

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	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
2	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
3	Wastewater sequencing reveals early cryptic SARS-CoV-2 variant transmission. <i>Nature</i> , 2022, 609, 101-108.	13.7	200
4	COVID-19 testing: One size does not fit all. <i>Science</i> , 2021, 371, 126-127.	6.0	159
5	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
6	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
7	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
8	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
9	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
10	The Origins and Future of Sentinel: An Early-Warning System for Pandemic Preemption and Response. <i>Viruses</i> , 2021, 13, 1605.	1.5	8
11	Emergence of an early SARS-CoV-2 epidemic in the United States. <i>Cell</i> , 2021, 184, 4939-4952.e15.	13.5	31
12	The origins of SARS-CoV-2: A critical review. <i>Cell</i> , 2021, 184, 4848-4856.	13.5	330
13	Zika Virus Non-Structural Protein 1 Antigen-Capture Immunoassay. <i>Viruses</i> , 2021, 13, 1771.	1.5	5
14	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
15	Epidemiological hypothesis testing using a phylogeographic and phylodynamic framework. <i>Nature Communications</i> , 2020, 11, 5620.	5.8	35
16	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
17	Lassa Virus Genetics. <i>Current Topics in Microbiology and Immunology</i> , 2020, , 1.	0.7	4
18	Survivors of Ebola Virus Disease Develop Polyfunctional Antibody Responses. <i>Journal of Infectious Diseases</i> , 2020, 221, 156-161.	1.9	35

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19	Genomic surveillance reveals multiple introductions of SARS-CoV-2 into Northern California. <i>Science</i> , 2020, 369, 582-587.	6.0	253
20	The proximal origin of SARS-CoV-2. <i>Nature Medicine</i> , 2020, 26, 450-452.	15.2	3,871
21	High crossreactivity of human T cell responses between Lassa virus lineages. <i>PLoS Pathogens</i> , 2020, 16, e1008352.	2.1	22
22	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
23	Identification of Common CD8 ⁺ T Cell Epitopes from Lassa Fever Survivors in Nigeria and Sierra Leone. <i>Journal of Virology</i> , 2020, 94, .	1.5	15
24	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
25	High crossreactivity of human T cell responses between Lassa virus lineages. , 2020, 16, e1008352.		0
26	High crossreactivity of human T cell responses between Lassa virus lineages. , 2020, 16, e1008352.		0
27	High crossreactivity of human T cell responses between Lassa virus lineages. , 2020, 16, e1008352.		0
28	High crossreactivity of human T cell responses between Lassa virus lineages. , 2020, 16, e1008352.		0
29	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
30	Travel Surveillance and Genomics Uncover a Hidden Zika Outbreak during the Waning Epidemic. <i>Cell</i> , 2019, 178, 1057-1071.e11.	13.5	68
31	Precision epidemiology for infectious disease control. <i>Nature Medicine</i> , 2019, 25, 206-211.	15.2	94
32	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
33	Tracking virus outbreaks in the twenty-first century. <i>Nature Microbiology</i> , 2019, 4, 10-19.	5.9	305
34	Genomic Insights into Zika Virus Emergence and Spread. <i>Cell</i> , 2018, 172, 1160-1162.	13.5	56
35	Fetal demise and failed antibody therapy during Zika virus infection of pregnant macaques. <i>Nature Communications</i> , 2018, 9, 1624.	5.8	68
36	Field validation of recombinant antigen immunoassays for diagnosis of Lassa fever. <i>Scientific Reports</i> , 2018, 8, 5939.	1.6	39

