

# Kristian G Andersen

## List of Publications by Year in descending order

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Version: 2024-02-01

84  
papers

15,180  
citations

50170

46  
h-index

62479

80  
g-index

101  
all docs

101  
docs citations

101  
times ranked

25566  
citing authors

#	ARTICLE	IF	CITATIONS
1	The proximal origin of SARS-CoV-2. <i>Nature Medicine</i> , 2020, 26, 450-452.	15.2	3,871
2	Genomic surveillance elucidates Ebola virus origin and transmission during the 2014 outbreak. <i>Science</i> , 2014, 345, 1369-1372.	6.0	1,083
3	Multiplex PCR method for MinION and Illumina sequencing of Zika and other virus genomes directly from clinical samples. <i>Nature Protocols</i> , 2017, 12, 1261-1276.	5.5	898
4	An amplicon-based sequencing framework for accurately measuring intrahost virus diversity using PrimalSeq and iVar. <i>Genome Biology</i> , 2019, 20, 8.	3.8	712
5	Clinical Illness and Outcomes in Patients with Ebola in Sierra Leone. <i>New England Journal of Medicine</i> , 2014, 371, 2092-2100.	13.9	471
6	Direct Identification of Hundreds of Expression-Modulating Variants using a Multiplexed Reporter Assay. <i>Cell</i> , 2016, 165, 1519-1529.	13.5	378
7	Virus genomes reveal factors that spread and sustained the Ebola epidemic. <i>Nature</i> , 2017, 544, 309-315.	13.7	346
8	The origins of SARS-CoV-2: A critical review. <i>Cell</i> , 2021, 184, 4848-4856.	13.5	330
9	Identifying Recent Adaptations in Large-Scale Genomic Data. <i>Cell</i> , 2013, 152, 703-713.	13.5	325
10	Zika virus evolution and spread in the Americas. <i>Nature</i> , 2017, 546, 411-415.	13.7	323
11	Tracking virus outbreaks in the twenty-first century. <i>Nature Microbiology</i> , 2019, 4, 10-19.	5.9	305
12	Genomic epidemiology reveals multiple introductions of Zika virus into the United States. <i>Nature</i> , 2017, 546, 401-405.	13.7	298
13	Neuropilin-1 Expression on Regulatory T Cells Enhances Their Interactions with Dendritic Cells during Antigen Recognition. <i>Immunity</i> , 2008, 28, 402-413.	6.6	296
14	Emergence and rapid transmission of SARS-CoV-2 B.1.1.7 in the United States. <i>Cell</i> , 2021, 184, 2587-2594.e7.	13.5	285
15	Ebola Virus Epidemiology, Transmission, and Evolution during Seven Months in Sierra Leone. <i>Cell</i> , 2015, 161, 1516-1526.	13.5	275
16	The evolution of Ebola virus: Insights from the 2013â€“2016 epidemic. <i>Nature</i> , 2016, 538, 193-200.	13.7	264
17	Genomic surveillance reveals multiple introductions of SARS-CoV-2 into Northern California. <i>Science</i> , 2020, 369, 582-587.	6.0	253
18	Clinical Sequencing Uncovers Origins and Evolution of Lassa Virus. <i>Cell</i> , 2015, 162, 738-750.	13.5	230

