James I Mullins

List of Publications by Year in descending order

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8755 12946 19,721 231 75 131 citations h-index g-index papers 234 234 234 12883 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	CD8+ T-cell responses to different HIV proteins have discordant associations with viral load. Nature Medicine, 2007, 13, 46-53.	30.7	910
2	Consistent Viral Evolutionary Changes Associated with the Progression of Human Immunodeficiency Virus Type 1 Infection. Journal of Virology, 1999, 73, 10489-10502.	3.4	875
3	Proliferation of cells with HIV integrated into cancer genes contributes to persistent infection. Science, 2014, 345, 570-573.	12.6	573
4	Photonic detection of bacterial pathogens in living hosts. Molecular Microbiology, 1995, 18, 593-603.	2.5	524
5	Towards an HIV cure: a global scientific strategy. Nature Reviews Immunology, 2012, 12, 607-614.	22.7	485
6	Production of hepatitis B virus by a differentiated human hepatoma cell line after transfection with cloned circular HBV DNA. Cell, 1986, 47, 37-47.	28.9	415
7	Fitness Cost of Escape Mutations in p24 Gag in Association with Control of Human Immunodeficiency Virus Type 1. Journal of Virology, 2006, 80, 3617-3623.	3.4	408
8	Increased HIV-1 vaccine efficacy against viruses with genetic signatures in Env V2. Nature, 2012, 490, 417-420.	27.8	405
9	Relationship between pre-existing viral reservoirs and the re-emergence of plasma viremia after discontinuation of highly active anti-retroviral therapy. Nature Medicine, 2000, 6, 757-761.	30.7	404
10	Improved Coreceptor Usage Prediction and GenotypicMonitoring of R5-to-X4 Transition by Motif Analysis of HumanImmunodeficiency Virus Type 1 env V3 LoopSequences. Journal of Virology, 2003, 77, 13376-13388.	3.4	390
11	Cellular Immune Responses and Viral Diversity in Individuals Treated during Acute and Early HIV-1 Infection. Journal of Experimental Medicine, 2001, 193, 169-180.	8.5	363
12	Evidence for Human Immunodeficiency Virus Type 1 Replication In Vivo in CD14 ⁺ Monocytes and Its Potential Role as a Source of Virus in Patients on Highly Active Antiretroviral Therapy. Journal of Virology, 2002, 76, 707-716.	3.4	282
13	Two Randomized Trials of Neutralizing Antibodies to Prevent HIV-1 Acquisition. New England Journal of Medicine, 2021, 384, 1003-1014.	27.0	270
14	Genital HIV-1 RNA Predicts Risk of Heterosexual HIV-1 Transmission. Science Translational Medicine, 2011, 3, 77ra29.	12.4	265
15	Sequence analysis and acute pathogenicity of molecularly cloned SIVSMM-PBj14. Nature, 1990, 345, 636-640.	27.8	250
16	HIV-infected individuals receiving effective antiviral therapy for extended periods of time continually replenish their viral reservoir. Journal of Clinical Investigation, 2005, 115, 3250-3255.	8.2	246
17	Founder Effects in the Assessment of HIV Polymorphisms and HLA Allele Associations. Science, 2007, 315, 1583-1586.	12.6	234
18	Genetic impact of vaccination on breakthrough HIV-1 sequences from the STEP trial. Nature Medicine, 2011, 17, 366-371.	30.7	220

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19	ViroBLAST: a stand-alone BLAST web server for flexible queries of multiple databases and user's datasets. Bioinformatics, 2007, 23, 2334-2336.	4.1	213
20	Cloning of HTLV-4 and its relation to simian and human immunodeficiency viruses. Nature, 1987, 326, 610-613.	27.8	209
21	Control of human immunodeficiency virus replication by cytotoxic T lymphocytes targeting subdominant epitopes. Nature Immunology, 2006, 7, 173-178.	14.5	209
