

Simon Rasmussen

List of Publications by Year in descending order

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Version: 2024-02-01

96
papers

24,664
citations

31902

53
h-index

37111

96
g-index

116
all docs

116
docs citations

116
times ranked

31028
citing authors

#	ARTICLE	IF	CITATIONS
1	Identification of acquired antimicrobial resistance genes. <i>Journal of Antimicrobial Chemotherapy</i> , 2012, 67, 2640-2644.	1.3	4,515
2	Richness of human gut microbiome correlates with metabolic markers. <i>Nature</i> , 2013, 500, 541-546.	13.7	3,641
3	Multilocus Sequence Typing of Total-Genome-Sequenced Bacteria. <i>Journal of Clinical Microbiology</i> , 2012, 50, 1355-1361.	1.8	1,925
4	Population genomics of Bronze Age Eurasia. <i>Nature</i> , 2015, 522, 167-172.	13.7	1,166
5	Identification and assembly of genomes and genetic elements in complex metagenomic samples without using reference genomes. <i>Nature Biotechnology</i> , 2014, 32, 822-828.	9.4	909
6	Upper Palaeolithic Siberian genome reveals dual ancestry of Native Americans. <i>Nature</i> , 2014, 505, 87-91.	13.7	821
7	An Aboriginal Australian Genome Reveals Separate Human Dispersals into Asia. <i>Science</i> , 2011, 334, 94-98.	6.0	675
8	Global monitoring of antimicrobial resistance based on metagenomics analyses of urban sewage. <i>Nature Communications</i> , 2019, 10, 1124.	5.8	612
9	The genome of a Late Pleistocene human from a Clovis burial site in western Montana. <i>Nature</i> , 2014, 506, 225-229.	13.7	500
10	Transcriptome Responses to Combinations of Stresses in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2013, 161, 1783-1794.	2.3	478
11	Genomic evidence for the Pleistocene and recent population history of Native Americans. <i>Science</i> , 2015, 349, aab3884.	6.0	449
12	Metagenomic species profiling using universal phylogenetic marker genes. <i>Nature Methods</i> , 2013, 10, 1196-1199.	9.0	442
13	A genomic history of Aboriginal Australia. <i>Nature</i> , 2016, 538, 207-214.	13.7	439
14	Early Divergent Strains of <i>Yersinia pestis</i> in Eurasia 5,000 Years Ago. <i>Cell</i> , 2015, 163, 571-582.	13.5	425
15	Derived immune and ancestral pigmentation alleles in a 7,000-year-old Mesolithic European. <i>Nature</i> , 2014, 507, 225-228.	13.7	328
16	137 ancient human genomes from across the Eurasian steppes. <i>Nature</i> , 2018, 557, 369-374.	13.7	325
17	Terminal Pleistocene Alaskan genome reveals first founding population of Native Americans. <i>Nature</i> , 2018, 553, 203-207.	13.7	304
18	The prehistoric peopling of Southeast Asia. <i>Science</i> , 2018, 361, 88-92.	6.0	291

