

Cecilio Lopez-Galindez

List of Publications by Year in descending order

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91
papers

3,591
citations

147801

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93
docs citations

93
times ranked

2981
citing authors

#	ARTICLE	IF	CITATIONS
1	Viral and Cellular Factors Leading to the Loss of CD4 Homeostasis in HIV-1 Viremic Nonprogressors. <i>Journal of Virology</i> , 2022, 96, JV0149921.	3.4	0
2	The Characteristics of the HIV-1 Env Glycoprotein Are Linked With Viral Pathogenesis. <i>Frontiers in Microbiology</i> , 2022, 13, 763039.	3.5	7
3	Immunescape of HIV-1 in Env-EL9 CD8 ⁺ T cell response restricted by HLA-B*14:02 in a Non progressor who lost twenty-seven years of HIV-1 control. <i>Retrovirology</i> , 2022, 19, 6.	2.0	3
4	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
5	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
6	Unintended HIV-1 Infection During Analytical Therapy Interruption. <i>Journal of Infectious Diseases</i> , 2020, 221, 1740-1742.	4.0	32
7	Persistent HIV controllers are more prone to spontaneously clear HCV: a retrospective cohort study. <i>Journal of the International AIDS Society</i> , 2020, 23, e25607.	3.0	2
8	High-Risk Sexual Practices Contribute to HIV-1 Double Infection Among Men Who Have Sex with Men in Madrid. <i>AIDS Research and Human Retroviruses</i> , 2020, 36, 896-904.	1.1	3
9	Characterizing the antiviral effect of an ATR inhibitor on human immunodeficiency virus type 1 replication. <i>Archives of Virology</i> , 2020, 165, 683-690.	2.1	0
10	Permanent control of HIV-1 pathogenesis in exceptional elite controllers: a model of spontaneous cure. <i>Scientific Reports</i> , 2020, 10, 1902.	3.3	50
11	HIV long-term non-progressors elite controllers: an interplay between host, immune and viral factors. <i>Future Virology</i> , 2019, 14, 287-297.	1.8	4
12	Elite controllers and lessons learned for HIV-1 cure. <i>Current Opinion in Virology</i> , 2019, 38, 31-36.	5.4	31
13	HIV-1 envelope glycoproteins isolated from Viremic Non-Progressor individuals are fully functional and cytopathic. <i>Scientific Reports</i> , 2019, 9, 5544.	3.3	17
14	Viral Characteristics Associated with the Clinical Nonprogressor Phenotype Are Inherited by Viruses from a Cluster of HIV-1 Elite Controllers. <i>MBio</i> , 2018, 9, .	4.1	37
15	Factors Leading to the Loss of Natural Elite Control of HIV-1 Infection. <i>Journal of Virology</i> , 2018, 92, .	3.4	58
16	Rate and predictors of progression in elite and viremic HIV-1 controllers. <i>Aids</i> , 2016, 30, 1209-1220.	2.2	69
17	Analysis of Non-AIDS-Defining Events in HIV Controllers. <i>Clinical Infectious Diseases</i> , 2016, 62, 1304-1309.	5.8	34
18	Influence of mutation and recombination on HIV-1 in vitro fitness recovery. <i>Molecular Phylogenetics and Evolution</i> , 2016, 94, 264-270.	2.7	31

