

Victor Greiff

List of Publications by Year in descending order

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Version: 2024-02-01

51
papers

2,656
citations

257357

24
h-index

243529

44
g-index

71
all docs

71
docs citations

71
times ranked

2663
citing authors

#	ARTICLE	IF	CITATIONS
1	Bioinformatic and Statistical Analysis of Adaptive Immune Repertoires. Trends in Immunology, 2015, 36, 738-749.	2.9	178
2	A bioinformatic framework for immune repertoire diversity profiling enables detection of immunological status. Genome Medicine, 2015, 7, 49.	3.6	177
3	Systems Analysis Reveals High Genetic and Antigen-Driven Predetermination of Antibody Repertoires throughout B Cell Development. Cell Reports, 2017, 19, 1467-1478.	2.9	172
4	Computational Strategies for Dissecting the High-Dimensional Complexity of Adaptive Immune Repertoires. Frontiers in Immunology, 2018, 9, 224.	2.2	164
5	Mucosal or systemic microbiota exposures shape the B cell repertoire. Nature, 2020, 584, 274-278.	13.7	132
6	Learning the High-Dimensional Immunogenomic Features That Predict Public and Private Antibody Repertoires. Journal of Immunology, 2017, 199, 2985-2997.	0.4	124
7	Large-scale network analysis reveals the sequence space architecture of antibody repertoires. Nature Communications, 2019, 10, 1321.	5.8	103
8	Resident memory CD8 T cells persist for years in human small intestine. Journal of Experimental Medicine, 2019, 216, 2412-2426.	4.2	101
9	A compact vocabulary of paratope-epitope interactions enables predictability of antibody-antigen binding. Cell Reports, 2021, 34, 108856.	2.9	101
10	Animal Immunization, in Vitro Display Technologies, and Machine Learning for Antibody Discovery. Trends in Biotechnology, 2021, 39, 1263-1273.	4.9	74
11	Single-cell BCR and transcriptome analysis after influenza infection reveals spatiotemporal dynamics of antigen-specific B cells. Cell Reports, 2021, 35, 109286.	2.9	67
12	Comprehensive Evaluation and Optimization of Amplicon Library Preparation Methods for High-Throughput Antibody Sequencing. PLoS ONE, 2014, 9, e96727.	1.1	63
13	Inferred Allelic Variants of Immunoglobulin Receptor Genes: A System for Their Evaluation, Documentation, and Naming. Frontiers in Immunology, 2019, 10, 435.	2.2	63
14	Quantitative assessment of the robustness of next-generation sequencing of antibody variable gene repertoires from immunized mice. BMC Immunology, 2014, 15, 40.	0.9	61
15	High-throughput antibody engineering in mammalian cells by CRISPR/Cas9-mediated homology-directed mutagenesis. Nucleic Acids Research, 2018, 46, 7436-7449.	6.5	61
16	Mining adaptive immune receptor repertoires for biological and clinical information using machine learning. Current Opinion in Systems Biology, 2020, 24, 109-119.	1.3	58
17	Augmenting adaptive immunity: progress and challenges in the quantitative engineering and analysis of adaptive immune receptor repertoires. Molecular Systems Design and Engineering, 2019, 4, 701-736.	1.7	57
18	Discrete populations of isotype-switched memory B lymphocytes are maintained in murine spleen and bone marrow. Nature Communications, 2020, 11, 2570.	5.8	54