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19	The genetic prehistory of the New World Arctic. <i>Science</i> , 2014, 345, 1255832.	6.0	264
20	Ancient genomes show social and reproductive behavior of early Upper Paleolithic foragers. <i>Science</i> , 2017, 358, 659-662.	6.0	263
21	The first horse herders and the impact of early Bronze Age steppe expansions into Asia. <i>Science</i> , 2018, 360, .	6.0	262
22	The population history of northeastern Siberia since the Pleistocene. <i>Nature</i> , 2019, 570, 182-188.	13.7	259
23	Global Network Reorganization During Dynamic Adaptations of <i>Bacillus subtilis</i> . <i>Metabolism</i> . <i>Science</i> , 2012, 335, 1099-1103.	6.0	255
24	Improved metagenome binning and assembly using deep variational autoencoders. <i>Nature Biotechnology</i> , 2021, 39, 555-560.	9.4	251
25	Benchmarking of Methods for Genomic Taxonomy. <i>Journal of Clinical Microbiology</i> , 2014, 52, 1529-1539.	1.8	241
26	Early human dispersals within the Americas. <i>Science</i> , 2018, 362, .	6.0	230
27	Metagenomic analysis of rapid gravity sand filter microbial communities suggests novel physiology of <i>Nitrospira</i> spp.. <i>ISME Journal</i> , 2016, 10, 2569-2581.	4.4	213
28	Microbial community structure of Arctic multiyear sea ice and surface seawater by 454 sequencing of the 16S RNA gene. <i>ISME Journal</i> , 2012, 6, 11-20.	4.4	175
29	Bacterial natural transformation by highly fragmented and damaged DNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 19860-19865.	3.3	170
30	Emergence and Spread of Basal Lineages of <i>Yersinia pestis</i> during the Neolithic Decline. <i>Cell</i> , 2019, 176, 295-305.e10.	13.5	168
31	Novel variation and de novo mutation rates in population-wide de novo assembled Danish trios. <i>Nature Communications</i> , 2015, 6, 5969.	5.8	164
32	Re-theorising mobility and the formation of culture and language among the Corded Ware Culture in Europe. <i>Antiquity</i> , 2017, 91, 334-347.	0.5	157
33	Ancient hepatitis B viruses from the Bronze Age to the Medieval period. <i>Nature</i> , 2018, 557, 418-423.	13.7	155
34	The transcriptionally active regions in the genome of <i>Bacillus subtilis</i> . <i>Molecular Microbiology</i> , 2009, 73, 1043-1057.	1.2	146
35	Population genomics of the Viking world. <i>Nature</i> , 2020, 585, 390-396.	13.7	143
36	<i>Lactobacillus acidophilus</i> induces virus immune defence genes in murine dendritic cells by a Toll-like receptor-dependent mechanism. <i>Immunology</i> , 2010, 131, 268-281.	2.0	138

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37	Critical Assessment of Metagenome Interpretation: the second round of challenges. <i>Nature Methods</i> , 2022, 19, 429-440.	9.0	133
38	Sequencing and de novo assembly of 150 genomes from Denmark as a population reference. <i>Nature</i> , 2017, 548, 87-91.	13.7	130
39	Physiological and Genetic Adaptations to Diving in Sea Nomads. <i>Cell</i> , 2018, 173, 569-580.e15.	13.5	129
40	Transcriptome analysis of root-knot nematode (<i>Meloidogyne incognita</i>)-infected tomato (<i>Solanum lycopersicum</i>) roots reveals complex gene expression profiles and metabolic networks of both host and nematode during susceptible and resistance responses. <i>Molecular Plant Pathology</i> , 2018, 19, 615-633.	2.0	127
41	A Selective Sweep on a Deleterious Mutation in CPT1A in Arctic Populations. <i>American Journal of Human Genetics</i> , 2014, 95, 584-589.	2.6	119
42	Unraveling ancestry, kinship, and violence in a Late Neolithic mass grave. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 10705-10710.	3.3	119
43	Transcriptome profiling of brown adipose tissue during cold exposure reveals extensive regulation of glucose metabolism. <i>American Journal of Physiology - Endocrinology and Metabolism</i> , 2015, 308, E380-E392.	1.8	105
44	Rare truncating variants in the sarcomeric protein titin associate with familial and early-onset atrial fibrillation. <i>Nature Communications</i> , 2018, 9, 4316.	5.8	93
45	Noninvasive proteomic biomarkers for alcohol-related liver disease. <i>Nature Medicine</i> , 2022, 28, 1277-1287.	15.2	91
46	snpTree - a web-server to identify and construct SNP trees from whole genome sequence data. <i>BMC Genomics</i> , 2012, 13, S6.	1.2	87
47	Meta-genomic analysis of toilet waste from long distance flights; a step towards global surveillance of infectious diseases and antimicrobial resistance. <i>Scientific Reports</i> , 2015, 5, 11444.	1.6	74
48	Genome-scale cold stress response regulatory networks in ten <i>Arabidopsis thaliana</i> ecotypes. <i>BMC Genomics</i> , 2013, 14, 722.	1.2	73
49	Two ancient human genomes reveal Polynesian ancestry among the indigenous Botocudos of Brazil. <i>Current Biology</i> , 2014, 24, R1035-R1037.	1.8	73
50	Biosynthesis of bioactive diterpenoids in the medicinal plant <i>Vitex agnus-castus</i> . <i>Plant Journal</i> , 2018, 93, 943-958.	2.8	68
51	Construction of a dairy microbial genome catalog opens new perspectives for the metagenomic analysis of dairy fermented products. <i>BMC Genomics</i> , 2014, 15, 1101.	1.2	64
52	Origins and genetic legacies of the Caribbean Taino. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 2341-2346.	3.3	64
53	Facilitation of pain sensitization in knee osteoarthritis and persistent post-operative pain: A cross-sectional study. <i>European Journal of Pain</i> , 2014, 18, 1024-1031.	1.4	61
54	A 5700 year-old human genome and oral microbiome from chewed birch pitch. <i>Nature Communications</i> , 2019, 10, 5520.	5.8	61

