

Simon Rasmussen

List of Publications by Citations

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103
papers

15,997
citations

47
h-index

116
g-index

116
ext. papers

21,507
ext. citations

18
avg, IF

5.86
L-index

#	Paper	IF	Citations
103	Identification of acquired antimicrobial resistance genes. <i>Journal of Antimicrobial Chemotherapy</i> , 2012 , 67, 2640-4	5.1	2855
102	Richness of human gut microbiome correlates with metabolic markers. <i>Nature</i> , 2013 , 500, 541-6	50.4	2584
101	Multilocus sequence typing of total-genome-sequenced bacteria. <i>Journal of Clinical Microbiology</i> , 2012 , 50, 1355-61	9.7	1163
100	Population genomics of Bronze Age Eurasia. <i>Nature</i> , 2015 , 522, 167-72	50.4	827
99	Identification and assembly of genomes and genetic elements in complex metagenomic samples without using reference genomes. <i>Nature Biotechnology</i> , 2014 , 32, 822-8	44.5	624
98	Upper Palaeolithic Siberian genome reveals dual ancestry of Native Americans. <i>Nature</i> , 2014 , 505, 87-91	50.4	581
97	An Aboriginal Australian genome reveals separate human dispersals into Asia. <i>Science</i> , 2011 , 334, 94-8	33.3	528
96	The genome of a Late Pleistocene human from a Clovis burial site in western Montana. <i>Nature</i> , 2014 , 506, 225-9	50.4	357
95	Metagenomic species profiling using universal phylogenetic marker genes. <i>Nature Methods</i> , 2013 , 10, 1196-9	21.6	340
94	Transcriptome responses to combinations of stresses in Arabidopsis. <i>Plant Physiology</i> , 2013 , 161, 1783-94	94.6	334
93	POPULATION GENETICS. Genomic evidence for the Pleistocene and recent population history of Native Americans. <i>Science</i> , 2015 , 349, aab3884	33.3	317
92	Early divergent strains of <i>Yersinia pestis</i> in Eurasia 5,000 years ago. <i>Cell</i> , 2015 , 163, 571-82	56.2	294
91	Global monitoring of antimicrobial resistance based on metagenomics analyses of urban sewage. <i>Nature Communications</i> , 2019 , 10, 1124	17.4	293
90	A genomic history of Aboriginal Australia. <i>Nature</i> , 2016 , 538, 207-214	50.4	268
89	Derived immune and ancestral pigmentation alleles in a 7,000-year-old Mesolithic European. <i>Nature</i> , 2014 , 507, 225-8	50.4	235
88	Global network reorganization during dynamic adaptations of <i>Bacillus subtilis</i> metabolism. <i>Science</i> , 2012 , 335, 1099-103	33.3	215
87	The genetic prehistory of the New World Arctic. <i>Science</i> , 2014 , 345, 1255832	33.3	204

86	137 ancient human genomes from across the Eurasian steppes. <i>Nature</i> , 2018 , 557, 369-374	50.4	197
85	Terminal Pleistocene Alaskan genome reveals first founding population of Native Americans. <i>Nature</i> , 2018 , 553, 203-207	50.4	178
84	The prehistoric peopling of Southeast Asia. <i>Science</i> , 2018 , 361, 88-92	33.3	174
83	The first horse herders and the impact of early Bronze Age steppe expansions into Asia. <i>Science</i> , 2018 , 360,	33.3	162
82	Ancient genomes show social and reproductive behavior of early Upper Paleolithic foragers. <i>Science</i> , 2017 , 358, 659-662	33.3	160
81	Benchmarking of methods for genomic taxonomy. <i>Journal of Clinical Microbiology</i> , 2014 , 52, 1529-39	9.7	141
80	The transcriptionally active regions in the genome of <i>Bacillus subtilis</i> . <i>Molecular Microbiology</i> , 2009 , 73, 1043-57	4.1	139
79	The population history of northeastern Siberia since the Pleistocene. <i>Nature</i> , 2019 , 570, 182-188	50.4	137
78	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	11.9	137
77	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	11.9	135
76	Novel variation and de novo mutation rates in population-wide de novo assembled Danish trios. <i>Nature Communications</i> , 2015 , 6, 5969	17.4	119
75	Early human dispersals within the Americas. <i>Science</i> , 2018 , 362,	33.3	118
74	Ancient hepatitis B viruses from the Bronze Age to the Medieval period. <i>Nature</i> , 2018 , 557, 418-423	50.4	112
73	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, 19860-5	11.5	111
72	<i>Lactobacillus acidophilus</i> induces virus immune defence genes in murine dendritic cells by a Toll-like receptor-2-dependent mechanism. <i>Immunology</i> , 2010 , 131, 268-81	7.8	110
71	Re-theorising mobility and the formation of culture and language among the Corded Ware Culture in Europe. <i>Antiquity</i> , 2017 , 91, 334-347	1	108
70	Emergence and Spread of Basal Lineages of <i>Yersinia pestis</i> during the Neolithic Decline. <i>Cell</i> , 2019 , 176, 295-305.e10	56.2	93
69	Sequencing and de novo assembly of 150 genomes from Denmark as a population reference. <i>Nature</i> , 2017 , 548, 87-91	50.4	87

