

Astrid Gall

List of Publications by Year in descending order

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Version: 2024-02-01

44
papers

8,149
citations

279798

23
h-index

276875

41
g-index

50
all docs

50
docs citations

50
times ranked

20869
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | The Ensembl COVID-19 resource: ongoing integration of public SARS-CoV-2 data. <i>Nucleic Acids Research</i> , 2022, 50, D765-D770. | 14.5 | 10 |
| 2 | Ensembl Genomes 2022: an expanding genome resource for non-vertebrates. <i>Nucleic Acids Research</i> , 2022, 50, D996-D1003. | 14.5 | 141 |
| 3 | Scripting Analyses of Genomes in Ensembl Plants. <i>Methods in Molecular Biology</i> , 2022, 2443, 27-55. | 0.9 | 6 |
| 4 | A highly virulent variant of HIV-1 circulating in the Netherlands. <i>Science</i> , 2022, 375, 540-545. | 12.6 | 39 |
| 5 | Phylogenetic estimation of the viral fitness landscape of HIV-1 set-point viral load. <i>Virus Evolution</i> , 2022, 8, veac022. | 4.9 | 1 |
| 6 | Ensembl 2021. <i>Nucleic Acids Research</i> , 2021, 49, D884-D891. | 14.5 | 1,231 |
| 7 | Accessing Livestock Resources in Ensembl. <i>Frontiers in Genetics</i> , 2021, 12, 650228. | 2.3 | 3 |
| 8 | Ensembl 2020. <i>Nucleic Acids Research</i> , 2020, 48, D682-D688. | 14.5 | 1,076 |
| 9 | Ensembl Genomes 2020â€”enabling non-vertebrate genomic research. <i>Nucleic Acids Research</i> , 2020, 48, D689-D695. | 14.5 | 416 |
| 10 | Pervasive and non-random recombination in near full-length HIV genomes from Uganda. <i>Virus Evolution</i> , 2020, 6, veaa004. | 4.9 | 9 |
| 11 | Quantifying HIV transmission flow between high-prevalence hotspots and surrounding communities: a population-based study in Rakai, Uganda. <i>Lancet HIV</i> , 2020, 7, e173-e183. | 4.7 | 59 |
| 12 | Inferring HIV-1 transmission networks and sources of epidemic spread in Africa with deep-sequence phylogenetic analysis. <i>Nature Communications</i> , 2019, 10, 1411. | 12.8 | 50 |
| 13 | Ensembl 2019. <i>Nucleic Acids Research</i> , 2019, 47, D745-D751. | 14.5 | 879 |
| 14 | Workup of Human Blood Samples for Deep Sequencing of HIV-1 Genomes. <i>Methods in Molecular Biology</i> , 2018, 1746, 55-61. | 0.9 | 0 |
| 15 | Ensembl 2018. <i>Nucleic Acids Research</i> , 2018, 46, D754-D761. | 14.5 | 2,710 |
| 16 | The evolution of subtype B HIV-1 tat in the Netherlands during 1985â€”2012. <i>Virus Research</i> , 2018, 250, 51-64. | 2.2 | 8 |
| 17 | Easy and accurate reconstruction of whole HIV genomes from short-read sequence data with shiver. <i>Virus Evolution</i> , 2018, 4, vey007. | 4.9 | 64 |
| 18 | PHYLOSCANNER: Inferring Transmission from Within- and Between-Host Pathogen Genetic Diversity. <i>Molecular Biology and Evolution</i> , 2018, 35, 719-733. | 8.9 | 122 |

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 19 | Rapid HIV disease progression following superinfection in an HLA-B*27:05/B*57:01-positive transmission recipient. <i>Retrovirology</i> , 2018, 15, 7. | 2.0 | 13 |
| 20 | 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. | 1.1 | 18 |
| 21 | 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. | 8.5 | 31 |
| 22 | 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. | 2.2 | 23 |
| 23 | Genome-wide evolutionary dynamics of influenza B viruses on a global scale. <i>PLoS Pathogens</i> , 2017, 13, e1006749. | 4.7 | 78 |
| 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. | 5.6 | 38 |
| 25 | Coalescent Inference Using Serially Sampled, High-Throughput Sequencing Data from Intra-host HIV Infection. <i>Genetics</i> , 2016, 202, 1449-1472. | 2.9 | 11 |
| 26 | Viral fossils. <i>Nature Reviews Microbiology</i> , 2016, 14, 66-66. | 28.6 | 0 |
| 27 | Dynamics of immunoglobulin sequence diversity in HIV-1 infected individuals. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20140241. | 4.0 | 33 |
| 28 | Disease progression despite protective HLA expression in an HIV-infected transmission pair. <i>Retrovirology</i> , 2015, 12, 55. | 2.0 | 11 |
| 29 | Bugs full of viruses. <i>Nature Reviews Microbiology</i> , 2015, 13, 253-253. | 28.6 | 2 |
| 30 | IVA: accurate <i>de novo</i> assembly of RNA virus genomes. <i>Bioinformatics</i> , 2015, 31, 2374-2376. | 4.1 | 179 |
| 31 | 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. | 2.5 | 14 |
| 32 | 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 |
| 33 | 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. | 1.1 | 0 |
| 34 | 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. | 2.0 | 17 |
| 35 | An elephantine viral problem. <i>Nature Reviews Microbiology</i> , 2013, 11, 512-512. | 28.6 | 1 |
| 36 | Transmission and evolution of the Middle East respiratory syndrome coronavirus in Saudi Arabia: a descriptive genomic study. <i>Lancet</i> , 2013, 382, 1993-2002. | 13.7 | 282 |

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|----|--|-----|-----------|
| 37 | Universal Amplification, Next-Generation Sequencing, and Assembly of HIV-1 Genomes. <i>Journal of Clinical Microbiology</i> , 2012, 50, 3838-3844. | 3.9 | 119 |
| 38 | Evolutionary Dynamics of Local Pandemic H1N1/2009 Influenza Virus Lineages Revealed by Whole-Genome Analysis. <i>Journal of Virology</i> , 2012, 86, 11-18. | 3.4 | 101 |
| 39 | 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. | 2.1 | 5 |
| 40 | Disease-associated XMRV sequences are consistent with laboratory contamination. <i>Retrovirology</i> , 2010, 7, 111. | 2.0 | 141 |
| 41 | Design and Validation of a Microarray for Detection, Hemagglutinin Subtyping, and Pathotyping of Avian Influenza Viruses. <i>Journal of Clinical Microbiology</i> , 2009, 47, 327-334. | 3.9 | 52 |
| 42 | 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. | 3.9 | 29 |
| 43 | Rapid haemagglutinin subtyping and pathotyping of avian influenza viruses by a DNA microarray. <i>Journal of Virological Methods</i> , 2009, 160, 200-205. | 2.1 | 28 |
| 44 | Universal Primer Set for Amplification and Sequencing of HA Cleavage Sites of All Influenza A Viruses. <i>Journal of Clinical Microbiology</i> , 2008, 46, 2561-2567. | 3.9 | 59 |