Rafael Sanjuan

List of Publications by Year
in descending order

106 papers	7,059 citations	94433 37 h-index	66911 78 g-index
108 all docs	108 docs citations	108 times ranked	7648 citing authors

#	Article	IF	Citations
1	Essential Topics for the Regulatory Consideration of Phages as Clinically Valuable Therapeutic Agents: A Perspective from Spain. Microorganisms, 2022, 10, 717.	3.6	12
2	Potential Influence of Helminth Molecules on COVID-19 Pathology. Trends in Parasitology, 2021, 37, 11-14.	3.3	29
3	Experimental Evolution Reveals a Genetic Basis for Membrane-Associated Virus Release. Molecular Biology and Evolution, 2021, 38, 358-367.	8.9	3
4	Genetic Diversity and Evolution of Viral Populations. , 2021, , 53-61.		43
5	Deep viral blood metagenomics reveals extensive anellovirus diversity in healthy humans. Scientific Reports, 2021, 11, 6921.	3.3	31
6	Five Challenges in the Field of Viral Diversity and Evolution. Frontiers in Virology, 2021, 1, .	1.4	6
7	The Social Life of Viruses. Annual Review of Virology, 2021, 8, 183-199.	6.7	25
8	Experimental virus evolution in cancer cell monolayers, spheroids, and tissue explants. Virus Evolution, 2021, 7, veab045.	4.9	0
9	Exploring the Diversity of the Human Blood Virome. Viruses, 2021, 13, 2322.	3.3	13
10	Cooperative nature of viral replication. Science Advances, 2020, 6, .	10.3	19
11	Isolation and Characterization of Two Klebsiella pneumoniae Phages Encoding Divergent Depolymerases. International Journal of Molecular Sciences, 2020, 21, 3160.	4.1	21
12	Fibrinogen Gamma Chain Promotes Aggregation of Vesicular Stomatitis Virus in Saliva. Viruses, 2020, 12, 282.	3.3	13
13	Isolation of Four Lytic Phages Infecting Klebsiella pneumoniae K22 Clinical Isolates from Spain. International Journal of Molecular Sciences, 2020, 21, 425.	4.1	19
14	Collective Viral Spread Mediated by Virion Aggregates Promotes the Evolution of Defective Interfering Particles. MBio, 2020, 11, .	4.1	27
15	Social Bacteriophages. Microorganisms, 2020, 8, 533.	3.6	16
16	The role of spatial structure in the evolution of viral innate immunity evasion: AÂdiffusion-reaction cellular automaton model. PLoS Computational Biology, 2020, 16, e1007656.	3.2	8
17	Social Interactions Among Bacteriophages. , 2020, , 103-119.		0
18	Why viruses sometimes disperse in groupsâ€. Virus Evolution, 2019, 5, vez014.	4.9	40

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19	Membrane-Associated Enteroviruses Undergo Intercellular Transmission as Pools of Sibling Viral Genomes. Cell Reports, 2019, 29, 714-723.e4.	6.4	28
20	The effect of genetic complementation on the fitness and diversity of viruses spreading as collective infectious units. Virus Research, 2019, 267, 41-48.	2.2	15
21	Directed Evolution of a Mycobacteriophage. Antibiotics, 2019, 8, 46.	3.7	9
22	Social evolution of innate immunity evasion in a virus. Nature Microbiology, 2019, 4, 1006-1013.	13.3	52
23	The evolution of collective infectious units in viruses. Virus Research, 2019, 265, 94-101.	2.2	31
24	High Fidelity Deep Sequencing Reveals No Effect of ATM, ATR, and DNA-PK Cellular DNA Damage Response Pathways on Adenovirus Mutation Rate. Viruses, 2019, 11, 938.	3.3	1
25	Beneficial coinfection can promote within-host viral diversity. Virus Evolution, 2018, 4, vey028.	4.9	29
26	Role of APOBEC3H in the Viral Control of HIV Elite Controller Patients. International Journal of Medical Sciences, 2018, 15, 95-100.	2.5	2
27	Collective Infection of Cells by Viral Aggregates Promotes Early Viral Proliferation and Reveals a Cellular-Level Allee Effect. Current Biology, 2018, 28, 3212-3219.e4.	3.9	53
28	Genome-scale analysis of evolutionary rate and selection in a fast-expanding Spanish cluster of HIV-1 subtype F1. Infection, Genetics and Evolution, 2018, 66, 43-47.	2.3	4
29	Collective properties of viral infectivity. Current Opinion in Virology, 2018, 33, 1-6.	5.4	44
30	Collective Infectious Units in Viruses. Trends in Microbiology, 2017, 25, 402-412.	7.7	101
31	Multi-virion infectious units arise from free viral particles in an enveloped virus. Nature Microbiology, 2017, 2, 17078.	13.3	50
32	Sociovirology: Conflict, Cooperation, and Communication among Viruses. Cell Host and Microbe, 2017, 22, 437-441.	11.0	98
33	Different rates of spontaneous mutation of chloroplastic and nuclear viroids as determined by high-fidelity ultra-deep sequencing. PLoS Pathogens, 2017, 13, e1006547.	4.7	41
34	Mechanisms of viral mutation. Cellular and Molecular Life Sciences, 2016, 73, 4433-4448.	5.4	621
35	Human norovirus hyper-mutation revealed by ultra-deep sequencing. Infection, Genetics and Evolution, 2016, 41, 233-239.	2.3	26
36	Constrained evolvability of interferon suppression in an RNA virus. Scientific Reports, 2016, 6, 24722.	3.3	8

