

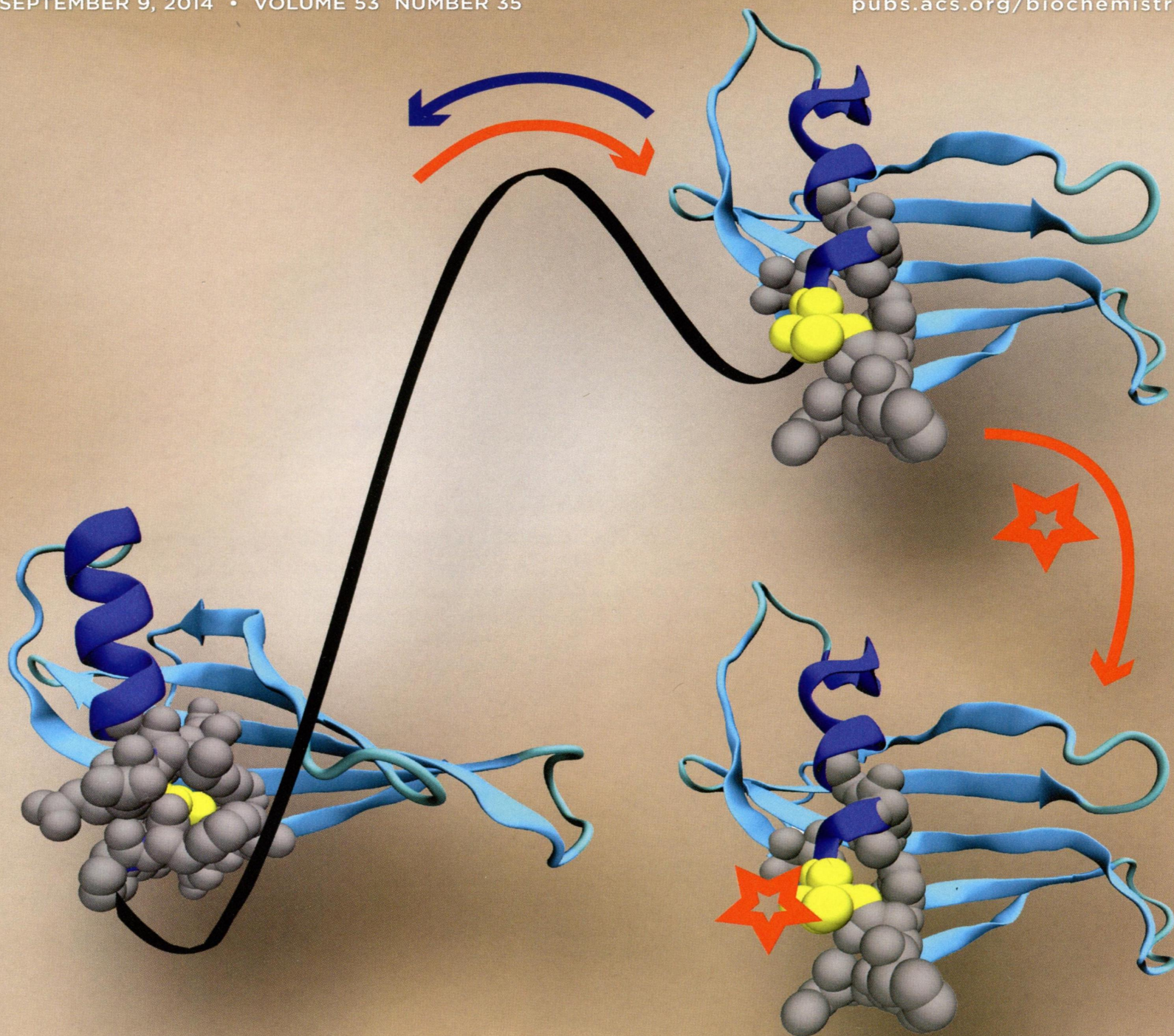
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ON THE COVER: The photosynthetic apparatus of the anoxygenic photosynthetic green sulfur bacterium *Chlorobaculum tepidum* includes the reaction center core (RCC) complex and the FMO antenna protein. The RCC complex is an FeS-type (type I) reaction 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.

