Jason A Vander Heiden

List of Publications by Year
in descending order

28 papers	3,314 citations	279798 23 h-index	501196 28 g-index
30 all docs	30 docs citations	30 times ranked	4704 citing authors

#	Article	IF	Citations
1	Change-O: a toolkit for analyzing large-scale B cell immunoglobulin repertoire sequencing data. Bioinformatics, 2015, 31, 3356-3358.	4.1	643
2	pRESTO: a toolkit for processing high-throughput sequencing raw reads of lymphocyte receptor repertoires. Bioinformatics, 2014, 30, 1930-1932.	4.1	417
3	B cells populating the multiple sclerosis brain mature in the draining cervical lymph nodes. Science Translational Medicine, 2014, 6, 248ra107.	12.4	394
4	Models of Somatic Hypermutation Targeting and Substitution Based on Synonymous Mutations from High-Throughput Immunoglobulin Sequencing Data. Frontiers in Immunology, 2013, 4, 358.	4.8	197
5	High-resolution antibody dynamics of vaccine-induced immune responses. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 4928-4933.	7.1	186
6	Salmonella Infection Drives Promiscuous B Cell Activation Followed by Extrafollicular Affinity Maturation. Immunity, 2015, 43, 120-131.	14.3	186
7	Interleukin-10 from CD4⁺ follicular regulatory T cells promotes the germinal center response. Science Immunology, 2017, 2, .	11.9	139
8	Individual heritable differences result in unique cell lymphocyte receptor repertoires of naïve and antigen-experienced cells. Nature Communications, 2016, 7, 11112.	12.8	123
9	Reproducibility and Reuse of Adaptive Immune Receptor Repertoire Data. Frontiers in Immunology, 2017, 8, 1418.	4.8	102
10	In vivo partial reprogramming alters age-associated molecular changes during physiological aging in mice. Nature Aging, 2022, 2, 243-253.	11.6	101
11	Dysregulation of B Cell Repertoire Formation in Myasthenia Gravis Patients Revealed through Deep Sequencing. Journal of Immunology, 2017, 198, 1460-1473.	0.8	92
12	Repertoire-wide phylogenetic models of B cell molecular evolution reveal evolutionary signatures of aging and vaccination. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 22664-22672.	7.1	71
13	Identification of Subject-Specific Immunoglobulin Alleles From Expressed Repertoire Sequencing Data. Frontiers in Immunology, 2019, 10, 129.	4.8	67
14	A Model of Somatic Hypermutation Targeting in Mice Based on High-Throughput Ig Sequencing Data. Journal of Immunology, 2016, 197, 3566-3574.	0.8	63
15	Early B cell tolerance defects in neuromyelitis optica favour anti-AQP4 autoantibody production. Brain, 2019, 142, 1598-1615.	7.6	62
16	A TRPA1 inhibitor suppresses neurogenic inflammation and airway contraction for asthma treatment. Journal of Experimental Medicine, 2021, 218, .	8.5	56
17	TGFβ2 and TGFβ3 isoforms drive fibrotic disease pathogenesis. Science Translational Medicine, 2021, 13, .	12.4	56
18	Influence of seasonal exposure to grass pollen on local and peripheral blood IgE repertoires in patients with allergic rhinitis. Journal of Allergy and Clinical Immunology, 2014, 134, 604-612.	2.9	55

#	Article	IF	Citations
19	The Repertoire Dissimilarity Index as a method to compare lymphocyte receptor repertoires. BMC Bioinformatics, 2017, 18, 155.	2.6	52
20	The mutation patterns in B-cell immunoglobulin receptors reflect the influence of selection acting at multiple time-scales. Philosophical Transactions of the Royal Society B: Biological Sciences, 2015, 370, 20140242.	4.0	49
21	Molecular mapping of interstitial lung disease reveals a phenotypically distinct senescent basal epithelial cell population. JCI Insight, 2021, 6, .	5.0	42
22	Compromised fidelity of B‑cell tolerance checkpoints in AChR and MuSK myasthenia gravis. Annals of Clinical and Translational Neurology, 2016, 3, 443-454.	3.7	39
23	Mechanisms underlying B cell immune dysregulation and autoantibody production in MuSK myasthenia gravis. Annals of the New York Academy of Sciences, 2018, 1412, 154-165.	3.8	34
24	sumrep: A Summary Statistic Framework for Immune Receptor Repertoire Comparison and Model Validation. Frontiers in Immunology, 2019, 10, 2533.	4.8	22
25	<i>In silico</i> tools for accurate HLA and KIR inference from clinical sequencing data empower immunogenetics on individual-patient and population scales. Briefings in Bioinformatics, 2021, 22, .	6.5	19
26	Oncostatin M expression induced by bacterial triggers drives airway inflammatory and mucus secretion in severe asthma. Science Translational Medicine, 2022, 14, eabf8188.	12.4	17
27	VDJML: a file format with tools for capturing the results of inferring immune receptor rearrangements. BMC Bioinformatics, 2016, 17, 333.	2.6	16
28	Mutant Cellular AP-1 Proteins Promote Expression of a Subset of Epstein-Barr Virus Late Genes in the Absence of Lytic Viral DNA Replication. Journal of Virology, 2018, 92, .	3.4	10