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37	Highly heterogeneous mutation rates in the hepatitis C virus genome. Nature Microbiology, 2016, 1, 16045.	13.3	44
38	Lamivudine/Adefovir Treatment Increases the Rate of Spontaneous Mutation of Hepatitis B Virus in Patients. PLoS ONE, 2016, 11, e0163363.	2.5	2
39	Genome-Wide Estimation of the Spontaneous Mutation Rate of Human Adenovirus 5 by High-Fidelity Deep Sequencing. PLoS Pathogens, 2016, 12, e1006013.	4.7	23
40	Extremely High Mutation Rate of HIV-1 In Vivo. PLoS Biology, 2015, 13, e1002251.	5.6	291
41	Experimental evolution of an RNA virus in cells with innate immunity defects. Virus Evolution, 2015, 1, vev008.	4.9	3
42	Effect of mismatch repair on the mutation rate of bacteriophage Ï•X174. Virus Evolution, 2015, 1, vev010.	4.9	5
43	The external domains of the HIV-1 envelope are a mutational cold spot. Nature Communications, 2015, 6, 8571.	12.8	39
44	Evolution of oncolytic viruses. Current Opinion in Virology, 2015, 13, 1-5.	5.4	13
45	Single-Cell Analysis of RNA Virus Infection Identifies Multiple Genetically Diverse Viral Genomes within Single Infectious Units. Cell Host and Microbe, 2015, 18, 424-432.	11.0	75
46	Variation in RNA Virus Mutation Rates across Host Cells. PLoS Pathogens, 2014, 10, e1003855.	4.7	59
47	Experimental Evolution of an Oncolytic Vesicular Stomatitis Virus with Increased Selectivity for p53-Deficient Cells. PLoS ONE, 2014, 9, e102365.	2.5	21
48	Changes in Protein Domains outside the Catalytic Site of the Bacteriophage QÂ Replicase Reduce the Mutagenic Effect of 5-Azacytidine. Journal of Virology, 2014, 88, 10480-10487.	3.4	6
49	Variability in the mutation rates of RNA viruses. Future Virology, 2014, 9, 605-615.	1.8	6
50	Delayed Lysis Confers Resistance to the Nucleoside Analogue 5-Fluorouracil and Alleviates Mutation Accumulation in the Single-Stranded DNA Bacteriophage Ï•X174. Journal of Virology, 2014, 88, 5042-5049.	3.4	11
51	Viroids: Survivors from the RNA World?. Annual Review of Microbiology, 2014, 68, 395-414.	7.3	142
52	Correlation Between Mutation Rate and Genome Size in Riboviruses: Mutation Rate of Bacteriophage QÎ². Genetics, 2013, 195, 243-251.	2.9	55
53	Natural selection fails to optimize mutation rates for long-term adaptation on rugged fitness landscapes. , 2013, , .		21
54	Immune Activation Promotes Evolutionary Conservation of T-Cell Epitopes in HIV-1. PLoS Biology, 2013, 11, e1001523.	5.6	16