68	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, E380-92	6	86
67	A Selective Sweep on a Deleterious Mutation in CPT1A in Arctic Populations. <i>American Journal of Human Genetics</i> , 2014 , 95, 584-589	11	86
66	Physiological and Genetic Adaptations to Diving in Sea Nomads. <i>Cell</i> , 2018 , 173, 569-580.e15	56.2	82
65	snpTree--a web-server to identify and construct SNP trees from whole genome sequence data. <i>BMC Genomics</i> , 2012 , 13 Suppl 7, S6	4.5	76
64	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	5.7	68
63	Two ancient human genomes reveal Polynesian ancestry among the indigenous Botocudos of Brazil. <i>Current Biology</i> , 2014 , 24, R1035-7	6.3	62
62	Rare truncating variants in the sarcomeric protein titin associate with familial and early-onset atrial fibrillation. <i>Nature Communications</i> , 2018 , 9, 4316	17.4	58
61	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	11.5	56
60	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	4.9	51
59	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	4.5	51
58	Facilitation of pain sensitization in knee osteoarthritis and persistent post-operative pain: a cross-sectional study. <i>European Journal of Pain</i> , 2014 , 18, 1024-31	3.7	50
57	Genome-scale cold stress response regulatory networks in ten <i>Arabidopsis thaliana</i> ecotypes. <i>BMC Genomics</i> , 2013 , 14, 722	4.5	50
56	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	11.5	45
55	Biosynthesis of bioactive diterpenoids in the medicinal plant <i>Vitex agnus-castus</i> . <i>Plant Journal</i> , 2018 , 93, 943-958	6.9	44
54	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	4.6	43
53	Genome-wide ancestry patterns in Rapanui suggest pre-European admixture with Native Americans. <i>Current Biology</i> , 2014 , 24, 2518-25	6.3	39
52	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	4.5	37
51	Population genomics of the Viking world. <i>Nature</i> , 2020 , 585, 390-396	50.4	35

50	Complete genes may pass from food to human blood. <i>PLoS ONE</i> , 2013 , 8, e69805	3.7	31
49	A 5700 year-old human genome and oral microbiome from chewed birch pitch. <i>Nature Communications</i> , 2019 , 10, 5520	17.4	31
48	Bifidobacterium bifidum actively changes the gene expression profile induced by Lactobacillus acidophilus in murine dendritic cells. <i>PLoS ONE</i> , 2010 , 5, e11065	3.7	29
47	Improved metagenome binning and assembly using deep variational autoencoders. <i>Nature Biotechnology</i> , 2021 , 39, 555-560	44.5	28
46	Ancient pathogen DNA in human teeth and petrous bones. <i>Ecology and Evolution</i> , 2018 , 8, 3534-3542	2.8	23
45	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	6	23
44	Alpha proteobacterial ancestry of the [Fe-Fe]-hydrogenases in anaerobic eukaryotes. <i>Biology Direct</i> , 2016 , 11, 34	7.2	22
43	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, 301-4		21
42	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	5.3	20
41	Transcriptional landscape estimation from tiling array data using a model of signal shift and drift. <i>Bioinformatics</i> , 2009 , 25, 2341-7	7.2	20
40	Gut microbial changes of patients with psychotic and affective disorders: A systematic review. <i>Schizophrenia Research</i> , 2021 , 234, 1-10	3.6	19
39	Ancient Jomon genome sequence analysis sheds light on migration patterns of early East Asian populations. <i>Communications Biology</i> , 2020 , 3, 437	6.7	19
38	Impaired uptake and/or utilization of leucine by <i>Saccharomyces cerevisiae</i> is suppressed by the SPT15-300 allele of the TATA-binding protein gene. <i>Applied and Environmental Microbiology</i> , 2009 , 75, 6055-61	4.8	18
37	A draft genome sequence of the elusive giant squid, <i>Architeuthis dux</i> . <i>GigaScience</i> , 2020 , 9,	7.6	17
36	Hybridization capture using short PCR products enriches small genomes by capturing flanking sequences (CapFlank). <i>PLoS ONE</i> , 2014 , 9, e109101	3.7	17
35	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	7.6	16
34	Ancient nuclear genomes enable repatriation of Indigenous human remains. <i>Science Advances</i> , 2018 , 4, eaau5064	14.3	16
33	assessment of virulence factors in strains of and isolated from patients with Infective Endocarditis. <i>Journal of Medical Microbiology</i> , 2017 , 66, 1316-1323	3.2	15

