

# Thierry Mora

## List of Publications by Year in descending order

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Version: 2024-02-01

83  
papers

5,765  
citations

126708

33  
h-index

102304

66  
g-index

126  
all docs

126  
docs citations

126  
times ranked

4880  
citing authors

#	ARTICLE	IF	CITATIONS
1	Are Biological Systems Poised at Criticality?. Journal of Statistical Physics, 2011, 144, 268-302.	0.5	537
2	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
3	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
4	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
5	High-throughput immune repertoire analysis with IGoR. Nature Communications, 2018, 9, 561.	5.8	217
6	Inferring processes underlying B-cell repertoire diversity. Philosophical Transactions of the Royal Society B: Biological Sciences, 2015, 370, 20140243.	1.8	180
7	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
8	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
9	The Past, Present, and Future of Immune Repertoire Biology – The Rise of Next-Generation Repertoire Analysis. Frontiers in Immunology, 2013, 4, 413.	2.2	164
10	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
11	Social interactions dominate speed control in poisoning natural flocks near criticality. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 7212-7217.	3.3	145
12	Detecting T cell receptors involved in immune responses from single repertoire snapshots. PLoS Biology, 2019, 17, e3000314.	2.6	116
13	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
14	Predicting the spectrum of TCR repertoire sharing with a data-driven model of recombination. Immunological Reviews, 2018, 284, 167-179.	2.8	112
15	Flocking and Turning: a New Model for Self-organized Collective Motion. Journal of Statistical Physics, 2015, 158, 601-627.	0.5	108
16	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
17	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
18	Measuring the sequence-affinity landscape of antibodies with massively parallel titration curves. ELife, 2016, 5, .	2.8	97

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19	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
20	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
21	Contribution of resident and circulating precursors to tumor-infiltrating CD8 <sup>+</sup> T cell populations in lung cancer. Science Immunology, 2021, 6, .	5.6	82
22	Persisting fetal clonotypes influence the structure and overlap of adult human T cell receptor repertoires. PLoS Computational Biology, 2017, 13, e1005572.	1.5	82
23	Local equilibrium in bird flocks. Nature Physics, 2016, 12, 1153-1157.	6.5	80
24	Neoantigen quality predicts immunoediting in survivors of pancreatic cancer. Nature, 2022, 606, 389-395.	13.7	80
25	Limits of Sensing Temporal Concentration Changes by Single Cells. Physical Review Letters, 2010, 104, 248101.	2.9	73
26	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
27	Genesis of the $\hat{I}^2$ T-cell receptor. PLoS Computational Biology, 2019, 15, e1006874.	1.5	72
28	Method for identification of condition-associated public antigen receptor sequences. ELife, 2018, 7, .	2.8	71
29	Dynamical Criticality in the Collective Activity of a Population of Retinal Neurons. Physical Review Letters, 2015, 114, 078105.	2.9	57
30	Dynamical maximum entropy approach to flocking. Physical Review E, 2014, 89, 042707.	0.8	55
31	Single molecule microscopy reveals key physical features of repair foci in living cells. ELife, 2021, 10, .	2.8	55
32	Physical Limit to Concentration Sensing Amid Spurious Ligands. Physical Review Letters, 2015, 115, 038102.	2.9	50
33	High Accuracy Decoding of Dynamical Motion from a Large Retinal Population. PLoS Computational Biology, 2015, 11, e1004304.	1.5	49
34	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
35	Primary and secondary anti-viral response captured by the dynamics and phenotype of individual T cell clones. ELife, 2020, 9, .	2.8	48
36	Fierce Selection and Interference in B-Cell Repertoire Response to Chronic HIV-1. Molecular Biology and Evolution, 2019, 36, 2184-2194.	3.5	46

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37	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
38	How many different clonotypes do immune repertoires contain?. Current Opinion in Systems Biology, 2019, 18, 104-110.	1.3	43
39	Epistasis in a Fitness Landscape Defined by Antibody-Antigen Binding Free Energy. Cell Systems, 2019, 8, 86-93.e3.	2.9	39
40	Quantitative immunology for physicists. Physics Reports, 2020, 849, 1-83.	10.3	39
41	repgenHMM: a dynamic programming tool to infer the rules of immune receptor generation from sequence data. Bioinformatics, 2016, 32, 1943-1951.	1.8	38
42	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
43	Population variability in the generation and selection of T-cell repertoires. PLoS Computational Biology, 2020, 16, e1008394.	1.5	36
44	Antigenic waves of virus-immune coevolution. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	29
45	Binding affinity landscapes constrain the evolution of broadly neutralizing anti-influenza antibodies. ELife, 2021, 10, .	2.8	28
46	A General Pairwise Interaction Model Provides an Accurate Description of In Vivo Transcription Factor Binding Sites. PLoS ONE, 2014, 9, e99015.	1.1	26
47	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
48	Rényi entropy, abundance distribution, and the equivalence of ensembles. Physical Review E, 2016, 93, 052418.	0.8	25
49	Inferring the immune response from repertoire sequencing. PLoS Computational Biology, 2020, 16, e1007873.	1.5	25
50	Capturing coevolutionary signals in repeat proteins. BMC Bioinformatics, 2015, 16, 207.	1.2	24
51	Receptor crosstalk improves concentration sensing of multiple ligands. Physical Review E, 2019, 99, 022423.	0.8	24
52	Transitions in optimal adaptive strategies for populations in fluctuating environments. Physical Review E, 2017, 96, 032412.	0.8	23
53	Physical Limit to Concentration Sensing in a Changing Environment. Physical Review Letters, 2019, 123, 198101.	2.9	23
54	Origin of Public Memory B Cell Clones in Fish After Antiviral Vaccination. Frontiers in Immunology, 2018, 9, 2115.	2.2	21

