

# Aleksandra M Walczak

## List of Publications by Year in descending order

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Version: 2024-02-01

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	Affinity maturation for an optimal balance between long-term immune coverage and short-term resource constraints. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	12
2	Renormalization group approach to connect discrete- and continuous-time descriptions of Gaussian processes. <i>Physical Review E</i> , 2022, 105, 044133.	2.1	1
3	Mutual information maximization for amortized likelihood inference from sampled trajectories: MINIMALIST. <i>Physical Review E</i> , 2022, 105, .	2.1	0
4	Learning the statistics and landscape of somatic mutation-induced insertions and deletions in antibodies. <i>PLoS Computational Biology</i> , 2022, 18, e1010167.	3.2	6
5	RBM-MHC: A Semi-Supervised Machine-Learning Method for Sample-Specific Prediction of Antigen Presentation by HLA-I Alleles. <i>Cell Systems</i> , 2021, 12, 195-202.e9.	6.2	26
6	Immune fingerprinting through repertoire similarity. <i>PLoS Genetics</i> , 2021, 17, e1009301.	3.5	12
7	Longitudinal high-throughput TCR repertoire profiling reveals the dynamics of T-cell memory formation after mild COVID-19 infection. <i>ELife</i> , 2021, 10, .	6.0	103
8	Single molecule microscopy reveals key physical features of repair foci in living cells. <i>ELife</i> , 2021, 10, .	6.0	55
9	Optimal prediction with resource constraints using the information bottleneck. <i>PLoS Computational Biology</i> , 2021, 17, e1008743.	3.2	5
10	Deep generative selection models of T and B cell receptor repertoires with soNNia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	46
11	Roadmap on biology in time varying environments. <i>Physical Biology</i> , 2021, 18, 041502.	1.8	23
12	Antigenic waves of virus-immune coevolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	29
13	Probing T-cell response by sequence-based probabilistic modeling. <i>PLoS Computational Biology</i> , 2021, 17, e1009297.	3.2	9
14	Binding affinity landscapes constrain the evolution of broadly neutralizing anti-influenza antibodies. <i>ELife</i> , 2021, 10, .	6.0	28
15	Population Dynamics of Immune Repertoires. , 2021, , 203-221.		4
16	Contribution of resident and circulating precursors to tumor-infiltrating CD8 <sup>+</sup> T cell populations in lung cancer. <i>Science Immunology</i> , 2021, 6, .	11.9	82
17	Physical observables to determine the nature of membrane-less cellular sub-compartments. <i>ELife</i> , 2021, 10, .	6.0	14
18	Learning the heterogeneous hypermutation landscape of immunoglobulins from high-throughput repertoire data. <i>Nucleic Acids Research</i> , 2020, 48, 10702-10712.	14.5	20

#	ARTICLE	IF	CITATIONS
19	Building General Langevin Models from Discrete Datasets. <i>Physical Review X</i> , 2020, 10, .	8.9	17
20	Generative models of T-cell receptor sequences. <i>Physical Review E</i> , 2020, 101, 062414.	2.1	9
21	Quantitative immunology for physicists. <i>Physics Reports</i> , 2020, 849, 1-83.	25.6	39
22	Inferring the immune response from repertoire sequencing. <i>PLoS Computational Biology</i> , 2020, 16, e1007873.	3.2	25
23	Constraints and limitations on the transcriptional response downstream of the Bicoid morphogen gradient. <i>Current Topics in Developmental Biology</i> , 2020, 137, 119-142.	2.2	4
24	Population variability in the generation and selection of T-cell repertoires. <i>PLoS Computational Biology</i> , 2020, 16, e1008394.	3.2	36
25	A mechanism for hunchback promoters to readout morphogenetic positional information in less than a minute. <i>ELife</i> , 2020, 9, .	6.0	21
26	Primary and secondary anti-viral response captured by the dynamics and phenotype of individual T cell clones. <i>ELife</i> , 2020, 9, .	6.0	48
27	Multi-Lineage Evolution in Viral Populations Driven by Host Immune Systems. <i>Pathogens</i> , 2019, 8, 115.	2.8	10
28	Fierce Selection and Interference in B-Cell Repertoire Response to Chronic HIV-1. <i>Molecular Biology and Evolution</i> , 2019, 36, 2184-2194.	8.9	46
29	Detecting T cell receptors involved in immune responses from single repertoire snapshots. <i>PLoS Biology</i> , 2019, 17, e3000314.	5.6	116
30	How a well-adapting immune system remembers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 8815-8823.	7.1	49
31	Genesis of the $\hat{I}\pm\hat{I}^2$ T-cell receptor. <i>PLoS Computational Biology</i> , 2019, 15, e1006874.	3.2	72
32	Cost and benefits of clustered regularly interspaced short palindromic repeats spacer acquisition. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019, 374, 20180095.	4.0	15
33	Dissipation in Non-Steady State Regulatory Circuits. <i>Entropy</i> , 2019, 21, 1212.	2.2	1
34	Epistasis in a Fitness Landscape Defined by Antibody-Antigen Binding Free Energy. <i>Cell Systems</i> , 2019, 8, 86-93.e3.	6.2	39
35	OLGA: fast computation of generation probabilities of B- and T-cell receptor amino acid sequences and motifs. <i>Bioinformatics</i> , 2019, 35, 2974-2981.	4.1	175
36	High-throughput immune repertoire analysis with IGoR. <i>Nature Communications</i> , 2018, 9, 561.	12.8	217