22	Disease-specific and tissue-specific production of unintegrated feline leukaemia virus variant DNA in feline AIDS. Nature, 1986, 319, 333-336.	27.8	206
23	The genome organization of STLV-3 is similar to that of the AIDS virus except for a truncated transmembrane protein. Cell, 1987, 49, 307-319.	28.9	199
24	Compensatory Mutation Partially Restores Fitness and Delays Reversion of Escape Mutation within the Immunodominant HLA-B*5703-Restricted Gag Epitope in Chronic Human Immunodeficiency Virus Type 1 Infection. Journal of Virology, 2007, 81, 8346-8351.	3.4	197
25	Evidence that Low-Level Viremias during Effective Highly Active Antiretroviral Therapy Result from Two Processes: Expression of Archival Virus and Replication of Virus. Journal of Virology, 2005, 79, 9625-9634.	3.4	194
26	Dual HIV-1 infection associated with rapid disease progression. Lancet, The, 2004, 363, 619-622.	13.7	189
27	DIVEIN: a web server to analyze phylogenies, sequence divergence, diversity, and informative sites. BioTechniques, 2010, 48, 405-408.	1.8	184
28	Changes in Human Immunodeficiency Virus Type 1 Fitness and Genetic Diversity during Disease Progression. Journal of Virology, 2005, 79, 9006-9018.	3.4	182
29	Decay of the HIV Reservoir in Patients Receiving Antiretroviral Therapy for Extended Periods: Implications for Eradication of Virus. Journal of Infectious Diseases, 2007, 195, 1762-1764.	4.0	180
30	Cellular Gene Expression upon Human Immunodeficiency Virus Type 1 Infection of CD4 + -T-Cell Lines. Journal of Virology, 2003, 77, 1392-1402.	3.4	173
31	Variable Fitness Impact of HIV-1 Escape Mutations to Cytotoxic T Lymphocyte (CTL) Response. PLoS Pathogens, 2009, 5, e1000365.	4.7	169
32	HIV-1 Group M Conserved Elements Vaccine. PLoS Pathogens, 2007, 3, e157.	4.7	168
33	Viral transduction of c-myc gene in naturally occurring feline leukaemias. Nature, 1984, 308, 856-858.	27.8	160
34	The evolving molecular epidemiology of HIV-1 envelope subtypes in injecting drug users in Bangkok, Thailand. Aids, 1995, 9, 851-858.	2.2	159
35	Potential impact of recombination on sitewise approaches for detecting positive natural selection. Genetical Research, 2003, 81, 115-121.	0.9	158
36	Human Immunodeficiency Virus Type 1 Populations in Blood and Semen. Journal of Virology, 1998, 72, 617-623.	3.4	157

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37	CD39/Adenosine Pathway Is Involved in AIDS Progression. PLoS Pathogens, 2011, 7, e1002110.	4.7	154
38	Polymorphisms of large effect explain the majority of the host genetic contribution to variation of HIV-1 virus load. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 14658-14663.	7.1	154
39	V3 Region Polymorphisms in HIV-1 from Brazil: Prevalence of Subtype B Strains Divergent from North American/European Prototype and Detection of Subtype F. AIDS Research and Human Retroviruses, 1994, 10, 569-576.	1.1	153
40	Central Role of Reverting Mutations in HLA Associations with Human Immunodeficiency Virus Set Point. Journal of Virology, 2008, 82, 8548-8559.	3.4	152
41	Nucleotide Sequence of the Envelope Gene of Gardner-Arnstein Feline Leukemia Virus B Reveals Unique Sequence Homologies with a Murine Mink Cell Focus-Forming Virus. Journal of Virology, 1983, 46, 871-880.	3.4	150
42	Broad and Gag-Biased HIV-1 Epitope Repertoires Are Associated with Lower Viral Loads. PLoS ONE, 2008, 3, e1424.	2.5	146
