

# Celia Belen Perales Viejo

## List of Publications by Year in descending order

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89  
papers

3,683  
citations

147801

31  
h-index

149698

56  
g-index

100  
all docs

100  
docs citations

100  
times ranked

3960  
citing authors

#	ARTICLE	IF	CITATIONS
1	Viral Quasispecies Evolution. <i>Microbiology and Molecular Biology Reviews</i> , 2012, 76, 159-216.	6.6	811
2	Viral quasispecies. <i>PLoS Genetics</i> , 2019, 15, e1008271.	3.5	220
3	HIV-1 protease cleaves eukaryotic initiation factor 4G and inhibits cap-dependent translation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 12966-12971.	7.1	115
4	Viral quasispecies complexity measures. <i>Virology</i> , 2016, 493, 227-237.	2.4	109
5	Viral Genome Segmentation Can Result from a Trade-Off between Genetic Content and Particle Stability. <i>PLoS Genetics</i> , 2011, 7, e1001344.	3.5	95
6	Insights into RNA Virus Mutant Spectrum and Lethal Mutagenesis Events: Replicative Interference and Complementation by Multiple Point Mutants. <i>Journal of Molecular Biology</i> , 2007, 369, 985-1000.	4.2	93
7	Response of Hepatitis C Virus to Long-Term Passage in the Presence of Alpha Interferon: Multiple Mutations and a Common Phenotype. <i>Journal of Virology</i> , 2013, 87, 7593-7607.	3.4	88
8	A Multi-Step Process of Viral Adaptation to a Mutagenic Nucleoside Analogue by Modulation of Transition Types Leads to Extinction-Escape. <i>PLoS Pathogens</i> , 2010, 6, e1001072.	4.7	83
9	Increased Replicative Fitness Can Lead to Decreased Drug Sensitivity of Hepatitis C Virus. <i>Journal of Virology</i> , 2014, 88, 12098-12111.	3.4	74
10	High-Resolution Hepatitis C Virus Subtyping Using NS5B Deep Sequencing and Phylogeny, an Alternative to Current Methods. <i>Journal of Clinical Microbiology</i> , 2015, 53, 219-226.	3.9	74
11	Potential Benefits of Sequential Inhibitor-Mutagen Treatments of RNA Virus Infections. <i>PLoS Pathogens</i> , 2009, 5, e1000658.	4.7	68
12	Mutation Rates, Mutation Frequencies, and Proofreading-Repair Activities in RNA Virus Genetics. <i>Viruses</i> , 2021, 13, 1882.	3.3	66
13	Quasispecies as a matter of fact: Viruses and beyond. <i>Virus Research</i> , 2011, 162, 203-215.	2.2	65
14	Lethal Mutagenesis of Hepatitis C Virus Induced by Favipiravir. <i>PLoS ONE</i> , 2016, 11, e0164691.	2.5	63
15	Extinction of Hepatitis C Virus by Ribavirin in Hepatoma Cells Involves Lethal Mutagenesis. <i>PLoS ONE</i> , 2013, 8, e71039.	2.5	60
16	Extracellular vesicles: Vehicles of en bloc viral transmission. <i>Virus Research</i> , 2019, 265, 143-149.	2.2	58
17	Ultra-Deep Pyrosequencing (UDPS) Data Treatment to Study Amplicon HCV Minor Variants. <i>PLoS ONE</i> , 2013, 8, e83361.	2.5	54
18	Quasispecies and virus. <i>European Biophysics Journal</i> , 2018, 47, 443-457.	2.2	51

