

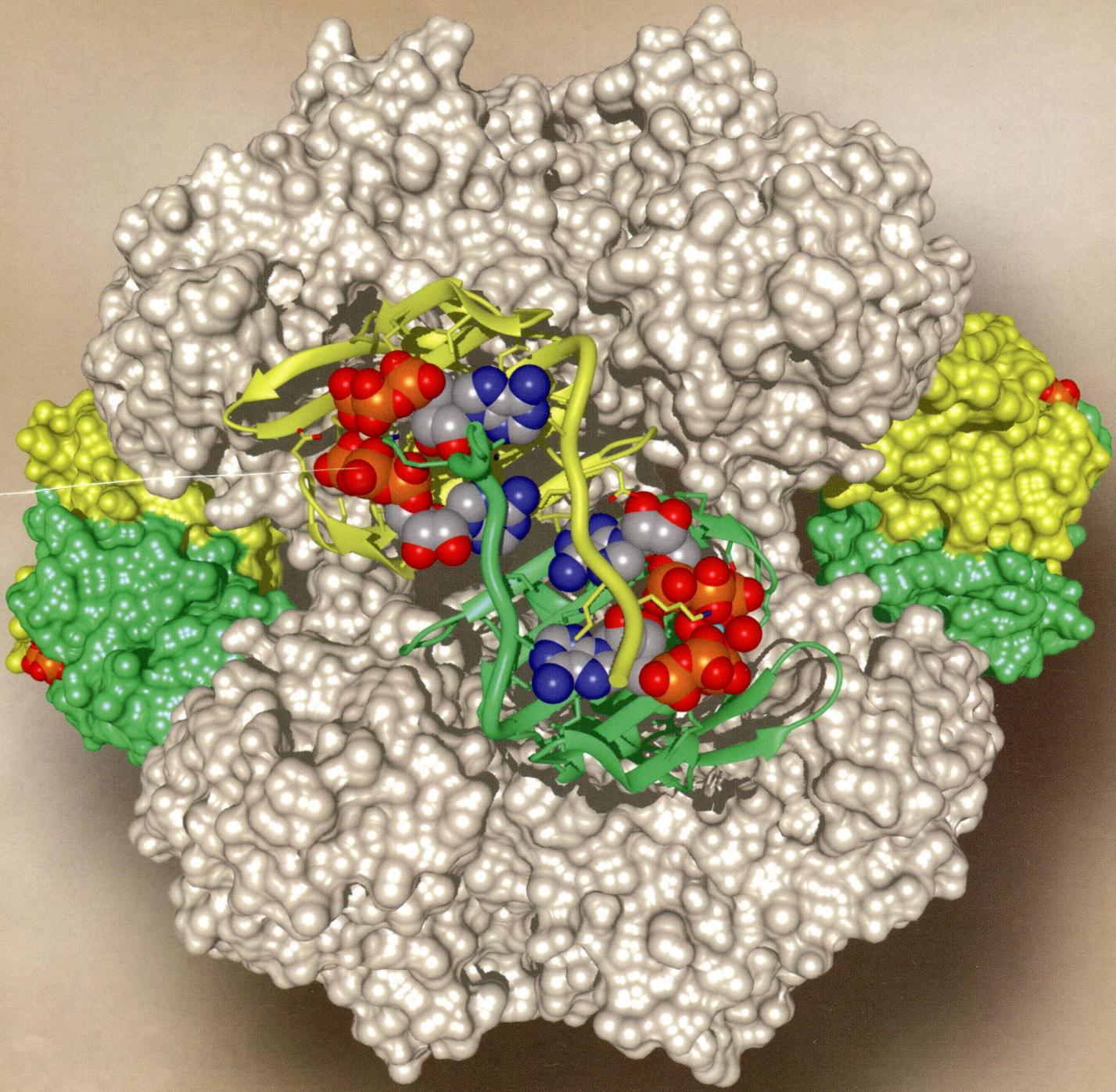
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ON THE COVER: Three-dimensional structure of the *Escherichia coli* aspartate transcarbamoylase holoenzyme in the R state with two ATP molecules and a Mg²⁺ cation bound to each regulatory chain. The two catalytic trimers are shown as surface representations (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 Mg²⁺ 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]

Articles

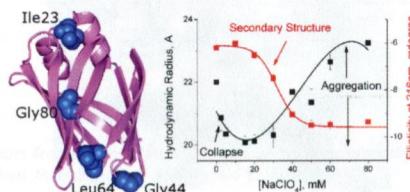
1393



[dx.doi.org/10.1021/bi4014837](https://doi.org/10.1021/bi4014837)

Studies of Early Events of Folding of a Predominately β -Sheet Protein Using Fluorescence Correlation Spectroscopy and Other Biophysical Methods

