

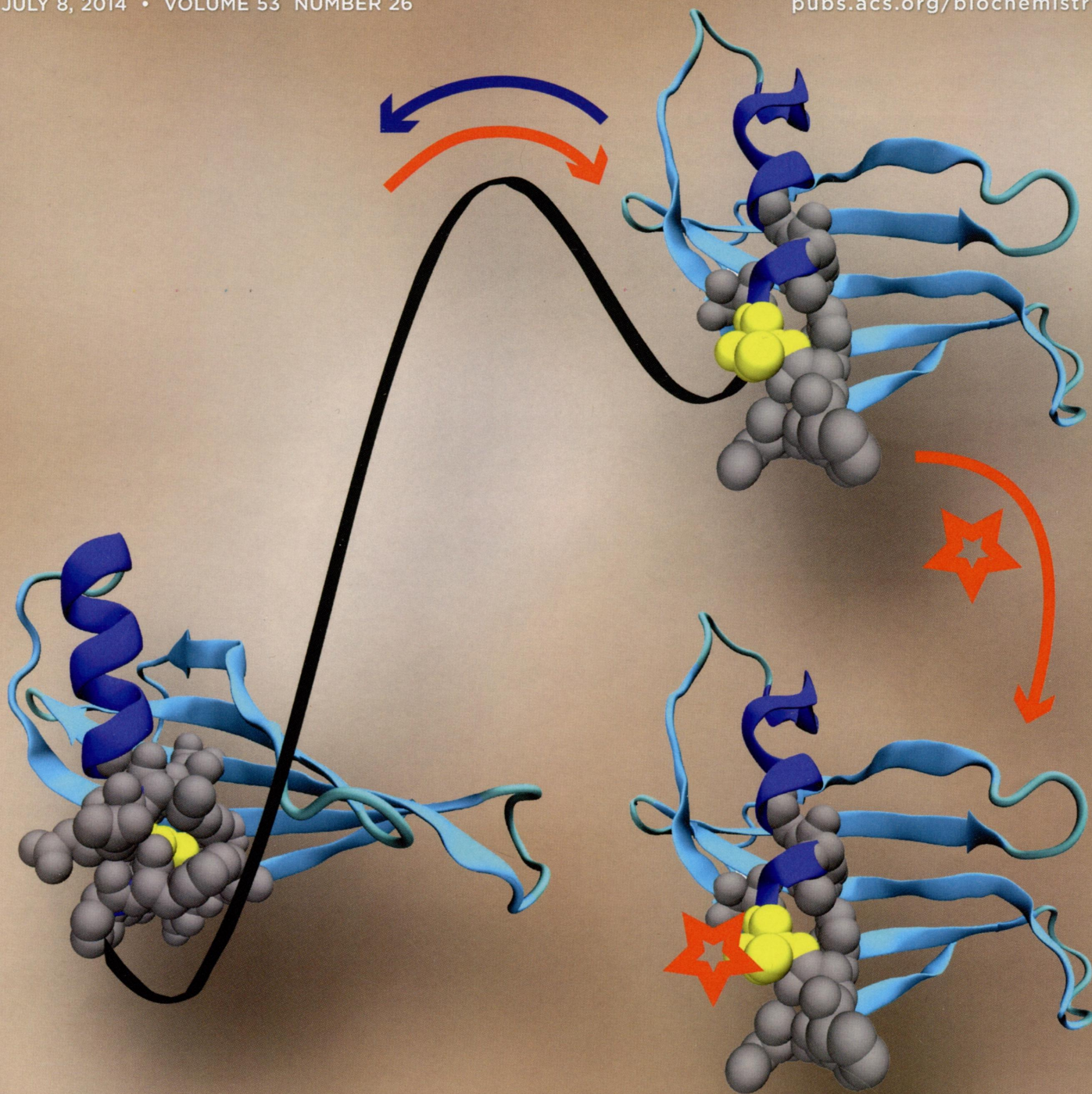
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JULY 8, 2014 • VOLUME 53 NUMBER 26

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ON THE COVER: Thiol labeling of a single cysteine residue (yellow spheres) has been used to monitor rare unfolding events in a protein under nativelike conditions. The residues (gray spheres) surrounding the buried cysteine move apart, resulting in solvent exposure and hence labeling of the side chain thiol. This deprotection of the side chain is associated with an energy barrier between the native state and a partially unfolded, labeling-competent intermediate. Such intermediates have been mapped onto the unfolding energy landscape of the protein monellin using the kinetic and thermodynamic information obtained from thiol labeling. [Malhotra, P., and Udgaonkar, J. B. (2014) *Biochemistry* 53, 3608–3620]

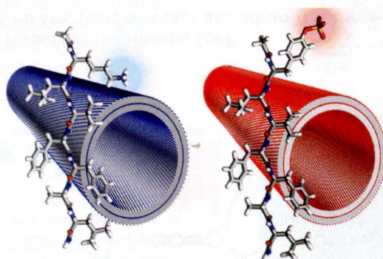
Rapid Reports

4225 **S**

dx.doi.org/10.1021/bi500599a

Neurofibrillar Tangle Surrogates: Histone H1 Binding to Patterned Phosphotyrosine Peptide Nanotubes