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19	Cleavage of eIF4G by HIV-1 protease: effects on translation. <i>FEBS Letters</i> , 2003, 533, 89-94.	2.8	49
20	The impact of quasispecies dynamics on the use of therapeutics. <i>Trends in Microbiology</i> , 2012, 20, 595-603.	7.7	48
21	Enhancement of DNA, cDNA synthesis and fidelity at high temperatures by a dimeric single-stranded DNA-binding protein. <i>Nucleic Acids Research</i> , 2003, 31, 6473-6480.	14.5	45
22	Resistance of Hepatitis C Virus to Inhibitors: Complexity and Clinical Implications. <i>Viruses</i> , 2015, 7, 5746-5766.	3.3	44
23	Barrier-Independent, Fitness-Associated Differences in Sofosbuvir Efficacy against Hepatitis C Virus. <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 3786-3793.	3.2	42
24	Internal Disequilibria and Phenotypic Diversification during Replication of Hepatitis C Virus in a Noncoevolving Cellular Environment. <i>Journal of Virology</i> , 2017, 91, .	3.4	42
25	Molecular Characterization of a Dual Inhibitory and Mutagenic Activity of 5-Fluorouridine Triphosphate on Viral RNA Synthesis. Implications for Lethal Mutagenesis. <i>Journal of Molecular Biology</i> , 2008, 382, 652-666.	4.2	41
26	Antiviral Strategies Based on Lethal Mutagenesis and Error Threshold. <i>Current Topics in Microbiology and Immunology</i> , 2015, 392, 323-339.	1.1	41
27	Deep-sequencing reveals broad subtype-specific HCV resistance mutations associated with treatment failure. <i>Antiviral Research</i> , 2020, 174, 104694.	4.1	39
28	Tempo and mode of inhibitor-“mutagen antiviral therapies: A multidisciplinary approach. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 16008-16013.	7.1	38
29	Counteracting Quasispecies Adaptability: Extinction of a Ribavirin-Resistant Virus Mutant by an Alternative Mutagenic Treatment. <i>PLoS ONE</i> , 2009, 4, e5554.	2.5	36
30	Viral fitness: history and relevance for viral pathogenesis and antiviral interventions. <i>Pathogens and Disease</i> , 2019, 77, .	2.0	36
31	Historical Perspective on the Discovery of the Quasispecies Concept. <i>Annual Review of Virology</i> , 2021, 8, 51-72.	6.7	35
32	Regulation of HIV-1 env mRNA translation by Rev protein. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2005, 1743, 169-175.	4.1	34
33	Favipiravir can evoke lethal mutagenesis and extinction of foot-and-mouth disease virus. <i>Virus Research</i> , 2017, 233, 105-112.	2.2	32
34	From Quasispecies Theory to Viral Quasispecies: How Complexity has Permeated Virology. <i>Mathematical Modelling of Natural Phenomena</i> , 2012, 7, 105-122.	2.4	30
35	Resistance of high fitness hepatitis C virus to lethal mutagenesis. <i>Virology</i> , 2018, 523, 100-109.	2.4	30
36	The increasing impact of lethal mutagenesis of viruses. <i>Future Medicinal Chemistry</i> , 2019, 11, 1645-1657.	2.3	30

