David W Borhani

List of Publications by Year
in descending order

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49 papers	5,769 citations	201674 27 h-index	233421 45 g-index
50 all docs	50 docs citations	50 times ranked	6945 citing authors

#	Article	IF	Citations
1	Pathway and mechanism of drug binding to G-protein-coupled receptors. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 13118-13123.	7.1	673
2	Activation mechanism of theÎ²₂-adrenergic receptor. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 18684-18689.	7.1	539
3	Mechanism of Voltage Gating in Potassium Channels. Science, 2012, 336, 229-233.	12.6	516
4	Crystal structure of truncated human apolipoprotein A-I suggests a lipid-bound conformation. Proceedings of the National Academy of Sciences of the United States of America, 1997, 94, 12291-12296.	7.1	422
5	Structural basis for modulation of a G-protein-coupled receptor by allosteric drugs. Nature, 2013, 503, 295-299.	27.8	365
6	Molecular determinants of drugâ€“receptor binding kinetics. Drug Discovery Today, 2013, 18, 667-673.	6.4	307
7	Crystal Structure of the Ectodomain of Human Transferrin Receptor. Science, 1999, 286, 779-782.	12.6	298
8	Identification of two distinct inactive conformations of the Î² ₂ -adrenergic receptor reconciles structural and biochemical observations. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 4689-4694.	7.1	298
9	Principles of conduction and hydrophobic gating in K ⁺ channels. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 5833-5838.	7.1	298
10	Structural basis for nucleotide exchange in heterotrimeric G proteins. Science, 2015, 348, 1361-1365.	12.6	250
11	The future of molecular dynamics simulations in drug discovery. Journal of Computer-Aided Molecular Design, 2012, 26, 15-26.	2.9	233
12	Structural models of human apolipoprotein A-I: a critical analysis and review. Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids, 2001, 1531, 4-46.	2.4	212
13	Exploring atomic resolution physiology on a femtosecond to millisecond timescale using molecular dynamics simulations. Journal of General Physiology, 2010, 135, 555-562.	1.9	168
14	Slow Polymerization of Mycobacterium tuberculosis FtsZ. Journal of Bacteriology, 2000, 182, 4028-4034.	2.2	122
15	Structure of Mycobacterium tuberculosis FtsZ Reveals Unexpected, G Protein-like Conformational Switches. Journal of Molecular Biology, 2004, 342, 953-970.	4.2	116
16	Crystal Structure of Toxoplasma gondii Hypoxanthine-Guanine Phosphoribosyltransferase with XMP, Pyrophosphate, and Two Mg2+ Ions Bound:â€‰ Insights into the Catalytic Mechanism,. Biochemistry, 1999, 38, 14495-14506.	2.5	92
17	Discovery and Characterization of Non-ATP Site Inhibitors of the Mitogen Activated Protein (MAP) Kinases. ACS Chemical Biology, 2011, 6, 234-244.	3.4	77
18	Substrate Deformation in a Hypoxanthine-Guanine Phosphoribosyltransferase Ternary Complex. Structure, 2000, 8, 1309-1318.	3.3	75