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37	Common PIEZO1 Allele in African Populations Causes RBC Dehydration and Attenuates Plasmodium Infection. <i>Cell</i> , 2018, 173, 443-455.e12.	13.5	176
38	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
39	Analysis of CD8 ⁺ T cell response during the 2013–2016 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
40	Pandemics: spend on surveillance, not prediction. <i>Nature</i> , 2018, 558, 180-182.	13.7	120
41	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
42	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
43	Virus genomes reveal factors that spread and sustained the Ebola epidemic. <i>Nature</i> , 2017, 544, 309-315.	13.7	346
44	Genomic epidemiology reveals multiple introductions of Zika virus into the United States. <i>Nature</i> , 2017, 546, 401-405.	13.7	298
45	Zika virus evolution and spread in the Americas. <i>Nature</i> , 2017, 546, 411-415.	13.7	323
46	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
47	Experimental Evolution to Study Virus Emergence. <i>Cell</i> , 2017, 169, 1-3.	13.5	39
48	High-Definition Medicine. <i>Cell</i> , 2017, 170, 828-843.	13.5	168
49	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
50	An Outbreak of Ebola Virus Disease in the Lassa Fever Zone. <i>Journal of Infectious Diseases</i> , 2016, 214, S110-S121.	1.9	34
51	Roots, Not Parachutes: Research Collaborations Combat Outbreaks. <i>Cell</i> , 2016, 166, 5-8.	13.5	48
52	Most neutralizing human monoclonal antibodies target novel epitopes requiring both Lassa virus glycoprotein subunits. <i>Nature Communications</i> , 2016, 7, 11544.	5.8	148
53	A laboratory in your pocket. <i>Lancet</i> , The, 2016, 388, 1875.	6.3	7
54	The evolution of Ebola virus: Insights from the 2013–2016 epidemic. <i>Nature</i> , 2016, 538, 193-200.	13.7	264

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55	Comment on "Mutation rate and genotype variation of Ebola virus from Mali case sequences" Science, 2016, 353, 658-658.	6.0	6
56	Structures of Ebola virus GP and sGP in complex with therapeutic antibodies. Nature Microbiology, 2016, 1, 16128.	5.9	92
57	Ebola Virus Glycoprotein with Increased Infectivity Dominated the 2013-2016 Epidemic. Cell, 2016, 167, 1088-1098.e6.	13.5	173
58	Direct Identification of Hundreds of Expression-Modulating Variants using a Multiplexed Reporter Assay. Cell, 2016, 165, 1519-1529.	13.5	378
59	Navigating the Zika panic. F1000Research, 2016, 5, 1914.	0.8	1
60	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.	1.5	35
61	GB Virus C Coinfections in West African Ebola Patients. Journal of Virology, 2015, 89, 2425-2429.	1.5	65
62	Evaluation of the Potential Impact of Ebola Virus Genomic Drift on the Efficacy of Sequence-Based Candidate Therapeutics. MBio, 2015, 6, .	1.8	62
63	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.	0.6	33
64	Ebola Virus Epidemiology, Transmission, and Evolution during Seven Months in Sierra Leone. Cell, 2015, 161, 1516-1526.	13.5	275
65	Discovery of Novel Rhabdoviruses in the Blood of Healthy Individuals from West Africa. PLoS Neglected Tropical Diseases, 2015, 9, e0003631.	1.3	56
66	Clinical Sequencing Uncovers Origins and Evolution of Lassa Virus. Cell, 2015, 162, 738-750.	13.5	230
67	Filovirus RefSeq Entries: Evaluation and Selection of Filovirus Type Variants, Type Sequences, and Names. Viruses, 2014, 6, 3663-3682.	1.5	49
68	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, 4760-4799.	1.5	83
69	Lassa Fever in Post-Conflict Sierra Leone. PLoS Neglected Tropical Diseases, 2014, 8, e2748.	1.3	172
70	Enhanced methods for unbiased deep sequencing of Lassa and Ebola RNA viruses from clinical and biological samples. Genome Biology, 2014, 15, 519.	3.8	129
71	Clinical Illness and Outcomes in Patients with Ebola in Sierra Leone. New England Journal of Medicine, 2014, 371, 2092-2100.	13.9	471
72	Genomic surveillance elucidates Ebola virus origin and transmission during the 2014 outbreak. Science, 2014, 345, 1369-1372.	6.0	1,083

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73	Identifying Recent Adaptations in Large-Scale Genomic Data. <i>Cell</i> , 2013, 152, 703-713.	13.5	325
74	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
75	Foxp3 Expression Is Required for the Induction of Therapeutic Tissue Tolerance. <i>Journal of Immunology</i> , 2012, 189, 3947-3956.	0.4	43
76	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
77	Emerging Disease or Diagnosis?. <i>Science</i> , 2012, 338, 750-752.	6.0	29
78	Activation rather than Foxp3 expression determines that TGF β -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
79	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
80	Foxp3 Interacts with c-Rel to Mediate NF- κ B Repression. <i>PLoS ONE</i> , 2011, 6, e18670.	1.1	24
81	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
82	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
83	Specific Immunosuppression with Inducible Foxp3-Transduced Polyclonal T cells. <i>PLoS Biology</i> , 2008, 6, e276.	2.6	28
84	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