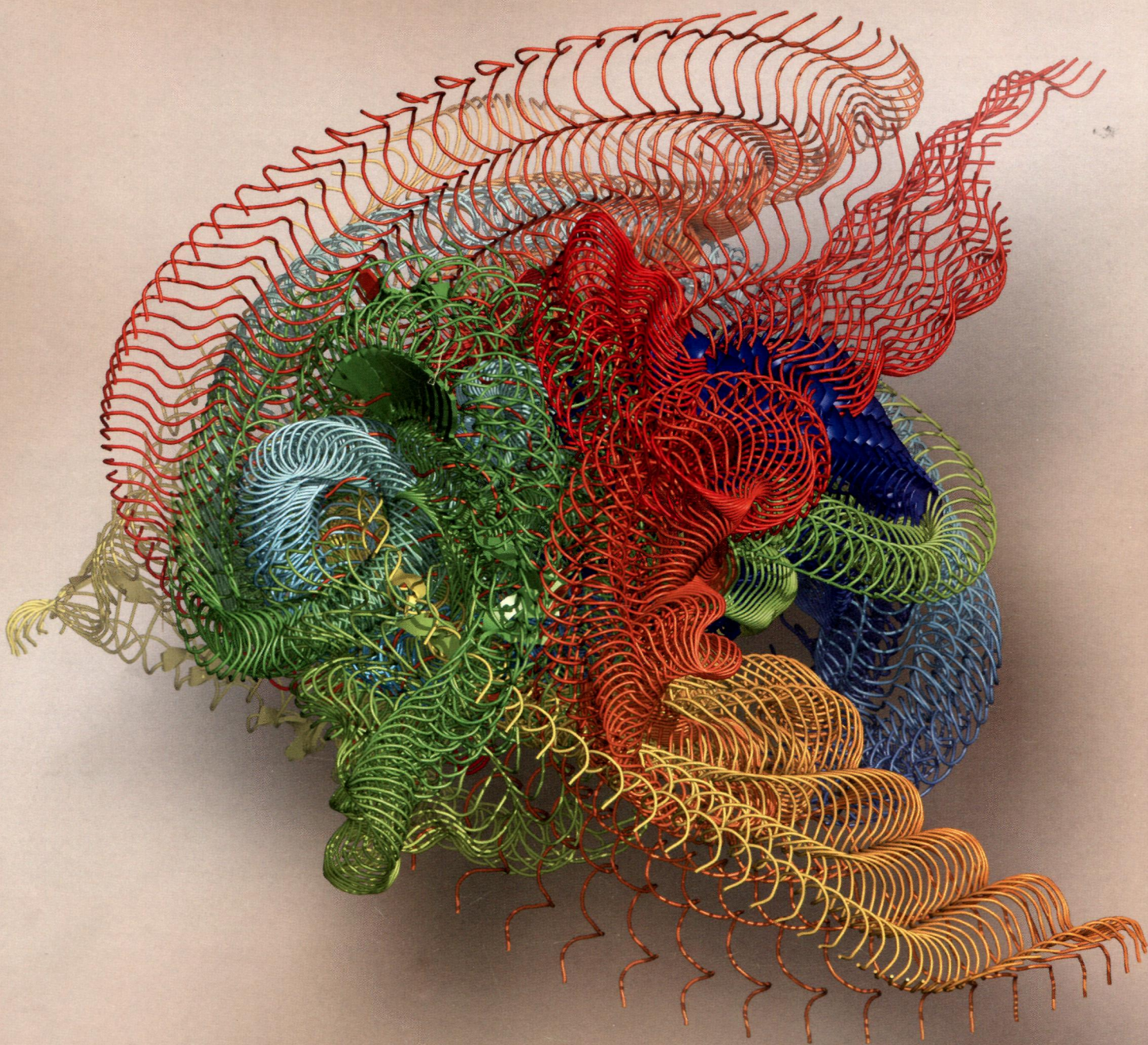


BIOCHEMISTRY

including biophysical chemistry & molecular biology

DECEMBER 10, 2013 • VOLUME 52 NUMBER 49

pubs.acs.org/biochemistry



ACS Publications

MOST TRUSTED. MOST CITED. MOST READ.

www.acs.org

ON THE COVER: Pictured is an overlay of 300 states of oxidized cytochrome *c*, starting from the “native” fully folded state to an unfolded state. Soffer et al. describe a previously unseen frustrated state of this protein produced under conditions that promote a misfolded ligation state of the heme iron. This image was rendered using PyMol (Schrödinger, LLC) [Soffer, J. B., et al. (2013) *Biochemistry* 52, 1397–1408].

