

Benjamin T Porebski

List of Publications by Year in descending order

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Version: 2024-02-01

26
papers

1,136
citations

471509

17
h-index

552781

26
g-index

29
all docs

29
docs citations

29
times ranked

2159
citing authors

#	ARTICLE	IF	CITATIONS
1	The role of protein dynamics in the evolution of new enzyme function. <i>Nature Chemical Biology</i> , 2016, 12, 944-950.	8.0	252
2	Consensus protein design. <i>Protein Engineering, Design and Selection</i> , 2016, 29, 245-251.	2.1	160
3	Germinal center antibody mutation trajectories are determined by rapid self/foreign discrimination. <i>Science</i> , 2018, 360, 223-226.	12.6	122
4	A synthetic genetic polymer with an uncharged backbone chemistry based on alkyl phosphonate nucleic acids. <i>Nature Chemistry</i> , 2019, 11, 533-542.	13.6	69
5	Epitope Flexibility and Dynamic Footprint Revealed by Molecular Dynamics of a pMHC-TCR Complex. <i>PLoS Computational Biology</i> , 2012, 8, e1002404.	3.2	54
6	Denisovan, modern human and mouse TNFAIP3 alleles tune A20 phosphorylation and immunity. <i>Nature Immunology</i> , 2019, 20, 1299-1310.	14.5	53
7	Random-sequence genetic oligomer pools display an innate potential for ligation and recombination. <i>ELife</i> , 2018, 7, .	6.0	43
8	Discovery and evolution of RNA and XNA reverse transcriptase function and fidelity. <i>Nature Chemistry</i> , 2020, 12, 683-690.	13.6	41
9	Modelling of Thyroid Peroxidase Reveals Insights into Its Enzyme Function and Autoantigenicity. <i>PLoS ONE</i> , 2015, 10, e0142615.	2.5	36
10	Cofactor-dependent conformational heterogeneity of GAD65 and its role in autoimmunity and neurotransmitter homeostasis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E2524-E2529.	7.1	34
11	Key determinants of selective binding and activation by the monocyte chemoattractant proteins at the chemokine receptor CCR2. <i>Science Signaling</i> , 2017, 10, .	3.6	33
12	Reactive centre loop dynamics and serpin specificity. <i>Scientific Reports</i> , 2019, 9, 3870.	3.3	33
13	Structural and dynamic properties that govern the stability of an engineered fibronectin type III domain. <i>Protein Engineering, Design and Selection</i> , 2015, 28, 67-78.	2.1	31
14	Direct and indirect mechanisms of KLK4 inhibition revealed by structure and dynamics. <i>Scientific Reports</i> , 2016, 6, 35385.	3.3	28
15	A Redundant Role of Human Thyroid Peroxidase Propeptide for Cellular, Enzymatic, and Immunological Activity. <i>Thyroid</i> , 2014, 24, 371-382.	4.5	25
16	Smoothing a rugged protein folding landscape by sequence-based redesign. <i>Scientific Reports</i> , 2016, 6, 33958.	3.3	22
17	Critical evaluation of <i>in silico</i> methods for prediction of coiled-coil domains in proteins. <i>Briefings in Bioinformatics</i> , 2016, 17, 270-282.	6.5	22
18	Circumventing the stability-function trade-off in an engineered FN3 domain. <i>Protein Engineering, Design and Selection</i> , 2016, 29, 541-550.	2.1	17

#	ARTICLE	IF	CITATIONS
19	Conformational diversity facilitates antibody mutation trajectories and discrimination between foreign and self-antigens. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 22341-22350.	7.1	15
20	Generation of AMBER force field parameters for zinc centres of M1 and M17 family aminopeptidases. Journal of Biomolecular Structure and Dynamics, 2018, 36, 2595-2604.	3.5	13
21	Structural reconstruction of protein ancestry. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 3897-3902.	7.1	12
22	Mapping the Pathway and Dynamics of Bestatin Inhibition of the <i>Plasmodium falciparum</i> M1 Aminopeptidase PfA-M1. ChemMedChem, 2018, 13, 2504-2513.	3.2	9
23	Interactive visualization tools for the structural biologist. Journal of Applied Crystallography, 2013, 46, 1518-1520.	4.5	4
24	Solution structure of a soluble fragment derived from a membrane protein by shotgun proteolysis. Protein Engineering, Design and Selection, 2015, 28, 445-450.	2.1	4
25	Structural Capacitance in Protein Evolution and Human Diseases. Journal of Molecular Biology, 2018, 430, 3200-3217.	4.2	3
26	Molecular basis of a redox switch: molecular dynamics simulations and surface plasmon resonance provide insight into reduced and oxidised angiotensinogen. Biochemical Journal, 2021, 478, 3319-3330.	3.7	1