Kristian G Andersen

List of Publications by Year in Descending Order

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Version: 2024-04-23

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

90 papers	10,062 citations	43 h-index	100 g-index
101 ext. papers	13,227 ext. citations	26.1 avg, IF	6.99 L-index

#	Paper	IF	Citations
90	Wastewater sequencing uncovers early, cryptic SARS-CoV-2 variant transmission. **2022**,		1
89	Inter-individual variation in objective measure of reactogenicity following COVID-19 vaccination via smartwatches and fitness bands.. *Npj Digital Medicine*, **2022**, 5, 49	15.7	0
88	Cross-Reactive Antibodies to SARS-CoV-2 and MERS-CoV in Pre-COVID-19 Blood Samples from Sierra Leoneans. *Viruses*, **2021**, 13,	6.2	3
87	A Fc engineering approach to define functional humoral correlates of immunity against Ebola virus. *Immunity*, **2021**, 54, 815-828.e5	32.3	7
86	Ebola Virus Transmission Initiated by Relapse of Systemic Ebola Virus Disease. *New England Journal of Medicine*, **2021**, 384, 1240-1247	59.2	16
85	Integration of genomic sequencing into the response to the Ebola virus outbreak in Nord Kivu, Democratic Republic of the Congo. *Nature Medicine*, **2021**, 27, 710-716	50.5	3
84	Emergence and rapid transmission of SARS-CoV-2 B.1.1.7 in the United States. *Cell*, **2021**, 184, 2587-2594.e7	56.2	132
83	Ebola vaccine-induced protection in nonhuman primates correlates with antibody specificity and Fc-mediated effects. *Science Translational Medicine*, **2021**, 13,	17.5	6
82	COVID-19 testing: One size does not fit all. *Science*, **2021**, 371, 126-127	33.3	85
81	Emergence of an early SARS-CoV-2 epidemic in the United States **2021**,		3
80	Genomic epidemiology identifies emergence and rapid transmission of SARS-CoV-2 B.1.1.7 in the United States **2021**,		44
79	Emergence of an early SARS-CoV-2 epidemic in the United States. *Cell*, **2021**, 184, 4939-4952.e15	56.2	2
78	The origins of SARS-CoV-2: A critical review. *Cell*, **2021**, 184, 4848-4856	56.2	103
77	Lassa Virus Genetics. *Current Topics in Microbiology and Immunology*, **2020**, 1	3.3	1
76	Survivors of Ebola Virus Disease Develop Polyfunctional Antibody Responses. *Journal of Infectious Diseases*, **2020**, 221, 156-161	7	19
75	Genomic surveillance reveals multiple introductions of SARS-CoV-2 into Northern California. *Science*, **2020**, 369, 582-587	33.3	162
74	The proximal origin of SARS-CoV-2. *Nature Medicine*, **2020**, 26, 450-452	50.5	2687

73	High crossreactivity of human T cell responses between Lassa virus lineages. *PLoS Pathogens*, **2020**, 16, e1008352	7.6	10
72	Reporter Assays for Ebola Virus Nucleoprotein Oligomerization, Virion-Like Particle Budding, and Minigenome Activity Reveal the Importance of Nucleoprotein Amino Acid Position 111. *Viruses*, **2020**, 12,	6.2	3
71	Two Sides of a Coin: a Zika Virus Mutation Selected in Pregnant Rhesus Macaques Promotes Fetal Infection in Mice but at a Cost of Reduced Fitness in Nonpregnant Macaques and Diminished Transmissibility by Vectors. *Journal of Virology*, **2020**, 94,	6.6	4
70	A Genomic Survey of SARS-CoV-2 Reveals Multiple Introductions into Northern California without a Predominant Lineage **2020**,		21
69	Accommodating individual travel history, global mobility, and unsampled diversity in phylogeography: a SARS-CoV-2 case study **2020**,		5
68	Epidemiological hypothesis testing using a phylogeographic and phylodynamic framework. *Nature Communications*, **2020**, 11, 5620	17.4	7
67	Accommodating individual travel history and unsampled diversity in Bayesian phylogeographic inference of SARS-CoV-2. *Nature Communications*, **2020**, 11, 5110	17.4	49
66	Identification of Common CD8 T Cell Epitopes from Lassa Fever Survivors in Nigeria and Sierra Leone. *Journal of Virology*, **2020**, 94,	6.6	6
65	High crossreactivity of human T cell responses between Lassa virus lineages **2020**, 16, e1008352		
64	High crossreactivity of human T cell responses between Lassa virus lineages **2020**, 16, e1008352		
63	High crossreactivity of human T cell responses between Lassa virus lineages **2020**, 16, e1008352		
62	High crossreactivity of human T cell responses between Lassa virus lineages **2020**, 16, e1008352		
61	Travel Surveillance and Genomics Uncover a Hidden Zika Outbreak during the Waning Epidemic. *Cell*, **2019**, 178, 1057-1071.e11	56.2	45
60	Precision epidemiology for infectious disease control. *Nature Medicine*, **2019**, 25, 206-211	50.5	52
59	Twenty years of West Nile virus spread and evolution in the Americas visualized by Nextstrain. *PLoS Pathogens*, **2019**, 15, e1008042	7.6	42
58	An amplicon-based sequencing framework for accurately measuring intrahost virus diversity using PrimalSeq and iVar. *Genome Biology*, **2019**, 20, 8	18.3	308
57	Tracking virus outbreaks in the twenty-first century. *Nature Microbiology*, **2019**, 4, 10-19	26.6	179
56	Genomic Insights into Zika Virus Emergence and Spread. *Cell*, **2018**, 172, 1160-1162	56.2	39

