

Thomas MacCarthy

List of Publications by Year in descending order

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516710

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39
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1121
citing authors

#	ARTICLE	IF	CITATIONS
1	Deep learning model of somatic hypermutation reveals importance of sequence context beyond hotspot targeting. <i>IScience</i> , 2022, 25, 103668.	4.1	6
2	#84: Evolutionary Pressure from APOBEC Causes an Underrepresentation of TC Motifs in Human Polyomavirus. <i>Journal of the Pediatric Infectious Diseases Society</i> , 2021, 10, S14-S15.	1.3	0
3	Mutational pressure by host APOBEC3s more strongly affects genes expressed early in the lytic phase of herpes simplex virus-1 (HSV-1) and human polyomavirus (HPyV) infection. <i>PLoS Pathogens</i> , 2021, 17, e1009560.	4.7	9
4	Post-Transformation IGHV-IGHD-IGHJ Mutations in Chronic Lymphocytic Leukemia B Cells: Implications for Mutational Mechanisms and Impact on Clinical Course. <i>Frontiers in Oncology</i> , 2021, 11, 640731.	2.8	12
5	Characterization of DNA G-Quadruplex Structures in Human Immunoglobulin Heavy Variable (IGHV) Genes. <i>Frontiers in Immunology</i> , 2021, 12, 671944.	4.8	10
6	Role of Dot1L and H3K79 methylation in regulating somatic hypermutation of immunoglobulin genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	6
7	A Bayesian model based computational analysis of the relationship between bisulfite accessible single-stranded DNA in chromatin and somatic hypermutation of immunoglobulin genes. <i>PLoS Computational Biology</i> , 2021, 17, e1009323.	3.2	4
8	The role of HIRA-dependent H3.3 deposition and its modifications in the somatic hypermutation of immunoglobulin variable regions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	8
9	STAT3 imparts BCRAness by impairing homologous recombination repair in Epstein-Barr virus-transformed B lymphocytes. <i>PLoS Pathogens</i> , 2020, 16, e1008849.	4.7	12
10	AID Overlapping and PolÎ Hotspots Are Key Features of Evolutionary Variation Within the Human Antibody Heavy Chain (IGHV) Genes. <i>Frontiers in Immunology</i> , 2020, 11, 788.	4.8	19
11	Correlations in Somatic Hypermutation Between Sites in IGHV Genes Can Be Explained by Interactions Between AID and/or PolÎ Hotspots. <i>Frontiers in Immunology</i> , 2020, 11, 618409.	4.8	2
12	A-to-I editing of Malacoherpesviridae RNAs supports the antiviral role of ADAR1 in mollusks. <i>BMC Evolutionary Biology</i> , 2019, 19, 149.	3.2	20
13	PD-1/PD-L1 immune checkpoint and p53 loss facilitate tumor progression in activated B-cell diffuse large B-cell lymphomas. <i>Blood</i> , 2019, 133, 2401-2412.	1.4	54
14	Evolutionary effects of the AID/APOBEC family of mutagenic enzymes on human gamma-herpesviruses. <i>Virus Evolution</i> , 2019, 5, vey040.	4.9	27
15	Combinatorial Loss of the Enzymatic Activities of Viral Uracil-DNA Glycosylase and Viral dUTPase Impairs Murine Gammaherpesvirus Pathogenesis and Leads to Increased Recombination-Based Deletion in the Viral Genome. <i>MBio</i> , 2018, 9, .	4.1	11
16	The cytidine deaminase under-representation reporter (CDUR) as a tool to study evolution of sequences under deaminase mutational pressure. <i>BMC Bioinformatics</i> , 2018, 19, 163.	2.6	8
17	The preferred nucleotide contexts of the AID/APOBEC cytidine deaminases have differential effects when mutating retrotransposon and virus sequences compared to host genes. <i>PLoS Computational Biology</i> , 2017, 13, e1005471.	3.2	46
18	The Number of Overlapping AID Hotspots in Germline IGHV Genes Is Inversely Correlated with Mutation Frequency in Chronic Lymphocytic Leukemia. <i>PLoS ONE</i> , 2017, 12, e0167602.	2.5	4

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19	Chronic lymphocytic leukemia cells diversify and differentiate in vivo via a nonclassical Th1-dependent, Bcl-6-deficient process. <i>JCI Insight</i> , 2016, 1, .	5.0	29
20	DNA polymerase δ functions in the generation of tandem mutations during somatic hypermutation of antibody genes. <i>Journal of Experimental Medicine</i> , 2016, 213, 1675-1683.	8.5	27
21	Potential for evolution of complex defense strategies in a multi-scale model of virus-host coevolution. <i>BMC Evolutionary Biology</i> , 2016, 16, 233.	3.2	7
22	Antagonistic Coevolution Drives Whack-a-Mole Sensitivity in Gene Regulatory Networks. <i>PLoS Computational Biology</i> , 2015, 11, e1004432.	3.2	8
23	Overlapping hotspots in CDRs are critical sites for V region diversification. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E728-37.	7.1	62
24	Regulatory Evolution and Voltage-Gated Ion Channel Expression in Squid Axon: Selection-Mutation Balance and Fitness Cliffs. <i>PLoS ONE</i> , 2015, 10, e0120785.	2.5	3
25	Epigenetics Decouples Mutational from Environmental Robustness. Did It Also Facilitate Multicellularity?. <i>PLoS Computational Biology</i> , 2014, 10, e1003450.	3.2	18
26	Host restriction of murine gammaherpesvirus 68 replication by human APOBEC3 cytidine deaminases but not murine APOBEC3. <i>Virology</i> , 2014, 454-455, 215-226.	2.4	20
27	The Underlying Molecular and Network Level Mechanisms in the Evolution of Robustness in Gene Regulatory Networks. <i>PLoS Computational Biology</i> , 2013, 9, e1002865.	3.2	17
28	IGHV-unmutated and IGHV-mutated chronic lymphocytic leukemia cells produce activation-induced deaminase protein with a full range of biologic functions. <i>Blood</i> , 2012, 120, 4802-4811.	1.4	52
29	Ultra-Deep Sequencing of De Novo IGHV Mutations in Activated CLL Cells: Evidence for Activation-Induced Deaminase Function.. <i>Blood</i> , 2012, 120, 2545-2545.	1.4	4
30	Recombinase-Mediated Cassette Exchange as a Novel Method To Study Somatic Hypermutation in Ramos Cells. <i>MBio</i> , 2011, 2, .	4.1	7
31	Differential regulation drives plasticity in sex determination gene networks. <i>BMC Evolutionary Biology</i> , 2010, 10, 388.	3.2	19
32	V-region mutation in vitro, in vivo, and in silico reveal the importance of the enzymatic properties of AID and the sequence environment. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 8629-8634.	7.1	37
33	SHMTool: A webserver for comparative analysis of somatic hypermutation datasets. <i>DNA Repair</i> , 2009, 8, 137-141.	2.8	36
34	Coevolution of robustness, epistasis, and recombination favors asexual reproduction. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 12801-12806.	7.1	43
35	The limits of subfunctionalization. <i>BMC Evolutionary Biology</i> , 2007, 7, 213.	3.2	38
36	Buffering Mechanisms in Aging: A systems approach towards uncovering the genetic component of aging. <i>PLoS Computational Biology</i> , 2005, preprint, e170.	3.2	2

#	ARTICLE	IF	CITATIONS
37	The evolutionary potential of the Drosophila sex determination gene network. Journal of Theoretical Biology, 2003, 225, 461-468.	1.7	17