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37	A model for the integration of conflicting exogenous and endogenous signals by dendritic cells. <i>Physical Biology</i> , 2018, 15, 056001.	1.8	3
38	Precision in a rush: Trade-offs between reproducibility and steepness of the hunchback expression pattern. <i>PLoS Computational Biology</i> , 2018, 14, e1006513.	3.2	32
39	Precise tracking of vaccine-responding T cell clones reveals convergent and personalized response in identical twins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 12704-12709.	7.1	108
40	3 minutes to precisely measure morphogen concentration. <i>PLoS Genetics</i> , 2018, 14, e1007676.	3.5	35
41	Live Imaging of mRNA Transcription in <i>Drosophila</i> Embryos. <i>Methods in Molecular Biology</i> , 2018, 1863, 165-182.	0.9	5
42	LiveFly: A Toolbox for the Analysis of Transcription Dynamics in Live <i>Drosophila</i> Embryos. <i>Methods in Molecular Biology</i> , 2018, 1863, 183-195.	0.9	4
43	Predicting the spectrum of TCR repertoire sharing with a data-driven model of recombination. <i>Immunological Reviews</i> , 2018, 284, 167-179.	6.0	112
44	Method for identification of condition-associated public antigen receptor sequences. <i>ELife</i> , 2018, 7, .	6.0	71
45	Quantifying lymphocyte receptor diversity. , 2018, , 183-198.		16
46	Predicting evolution. <i>Nature Ecology and Evolution</i> , 2017, 1, 77.	7.8	272
47	Transitions in optimal adaptive strategies for populations in fluctuating environments. <i>Physical Review E</i> , 2017, 96, 032412.	2.1	23
48	Persisting fetal clonotypes influence the structure and overlap of adult human T cell receptor repertoires. <i>PLoS Computational Biology</i> , 2017, 13, e1005572.	3.2	82
49	Diversity of immune strategies explained by adaptation to pathogen statistics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 8630-8635.	7.1	95
50	New methods to image transcription in living fly embryos: the insights so far, and the prospects. <i>Wiley Interdisciplinary Reviews: Developmental Biology</i> , 2016, 5, 296-310.	5.9	27
51	Local equilibrium in bird flocks. <i>Nature Physics</i> , 2016, 12, 1153-1157.	16.7	80
52	Fluctuating fitness shapes the clone-size distribution of immune repertoires. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 274-279.	7.1	73
53	Transcriptional Memory in the <i>Drosophila</i> Embryo. <i>Current Biology</i> , 2016, 26, 212-218.	3.9	63
54	Precision of Readout at the hunchback Gene: Analyzing Short Transcription Time Traces in Living Fly Embryos. <i>PLoS Computational Biology</i> , 2016, 12, e1005256.	3.2	48

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55	Measuring the sequence-affinity landscape of antibodies with massively parallel titration curves. <i>ELife</i> , 2016, 5, .	6.0	97
56	Inferring processes underlying B-cell repertoire diversity. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20140243.	4.0	180
57	Flocking and Turning: a New Model for Self-organized Collective Motion. <i>Journal of Statistical Physics</i> , 2015, 158, 601-627.	1.2	108
58	Combinatorial code governing cellular responses to complex stimuli. <i>Nature Communications</i> , 2015, 6, 6847.	12.8	32
59	How a well-adapted immune system is organized. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 5950-5955.	7.1	114
60	Quantifying selection in immune receptor repertoires. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 9875-9880.	7.1	153
61	Dynamical maximum entropy approach to flocking. <i>Physical Review E</i> , 2014, 89, 042707.	2.1	55
62	Live Imaging of Bicoid-Dependent Transcription in <i>Drosophila</i> Embryos. <i>Current Biology</i> , 2013, 23, 2135-2139.	3.9	159
63	The Past, Present, and Future of Immune Repertoire Biology – The Rise of Next-Generation Repertoire Analysis. <i>Frontiers in Immunology</i> , 2013, 4, 413.	4.8	164
64	Statistical mechanics for natural flocks of birds. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 4786-4791.	7.1	519
65	Statistical inference of the generation probability of T-cell receptors from sequence repertoires. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 16161-16166.	7.1	283
66	Optimizing information flow in small genetic networks. II. Feed-forward interactions. <i>Physical Review E</i> , 2010, 81, 041905.	2.1	84
67	Maximum entropy models for antibody diversity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 5405-5410.	7.1	283
68	Abduction and asylum in the lives of transcription factors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 4016-4021.	7.1	73