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19	HIV-1 Dual Infected LTNP-EC Patients Developed an Unexpected Antibody Cross-Neutralizing Activity. PLoS ONE, 2015, 10, e0134054.	2.5	5
20	Differential MicroRNA Expression Profile between Stimulated PBMCs from HIV-1 Infected Elite Controllers and Viremic Progressors. PLoS ONE, 2014, 9, e106360.	2.5	52
21	Realistic Three Dimensional Fitness Landscapes Generated by Self Organizing Maps for the Analysis of Experimental HIV-1 Evolution. PLoS ONE, 2014, 9, e88579.	2.5	17
22	IL28B Single-Nucleotide Polymorphism rs12979860 Is Associated With Spontaneous HIV Control in White Subjects. Journal of Infectious Diseases, 2013, 207, 651-655.	4.0	22
23	Evidence of ongoing replication in a human immunodeficiency virus type 1 persistently infected cell line. Journal of General Virology, 2013, 94, 944-954.	2.9	5
24	Identification of a Cluster of HIV-1 Controllers Infected with Low Replicating Viruses. PLoS ONE, 2013, 8, e77663.	2.5	19
25	A genome-to-genome analysis of associations between human genetic variation, HIV-1 sequence diversity, and viral control. ELife, 2013, 2, e01123.	6.0	126
26	Circulation of HIV-1 subtype A within the subtype C HIV-1 epidemic in Tamil Nadu, India. Journal of Medical Virology, 2012, 84, 1507-1513.	5.0	0
27	Viremic HIV Infected Individuals with High CD4 T Cells and Functional Envelope Proteins Show Anti-gp41 Antibodies with Unique Specificity and Function. PLoS ONE, 2012, 7, e30330.	2.5	13
28	Mutagen-mediated enhancement of HIV-1 replication in persistently infected cells. Virology, 2012, 424, 147-153.	2.4	8
29	Low-Replicating Viruses and Strong Anti-Viral Immune Response Associated with Prolonged Disease Control in a Superinfected HIV-1 LTNP Elite Controller. PLoS ONE, 2012, 7, e31928.	2.5	21
30	A Bayesian network approach to study host and viral genetic correlates of HIV-1 disease progression. Retrovirology, 2011, 8, .	2.0	1
31	Dynamics of In Vitro Fitness Recovery of HIV-1. Journal of Virology, 2011, 85, 1861-1870.	3.4	23
32	Challenges and perspectives for improved management of HIV/Mycobacterium tuberculosis co-infection. European Respiratory Journal, 2010, 36, 1242-1247.	6.7	39
33	Phylogenetics of HIV-1 Circulating Recombinant Forms 12_BF and 38_BF in Argentina and Uruguay. Retrovirology, 2010, 7, 22.	2.0	41
34	Host and Viral Genetic Correlates of Clinical Definitions of HIV-1 Disease Progression. PLoS ONE, 2010, 5, e11079.	2.5	78
35	Mutant spectra in virus behavior. Future Virology, 2010, 5, 679-698.	1.8	26
36	Unfinished Stories on Viral Quasispecies and Darwinian Views of Evolution. Journal of Molecular Biology, 2010, 397, 865-877.	4.2	82

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37	Initial Fitness Recovery of HIV-1 Is Associated with Quasispecies Heterogeneity and Can Occur without Modifications in the Consensus Sequence. <i>PLoS ONE</i> , 2010, 5, e10319.	2.5	28
38	Identification of a new HIV Type 1 Circulating Recombinant Form (CRF38_BF1) in Uruguay. <i>AIDS Research and Human Retroviruses</i> , 2009, 25, 351-356.	1.1	22
39	A combination of defective DNA and protective host factors are found in a set of HIV-1 ancestral LTNPs. <i>Virology</i> , 2009, 391, 73-82.	2.4	31
40	Human immunodeficiency virus type 1 chronic infection is associated with different gene expression in MT-4, H9 and U937 cell lines. <i>Virus Research</i> , 2009, 139, 22-31.	2.2	16
41	An HIV-1 215V mutant shows increased phenotypic resistance to d4T. <i>Virus Research</i> , 2008, 135, 340-344.	2.2	1
42	High Divergence within the Major HIV Type 1 Subtype B Epidemic in Panama. <i>AIDS Research and Human Retroviruses</i> , 2008, 24, 1461-1466.	1.1	10
43	Plasma Viral Load Threshold for Sustaining Intra-host HIV Type 1 Evolution. <i>AIDS Research and Human Retroviruses</i> , 2007, 23, 1242-1250.	1.1	21
44	Genetic Changes Associated with Distinct Patterns of HIV Type 1 Persistence in Chronically Infected Cell Lines. <i>AIDS Research and Human Retroviruses</i> , 2007, 23, 251-260.	1.1	3
45	Coinfection and Superinfection in Patients with Long-Term, Nonprogressive HIV-1 Disease. <i>Journal of Infectious Diseases</i> , 2007, 196, 895-899.	4.0	39
46	HIV-1 Protease Dimer Interface Mutations that Compensate for Viral Reverse Transcriptase Instability in Infectious Virions. <i>Journal of Molecular Biology</i> , 2007, 372, 369-381.	4.2	14
47	Lack of temporal structure in the short term HIV-1 evolution within asymptomatic naïve patients. <i>Virology</i> , 2007, 362, 294-303.	2.4	20
48	A Dual Superinfection and Recombination Within HIV-1 Subtype B 12 Years After Primary Infection. <i>Journal of Acquired Immune Deficiency Syndromes</i> (1999), 2006, 42, 12-18.	2.1	59
49	Each genomic RNA in HIV-1 heterozygous virus generate new virions. <i>Virology</i> , 2005, 333, 316-323.	2.4	5
50	A subset of human immunodeficiency virus type 1 long-term non-progressors is characterized by the unique presence of ancestral sequences in the viral population. <i>Journal of General Virology</i> , 2005, 86, 355-364.	2.9	27
51	Few Mutations in the 5' Leader Region Mediate Fitness Recovery of Debilitated Human Immunodeficiency Type 1 Viruses. <i>Journal of Virology</i> , 2005, 79, 5421-5427.	3.4	18
52	Co-existence of recent and ancestral nucleotide sequences in viral quasispecies of human immunodeficiency virus type 1 patients. <i>Journal of General Virology</i> , 2004, 85, 399-407.	2.9	18
53	Tryptophan scanning mutagenesis of aromatic residues within the polymerase domain of HIV-1 reverse transcriptase: critical role of Phe-130 for p51 function and second-site revertant restoring viral replication capacity. <i>Virology</i> , 2004, 324, 400-411.	2.4	10
54	Plasma RNA viral load is not associated with inpatient quasispecies heterogeneity in HIV-1 infection. <i>Archives of Virology</i> , 2004, 149, 1761-71.	2.1	12

