

# 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	Whole-Exome Sequencing Implicates Neuronal Calcium Channel with Familial Atrial Fibrillation. <i>Frontiers in Genetics</i> , 2022, 13, 806429.	1.1	1
2	SCAI promotes error-free repair of DNA interstrand crosslinks via the Fanconi anemia pathway. <i>EMBO Reports</i> , 2022, 23, e53639.	2.0	12
3	Genome binning of viral entities from bulk metagenomics data. <i>Nature Communications</i> , 2022, 13, 965.	5.8	41
4	Critical Assessment of Metagenome Interpretation: the second round of challenges. <i>Nature Methods</i> , 2022, 19, 429-440.	9.0	133
5	Noninvasive proteomic biomarkers for alcohol-related liver disease. <i>Nature Medicine</i> , 2022, 28, 1277-1287.	15.2	91
6	Deep learning-based integration of genetics with registry data for stratification of schizophrenia and depression. <i>Science Advances</i> , 2022, 8, .	4.7	6
7	Gut microbial changes of patients with psychotic and affective disorders: A systematic review. <i>Schizophrenia Research</i> , 2021, 234, 41-50.	1.1	34
8	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
9	<i>Streptococcus pseudopneumoniae</i> : Use of Whole-Genome Sequences To Validate Species Identification Methods. <i>Journal of Clinical Microbiology</i> , 2021, 59, .	1.8	4
10	The ubiquitin ligase RFWD3 is required for translesion DNA synthesis. <i>Molecular Cell</i> , 2021, 81, 442-458.e9.	4.5	43
11	Improved metagenome binning and assembly using deep variational autoencoders. <i>Nature Biotechnology</i> , 2021, 39, 555-560.	9.4	251
12	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
13	Extension of Plant Phenotypes by the Foliar Microbiome. <i>Annual Review of Plant Biology</i> , 2021, 72, 823-846.	8.6	27
14	Defining NASH from a Multi-Omics Systems Biology Perspective. <i>Journal of Clinical Medicine</i> , 2021, 10, 4673.	1.0	9
15	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
16	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
17	Population genomics of the Viking world. <i>Nature</i> , 2020, 585, 390-396.	13.7	143
18	Re-theorising mobility and the formation of culture and language among the Corded Ware Culture in Europe – CORRIGENDUM. <i>Antiquity</i> , 2020, 94, 839-839.	0.5	0

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19	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
20	A draft genome sequence of the elusive giant squid, <i>Architeuthis dux</i> . <i>GigaScience</i> , 2020, 9, .	3.3	37
21	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
22	The population history of northeastern Siberia since the Pleistocene. <i>Nature</i> , 2019, 570, 182-188.	13.7	259
23	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
24	Global monitoring of antimicrobial resistance based on metagenomics analyses of urban sewage. <i>Nature Communications</i> , 2019, 10, 1124.	5.8	612
25	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
26	A 5700 year-old human genome and oral microbiome from chewed birch pitch. <i>Nature Communications</i> , 2019, 10, 5520.	5.8	61
27	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
28	L'identification génétique de la peste sur les squelettes préhistoriques. , 2019, , 50-58.		0
29	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
30	Ancient pathogen DNA in human teeth and petrous bones. <i>Ecology and Evolution</i> , 2018, 8, 3534-3542.	0.8	38
31	Physiological and Genetic Adaptations to Diving in Sea Nomads. <i>Cell</i> , 2018, 173, 569-580.e15.	13.5	129
32	Biosynthesis of bioactive diterpenoids in the medicinal plant <i>Vitex agnus-castus</i> . <i>Plant Journal</i> , 2018, 93, 943-958.	2.8	68
33	Terminal Pleistocene Alaskan genome reveals first founding population of Native Americans. <i>Nature</i> , 2018, 553, 203-207.	13.7	304
34	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
35	Early human dispersals within the Americas. <i>Science</i> , 2018, 362, .	6.0	230
36	Ancient nuclear genomes enable repatriation of Indigenous human remains. <i>Science Advances</i> , 2018, 4, eaau5064.	4.7	41

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37	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
38	The prehistoric peopling of Southeast Asia. <i>Science</i> , 2018, 361, 88-92.	6.0	291
39	137 ancient human genomes from across the Eurasian steppes. <i>Nature</i> , 2018, 557, 369-374.	13.7	325
40	Ancient hepatitis B viruses from the Bronze Age to the Medieval period. <i>Nature</i> , 2018, 557, 418-423.	13.7	155
41	The first horse herders and the impact of early Bronze Age steppe expansions into Asia. <i>Science</i> , 2018, 360, .	6.0	262
42	The CGE Tool Box. , 2017, , 65-90.		3
43	Genome Sequence of <i>Talaromyces atrovirens</i> , Which Produces Red Colorants for the Food Industry. <i>Genome Announcements</i> , 2017, 5, .	0.8	7
44	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
45	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
46	Ancient genomes show social and reproductive behavior of early Upper Paleolithic foragers. <i>Science</i> , 2017, 358, 659-662.	6.0	263
47	Assembly and analysis of 100 full MHC haplotypes from the Danish population. <i>Genome Research</i> , 2017, 27, 1597-1607.	2.4	15
48	Sequencing and de novo assembly of 150 genomes from Denmark as a population reference. <i>Nature</i> , 2017, 548, 87-91.	13.7	130
49	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
50	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
51	Gene expression plasticity across hosts of an invasive scale insect species. <i>PLoS ONE</i> , 2017, 12, e0176956.	1.1	20
52	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
53	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
54	A genomic history of Aboriginal Australia. <i>Nature</i> , 2016, 538, 207-214.	13.7	439

