

Astrid Gall

List of Publications by Year in Descending Order

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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.

47
papers

4,795
citations

21
h-index

50
g-index

50
ext. papers

7,188
ext. citations

10.5
avg, IF

4.51
L-index

#	Paper	IF	Citations
47	Scripting Analyses of Genomes in Ensembl Plants.. <i>Methods in Molecular Biology</i> , 2022 , 2443, 27-55	1.4	0
46	A highly virulent variant of HIV-1 circulating in the Netherlands.. <i>Science</i> , 2022 , 375, 540-545	33.3	5
45	Phylogenetic estimation of the viral fitness landscape of HIV-1 set-point viral load.. <i>Virus Evolution</i> , 2022 , 8, veac022	3.7	
44	Ensembl Genomes 2022: an expanding genome resource for non-vertebrates. <i>Nucleic Acids Research</i> , 2021 ,	20.1	12
43	Accessing Livestock Resources in Ensembl. <i>Frontiers in Genetics</i> , 2021 , 12, 650228	4.5	2
42	Ensembl 2021. <i>Nucleic Acids Research</i> , 2021 , 49, D884-D891	20.1	324
41	The Ensembl COVID-19 resource: ongoing integration of public SARS-CoV-2 data. <i>Nucleic Acids Research</i> , 2021 ,	20.1	3
40	Pervasive and non-random recombination in near full-length HIV genomes from Uganda. <i>Virus Evolution</i> , 2020 , 6, veaa004	3.7	3
39	Quantifying HIV transmission flow between high-prevalence hotspots and surrounding communities: a population-based study in Rakai, Uganda. <i>Lancet HIV,the</i> , 2020 , 7, e173-e183	7.8	26
38	Ensembl 2020. <i>Nucleic Acids Research</i> , 2020 , 48, D682-D688	20.1	645
37	Ensembl Genomes 2020-enabling non-vertebrate genomic research. <i>Nucleic Acids Research</i> , 2020 , 48, D689-D695	20.1	214
36	Inferring HIV-1 transmission networks and sources of epidemic spread in Africa with deep-sequence phylogenetic analysis. <i>Nature Communications</i> , 2019 , 10, 1411	17.4	26
35	Ensembl 2019. <i>Nucleic Acids Research</i> , 2019 , 47, D745-D751	20.1	554
34	Workup of Human Blood Samples for Deep Sequencing of HIV-1 Genomes. <i>Methods in Molecular Biology</i> , 2018 , 1746, 55-61	1.4	
33	Ensembl 2018. <i>Nucleic Acids Research</i> , 2018 , 46, D754-D761	20.1	1822
32	The evolution of subtype B HIV-1 tat in the Netherlands during 1985-2012. <i>Virus Research</i> , 2018 , 250, 51-64	6.4	4
31	Rapid HIV disease progression following superinfection in an HLA-B*27:05/B*57:01-positive transmission recipient. <i>Retrovirology</i> , 2018 , 15, 7	3.6	11