43	Definition of the viral targets of protective HIV-1-specific T cell responses. Journal of Translational Medicine, 2011, 9, 208. Pervasive Genomic Recombination of HIV-1 in VivoSequence data from this article have been deposited	4.4	143
44	with the EMBL/GenBank Data Libraries under accession nos. AY496645, AY496646, AY496647, AY496648, AY496649, AY496650, AY496651, AY496652, AY496653, AY496654, AY496655, AY496656, AY496657, AY496659, AY496660, AY496661, AY496662, AY496663, AY496664, AY496665, AY496666, AY496671, AY496672, AY496673, AY496674, AY496675, AY496676, AY496677, AY4966	68,	139
45	AY496679, AY49. Genetics, 2004, 167, 1573-1583. Control of Human Immunodeficiency Virus Type 1 Is Associated with HLA-B*13 and Targeting of Multiple Gag-Specific CD8 + T-Cell Epitopes. Journal of Virology, 2007, 81, 3667-3672.	3.4	138
46	Quantitation of Target Molecules from Polymerase Chain Reaction-Based Limiting Dilution Assays. AIDS Research and Human Retroviruses, 1997, 13, 737-742.	1.1	137
47	Enhanced Detection of Human Immunodeficiency Virus Type 1-Specific T-Cell Responses to Highly Variable Regions by Using Peptides Based on Autologous Virus Sequences. Journal of Virology, 2003, 77, 7330-7340.	3.4	133
48	Evolution of Hepatitis C Virus Quasispecies in Hypervariable Region 1 and the Putative Interferon Sensitivity-Determining Region during Interferon Therapy and Natural Infection. Journal of Virology, 1998, 72, 4288-4296.	3.4	131
49	Transduction of endogenous envelope genes by feline leukaemia virus in vitro. Nature, 1988, 332, 731-734.	27.8	130
50	Estimating the Impact of Plasma HIV-1 RNA Reductions on Heterosexual HIV-1 Transmission Risk. PLoS ONE, 2010, 5, e12598.	2.5	129
51	HLA Class I-Driven Evolution of Human Immunodeficiency Virus Type 1 Subtype C Proteome: Immune Escape and Viral Load. Journal of Virology, 2008, 82, 6434-6446.	3.4	126
52	A Reliable Phenotype Predictor for Human Immunodeficiency Virus Type 1 Subtype C Based on Envelope V3 Sequences. Journal of Virology, 2006, 80, 4698-4704.	3.4	124
53	Consensus and Ancestral State HIV Vaccines. Science, 2003, 299, 1515c-1518.	12.6	121
54	Selection on the Human Immunodeficiency Virus Type 1 Proteome following Primary Infection. Journal of Virology, 2006, 80, 9519-9529.	3.4	118

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55	CTL Responses of High Functional Avidity and Broad Variant Cross-Reactivity Are Associated with HIV Control. PLoS ONE, 2012, 7, e29717.	2.5	117
56	Phylogenetic Dependency Networks: Inferring Patterns of CTL Escape and Codon Covariation in HIV-1 Gag. PLoS Computational Biology, 2008, 4, e1000225.	3.2	116
57	Association Study of Common Genetic Variants and HIV-1 Acquisition in 6,300 Infected Cases and 7,200 Controls. PLoS Pathogens, 2013, 9, e1003515.	4.7	109
58	Human Immunodeficiency Virus Type 1 env Evolves toward Ancestral States upon Transmission to a New Host. Journal of Virology, 2006, 80, 1637-1644.	3.4	103
59	Virus Population Homogenization following Acute Human Immunodeficiency Virus Type 1 Infection. Journal of Virology, 2002, 76, 11953-11959.	3.4	100
60	Evolutionary Indicators of Human Immunodeficiency Virus Type 1 Reservoirs and Compartments. Journal of Virology, 2003, 77, 5540-5546.	3.4	97
61	HIV-Specific Probabilistic Models of Protein Evolution. PLoS ONE, 2007, 2, e503.	2.5	96
62	Rapid Genetic Characterization of HIV Type 1 Strains from Four World Health Organization-Sponsored Vaccine Evaluation Sites Using a Heteroduplex Mobility Assay. AIDS Research and Human Retroviruses, 1994, 10, 1345-1353.	1.1	94