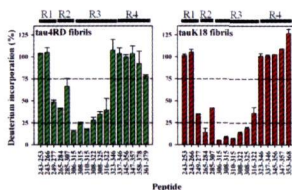
Rapid Reports

8787 **S**

[dx.doi.org/10.1021/bi4014352](https://doi.org/10.1021/bi4014352)

Difference in Fibril Core Stability between Two Tau Four-Repeat Domain Proteins: A Hydrogen–Deuterium Exchange Coupled to Mass Spectrometry Study

Gayathri Ramachandran and Jayant B. Udgaonkar*



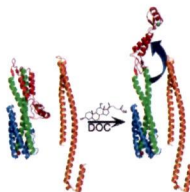
Articles

8790 **S**

[dx.doi.org/10.1021/bi400755f](https://doi.org/10.1021/bi400755f)

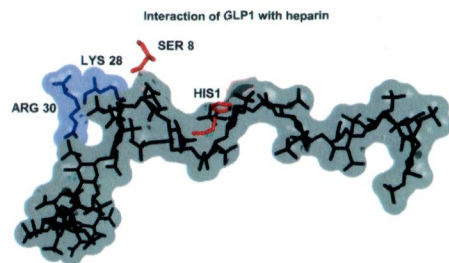
N-Terminus of IpaB Provides a Potential Anchor to the *Shigella* Type III Secretion System Tip Complex Protein IpaD

Nicholas E. Dickenson, Olivia Arizmendi, Mrinalini K. Patil, Ronald T. Toth IV, C. Russell Middaugh, William D. Picking, and Wendy L. Picking*



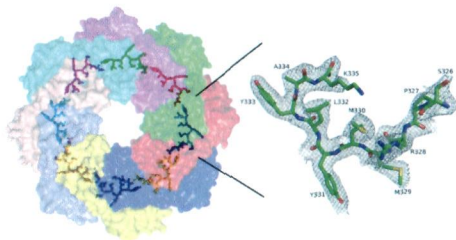
Characterization of Amyloid Formation by Glucagon-Like Peptides: Role of Basic Residues in Heparin-Mediated Aggregation

Narendra Nath Jha, A. Anoop, Srivastav Ranganathan, Ganesh M. Mohite, Ranjith Padinhateeri, and Samir K. Maji*



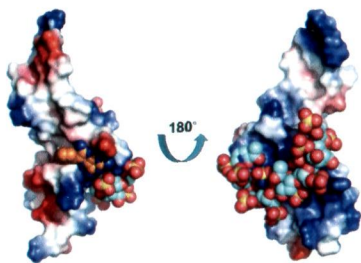
Structure of Signal Peptide Peptidase A with C-Termini Bound in the Active Sites: Insights into Specificity, Self-Processing, and Regulation

Sung-Eun Nam and Mark Paetzel*



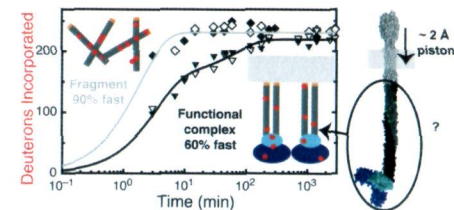
Relationship between Structural Flexibility and Function in the C-Terminal Region of the Heparin-Binding Domain of VEGF₁₆₅

Ki-Woong Jeong, Min-Cheol Jeong, Bonghwan Jin, and Yangmee Kim*



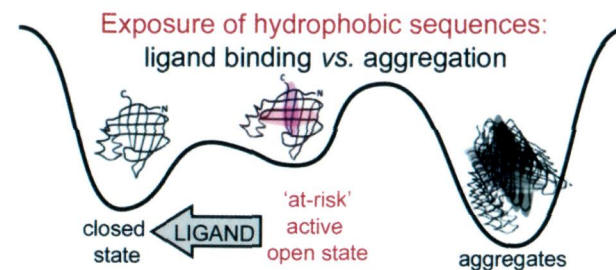
Hydrogen Exchange Mass Spectrometry of Functional Membrane-Bound Chemotaxis Receptor Complexes

Seena S. Koshy, Stephen J. Eyles, Robert M. Weis, and Lynmarie K. Thompson*



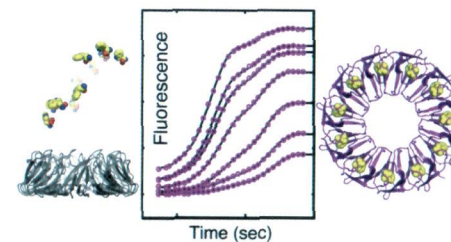
Delicate Balance between Functionally Required Flexibility and Aggregation Risk in a β -Rich Protein

Mylene C. Ferrolino, Anastasia Zhuravleva, Ivan L. Budyak, Beena Krishnan, and Lila M. Gierasch*



Homotropic Cooperativity from the Activation Pathway of the Allosteric Ligand-Responsive Regulatory *trp* RNA-Binding Attenuation Protein

Ian R. Kleckner, Craig A. McElroy, Petr Kuzmic, Paul Gollnick, and Mark P. Foster*

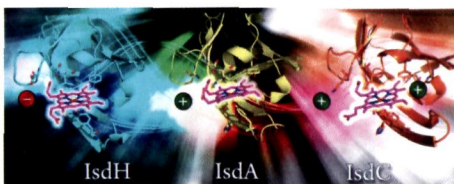


8866 5

dx.doi.org/10.1021/bi4008325

Heme Binding Mechanism of Structurally Similar Iron-Regulated Surface Determinant Near Transporter Domains of *Staphylococcus aureus* Exhibiting Different Affinities for Heme