Suparna Sarkar and Krishnananda Chattopadhyay*



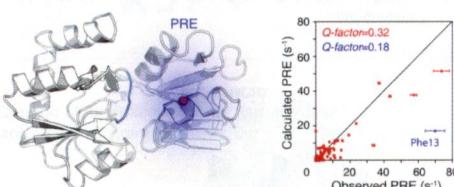
1403



[dx.doi.org/10.1021/bi4015715](https://doi.org/10.1021/bi4015715)

Subtle Dynamics of *holo* Glutamine Binding Protein Revealed with a Rigid Paramagnetic Probe

Zhu Liu, Zhou Gong, Da-Chuan Guo, Wei-Ping Zhang,* and Chun Tang*



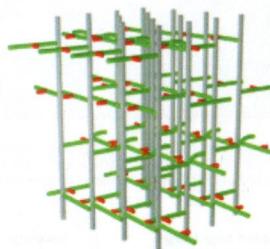
A Minimal Hydrophobicity Is Needed To Employ Amphiphilic p(HPMA)-co-p(LMA) Random Copolymers in Membrane Research

Michael Stangl, Mirjam Hemmelmann, Mareli Allmeroth, Rudolf Zentel, and Dirk Schneider*



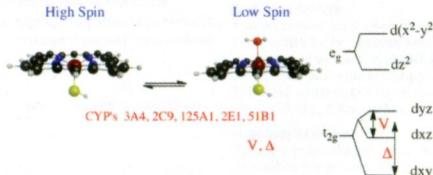
Cross-Link Formation and Peptidoglycan Lattice Assembly in the FemA Mutant of *Staphylococcus aureus*

Sung Joon Kim, Manmohan Singh, Shasad Sharif, and Jacob Schaefer*



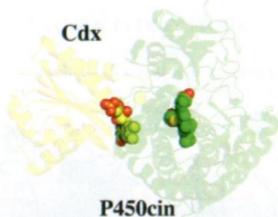
Strength of Axial Water Ligation in Substrate-Free Cytochrome P450s Is Isoform Dependent

Kip P. Conner, Alina M. Schimpf, Alex A. Cruce, Kirsty J. McLean, Andrew W. Munro, Daniel J. Frank, Matthew D. Krzyaniak, Paul Ortiz de Montellano, Michael K. Bowman, and William M. Atkins*

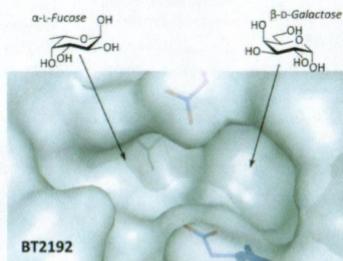


Crystal Structure of Cindoxin, the P450cin Redox Partner

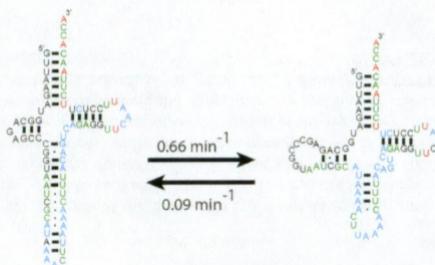
Yarrow Madrona, Scott A. Hollingsworth, Sarvind Tripathi, James B. Fields, Jean-Christophe N. Rwigema, Douglas J. Tobias, and Thomas L. Poulos*

**Unraveling the Substrate Recognition Mechanism and Specificity of the Unusual Glycosyl Hydrolase Family 29 BT2192 from *Bacteroides thetaiotaomicron***

Laure Guillotin, Pierre Lafite, and Richard Daniellou*

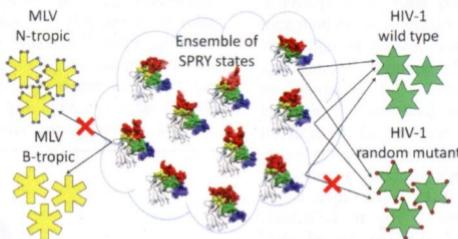
**Structural Dynamics of a Mitochondrial tRNA Possessing Weak Thermodynamic Stability**

Hari Bhaskaran, Takaaki Taniguchi, Takeo Suzuki, Tsutomu Suzuki, and John J. Perona*



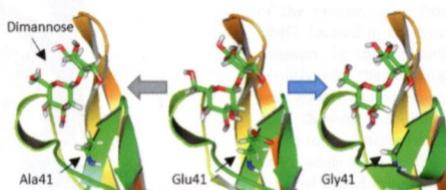
Recognition of the HIV Capsid by the TRIM5 α Restriction Factor Is Mediated by a Subset of Pre-Existing Conformations of the TRIM5 α SPRY Domain