32	Critical Assessment of Metagenome Interpretation: the second round of challenges.. <i>Nature Methods</i> , 2022 ,	21.6	14
31	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, 1615-25	5.3	11
30	The ubiquitin ligase RFWD3 is required for translesion DNA synthesis. <i>Molecular Cell</i> , 2021 , 81, 442-458.	9.6	11
29	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	13.4	10
28	Assembly and analysis of 100 full MHC haplotypes from the Danish population. <i>Genome Research</i> , 2017 , 27, 1597-1607	9.7	10
27	Gene expression plasticity across hosts of an invasive scale insect species. <i>PLoS ONE</i> , 2017 , 12, e0176956.	3.7	10
26	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	3.8	9
25	Binning microbial genomes using deep learning		9
24	Extension of Plant Phenotypes by the Foliar Microbiome. <i>Annual Review of Plant Biology</i> , 2021 , 72, 823-847	16.7	7
23	Jomon genome sheds light on East Asian population history		6
22	Paleogenomic insights into the red complex bacteria in Pre-Hispanic and Colonial individuals from Mexico. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020 , 375, 20190580	5.8	6
21	Genome Sequence of , Which Produces Red Colorants for the Food Industry. <i>Genome Announcements</i> , 2017 , 5,		5
20	Reads2Type: a web application for rapid microbial taxonomy identification. <i>BMC Bioinformatics</i> , 2015 , 16, 398	3.6	5
19	A paired liver biopsy and plasma proteomics study reveals circulating biomarkers for alcohol-related liver disease		5
18	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	16.6	4
17	The CGE Tool Box 2017 , 65-90		3
16	Critical Assessment of Metagenome Interpretation - the second round of challenges		3
15	Genome binning of viral entities from bulk metagenomics data.. <i>Nature Communications</i> , 2022 , 13, 965	17.4	3

14	Ancient Genomics Reveals Four Prehistoric Migration Waves into Southeast Asia		2
13	Genetic factors underlying the bidirectional relationship between autoimmune and mental disorders [findings from a Danish population-based study		2
12	Population genomics of the Viking world		2
11	Defining NASH from a Multi-Omics Systems Biology Perspective. <i>Journal of Clinical Medicine</i> , 2021 , 10,	5.1	1
10	The population history of northeastern Siberia since the Pleistocene		1
9	Genome binning of viral entities from bulk metagenomics data		1
8	<i>Streptococcus pseudopneumoniae</i> : Use of Whole-Genome Sequences To Validate Species Identification Methods. <i>Journal of Clinical Microbiology</i> , 2021 , 59,	9.7	1
7	SCAI promotes error-free repair of DNA interstrand crosslinks via the Fanconi anemia pathway.. <i>EMBO Reports</i> , 2022 , e53639	6.5	1
6	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	4.9	0
5	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	8.5	0
4	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	1	
3	Targeted metabolic engineering guided by computational analysis of single-nucleotide polymorphisms (SNPs). <i>Methods in Molecular Biology</i> , 2013 , 985, 409-28	1.4	
2	Whole-Exome Sequencing Implicates Neuronal Calcium Channel with Familial Atrial Fibrillation.. <i>Frontiers in Genetics</i> , 2022 , 13, 806429	4.5	
1	L'identification génétique de la peste sur les squelettes préhistoriques 2019 , 50-58		