

David D Boehr

List of Publications by Year in descending order

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Version: 2024-02-01

49
papers

4,109
citations

394421

19
h-index

214800

47
g-index

51
all docs

51
docs citations

51
times ranked

4993
citing authors

#	ARTICLE	IF	CITATIONS
1	The role of dynamic conformational ensembles in biomolecular recognition. <i>Nature Chemical Biology</i> , 2009, 5, 789-796.	8.0	1,649
2	The Dynamic Energy Landscape of Dihydrofolate Reductase Catalysis. <i>Science</i> , 2006, 313, 1638-1642.	12.6	877
3	An NMR Perspective on Enzyme Dynamics. <i>Chemical Reviews</i> , 2006, 106, 3055-3079.	47.7	424
4	How Do Proteins Interact?. <i>Science</i> , 2008, 320, 1429-1430.	12.6	174
5	Millisecond timescale fluctuations in dihydrofolate reductase are exquisitely sensitive to the bound ligands. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 1373-1378.	7.1	133
6	Motif D of Viral RNA-Dependent RNA Polymerases Determines Efficiency and Fidelity of Nucleotide Addition. <i>Structure</i> , 2012, 20, 1519-1527.	3.3	80
7	A Distal Mutation Perturbs Dynamic Amino Acid Networks in Dihydrofolate Reductase. <i>Biochemistry</i> , 2013, 52, 4605-4619.	2.5	77
8	The RNA Template Channel of the RNA-Dependent RNA Polymerase as a Target for Development of Antiviral Therapy of Multiple Genera within a Virus Family. <i>PLoS Pathogens</i> , 2015, 11, e1004733.	4.7	55
9	Biophysical and computational methods to analyze amino acid interaction networks in proteins. <i>Computational and Structural Biotechnology Journal</i> , 2016, 14, 245-251.	4.1	55
10	Conformational Relaxation following Hydride Transfer Plays a Limiting Role in Dihydrofolate Reductase Catalysis. <i>Biochemistry</i> , 2008, 47, 9227-9233.	2.5	53
11	Long-Range Interaction Networks in the Function and Fidelity of Poliovirus RNA-Dependent RNA Polymerase Studied by Nuclear Magnetic Resonance. <i>Biochemistry</i> , 2010, 49, 9361-9371.	2.5	46
12	Amino Acid Networks in a $(\beta/\beta)_8$ Barrel Enzyme Change during Catalytic Turnover. <i>Journal of the American Chemical Society</i> , 2014, 136, 6818-6821.	13.7	41
13	Long-Range Interactions in the Alpha Subunit of Tryptophan Synthase Help to Coordinate Ligand Binding, Catalysis, and Substrate Channeling. <i>Journal of Molecular Biology</i> , 2013, 425, 1527-1545.	4.2	36
14	Vaccine-derived Mutation in Motif D of Poliovirus RNA-dependent RNA Polymerase Lowers Nucleotide Incorporation Fidelity. <i>Journal of Biological Chemistry</i> , 2013, 288, 32753-32765.	3.4	35
15	Structural Dynamics as a Contributor to Error-prone Replication by an RNA-dependent RNA Polymerase. <i>Journal of Biological Chemistry</i> , 2014, 289, 36229-36248.	3.4	31
16	Engineered control of enzyme structural dynamics and function. <i>Protein Science</i> , 2018, 27, 825-838.	7.6	30
17	Conformational selection and induced changes along the catalytic cycle of <i>Escherichia coli</i> dihydrofolate reductase. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 2369-2383.	2.6	20
18	The RNA-Binding Site of Poliovirus 3C Protein Doubles as a Phosphoinositide-Binding Domain. <i>Structure</i> , 2017, 25, 1875-1886.e7.	3.3	20

