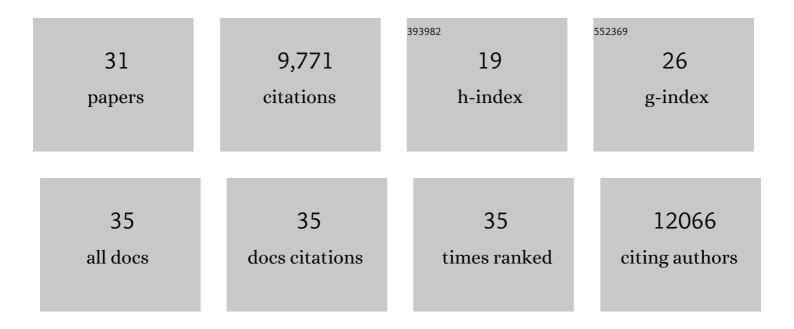
Philip L F Johnson

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/520463/publications.pdf Version: 2024-02-01



#	Article	lF	CITATIONS
1	A Draft Sequence of the Neandertal Genome. Science, 2010, 328, 710-722.	6.0	3,588
2	The complete genome sequence of a Neanderthal from the Altai Mountains. Nature, 2014, 505, 43-49.	13.7	1,830
3	mapDamage2.0: fast approximate Bayesian estimates of ancient DNA damage parameters. Bioinformatics, 2013, 29, 1682-1684.	1.8	1,174
4	Genome sequence of a 45,000-year-old modern human from western Siberia. Nature, 2014, 514, 445-449.	13.7	856
5	Patterns of damage in genomic DNA sequences from a Neandertal. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 14616-14621.	3.3	799
6	A Revised Timescale for Human Evolution Based on Ancient Mitochondrial Genomes. Current Biology, 2013, 23, 553-559.	1.8	540
7	Duelling timescales of host movement and disease recovery determine invasion of disease in structured populations. Ecology Letters, 2005, 8, 587-595.	3.0	172
8	Initial viral load determines the magnitude of the human CD8 T cell response to yellow fever vaccination. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 3050-3055.	3.3	111
9	Genome-wide ancestry of 17th-century enslaved Africans from the Caribbean. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 3669-3673.	3.3	110
10	Utility of R 0 as a predictor of disease invasion in structured populations. Journal of the Royal Society Interface, 2007, 4, 315-324.	1.5	84
11	Peripheral selection rather than thymic involution explains sudden contraction in naive CD4 T-cell diversity with age. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 21432-21437.	3.3	80
12	Two ancient human genomes reveal Polynesian ancestry among the indigenous Botocudos of Brazil. Current Biology, 2014, 24, R1035-R1037.	1.8	73
13	Immune loss as a driver of coexistence during host-phage coevolution. ISME Journal, 2018, 12, 585-597.	4.4	50
14	Linking high GC content to the repair of double strand breaks in prokaryotic genomes. PLoS Genetics, 2019, 15, e1008493.	1.5	43
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. Genes, 2018, 9, 135.	1.0	39
16	Vaccination Alters the Balance between Protective Immunity, Exhaustion, Escape, and Death in Chronic Infections. Journal of Virology, 2011, 85, 5565-5570.	1.5	37
17	Visualization and prediction of CRISPR incidence in microbial trait-space to identify drivers of antiviral immune strategy. ISME Journal, 2019, 13, 2589-2602.	4.4	34
18	Inference of Microbial Recombination Rates from Metagenomic Data. PLoS Genetics, 2009, 5, e1000674.	1.5	31

Philip L F Johnson

#	Article	IF	CITATIONS
19	Mutation Rate Distribution Inferred from Coincident SNPs and Coincident Substitutions. Genome Biology and Evolution, 2011, 3, 842-850.	1.1	30
20	Avoidance of Self during CRISPR Immunization. Trends in Microbiology, 2020, 28, 543-553.	3.5	19
21	Selective Maintenance of Multiple CRISPR Arrays Across Prokaryotes. CRISPR Journal, 2018, 1, 405-413.	1.4	17
22	How do antigenically varying pathogens avoid cross-reactive responses to invariant antigens?. Proceedings of the Royal Society B: Biological Sciences, 2012, 279, 2777-2785.	1.2	16
23	Dynamics and turnover of memory CD8 T cell responses following yellow fever vaccination. PLoS Computational Biology, 2021, 17, e1009468.	1.5	9
24	Exploring the functional composition of the human microbiome using a hand-curated microbial trait database. BMC Bioinformatics, 2021, 22, 306.	1.2	8
25	Population structure, intergroup interaction, and human contact govern infectious disease impacts in mountain gorilla populations. American Journal of Primatology, 2022, 84, e23350.	0.8	4
26	Network-Based Prediction of Novel CRISPR-Associated Genes in Metagenomes. MSystems, 2020, 5, .	1.7	1
27	Selection influences naive CD8+ TCRâ€Î² repertoire sharing. Immunology, 2021, 162, 464-475.	2.0	0
28	Linking high GC content to the repair of double strand breaks in prokaryotic genomes. , 2019, 15, e1008493.		0
29	Linking high GC content to the repair of double strand breaks in prokaryotic genomes. , 2019, 15, e1008493.		0
30	Linking high GC content to the repair of double strand breaks in prokaryotic genomes. , 2019, 15, e1008493.		0
31	Linking high GC content to the repair of double strand breaks in prokaryotic genomes. , 2019, 15, e1008493.		0