Yoshitaka Moriwaki,* Tohru Terada, Jose M. M. Caaveiro, Yousuke Takaoka, Itaru Hamachi, Kouhei Tsumoto, and Kentaro Shimizu

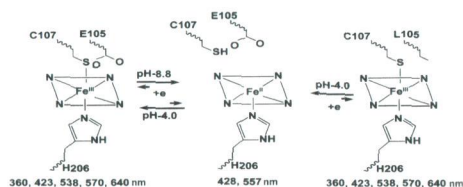


8878 5

dx.doi.org/10.1021/bi401343t

Identification of Proximal and Distal Axial Ligands in *Leishmania major* Pseudoperoxidase

Rina Saha, Moumita Bose, Sumit Sen Santara, Jayasree Roy, and Subrata Adak*

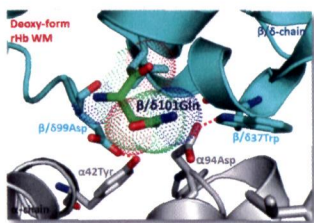


8888 5

dx.doi.org/10.1021/bi401087d

Role of $\beta/\delta 101$ Gln in Regulating the Effect of Temperature and Allosteric Effectors on Oxygen Affinity in Woolly Mammoth Hemoglobin

Yue Yuan, Catherine Byrd, Tong-Jian Shen, Virgil Simplaceanu, Tsuey Chyi S. Tam, and Chien Ho*

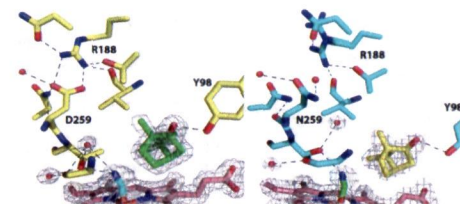


8898

dx.doi.org/10.1021/bi401330c

Crystal Structures and Functional Characterization of Wild-Type CYP101D1 and Its Active Site Mutants

Dipanwita Batabyal and Thomas L. Poulos*

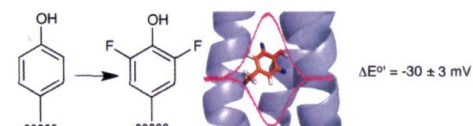


8907 5

dx.doi.org/10.1021/bi401494f

Formal Reduction Potential of 3,5-Difluorotyrosine in a Structured Protein: Insight into Multistep Radical Transfer

Kanchana R. Ravichandran, Li Liang, JoAnne Stubbe, and Cecilia Tommos*

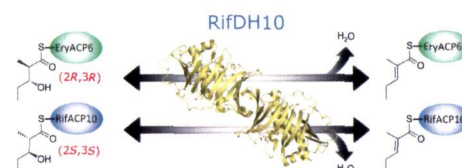


8916 5

dx.doi.org/10.1021/bi400988t

Structure and Stereospecificity of the Dehydratase Domain from the Terminal Module of the Rifamycin Polyketide Synthase

Darren Gay, Young-Ok You, Adrian Keatinge-Clay,* and David E. Cane*

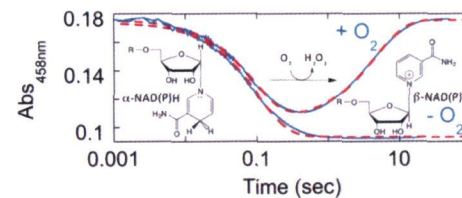


8929

dx.doi.org/10.1021/bi401185m

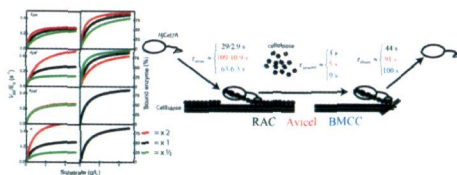
Kinetics and Equilibria of the Reductive and Oxidative Half-Reactions of Human Renalase with α -NADPH

Brett A. Beaupre, Matthew R. Hoag, Brenton R. Carmichael, and Graham R. Moran*



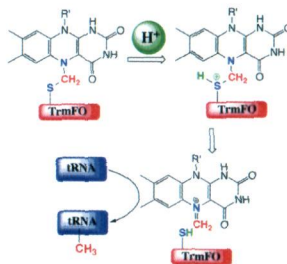
Transient Kinetics and Rate-Limiting Steps for the Processive Cellobiohydrolase Cel7A: Effects of Substrate Structure and Carbohydrate Binding Domain

Nicolaj Cruys-Bagger, Hirosuke Tatsumi, Guilin Robin Ren, Kim Borch, and Peter Westh*



Activation of a Unique Flavin-Dependent tRNA-Methylating Agent

Djemel Hamdane,* Eduardo Bruch, Sun Un, Martin Field, and Marc Fontecave



Multiple Exosites Distributed across the Three Domains of Streptokinase Co-Operate to Generate High Catalytic Rates in the Streptokinase–Plasmin Activator Complex

Rachna Aneja, Manish Datt, Suman Yadav, and Girish Sahni*