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55	Dhurrin metabolism in the developing grain of <i>Sorghum bicolor</i> (L.) Moench investigated by metabolite profiling and novel clustering analyses of time-resolved transcriptomic data. <i>BMC Genomics</i> , 2016, 17, 1021.	1.2	56
56	Complete Genes May Pass from Food to Human Blood. <i>PLoS ONE</i> , 2013, 8, e69805.	1.1	52
57	Arthroscopic treatment of impingement of the ankle reduces pain and enhances function. <i>Scandinavian Journal of Medicine and Science in Sports</i> , 2002, 12, 69-72.	1.3	50
58	Genome-wide Ancestry Patterns in Rapanui Suggest Pre-European Admixture with Native Americans. <i>Current Biology</i> , 2014, 24, 2518-2525.	1.8	50
59	Ancient Jomon genome sequence analysis sheds light on migration patterns of early East Asian populations. <i>Communications Biology</i> , 2020, 3, 437.	2.0	44
60	The ubiquitin ligase RFW3 is required for translesion DNA synthesis. <i>Molecular Cell</i> , 2021, 81, 442-458.e9.	4.5	43
61	Analysis of 62 hybrid assembled human Y chromosomes exposes rapid structural changes and high rates of gene conversion. <i>PLoS Genetics</i> , 2017, 13, e1006834.	1.5	42
62	Ancient nuclear genomes enable repatriation of Indigenous human remains. <i>Science Advances</i> , 2018, 4, eaau5064.	4.7	41
63	In silico assessment of virulence factors in strains of <i>Streptococcus oralis</i> and <i>Streptococcus mitis</i> isolated from patients with Infective Endocarditis. <i>Journal of Medical Microbiology</i> , 2017, 66, 1316-1323.	0.7	41
64	Genome binning of viral entities from bulk metagenomics data. <i>Nature Communications</i> , 2022, 13, 965.	5.8	41
65	Ancient pathogen <scp>DNA</scp> in human teeth and petrous bones. <i>Ecology and Evolution</i> , 2018, 8, 3534-3542.	0.8	38
66	Immunity and mental illness: findings from a Danish population-based immunogenetic study of seven psychiatric and neurodevelopmental disorders. <i>European Journal of Human Genetics</i> , 2019, 27, 1445-1455.	1.4	38
67	A draft genome sequence of the elusive giant squid, <i>Architeuthis dux</i> . <i>GigaScience</i> , 2020, 9, .	3.3	37
68	Gut microbial changes of patients with psychotic and affective disorders: A systematic review. <i>Schizophrenia Research</i> , 2021, 234, 41-50.	1.1	34
69	Alpha proteobacterial ancestry of the [Fe-Fe]-hydrogenases in anaerobic eukaryotes. <i>Biology Direct</i> , 2016, 11, 34.	1.9	33
70	<i>Bifidobacterium bifidum</i> Actively Changes the Gene Expression Profile Induced by <i>Lactobacillus acidophilus</i> in Murine Dendritic Cells. <i>PLoS ONE</i> , 2010, 5, e11065.	1.1	30
71	Discovery, genotyping and characterization of structural variation and novel sequence at single nucleotide resolution from de novo genome assemblies on a population scale. <i>GigaScience</i> , 2015, 4, 64.	3.3	30
72	Extension of Plant Phenotypes by the Foliar Microbiome. <i>Annual Review of Plant Biology</i> , 2021, 72, 823-846.	8.6	27