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37	Biological Effect of Muller's Ratchet: Distant Capsid Site Can Affect Picornavirus Protein Processing. <i>Journal of Virology</i> , 2009, 83, 6748-6756.	3.4	29
38	Lethal mutagenesis of viruses. <i>Current Opinion in Virology</i> , 2011, 1, 419-422.	5.4	29
39	Exploration of sequence space as the basis of viral RNA genome segmentation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 6678-6683.	7.1	29
40	Pipeline for specific subtype amplification and drug resistance detection in hepatitis C virus. <i>BMC Infectious Diseases</i> , 2018, 18, 446.	2.9	29
41	Monitoring Sequence Space as a Test for the Target of Selection in Viruses. <i>Journal of Molecular Biology</i> , 2005, 345, 451-459.	4.2	28
42	Viral Quasispecies: Dynamics, Interactions, and Pathogenesis**Dedicated to Manfred Eigen on the occasion of his 80th birthday, for the insights that his pioneer studies have represented for virology.. , 2008, , 87-118.		27
43	Mutant spectra in virus behavior. <i>Future Virology</i> , 2010, 5, 679-698.	1.8	26
44	Lethal Mutagenesis of Foot-and-Mouth Disease Virus Involves Shifts in Sequence Space. <i>Journal of Virology</i> , 2011, 85, 12227-12240.	3.4	26
45	Clonality and intracellular polyploidy in virus evolution and pathogenesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 8887-8892.	7.1	26
46	Baseline hepatitis C virus resistance-associated substitutions present at frequencies lower than 15% may be clinically significant. <i>Infection and Drug Resistance</i> , 2018, Volume 11, 2207-2210.	2.7	26
47	Persistence of foot-and-mouth disease virus in cell culture revisited: implications for contingency in evolution. <i>Journal of General Virology</i> , 2008, 89, 232-244.	2.9	25
48	Influence of Mutagenesis and Viral Load on the Sustained Low-Level Replication of an RNA Virus. <i>Journal of Molecular Biology</i> , 2011, 407, 60-78.	4.2	25
49	Deep sequencing in the management of hepatitis virus infections. <i>Virus Research</i> , 2017, 239, 115-125.	2.2	23
50	Molecular basis of interferon resistance in hepatitis C virus. <i>Current Opinion in Virology</i> , 2014, 8, 38-44.	5.4	22
51	Multifunctionality of a Picornavirus Polymerase Domain: Nuclear Localization Signal and Nucleotide Recognition. <i>Journal of Virology</i> , 2015, 89, 6848-6859.	3.4	22
52	Broad and Dynamic Diversification of Infectious Hepatitis C Virus in a Cell Culture Environment. <i>Journal of Virology</i> , 2020, 94, .	3.4	20
53	A new implication of quasispecies dynamics: Broad virus diversification in absence of external perturbations. <i>Infection, Genetics and Evolution</i> , 2020, 82, 104278.	2.3	20
54	Deletion Mutants of VPg Reveal New Cytopathology Determinants in a Picornavirus. <i>PLoS ONE</i> , 2010, 5, e10735.	2.5	19

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55	Hepatitis C virus-mediated Aurora B kinase inhibition modulates inflammatory pathway and viral infectivity. <i>Journal of Hepatology</i> , 2015, 63, 312-319.	3.7	17
56	Microarray-based identification of antigenic variants of foot-and-mouth disease virus: a bioinformatics quality assessment. <i>BMC Genomics</i> , 2006, 7, 117.	2.8	16
57	SARS-CoV-2 Mutant Spectra at Different Depth Levels Reveal an Overwhelming Abundance of Low Frequency Mutations. <i>Pathogens</i> , 2022, 11, 662.	2.8	16
58	Amino Acid Substitutions Associated with Treatment Failure for Hepatitis C Virus Infection. <i>Journal of Clinical Microbiology</i> , 2020, 58, .	3.9	15
59	Quasispecies dynamics and clinical significance of hepatitis C virus (HCV) antiviral resistance. <i>International Journal of Antimicrobial Agents</i> , 2020, 56, 105562.	2.5	14
60	Viral Fitness Can Influence the Repertoire of Virus Variants Selected by Antibodies. <i>Journal of Molecular Biology</i> , 2006, 362, 44-54.	4.2	13
61	Molecular and Functional Bases of Selection against a Mutation Bias in an RNA Virus. <i>Genome Biology and Evolution</i> , 2017, 9, 1212-1228.	2.5	13
62	High SARS-CoV-2 viral load is associated with a worse clinical outcome of COVID-19 disease. <i>Access Microbiology</i> , 2021, 3, 000259.	0.5	13
63	In vitro Selection of High Affinity DNA and RNA Aptamers that Detect Hepatitis C Virus Core Protein of Genotypes 1 to 4 and Inhibit Virus Production in Cell Culture. <i>Journal of Molecular Biology</i> , 2022, 434, 167501.	4.2	13
64	Dissimilar Conservation Pattern in Hepatitis C Virus Mutant Spectra, Consensus Sequences, and Data Banks. <i>Journal of Clinical Medicine</i> , 2020, 9, 3450.	2.4	12
65	Identification of host and viral factors involved in a dissimilar resolution of a hepatitis C virus infection. <i>Liver International</i> , 2014, 34, 896-906.	3.9	10
66	Hepatitis C virus early kinetics and resistance-associated substitution dynamics during antiviral therapy with direct-acting antivirals. <i>Journal of Viral Hepatitis</i> , 2018, 25, 1515-1525.	2.0	10
67	The archaeology of coding RNA. <i>Annals of the New York Academy of Sciences</i> , 2019, 1447, 119-134.	3.8	10
68	Synergistic Lethal Mutagenesis of Hepatitis C Virus. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	3.2	10
69	SARS-CoV-2 Point Mutation and Deletion Spectra and Their Association with Different Disease Outcomes. <i>Microbiology Spectrum</i> , 2022, 10, e0022122.	3.0	10
70	Vaccine breakthrough infections with SARS-CoV-2 Alpha mirror mutations in Delta Plus, Iota, and Omicron. <i>Journal of Clinical Investigation</i> , 2022, 132, .	8.2	10
71	Rare haplotype load as marker for lethal mutagenesis. <i>PLoS ONE</i> , 2018, 13, e0204877.	2.5	8
72	The Time for COVID-19 Vaccination. <i>Journal of Virology</i> , 2021, 95, .	3.4	8