Sha Li, Anton N. Sidorov, Anil K. Mehta, Anthony J. Bisignano, Dibyendu Das, W. Seth Childers, Erin Schuler, Zhigang Jiang, Thomas M. Orlando, Keith Berland, and David G. Lynn*



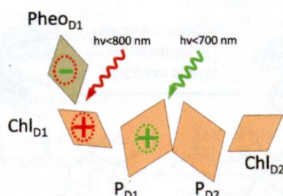
Articles

4228 **S**

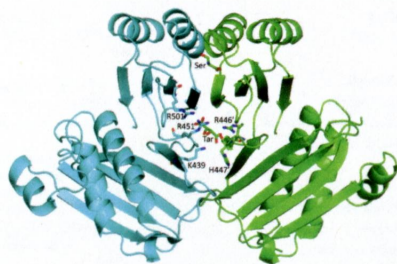
dx.doi.org/10.1021/bi5006392

The Photochemistry in Photosystem II at 5 K Is Different in Visible and Far-Red Light

Fredrik Møkvist, Johannes Sjöholm, Fikret Mamedov, and Stenbjörn Styring*



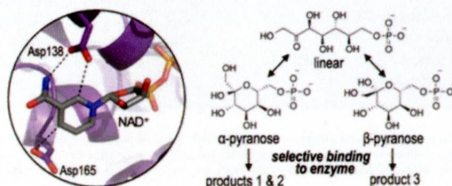
Regulation of *Mycobacterium tuberculosis* D-3-Phosphoglycerate Dehydrogenase by Phosphate-Modulated Quaternary Structure Dynamics and a Potential Role for Polyphosphate in Enzyme Regulation
Xiao Lan Xu and Gregory A. Grant*



4250

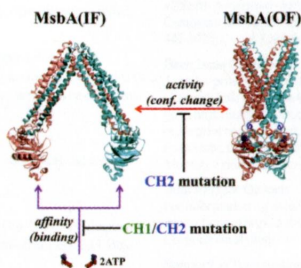
dx.doi.org/10.1021/bi5003508

Structure of a Sedoheptulose 7-Phosphate Cyclase: ValA from *Streptomyces hygroscopicus*
Kelsey M. Kean, Sara J. Coddling, Shumpei Asamizu, Taifo Mahmud, and P. Andrew Karplus*

4261 **S**

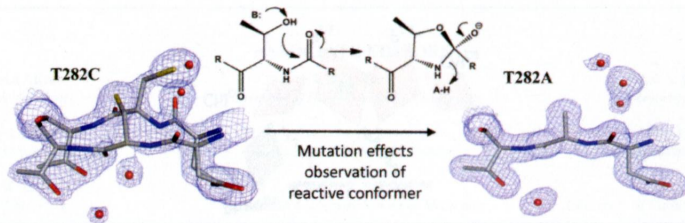
dx.doi.org/10.1021/bi500255j

Analysis of the Structural and Functional Roles of Coupling Helices in the ATP-Binding Cassette Transporter MsbA through Enzyme Assays and Molecular Dynamics Simulations
Tadaomi Furuta, Tomohiro Yamaguchi, Hiroaki Kato, and Minoru Sakurai*



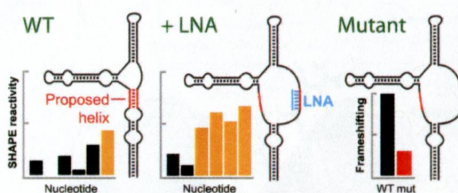
Exploring the Role of Conformational Heterogeneity in *cis*-Autoproteolytic Activation of ThnT

Andrew R. Buller, Michael F. Freeman, Joel F. Schildbach, and Craig A. Townsend*



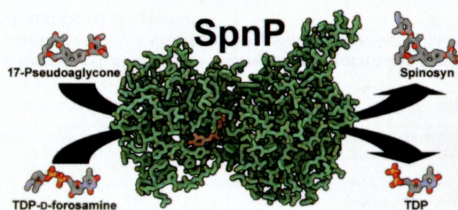
Structure and Dynamics of the HIV-1 Frameshift Element RNA

Justin T. Low, Pablo Garcia-Miranda, Kathryn D. Mouzakis, Robert J. Gorelick, Samuel E. Butcher, and Kevin M. Weeks*

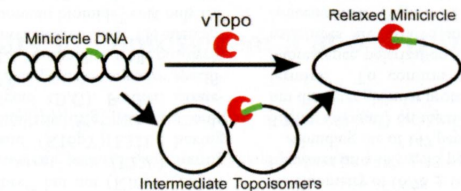


Structural Studies of the Spinosyn Forsaminyltransferase, SpnP

Eta A. Isiorho, Byung-Sun Jeon, Nam Ho Kim, Hung-wen Liu,* and Adrian T. Keatinge-Clay*



Variola Type IB DNA Topoisomerase: DNA Binding and Supercoil Unwinding Using Engineered DNA Minicircles
Breeana G. Anderson and James T. Stivers*



Additions and Corrections

4316

dx.doi.org/10.1021/bi5007496

Correction to Structure of a Sedoheptulose 7-Phosphate Cyclase: ValA from *Streptomyces hygroscopicus*
Kelsey M. Kean, Sara J. Coddling, Shumpei Asamizu, Taifo Mahmud, and P. Andrew Karplus*