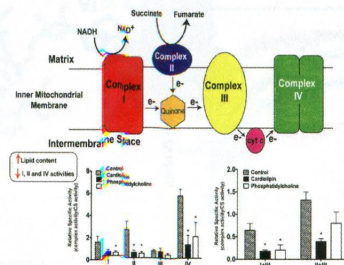
Rapid Reports

5589 

[dx.doi.org/10.1021/bi500868g](https://doi.org/10.1021/bi500868g)

Increasing Mitochondrial Membrane Phospholipid Content Lowers the Enzymatic Activity of Electron Transport Complexes

Saame Raza Shaikh, E. Madison Sullivan, Rick J. Allenman, David A. Brown, and Tonya N. Zeczycki*



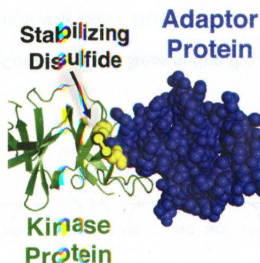
Accelerated Publications

5592

[dx.doi.org/10.1021/bi500849p](https://doi.org/10.1021/bi500849p)

Increasing and Decreasing the Ultrastability of Bacterial Chemotaxis Core Signaling Complexes by Modifying Protein–Protein Contacts

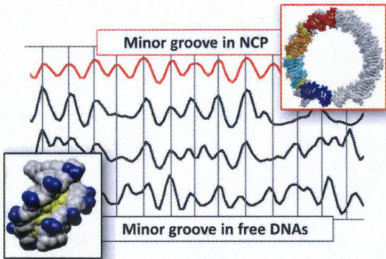
Kene N. Piasta and Joseph J. Falke*



5601 **S**

[dx.doi.org/10.1021/bi500504y](https://doi.org/10.1021/bi500504y)

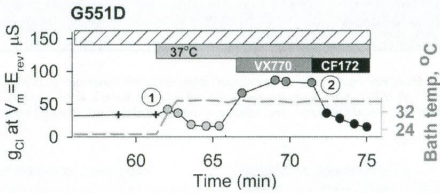
NMR Studies of DNA Support the Role of Pre-Existing Minor Groove Variations in Nucleosome Indirect Readout
Xiaoqian Xu, Akli Ben Imeddourene, Louissin  Zargarian, Nicolas Foloppe, Olivier Mauffret,* and Brigitte Hartmann*



5613

[dx.doi.org/10.1021/bi501007v](https://doi.org/10.1021/bi501007v)

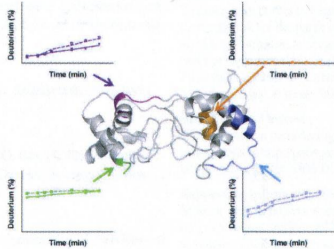
Cystic Fibrosis Transmembrane Conductance Regulator (CFTR) Potentiators Protect G551D but Not Δ F508 CFTR from Thermal Instability
Xuehong Liu* and David C. Dawson



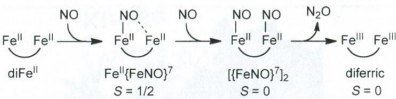
5619 **S**

[dx.doi.org/10.1021/bi500420y](https://doi.org/10.1021/bi500420y)

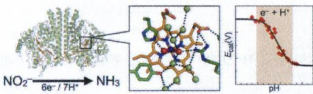
Structural Analysis of Diheme Cytochrome c by Hydrogen–Deuterium Exchange Mass Spectrometry and Homology Modeling
Ying Zhang, Erica L.-W. Majumder, Hai Yue, Robert E. Blankenship,* and Michael L. Gross*