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55	SHAPE MATTERS: EFFECT OF POINT MUTATIONS ON RNA SECONDARY STRUCTURE. International Journal of Modeling, Simulation, and Scientific Computing, 2013, 16, 1250052.	1.4	5
56	From Molecular Genetics to Phylodynamics: Evolutionary Relevance of Mutation Rates Across Viruses. PLoS Pathogens, 2012, 8, e1002685.	4.7	124
57	Relationship between within-Host Fitness and Virulence in the Vesicular Stomatitis Virus: Correlation with Partial Decoupling. Journal of Virology, 2012, 86, 12228-12236.	3.4	23
58	Biomedical implications of viral mutation and evolution. Future Virology, 2012, 7, 391-402.	1.8	4
59	The Fitness Effects of Synonymous Mutations in DNA and RNA Viruses. Molecular Biology and Evolution, 2012, 29, 17-20.	8.9	101
60	Nucleoside Analogue Mutagenesis of a Single-Stranded DNA Virus: Evolution and Resistance. Journal of Virology, 2012, 86, 9640-9646.	3.4	10
61	THE DISTRIBUTION OF MUTATIONAL FITNESS EFFECTS OF PHAGE Ï†X174 ON DIFFERENT HOSTS. Evolution; International Journal of Organic Evolution, 2012, 66, 3495-3507.	2.3	26
62	Interplay between RNA Structure and Protein Evolution in HIV-1. Molecular Biology and Evolution, 2011, 28, 1333-1338.	8.9	31
63	Viral mutation and substitution: units and levels. Current Opinion in Virology, 2011, 1, 430-435.	5.4	24
64	EXPERIMENTAL EVOLUTION OF RNA VERSUS DNA VIRUSES. Evolution; International Journal of Organic Evolution, 2011, 65, 2987-2994.	2.3	18
65	Mutation rate of bacteriophage Î¦X174 modified through changes in GATC sequence context. Infection, Genetics and Evolution, 2011, 11, 1820-1822.	2.3	6
66	Distribution of Fitness Effects Caused by Single-Nucleotide Substitutions in Bacteriophage f1. Genetics, 2010, 185, 603-609.	2.9	68
67	Mutational fitness effects in RNA and single-stranded DNA viruses: common patterns revealed by site-directed mutagenesis studies. Philosophical Transactions of the Royal Society B: Biological Sciences, 2010, 365, 1975-1982.	4.0	161
68	Viral Mutation Rates. Journal of Virology, 2010, 84, 9733-9748.	3.4	1,078
69	The Fitness Effects of Random Mutations in Single-Stranded DNA and RNA Bacteriophages. PLoS Genetics, 2009, 5, e1000742.	3.5	100
70	Extremely High Mutation Rate of a Hammerhead Viroid. Science, 2009, 323, 1308-1308.	12.6	215
71	Effect of Ribavirin on the Mutation Rate and Spectrum of Hepatitis C Virus In Vivo. Journal of Virology, 2009, 83, 5760-5764.	3.4	141
72	Point Mutation Rate of Bacteriophage Î¦X174. Genetics, 2009, 183, 747-749.	2.9	37

