

Robert Paul Bywater

List of Publications by Year in descending order

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25
papers

797
citations

840776

11
h-index

580821

25
g-index

26
all docs

26
docs citations

26
times ranked

1102
citing authors

#	ARTICLE	IF	CITATIONS
1	Recognition of Privileged Structures by G-Protein Coupled Receptors. <i>Journal of Medicinal Chemistry</i> , 2004, 47, 888-899.	6.4	199
2	CURRENT PROGRESS IN STRUCTURE-BASED RATIONAL DRUG DESIGN MARKS A NEW MINDSET IN DRUG DISCOVERY. <i>Computational and Structural Biotechnology Journal</i> , 2013, 5, e201302011.	4.1	173
3	Conformation of Alamethicin in Oriented Phospholipid Bilayers Determined by ¹⁵ N Solid-State Nuclear Magnetic Resonance. <i>Biophysical Journal</i> , 2001, 81, 1684-1698.	0.5	109
4	Prediction of protein residue contacts with a PDB-derived likelihood matrix. <i>Protein Engineering, Design and Selection</i> , 2002, 15, 721-725.	2.1	55
5	Location and nature of the residues important for ligand recognition in G-protein coupled receptors. <i>Journal of Molecular Recognition</i> , 2005, 18, 60-72.	2.1	52
6	A sequence and structural study of transmembrane helices. <i>Journal of Computer-Aided Molecular Design</i> , 2001, 15, 533-552.	2.9	37
7	Protein folding: a problem with multiple solutions. <i>Journal of Biomolecular Structure and Dynamics</i> , 2013, 31, 351-362.	3.5	25
8	Did Life Begin on the Beach?. <i>Astrobiology</i> , 2005, 5, 568-574.	3.0	23
9	Melody discrimination and protein fold classification. <i>Heliyon</i> , 2016, 2, e00175.	3.2	19
10	Prediction of Protein Structural Features from Sequence Data Based on Shannon Entropy and Kolmogorov Complexity. <i>PLoS ONE</i> , 2015, 10, e0119306.	2.5	18
11	Essential motions in a fungal lipase with bound substrate, covalently attached inhibitor and product. <i>Journal of Molecular Recognition</i> , 2002, 15, 393-404.	2.1	15
12	Membrane-spanning peptides and the origin of life. <i>Journal of Theoretical Biology</i> , 2009, 261, 407-413.	1.7	10
13	Accelerated simulation of unfolding and refolding of a large single chain globular protein. <i>Open Biology</i> , 2012, 2, 120087.	3.6	10
14	On dating stages in prebiotic chemical evolution. <i>Die Naturwissenschaften</i> , 2012, 99, 167-176.	1.6	10
15	The dipeptide conformations of all twenty amino acid types in the context of biosynthesis. <i>SpringerPlus</i> , 2015, 4, 668.	1.2	7
16	PLIM: A protein-ligand interaction modeller. <i>Journal of Molecular Recognition</i> , 1993, 6, 111-115.	2.1	6
17	The preferred conformation of dipeptides in the context of biosynthesis. <i>Die Naturwissenschaften</i> , 2013, 100, 853-859.	1.6	6
18	Why twenty amino acid residue types suffice(d) to support all living systems. <i>PLoS ONE</i> , 2018, 13, e0204883.	2.5	6

#	ARTICLE	IF	CITATIONS
19	De Novo Generation of Molecular Structures Using Optimization To Select Graphs on a Given Lattice. Journal of Chemical Information and Computer Sciences, 2004, 44, 856-861.	2.8	5
20	Inactivation and reactivation of ribonuclease A studied by computer simulation. Open Biology, 2012, 2, 120088.	3.6	3
21	A tensegrity model for hydrogen bond networks in proteins. Heliyon, 2017, 3, e00307.	3.2	3
22	The fate of proteins in outer space. International Journal of Astrobiology, 2017, 16, 19-27.	1.6	2
23	Essential Motions and Energetic Contributions of Individual Residues in a Peptide Bound to an SH3 Domain. Biophysical Journal, 2000, 79, 646-655.	0.5	1
24	Comparison of Algorithms for Prediction of Protein Structural Features from Evolutionary Data. PLoS ONE, 2016, 11, e0150769.	2.5	1
25	GPCRs: Past, present, and future. , 2010, , 251-278.		1