

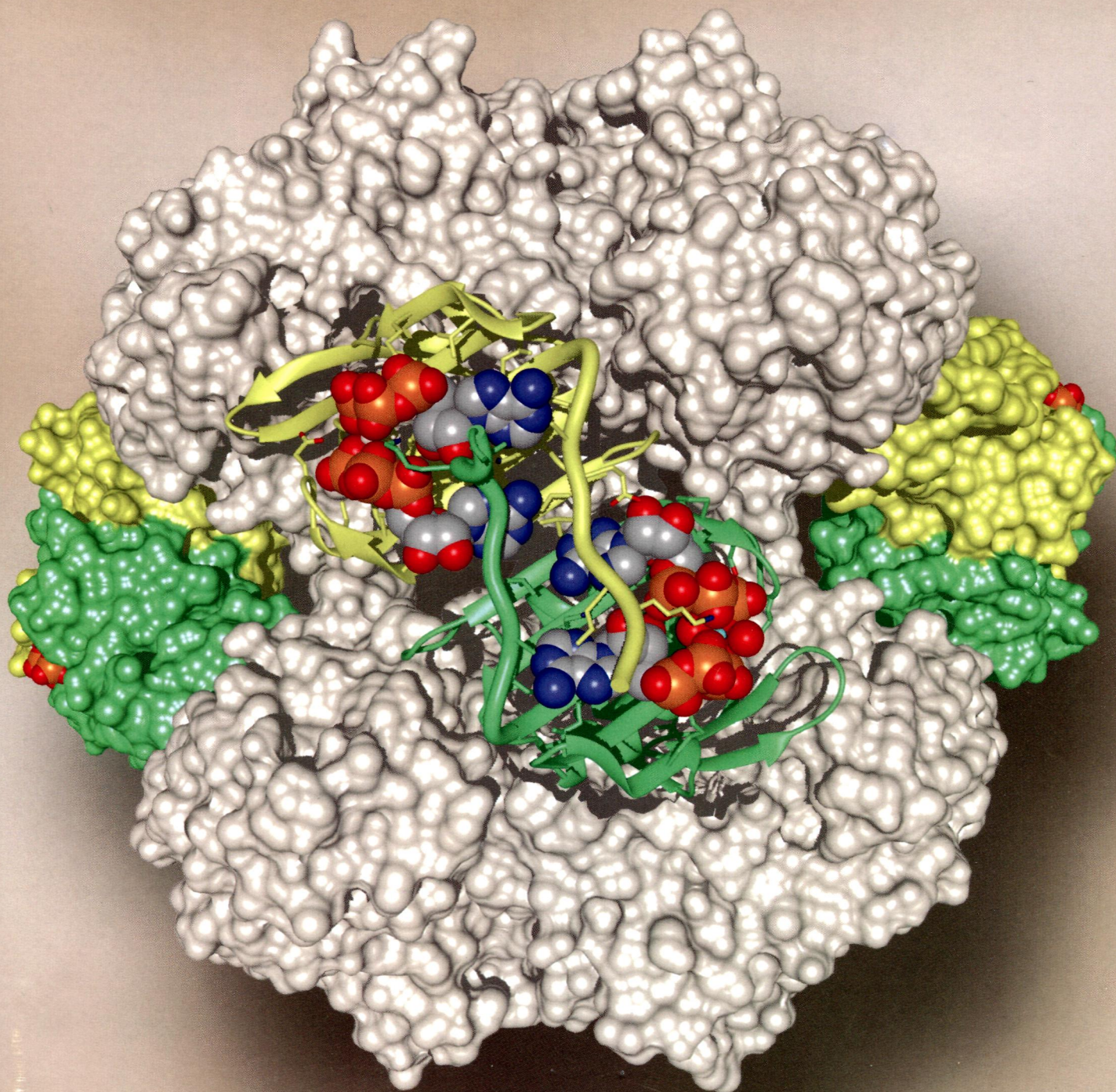
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JANUARY 21, 2014 • VOLUME 53 NUMBER 2

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ON THE COVER: Three-dimensional structure of the *Escherichia coli* aspartate transcarbamoylase holoenzyme in the R state with two ATP molecules and a Mg^{2+} cation bound to each regulatory chain. The two catalytic trimers are shown as surface representations (tan). One chain of each of the three regulatory dimers is colored yellow, while the other is colored green. The two regulatory dimers on the sides are shown as surface representations, while the third, in front, is shown as a ribbon trace. The binding of the two ATP molecules and one Mg^{2+} molecule induces an alteration of the N-termini of the regulatory chains (thick lines), displacing them into the adjacent regulatory chain and thereby strengthening the dimer interface and further stabilizing the R state of the enzyme. This figure was generated using UCSF Chimera. [Cockrell, G. M., et al. (2013) *Biochemistry* 52, 8036–8047]

Rapid Reports

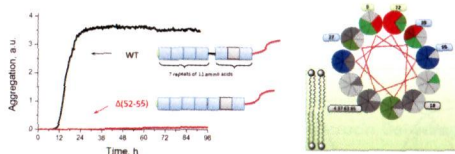
279

5

dx.doi.org/10.1021/bi401427t

A Four-Amino Acid Linker between Repeats in the α -Synuclein Sequence Is Important for Fibril Formation