63	Multiple Viral Genetic Analyses Detect Low-Level Human Immunodeficiency Virus Type 1 Replication during Effective Highly Active Antiretroviral Therapy. Journal of Virology, 2003, 77, 5721-5730.	3.4	93
64	Conflicting selective forces affect T cell receptor contacts in an immunodominant human immunodeficiency virus epitope. Nature Immunology, 2006, 7, 179-189.	14.5	91
65	An Increasing Proportion of Monotypic HIV-1 DNA Sequences during Antiretroviral Treatment Suggests Proliferation of HIV-Infected Cells. Journal of Virology, 2013, 87, 1770-1778.	3.4	91
66	Human Immunodeficiency Virus Type 1 Env Sequences from Calcutta in Eastern India: Identification of Features That Distinguish Subtype C Sequences in India from Other Subtype C Sequences. Journal of Virology, 2001, 75, 10479-10487.	3.4	90
67	Nef Induces Multiple Genes Involved in Cholesterol Synthesis and Uptake in Human Immunodeficiency Virus Type 1-Infected T Cells. Journal of Virology, 2005, 79, 10053-10058.	3.4	89
68	Evolution of Human Immunodeficiency Virus Type 1 Envelope Sequences in Infected Individuals with Differing Disease Progression Profiles. Virology, 1998, 241, 251-259.	2.4	88
69	Large-scale amplification, cloning and sequencing of near full-length HIV-1 subtype C genomes. Journal of Virological Methods, 2006, 136, 118-125.	2.1	88
70	Demographic Processes Affect HIV-1 Evolution in Primary Infection before the Onset of Selective Processes. Journal of Virology, 2011, 85, 7523-7534.	3.4	86
71	A human immune data-informed vaccine concept elicits strong and broad T-cell specificities associated with HIV-1 control in mice and macaques. Journal of Translational Medicine, 2015, 13, 60.	4.4	84
72	Persistence of Extraordinarily Low Levels of Genetically Homogeneous Human Immunodeficiency Virus Type 1 in Exposed Seronegative Individuals. Journal of Virology, 2003, 77, 6108-6116.	3.4	83

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73	Compartmentalization of Human Immunodeficiency Virus Type 1 between Blood Monocytes and CD4 + T Cells during Infection. Journal of Virology, 2004, 78, 7883-7893.	3.4	83
74	Coping with Viral Diversity in HIV Vaccine Design. PLoS Computational Biology, 2007, 3, e75.	3.2	83
75	Clinical and immunological impact of HIV envelope V3 sequence variation after starting initial triple antiretroviral therapy. Aids, 2004, 18, F1-F9.	2.2	80
76	Viral Linkage in HIV-1 Seroconverters and Their Partners in an HIV-1 Prevention Clinical Trial. PLoS ONE, 2011, 6, e16986.	2.5	80
77	Genomewide Association Study for Determinants of HIV-1 Acquisition and Viral Set Point in HIV-1 Serodiscordant Couples with Quantified Virus Exposure. PLoS ONE, 2011, 6, e28632.	2.5	80
78	Differential Selection Pressure Exerted on HIV by CTL Targeting Identical Epitopes but Restricted by Distinct HLA Alleles from the Same HLA Supertype. Journal of Immunology, 2006, 177, 4699-4708.	0.8	79
79	HIV-1 Envelope Subregion Length Variation during Disease Progression. PLoS Pathogens, 2010, 6, e1001228.	4.7	79
80	Emergence of Multiclass Drug–Resistance in HIVâ€2 in Antiretroviralâ€Treated Individuals in Senegal: Implications for HIVâ€2 Treatment in Resouceâ€Limited West Africa. Clinical Infectious Diseases, 2009, 48, 476-483.	5. 8	75
81	Env length and N-linked glycosylation following transmission of human immunodeficiency virus Type 1 subtype B viruses. Virology, 2008, 374, 229-233.	2.4	7 3
82	Perspective - Lethal Mutagenesis of HIV by Mutagenic Ribonucleoside Analogs. AIDS Research and Human Retroviruses, 2000, 16 , 1 -3.	1.1	72
