In addition, 14 structure-based mutants were produced and characterized at 0.93 Å resolution, allowing a very detailed analysis of fatty acid binding. The crystal structure of the wild-type human P2 protein was determined at the University of Hamburg, Hamburg, Germany. 

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The myelin sheath is a multilayered, tightly packed membrane wrapped around axons, enabling the rapid saltatory transmission of nerve impulses. Myelin carries a set of specific proteins, most of which are either integral or peripheral membrane proteins. In the peripheral nervous system, one of the myelin-specific proteins is P2, a member of the fatty acid binding protein (FABP) family that binds monomeric lipids inside its barrel structure. P2 is a small probability.

We show that most of native complexes can find an artificial counterpart, structural relationships between retaining and inverting GT-B glycosyltransferases as revealed by structure analysis of Sucrose Synthase-1 from Arabidopsis Thaliana.

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Sucrose synthase-1 from Arabidopsis thaliana (AtSus1) is a member of the retaining GT-4 glycosyltransferase subfamily (i.e., the product sucrose has the same alpha configuration as the sugar donor UDP-glucose) within the larger family of metal-independent GT-B glycosyltransferases. A typical GT-B fold comprises of two structurally similar Rossmann folds (GT-Bα and GT-Bβ) connected by two hinge regions. We have determined the structure of AtSus1 in catalytically competent closed state with UDP-glucose or fructose and UDP bound at the active site. Active site analysis provides future evidence for S0/S1-like reaction mechanism and functions of conserved residues His438, Glu675, Lys585 and Arg589. Structural Comparison of AtSus1 with inverting and retaining GTs of known structures revealed two interesting features of GT-B glycosyltransferase. First, three loop regions have distinct lengths and differing positions between the inverting and retaining GTs and play an important role in determining the direction of attack on the anomeric carbon of the sugar moiety by the sugar acceptor. Second, a simple rigid body motion of GT-Bα domain relative to GT-Bβ domain may be sufficient for the movement of the loops to open or close the attacking route. This domain motion suggests the two hinge regions connecting the two individual Rossmann folds in a particular orientation will stabilize either retaining or inverting reaction outcome over the other. Further understanding of the hinge region will provide new insights for glycosyltransferase engineering and may open up a broader substrate spectrum for glycosyltransferase reactions.

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Protein unfolding, disassembly, and aggregation underlie many diseases, but detailed study of these processes in intact cells has been limited. Cysteine Shot-gun labeling utilizes cell-permeable fluorescent dyes to label exposed cysteine residues. We applied it to study protein structure changes in response to mechanical stress on red blood cell ghosts in live mice and in whole-cell lysates in native versus urea-denaturing conditions. Labeling rate constants are calculated for any given Cys site by normalizing the protein labeling kinetics to the rapid labeling under denaturing conditions. Proteins can be identified and further analyzed by mass spectrometry to pinpoint specific, susceptible domains involved. A number of proteins contain cys with a wide variety of rate constants. This study focuses on human and mouse spectrin, Filamin A and B, Talin, and pyruvate kinase. These various proteins contain many cysteine-rich domains and have been amenable to studying by this in-cell technique. Results are confirmed by studies of purified protein.