55	Fetal demise and failed antibody therapy during Zika virus infection of pregnant macaques. *Nature Communications*, **2018**, 9, 1624	17.4	50
54	Field validation of recombinant antigen immunoassays for diagnosis of Lassa fever. *Scientific Reports*, **2018**, 8, 5939	4.9	26
53	Common PIEZO1 Allele in African Populations Causes RBC Dehydration and Attenuates Plasmodium Infection. *Cell*, **2018**, 173, 443-455.e12	56.2	104
52	Analysis of CD8 T cell response during the 2013-2016 Ebola epidemic in West Africa. *Proceedings of the National Academy of Sciences of the United States of America*, **2018**, 115, E7578-E7586	11.5	38
51	Pandemics: spend on surveillance, not prediction. *Nature*, **2018**, 558, 180-182	50.4	77
50	A Role for Fc Function in Therapeutic Monoclonal Antibody-Mediated Protection against Ebola Virus. *Cell Host and Microbe*, **2018**, 24, 221-233.e5	23.4	121
49	Systematic Analysis of Monoclonal Antibodies against Ebola Virus GP Defines Features that Contribute to Protection. *Cell*, **2018**, 174, 938-952.e13	56.2	126
48	Genomic Analysis of Lassa Virus during an Increase in Cases in Nigeria in 2018. *New England Journal of Medicine*, **2018**, 379, 1745-1753	59.2	82
47	Virus genomes reveal factors that spread and sustained the Ebola epidemic. *Nature*, **2017**, 544, 309-315	50.4	238
46	Genomic epidemiology reveals multiple introductions of Zika virus into the United States. *Nature*, **2017**, 546, 401-405	50.4	235
45	Zika virus evolution and spread in the Americas. *Nature*, **2017**, 546, 411-415	50.4	253
44	Multiplex PCR method for MinION and Illumina sequencing of Zika and other virus genomes directly from clinical samples. *Nature Protocols*, **2017**, 12, 1261-1276	18.8	529
43	Experimental Evolution to Study Virus Emergence. *Cell*, **2017**, 169, 1-3	56.2	33
42	Ontogeny of the B- and T-cell response in a primary Zika virus infection of a dengue-naïve individual during the 2016 outbreak in Miami, FL. *PLoS Neglected Tropical Diseases*, **2017**, 11, e0006000	4.8	31
41	High-Definition Medicine. *Cell*, **2017**, 170, 828-843	56.2	114
40	Comment on "Mutation rate and genotype variation of Ebola virus from Mali case sequences". *Science*, **2016**, 353, 658	33.3	5
39	Structures of Ebola virus GP and sGP in complex with therapeutic antibodies. *Nature Microbiology*, **2016**, 1, 16128	26.6	78
38	Ebola Virus Glycoprotein with Increased Infectivity Dominated the 2013-2016 Epidemic. *Cell*, **2016**, 167, 1088-1098.e6	56.2	135

