Philip Bradley

List of Publications by Year
in descending order

35 papers	**8,219** citations	279798 **23** h-index	377865 **34** g-index
45 all docs	**45** docs citations	**45** times ranked	**10588** citing authors

#	ARTICLE	IF	CITATIONS
1	Integrating T cell receptor sequences and transcriptional profiles by clonotype neighbor graph analysis (CoNGA). Nature Biotechnology, 2022, 40, 54-63.	17.5	65
2	Convergent clonal selection of donor- and recipient-derived CMV-specific T cells in hematopoietic stem cell transplant patients. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	2
3	Combining genotypes and T cell receptor distributions to infer genetic loci determining V(D)J recombination probabilities. ELife, 2022, 11, .	6.0	12
4	Computational design of mechanically coupled axle-rotor protein assemblies. Science, 2022, 376, 383-390.	12.6	33
5	Design of functionalised circular tandem repeat proteins with longer repeat topologies and enhanced subunit contact surfaces. Communications Biology, 2021, 4, 1240.	4.4	8
6	Non-Genetic Determinants of Clonotypic T Cell Expansion Following Allogeneic Stem Cell Transplant. Blood, 2021, 138, 646-646.	1.4	0
7	TCR meta-clonotypes for biomarker discovery with tcrdist3 enabled identification of public, HLA-restricted clusters of SARS-CoV-2 TCRs. ELife, 2021, 10, .	6.0	76
8	Better together: Elements of successful scientific software development in a distributed collaborative community. PLoS Computational Biology, 2020, 16, e1007507.	3.2	27
9	Macromolecular modeling and design in Rosetta: recent methods and frameworks. Nature Methods, 2020, 17, 665-680.	19.0	513
10	Engineering and functionalization of large circular tandem repeat protein nanoparticles. Nature Structural and Molecular Biology, 2020, 27, 342-350.	8.2	26
11	Advances in protein structure prediction and design. Nature Reviews Molecular Cell Biology, 2019, 20, 681-697.	37.0	489
12	Using T Cell Receptor Repertoires to Understand the Principles of Adaptive Immune Recognition. Annual Review of Immunology, 2019, 37, 547-570.	21.8	122
13	Deep generative models for T cell receptor protein sequences. ELife, 2019, 8, .	6.0	60
14	Human T cell receptor occurrence patterns encode immune history, genetic background, and receptor specificity. ELife, 2018, 7, .	6.0	124
15	A Diverse Lipid Antigen–Specific TCR Repertoire Is Clonally Expanded during Active Tuberculosis. Journal of Immunology, 2018, 201, 888-896.	0.8	30
16	The Rosetta All-Atom Energy Function for Macromolecular Modeling and Design. Journal of Chemical Theory and Computation, 2017, 13, 3031-3048.	5.3	1,032
17	Quantifiable predictive features define epitope-specific T cell receptor repertoires. Nature, 2017, 547, 89-93.	27.8	723
18	Mammalian display screening of diverse cystine-dense peptides for difficult to drug targets. Nature Communications, 2017, 8, 2244.	12.8	56

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19	Simultaneous Optimization of Biomolecular Energy Functions on Features from Small Molecules and Macromolecules. Journal of Chemical Theory and Computation, 2016, 12, 6201-6212.	5.3	382
20	Rational design of Î±-helical tandem repeat proteins with closed architectures. Nature, 2015, 528, 585-588.	27.8	113
21	Combined Covalent-Electrostatic Model of Hydrogen Bonding Improves Structure Prediction with Rosetta. Journal of Chemical Theory and Computation, 2015, 11, 609-622.	5.3	204
22	Quantifying evolutionary constraints on B-cell affinity maturation. Philosophical Transactions of the Royal Society B: Biological Sciences, 2015, 370, 20140244.	4.0	45
23	<i>U2AF1</i> mutations alter splice site recognition in hematological malignancies. Genome Research, 2015, 25, 14-26.	5.5	238
24	Massively parallel determination and modeling of endonuclease substrate specificity. Nucleic Acids Research, 2014, 42, 13839-13852.	14.5	10
25	Improved Modeling of Side-Chainâ€"Base Interactions and Plasticity in Proteinâ€"DNA Interface Design. Journal of Molecular Biology, 2012, 419, 255-274.	4.2	20
26	The Crystal Structure of TAL Effector PthXo1 Bound to Its DNA Target. Science, 2012, 335, 716-719.	12.6	505
27	Structural modeling of TAL effectorâ€"DNA interactions. Protein Science, 2012, 21, 471-474.	7.6	17
28	Rosetta3. Methods in Enzymology, 2011, 487, 545-574.	1.0	1,620
29	Extensive protein and DNA backbone sampling improves structure-based specificity prediction for C2H2 zinc fingers. Nucleic Acids Research, 2011, 39, 4564-4576.	14.5	41
30	Modeling Symmetric Macromolecular Structures in Rosetta3. PLoS ONE, 2011, 6, e20450.	2.5	197
31	HLA mismatches and hematopoietic cell transplantation: structural simulations assess the impact of changes in pep-tide binding specificity on transplant outcome. Immunome Research, 2011, 7, 4.	0.1	9
32	Proteinâ€"Protein Docking with Backbone Flexibility. Journal of Molecular Biology, 2007, 373, 503-519.	4.2	401
33	Toward High-Resolution de Novo Structure Prediction for Small Proteins. Science, 2005, 309, 1868-1871.	12.6	797
34	Rosetta predictions in CASP5: Successes, failures, and prospects for complete automation. Proteins: Structure, Function and Bioinformatics, 2003, 53, 457-468.	2.6	162
35	Intestinal Intraepithelial Lymphocyte Repertoires are Imprinted Clonal Structures Selected for MHC Reactivity. SSRN Electronic Journal, 0, , .	0.4	3