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CMP-Induced Structural Changes in a Multifunctional Sialyltransferase from *Pasteurella multocida*. Lisheng Ni,¹ Mingchi Sun,¹ Harshal Chokhawala,¹ Xi Chen,¹ Andrew J. Fisher^{1,2}, ¹Dept. of Chemistry, ²Section of Molecular and Cellular Biology, Univ. of California, Davis, CA 95616 USA.

Sialyltransferases catalyze the transfer a sialic acid from CMP-sialic acid to an acceptor (galactose, N-acetylgalactosamine, or sialic acid). They are key enzymes in the synthesis of sialic acid-containing oligosaccharides, polysaccharides, and glycoconjugates and play pivotal roles in many physiological processes including cell recognition, bacterial infection, and tumor metastasis. The structures of truncated multifunctional *Pasteurella multocida* sialyltransferase, with and without CMP, have been determined at 2.0 and 1.65 Å resolution, respectively. The structure represents the first sialyltransferase structure that belongs to glycosyltransferase-B structural group. The CMP binding site is located in a cleft between the two Rossmann domains. Yet, the CMP only interacts with residues in the C-terminal domain. The binding of CMP to the protein causes a large closure movement of the N-terminal Rossmann domain towards the C-terminal nucleotide-binding domain. Additionally, a short helix near the active site seen in the apo structure becomes disordered upon binding to CMP. This helix may swing down upon binding to donor CMP-sialic acid to form the binding pocket for an acceptor.