

Robert Paul Bywater

List of Publications by Year in descending order

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Version: 2024-02-01

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	Why twenty amino acid residue types suffice(d) to support all living systems. PLoS ONE, 2018, 13, e0204883.	2.5	6
2	The fate of proteins in outer space. International Journal of Astrobiology, 2017, 16, 19-27.	1.6	2
3	A tensegrity model for hydrogen bond networks in proteins. Heliyon, 2017, 3, e00307.	3.2	3
4	Comparison of Algorithms for Prediction of Protein Structural Features from Evolutionary Data. PLoS ONE, 2016, 11, e0150769.	2.5	1
5	Melody discrimination and protein fold classification. Heliyon, 2016, 2, e00175.	3.2	19
6	The dipeptide conformations of all twenty amino acid types in the context of biosynthesis. SpringerPlus, 2015, 4, 668.	1.2	7
7	Prediction of Protein Structural Features from Sequence Data Based on Shannon Entropy and Kolmogorov Complexity. PLoS ONE, 2015, 10, e0119306.	2.5	18
8	Protein folding: a problem with multiple solutions. Journal of Biomolecular Structure and Dynamics, 2013, 31, 351-362.	3.5	25
9	CURRENT PROGRESS IN STRUCTURE-BASED RATIONAL DRUG DESIGN MARKS A NEW MINDSET IN DRUG DISCOVERY. Computational and Structural Biotechnology Journal, 2013, 5, e201302011.	4.1	173
10	The preferred conformation of dipeptides in the context of biosynthesis. Die Naturwissenschaften, 2013, 100, 853-859.	1.6	6
11	Inactivation and reactivation of ribonuclease A studied by computer simulation. Open Biology, 2012, 2, 120088.	3.6	3
12	Accelerated simulation of unfolding and refolding of a large single chain globular protein. Open Biology, 2012, 2, 120087.	3.6	10
13	On dating stages in prebiotic chemical evolution. Die Naturwissenschaften, 2012, 99, 167-176.	1.6	10
14	GPCRs: Past, present, and future. , 2010, , 251-278.		1
15	Membrane-spanning peptides and the origin of life. Journal of Theoretical Biology, 2009, 261, 407-413.	1.7	10
16	Location and nature of the residues important for ligand recognition in G-protein coupled receptors. Journal of Molecular Recognition, 2005, 18, 60-72.	2.1	52
17	Did Life Begin on the Beach?. Astrobiology, 2005, 5, 568-574.	3.0	23
18	Recognition of Privileged Structures by G-Protein Coupled Receptors. Journal of Medicinal Chemistry, 2004, 47, 888-899.	6.4	199

#	ARTICLE	IF	CITATIONS
19	De Novo Generation of Molecular Structures Using Optimization To Select Graphs on a Given Lattice. <i>Journal of Chemical Information and Computer Sciences</i> , 2004, 44, 856-861.	2.8	5
20	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
21	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
22	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
23	A sequence and structural study of transmembrane helices. <i>Journal of Computer-Aided Molecular Design</i> , 2001, 15, 533-552.	2.9	37
24	Essential Motions and Energetic Contributions of Individual Residues in a Peptide Bound to an SH3 Domain. <i>Biophysical Journal</i> , 2000, 79, 646-655.	0.5	1
25	PLIM: A protein-ligand interaction modeller. <i>Journal of Molecular Recognition</i> , 1993, 6, 111-115.	2.1	6