

# Marco Vignuzzi

## List of Publications by Year in descending order

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93  
papers

12,589  
citations

53751

45  
h-index

46771

89  
g-index

108  
all docs

108  
docs citations

108  
times ranked

19245  
citing authors

#	ARTICLE	IF	CITATIONS
1	Chemical Evolution of Rhinovirus Identifies Capsid-Destabilizing Mutations Driving Low-pH-Independent Genome Uncoating. <i>Journal of Virology</i> , 2022, 96, JVI0106021.	1.5	12
2	BRD2 inhibition blocks SARS-CoV-2 infection by reducing transcription of the host cell receptor ACE2. <i>Nature Cell Biology</i> , 2022, 24, 24-34.	4.6	47
3	APOBEC3C S188I Polymorphism Enhances Context-Specific Editing of Hepatitis B Virus Genome. <i>Journal of Infectious Diseases</i> , 2022, 226, 891-895.	1.9	1
4	An alphavirus-derived self-amplifying mRNA encoding PpSP15-LmSTI1 fusion protein for the design of a vaccine against leishmaniasis. <i>Parasitology International</i> , 2022, 89, 102577.	0.6	1
5	Identification of DAXX as a restriction factor of SARS-CoV-2 through a CRISPR/Cas9 screen. <i>Nature Communications</i> , 2022, 13, 2442.	5.8	25
6	Interactions between vector competence to chikungunya virus and resistance to deltamethrin in <i>Aedes aegypti</i> laboratory lines?. <i>Medical and Veterinary Entomology</i> , 2022, 36, 486-495.	0.7	3
7	Defective viral genomes from chikungunya virus are broad-spectrum antivirals and prevent virus dissemination in mosquitoes. <i>PLoS Pathogens</i> , 2021, 17, e1009110.	2.1	23
8	Plitidepsin has potent preclinical efficacy against SARS-CoV-2 by targeting the host protein eEF1A. <i>Science</i> , 2021, 371, 926-931.	6.0	247
9	Defective viral genomes as therapeutic interfering particles against flavivirus infection in mammalian and mosquito hosts. <i>Nature Communications</i> , 2021, 12, 2290.	5.8	32
10	Host PDZ-containing proteins targeted by SARS-CoV-2. <i>FEBS Journal</i> , 2021, 288, 5148-5162.	2.2	48
11	Drug-induced phospholipidosis confounds drug repurposing for SARS-CoV-2. <i>Science</i> , 2021, 373, 541-547.	6.0	148
12	Masitinib is a broad coronavirus 3CL inhibitor that blocks replication of SARS-CoV-2. <i>Science</i> , 2021, 373, 931-936.	6.0	173
13	Intra and inter-cellular modeling of dynamic interaction between Zika virus and its naturally occurring defective viral genomes. <i>Journal of Virology</i> , 2021, 95, e0097721.	1.5	0
14	Characterising proteolysis during SARS-CoV-2 infection identifies viral cleavage sites and cellular targets with therapeutic potential. <i>Nature Communications</i> , 2021, 12, 5553.	5.8	76
15	Quantitative evaluation of PpSP15-LmSTI1 fusion gene expression following transfection with an alphavirus-derived self-amplifying mRNA and conventional DNA vaccine platforms. <i>Molecular and Cellular Probes</i> , 2021, 59, 101749.	0.9	9
16	Mathematical modelling of SARS-CoV-2 infection of human and animal host cells reveals differences in the infection rates and delays in viral particle production by infected cells. <i>Journal of Theoretical Biology</i> , 2021, 531, 110895.	0.8	5
17	Induced intra- and intermolecular template switching as a therapeutic mechanism against RNA viruses. <i>Molecular Cell</i> , 2021, 81, 4467-4480.e7.	4.5	10
18	Herpes Simplex Virus Type 1 Infection Disturbs the Mitochondrial Network, Leading to Type I Interferon Production through the RNA Polymerase III/RIG-I Pathway. <i>MBio</i> , 2021, 12, e0255721.	1.8	16