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19	Wastewater sequencing reveals early cryptic SARS-CoV-2 variant transmission. <i>Nature</i> , 2022, 609, 101-108.	13.7	200
20	A Role for Fc Function in Therapeutic Monoclonal Antibody-Mediated Protection against Ebola Virus. <i>Cell Host and Microbe</i> , 2018, 24, 221-233.e5.	5.1	182
21	Common PIEZO1 Allele in African Populations Causes RBC Dehydration and Attenuates Plasmodium Infection. <i>Cell</i> , 2018, 173, 443-455.e12.	13.5	176
22	Ebola Virus Glycoprotein with Increased Infectivity Dominated the 2013â€“2016 Epidemic. <i>Cell</i> , 2016, 167, 1088-1098.e6.	13.5	173
23	Systematic Analysis of Monoclonal Antibodies against Ebola Virus GP Defines Features that Contribute to Protection. <i>Cell</i> , 2018, 174, 938-952.e13.	13.5	173
24	Lassa Fever in Post-Conflict Sierra Leone. <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e2748.	1.3	172
25	High-Definition Medicine. <i>Cell</i> , 2017, 170, 828-843.	13.5	168
26	COVID-19 testing: One size does not fit all. <i>Science</i> , 2021, 371, 126-127.	6.0	159
27	Most neutralizing human monoclonal antibodies target novel epitopes requiring both Lassa virus glycoprotein subunits. <i>Nature Communications</i> , 2016, 7, 11544.	5.8	148
28	Genomic Analysis of Lassa Virus during an Increase in Cases in Nigeria in 2018. <i>New England Journal of Medicine</i> , 2018, 379, 1745-1753.	13.9	135
29	Enhanced methods for unbiased deep sequencing of Lassa and Ebola RNA viruses from clinical and biological samples. <i>Genome Biology</i> , 2014, 15, 519.	3.8	129
30	Alloantigen-enhanced accumulation of CCR5+ 'effector' regulatory T cells in the gravid uterus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 594-599.	3.3	124
31	Pandemics: spend on surveillance, not prediction. <i>Nature</i> , 2018, 558, 180-182.	13.7	120
32	Accommodating individual travel history and unsampled diversity in Bayesian phylogeographic inference of SARS-CoV-2. <i>Nature Communications</i> , 2020, 11, 5110.	5.8	118
33	Precision epidemiology for infectious disease control. <i>Nature Medicine</i> , 2019, 25, 206-211.	15.2	94
34	Genome-wide scans provide evidence for positive selection of genes implicated in Lassa fever. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2012, 367, 868-877.	1.8	93
35	Structures of Ebola virus GP and sGP in complex with therapeutic antibodies. <i>Nature Microbiology</i> , 2016, 1, 16128.	5.9	92
36	Twenty years of West Nile virus spread and evolution in the Americas visualized by Nextstrain. <i>PLoS Pathogens</i> , 2019, 15, e1008042.	2.1	87

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37	Nomenclature- and Database-Compatible Names for the Two Ebola Virus Variants that Emerged in Guinea and the Democratic Republic of the Congo in 2014. <i>Viruses</i> , 2014, 6, 4760-4799.	1.5	83
38	Fetal demise and failed antibody therapy during Zika virus infection of pregnant macaques. <i>Nature Communications</i> , 2018, 9, 1624.	5.8	68
39	Travel Surveillance and Genomics Uncover a Hidden Zika Outbreak during the Waning Epidemic. <i>Cell</i> , 2019, 178, 1057-1071.e11.	13.5	68
40	GB Virus C Coinfections in West African Ebola Patients. <i>Journal of Virology</i> , 2015, 89, 2425-2429.	1.5	65
41	Evaluation of the Potential Impact of Ebola Virus Genomic Drift on the Efficacy of Sequence-Based Candidate Therapeutics. <i>MBio</i> , 2015, 6, .	1.8	62
42	Ebola Virus Transmission Initiated by Relapse of Systemic Ebola Virus Disease. <i>New England Journal of Medicine</i> , 2021, 384, 1240-1247.	13.9	57
43	Comparative Genomics Reveals Key Gain-of-Function Events in Foxp3 during Regulatory T Cell Evolution. <i>Frontiers in Immunology</i> , 2012, 3, 113.	2.2	56
44	Discovery of Novel Rhabdoviruses in the Blood of Healthy Individuals from West Africa. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0003631.	1.3	56
45	Genomic Insights into Zika Virus Emergence and Spread. <i>Cell</i> , 2018, 172, 1160-1162.	13.5	56
46	Analysis of CD8 <sup>+</sup> T cell response during the 2013â€“2016 Ebola epidemic in West Africa. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E7578-E7586.	3.3	55
47	Lassa hemorrhagic fever in a late term pregnancy from northern sierra leone with a positive maternal outcome: case report. <i>Virology Journal</i> , 2011, 8, 404.	1.4	53
48	Filovirus RefSeq Entries: Evaluation and Selection of Filovirus Type Variants, Type Sequences, and Names. <i>Viruses</i> , 2014, 6, 3663-3682.	1.5	49
49	Roots, Not Parachutes: Research Collaborations Combat Outbreaks. <i>Cell</i> , 2016, 166, 5-8.	13.5	48
50	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. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0006000.	1.3	48
51	Foxp3 Expression Is Required for the Induction of Therapeutic Tissue Tolerance. <i>Journal of Immunology</i> , 2012, 189, 3947-3956.	0.4	43
52	Experimental Evolution to Study Virus Emergence. <i>Cell</i> , 2017, 169, 1-3.	13.5	39
53	Field validation of recombinant antigen immunoassays for diagnosis of Lassa fever. <i>Scientific Reports</i> , 2018, 8, 5939.	1.6	39
54	The Regulatory T Cell Lineage Factor Foxp3 Regulates Gene Expression through Several Distinct Mechanisms Mostly Independent of Direct DNA Binding. <i>PLoS Genetics</i> , 2015, 11, e1005251.	1.5	35