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73	A Two-Level, Intramutant Spectrum Haplotype Profile of Hepatitis C Virus Revealed by Self-Organized Maps. <i>Microbiology Spectrum</i> , 2021, 9, e0145921.	3.0	8
74	Hepatitis C Virus RNA-Dependent RNA Polymerase Interacts with the Akt/PKB Kinase and Induces Its Subcellular Relocalization. <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 3540-3550.	3.2	7
75	Population Disequilibrium as Promoter of Adaptive Explorations in Hepatitis C Virus. <i>Viruses</i> , 2021, 13, 616.	3.3	7
76	An Efficient Microarray-Based Genotyping Platform for the Identification of Drug-Resistance Mutations in Majority and Minority Subpopulations of HIV-1 Quasispecies. <i>PLoS ONE</i> , 2016, 11, e0166902.	2.5	7
77	Partial restoration of immune response in Hepatitis C patients after viral clearance by direct-acting antiviral therapy. <i>PLoS ONE</i> , 2021, 16, e0254243.	2.5	6
78	New hepatitis C virus genotype 1 subtype naturally harbouring resistance-associated mutations to NS5A inhibitors. <i>Journal of General Virology</i> , 2018, 99, 97-102.	2.9	6
79	Contribution of a Multifunctional Polymerase Region of Foot-and-Mouth Disease Virus to Lethal Mutagenesis. <i>Journal of Virology</i> , 2018, 92, .	3.4	5
80	New real-time-PCR method to identify single point mutations in hepatitis C virus. <i>World Journal of Gastroenterology</i> , 2016, 22, 9604.	3.3	5
81	Guanosine inhibits hepatitis C virus replication and increases indel frequencies, associated with altered intracellular nucleotide pools. <i>PLoS Pathogens</i> , 2022, 18, e1010210.	4.7	3
82	Akt Phosphorylation of Hepatitis C Virus NS5B Regulates Polymerase Activity and Hepatitis C Virus Infection. <i>Frontiers in Microbiology</i> , 2021, 12, 754664.	3.5	2
83	Quasispecies and Drug Resistance. , 2017, , 123-147.		2
84	Viral Quasispecies and Lethal Mutagenesis. <i>European Review</i> , 2016, 24, 39-48.	0.7	1
85	Distance effects during polyprotein processing in the complementation between defective FMDV RNAs. <i>Journal of General Virology</i> , 2016, 97, 1575-1583.	2.9	1
86	Quasispecies Dynamics Taught by Natural and Experimental Evolution of Foot-and-mouth Disease Virus. , 2017, , 147-170.		1
87	Quasispecies and Drug Resistance. , 2014, , 1-22.		0
88	Mutation, Quasispecies, and Lethal Mutagenesis. , 0, , 195-211.		0
89	Study of Quasispecies Complexity and Liver Damage Progression after Liver Transplantation in Hepatitis C Virus Infected Patients. <i>Genes</i> , 2021, 12, 1731.	2.4	0