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19	Comparative host-coronavirus protein interaction networks reveal pan-viral disease mechanisms. <i>Science</i> , 2020, 370, .	6.0	508
20	RNA-seq accuracy and reproducibility for the mapping and quantification of influenza defective viral genomes. <i>Rna</i> , 2020, 26, 1905-1918.	1.6	18
21	An ultrapotent synthetic nanobody neutralizes SARS-CoV-2 by stabilizing inactive Spike. <i>Science</i> , 2020, 370, 1473-1479.	6.0	336
22	Modelling Degradation and Replication Kinetics of the Zika Virus In Vitro Infection. <i>Viruses</i> , 2020, 12, 547.	1.5	6
23	High-Throughput Fluorescence-Based Screen Identifies the Neuronal MicroRNA miR-124 as a Positive Regulator of Alphavirus Infection. <i>Journal of Virology</i> , 2020, 94, .	1.5	10
24	The Global Phosphorylation Landscape of SARS-CoV-2 Infection. <i>Cell</i> , 2020, 182, 685-712.e19.	13.5	825
25	A SARS-CoV-2 protein interaction map reveals targets for drug repurposing. <i>Nature</i> , 2020, 583, 459-468.	13.7	3,542
26	Chikungunya virus superinfection exclusion is mediated by a block in viral replication and does not rely on non-structural protein 2. <i>PLoS ONE</i> , 2020, 15, e0241592.	1.1	12
27	Usutu Virus: An Arbovirus on the Rise. <i>Viruses</i> , 2019, 11, 640.	1.5	77
28	Chikungunya Virus Vaccine Candidates with Decreased Mutational Robustness Are Attenuated <i>In Vivo</i> and Have Compromised Transmissibility. <i>Journal of Virology</i> , 2019, 93, .	1.5	27
29	Host nutritional status affects alphavirus virulence, transmission, and evolution. <i>PLoS Pathogens</i> , 2019, 15, e1008089.	2.1	34
30	Defective viral genomes are key drivers of the virusâ€™ host interaction. <i>Nature Microbiology</i> , 2019, 4, 1075-1087.	5.9	229
31	Arthritogenic Alphaviruses: A Worldwide Emerging Threat?. <i>Microorganisms</i> , 2019, 7, 133.	1.6	56
32	Long-term context-dependent genetic adaptation of the viral genetic cloud. <i>Bioinformatics</i> , 2019, 35, 1907-1915.	1.8	7
33	Dicer-2-Dependent Generation of Viral DNA from Defective Genomes of RNA Viruses Modulates Antiviral Immunity in Insects. <i>Cell Host and Microbe</i> , 2018, 23, 353-365.e8.	5.1	124
34	Seasonal Genetic Drift of Human Influenza A Virus Quasispecies Revealed by Deep Sequencing. <i>Frontiers in Microbiology</i> , 2018, 9, 2596.	1.5	27
35	Homologous recombination is an intrinsic defense against antiviral RNA interference. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E9211-E9219.	3.3	17
36	Complete Genome Sequence of a Novel Recombinant Citrus Tristeza Virus , a Resistance-Breaking Isolate from Uruguay. <i>Genome Announcements</i> , 2018, 6, .	0.8	5

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37	Chikungunya virus evolution following a large 3'UTR deletion results in host-specific molecular changes in protein-coding regions. <i>Virus Evolution</i> , 2018, 4, vey012.	2.2	24
38	Monitoring and redirecting virus evolution. <i>PLoS Pathogens</i> , 2018, 14, e1006979.	2.1	13
39	Differential Transmission of Antiviral Drug-Resistant Chikungunya Viruses by <i>Aedes</i> Mosquitoes. <i>MSphere</i> , 2018, 3, .	1.3	8
40	The defective component of viral populations. <i>Current Opinion in Virology</i> , 2018, 33, 74-80.	2.6	79
41	Taking a bite out of nutrition and arbovirus infection. <i>PLoS Neglected Tropical Diseases</i> , 2018, 12, e0006247.	1.3	31
42	Imaging of viral neuroinvasion in the zebrafish reveals that Sindbis and chikungunya viruses favour different entry routes. <i>DMM Disease Models and Mechanisms</i> , 2017, 10, 847-857.	1.2	46
43	Virus population dynamics during infection. <i>Current Opinion in Virology</i> , 2017, 23, 82-87.	2.6	65
44	Chikungunya Virus Overcomes Polyamine Depletion by Mutation of nsP1 and the Opal Stop Codon To Confer Enhanced Replication and Fitness. <i>Journal of Virology</i> , 2017, 91, .	1.5	35
45	Pathogenic Events in a Nonhuman Primate Model of Oral Poliovirus Infection Leading to Paralytic Poliomyelitis. <i>Journal of Virology</i> , 2017, 91, .	1.5	34
46	Understanding the Mechanism of the Broad-Spectrum Antiviral Activity of Favipiravir (T-705): Key Role of the F1 Motif of the Viral Polymerase. <i>Journal of Virology</i> , 2017, 91, .	1.5	62
47	Curcumin inhibits Zika and chikungunya virus infection by inhibiting cell binding. <i>Antiviral Research</i> , 2017, 142, 148-157.	1.9	246
48	The Bridges and Blockades to Evolutionary Convergence on the Road to Predicting Chikungunya Virus Evolution. <i>Annual Review of Virology</i> , 2017, 4, 181-200.	3.0	15
49	Drivers of Dengue Intrahost Evolution. <i>Cell Host and Microbe</i> , 2017, 22, 260-261.	5.1	0
50	Polyamines and Their Role in Virus Infection. <i>Microbiology and Molecular Biology Reviews</i> , 2017, 81, .	2.9	82
51	Uptake and metabolism of arginine impact Plasmodium development in the liver. <i>Scientific Reports</i> , 2017, 7, 4072.	1.6	29
52	Attenuation of RNA viruses by redirecting their evolution in sequence space. <i>Nature Microbiology</i> , 2017, 2, 17088.	5.9	77
53	Cell-Based High-Throughput Screening Assay Identifies 2',2'-Difluoro-2'-deoxycytidine Gemcitabine as a Potential Antipoliovirus Agent. <i>ACS Infectious Diseases</i> , 2017, 3, 45-53.	1.8	17
54	Design of a Genetically Stable High Fidelity Coxsackievirus B3 Polymerase That Attenuates Virus Growth in Vivo. <i>Journal of Biological Chemistry</i> , 2016, 291, 13999-14011.	1.6	41