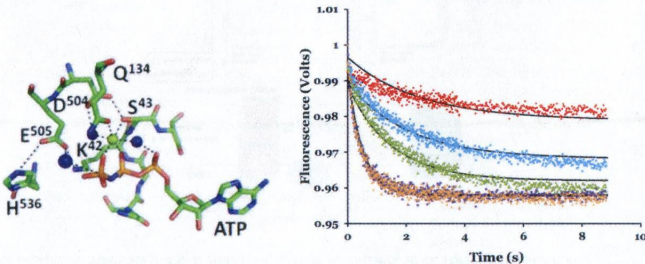
A Diferrous-Dinitrosyl Intermediate in the N₂O-Generating Pathway of a Deflavinated Flavo-Diiron Protein
Jonathan D. Caranto, Andrew Weitz, Nitai Giri, Michael P. Hendrich,* and Donald M. Kurtz Jr.*



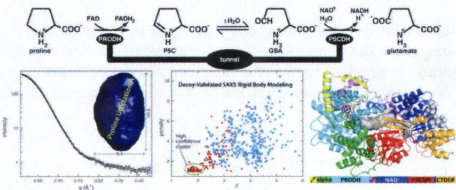
Hydrogen Bonding Networks Tune Proton-Coupled Redox Steps during the Enzymatic Six-Electron Conversion of Nitrite to Ammonia
Evan T. Judd, Natalia Stein, A. Andrew Pacheco, and Sean J. Elliott*



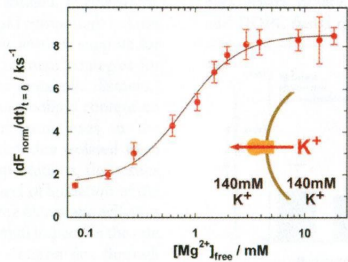
Catalytic Mechanism of Bacteriophage T4 Rad50 ATP Hydrolysis
Timothy J. Herdendorf and Scott W. Nelson*



Evidence That the C-Terminal Domain of a Type B PutA Protein Contributes to Aldehyde Dehydrogenase Activity and Substrate Channeling
Min Luo, Shelbi Christgen, Nikhilesh Sanyal, Benjamin W. Arentson, Donald F. Becker, and John J. Tanner*

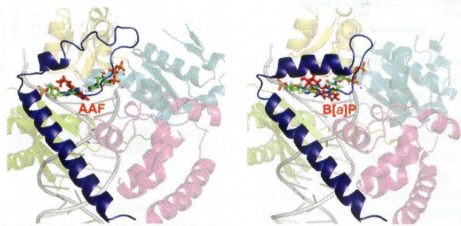


KdpFABC Reconstituted in *Escherichia coli* Lipid Vesicles: Substrate Dependence of the Transport Rate
Bojana Damjanovic and Hans-Jürgen Apell*



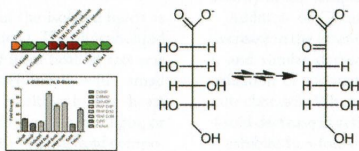
Structural and Dynamic Characterization of Polymerase κ 's Minor Groove Lesion Processing Reveals How Adduct Topology Impacts Fidelity

Lee Lior-Hoffmann, Shuang Ding, Nicholas E. Geacintov, Yingkai Zhang, and Suse Broyde*



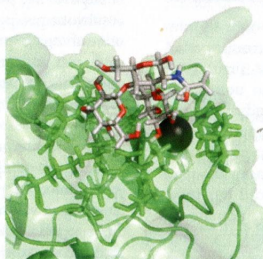
Investigating the Physiological Roles of Low-Efficiency D-Mannonate and D-Gluconate Dehydratases in the Enolase Superfamily: Pathways for the Catabolism of L-Gulonate and L-Isonate

Daniel J. Wichelecki, Jean Alyxa Ferolin Vendiola, Amy M. Jones, Nawar Al-Obaidi, Steven C. Almo, and John A. Gerlt*



Structural Characterization of the DC-SIGN–Lewis^X Complex

Kari Pederson, Daniel A. Mitchell, and James H. Prestegard*



The Interface between *Escherichia coli* Elongation Factor Tu and Aminoacyl-tRNA

Emine Yikilmaz, Stephen J. Chapman, Jared M. Schrader, and Olke C. Uhlenbeck*

