

Astrid Gall

List of Publications by Year in descending order

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Version: 2024-02-01

44
papers

8,149
citations

279701

23
h-index

276775

41
g-index

50
all docs

50
docs citations

50
times ranked

20869
citing authors

#	ARTICLE	IF	CITATIONS
1	Ensembl 2018. Nucleic Acids Research, 2018, 46, D754-D761.	6.5	2,710
2	Ensembl 2021. Nucleic Acids Research, 2021, 49, D884-D891.	6.5	1,231
3	Ensembl 2020. Nucleic Acids Research, 2020, 48, D682-D688.	6.5	1,076
4	Ensembl 2019. Nucleic Acids Research, 2019, 47, D745-D751.	6.5	879
5	Ensembl Genomes 2020â€”enabling non-vertebrate genomic research. Nucleic Acids Research, 2020, 48, D689-D695.	6.5	416
6	Transmission and evolution of the Middle East respiratory syndrome coronavirus in Saudi Arabia: a descriptive genomic study. Lancet, The, 2013, 382, 1993-2002.	6.3	282
7	IVA: accurate <i>de novo</i> assembly of RNA virus genomes. Bioinformatics, 2015, 31, 2374-2376.	1.8	179
8	Disease-associated XMRV sequences are consistent with laboratory contamination. Retrovirology, 2010, 7, 111.	0.9	141
9	Ensembl Genomes 2022: an expanding genome resource for non-vertebrates. Nucleic Acids Research, 2022, 50, D996-D1003.	6.5	141
10	PHYLOSCANNER: Inferring Transmission from Within- and Between-Host Pathogen Genetic Diversity. Molecular Biology and Evolution, 2018, 35, 719-733.	3.5	122
11	Universal Amplification, Next-Generation Sequencing, and Assembly of HIV-1 Genomes. Journal of Clinical Microbiology, 2012, 50, 3838-3844.	1.8	119
12	Evolutionary Dynamics of Local Pandemic H1N1/2009 Influenza Virus Lineages Revealed by Whole-Genome Analysis. Journal of Virology, 2012, 86, 11-18.	1.5	101
13	Genome-wide evolutionary dynamics of influenza B viruses on a global scale. PLoS Pathogens, 2017, 13, e1006749.	2.1	78
14	Easy and accurate reconstruction of whole HIV genomes from short-read sequence data with shiver. Virus Evolution, 2018, 4, vey007.	2.2	64
15	Universal Primer Set for Amplification and Sequencing of HA ₀ Cleavage Sites of All Influenza A Viruses. Journal of Clinical Microbiology, 2008, 46, 2561-2567.	1.8	59
16	Quantifying HIV transmission flow between high-prevalence hotspots and surrounding communities: a population-based study in Rakai, Uganda. Lancet HIV, the, 2020, 7, e173-e183.	2.1	59
17	Design and Validation of a Microarray for Detection, Hemagglutinin Subtyping, and Pathotyping of Avian Influenza Viruses. Journal of Clinical Microbiology, 2009, 47, 327-334.	1.8	52
18	Inferring HIV-1 transmission networks and sources of epidemic spread in Africa with deep-sequence phylogenetic analysis. Nature Communications, 2019, 10, 1411.	5.8	50

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19	A highly virulent variant of HIV-1 circulating in the Netherlands. <i>Science</i> , 2022, 375, 540-545.	6.0	39
20	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.	2.6	38
21	Dynamics of immunoglobulin sequence diversity in HIV-1 infected individuals. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20140241.	1.8	33
22	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.	4.2	31
23	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, 2985-2988.	1.8	29
24	Rapid haemagglutinin subtyping and pathotyping of avian influenza viruses by a DNA microarray. <i>Journal of Virological Methods</i> , 2009, 160, 200-205.	1.0	28
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.	1.1	23
26	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.	0.5	18
27	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.	0.9	17
28	Complete Genome Sequence of the WHO International Standard for HIV-1 RNA Determined by Deep Sequencing. <i>Genome Announcements</i> , 2014, 2, .	0.8	16
29	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.	1.1	14
30	Rapid HIV disease progression following superinfection in an HLA-B*27:05/B*57:01-positive transmission recipient. <i>Retrovirology</i> , 2018, 15, 7.	0.9	13
31	Disease progression despite protective HLA expression in an HIV-infected transmission pair. <i>Retrovirology</i> , 2015, 12, 55.	0.9	11
32	Coalescent Inference Using Serially Sampled, High-Throughput Sequencing Data from Intrahost HIV Infection. <i>Genetics</i> , 2016, 202, 1449-1472.	1.2	11
33	The Ensembl COVID-19 resource: ongoing integration of public SARS-CoV-2 data. <i>Nucleic Acids Research</i> , 2022, 50, D765-D770.	6.5	10
34	Pervasive and non-random recombination in near full-length HIV genomes from Uganda. <i>Virus Evolution</i> , 2020, 6, veaa004.	2.2	9
35	The evolution of subtype B HIV-1 tat in the Netherlands during 1985–2012. <i>Virus Research</i> , 2018, 250, 51-64.	1.1	8
36	Scripting Analyses of Genomes in Ensembl Plants. <i>Methods in Molecular Biology</i> , 2022, 2443, 27-55.	0.4	6

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37	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.	0.9	5
38	Accessing Livestock Resources in Ensembl. <i>Frontiers in Genetics</i> , 2021, 12, 650228.	1.1	3
39	Bugs full of viruses. <i>Nature Reviews Microbiology</i> , 2015, 13, 253-253.	13.6	2
40	An elephantine viral problem. <i>Nature Reviews Microbiology</i> , 2013, 11, 512-512.	13.6	1
41	Phylogenetic estimation of the viral fitness landscape of HIV-1 set-point viral load. <i>Virus Evolution</i> , 2022, 8, veac022.	2.2	1
42	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.	0.5	0
43	Viral fossils. <i>Nature Reviews Microbiology</i> , 2016, 14, 66-66.	13.6	0
44	Workup of Human Blood Samples for Deep Sequencing of HIV-1 Genomes. <i>Methods in Molecular Biology</i> , 2018, 1746, 55-61.	0.4	0