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55	Virus-derived DNA drives mosquito vector tolerance to arboviral infection. <i>Nature Communications</i> , 2016, 7, 12410.	5.8	199
56	Inhibition of Polyamine Biosynthesis Is a Broad-Spectrum Strategy against RNA Viruses. <i>Journal of Virology</i> , 2016, 90, 9683-9692.	1.5	71
57	Interferon-Induced Spermidine-Spermine Acetyltransferase and Polyamine Depletion Restrict Zika and Chikungunya Viruses. <i>Cell Host and Microbe</i> , 2016, 20, 167-177.	5.1	105
58	Homology-Based Identification of a Mutation in the Coronavirus RNA-Dependent RNA Polymerase That Confers Resistance to Multiple Mutagens. <i>Journal of Virology</i> , 2016, 90, 7415-7428.	1.5	137
59	Increasing Clinical Severity during a Dengue Virus Type 3 Cuban Epidemic: Deep Sequencing of Evolving Viral Populations. <i>Journal of Virology</i> , 2016, 90, 4320-4333.	1.5	32
60	Low-Fidelity Polymerases of Alphaviruses Recombine at Higher Rates To Overproduce Defective Interfering Particles. <i>Journal of Virology</i> , 2016, 90, 2446-2454.	1.5	57
61	Whole-Genome Sequencing Analysis from the Chikungunya Virus Caribbean Outbreak Reveals Novel Evolutionary Genomic Elements. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004402.	1.3	96
62	Viral Polymerase-Helicase Complexes Regulate Replication Fidelity To Overcome Intracellular Nucleotide Depletion. <i>Journal of Virology</i> , 2015, 89, 11233-11244.	1.5	36
63	Group Selection and Contribution of Minority Variants during Virus Adaptation Determines Virus Fitness and Phenotype. <i>PLoS Pathogens</i> , 2015, 11, e1004838.	2.1	106
64	Mutations in Coronavirus Nonstructural Protein 10 Decrease Virus Replication Fidelity. <i>Journal of Virology</i> , 2015, 89, 6418-6426.	1.5	56
65	Deep sequencing analysis of viral infection and evolution allows rapid and detailed characterization of viral mutant spectrum. <i>Bioinformatics</i> , 2015, 31, 2141-2150.	1.8	62
66	Fidelity Variants and RNA Quasispecies. <i>Current Topics in Microbiology and Immunology</i> , 2015, 392, 303-322.	0.7	54
67	Structure-Function Relationships Underlying the Replication Fidelity of Viral RNA-Dependent RNA Polymerases. <i>Journal of Virology</i> , 2015, 89, 275-286.	1.5	95
68	Phylogenetic and Genome-Wide Deep-Sequencing Analyses of Canine Parvovirus Reveal Co-Infection with Field Variants and Emergence of a Recent Recombinant Strain. <i>PLoS ONE</i> , 2014, 9, e111779.	1.1	73
69	Alphavirus Mutator Variants Present Host-Specific Defects and Attenuation in Mammalian and Insect Models. <i>PLoS Pathogens</i> , 2014, 10, e1003877.	2.1	94
70	RNA Virus Population Diversity, an Optimum for Maximal Fitness and Virulence. <i>Journal of Biological Chemistry</i> , 2014, 289, 29531-29544.	1.6	94
71	Emergence and Transmission of Arbovirus Evolutionary Intermediates with Epidemic Potential. <i>Cell Host and Microbe</i> , 2014, 15, 706-716.	5.1	107
72	Ribavirin: a drug active against many viruses with multiple effects on virus replication and propagation. Molecular basis of ribavirin resistance. <i>Current Opinion in Virology</i> , 2014, 8, 10-15.	2.6	102

