

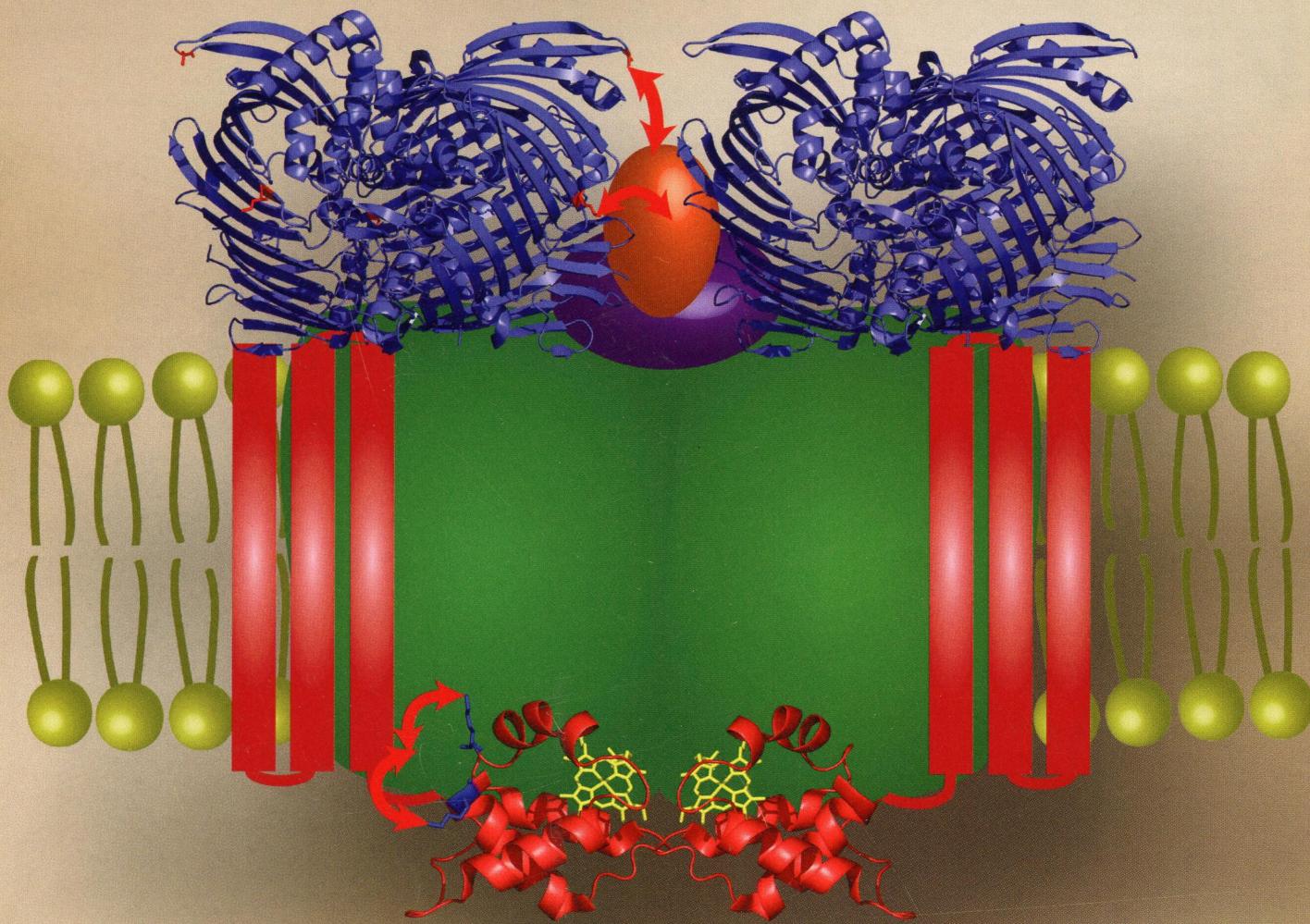
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DECEMBER 23, 2014 • VOLUME 53 NUMBER 50

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ON THE COVER: The photosynthetic apparatus of the anoxygenic photosynthetic green sulfur bacterium *Chlorobaculum tepidum* includes the reaction center core (RCC) complex and the FMO antenna protein. The RCC complex is an FeS-type (type I) reaction center, which is composed of a homodimeric core structure formed by two PscA proteins, PscB Fe-S protein, a cytochrome *c*₅₅₁ (PscC) protein, and a PscD protein. A structural model of the FMO/RCC complex is proposed on the basis of chemical cross-linking results.

