Angela Ciuffi

List of Publications by Year
in descending order

65 papers	4,276 citations	182225 30 h-index	145109 60 g-index
72 all docs	72 docs citations	72 times ranked	5952 citing authors

#	Article	IF	Citations
1	Role of the cellular factor CTCF in the regulation of bovine leukemia virus latency and three-dimensional chromatin organization. Nucleic Acids Research, 2022, 50, 3190-3202.	6.5	5
2	Exploring m⁶A and m⁵C Epitranscriptomes upon Viral Infection: an Example with HIV. Journal of Visualized Experiments, 2022, , .	0.2	1
3	HIV Modifies the m6A and m5C Epitranscriptomic Landscape of the Host Cell. Frontiers in Virology, 2021, 1, .	0.7	6
4	Single-Cell Analysis Reveals Heterogeneity of Virus Infection, Pathogenicity, and Host Responses: HIV as a Pioneering Example. Annual Review of Virology, 2020, 7, 333-350.	3.0	15
5	Proteo-Transcriptomic Dynamics of Cellular Response to HIV-1 Infection. Scientific Reports, 2019, 9, 213.	1.6	24
6	Entry of Polarized Effector Cells into Quiescence Forces HIV Latency. MBio, 2019, 10, .	1.8	41
7	Single-Cell RNA-Seq Reveals Transcriptional Heterogeneity in Latent and Reactivated HIV-Infected Cells. Cell Reports, 2018, 23, 942-950.	2.9	89
8	The use of single-cell RNA-Seq to understand virusâ€“host interactions. Current Opinion in Virology, 2018, 29, 39-50.	2.6	46
9	Viral Fitness in Hosts. , 2018, , 2150-2158.		0
10	Single-virus tracking uncovers the missing link between HIV integration site location and viral gene expression. Nature Structural and Molecular Biology, 2017, 24, 8-11.	3.6	5
11	Unravelling HIV-1 Latency, One Cell at a Time. Trends in Microbiology, 2017, 25, 932-941.	3.5	17
12	Exploring viral infection using single-cell sequencing. Virus Research, 2017, 239, 55-68.	1.1	23
13	Single-cell analysis identifies cellular markers of the HIV permissive cell. PLoS Pathogens, 2017, 13, e1006678.	2.1	44
14	Single-Cell Genomics for Virology. Viruses, 2016, 8, 123.	1.5	32
15	Innate immune defects in HIV permissive cell lines. Retrovirology, 2016, 13, 43.	0.9	17
16	HIV-1 latent reservoir: size matters. Future Virology, 2016, 11, 785-794.	0.9	18
17	Differential expression of lncRNAs during the HIV replication cycle: an underestimated layer in the HIV-host interplay. Scientific Reports, 2016, 6, 36111.	1.6	28
18	Viral cell biology: HIV RNA gets methylated. Nature Microbiology, 2016, 1, 16037.	5.9	6

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19	The benefits of integration. Clinical Microbiology and Infection, 2016, 22, 324-332.	2.8	23
20	Guanylate Binding Protein (GBP) 5 Is an Interferon-Inducible Inhibitor of HIV-1 Infectivity. Cell Host and Microbe, 2016, 19, 504-514.	5.1	211
21	HIV-1 immune activation induces Siglec-1 expression and enhances viral trans-infection in blood and tissue myeloid cells. Retrovirology, 2015, 12, 37.	0.9	85
22	Identification of potential HIV restriction factors by combining evolutionary genomic signatures with functional analyses. Retrovirology, 2015, 12, 41.	0.9	78
23	Dual and Opposite Effects of hRAD51 Chemical Modulation on HIV-1 Integration. Chemistry and Biology, 2015, 22, 712-723.	6.2	8
24	Bioinformatics and HIV Latency. Current HIV/AIDS Reports, 2015, 12, 97-106.	1.1	12
25	Dynamic models of viral replication and latency. Current Opinion in HIV and AIDS, 2015, 10, 90-95.	1.5	8
26	Viral Fitness in Hosts. , 2015, , 1-11.		0
27	Dynamics of HIV Latency and Reactivation in a Primary CD4+ T Cell Model. PLoS Pathogens, 2014, 10, e1004156.	2.1	70
28	GuavaH: a compendium of host genomic data in HIV biology and disease. Retrovirology, 2014, 11, 6.	0.9	13
29	Susceptibility and adaptation to human TRIM5Î± alleles at positive selected sites in HIV-1 capsid. Virology, 2013, 441, 162-170.	1.1	12
30	24 Hours in the Life of HIV-1 in a T Cell Line. PLoS Pathogens, 2013, 9, e1003161.	2.1	134
31	State of genomics and epigenomics research in the perspective of HIV cure. Current Opinion in HIV and AIDS, 2013, 8, 176-181.	1.5	5
32	Viral Integration and Consequences on Host Gene Expression. , 2012, , 147-175.		16
33	LEDGF/p75 TATA-Less Promoter Is Driven by the Transcription Factor Sp1. Journal of Molecular Biology, 2011, 414, 177-193.	2.0	13
34	Identification of HIV integration sites in infected host genomic DNA. Methods, 2011, 53, 39-46.	1.9	25
35	A gene-rich, transcriptionally active environment and the pre-deposition of repressive marks are predictive of susceptibility to KRAB/KAP1-mediated silencing. BMC Genomics, 2011, 12, 378.	1.2	26
36	Estimating the net contribution of interleukinâ€28B variation to spontaneous hepatitis C virus clearance. Hepatology, 2011, 53, 1446-1454.	3.6	56