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55	Epidemiological hypothesis testing using a phylogeographic and phylodynamic framework. <i>Nature Communications</i> , 2020, 11, 5620.	5.8	35
56	Survivors of Ebola Virus Disease Develop Polyfunctional Antibody Responses. <i>Journal of Infectious Diseases</i> , 2020, 221, 156-161.	1.9	35
57	Integration of genomic sequencing into the response to the Ebola virus outbreak in Nord Kivu, Democratic Republic of the Congo. <i>Nature Medicine</i> , 2021, 27, 710-716.	15.2	35
58	An Outbreak of Ebola Virus Disease in the Lassa Fever Zone. <i>Journal of Infectious Diseases</i> , 2016, 214, S110-S121.	1.9	34
59	A Fc engineering approach to define functional humoral correlates of immunity against Ebola virus. <i>Immunity</i> , 2021, 54, 815-828.e5.	6.6	34
60	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. <i>Viral Immunology</i> , 2015, 28, 19-31.	0.6	33
61	Emergence of an early SARS-CoV-2 epidemic in the United States. <i>Cell</i> , 2021, 184, 4939-4952.e15.	13.5	31
62	Emerging Disease or Diagnosis?. <i>Science</i> , 2012, 338, 750-752.	6.0	29
63	Specific Immunosuppression with Inducible Foxp3-Transduced Polyclonal T cells. <i>PLoS Biology</i> , 2008, 6, e276.	2.6	28
64	LEF-1 Negatively Controls Interleukin-4 Expression through a Proximal Promoter Regulatory Element. <i>Journal of Biological Chemistry</i> , 2008, 283, 22490-22497.	1.6	24
65	Foxp3 Interacts with c-Rel to Mediate NF- $\kappa$ B Repression. <i>PLoS ONE</i> , 2011, 6, e18670.	1.1	24
66	Cross-Reactive Antibodies to SARS-CoV-2 and MERS-CoV in Pre-COVID-19 Blood Samples from Sierra Leoneans. <i>Viruses</i> , 2021, 13, 2325.	1.5	24
67	Inter-individual variation in objective measure of reactogenicity following COVID-19 vaccination via smartwatches and fitness bands. <i>Npj Digital Medicine</i> , 2022, 5, 49.	5.7	24
68	High crossreactivity of human T cell responses between Lassa virus lineages. <i>PLoS Pathogens</i> , 2020, 16, e1008352.	2.1	22
69	Ebola vaccine-induced protection in nonhuman primates correlates with antibody specificity and Fc-mediated effects. <i>Science Translational Medicine</i> , 2021, 13, .	5.8	22
70	Identification of Common CD8 <sup>+</sup> T Cell Epitopes from Lassa Fever Survivors in Nigeria and Sierra Leone. <i>Journal of Virology</i> , 2020, 94, .	1.5	15
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. <i>Journal of Virology</i> , 2020, 94, .	1.5	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. <i>Viruses</i> , 2020, 12, 105.	1.5	9

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73	The Origins and Future of Sentinel: An Early-Warning System for Pandemic Preemption and Response. <i>Viruses</i> , 2021, 13, 1605.	1.5	8
74	A laboratory in your pocket. <i>Lancet, The</i> , 2016, 388, 1875.	6.3	7
75	Comment on "Mutation rate and genotype variation of Ebola virus from Mali case sequences". <i>Science</i> , 2016, 353, 658-658.	6.0	6
76	Zika Virus Non-Structural Protein 1 Antigen-Capture Immunoassay. <i>Viruses</i> , 2021, 13, 1771.	1.5	5
77	Introduction and Establishment of SARS-CoV-2 Gamma Variant in New York City in Early 2021. <i>Journal of Infectious Diseases</i> , 2022, 226, 2142-2149.	1.9	5
78	Lassa Virus Genetics. <i>Current Topics in Microbiology and Immunology</i> , 2020, , 1.	0.7	4
79	Activation rather than $Foxp3$ expression determines that $TGF\beta$ -induced regulatory $T$ cells outcompete naive $T$ cells in dendritic cell clustering. <i>European Journal of Immunology</i> , 2012, 42, 1436-1448.	1.6	2
80	Navigating the Zika panic. <i>F1000Research</i> , 2016, 5, 1914.	0.8	1
81	High crossreactivity of human T cell responses between Lassa virus lineages. , 2020, 16, e1008352.		0
82	High crossreactivity of human T cell responses between Lassa virus lineages. , 2020, 16, e1008352.		0
83	High crossreactivity of human T cell responses between Lassa virus lineages. , 2020, 16, e1008352.		0
84	High crossreactivity of human T cell responses between Lassa virus lineages. , 2020, 16, e1008352.		0