#	ARTICLE	IF	CITATIONS
19	Severing of a hydrogen bond disrupts amino acid networks in the catalytically active state of the alpha subunit of tryptophan synthase. <i>Protein Science</i> , 2015, 24, 484-494.	7.6	19
20	Assigning methyl resonances for protein solution-state NMR studies. <i>Methods</i> , 2018, 148, 88-99.	3.8	18
21	Triphosphate Reorientation of the Incoming Nucleotide as a Fidelity Checkpoint in Viral RNA-dependent RNA Polymerases. <i>Journal of Biological Chemistry</i> , 2017, 292, 3810-3826.	3.4	16
22	Differences in the catalytic mechanisms of mesophilic and thermophilic indole-3-glycerol phosphate synthase enzymes at their adaptive temperatures. <i>Biochemical and Biophysical Research Communications</i> , 2012, 418, 324-329.	2.1	14
23	Rational Control of Poliovirus RNA-Dependent RNA Polymerase Fidelity by Modulating Motif-D Loop Conformational Dynamics. <i>Biochemistry</i> , 2019, 58, 3735-3743.	2.5	14
24	Promiscuity in protein-RNA interactions: Conformational ensembles facilitate molecular recognition in the spliceosome. <i>BioEssays</i> , 2012, 34, 174-180.	2.5	13
25	2-C-methylated nucleotides terminate virus RNA synthesis by preventing active site closure of the viral RNA-dependent RNA polymerase. <i>Journal of Biological Chemistry</i> , 2019, 294, 16897-16907.	3.4	12
26	Engineering Allostery into Proteins. <i>Advances in Experimental Medicine and Biology</i> , 2019, 1163, 359-384.	1.6	12
27	Loop-loop interactions govern multiple steps in indole-3-glycerol phosphate synthase catalysis. <i>Protein Science</i> , 2014, 23, 302-311.	7.6	11
28	During Transitions Proteins Make Fleeting Bonds. <i>Cell</i> , 2009, 139, 1049-1051.	28.9	10
29	Targeting structural dynamics of the RNA-dependent RNA polymerase for anti-viral strategies. <i>Current Opinion in Virology</i> , 2014, 9, 194-200.	5.4	10
30	Long-Range Communication between Different Functional Sites in the Picornaviral 3C Protein. <i>Structure</i> , 2016, 24, 509-517.	3.3	10
31	Coordinated Network Changes across the Catalytic Cycle of Alpha Tryptophan Synthase. <i>Structure</i> , 2019, 27, 1405-1415.e5.	3.3	9
32	The Picornavirus Precursor 3CD Has Different Conformational Dynamics Compared to 3Cpro and 3Dpol in Functionally Relevant Regions. <i>Viruses</i> , 2021, 13, 442.	3.3	9
33	Structure, Dynamics, and Fidelity of RNA-Dependent RNA Polymerases. <i>Nucleic Acids and Molecular Biology</i> , 2014, , 309-333.	0.2	9
34	Functional Identification of the General Acid and Base in the Dehydration Step of Indole-3-glycerol Phosphate Synthase Catalysis. <i>Journal of Biological Chemistry</i> , 2013, 288, 26350-26356.	3.4	8
35	Controlling Active Site Loop Dynamics in the (12/1±)8 Barrel Enzyme Indole-3-Glycerol Phosphate Synthase. <i>Catalysts</i> , 2016, 6, 129.	3.5	8
36	Energy and Enzyme Activity Landscapes of Yeast Chorismate Mutase at Cellular Concentrations of Allosteric Effectors. <i>Biochemistry</i> , 2019, 58, 4058-4069.	2.5	7

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37	Distinct conformational dynamics and allosteric networks in alpha tryptophan synthase during active catalysis. <i>Protein Science</i> , 2021, 30, 543-557.	7.6	7
38	Substitution of a Surface-Exposed Residue Involved in an Allosteric Network Enhances Tryptophan Synthase Function in Cells. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 679915.	3.5	7
39	Millisecond Timescale Motions Connect Amino Acid Interaction Networks in Alpha Tryptophan Synthase. <i>Frontiers in Molecular Biosciences</i> , 2018, 5, 92.	3.5	6
40	Different Solvent and Conformational Entropy Contributions to the Allosteric Activation and Inhibition Mechanisms of Yeast Chorismate Mutase. <i>Biochemistry</i> , 2020, 59, 2528-2540.	2.5	6
41	Nucleobase but not Sugar Fidelity is Maintained in the Sabin I RNA-Dependent RNA Polymerase. <i>Viruses</i> , 2015, 7, 5571-5586.	3.3	4
42	Conformational Transitions in Yeast Chorismate Mutase Important for Allosteric Regulation as Identified by Nuclear Magnetic Resonance Spectroscopy. <i>Journal of Molecular Biology</i> , 2022, 434, 167531.	4.2	4
43	The Ins and Outs of Viral RNA Polymerase Translocation. <i>Journal of Molecular Biology</i> , 2014, 426, 1373-1376.	4.2	2
44	NMR Methods of Characterizing Biomolecular Structural Dynamics and Conformational Ensembles. <i>Methods</i> , 2018, 148, 1-3.	3.8	2
45	Driving Protein Conformational Cycles in Physiology and Disease: "Frustrated" Amino Acid Interaction Networks Define Dynamic Energy Landscapes. <i>BioEssays</i> , 2020, 42, 2000092.	2.5	2
46	Catalyst-Based Biomolecular Logic Gates. <i>Catalysts</i> , 2022, 12, 712.	3.5	2
47	Allosteric and dynamic control of RNA-dependent RNA polymerase function and fidelity. <i>The Enzymes</i> , 2021, 49, 149-193.	1.7	0
48	Triphosphate Reorientation of the Incoming Nucleotide as A Fidelity Checkpoint in Viral RNA-dependent RNA Polymerases. <i>FASEB Journal</i> , 2015, 29, 572.14.	0.5	0
49	The evolution of dynamic amino acid interaction networks around the catalytic cycle of $\hat{\pm}$ tryptophan synthase. <i>FASEB Journal</i> , 2018, 32, 527.6.	0.5	0