

# Benjamin T Porebski

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7850092/publications.pdf>

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	Molecular basis of a redox switch: molecular dynamics simulations and surface plasmon resonance provide insight into reduced and oxidised angiotensinogen. <i>Biochemical Journal</i> , 2021, 478, 3319-3330.	3.7	1
2	Discovery and evolution of RNA and XNA reverse transcriptase function and fidelity. <i>Nature Chemistry</i> , 2020, 12, 683-690.	13.6	41
3	Conformational diversity facilitates antibody mutation trajectories and discrimination between foreign and self-antigens. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 22341-22350.	7.1	15
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	Reactive centre loop dynamics and serpin specificity. <i>Scientific Reports</i> , 2019, 9, 3870.	3.3	33
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	Germinal center antibody mutation trajectories are determined by rapid self/foreign discrimination. <i>Science</i> , 2018, 360, 223-226.	12.6	122
8	Generation of AMBER force field parameters for zinc centres of M1 and M17 family aminopeptidases. <i>Journal of Biomolecular Structure and Dynamics</i> , 2018, 36, 2595-2604.	3.5	13
9	Mapping the Pathway and Dynamics of Bestatin Inhibition of the <i>Plasmodium falciparum</i> M1 Aminopeptidase PfAEM1. <i>ChemMedChem</i> , 2018, 13, 2504-2513.	3.2	9
10	Structural Capacitance in Protein Evolution and Human Diseases. <i>Journal of Molecular Biology</i> , 2018, 430, 3200-3217.	4.2	3
11	Random-sequence genetic oligomer pools display an innate potential for ligation and recombination. <i>ELife</i> , 2018, 7, .	6.0	43
12	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
13	Structural reconstruction of protein ancestry. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 3897-3902.	7.1	12
14	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
15	The role of protein dynamics in the evolution of new enzyme function. <i>Nature Chemical Biology</i> , 2016, 12, 944-950.	8.0	252
16	Smoothing a rugged protein folding landscape by sequence-based redesign. <i>Scientific Reports</i> , 2016, 6, 33958.	3.3	22
17	Direct and indirect mechanisms of KLK4 inhibition revealed by structure and dynamics. <i>Scientific Reports</i> , 2016, 6, 35385.	3.3	28
18	Consensus protein design. <i>Protein Engineering, Design and Selection</i> , 2016, 29, 245-251.	2.1	160

#	ARTICLE	IF	CITATIONS
19	Critical evaluation of <i>in silico</i> methods for prediction of coiled-coil domains in proteins. Briefings in Bioinformatics, 2016, 17, 270-282.	6.5	22
20	Modelling of Thyroid Peroxidase Reveals Insights into Its Enzyme Function and Autoantigenicity. PLoS ONE, 2015, 10, e0142615.	2.5	36
21	Structural and dynamic properties that govern the stability of an engineered fibronectin type III domain. Protein Engineering, Design and Selection, 2015, 28, 67-78.	2.1	31
22	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
23	A Redundant Role of Human Thyroid Peroxidase Propeptide for Cellular, Enzymatic, and Immunological Activity. Thyroid, 2014, 24, 371-382.	4.5	25
24	Cofactor-dependent conformational heterogeneity of GAD65 and its role in autoimmunity and neurotransmitter homeostasis. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E2524-E2529.	7.1	34
25	Interactive visualization tools for the structural biologist. Journal of Applied Crystallography, 2013, 46, 1518-1520.	4.5	4
26	Epitope Flexibility and Dynamic Footprint Revealed by Molecular Dynamics of a pMHC-TCR Complex. PLoS Computational Biology, 2012, 8, e1002404.	3.2	54