

# Astrid Gall

## List of Publications by Citations

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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	Ensembl 2018. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, D754-D761	20.1	1822
46	Ensembl 2020. <i>Nucleic Acids Research</i> , <b>2020</b> , 48, D682-D688	20.1	645
45	Ensembl 2019. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, D745-D751	20.1	554
44	Ensembl 2021. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, D884-D891	20.1	324
43	Transmission and evolution of the Middle East respiratory syndrome coronavirus in Saudi Arabia: a descriptive genomic study. <i>Lancet, The</i> , <b>2013</b> , 382, 1993-2002	4.0	234
42	Ensembl Genomes 2020-enabling non-vertebrate genomic research. <i>Nucleic Acids Research</i> , <b>2020</b> , 48, D689-D695	20.1	214
41	Disease-associated XMRV sequences are consistent with laboratory contamination. <i>Retrovirology</i> , <b>2010</b> , 7, 111	3.6	128
40	IVA: accurate de novo assembly of RNA virus genomes. <i>Bioinformatics</i> , <b>2015</b> , 31, 2374-6	7.2	123
39	Universal amplification, next-generation sequencing, and assembly of HIV-1 genomes. <i>Journal of Clinical Microbiology</i> , <b>2012</b> , 50, 3838-44	9.7	96
38	Evolutionary dynamics of local pandemic H1N1/2009 influenza virus lineages revealed by whole-genome analysis. <i>Journal of Virology</i> , <b>2012</b> , 86, 11-8	6.6	87
37	PHYLOSCANNER: Inferring Transmission from Within- and Between-Host Pathogen Genetic Diversity. <i>Molecular Biology and Evolution</i> , <b>2018</b> , 35, 719-733	8.3	68
36	Genome-wide evolutionary dynamics of influenza B viruses on a global scale. <i>PLoS Pathogens</i> , <b>2017</b> , 13, e1006749	7.6	55
35	Universal primer set for amplification and sequencing of HA0 cleavage sites of all influenza A viruses. <i>Journal of Clinical Microbiology</i> , <b>2008</b> , 46, 2561-7	9.7	50
34	Design and validation of a microarray for detection, hemagglutinin subtyping, and pathotyping of avian influenza viruses. <i>Journal of Clinical Microbiology</i> , <b>2009</b> , 47, 327-34	9.7	42
33	Easy and accurate reconstruction of whole HIV genomes from short-read sequence data with shiver. <i>Virus Evolution</i> , <b>2018</b> , 4, vey007	3.7	38
32	Rapid and highly sensitive neuraminidase subtyping of avian influenza viruses by use of a diagnostic DNA microarray. <i>Journal of Clinical Microbiology</i> , <b>2009</b> , 47, 2985-8	9.7	29
31	Rapid haemagglutinin subtyping and pathotyping of avian influenza viruses by a DNA microarray. <i>Journal of Virological Methods</i> , <b>2009</b> , 160, 200-5	2.6	27

30	Inferring HIV-1 transmission networks and sources of epidemic spread in Africa with deep-sequence phylogenetic analysis. <i>Nature Communications</i> , <b>2019</b> , 10, 1411	17.4	26
29	Quantifying HIV transmission flow between high-prevalence hotspots and surrounding communities: a population-based study in Rakai, Uganda. <i>Lancet HIV</i> , <b>2020</b> , 7, e173-e183	7.8	26
28	Dynamics of immunoglobulin sequence diversity in HIV-1 infected individuals. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , <b>2015</b> , 370,	5.8	23
27	From clinical sample to complete genome: Comparing methods for the extraction of HIV-1 RNA for high-throughput deep sequencing. <i>Virus Research</i> , <b>2017</b> , 239, 10-16	6.4	21
26	Viral genetic variation accounts for a third of variability in HIV-1 set-point viral load in Europe. <i>PLoS Biology</i> , <b>2017</b> , 15, e2001855	9.7	21
25	Role of HIV-specific CD8 T cells in pediatric HIV cure strategies after widespread early viral escape. <i>Journal of Experimental Medicine</i> , <b>2017</b> , 214, 3239-3261	16.6	15
24	Restriction of V3 region sequence divergence in the HIV-1 envelope gene during antiretroviral treatment in a cohort of recent seroconverters. <i>Retrovirology</i> , <b>2013</b> , 10, 8	3.6	15
23	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> , <b>2017</b> , 33, 1083-1098	1.6	13
22	Host genetic variants and gene expression patterns associated with Epstein-Barr virus copy number in lymphoblastoid cell lines. <i>PLoS ONE</i> , <b>2014</b> , 9, e108384	3.7	12
21	Complete Genome Sequence of the WHO International Standard for HIV-1 RNA Determined by Deep Sequencing. <i>Genome Announcements</i> , <b>2014</b> , 2,		12
20	Ensembl Genomes 2022: an expanding genome resource for non-vertebrates. <i>Nucleic Acids Research</i> , <b>2021</b> ,	20.1	12
19	Rapid HIV disease progression following superinfection in an HLA-B*27:05/B*57:01-positive transmission recipient. <i>Retrovirology</i> , <b>2018</b> , 15, 7	3.6	11
18	Disease progression despite protective HLA expression in an HIV-infected transmission pair. <i>Retrovirology</i> , <b>2015</b> , 12, 55	3.6	10
17	Coalescent Inference Using Serially Sampled, High-Throughput Sequencing Data from Intra-host HIV Infection. <i>Genetics</i> , <b>2016</b> , 202, 1449-72	4	8
16	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> , <b>2012</b> , 26, 6-10	3.3	5
15	A highly virulent variant of HIV-1 circulating in the Netherlands.. <i>Science</i> , <b>2022</b> , 375, 540-545	33.3	5
14	The evolution of subtype B HIV-1 tat in the Netherlands during 1985-2012. <i>Virus Research</i> , <b>2018</b> , 250, 51-64	6.4	4
13	Easy and Accurate Reconstruction of Whole HIV Genomes from Short-Read Sequence Data		4

12	Pervasive and non-random recombination in near full-length HIV genomes from Uganda. <i>Virus Evolution</i> , <b>2020</b> , 6, veaa004	3.7	3
11	The Ensembl COVID-19 resource: ongoing integration of public SARS-CoV-2 data. <i>Nucleic Acids Research</i> , <b>2021</b> ,	20.1	3
10	Bugs full of viruses. <i>Nature Reviews Microbiology</i> , <b>2015</b> , 13, 253	22.2	2
9	PHYLOSCANNER: Inferring Transmission from Within- and Between-Host Pathogen Genetic Diversity		2
8	Accessing Livestock Resources in Ensembl. <i>Frontiers in Genetics</i> , <b>2021</b> , 12, 650228	4.5	2
7	An elephantine viral problem. <i>Nature Reviews Microbiology</i> , <b>2013</b> , 11, 512	22.2	1
6	Coalescent inference using serially sampled, high-throughput sequencing data from intra-host HIV infection		1
5	Scripting Analyses of Genomes in Ensembl Plants.. <i>Methods in Molecular Biology</i> , <b>2022</b> , 2443, 27-55	1.4	0
4	Workup of Human Blood Samples for Deep Sequencing of HIV-1 Genomes. <i>Methods in Molecular Biology</i> , <b>2018</b> , 1746, 55-61	1.4	
3	Viral fossils. <i>Nature Reviews Microbiology</i> , <b>2016</b> , 14, 66	22.2	
2	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> , <b>2014</b> , 30, A180-A181		16
1	Phylogenetic estimation of the viral fitness landscape of HIV-1 set-point viral load.. <i>Virus Evolution</i> , <b>2022</b> , 8, veac022	3.7	