Crystal structure and kinetic analysis of N-acetylmannosamine-6-phosphate 2-epimerase from *Fusobacterium nucleatum* and *Vibrio cholerae*

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Figure S1  (S1a) Malonate (a component of the crystallization buffer condition) in the binding pocket of VcNanE (S1b) ManNAc-6-P in the binding site of VcNanE (S1c) Comparison of active site interactions with malonate and ManNAc-6-P. The O1 and O2 of malonate hydrogen bond with amide backbones of R188 and G209, O3 can hydrogen bond with guanidinium group of R214. The O4 can hydrogen bond with ε-amine K76 via a water molecule (depicted as a blue spheres) and can also hydrogen bond with carboxyl group of E186 via a water molecule. Amino acids of apo- VcNanE and VcNanE/ManNAc-6-P are depicted in green and magenta respectively. Hydrogen bonds are represented as dashed red lines. Figures were made using Pymol.
**Figure S2**  Electron density for open chain sugar phosphate in VcNanE co crystallized with GlcNAc-6-P. The Fo-Fc electron density modeled with both ManNAc-6-P and GlcNAc-6-P (depicted in cyan and yellow respectively). The density is contoured at 2σ. Figure was made using Pymol.
**Figure S3** Active site is rigid. Superposition of apo SpNanE (1YXY) with VcNanE-ManNAc-6-P shows the spatial orientations of the active site amino acids. Arg-220 of SpNanE has moved away from the ligand binding site as there is no ligand for it to anchor. Amino acids of VcNanE-ManNAc-6-P and SpNanE are represented in magenta and orange respectively. ManNAc-6-P is depicted in cyan. Figures were made using Pymol.