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55	Long-term suppression of plasma viremia with highly active antiretroviral therapy despite virus evolution and very limited selection of drug-resistant genotypes. <i>Journal of Medical Virology</i> , 2004, 73, 350-361.	5.0	6
56	Genetic Analysis of Culture-Negative UNAIDS Subtype C Samples. <i>AIDS Research and Human Retroviruses</i> , 2003, 19, 49-55.	1.1	9
57	Intrafamilial transmission of HIV-1. <i>Aids</i> , 2003, 17, 2673-2674.	2.2	0
58	Analysis, Quantification, and Evolutionary Consequences of HIV-1 in Vitro Recombination. <i>Virology</i> , 2002, 304, 392-402.	2.4	17
59	Frequency-dependent selection in human immunodeficiency virus type 1. <i>Journal of General Virology</i> , 2002, 83, 103-106.	2.9	17
60	In vitro analysis of human immunodeficiency virus type 1 resistance to nevirapine and fitness determination of resistant variants. <i>Journal of General Virology</i> , 2002, 83, 93-101.	2.9	44
61	Resistance to Nucleoside Analog Reverse Transcriptase Inhibitors Mediated by Human Immunodeficiency Virus Type 1 p6 Protein. <i>Journal of Virology</i> , 2001, 75, 9644-9653.	3.4	73
62	Different evolutionary patterns are found within human immunodeficiency virus type 1-infected patients. <i>Journal of General Virology</i> , 2001, 82, 2495-2508.	2.9	21
63	Genetic Analysis of HIV-1 Samples From Spain. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2000, 23, 68-74.	2.1	3
64	Genetic Analysis of HIV-1 Samples From Spain. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2000, 23, 68-74.	2.1	19
65	Different Distribution of HIV Type 1 Genetic Variants in European Patients with Distinct Risk Practices. <i>AIDS Research and Human Retroviruses</i> , 2000, 16, 299-304.	1.1	20
66	Unusual Distribution of Mutations Associated with Serial Bottleneck Passages of Human Immunodeficiency Virus Type 1. <i>Journal of Virology</i> , 2000, 74, 9546-9552.	3.4	49
67	Drastic Fitness Loss in Human Immunodeficiency Virus Type 1 upon Serial Bottleneck Events. <i>Journal of Virology</i> , 1999, 73, 2745-2751.	3.4	160
68	Complete Sequence of an Infectious Molecular Clone Derived from a Spanish HIV Type 1 Isolate. <i>AIDS Research and Human Retroviruses</i> , 1998, 14, 1649-1651.	1.1	14
69	Phenotypic Switch in a Spanish HIV Type 1 Isolate on Serial Passage on MT-4 Cells. <i>AIDS Research and Human Retroviruses</i> , 1997, 13, 979-984.	1.1	14
70	Sequence analysis of HIV-1 vif gene in Spanish isolates. <i>Virus Genes</i> , 1995, 9, 283-288.	1.6	6
71	Primary genetic characterization of HIV-1 isolates from WHO-sponsored vaccine evaluation sites by the RNase-A mismatch method. <i>Virus Research</i> , 1995, 39, 251-259.	2.2	15
72	Comparative study of the genetic variability in thymidine kinase and glycoprotein B genes of herpes simplex viruses by the RNase A mismatch cleavage method. <i>Virus Research</i> , 1995, 35, 205-214.	2.2	10