Volodymyr V. Shvadchak and Vinod Subramaniam*



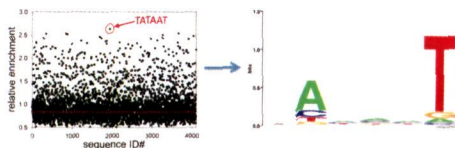
Articles

282

dx.doi.org/10.1021/bi401277w

Next Generation Sequencing-Based Parallel Analysis of Melting Kinetics of 4096 Variants of a Bacterial Promoter

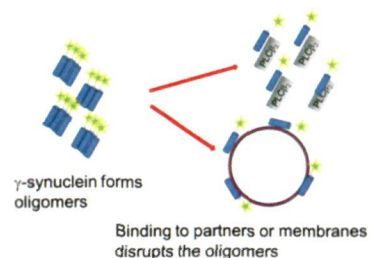
Ewa Heyduk and Tomasz Heyduk*



Defining the Oligomerization State of γ -Synuclein in Solution and in Cells

Urszula Golebiewska,* Cassandra Zurawsky, and Suzanne Scarlata

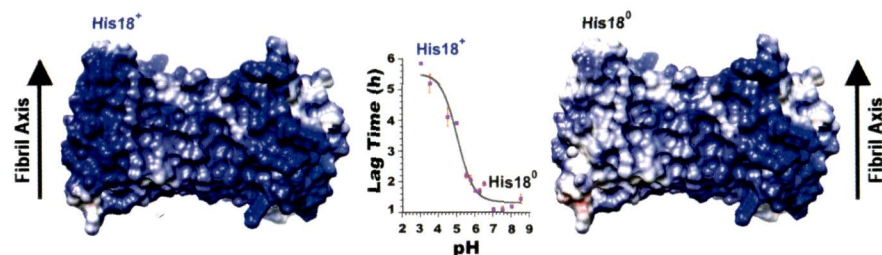
dx.doi.org/10.1021/bi401479a



pH Dependence of Amylin Fibrillization

Suman Jha, Jessica M. Snell, Sarah R. Sheftic, Sharadrao M. Patil, Stephen B. Daniels, Frederick W. Kolling, and Andrei T. Alexandrescu*

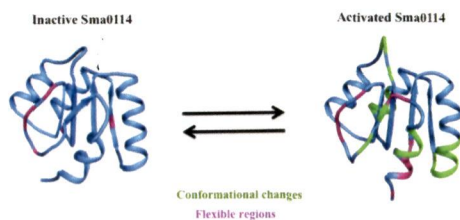
dx.doi.org/10.1021/bi401164k



NMR Structure of the HWE Kinase Associated Response Regulator Sma0114 in Its Activated State

Sarah R. Sheftic, Emma White, Daniel J. Gage, and Andrei T. Alexandrescu*

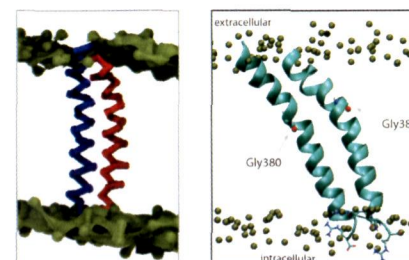
dx.doi.org/10.1021/bi401497h



Primary and Secondary Dimer Interfaces of the Fibroblast Growth Factor Receptor 3 Transmembrane Domain: Characterization via Multiscale Molecular Dynamics Simulations

Tyler Reddy, Santiago Manrique, Amanda Buyan, Benjamin A. Hall, Alan Chetwynd, and Mark S. P. Sansom*

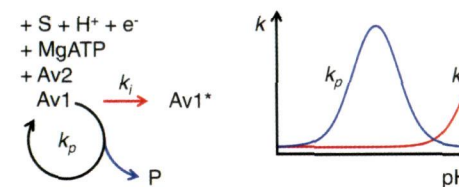
dx.doi.org/10.1021/bi401576k



Turnover-Dependent Inactivation of the Nitrogenase MoFe-Protein at High pH

Kun-Yun Yang, Chad A. Haynes, Thomas Spatzal, Douglas C. Rees,* and James B. Howard*

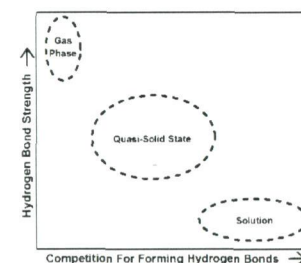
dx.doi.org/10.1021/bi4014769



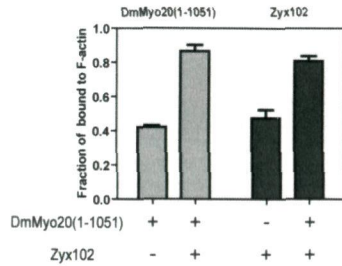
Strong, Low-Barrier Hydrogen Bonds May Be Available to Enzymes

