Thierry Mora

List of Publications by Year
in descending order

83	5,765	126708	102304
papers	citations	33	66
		h-index	g-index

126	126	126	4880
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	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, .	3.3	12
2	Renormalization group approach to connect discrete- and continuous-time descriptions of Gaussian processes. Physical Review E, 2022, 105, 044133.	0.8	1
3	Neoantigen quality predicts immunoediting in survivors of pancreatic cancer. Nature, 2022, 606, 389-395.	13.7	80
4	Mutual information maximization for amortized likelihood inference from sampled trajectories: MINIMALIST. Physical Review E, 2022, 105, .	0.8	0
5	Learning the statistics and landscape of somatic mutation-induced insertions and deletions in antibodies. PLoS Computational Biology, 2022, 18, e1010167.	1.5	6
6	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.	2.9	26
7	Immune fingerprinting through repertoire similarity. PLoS Genetics, 2021, 17, e1009301.	1.5	12
8	Longitudinal high-throughput TCR repertoire profiling reveals the dynamics of T-cell memory formation after mild COVID-19 infection. ELife, 2021, 10, .	2.8	103
9	Single molecule microscopy reveals key physical features of repair foci in living cells. ELife, 2021, 10, .	2.8	55
10	Optimal prediction with resource constraints using the information bottleneck. PLoS Computational Biology, 2021, 17, e1008743.	1.5	5
11	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, .	3.3	46
12	Antigenic waves of virus–immune coevolution. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	29
13	Probing T-cell response by sequence-based probabilistic modeling. PLoS Computational Biology, 2021, 17, e1009297.	1.5	9
14	Binding affinity landscapes constrain the evolution of broadly neutralizing anti-influenza antibodies. ELife, 2021, 10, .	2.8	28
15	Population Dynamics of Immune Repertoires. , 2021, , 203-221.		4
16	Contribution of resident and circulating precursors to tumor-infiltrating CD8 [+] T cell populations in lung cancer. Science Immunology, 2021, 6, .	5.6	82
17	Physical observables to determine the nature of membrane-less cellular sub-compartments. ELife, 2021, 10, .	2.8	14
18	Exploiting B Cell Receptor Analyses to Inform on HIV-1 Vaccination Strategies. Vaccines, 2020, 8, 13.	2.1	18

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19	Learning the heterogeneous hypermutation landscape of immunoglobulins from high-throughput repertoire data. Nucleic Acids Research, 2020, 48, 10702-10712.	6.5	20
20	Building General Langevin Models from Discrete Datasets. Physical Review X, 2020, 10, .	2.8	17
21	Generative models of T-cell receptor sequences. Physical Review E, 2020, 101, 062414.	0.8	9
22	SOS: online probability estimation and generation of T-and B-cell receptors. Bioinformatics, 2020, 36, 4510-4512.	1.8	4
23	Quantitative immunology for physicists. Physics Reports, 2020, 849, 1-83.	10.3	39
24	Inferring the immune response from repertoire sequencing. PLoS Computational Biology, 2020, 16, e1007873.	1.5	25
25	Population variability in the generation and selection of T-cell repertoires. PLoS Computational Biology, 2020, 16, e1008394.	1.5	36
26	Primary and secondary anti-viral response captured by the dynamics and phenotype of individual T cell clones. ELife, 2020, 9, .	2.8	48
27	Multi-Lineage Evolution in Viral Populations Driven by Host Immune Systems. Pathogens, 2019, 8, 115.	1.2	10
28	How many different clonotypes do immune repertoires contain?. Current Opinion in Systems Biology, 2019, 18, 104-110.	1.3	43
29	Physical Limit to Concentration Sensing in a Changing Environment. Physical Review Letters, 2019, 123, 198101.	2.9	23
30	Size and structure of the sequence space of repeat proteins. PLoS Computational Biology, 2019, 15, e1007282.	1.5	14
31	Fierce Selection and Interference in B-Cell Repertoire Response to Chronic HIV-1. Molecular Biology and Evolution, 2019, 36, 2184-2194.	3.5	46
32	Detecting T cell receptors involved in immune responses from single repertoire snapshots. PLoS Biology, 2019, 17, e3000314.	2.6	116
33	How a well-adapting immune system remembers. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 8815-8823.	3.3	49
34	Genesis of the $\alpha\beta$ T-cell receptor. PLoS Computational Biology, 2019, 15, e1006874.	1.5	72
35	Receptor crosstalk improves concentration sensing of multiple ligands. Physical Review E, 2019, 99, 022423.	0.8	24
36	Cost and benefits of clustered regularly interspaced short palindromic repeats spacer acquisition. Philosophical Transactions of the Royal Society B: Biological Sciences, 2019, 374, 20180095.	1.8	15