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55	Alpha proteobacterial ancestry of the [Fe-Fe]-hydrogenases in anaerobic eukaryotes. <i>Biology Direct</i> , 2016, 11, 34.	1.9	33
56	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
57	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
58	Reads2Type: a web application for rapid microbial taxonomy identification. <i>BMC Bioinformatics</i> , 2015, 16, 398.	1.2	5
59	Population genomics of Bronze Age Eurasia. <i>Nature</i> , 2015, 522, 167-172.	13.7	1,166
60	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
61	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
62	Genomic evidence for the Pleistocene and recent population history of Native Americans. <i>Science</i> , 2015, 349, aab3884.	6.0	449
63	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
64	Early Divergent Strains of <i>Yersinia pestis</i> in Eurasia 5,000 Years Ago. <i>Cell</i> , 2015, 163, 571-582.	13.5	425
65	Facilitation of pain sensitization in knee osteoarthritis and persistent postoperative pain: A cross-sectional study. <i>European Journal of Pain</i> , 2014, 18, 1024-1031.	1.4	61
66	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
67	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
68	Derived immune and ancestral pigmentation alleles in a 7,000-year-old Mesolithic European. <i>Nature</i> , 2014, 507, 225-228.	13.7	328
69	Upper Palaeolithic Siberian genome reveals dual ancestry of Native Americans. <i>Nature</i> , 2014, 505, 87-91.	13.7	821
70	Genome-wide Ancestry Patterns in Rapanui Suggest Pre-European Admixture with Native Americans. <i>Current Biology</i> , 2014, 24, 2518-2525.	1.8	50
71	Two ancient human genomes reveal Polynesian ancestry among the indigenous Botocudos of Brazil. <i>Current Biology</i> , 2014, 24, R1035-R1037.	1.8	73
72	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

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73	Benchmarking of Methods for Genomic Taxonomy. <i>Journal of Clinical Microbiology</i> , 2014, 52, 1529-1539.	1.8	241
74	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
75	The genetic prehistory of the New World Arctic. <i>Science</i> , 2014, 345, 1255832.	6.0	264
76	Hybridization Capture Using Short PCR Products Enriches Small Genomes by Capturing Flanking Sequences (CapFlank). <i>PLoS ONE</i> , 2014, 9, e109101.	1.1	21
77	Richness of human gut microbiome correlates with metabolic markers. <i>Nature</i> , 2013, 500, 541-546.	13.7	3,641
78	Metagenomic species profiling using universal phylogenetic marker genes. <i>Nature Methods</i> , 2013, 10, 1196-1199.	9.0	442
79	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
80	Targeted Metabolic Engineering Guided by Computational Analysis of Single-Nucleotide Polymorphisms (SNPs). <i>Methods in Molecular Biology</i> , 2013, 985, 409-428.	0.4	0
81	Transcriptome Responses to Combinations of Stresses in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2013, 161, 1783-1794.	2.3	478
82	Genome-scale cold stress response regulatory networks in ten <i>Arabidopsis thaliana</i> ecotypes. <i>BMC Genomics</i> , 2013, 14, 722.	1.2	73
83	Complete Genes May Pass from Food to Human Blood. <i>PLoS ONE</i> , 2013, 8, e69805.	1.1	52
84	Identification of acquired antimicrobial resistance genes. <i>Journal of Antimicrobial Chemotherapy</i> , 2012, 67, 2640-2644.	1.3	4,515
85	Global Network Reorganization During Dynamic Adaptations of <i>Bacillus subtilis</i> . <i>Metabolism. Science</i> , 2012, 335, 1099-1103.	6.0	255
86	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
87	Multilocus Sequence Typing of Total-Genome-Sequenced Bacteria. <i>Journal of Clinical Microbiology</i> , 2012, 50, 1355-1361.	1.8	1,925
88	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
89	An Aboriginal Australian Genome Reveals Separate Human Dispersals into Asia. <i>Science</i> , 2011, 334, 94-98.	6.0	675
90	<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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91	Bifidobacterium bifidum Actively Changes the Gene Expression Profile Induced by Lactobacillus acidophilus in Murine Dendritic Cells. PLoS ONE, 2010, 5, e11065.	1.1	30
92	Transcriptional landscape estimation from tiling array data using a model of signal shift and drift. Bioinformatics, 2009, 25, 2341-2347.	1.8	23
93	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. Applied and Environmental Microbiology, 2009, 75, 6055-6061.	1.4	19
94	The transcriptionally active regions in the genome of <i>Bacillus subtilis</i> . Molecular Microbiology, 2009, 73, 1043-1057.	1.2	146
95	Arthroscopic treatment of impingement of the ankle reduces pain and enhances function. Scandinavian Journal of Medicine and Science in Sports, 2002, 12, 69-72.	1.3	50
96	Intraarticular glucocorticoid, morphine and bupivacaine reduces pain and convalescence after arthroscopic ankle surgery: A randomized study of 36 patients. Acta Orthopaedica, 2000, 71, 301-304.	1.4	25