#	ARTICLE	IF	CITATIONS
55	Learning the heterogeneous hypermutation landscape of immunoglobulins from high-throughput repertoire data. <i>Nucleic Acids Research</i> , 2020, 48, 10702-10712.	6.5	20
56	Exploiting B Cell Receptor Analyses to Inform on HIV-1 Vaccination Strategies. <i>Vaccines</i> , 2020, 8, 13.	2.1	18
57	A Tractable Method for Describing Complex Couplings between Neurons and Population Rate. <i>ENeuro</i> , 2016, 3, ENEURO.0160-15.2016.	0.9	18
58	Random versus maximum entropy models of neural population activity. <i>Physical Review E</i> , 2017, 95, 042321.	0.8	17
59	Building General Langevin Models from Discrete Datasets. <i>Physical Review X</i> , 2020, 10, .	2.8	17
60	Quantifying lymphocyte receptor diversity. , 2018, , 183-198.		16
61	Separating intrinsic interactions from extrinsic correlations in a network of sensory neurons. <i>Physical Review E</i> , 2018, 98, .	0.8	15
62	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.	1.8	15
63	Size and structure of the sequence space of repeat proteins. <i>PLoS Computational Biology</i> , 2019, 15, e1007282.	1.5	14
64	Physical observables to determine the nature of membrane-less cellular sub-compartments. <i>ELife</i> , 2021, 10, .	2.8	14
65	Modeling the Correlated Activity of Neural Populations: A Review. <i>Neural Computation</i> , 2019, 31, 233-269.	1.3	12
66	Immune fingerprinting through repertoire similarity. <i>PLoS Genetics</i> , 2021, 17, e1009301.	1.5	12
67	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, .	3.3	12
68	Inferring repeat-protein energetics from evolutionary information. <i>PLoS Computational Biology</i> , 2017, 13, e1005584.	1.5	11
69	Active degradation of MarA controls coordination of its downstream targets. <i>PLoS Computational Biology</i> , 2018, 14, e1006634.	1.5	10
70	Multi-Lineage Evolution in Viral Populations Driven by Host Immune Systems. <i>Pathogens</i> , 2019, 8, 115.	1.2	10
71	Blindfold learning of an accurate neural metric. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 3267-3272.	3.3	9
72	Generative models of T-cell receptor sequences. <i>Physical Review E</i> , 2020, 101, 062414.	0.8	9

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73	Probing T-cell response by sequence-based probabilistic modeling. PLoS Computational Biology, 2021, 17, e1009297.	1.5	9
74	Evidence for Shaping of Light Chain Repertoire by Structural Selection. Frontiers in Immunology, 2018, 9, 1307.	2.2	8
75	Learning the statistics and landscape of somatic mutation-induced insertions and deletions in antibodies. PLoS Computational Biology, 2022, 18, e1010167.	1.5	6
76	Optimal prediction with resource constraints using the information bottleneck. PLoS Computational Biology, 2021, 17, e1008743.	1.5	5
77	SOS: online probability estimation and generation of T-and B-cell receptors. Bioinformatics, 2020, 36, 4510-4512.	1.8	4
78	Population Dynamics of Immune Repertoires. , 2021, , 203-221.		4
79	Closed-Loop Estimation of Retinal Network Sensitivity by Local Empirical Linearization. ENeuro, 2017, 4, ENEURO.0166-17.2017.	0.9	4
80	A model for the integration of conflicting exogenous and endogenous signals by dendritic cells. Physical Biology, 2018, 15, 056001.	0.8	3
81	Renormalization group approach to connect discrete- and continuous-time descriptions of Gaussian processes. Physical Review E, 2022, 105, 044133.	0.8	1
82	JSP Special Issue on Information Processing in Living Systems. Journal of Statistical Physics, 2016, 162, 1085-1087.	0.5	0
83	Mutual information maximization for amortized likelihood inference from sampled trajectories: MINIMALIST. Physical Review E, 2022, 105, .	0.8	0