30	Easy and accurate reconstruction of whole HIV genomes from short-read sequence data with shiver. <i>Virus Evolution</i> , 2018 , 4, vey007	3.7	38
29	PHYLOSCANNER: Inferring Transmission from Within- and Between-Host Pathogen Genetic Diversity. <i>Molecular Biology and Evolution</i> , 2018 , 35, 719-733	8.3	68
28	HIV-1 full-genome phylogenetics of generalized epidemics in sub-Saharan Africa: impact of missing nucleotide characters in next-generation sequences. <i>AIDS Research and Human Retroviruses</i> , 2017 , 33, 1083-1098	1.6	13
27	Role of HIV-specific CD8 T cells in pediatric HIV cure strategies after widespread early viral escape. <i>Journal of Experimental Medicine</i> , 2017 , 214, 3239-3261	16.6	15
26	Genome-wide evolutionary dynamics of influenza B viruses on a global scale. <i>PLoS Pathogens</i> , 2017 , 13, e1006749	7.6	55
25	From clinical sample to complete genome: Comparing methods for the extraction of HIV-1 RNA for high-throughput deep sequencing. <i>Virus Research</i> , 2017 , 239, 10-16	6.4	21
24	Viral genetic variation accounts for a third of variability in HIV-1 set-point viral load in Europe. <i>PLoS Biology</i> , 2017 , 15, e2001855	9.7	21
23	Coalescent Inference Using Serially Sampled, High-Throughput Sequencing Data from Intrahost HIV Infection. <i>Genetics</i> , 2016 , 202, 1449-72	4	8
22	Viral fossils. <i>Nature Reviews Microbiology</i> , 2016 , 14, 66	22.2	
21	Bugs full of viruses. <i>Nature Reviews Microbiology</i> , 2015 , 13, 253	22.2	2
20	IVA: accurate de novo assembly of RNA virus genomes. <i>Bioinformatics</i> , 2015 , 31, 2374-6	7.2	123
19	Dynamics of immunoglobulin sequence diversity in HIV-1 infected individuals. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015 , 370,	5.8	23
18	Disease progression despite protective HLA expression in an HIV-infected transmission pair. <i>Retrovirology</i> , 2015 , 12, 55	3.6	10
17	HIV Minor Variants Detected by Next Generation Sequencing: Impact on Immune Control of HIV in the Context of HLA-B*27:05 and HLA-B*57:01. <i>AIDS Research and Human Retroviruses</i> , 2014 , 30, A180-A181	1.6	13
16	Host genetic variants and gene expression patterns associated with Epstein-Barr virus copy number in lymphoblastoid cell lines. <i>PLoS ONE</i> , 2014 , 9, e108384	3.7	12
15	Complete Genome Sequence of the WHO International Standard for HIV-1 RNA Determined by Deep Sequencing. <i>Genome Announcements</i> , 2014 , 2,		12
14	Restriction of V3 region sequence divergence in the HIV-1 envelope gene during antiretroviral treatment in a cohort of recent seroconverters. <i>Retrovirology</i> , 2013 , 10, 8	3.6	15
13	An elephantine viral problem. <i>Nature Reviews Microbiology</i> , 2013 , 11, 512	22.2	1

12	Transmission and evolution of the Middle East respiratory syndrome coronavirus in Saudi Arabia: a descriptive genomic study. <i>Lancet, The</i> , 2013 , 382, 1993-2002	40	234
11	Economic high-throughput-identification of influenza A subtypes from clinical specimens with a DNA-oligonucleotide microarray in an outbreak situation. <i>Molecular and Cellular Probes</i> , 2012 , 26, 6-10	33	5
10	Universal amplification, next-generation sequencing, and assembly of HIV-1 genomes. <i>Journal of Clinical Microbiology</i> , 2012 , 50, 3838-44	97	96
9	Evolutionary dynamics of local pandemic H1N1/2009 influenza virus lineages revealed by whole-genome analysis. <i>Journal of Virology</i> , 2012 , 86, 11-8	66	87
8	Disease-associated XMRV sequences are consistent with laboratory contamination. <i>Retrovirology</i> , 2010 , 7, 111	36	128
7	Design and validation of a microarray for detection, hemagglutinin subtyping, and pathotyping of avian influenza viruses. <i>Journal of Clinical Microbiology</i> , 2009 , 47, 327-34	97	42
6	Rapid and highly sensitive neuraminidase subtyping of avian influenza viruses by use of a diagnostic DNA microarray. <i>Journal of Clinical Microbiology</i> , 2009 , 47, 2985-8	97	29
5	Rapid haemagglutinin subtyping and pathotyping of avian influenza viruses by a DNA microarray. <i>Journal of Virological Methods</i> , 2009 , 160, 200-5	26	27
4	Universal primer set for amplification and sequencing of HA0 cleavage sites of all influenza A viruses. <i>Journal of Clinical Microbiology</i> , 2008 , 46, 2561-7	97	50
3	Easy and Accurate Reconstruction of Whole HIV Genomes from Short-Read Sequence Data		4
2	PHYLOSCANNER: Inferring Transmission from Within- and Between-Host Pathogen Genetic Diversity		2
1	Coalescent inference using serially sampled, high-throughput sequencing data from intra-host HIV infection		1