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73	Upper-limit mutation rate estimation for a plant RNA virus. Biology Letters, 2009, 5, 394-396.	2.3	36
74	Unequal distribution of RT-PCR artifacts along the E1â€“E2 region of Hepatitis C virus. Journal of Virological Methods, 2009, 161, 136-140.	2.1	3
75	Enhanced adaptation of vesicular stomatitis virus in cells infected with vaccinia virus. Infection, Genetics and Evolution, 2008, 8, 614-620.	2.3	2
76	The effect of genetic robustness on evolvability in digital organisms. BMC Evolutionary Biology, 2008, 8, 284.	3.2	43
77	Natural Selection Fails to Optimize Mutation Rates for Long-Term Adaptation on Rugged Fitness Landscapes. PLoS Computational Biology, 2008, 4, e1000187.	3.2	80
78	Lethal Mutagenesis. , 2008, , 207-218.		9
79	A Network Model for the Correlation between Epistasis and Genomic Complexity. PLoS ONE, 2008, 3, e2663.	2.5	36
80	Virus Evolution: Insights from an Experimental Approach. Annual Review of Ecology, Evolution, and Systematics, 2007, 38, 27-52.	8.3	103
81	Selection for Robustness in Mutagenized RNA Viruses. PLoS Genetics, 2007, 3, e93.	3.5	149
82	The cost of replication fidelity in human immunodeficiency virus type 1. Proceedings of the Royal Society B: Biological Sciences, 2007, 274, 225-230.	2.6	38
83	Gibberellin Regulation of Fruit Set and Growth in Tomato. Plant Physiology, 2007, 145, 246-257.	4.8	200
84	The effect of co- and superinfection on the adaptive dynamics of vesicular stomatitis virus. Infection, Genetics and Evolution, 2007, 7, 69-73.	2.3	16
85	SELECTION PROMOTES ORGAN COMPARTMENTALIZATION IN HIV-1: EVIDENCE FROMGAGANDPOLGENES. Evolution; International Journal of Organic Evolution, 2007, 61, 272-279.	2.3	10
86	One-step site-directed mutagenesis of viroid dimeric cDNA. Journal of Virological Methods, 2007, 145, 71-75.	2.1	4
87	Mechanisms of genetic robustness in RNA viruses. EMBO Reports, 2006, 7, 168-173.	4.5	136
88	Topology testing of phylogenies using least squares methods. BMC Evolutionary Biology, 2006, 6, 105.	3.2	7
89	Quantifying antagonistic epistasis in a multifunctional RNA secondary structure of the Rous sarcoma virus. Journal of General Virology, 2006, 87, 1595-1602.	2.9	17
90	In Silico Predicted Robustness of Viroids RNA Secondary Structures. I. The Effect of Single Mutations. Molecular Biology and Evolution, 2006, 23, 1427-1436.	8.9	43

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91	In Silico Predicted Robustness of Viroid RNA Secondary Structures. II. Interaction between Mutation Pairs. Molecular Biology and Evolution, 2006, 23, 2123-2130.	8.9	28
92	Epistasis correlates to genomic complexity. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 14402-14405.	7.1	146
93	Mode of selection and experimental evolution of antiviral drugs resistance in vesicular stomatitis virus. Infection, Genetics and Evolution, 2005, 5, 55-65.	2.3	3
94	RNA viruses as complex adaptive systems. BioSystems, 2005, 81, 31-41.	2.0	19
95	Following the very initial growth of biological RNA viral clones. Journal of General Virology, 2005, 86, 435-443.	2.9	25
96	Epistasis and the Adaptability of an RNA Virus. Genetics, 2005, 170, 1001-1008.	2.9	86
97	Weighted Least-Squares Likelihood Ratio Test for Branch Testing in Phylogenies Reconstructed from Distance Measures. Systematic Biology, 2005, 54, 218-229.	5.6	22
98	The cost of replication fidelity in an RNA virus. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 10233-10237.	7.1	91
99	Adaptive Value of High Mutation Rates of RNA Viruses: Separating Causes from Consequences. Journal of Virology, 2005, 79, 11555-11558.	3.4	265
100	The contribution of epistasis to the architecture of fitness in an RNA virus. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 15376-15379.	7.1	216
101	The distribution of fitness effects caused by single-nucleotide substitutions in an RNA virus. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 8396-8401.	7.1	513
102	NATURAL SELECTION AND THE ORGAN-SPECIFIC DIFFERENTIATION OF HIV-1 V3 HYPERVARIABLE REGION. Evolution; International Journal of Organic Evolution, 2004, 58, 1185-1194.	2.3	29
103	Intraclonal variation in RNA viruses: generation, maintenance and consequences. Biological Journal of the Linnean Society, 2003, 79, 17-26.	1.6	5
104	EVOLUTION: Climb Every Mountain?. Science, 2003, 302, 2074-2075.	12.6	46
105	Tracing the Origin of the Compensasome: Evolutionary History of DEAH Helicase and MYST Acetyltransferase Gene Families. Molecular Biology and Evolution, 2001, 18, 330-343.	8.9	44
106	Transmission bottlenecks and the evolution of fitness in rapidly evolving RNA viruses. Infection, Genetics and Evolution, 2001, 1, 41-48.	2.3	45