Rapid Reports

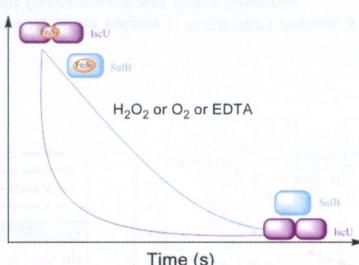
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DOI: 10.1021/bi5012496

Molecular Investigation of Iron–Sulfur Cluster Assembly Scaffolds under Stress

Béatrice Blanc, Martin Clémancey, Jean-Marc Latour, Marc Fontecave,* and Sandrine Ollagnier de Choudens*



Articles

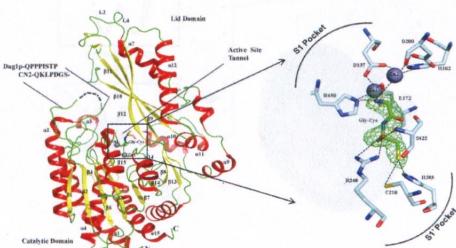
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DOI: 10.1021/bi501263u

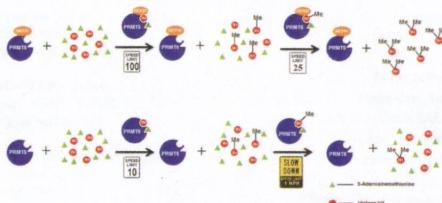
Molecular Basis of Peptide Recognition in Metallopeptidase Dug1p from *Saccharomyces cerevisiae*

Appu Kumar Singh, Mirage Singh, Vaibhav Kumar Pandya, Balasubramani G L, Vijay Singh, Mary Krishna Ekka, Monica Mittal, and S. Kumaran*



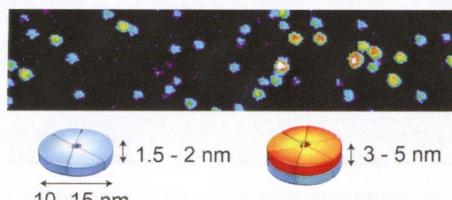
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Protein Arginine Methyltransferase 5 Catalyzes Substrate Dimethylation in a Distributive Fashion
Min Wang, Jakob Fuhrmann, and Paul R. Thompson*

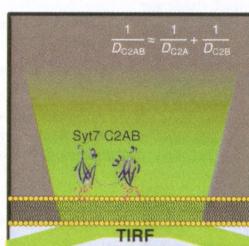


Capping of A_β42 Oligomers by Small Molecule Inhibitors

Ziao Fu, Darryl Aucoin, Mahiuddin Ahmed, Martine Ziliox, William E. Van Nostrand, and Steven O. Smith*

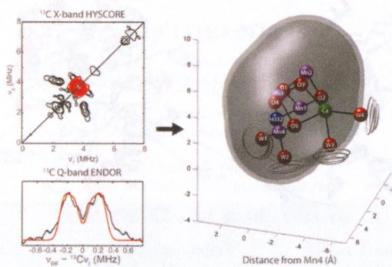


Lateral Diffusion of Proteins on Supported Lipid Bilayers: Additive Friction of Synaptotagmin 7 C2A–C2B Tandem Domains
Joseph K. Vasquez, Kan Chantranuvatana, Daniel T. Giardina, Matthew D. Coffman, and Jefferson D. Knight*



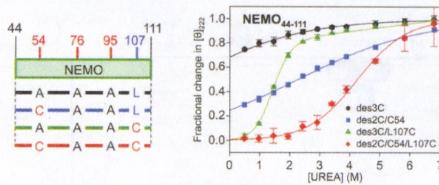
Pulse Electron Paramagnetic Resonance Studies of the Interaction of Methanol with the S₂ State of the Mn₄O₅Ca Cluster of Photosystem II