Jacob D. Graham, Allyson M. Buytendyk, Di Wang, Kit H. Bowen,* and Kim D. Collins*

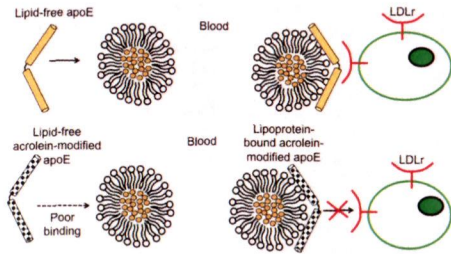
dx.doi.org/10.1021/bi4014566



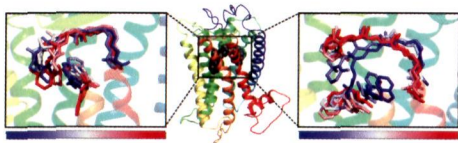
350 **S** [dx.doi.org/10.1021/bi401236c](https://doi.org/10.1021/bi401236c)
Drosophila Myosin-XX Functions as an Actin-Binding Protein To Facilitate the Interaction between Zyx102 and Actin
Yang Cao, Howard D. White, and Xiang-dong Li*



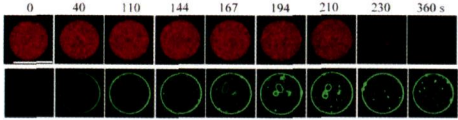
361 **S** [dx.doi.org/10.1021/bi401404u](https://doi.org/10.1021/bi401404u)
Acrolein Modification Impairs Key Functional Features of Rat Apolipoprotein E: Identification of Modified Sites by Mass Spectrometry
Tuyen N. Tran, Malathi G. Kosaraju, Shiori Tamamizu-Kato, Olayemi Akintunde, Ying Zheng, John K. Bielicki, Kent Pinkerton, Koji Uchida, Yuan Yu Lee,* and Vasanthy Narayanaswami*



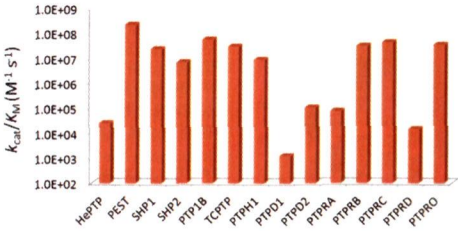
376 **S W** [dx.doi.org/10.1021/bi4013947](https://doi.org/10.1021/bi4013947)
Retinal Ligand Mobility Explains Internal Hydration and Reconciles Active Rhodopsin Structures
Nicholas Leioatts, Blake Mertz, Karina Martinez-Mayorga, Tod D. Romo, Michael C. Pitman, Scott E. Feller, Alan Grossfield,* and Michael F. Brown*



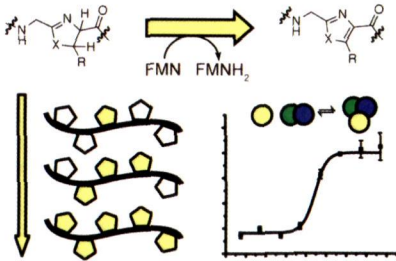
386 **S** [dx.doi.org/10.1021/bi401406p](https://doi.org/10.1021/bi401406p)
Entry of Cell-Penetrating Peptide Transporter 10 into a Single Vesicle by Translocating Across Lipid Membrane and Its Induced Pores
Md. Zahidul Islam, Hiroataka Ariyama, Jahangir Md. Alam, and Masahito Yamazaki*



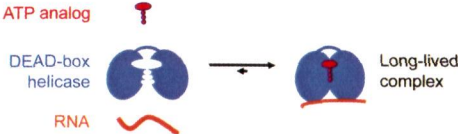
397 **S** [dx.doi.org/10.1021/bi401223r](https://doi.org/10.1021/bi401223r)
Diverse Levels of Sequence Selectivity and Catalytic Efficiency of Protein-Tyrosine Phosphatases
Nicholas G. Selner, Rinrada Luechapanichkul, Xianwen Chen, Benjamin G. Neel, Zhong-Yin Zhang, Stefan Knapp, Charles E. Bell, and Dehua Pei*



413 **S** [dx.doi.org/10.1021/bi401529y](https://doi.org/10.1021/bi401529y)
Orchestration of Enzymatic Processing by Thiazole/Oxazole-Modified Microcin Dehydrogenases
Joel O. Melby, Xiangpo Li, and Douglas A. Mitchell*



423 **S** [dx.doi.org/10.1021/bi401540q](https://doi.org/10.1021/bi401540q)
DEAD-Box Helicases Form Nucleotide-Dependent, Long-Lived Complexes with RNA
Fei Liu, Andrea A. Putnam, and Eckhard Jankowsky*



Targeted Reengineering of Protein Geranylgeranyltransferase Type I Selectivity Functionally Implicates Active-Site Residues in Protein-Substrate Recognition

Soumyashree A. Gangopadhyay, Erica L. Losito, and James L. Houglund*

