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The NMR studies of the interaction between polysialic acid (polySA) and the PSTD peptide in ST8Sia IV polysialyltransferase

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The α 2,8-sialyltransferase (ST8Sia) family consists of 6 sialyltransferases, which are related to forms of polysialic acid chains (PSA) on neural cell adhesion molecule (NCAM) and NCAM polysialylation, and have important effects on formation of sialic acid storage diseases, neural system diseases and invasive cancers. It has been known that synthesis of PSA chains is catalyzed by two polysialyltransferases, ST8Sia II (STX) and ST8Sia IV (PST). In addition, a polybasic motif of 32 amino acids in both ST8Sia II and ST8Sia IV has been designated as “polysialyltransferase domain” (PSTD), which is essential for NCAM polysialylation. In this study, we have determined the 3D structure of the PSTD peptide containing 22 amino acids (22AA) in ST8Sia IV using NMR spectroscopy. This NMR-based model displays that the PSTD domain consists of an α -helical segment, two unstructured domains in both N- and C-terminus, and two three-residue-loops near the C-terminus of the peptide. Our overlaid 2D ¹H-¹⁵N-HSQC spectra of the 22AA-PSTD peptide show that the amide proton chemical shifts of some amino acids such as I260, I261, H262, R265, L269 and K272 have been changed after polySA was mixed with the PSTD peptide. In addition, the peak intensity of A263, V264, R265, Y267, L269 and K272 were also decreased after adding polySA. However, there is no any change in both chemical shift and the amide proton peak intensity for all other residues located on outside of the helix. Above NMR results indicate a weak interaction exists between the helix of the PSTD and the PolySA, which may play a vital role in modulating biosynthesis of polySA chain and NCAM polysialylation.

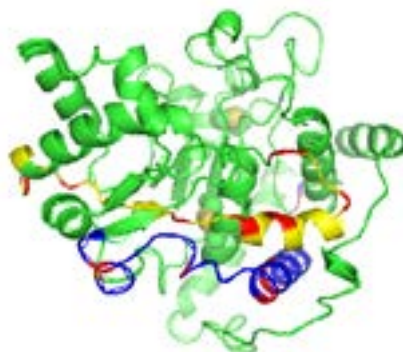


Figure1: The 3D models of ST8Sia IV. The PSTD domain is shown by yellow. All basic residues in PSTD and PBR motifs are shown by red.

Biography

Guo-Ping Zhou is currently a Distinguished Professor of Gordon Life Science Institute, USA. He is also an Adjunct Professor of several academics in the United States and China. He received his PhD in Biophysics from University of California at Davis, and completed his Postdoctoral training at Stanford University and Harvard University, respectively. He has determined the 3D NMR structures of some important proteins, protein-DNA complexes, and super lipids. He has successfully introduced the elegant wenxiang diagrams to elucidate the biological mechanisms of protein-protein/ligands interactions observed by NMR. Meanwhile, he has also published many papers in bioinformatics, and edited some special issues on structural biology for several influential scientific journals.

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