Paul H. Oyala, Troy A. Stich, Jamie A. Stull, Fangting Yu, Vincent L. Pecoraro, and R. David Britt*



Disulfide-Mediated Stabilization of the IκB Kinase Binding Domain of NF-κB Essential Modulator (NEMO)

Li Zhou, Alan T. Yeo, Carmine Ballarano, Urs Weber, Karen N. Allen,* Thomas D. Gilmore,* and Adrian Whitty*

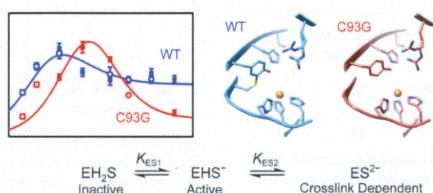


Structural and Biochemical Analysis of the *Hordeum vulgare* L. HvGR-RBP1 Protein, a Glycine-Rich RNA-Binding Protein Involved in the Regulation of Barley Plant Development and Stress Response

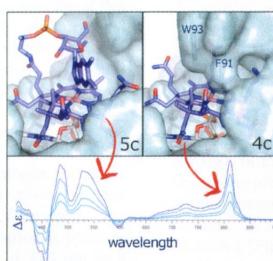
Brian P. Tripet, Katelyn E. Mason, Brian J. Eilers, Jennifer Burns, Paul Powell, Andreas M. Fischer, and Valérie Copié*



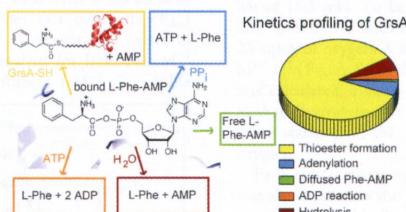
The Cys-Tyr Cross-Link of Cysteine Dioxygenase Changes the Optimal pH of the Reaction without a Structural Change
Casey G. Davies, Matthias Fellner, Egor P. Tchesnokov, Sigurd M. Wilbanks, and Guy N. L. Jameson*



Spectroscopic Studies of the *Salmonella enterica* Adenosyltransferase Enzyme SeCobA: Molecular-Level Insight into the Mechanism of Substrate Cob(II)alamin Activation
Ivan G. Pallares, Theodore C. Moore, Jorge C. Escalante-Semerena, and Thomas C. Brunold*

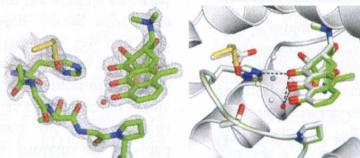


Kinetics Profiling of Gramicidin S Synthetase A, a Member of Nonribosomal Peptide Synthetases
Xun Sun, Hao Li, Jonas Alfermann, Henning D. Mootz, and Haw Yang*



Tetracycline Repressor Allostery Does Not Depend on Divalent Metal Recognition

Sebastiaan Werten,* Daniela Dalm, Gottfried Julius Palm, Christopher Cornelius Grimm, and Winfried Hinrichs*

**Additions and Corrections****Correction to The Specialized Hsp70 (HscA) Interdomain Linker Binds to Its Nucleotide-Binding Domain and Stimulates ATP Hydrolysis in Both *cis* and *trans* Configurations**

T. Reid Alderson, Jin Hae Kim, Kai Cai, Ronnie O. Frederick, Marco Tonelli, and John L. Markley*

The authors would like to correct the following statement in their article, published in Biochemistry, 2015, 54(29), 7999–8009: "The nucleotide-binding domain (NBD) of the HscA interdomain linker binds to the NBD in both *cis* and *trans* configurations, which stimulates ATP hydrolysis." In the original article, the authors used the term "linker" to describe the polypeptide chain connecting the two domains of the HscA protein. This term is misleading because the linker is not a separate domain; it is part of the NBD. The corrected statement is: "The NBD of the HscA interdomain linker binds to the NBD in both *cis* and *trans* configurations, which stimulates ATP hydrolysis." The authors apologize for any confusion this may have caused.

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