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37	Epistasis in a Fitness Landscape Defined by Antibody-Antigen Binding Free Energy. Cell Systems, 2019, 8, 86-93.e3.	2.9	39
38	Modeling the Correlated Activity of Neural Populations: A Review. Neural Computation, 2019, 31, 233-269.	1.3	12
39	OLGA: fast computation of generation probabilities of B- and T-cell receptor amino acid sequences and motifs. Bioinformatics, 2019, 35, 2974-2981.	1.8	175
40	High-throughput immune repertoire analysis with IGoR. Nature Communications, 2018, 9, 561.	5.8	217
41	Blindfold learning of an accurate neural metric. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 3267-3272.	3.3	9
42	A model for the integration of conflicting exogenous and endogenous signals by dendritic cells. Physical Biology, 2018, 15, 056001.	0.8	3
43	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.	3.3	108
44	Active degradation of MarA controls coordination of its downstream targets. PLoS Computational Biology, 2018, 14, e1006634.	1.5	10
45	Origin of Public Memory B Cell Clones in Fish After Antiviral Vaccination. Frontiers in Immunology, 2018, 9, 2115.	2.2	21
46	Separating intrinsic interactions from extrinsic correlations in a network of sensory neurons. Physical Review E, 2018, 98, .	0.8	15
47	Predicting the spectrum of TCR repertoire sharing with a dataâ€‘driven model of recombination. Immunological Reviews, 2018, 284, 167-179.	2.8	112
48	Evidence for Shaping of Light Chain Repertoire by Structural Selection. Frontiers in Immunology, 2018, 9, 1307.	2.2	8
49	Method for identification of condition-associated public antigen receptor sequences. ELife, 2018, 7, .	2.8	71
50	Quantifying lymphocyte receptor diversity. , 2018, , 183-198.		16
51	Insights into immune system development and function from mouse T-cell repertoires. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 2253-2258.	3.3	38
52	Transitions in optimal adaptive strategies for populations in fluctuating environments. Physical Review E, 2017, 96, 032412.	0.8	23
53	Random versus maximum entropy models of neural population activity. Physical Review E, 2017, 95, 042321.	0.8	17
54	Inferring repeat-protein energetics from evolutionary information. PLoS Computational Biology, 2017, 13, e1005584.	1.5	11

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55	Persisting fetal clonotypes influence the structure and overlap of adult human T cell receptor repertoires. PLoS Computational Biology, 2017, 13, e1005572.	1.5	82
56	Closed-Loop Estimation of Retinal Network Sensitivity by Local Empirical Linearization. ENeuro, 2017, 4, ENEURO.0166-17.2017.	0.9	4
57	JSP Special Issue on Information Processing in Living Systems. Journal of Statistical Physics, 2016, 162, 1085-1087.	0.5	0
58	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.	3.3	95
59	Local equilibrium in bird flocks. Nature Physics, 2016, 12, 1153-1157.	6.5	80
60	Rényi entropy, abundance distribution, and the equivalence of ensembles. Physical Review E, 2016, 93, 052418.	0.8	25
61	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.	3.3	73
62	repgenHMM: a dynamic programming tool to infer the rules of immune receptor generation from sequence data. Bioinformatics, 2016, 32, 1943-1951.	1.8	38
63	A Tractable Method for Describing Complex Couplings between Neurons and Population Rate. ENeuro, 2016, 3, ENEURO.0160-15.2016.	0.9	18
64	Measuring the sequence-affinity landscape of antibodies with massively parallel titration curves. ELife, 2016, 5, .	2.8	97
65	Physical Limit to Concentration Sensing Amid Spurious Ligands. Physical Review Letters, 2015, 115, 038102.	2.9	50
66	Inferring processes underlying B-cell repertoire diversity. Philosophical Transactions of the Royal Society B: Biological Sciences, 2015, 370, 20140243.	1.8	180
67	High Accuracy Decoding of Dynamical Motion from a Large Retinal Population. PLoS Computational Biology, 2015, 11, e1004304.	1.5	49
68	Flocking and Turning: a New Model for Self-organized Collective Motion. Journal of Statistical Physics, 2015, 158, 601-627.	0.5	108
69	Dynamical Criticality in the Collective Activity of a Population of Retinal Neurons. Physical Review Letters, 2015, 114, 078105.	2.9	57
70	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.	3.3	114
71	Capturing coevolutionary signals inrepeat proteins. BMC Bioinformatics, 2015, 16, 207.	1.2	24
72	Thermodynamics and signatures of criticality in a network of neurons. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 11508-11513.	3.3	169

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73	A General Pairwise Interaction Model Provides an Accurate Description of In Vivo Transcription Factor Binding Sites. PLoS ONE, 2014, 9, e99015.	1.1	26
74	Social interactions dominate speed control in poising natural flocks near criticality. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 7212-7217.	3.3	145
75	Quantifying selection in immune receptor repertoires. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 9875-9880.	3.3	153
76	Dynamical maximum entropy approach to flocking. Physical Review E, 2014, 89, 042707.	0.8	55
77	The simplest maximum entropy model for collective behavior in a neural network. Journal of Statistical Mechanics: Theory and Experiment, 2013, 2013, P03011.	0.9	89
78	The Past, Present, and Future of Immune Repertoire Biology â€" The Rise of Next-Generation Repertoire Analysis. Frontiers in Immunology, 2013, 4, 413.	2.2	164
79	Statistical mechanics for natural flocks of birds. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 4786-4791.	3.3	519
80	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.	3.3	283
81	Are Biological Systems Poised at Criticality?. Journal of Statistical Physics, 2011, 144, 268-302.	0.5	537
82	Maximum entropy models for antibody diversity. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 5405-5410.	3.3	283
83	Limits of Sensing Temporal Concentration Changes by Single Cells. Physical Review Letters, 2010, 104, 248101.	2.9	73