

Philip L F Johnson

List of Publications by Year in descending order

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31
papers

9,771
citations

394421

19
h-index

552781

26
g-index

35
all docs

35
docs citations

35
times ranked

12066
citing authors

#	ARTICLE	IF	CITATIONS
1	Population structure, intergroup interaction, and human contact govern infectious disease impacts in mountain gorilla populations. <i>American Journal of Primatology</i> , 2022, 84, e23350.	1.7	4
2	Selection influences naive CD8+ TCR α ^{hi} repertoire sharing. <i>Immunology</i> , 2021, 162, 464-475.	4.4	0
3	Exploring the functional composition of the human microbiome using a hand-curated microbial trait database. <i>BMC Bioinformatics</i> , 2021, 22, 306.	2.6	8
4	Dynamics and turnover of memory CD8 T cell responses following yellow fever vaccination. <i>PLoS Computational Biology</i> , 2021, 17, e1009468.	3.2	9
5	Network-Based Prediction of Novel CRISPR-Associated Genes in Metagenomes. <i>MSystems</i> , 2020, 5, .	3.8	1
6	Avoidance of Self during CRISPR Immunization. <i>Trends in Microbiology</i> , 2020, 28, 543-553.	7.7	19
7	Linking high GC content to the repair of double strand breaks in prokaryotic genomes. <i>PLoS Genetics</i> , 2019, 15, e1008493.	3.5	43
8	Visualization and prediction of CRISPR incidence in microbial trait-space to identify drivers of antiviral immune strategy. <i>ISME Journal</i> , 2019, 13, 2589-2602.	9.8	34
9	Linking high GC content to the repair of double strand breaks in prokaryotic genomes. , 2019, 15, e1008493.		0
10	Linking high GC content to the repair of double strand breaks in prokaryotic genomes. , 2019, 15, e1008493.		0
11	Linking high GC content to the repair of double strand breaks in prokaryotic genomes. , 2019, 15, e1008493.		0
12	Linking high GC content to the repair of double strand breaks in prokaryotic genomes. , 2019, 15, e1008493.		0
13	Immune loss as a driver of coexistence during host-phage coevolution. <i>ISME Journal</i> , 2018, 12, 585-597.	9.8	50
14	Selective Maintenance of Multiple CRISPR Arrays Across Prokaryotes. <i>CRISPR Journal</i> , 2018, 1, 405-413.	2.9	17
15	Biological Sexing of a 4000-Year-Old Egyptian Mummy Head to Assess the Potential of Nuclear DNA Recovery from the Most Damaged and Limited Forensic Specimens. <i>Genes</i> , 2018, 9, 135.	2.4	39
16	Genome-wide ancestry of 17th-century enslaved Africans from the Caribbean. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 3669-3673.	7.1	110
17	Initial viral load determines the magnitude of the human CD8 T cell response to yellow fever vaccination. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 3050-3055.	7.1	111
18	The complete genome sequence of a Neanderthal from the Altai Mountains. <i>Nature</i> , 2014, 505, 43-49.	27.8	1,830

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19	Two ancient human genomes reveal Polynesian ancestry among the indigenous Botocudos of Brazil. <i>Current Biology</i> , 2014, 24, R1035-R1037.	3.9	73
20	Genome sequence of a 45,000-year-old modern human from western Siberia. <i>Nature</i> , 2014, 514, 445-449.	27.8	856
21	A Revised Timescale for Human Evolution Based on Ancient Mitochondrial Genomes. <i>Current Biology</i> , 2013, 23, 553-559.	3.9	540
22	mapDamage2.0: fast approximate Bayesian estimates of ancient DNA damage parameters. <i>Bioinformatics</i> , 2013, 29, 1682-1684.	4.1	1,174
23	Peripheral selection rather than thymic involution explains sudden contraction in naive CD4 T-cell diversity with age. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 21432-21437.	7.1	80
24	How do antigenically varying pathogens avoid cross-reactive responses to invariant antigens?. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2012, 279, 2777-2785.	2.6	16
25	Mutation Rate Distribution Inferred from Coincident SNPs and Coincident Substitutions. <i>Genome Biology and Evolution</i> , 2011, 3, 842-850.	2.5	30
26	Vaccination Alters the Balance between Protective Immunity, Exhaustion, Escape, and Death in Chronic Infections. <i>Journal of Virology</i> , 2011, 85, 5565-5570.	3.4	37
27	A Draft Sequence of the Neandertal Genome. <i>Science</i> , 2010, 328, 710-722.	12.6	3,588
28	Inference of Microbial Recombination Rates from Metagenomic Data. <i>PLoS Genetics</i> , 2009, 5, e1000674.	3.5	31
29	Patterns of damage in genomic DNA sequences from a Neandertal. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 14616-14621.	7.1	799
30	Utility of R_0 as a predictor of disease invasion in structured populations. <i>Journal of the Royal Society Interface</i> , 2007, 4, 315-324.	3.4	84
31	Duelling timescales of host movement and disease recovery determine invasion of disease in structured populations. <i>Ecology Letters</i> , 2005, 8, 587-595.	6.4	172