

# Francesca Di Giallonardo

## List of Publications by Year in descending order

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Version: 2024-02-01

41  
papers

1,471  
citations

304743

22  
h-index

361022

35  
g-index

45  
all docs

45  
docs citations

45  
times ranked

2988  
citing authors

#	ARTICLE	IF	CITATIONS
1	Full-length haplotype reconstruction to infer the structure of heterogeneous virus populations. <i>Nucleic Acids Research</i> , 2014, 42, e115-e115.	14.5	126
2	Virological factors that increase the transmissibility of emerging human viruses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 4170-4175.	7.1	121
3	Low-frequency drug-resistant HIV-1 and risk of virological failure to first-line NNRTI-based ART: a multicohort European caseâ€“control study using centralized ultrasensitive 454 pyrosequencing. <i>Journal of Antimicrobial Chemotherapy</i> , 2015, 70, 930-940.	3.0	102
4	RNA-Seq analysis of chikungunya virus infection and identification of granzyme A as a major promoter of arthritic inflammation. <i>PLoS Pathogens</i> , 2017, 13, e1006155.	4.7	98
5	Dinucleotide Composition in Animal RNA Viruses Is Shaped More by Virus Family than by Host Species. <i>Journal of Virology</i> , 2017, 91, .	3.4	86
6	Distinct Viral Lineages from Fish and Amphibians Reveal the Complex Evolutionary History of Hepadnaviruses. <i>Journal of Virology</i> , 2016, 90, 7920-7933.	3.4	71
7	EH3 (ABHD9): the first member of a new epoxide hydrolase family with high activity for fatty acid epoxides. <i>Journal of Lipid Research</i> , 2012, 53, 2038-2045.	4.2	64
8	Virome composition in marine fish revealed by meta-transcriptomics. <i>Virus Evolution</i> , 2021, 7, veab005.	4.9	58
9	Next-Generation Sequencing of HIV-1 RNA Genomes: Determination of Error Rates and Minimizing Artificial Recombination. <i>PLoS ONE</i> , 2013, 8, e74249.	2.5	55
10	Hidden diversity and evolution of viruses in market fish. <i>Virus Evolution</i> , 2018, 4, vey031.	4.9	54
11	Fluid Spatial Dynamics of West Nile Virus in the United States: Rapid Spread in a Permissive Host Environment. <i>Journal of Virology</i> , 2016, 90, 862-872.	3.4	42
12	Tailored enrichment strategy detects low abundant small noncoding RNAs in HIV-1 infected cells. <i>Retrovirology</i> , 2012, 9, 27.	2.0	39
13	Genomic Epidemiology of the First Wave of SARS-CoV-2 in Italy. <i>Viruses</i> , 2020, 12, 1438.	3.3	39
14	Viral biocontrol: grand experiments in disease emergence and evolution. <i>Trends in Microbiology</i> , 2015, 23, 83-90.	7.7	38
15	Exploring Hostâ€“Pathogen Interactions through Biological Control. <i>PLoS Pathogens</i> , 2015, 11, e1004865.	4.7	37
16	Emergence and Spread of SARS-CoV-2 Lineages B.1.1.7 and P.1 in Italy. <i>Viruses</i> , 2021, 13, 794.	3.3	32
17	An international multicenter study on HIV-1 drug resistance testing by 454 ultra-deep pyrosequencing. <i>Journal of Virological Methods</i> , 2014, 204, 31-37.	2.1	31
18	A Framework for Inferring Fitness Landscapes of Patient-Derived Viruses Using Quasispecies Theory. <i>Genetics</i> , 2015, 199, 191-203.	2.9	28

