Aleksandra M Walczak

List of Publications by Year
in descending order

68 papers	4,961 citations	159585 30 h-index	123424 61 g-index
98 all docs	98 docs citations	98 times ranked	4660 citing authors

#	ARTICLE	IF	CITATIONS
1	Statistical mechanics for natural flocks of birds. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 4786-4791.	7.1	519
2	Maximum entropy models for antibody diversity. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 5405-5410.	7.1	283
3	Statistical inference of the generation probability of T-cell receptors from sequence repertoires. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 16161-16166.	7.1	283
4	Predicting evolution. Nature Ecology and Evolution, 2017, 1, 77.	7.8	272
5	High-throughput immune repertoire analysis with IGoR. Nature Communications, 2018, 9, 561.	12.8	217
6	Inferring processes underlying B-cell repertoire diversity. Philosophical Transactions of the Royal Society B: Biological Sciences, 2015, 370, 20140243.	4.0	180
7	OLGA: fast computation of generation probabilities of B- and T-cell receptor amino acid sequences and motifs. Bioinformatics, 2019, 35, 2974-2981.	4.1	175
8	The Past, Present, and Future of Immune Repertoire Biology â€" The Rise of Next-Generation Repertoire Analysis. Frontiers in Immunology, 2013, 4, 413.	4.8	164
9	Live Imaging of Bicoid-Dependent Transcription in Drosophila Embryos. Current Biology, 2013, 23, 2135-2139.	3.9	159
10	Quantifying selection in immune receptor repertoires. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 9875-9880.	7.1	153
11	Detecting T cell receptors involved in immune responses from single repertoire snapshots. PLoS Biology, 2019, 17, e3000314.	5.6	116
12	How a well-adapted immune system is organized. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 5950-5955.	7.1	114
13	Predicting the spectrum of TCR repertoire sharing with a dataâ€'driven model of recombination. Immunological Reviews, 2018, 284, 167-179.	6.0	112
14	Flocking and Turning: a New Model for Self-organized Collective Motion. Journal of Statistical Physics, 2015, 158, 601-627.	1.2	108
15	Precise tracking of vaccine-responding T cell clones reveals convergent and personalized response in identical twins. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 12704-12709.	7.1	108
16	Longitudinal high-throughput TCR repertoire profiling reveals the dynamics of T-cell memory formation after mild COVID-19 infection. ELife, 2021, 10, .	6.0	103
17	Measuring the sequence-affinity landscape of antibodies with massively parallel titration curves. ELife, 2016, 5, .	6.0	97
18	Diversity of immune strategies explained by adaptation to pathogen statistics. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 8630-8635.	7.1	95

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19	Optimizing information flow in small genetic networks. II. Feed-forward interactions. Physical Review E, 2010, 81, 041905.	2.1	84
20	Contribution of resident and circulating precursors to tumor-infiltrating CD8 [+] T cell populations in lung cancer. Science Immunology, 2021, 6, .	11.9	82
21	Persisting fetal clonotypes influence the structure and overlap of adult human T cell receptor repertoires. PLoS Computational Biology, 2017, 13, e1005572.	3.2	82
22	Local equilibrium in bird flocks. Nature Physics, 2016, 12, 1153-1157.	16.7	80
23	Abduction and asylum in the lives of transcription factors. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 4016-4021.	7.1	73
24	Fluctuating fitness shapes the clone-size distribution of immune repertoires. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 274-279.	7.1	73
25	Genesis of the αβ T-cell receptor. PLoS Computational Biology, 2019, 15, e1006874.	3.2	72
26	Method for identification of condition-associated public antigen receptor sequences. ELife, 2018, 7, .	6.0	71
27	Transcriptional Memory in the Drosophila Embryo. Current Biology, 2016, 26, 212-218.	3.9	63
28	Dynamical maximum entropy approach to flocking. Physical Review E, 2014, 89, 042707.	2.1	55
29	Single molecule microscopy reveals key physical features of repair foci in living cells. ELife, 2021, 10, .	6.0	55
30	How a well-adapting immune system remembers. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 8815-8823.	7.1	49
31	Precision of Readout at the hunchback Gene: Analyzing Short Transcription Time Traces in Living Fly Embryos. PLoS Computational Biology, 2016, 12, e1005256.	3.2	48
32	Primary and secondary anti-viral response captured by the dynamics and phenotype of individual T cell clones. ELife, 2020, 9, .	6.0	48
33	Fierce Selection and Interference in B-Cell Repertoire Response to Chronic HIV-1. Molecular Biology and Evolution, 2019, 36, 2184-2194.	8.9	46
34	Deep generative selection models of T and B cell receptor repertoires with soNNia. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	46
35	Epistasis in a Fitness Landscape Defined by Antibody-Antigen Binding Free Energy. Cell Systems, 2019, 8, 86-93.e3.	6.2	39
36	Quantitative immunology for physicists. Physics Reports, 2020, 849, 1-83.	25.6	39