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73	Standard Conditions of Virus Isolation Reveal Biological Variability of HIV Type 1 in Different Regions of the World. <i>AIDS Research and Human Retroviruses</i> , 1994, 10, 1401-1408.	1.1	62
74	Rapid Genetic Characterization of HIV Type 1 Strains from Four World Health Organization-Sponsored Vaccine Evaluation Sites Using a Heteroduplex Mobility Assay. <i>AIDS Research and Human Retroviruses</i> , 1994, 10, 1345-1353.	1.1	94
75	Genetic Variation of HIV Type 1 in Four World Health Organization-Sponsored Vaccine Evaluation Sites: Generation of Functional Envelope (Glycoprotein 160) Clones Representative of Sequence Subtypes A, B, C, and E. <i>AIDS Research and Human Retroviruses</i> , 1994, 10, 1359-1368.	1.1	134
76	Antigenic Variation and Serotyping of HIV Type 1 from Four World Health Organization-Sponsored HIV Vaccine Sites. <i>AIDS Research and Human Retroviruses</i> , 1994, 10, 1369-1377.	1.1	71
77	Serotyping HIV Type 1 by Antibody Binding to the V3 Loop: Relationship to Viral Genotype. <i>AIDS Research and Human Retroviruses</i> , 1994, 10, 1379-1386.	1.1	110
78	Syncytium-Inducing and Non-Syncytium-Inducing Capacity of Human Immunodeficiency Virus Type 1 Subtypes Other Than B: Phenotypic and Genotypic Characteristics. <i>AIDS Research and Human Retroviruses</i> , 1994, 10, 1387-1400.	1.1	173
79	Natural Occurrence of Drug Resistance Mutations in the Reverse Transcriptase of Human Immunodeficiency Virus Type 1 Isolates. <i>AIDS Research and Human Retroviruses</i> , 1994, 10, 1479-1488.	1.1	89
80	HIV Type 1 Variation in World Health Organization-Sponsored Vaccine Evaluation Sites: Genetic Screening, Sequence Analysis, and Preliminary Biological Characterization of Selected Viral Strains. <i>AIDS Research and Human Retroviruses</i> , 1994, 10, 1327-1343.	1.1	186
81	Molecular epidemiology of HIV-1 in Madrid. <i>Virus Research</i> , 1994, 31, 331-342.	2.2	18
82	The World Health Organization Global Programme on AIDS Proposal for Standardization of HIV Sequence Nomenclature. <i>AIDS Research and Human Retroviruses</i> , 1994, 10, 1355-1358.	1.1	57
83	Analysis of genetic variability of populations of herpes simplex viruses. <i>Virus Research</i> , 1993, 28, 249-261.	2.2	10
84	Estimates by computer simulation of genetic distances from comparisons of RNase A mismatch cleavage patterns. <i>Journal of Virological Methods</i> , 1993, 45, 73-82.	2.1	12
85	Characterization of genetic variation and 3'-azido-3'-deoxythymidine- resistance mutations of human immunodeficiency virus by the RNase A mismatch cleavage method.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1991, 88, 4280-4284.	7.1	69
86	Participation of cytoskeletal intermediate filaments in the infectious cycle of human respiratory syncytial virus (RSV). <i>Virus Research</i> , 1988, 9, 307-321.	2.2	72
87	Analysis of genetic variability and mapping of point mutations in influenza virus by the RNase A mismatch cleavage method.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1988, 85, 3522-3526.	7.1	53
88	Heterogeneity among influenza H3N2 isolates recovered during an outbreak. <i>Archives of Virology</i> , 1985, 85, 139-144.	2.1	6
89	The quasispecies (extremely heterogeneous) nature of viral RNA genome populations: biological relevance "a review. <i>Gene</i> , 1985, 40, 1-8.	2.2	484
90	Evolution of the nucleotide sequence of influenza virus RNA segment 7 during drift of the H3N2 subtype. <i>Gene</i> , 1983, 23, 233-239.	2.2	59

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91	HIV-1 Super Infection. , 0, , .		0