

Thomas MacCarthy

List of Publications by Year in descending order

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Version: 2024-02-01

37
papers

707
citations

516710

16
h-index

610901

24
g-index

39
all docs

39
docs citations

39
times ranked

1121
citing authors

#	ARTICLE	IF	CITATIONS
1	Overlapping hotspots in CDRs are critical sites for V region diversification. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E728-37.	7.1	62
2	PD-1/PD-L1 immune checkpoint and p53 loss facilitate tumor progression in activated B-cell diffuse large B-cell lymphomas. Blood, 2019, 133, 2401-2412.	1.4	54
3	IGHV-unmutated and IGHV-mutated chronic lymphocytic leukemia cells produce activation-induced deaminase protein with a full range of biologic functions. Blood, 2012, 120, 4802-4811.	1.4	52
4	The preferred nucleotide contexts of the AID/APOBEC cytidine deaminases have differential effects when mutating retrotransposon and virus sequences compared to host genes. PLoS Computational Biology, 2017, 13, e1005471.	3.2	46
5	Coevolution of robustness, epistasis, and recombination favors asexual reproduction. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 12801-12806.	7.1	43
6	The limits of subfunctionalization. BMC Evolutionary Biology, 2007, 7, 213.	3.2	38
7	V-region mutation in vitro, in vivo, and in silico reveal the importance of the enzymatic properties of AID and the sequence environment. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 8629-8634.	7.1	37
8	SHMTool: A webserver for comparative analysis of somatic hypermutation datasets. DNA Repair, 2009, 8, 137-141.	2.8	36
9	Chronic lymphocytic leukemia cells diversify and differentiate in vivo via a nonclassical Th1-dependent, Bcl-6-deficient process. JCI Insight, 2016, 1, .	5.0	29
10	DNA polymerase $\hat{1}$ functions in the generation of tandem mutations during somatic hypermutation of antibody genes. Journal of Experimental Medicine, 2016, 213, 1675-1683.	8.5	27
11	Evolutionary effects of the AID/APOBEC family of mutagenic enzymes on human gamma-herpesviruses. Virus Evolution, 2019, 5, vey040.	4.9	27
12	Host restriction of murine gammaherpesvirus 68 replication by human APOBEC3 cytidine deaminases but not murine APOBEC3. Virology, 2014, 454-455, 215-226.	2.4	20
13	A-to-I editing of Malacoherpesviridae RNAs supports the antiviral role of ADAR1 in mollusks. BMC Evolutionary Biology, 2019, 19, 149.	3.2	20
14	Differential regulation drives plasticity in sex determination gene networks. BMC Evolutionary Biology, 2010, 10, 388.	3.2	19
15	AID Overlapping and Pol $\hat{1}$ Hotspots Are Key Features of Evolutionary Variation Within the Human Antibody Heavy Chain (IGHV) Genes. Frontiers in Immunology, 2020, 11, 788.	4.8	19
16	Epigenetics Decouples Mutational from Environmental Robustness. Did It Also Facilitate Multicellularity?. PLoS Computational Biology, 2014, 10, e1003450.	3.2	18
17	The evolutionary potential of the Drosophila sex determination gene network. Journal of Theoretical Biology, 2003, 225, 461-468.	1.7	17
18	The Underlying Molecular and Network Level Mechanisms in the Evolution of Robustness in Gene Regulatory Networks. PLoS Computational Biology, 2013, 9, e1002865.	3.2	17

#	ARTICLE	IF	CITATIONS
19	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
20	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
21	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
22	Characterization of DNA G-Quadruplex Structures in Human Immunoglobulin Heavy Variable (IGHV) Genes. <i>Frontiers in Immunology</i> , 2021, 12, 671944.	4.8	10
23	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
24	Antagonistic Coevolution Drives Whack-a-Mole Sensitivity in Gene Regulatory Networks. <i>PLoS Computational Biology</i> , 2015, 11, e1004432.	3.2	8
25	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
26	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
27	Recombinase-Mediated Cassette Exchange as a Novel Method To Study Somatic Hypermutation in Ramos Cells. <i>MBio</i> , 2011, 2, .	4.1	7
28	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
29	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
30	Deep learning model of somatic hypermutation reveals importance of sequence context beyond hotspot targeting. <i>IScience</i> , 2022, 25, 103668.	4.1	6
31	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
32	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
33	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
34	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
35	Correlations in Somatic Hypermutation Between Sites in IGHV Genes Can Be Explained by Interactions Between AID and/or PolI Hotspots. <i>Frontiers in Immunology</i> , 2020, 11, 618409.	4.8	2
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	#84: Evolutionary Pressure from APOBEC Causes an Underrepresentation of TC Motifs in Human Polyomavirus. Journal of the Pediatric Infectious Diseases Society, 2021, 10, S14-S15.	1.3	0