37	Direct Identification of Hundreds of Expression-Modulating Variants using a Multiplexed Reporter Assay. *Cell*, **2016**, 165, 1519-1529	56.2	228
36	Navigating the Zika panic. *F1000Research*, **2016**, 5, 1914	3.6	1
35	An Outbreak of Ebola Virus Disease in the Lassa Fever Zone. *Journal of Infectious Diseases*, **2016**, 214, S110-S121	7	25
34	Roots, Not Parachutes: Research Collaborations Combat Outbreaks. *Cell*, **2016**, 166, 5-8	56.2	35
33	Most neutralizing human monoclonal antibodies target novel epitopes requiring both Lassa virus glycoprotein subunits. *Nature Communications*, **2016**, 7, 11544	17.4	99
32	A laboratory in your pocket. *Lancet, The*, **2016**, 388, 1875	40	6
31	The evolution of Ebola virus: Insights from the 2013-2016 epidemic. *Nature*, **2016**, 538, 193-200	50.4	185
30	Ebola Virus Epidemiology, Transmission, and Evolution during Seven Months in Sierra Leone. *Cell*, **2015**, 161, 1516-26	56.2	210
29	Discovery of novel rhabdoviruses in the blood of healthy individuals from West Africa. *PLoS Neglected Tropical Diseases*, **2015**, 9, e0003631	4.8	36
28	Clinical Sequencing Uncovers Origins and Evolution of Lassa Virus. *Cell*, **2015**, 162, 738-50	56.2	176
27	The Regulatory T Cell Lineage Factor Foxp3 Regulates Gene Expression through Several Distinct Mechanisms Mostly Independent of Direct DNA Binding. *PLoS Genetics*, **2015**, 11, e1005251	6	27
26	GB virus C coinfections in west African Ebola patients. *Journal of Virology*, **2015**, 89, 2425-9	6.6	47
25	Evaluation of the potential impact of Ebola virus genomic drift on the efficacy of sequence-based candidate therapeutics. *MBio*, **2015**, 6,	7.8	54
24	Multiple circulating infections can mimic the early stages of viral hemorrhagic fevers and possible human exposure to filoviruses in Sierra Leone prior to the 2014 outbreak. *Viral Immunology*, **2015**, 28, 19-31	1.7	29
23	Clinical illness and outcomes in patients with Ebola in Sierra Leone. *New England Journal of Medicine*, **2014**, 371, 2092-100	59.2	392
22	Genomic surveillance elucidates Ebola virus origin and transmission during the 2014 outbreak. *Science*, **2014**, 345, 1369-72	33.3	847
21	Filovirus RefSeq entries: evaluation and selection of filovirus type variants, type sequences, and names. *Viruses*, **2014**, 6, 3663-82	6.2	44
20	Nomenclature- and database-compatible names for the two Ebola virus variants that emerged in Guinea and the Democratic Republic of the Congo in 2014. *Viruses*, **2014**, 6, 4760-99	6.2	70

19	Lassa fever in post-conflict sierra leone. *PLoS Neglected Tropical Diseases*, **2014**, 8, e2748	4.8	126
18	Enhanced methods for unbiased deep sequencing of Lassa and Ebola RNA viruses from clinical and biological samples. *Genome Biology*, **2014**, 15, 519	18.3	97
17	Identifying recent adaptations in large-scale genomic data. *Cell*, **2013**, 152, 703-13	56.2	259
16	Epidemiology. Emerging disease or diagnosis?. *Science*, **2012**, 338, 750-2	33.3	23
15	Activation rather than Foxp3 expression determines that TGF-nduced regulatory T cells out-compete naïve T cells in dendritic cell clustering. *European Journal of Immunology*, **2012**, 42, 1436-48	6.1	0
14	Comparative Genomics Reveals Key Gain-of-Function Events in Foxp3 during Regulatory T Cell Evolution. *Frontiers in Immunology*, **2012**, 3, 113	8.4	46
13	Foxp3 expression is required for the induction of therapeutic tissue tolerance. *Journal of Immunology*, **2012**, 189, 3947-56	5.3	31
12	Genome-wide scans provide evidence for positive selection of genes implicated in Lassa fever. *Philosophical Transactions of the Royal Society B: Biological Sciences*, **2012**, 367, 868-77	5.8	73
11	Lassa hemorrhagic fever in a late term pregnancy from northern Sierra Leone with a positive maternal outcome: case report. *Virology Journal*, **2011**, 8, 404	6.1	42
10	Correction: Lassa hemorrhagic fever in a late term pregnancy from northern Sierra Leone with a positive maternal outcome: case report. *Virology Journal*, **2011**, 8, 480	6.1	78
9	Foxp3 interacts with c-Rel to mediate NF-B repression. *PLoS ONE*, **2011**, 6, e18670	3.7	23
8	Neuropilin-1 expression on regulatory T cells enhances their interactions with dendritic cells during antigen recognition. *Immunity*, **2008**, 28, 402-13	32.3	255
7	LEF-1 negatively controls interleukin-4 expression through a proximal promoter regulatory element. *Journal of Biological Chemistry*, **2008**, 283, 22490-7	5.4	22
6	Specific immunosuppression with inducible Foxp3-transduced polyclonal T cells. *PLoS Biology*, **2008**, 6, e276	9.7	21
5	Alloantigen-enhanced accumulation of CCR5+ VeffectorVregulatory T cells in the gravid uterus. *Proceedings of the National Academy of Sciences of the United States of America*, **2007**, 104, 594-9	11.5	107
4	Outbreak.info genomic reports: scalable and dynamic surveillance of SARS-CoV-2 variants and mutations		6
3	Multiplex PCR method for MinION and Illumina sequencing of Zika and other virus genomes directly from clinical samples		6
2	Genetic characterization of the Zika virus epidemic in the US Virgin Islands		2

LIST OF PUBLICATIONS