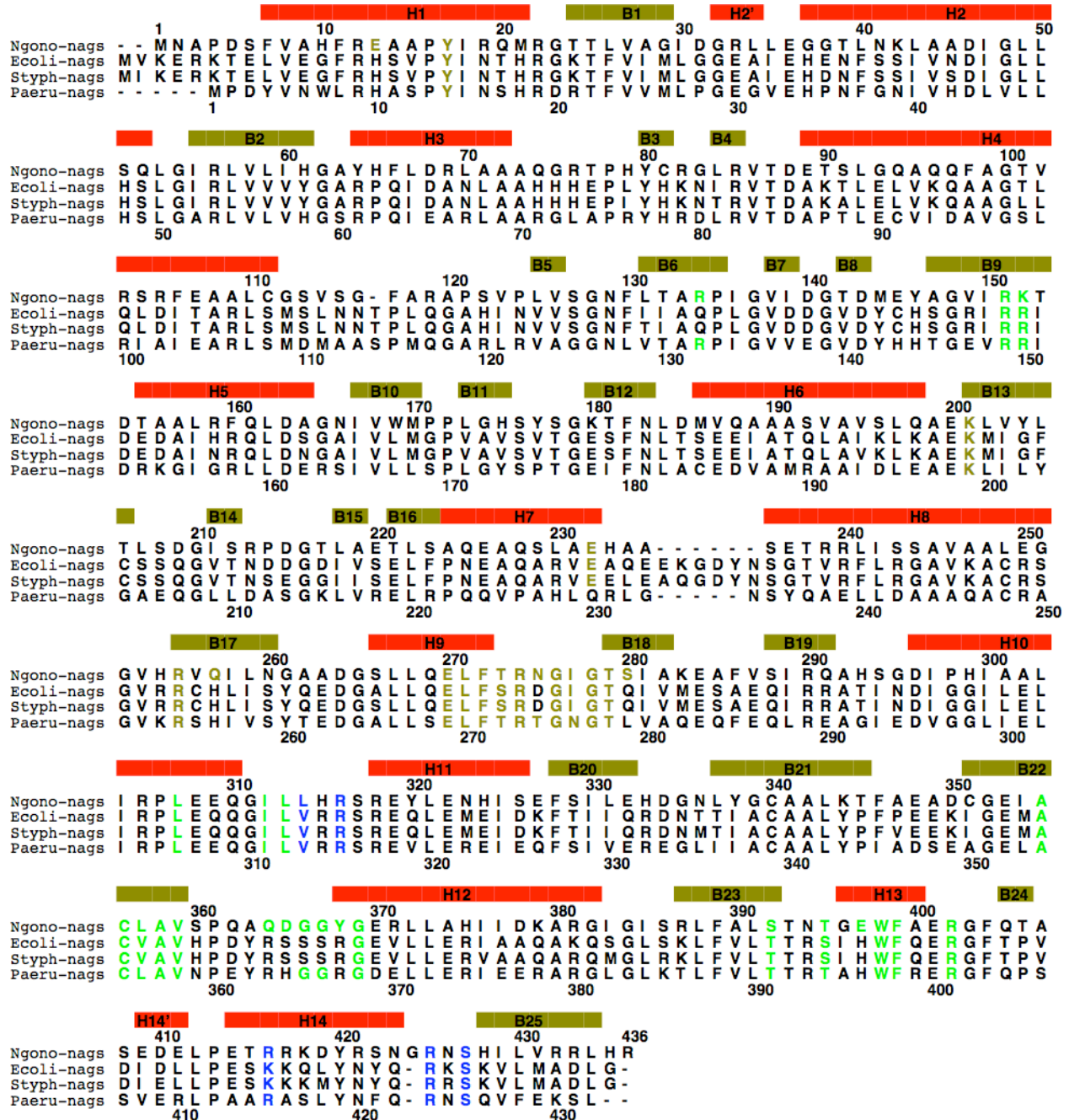


Figure S2. Superimposition of structures of *N. gonorrhoeae* NAGS AAK domain (shown in red), *E. coli* NAGK (PDB code 1OH9, shown in light blue), *P. aeruginosa* NAGK (PDB code 2BUF chain A, shown in pink) and *T. maritima* NAGK (PDB code 2BTY chain A, shown in yellow).