Dmytro B. Kovalsky and Dmitri N. Ivanov*



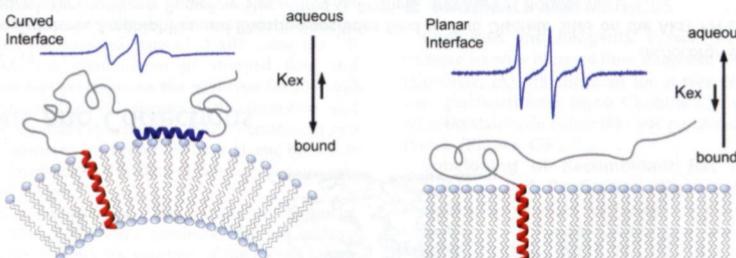
The Role of Glu41 in the Binding of Dimannose to P51G-m4-CVN

Sai Kumar Ramadugu, Zhen Li, Hemant K. Kashyap, and Claudio J. Margulis*



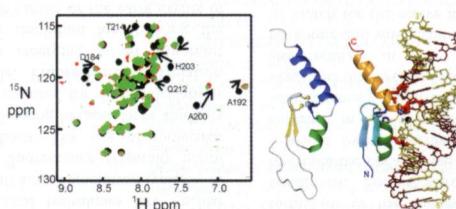
The SNARE Motif of Synaptobrevin Exhibits an Aqueous–Interfacial Partitioning That Is Modulated by Membrane Curvature

Binyong Liang, Damian Dawidowski, Jeffrey F. Ellena, Lukas K. Tamm,* and David S. Cafiso*



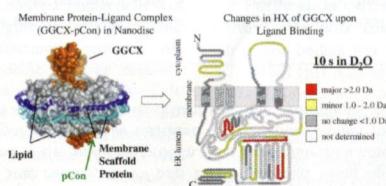
Structural Characterization of Interactions between the Double-Stranded RNA-Binding Zinc Finger Protein JAZ and Nucleic Acids

Russell G. Burge, Maria A. Martinez-Yamout, H. Jane Dyson,* and Peter E. Wright*



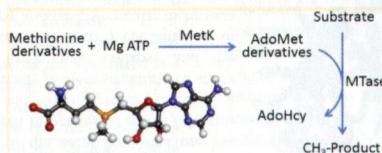
A Conformational Investigation of Propeptide Binding to the Integral Membrane Protein γ -Glutamyl Carboxylase Using Nanodisc Hydrogen Exchange Mass Spectrometry

Christine H. Parker,* Christopher R. Morgan, Kasper D. Rand, John R. Engen, James W. Jorgenson, and Darrel W. Stafford



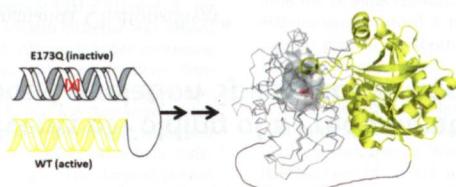
Producing Proficient Methyl Donors from Alternative Substrates of S-Adenosylmethionine Synthetase

Yasanandana S. Wijayasinghe, Robert M. Blumenthal, and Ronald E. Viola*



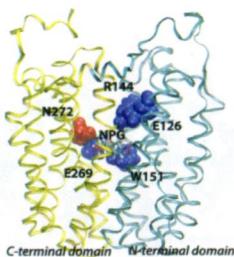
Catalytic Site Cooperativity in Dimeric Methylthioadenosine Nucleosidase

Shanzhi Wang, Keisha Thomas, and Vern L. Schramm*



Galactoside-Binding Site in LacY

Xiaoxu Jiang, Maria Katerina R. Villafuerte, Magnus Andersson, Stephen H. White, and H. Ronald Kaback*

**Additions and Corrections**

1544

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Correction to Cytotoxic Amphiphiles and Phosphoinositides Bind to Two Discrete Sites on the Akt1 PH Domain

Cheryl S. Gradziel, Yanling Wang, Boguslaw Stec, Alfred G. Redfield, and Mary F. Roberts*

The authors would like to correct their article, "Cytotoxic Amphiphiles and Phosphoinositides Bind to Two Discrete Sites on the Akt1 PH Domain," published in Biochemistry, 2014, 53(1), 1544–1552. In the original article, the authors reported that the binding of phosphoinositides to the Akt1 PH domain was dependent on the presence of a single conserved tyrosine residue, Y115. This finding was based on a mutagenesis study where the Y115 residue was mutated to phenylalanine (F115). However, upon closer examination, it was found that the Y115 residue is part of a larger hydrophobic cluster of residues, including I113, V114, and F115, which are involved in the binding of phosphoinositides. The authors apologize for this error and thank the reviewers for bringing this to their attention.

Supporting Information available via online article.