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37	Analysis of HIV-1 Expression Level and Sense of Transcription by High-Throughput Sequencing of the Infected Cell. Journal of Virology, 2011, 85, 6205-6211.	1.5	62
38	Unique Spectrum of Activity of Prosimian TRIM5Â against Exogenous and Endogenous Retroviruses. Journal of Virology, 2011, 85, 4173-4183.	1.5	25
39	ZNRD1 (Zinc Ribbon Domainâ€“Containing 1) Is a Host Cellular Factor That Influences HIVâ€1 Replication and Disease Progression. Clinical Infectious Diseases, 2010, 50, 1022-1032.	2.9	42
40	KRABâ€“Zinc Finger Proteins and KAP1 Can Mediate Long-Range Transcriptional Repression through Heterochromatin Spreading. PLoS Genetics, 2010, 6, e1000869.	1.5	309
41	Retroviral Integration Site Selection. Viruses, 2010, 2, 111-130.	1.5	62
42	Evolutionary Trajectories of Primate Genes Involved in HIV Pathogenesis. Molecular Biology and Evolution, 2009, 26, 2865-2875.	3.5	50
43	Methods for integration site distribution analyses in animal cell genomes. Methods, 2009, 47, 261-268.	1.9	42
44	Analysis of LEDGF/p75 expression regulation. Retrovirology, 2009, 6, .	0.9	0
45	Activity of ancestral restriction factors against ancient retroviruses. Retrovirology, 2009, 6, .	0.9	0
46	DNA bar coding and pyrosequencing to analyze adverse events in therapeutic gene transfer. Nucleic Acids Research, 2008, 36, e49-e49.	6.5	91
47	Genomic determinants of the efficiency of internal ribosomal entry sites of viral and cellular origin. Nucleic Acids Research, 2008, 36, 6918-6925.	6.5	13
48	Antiretroviral Activity of Ancestral TRIM5Î±. Journal of Virology, 2008, 82, 2089-2096.	1.5	27
49	In Vitro Whole-Genome Analysis Identifies a Susceptibility Locus for HIV-1. PLoS Biology, 2008, 6, e32.	2.6	63
50	Mechanisms Governing Lentivirus Integration Site Selection. Current Gene Therapy, 2008, 8, 419-429.	0.9	87
51	HIV integration site selection: Analysis by massively parallel pyrosequencing reveals association with epigenetic modifications. Genome Research, 2007, 17, 1186-1194.	2.4	396
52	Retroviral DNA integration: HIV and the role of LEDGF/p75. Trends in Genetics, 2006, 22, 388-395.	2.9	100
53	Retroviral DNA Integration: Viral and Cellular Determinants of Target-Site Selection. PLoS Pathogens, 2006, 2, e60.	2.1	310
54	Modulating Target Site Selection During Human Immunodeficiency Virus DNA IntegrationIn Vitrowith an Engineered Tethering Factor. Human Gene Therapy, 2006, 17, 960-967.	1.4	62

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55	HIV Integration Site Selection: Targeting in Macrophages and the Effects of Different Routes of Viral Entry. Molecular Therapy, 2006, 14, 218-225.	3.7	83
56	Integration Site Selection by HIV-Based Vectors in Dividing and Growth-Arrested IMR-90 Lung Fibroblasts. Molecular Therapy, 2006, 13, 366-373.	3.7	57
57	Modulating Target Site Selection During Human Immunodeficiency Virus DNA IntegrationIn Vitrowith an Engineered Tethering Factor. Human Gene Therapy, 2006, .	1.4	0
58	A role for LEDGF/p75 in targeting HIV DNA integration. Nature Medicine, 2005, 11, 1287-1289.	15.2	583
59	Genome-wide analysis of retroviral DNA integration. Nature Reviews Microbiology, 2005, 3, 848-858.	13.6	390
60	Interactions of Processed Nef (58-206) with Virion Proteins of HIV Type 1. AIDS Research and Human Retroviruses, 2004, 20, 399-407.	0.5	6
61	Entry and Transcription as Key Determinants of Differences in CD4 T-Cell Permissiveness to Human Immunodeficiency Virus Type 1 Infection. Journal of Virology, 2004, 78, 10747-10754.	1.5	46
62	Protection from HIV-1 infection of primary CD4 T cells by CCR5 silencing is effective for the full spectrum of CCR5 expression. Antiviral Therapy, 2003, 8, 373-7.	0.6	16
63	Protection from HIV-1 Infection of Primary Cd4 T Cells by Ccr5 Silencing is Effective for the Full Spectrum of Ccr5 Expression. Antiviral Therapy, 2003, 8, 373-377.	0.6	39
64	Individual Contributions of Mutant Protease and Reverse Transcriptase to Viral Infectivity, Replication, and Protein Maturation of Antiretroviral Drug-Resistant Human Immunodeficiency Virus Type 1. Journal of Virology, 2001, 75, 3291-3300.	1.5	79
65	The nef Gene Controls Syncytium Formation in Primary Human Lymphocytes and Macrophages Infected by HIV Type 1. AIDS Research and Human Retroviruses, 1998, 14, 1531-1542.	0.5	11