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73	Coronaviruses Lacking Exoribonuclease Activity Are Susceptible to Lethal Mutagenesis: Evidence for Proofreading and Potential Therapeutics. <i>PLoS Pathogens</i> , 2013, 9, e1003565.	2.1	392
74	Mutational Robustness of an RNA Virus Influences Sensitivity to Lethal Mutagenesis. <i>Journal of Virology</i> , 2012, 86, 2869-2873.	1.5	55
75	Coxsackievirus B3 mutator strains are attenuated in vivo. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E2294-303.	3.3	129
76	Biomedical implications of viral mutation and evolution. <i>Future Virology</i> , 2012, 7, 391-402.	0.9	4
77	Closing the gap: the challenges in converging theoretical, computational, experimental and real-life studies in virus evolution. <i>Current Opinion in Virology</i> , 2012, 2, 515-518.	2.6	15
78	Viruses: foe, freeloader or friend?. <i>Current Opinion in Microbiology</i> , 2012, 15, 486-489.	2.3	1
79	RNA virus population diversity: implications for inter-species transmission. <i>Current Opinion in Virology</i> , 2011, 1, 643-648.	2.6	44
80	Isolation of Fidelity Variants of RNA Viruses and Characterization of Virus Mutation Frequency. <i>Journal of Visualized Experiments</i> , 2011, , .	0.2	33
81	Host Alternation of Chikungunya Virus Increases Fitness while Restricting Population Diversity and Adaptability to Novel Selective Pressures. <i>Journal of Virology</i> , 2011, 85, 1025-1035.	1.5	152
82	Arbovirus high fidelity variant loses fitness in mosquitoes and mice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 16038-16043.	3.3	222
83	Fidelity Variants of RNA Dependent RNA Polymerases Uncover an Indirect, Mutagenic Activity of Amiloride Compounds. <i>PLoS Pathogens</i> , 2010, 6, e1001163.	2.1	75
84	Delivery of mengovirus-derived RNA replicons into tumoural liver enhances the anti-tumour efficacy of a peripheral peptide-based vaccine. <i>Cancer Immunology, Immunotherapy</i> , 2008, 57, 1161-1171.	2.0	5
85	Engineering attenuated virus vaccines by controlling replication fidelity. <i>Nature Medicine</i> , 2008, 14, 154-161.	15.2	247
86	Harnessing Endogenous miRNAs to Control Virus Tissue Tropism as a Strategy for Developing Attenuated Virus Vaccines. <i>Cell Host and Microbe</i> , 2008, 4, 239-248.	5.1	147
87	Evolutionary constraints on chaperone-mediated folding provide an antiviral approach refractory to development of drug resistance. <i>Genes and Development</i> , 2007, 21, 195-205.	2.7	246
88	Quasispecies diversity determines pathogenesis through cooperative interactions in a viral population. <i>Nature</i> , 2006, 439, 344-348.	13.7	982
89	Remote Site Control of an Active Site Fidelity Checkpoint in a Viral RNA-dependent RNAPolymerase. <i>Journal of Biological Chemistry</i> , 2005, 280, 25706-25716.	1.6	150
90	Ribavirin and lethal mutagenesis of poliovirus: molecular mechanisms, resistance and biological implications. <i>Virus Research</i> , 2005, 107, 173-181.	1.1	132

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91	Expression of a Membrane-Anchored Glycoprotein, the Influenza Virus Hemagglutinin, by Dicistronic Replicons Derived from the Poliovirus Genome. <i>Journal of Virology</i> , 2002, 76, 5285-5290.	1.5	3
92	Naked RNA immunization with replicons derived from poliovirus and Semliki Forest virus genomes for the generation of a cytotoxic T cell response against the influenza A virus nucleoprotein. <i>Journal of General Virology</i> , 2001, 82, 1737-1747.	1.3	37
93	Biological Implications of Picornavirus Fidelity Mutants. , 0, , 213-227.		3