#	ARTICLE	IF	CITATIONS
19	Progress and challenges for the machine learning-based design of fit-for-purpose monoclonal antibodies. <i>MABs</i> , 2022, 14, 2008790.	2.6	51
20	Comparison of methods for phylogenetic B-cell lineage inference using time-resolved antibody repertoire simulations (AbSim). <i>Bioinformatics</i> , 2017, 33, 3938-3946.	1.8	50
21	immuneSIM: tunable multi-feature simulation of B- and T-cell receptor repertoires for immunoinformatics benchmarking. <i>Bioinformatics</i> , 2020, 36, 3594-3596.	1.8	48
22	Immunoglobulin germline gene variation and its impact on human disease. <i>Genes and Immunity</i> , 2021, 22, 205-217.	2.2	48
23	Diversity in immunogenomics: the value and the challenge. <i>Nature Methods</i> , 2021, 18, 588-591.	9.0	40
24	In silico proof of principle of machine learning-based antibody design at unconstrained scale. <i>MABs</i> , 2022, 14, 2031482.	2.6	40
25	Benchmarking immunoinformatic tools for the analysis of antibody repertoire sequences. <i>Bioinformatics</i> , 2020, 36, 1731-1739.	1.8	39
26	The immuneML ecosystem for machine learning analysis of adaptive immune receptor repertoires. <i>Nature Machine Intelligence</i> , 2021, 3, 936-944.	8.3	35
27	Quantitative and Qualitative Analysis of Humoral Immunity Reveals Continued and Personalized Evolution in Chronic Viral Infection. <i>Cell Reports</i> , 2020, 30, 997-1012.e6.	2.9	34
28	Machine-designed biotherapeutics: opportunities, feasibility and advantages of deep learning in computational antibody discovery. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	29
29	Chronic Viral Infection Promotes Efficient Germinal Center B Cell Responses. <i>Cell Reports</i> , 2020, 30, 1013-1026.e7.	2.9	27
30	The TCR Repertoire Reconstitution in Multiple Sclerosis: Comparing One-Shot and Continuous Immunosuppressive Therapies. <i>Frontiers in Immunology</i> , 2020, 11, 559.	2.2	25
31	Progress and challenges in mass spectrometry-based analysis of antibody repertoires. <i>Trends in Biotechnology</i> , 2022, 40, 463-481.	4.9	23
32	Antibody variable sequences have a pronounced effect on cellular transport and plasma half-life. <i>IScience</i> , 2022, 25, 103746.	1.9	23
33	Individualized VDJ recombination predisposes the available Ig sequence space. <i>Genome Research</i> , 2021, 31, 2209-2224.	2.4	22
34	Modeling the Dynamics of T-Cell Development in the Thymus. <i>Entropy</i> , 2021, 23, 437.	1.1	19
35	TCR repertoire diversity in Multiple Sclerosis: High-dimensional bioinformatics analysis of sequences from brain, cerebrospinal fluid and peripheral blood. <i>EBioMedicine</i> , 2021, 68, 103429.	2.7	18
36	A minimal model of peptide binding predicts ensemble properties of serum antibodies. <i>BMC Genomics</i> , 2012, 13, 79.	1.2	16

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37	Persistence of intrathecal oligoclonal B cells and IgG in multiple sclerosis. <i>Journal of Neuroimmunology</i> , 2019, 333, 576966.	1.1	16
38	Extended plasma half-life of albumin-binding domain fused human IgA upon pH-dependent albumin engagement of human FcRn <i>in vitro</i> and <i>in vivo</i> . <i>MAbs</i> , 2021, 13, 1893888.	2.6	16
39	Influenza vaccine response profiles are affected by vaccine preparation and preexisting immunity, but not HIV infection. <i>Human Vaccines and Immunotherapeutics</i> , 2015, 11, 391-396.	1.4	15
40	Low immunoglobulin E flags two distinct types of immune dysregulation. <i>Clinical and Experimental Immunology</i> , 2017, 187, 345-352.	1.1	15
41	Germline polymorphisms and alternative splicing of human immunoglobulin light chain genes. <i>IScience</i> , 2021, 24, 103192.	1.9	14
42	Profiling the specificity of clonally expanded plasma cells during chronic viral infection by single-cell analysis. <i>European Journal of Immunology</i> , 2022, 52, 297-311.	1.6	11
43	Profiling the baseline performance and limits of machine learning models for adaptive immune receptor repertoire classification. <i>GigaScience</i> , 2022, 11, .	3.3	10
44	Inter- and intraspecies comparison of phylogenetic fingerprints and sequence diversity of immunoglobulin variable genes. <i>Immunogenetics</i> , 2020, 72, 279-294.	1.2	5
45	IgM Antibody Repertoire Fingerprints in Mice Are Personalized but Robust to Viral Infection Status. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 254.	1.8	5
46	Dynamic changes in the T cell receptor repertoire during treatment with radiotherapy combined with an immune checkpoint inhibitor. <i>Molecular Oncology</i> , 2021, 15, 2958-2968.	2.1	5
47	TCRpower: quantifying the detection power of T-cell receptor sequencing with a novel computational pipeline calibrated by spike-in sequences. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	5
48	Adaptive Immune Receptor Repertoire (AIRR) Community Guide to Repertoire Analysis. <i>Methods in Molecular Biology</i> , 2022, , 297-316.	0.4	5
49	A Nextflow pipeline for T-cell receptor repertoire reconstruction and analysis from RNA sequencing data. <i>Immuninformatics</i> , 2022, 6, 100012.	1.2	4
50	Ancestral diversity is limited in published T cell receptor sequencing studies. <i>Immunity</i> , 2021, 54, 2177-2179.	6.6	3
51	Editorial: Methods and Applications of Computational Immunology. <i>Frontiers in Immunology</i> , 2019, 10, 2818.	2.2	1