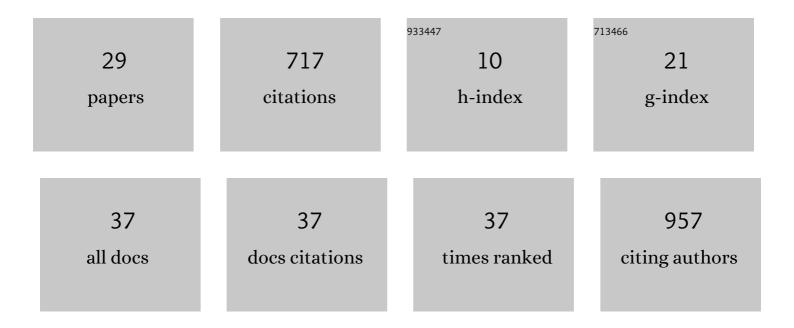
## Rahul Siddharthan

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/3464745/publications.pdf

Version: 2024-02-01



#	Article	IF	CITATIONS
1	ClaID: a Rapid Method of Clade-Level Identification of the Multidrug Resistant Human Fungal Pathogen Candida auris. Microbiology Spectrum, 2022, 10, e0063422.	3.0	7
2	Machine learning prediction of non-attendance to postpartum glucose screening and subsequent risk of type 2 diabetes following gestational diabetes. PLoS ONE, 2022, 17, e0264648.	2.5	7
3	Functional and Comparative Analysis of Centromeres Reveals Clade-Specific Genome Rearrangements in <i>Candida auris</i> and a Chromosome Number Change in Related Species. MBio, 2021, 12, .	4.1	11
4	Orc4 spatiotemporally stabilizes centromeric chromatin. Genome Research, 2021, 31, 607-621.	5.5	5
5	Loss of centromere function drives karyotype evolution in closely related Malassezia species. ELife, 2020, 9, .	6.0	45
6	Altered kinetics of circulating progenitor cells in cardiopulmonary bypass (CPB) associated vasoplegic patients: A pilot study. PLoS ONE, 2020, 15, e0242375.	2.5	0
7	Title is missing!. , 2020, 15, e0242375.		0
8	Title is missing!. , 2020, 15, e0242375.		0
9	Title is missing!. , 2020, 15, e0242375.		0
10	Title is missing!. , 2020, 15, e0242375.		0
11	Title is missing!. , 2020, 15, e0242375.		0
12	Title is missing!. , 2020, 15, e0242375.		0
13	ChIPulate: A comprehensive ChIP-seq simulation pipeline. PLoS Computational Biology, 2019, 15, e1006921.	3.2	9
14	THiCweed: fast, sensitive detection of sequence features by clustering big datasets. Nucleic Acids Research, 2018, 46, e29-e29.	14.5	4
15	Detection of cooperatively bound transcription factor pairs using ChIP-seq peak intensities and expectation maximization. PLoS ONE, 2018, 13, e0199771.	2.5	9
16	Proteogenomics produces comprehensive and highly accurate protein-coding gene annotation in a complete genome assembly ofMalassezia sympodialis. Nucleic Acids Research, 2017, 45, gkx006.	14.5	47
17	Repeat-Associated Fission Yeast-Like Regional Centromeres in the Ascomycetous Budding Yeast Candida tropicalis. PLoS Genetics, 2016, 12, e1005839.	3.5	56
18	The TAF9 C-Terminal Conserved Region Domain Is Required for SAGA and TFIID Promoter Occupancy To Promote Transcriptional Activation. Molecular and Cellular Biology, 2014, 34, 1547-1563.	2.3	21

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#	Article	IF	CITATIONS
19	Dinucleotide Weight Matrices for Predicting Transcription Factor Binding Sites: Generalizing the Position Weight Matrix. PLoS ONE, 2010, 5, e9722.	2.5	80
20	The Complex Spatio-Temporal Regulation of the Drosophila Myoblast Attractant Gene duf/kirre. PLoS ONE, 2009, 4, e6960.	2.5	9
21	Rapid evolution of Cse4p-rich centromeric DNA sequences in closely related pathogenic yeasts, <i>Candida albicans</i> and <i>Candida dubliniensis</i> . Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 19797-19802.	7.1	81
22	PhyloGibbs-MP: Module Prediction and Discriminative Motif-Finding by Gibbs Sampling. PLoS Computational Biology, 2008, 4, e1000156.	3.2	22
23	Parsing regulatory DNA: General tasks, techniques, and the PhyloGibbs approach. Journal of Biosciences, 2007, 32, 863-870.	1.1	2
24	Gene Expression From Random Libraries of Yeast Promoters. Genetics, 2006, 172, 2113-2122.	2.9	26
25	Eastern creeds are less dogmatic about scripture. Nature, 2005, 433, 355-355.	27.8	0
26	PhyloGibbs: A Gibbs Sampling Motif Finder That Incorporates Phylogeny. PLoS Computational Biology, 2005, 1, e67.	3.2	236
27	Dynamical Mean-Field Theory of Resonating-Valence-Bond Antiferromagnets. Physical Review Letters, 2001, 87, 277203.	7.8	20
28	Exact ground state and kink-like excitations of a two-dimensional Heisenberg antiferromagnet. Physical Review B, 1999, 60, R9904-R9907.	3.2	2
20	Quantizing the Toda lattice Physical Review B 1997 55 12196-12209	3.2	6