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37	Population variability in the generation and selection of T-cell repertoires. PLoS Computational Biology, 2020, 16, e1008394.	3.2	36
38	3 minutes to precisely measure morphogen concentration. PLoS Genetics, 2018, 14, e1007676.	3.5	35
39	Combinatorial code governing cellular responses to complex stimuli. Nature Communications, 2015, 6, 6847.	12.8	32
40	Precision in a rush: Trade-offs between reproducibility and steepness of the hunchback expression pattern. PLoS Computational Biology, 2018, 14, e1006513.	3.2	32
41	Antigenic waves of virusâ€"immune coevolution. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	29
42	Binding affinity landscapes constrain the evolution of broadly neutralizing anti-influenza antibodies. ELife, 2021, 10, .	6.0	28
43	New methods to image transcription in living fly embryos: the insights so far, and the prospects. Wiley Interdisciplinary Reviews: Developmental Biology, 2016, 5, 296-310.	5.9	27
44	RBM-MHC: A Semi-Supervised Machine-Learning Method for Sample-Specific Prediction of Antigen Presentation by HLA-I Alleles. Cell Systems, 2021, 12, 195-202.e9.	6.2	26
45	Inferring the immune response from repertoire sequencing. PLoS Computational Biology, 2020, 16, e1007873.	3.2	25
46	Transitions in optimal adaptive strategies for populations in fluctuating environments. Physical Review E, 2017, 96, 032412.	2.1	23
47	Roadmap on biology in time varying environments. Physical Biology, 2021, 18, 041502.	1.8	23
48	A mechanism for hunchback promoters to readout morphogenetic positional information in less than a minute. ELife, 2020, 9, .	6.0	21
49	Learning the heterogeneous hypermutation landscape of immunoglobulins from high-throughput repertoire data. Nucleic Acids Research, 2020, 48, 10702-10712.	14.5	20
50	Building General Langevin Models from Discrete Datasets. Physical Review X, 2020, 10, .	8.9	17
51	Quantifying lymphocyte receptor diversity. , 2018, , 183-198.		16
52	Cost and benefits of clustered regularly interspaced short palindromic repeats spacer acquisition. Philosophical Transactions of the Royal Society B: Biological Sciences, 2019, 374, 20180095.	4.0	15
53	Physical observables to determine the nature of membrane-less cellular sub-compartments. ELife, 2021, 10, .	6.0	14
54	Immune fingerprinting through repertoire similarity. PLoS Genetics, 2021, 17, e1009301.	3.5	12

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55	Affinity maturation for an optimal balance between long-term immune coverage and short-term resource constraints. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	12
56	Multi-Lineage Evolution in Viral Populations Driven by Host Immune Systems. Pathogens, 2019, 8, 115.	2.8	10
57	Generative models of T-cell receptor sequences. Physical Review E, 2020, 101, 062414.	2.1	9
58	Probing T-cell response by sequence-based probabilistic modeling. PLoS Computational Biology, 2021, 17, e1009297.	3.2	9
59	Learning the statistics and landscape of somatic mutation-induced insertions and deletions in antibodies. PLoS Computational Biology, 2022, 18, e1010167.	3.2	6
60	Live Imaging of mRNA Transcription in Drosophila Embryos. Methods in Molecular Biology, 2018, 1863, 165-182.	0.9	5
61	Optimal prediction with resource constraints using the information bottleneck. PLoS Computational Biology, 2021, 17, e1008743.	3.2	5
62	LiveFly: A Toolbox for the Analysis of Transcription Dynamics in Live Drosophila Embryos. Methods in Molecular Biology, 2018, 1863, 183-195.	0.9	4
63	Constraints and limitations on the transcriptional response downstream of the Bicoid morphogen gradient. Current Topics in Developmental Biology, 2020, 137, 119-142.	2.2	4
64	Population Dynamics of Immune Repertoires. , 2021, , 203-221.		4
65	A model for the integration of conflicting exogenous and endogenous signals by dendritic cells. Physical Biology, 2018, 15, 056001.	1.8	3
66	Dissipation in Non-Steady State Regulatory Circuits. Entropy, 2019, 21, 1212.	2.2	1
67	Renormalization group approach to connect discrete- and continuous-time descriptions of Gaussian processes. Physical Review E, 2022, 105, 044133.	2.1	1
68	Mutual information maximization for amortized likelihood inference from sampled trajectories: MINIMALIST. Physical Review E, 2022, 105, .	2.1	0