

Philip Bradley

List of Publications by Year in descending order

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Version: 2024-02-01

35
papers

8,219
citations

279701

23
h-index

377752

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). <i>Nature Biotechnology</i> , 2022, 40, 54-63.	9.4	65
2	Convergent clonal selection of donor- and recipient-derived CMV-specific T cells in hematopoietic stem cell transplant patients. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	2
3	Combining genotypes and T cell receptor distributions to infer genetic loci determining V(D)J recombination probabilities. <i>ELife</i> , 2022, 11, .	2.8	12
4	Computational design of mechanically coupled axle-rotor protein assemblies. <i>Science</i> , 2022, 376, 383-390.	6.0	33
5	Design of functionalised circular tandem repeat proteins with longer repeat topologies and enhanced subunit contact surfaces. <i>Communications Biology</i> , 2021, 4, 1240.	2.0	8
6	Non-Genetic Determinants of Clonotypic T Cell Expansion Following Allogeneic Stem Cell Transplant. <i>Blood</i> , 2021, 138, 646-646.	0.6	0
7	TCR meta-clonotypes for biomarker discovery with tcrdist3 enabled identification of public, HLA-restricted clusters of SARS-CoV-2 TCRs. <i>ELife</i> , 2021, 10, .	2.8	76
8	Better together: Elements of successful scientific software development in a distributed collaborative community. <i>PLoS Computational Biology</i> , 2020, 16, e1007507.	1.5	27
9	Macromolecular modeling and design in Rosetta: recent methods and frameworks. <i>Nature Methods</i> , 2020, 17, 665-680.	9.0	513
10	Engineering and functionalization of large circular tandem repeat protein nanoparticles. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 342-350.	3.6	26
11	Advances in protein structure prediction and design. <i>Nature Reviews Molecular Cell Biology</i> , 2019, 20, 681-697.	16.1	489
12	Using T Cell Receptor Repertoires to Understand the Principles of Adaptive Immune Recognition. <i>Annual Review of Immunology</i> , 2019, 37, 547-570.	9.5	122
13	Deep generative models for T cell receptor protein sequences. <i>ELife</i> , 2019, 8, .	2.8	60
14	Human T cell receptor occurrence patterns encode immune history, genetic background, and receptor specificity. <i>ELife</i> , 2018, 7, .	2.8	124
15	A Diverse Lipid Antigen-Specific TCR Repertoire Is Clonally Expanded during Active Tuberculosis. <i>Journal of Immunology</i> , 2018, 201, 888-896.	0.4	30
16	The Rosetta All-Atom Energy Function for Macromolecular Modeling and Design. <i>Journal of Chemical Theory and Computation</i> , 2017, 13, 3031-3048.	2.3	1,082
17	Quantifiable predictive features define epitope-specific T cell receptor repertoires. <i>Nature</i> , 2017, 547, 89-93.	13.7	723
18	Mammalian display screening of diverse cysteine-dense peptides for difficult to drug targets. <i>Nature Communications</i> , 2017, 8, 2244.	5.8	56

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19	Simultaneous Optimization of Biomolecular Energy Functions on Features from Small Molecules and Macromolecules. <i>Journal of Chemical Theory and Computation</i> , 2016, 12, 6201-6212.	2.3	382
20	Rational design of α -helical tandem repeat proteins with closed architectures. <i>Nature</i> , 2015, 528, 585-588.	13.7	113
21	Combined Covalent-Electrostatic Model of Hydrogen Bonding Improves Structure Prediction with Rosetta. <i>Journal of Chemical Theory and Computation</i> , 2015, 11, 609-622.	2.3	204
22	Quantifying evolutionary constraints on B-cell affinity maturation. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20140244.	1.8	45
23	<i>U2AF1</i> mutations alter splice site recognition in hematological malignancies. <i>Genome Research</i> , 2015, 25, 14-26.	2.4	238
24	Massively parallel determination and modeling of endonuclease substrate specificity. <i>Nucleic Acids Research</i> , 2014, 42, 13839-13852.	6.5	10
25	Improved Modeling of Side-Chain-Base Interactions and Plasticity in Protein-DNA Interface Design. <i>Journal of Molecular Biology</i> , 2012, 419, 255-274.	2.0	20
26	The Crystal Structure of TAL Effector PthXo1 Bound to Its DNA Target. <i>Science</i> , 2012, 335, 716-719.	6.0	505
27	Structural modeling of TAL effector-DNA interactions. <i>Protein Science</i> , 2012, 21, 471-474.	3.1	17
28	Rosetta3. <i>Methods in Enzymology</i> , 2011, 487, 545-574.	0.4	1,620
29	Extensive protein and DNA backbone sampling improves structure-based specificity prediction for C2H2 zinc fingers. <i>Nucleic Acids Research</i> , 2011, 39, 4564-4576.	6.5	41
30	Modeling Symmetric Macromolecular Structures in Rosetta3. <i>PLoS ONE</i> , 2011, 6, e20450.	1.1	197
31	HLA mismatches and hematopoietic cell transplantation: structural simulations assess the impact of changes in pep-tide binding specificity on transplant outcome. <i>Immunome Research</i> , 2011, 7, 4.	0.1	9
32	Protein-Protein Docking with Backbone Flexibility. <i>Journal of Molecular Biology</i> , 2007, 373, 503-519.	2.0	401
33	Toward High-Resolution de Novo Structure Prediction for Small Proteins. <i>Science</i> , 2005, 309, 1868-1871.	6.0	797
34	Rosetta predictions in CASP5: Successes, failures, and prospects for complete automation. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 53, 457-468.	1.5	162
35	Intestinal Intraepithelial Lymphocyte Repertoires are Imprinted Clonal Structures Selected for MHC Reactivity. <i>SSRN Electronic Journal</i> , 0, , .	0.4	3