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19	Novel Boron-Containing, Nonclassical Antifolates:â€‰ Synthesis and Preliminary Biological and Structural Evaluation. Journal of Medicinal Chemistry, 2007, 50, 3283-3289.	6.4	74
20	Dynamic control of slow water transport by aquaporin 0: Implications for hydration and junction stability in the eye lens. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 14430-14435.	7.1	74
21	Discovery of A-770041, a src-family selective orally active lck inhibitor that prevents organ allograft rejection. Bioorganic and Medicinal Chemistry Letters, 2006, 16, 118-122.	2.2	73
22	Crystal Structures of the Toxoplasma gondii Hypoxanthine-Guanine Phosphoribosyltransferaseâ^'GMP and â^'IMP Complexes:â€‰ Comparison of Purine Binding Interactions with the XMP Complex,. Biochemistry, 1999, 38, 14485-14494.	2.5	72
23	Atomic Structures of Human Dihydrofolate Reductase Complexed with NADPH and Two Lipophilic Antifolates at 1.09Ã... and 1.05Ã... Resolution. Journal of Molecular Biology, 2002, 320, 677-693.	4.2	68
24	Triazolinediones. Conversion to deaza dimers by electron-transfer catalysis. A possible radical anion Diels-Alder reaction. Journal of Organic Chemistry, 1986, 51, 1563-1570.	3.2	52
25	A-420983: a potent, orally active inhibitor of lck with efficacy in a model of transplant rejection. Bioorganic and Medicinal Chemistry Letters, 2004, 14, 2613-2616.	2.2	39
26	Comment on â€œA Bacterium That Can Grow by Using Arsenic Instead of Phosphorusâ€. Science, 2011, 332, 1149-1149.	12.6	30
27	Crystallization and X-ray diffraction studies of a soluble form of the human transferrin receptor. Journal of Molecular Biology, 1991, 218, 685-689.	4.2	28
28	Unusual Water-mediated Antigenic Recognition of the Proinflammatory Cytokine Interleukin-18. Journal of Biological Chemistry, 2009, 284, 24478-24489.	3.4	27
29	Crystallization of truncated human apolipoprotein A-I in a novel conformation. Acta Crystallographica Section D: Biological Crystallography, 1999, 55, 1578-1583.	2.5	26
30	2,4-Diaminopyrimidine MK2 inhibitors. Part I: Observation of an unexpected inhibitor binding mode. Bioorganic and Medicinal Chemistry Letters, 2010, 20, 330-333.	2.2	24
31	Michellamine Alkaloids Inhibit Protein Kinase C. Archives of Biochemistry and Biophysics, 1999, 365, 25-30.	3.0	21
32	2,4-Diaminopyrimidine MK2 inhibitors. Part II: Structure-based inhibitor optimization. Bioorganic and Medicinal Chemistry Letters, 2010, 20, 334-337.	2.2	19
33	The Two Toxoplasma gondii Hypoxanthine-Guanine Phosphoribosyltransferase Isozymes Form Heterotetramers. Journal of Biological Chemistry, 2000, 275, 19218-19223.	3.4	12
34	Enabling structure-based drug design of Tyk2 through co-crystallization with a stabilizing aminoindazole inhibitor. BMC Structural Biology, 2012, 12, 22.	2.3	12
35	Crystallization of theMycobacterium tuberculosiscell-division protein FtsZ. Acta Crystallographica Section D: Biological Crystallography, 2000, 56, 1634-1637.	2.5	11
36	Rational mutagenesis to support structure-based drug design: MAPKAP kinase 2 as a case study. BMC Structural Biology, 2009, 9, 16.	2.3	10

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37	Rethinking Clinical Trials: Biology's Mysteries. Science, 2011, 334, 1346-1347.	12.6	6
38	Enantioselective route to key intermediates in the synthesis of carbocyclic phosphoribosyltransferase transition state analogues. Tetrahedron, 2001, 57, 9899-9909.	1.9	5
39	Covalent JNK inhibitors?. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, E18; author reply E19.	7.1	4
40	Activation Mechanism of the Î²2-Adrenergic Receptor. Biophysical Journal, 2012, 102, 239a.	0.5	4
41	Kinetic Alteration of Human Aldose Reductase by Mutagenesis of Cysteine Residues. Advances in Experimental Medicine and Biology, 1993, 328, 289-300.	1.6	4
42	Human apolipoprotein A-I: structure determination and analysis of unusual diffraction characteristics. Acta Crystallographica Section D: Biological Crystallography, 1999, 55, 2013-2021.	2.5	3
43	Polymerization of C-terminally truncated Mycobacterium tuberculosis FtsZ is unlikely to be physiologically relevant. Microbiology (United Kingdom), 2004, 150, 3903-3906.	1.8	3
44	Pathway and Mechanism of Drug Binding to G-Protein-Coupled Receptors. Biophysical Journal, 2012, 102, 410a.	0.5	3
45	A scalable parallel framework for analyzing terascale molecular dynamics simulation trajectories. , 2008, , .		2
46	Identification Of Two Distinct Inactive Conformations Of The Beta-2 Adrenergic Receptor Reconciles Structural And Biochemical Observations. Biophysical Journal, 2009, 96, 365a.	0.5	2
47	Permeation And Conformational Changes Of The Pore Domain Of The Kv1.2 Potassium Channel. Biophysical Journal, 2009, 96, 176a.	0.5	0
48	Reply to Domene and Furini: Distinguishing knock-on and vacancy diffusion mechanisms. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, .	7.1	0
49	Include Israel when comparing metrics. Nature, 2011, 471, 37-37.	27.8	0