

David D Boehr

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

47
papers

3,525
citations

18
h-index

51
g-index

51
ext. papers

3,854
ext. citations

8.6
avg, IF

5.47
L-index

#	Paper	IF	Citations
47	The role of dynamic conformational ensembles in biomolecular recognition. <i>Nature Chemical Biology</i> , 2009 , 5, 789-96	11.7	1420
46	The dynamic energy landscape of dihydrofolate reductase catalysis. <i>Science</i> , 2006 , 313, 1638-42	33.3	778
45	An NMR perspective on enzyme dynamics. <i>Chemical Reviews</i> , 2006 , 106, 3055-79	68.1	369
44	Biochemistry. How do proteins interact?. <i>Science</i> , 2008 , 320, 1429-30	33.3	155
43	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, 1373-8	11.5	118
42	Motif D of viral RNA-dependent RNA polymerases determines efficiency and fidelity of nucleotide addition. <i>Structure</i> , 2012 , 20, 1519-27	5.2	75
41	A distal mutation perturbs dynamic amino acid networks in dihydrofolate reductase. <i>Biochemistry</i> , 2013 , 52, 4605-19	3.2	68
40	Conformational relaxation following hydride transfer plays a limiting role in dihydrofolate reductase catalysis. <i>Biochemistry</i> , 2008 , 47, 9227-33	3.2	50
39	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, 9361-71	3.2	45
38	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	7.6	44
37	Biophysical and computational methods to analyze amino acid interaction networks in proteins. <i>Computational and Structural Biotechnology Journal</i> , 2016 , 14, 245-51	6.8	39
36	Amino acid networks in a β -barrel enzyme change during catalytic turnover. <i>Journal of the American Chemical Society</i> , 2014 , 136, 6818-21	16.4	34
35	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	5.4	30
34	Long-range interactions in the β -subunit of tryptophan synthase help to coordinate ligand binding, catalysis, and substrate channeling. <i>Journal of Molecular Biology</i> , 2013 , 425, 1527-45	6.5	30
33	Structural dynamics as a contributor to error-prone replication by an RNA-dependent RNA polymerase. <i>Journal of Biological Chemistry</i> , 2014 , 289, 36229-48	5.4	27
32	Engineered control of enzyme structural dynamics and function. <i>Protein Science</i> , 2018 , 27, 825-838	6.3	19
31	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, 484-94	6.3	18

30	Conformational selection and induced changes along the catalytic cycle of Escherichia coli dihydrofolate reductase. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012 , 80, 2369-83	4.2	18
29	The RNA-Binding Site of Poliovirus 3C Protein Doubles as a Phosphoinositide-Binding Domain. <i>Structure</i> , 2017 , 25, 1875-1886.e7	5.2	14
28	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	5.4	13
27	Promiscuity in protein-RNA interactions: conformational ensembles facilitate molecular recognition in the spliceosome: conformational diversity in U2AF1 facilitates binding to diverse RNA sequences. <i>BioEssays</i> , 2012 , 34, 174-80	4.1	12
26	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, 324-9	3.4	12
25	Assigning methyl resonances for protein solution-state NMR studies. <i>Methods</i> , 2018 , 148, 88-99	4.6	10
24	During transitions proteins make fleeting bonds. <i>Cell</i> , 2009 , 139, 1049-51	56.2	10
23	Rational Control of Poliovirus RNA-Dependent RNA Polymerase Fidelity by Modulating Motif-D Loop Conformational Dynamics. <i>Biochemistry</i> , 2019 , 58, 3735-3743	3.2	9
22	Loop-loop interactions govern multiple steps in indole-3-glycerol phosphate synthase catalysis. <i>Protein Science</i> , 2014 , 23, 302-11	6.3	8
21	Targeting structural dynamics of the RNA-dependent RNA polymerase for anti-viral strategies. <i>Current Opinion in Virology</i> , 2014 , 9, 194-200	7.5	7
20	Coordinated Network Changes across the Catalytic Cycle of Alpha Tryptophan Synthase. <i>Structure</i> , 2019 , 27, 1405-1415.e5	5.2	6
19	Structure, Dynamics, and Fidelity of RNA-Dependent RNA Polymerases. <i>Nucleic Acids and Molecular Biology</i> , 2014 , 309-333		6
18	Engineering Allostery into Proteins. <i>Advances in Experimental Medicine and Biology</i> , 2019 , 1163, 359-384	3.6	6
17	Controlling Active Site Loop Dynamics in the (7)8 Barrel Enzyme Indole-3-Glycerol Phosphate Synthase. <i>Catalysts</i> , 2016 , 6, 129	4	6
16	Long-Range Communication between Different Functional Sites in the Picornaviral 3C Protein. <i>Structure</i> , 2016 , 24, 509-517	5.2	6
15	Energy and Enzyme Activity Landscapes of Yeast Chorismate Mutase at Cellular Concentrations of Allosteric Effectors. <i>Biochemistry</i> , 2019 , 58, 4058-4069	3.2	5
14	2VC-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	5.4	5
13	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, 26350-6	5.4	5

12	Millisecond Timescale Motions Connect Amino Acid Interaction Networks in Alpha Tryptophan Synthase. <i>Frontiers in Molecular Biosciences</i> , 2018 , 5, 92	5.6	5
11	Different Solvent and Conformational Entropy Contributions to the Allosteric Activation and Inhibition Mechanisms of Yeast Chorismate Mutase. <i>Biochemistry</i> , 2020 , 59, 2528-2540	3.2	4
10	Nucleobase but not Sugar Fidelity is Maintained in the Sabin I RNA-Dependent RNA Polymerase. <i>Viruses</i> , 2015 , 7, 5571-86	6.2	4
9	The Picornavirus Precursor 3CD Has Different Conformational Dynamics Compared to 3C and 3D in Functionally Relevant Regions. <i>Viruses</i> , 2021 , 13,	6.2	4
8	Distinct conformational dynamics and allosteric networks in alpha tryptophan synthase during active catalysis. <i>Protein Science</i> , 2021 , 30, 543-557	6.3	4
7	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	5.6	3
6	The ins and outs of viral RNA polymerase translocation. <i>Journal of Molecular Biology</i> , 2014 , 426, 1373-6	6.5	2
5	Driving Protein Conformational Cycles in Physiology and Disease: "Frustrated" Amino Acid Interaction Networks Define Dynamic Energy Landscapes: Amino Acid Interaction Networks Change Progressively Along Alpha Tryptophan Synthase's Catalytic Cycle. <i>BioEssays</i> , 2020 , 42, e2000092	4.1	1
4	Conformational transitions in yeast chorismate mutase important for allosteric regulation as identified by nuclear magnetic resonance spectroscopy.. <i>Journal of Molecular Biology</i> , 2022 , 167531	6.5	0
3	Allosteric and dynamic control of RNA-dependent RNA polymerase function and fidelity. <i>The Enzymes</i> , 2021 , 49, 149-193	2.3	
2	The evolution of dynamic amino acid interaction networks around the catalytic cycle of β tryptophan synthase. <i>FASEB Journal</i> , 2018 , 32, 527.6	0.9	
1	Triphosphate Re-orientation of the Incoming Nucleotide as A Fidelity Checkpoint in Viral RNA-dependent RNA Polymerases. <i>FASEB Journal</i> , 2015 , 29, 572.14	0.9	