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19	Substitution Model Adequacy and Assessing the Reliability of Estimates of Virus Evolutionary Rates and Time Scales. <i>Molecular Biology and Evolution</i> , 2016, 33, 255-267.	8.9	28
20	Evolution of Human Respiratory Syncytial Virus (RSV) over Multiple Seasons in New South Wales, Australia. <i>Viruses</i> , 2018, 10, 476.	3.3	28
21	Contribution of APOBEC3G/F activity to the development of low-abundance drug-resistant human immunodeficiency virus type 1 variants. <i>Clinical Microbiology and Infection</i> , 2016, 22, 191-200.	6.0	27
22	Red fox viromes in urban and rural landscapes. <i>Virus Evolution</i> , 2020, 6, veaa065.	4.9	27
23	A Comprehensive Analysis of Primer IDs to Study Heterogeneous HIV-1 Populations. <i>Journal of Molecular Biology</i> , 2016, 428, 238-250.	4.2	25
24	Monocyte-derived macrophages exhibit distinct and more restricted HIV-1 integration site repertoire than CD4+ T cells. <i>Scientific Reports</i> , 2016, 6, 24157.	3.3	21
25	Multiple detection and spread of novel strains of the SARS-CoV-2 B.1.177 (B.1.177.75) lineage that test negative by a commercially available nucleocapsid gene real-time RT-PCR. <i>Emerging Microbes and Infections</i> , 2021, 10, 1148-1155.	6.5	21
26	Cross-validation to select Bayesian hierarchical models in phylogenetics. <i>BMC Evolutionary Biology</i> , 2016, 16, 115.	3.2	19
27	Sustained Wolbachia-mediated blocking of dengue virus isolates following serial passage in <i>Aedes aegypti</i> cell culture. <i>Virus Evolution</i> , 2019, 5, vez012.	4.9	19
28	Punctuated Evolution of Myxoma Virus: Rapid and Disjunct Evolution of a Recent Viral Lineage in Australia. <i>Journal of Virology</i> , 2019, 93, .	3.4	17
29	In-depth analysis of G-to-A hypermutation rate in HIV-1 env DNA induced by endogenous APOBEC3 proteins using massively parallel sequencing. <i>Journal of Virological Methods</i> , 2011, 171, 329-338.	2.1	16
30	A Follow-Up of the Multicenter Collaborative Study on HIV-1 Drug Resistance and Tropism Testing Using 454 Ultra Deep Pyrosequencing. <i>PLoS ONE</i> , 2016, 11, e0146687.	2.5	15
31	A suicide gene approach using the human pro-apoptotic protein tBid inhibits HIV-1 replication. <i>BMC Biotechnology</i> , 2011, 11, 4.	3.3	14
32	Infectious disease phylodynamics with occurrence data. <i>Methods in Ecology and Evolution</i> , 2021, 12, 1498-1507.	5.2	14
33	Complete genome of <i>Aedes aegypti</i> anphevirus in the Aag2 mosquito cell line. <i>Journal of General Virology</i> , 2018, 99, 832-836.	2.9	13
34	Reappearance of Minority K103N HIV-1 Variants after Interruption of ART Initiated during Primary HIV-1 Infection. <i>PLoS ONE</i> , 2011, 6, e21734.	2.5	9
35	HIV-1 integration sites in CD4+ T-cells during primary, chronic, and late presentation of HIV-1 infection. <i>JCI Insight</i> , 2021, 6, .	5.0	7
36	Subtype-specific differences in transmission cluster dynamics of HIV-1 B and CRF01_AE in New South Wales, Australia. <i>Journal of the International AIDS Society</i> , 2021, 24, e25655.	3.0	7

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37	HIV-1 subtype diversity, transmitted drug resistance and phylogenetics in Australia. <i>Future Virology</i> , 2018, 13, 575-584.	1.8	4
38	Limited Sustained Local Transmission of HIV-1 CRF01_AE in New South Wales, Australia. <i>Viruses</i> , 2019, 11, 482.	3.3	4
39	Increased HIV Subtype Diversity Reflecting Demographic Changes in the HIV Epidemic in New South Wales, Australia. <i>Viruses</i> , 2020, 12, 1402.	3.3	4
40	Characterisation of a new human epoxide hydrolase capable of metabolizing epoxyeicosatrienoic acids. <i>FASEB Journal</i> , 2008, 22, 479.49.	0.5	0
41	Full Genome Characterization of Respiratory Syncytial Virus Causing a Fatal Infection in an Immunocompromised Patient in Tunisia. <i>Pathogens</i> , 2022, 11, 758.	2.8	0