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73	Intraarticular glucocorticoid, morphine and bupivacaine reduces pain and convalescence after arthroscopic ankle surgery: A randomized study of 36 patients. <i>Acta Orthopaedica</i> , 2000, 71, 301-304.	1.4	25
74	Whole genome sequencing as a tool for phylogenetic analysis of clinical strains of Mitis group streptococci. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2016, 35, 1615-1625.	1.3	25
75	Transcriptional landscape estimation from tiling array data using a model of signal shift and drift. <i>Bioinformatics</i> , 2009, 25, 2341-2347.	1.8	23
76	Genetic studies of abdominal MRI data identify genes regulating hepcidin as major determinants of liver iron concentration. <i>Journal of Hepatology</i> , 2019, 71, 594-602.	1.8	23
77	Hybridization Capture Using Short PCR Products Enriches Small Genomes by Capturing Flanking Sequences (CapFlank). <i>PLoS ONE</i> , 2014, 9, e109101.	1.1	21
78	Gene expression plasticity across hosts of an invasive scale insect species. <i>PLoS ONE</i> , 2017, 12, e0176956.	1.1	20
79	Impaired Uptake and/or Utilization of Leucine by <i>Saccharomyces cerevisiae</i> Is Suppressed by the <i>SPT15-300</i> Allele of the TATA-Binding Protein Gene. <i>Applied and Environmental Microbiology</i> , 2009, 75, 6055-6061.	1.4	19
80	Paleogenomic insights into the red complex bacteria <i>Tannerella forsythia</i> in Pre-Hispanic and Colonial individuals from Mexico. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020, 375, 20190580.	1.8	18
81	Assembly and analysis of 100 full MHC haplotypes from the Danish population. <i>Genome Research</i> , 2017, 27, 1597-1607.	2.4	15
82	Genomic characterization, phylogenetic analysis, and identification of virulence factors in <i>Aerococcus sanguinicola</i> and <i>Aerococcus urinae</i> strains isolated from infection episodes. <i>Microbial Pathogenesis</i> , 2017, 112, 327-340.	1.3	14
83	SCAI promotes error-free repair of DNA interstrand crosslinks via the Fanconi anemia pathway. <i>EMBO Reports</i> , 2022, 23, e53639.	2.0	12
84	Defining NASH from a Multi-Omics Systems Biology Perspective. <i>Journal of Clinical Medicine</i> , 2021, 10, 4673.	1.0	9
85	Similar genomic patterns of clinical infective endocarditis and oral isolates of <i>Streptococcus sanguinis</i> and <i>Streptococcus gordonii</i> . <i>Scientific Reports</i> , 2020, 10, 2728.	1.6	8
86	Genetic factors underlying the bidirectional relationship between autoimmune and mental disorders – Findings from a Danish population-based study. <i>Brain, Behavior, and Immunity</i> , 2021, 91, 10-23.	2.0	8
87	Genome Sequence of <i>Talaromyces atroroseus</i> , Which Produces Red Colorants for the Food Industry. <i>Genome Announcements</i> , 2017, 5, .	0.8	7
88	Deep learning-based integration of genetics with registry data for stratification of schizophrenia and depression. <i>Science Advances</i> , 2022, 8, .	4.7	6
89	Reads2Type: a web application for rapid microbial taxonomy identification. <i>BMC Bioinformatics</i> , 2015, 16, 398.	1.2	5
90	A large-scale investigation into the role of classical HLA loci in multiple types of severe infections, with a focus on overlaps with autoimmune and mental disorders. <i>Journal of Translational Medicine</i> , 2021, 19, 230.	1.8	5

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91	Streptococcus pseudopneumoniae: Use of Whole-Genome Sequences To Validate Species Identification Methods. Journal of Clinical Microbiology, 2021, 59, .	1.8	4
92	The CGE Tool Box. , 2017, , 65-90.		3
93	Whole-Exome Sequencing Implicates Neuronal Calcium Channel with Familial Atrial Fibrillation. Frontiers in Genetics, 2022, 13, 806429.	1.1	1
94	Targeted Metabolic Engineering Guided by Computational Analysis of Single-Nucleotide Polymorphisms (SNPs). Methods in Molecular Biology, 2013, 985, 409-428.	0.4	0
95	Re-theorising mobility and the formation of culture and language among the Corded Ware Culture in Europeâ€”CORRIGENDUM. Antiquity, 2020, 94, 839-839.	0.5	0
96	Lâ€™identification gÃ©nÃ©tique de la peste sur les squelettes prÃ©historiques. , 2019, , 50-58.		0