83	Evolution of Human Immunodeficiency Virus Type 1 Cytotoxic T-Lymphocyte Epitopes: Fitness-Balanced Escape. Journal of Virology, 2007, 81, 12179-12188.	3.4	72
84	Mutation of HIV-1 Genomes in a Clinical Population Treated with the Mutagenic Nucleoside KP1461. PLoS ONE, 2011, 6, e15135.	2.5	71
85	Selection against CpG dinucleotides in lentiviral genes: a possible role of methylation in regulation of viral expression. Nucleic Acids Research, 1990, 18, 5793-5797.	14.5	68
86	Genetic Evaluation of Suspected Cases of Transient HIV-1 Infection of Infants. Science, 1998, 280, 1073-1077.	12.6	68
87	Selection for Human Immunodeficiency Virus Type 1 Recombinants in a Patient with Rapid Progression to AIDS. Journal of Virology, 2002, 76, 10674-10684.	3.4	68
88	Sequence organization of feline leukemis virus DNA in infected cells. Nucleic Acids Research, 1980, 8, 3287-3305.	14.5	67
89	Testing the Hypothesis of a Recombinant Origin of Human Immunodeficiency Virus Type 1 Subtype E. Journal of Virology, 2000, 74, 10752-10765.	3.4	65
90	Influence of Random Genetic Drift on Human Immunodeficiency Virus Type 1 env Evolution During Chronic Infection. Genetics, 2004, 166, 1155-1164.	2.9	65

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91	Extensive Intrasubtype Recombination in South African Human Immunodeficiency Virus Type 1 Subtype C Infections. Journal of Virology, 2007, 81, 4492-4500.	3.4	62
92	HIV‹ Variation before Seroconversion in Men Who Have Sex with Men: Analysis of Acute/Early HIV Infection in the Multicenter AIDS Cohort Study. Journal of Infectious Diseases, 2008, 197, 1011-1015.	4.0	62
93	Virologic Studies in a Case of Transfusion-Associated AIDS. New England Journal of Medicine, 1984, 311, 1419-1422.	27.0	60
94	Phylogenetic Analysis of Population-Based and Deep Sequencing Data to Identify Coevolving Sites in the nef Gene of HIV-1. Molecular Biology and Evolution, 2010, 27, 819-832.	8.9	59
95	Lack of Resistance to Integrase Inhibitors among Antiretroviral-Naive Subjects with Primary HIV-1 Infection, 2007–2013. Antiviral Therapy, 2015, 20, 77-80.	1.0	59
96	Rapid Molecular Epidemiology of Human Immunodeficiency Virus Transmission. AIDS Research and Human Retroviruses, 1995, 11, 1081-1093.	1.1	58
97	Dynamics of Viral Evolution and CTL Responses in HIV-1 Infection. PLoS ONE, 2011, 6, e15639.	2.5	58
98	Vaccine-induced Human Antibodies Specific for the Third Variable Region of HIV-1 gp120 Impose Immune Pressure on Infecting Viruses. EBioMedicine, 2014, 1, 37-45.	6.1	55
99	Analysis of HLA A*02 Association with Vaccine Efficacy in the RV144 HIV-1 Vaccine Trial. Journal of Virology, 2014, 88, 8242-8255.	3.4	55
100	Curiously Modern DNA for a ``250 Million-Year-Old'' Bacterium. Journal of Molecular Evolution, 2002, 54, 134-137.	1.8	53
101	Reconstruction and Function of Ancestral Center-of-Tree Human Immunodeficiency Virus Type 1 Proteins. Journal of Virology, 2007, 81, 8507-8514.	3.4	53
102	Superior Control of HIV-1 Replication by CD8+ T Cells Targeting Conserved Epitopes: Implications for HIV Vaccine Design. PLoS ONE, 2013, 8, e64405.	2.5	53
103	Early Pathogenesis of Disease Caused by SIVsmmPBjl4 Molecular Clone 1.9 in Macaques. AIDS Research and Human Retroviruses, 1993, 9, 277-286.	1.1	52
104	Male Genital Tract Compartmentalization of Human Immunodeficiency Virus Type 1 (HIV). AIDS Research and Human Retroviruses, 2008, 24, 561-571.	1.1	51
105	Comprehensive Sieve Analysis of Breakthrough HIV-1 Sequences in the RV144 Vaccine Efficacy Trial. PLoS Computational Biology, 2015, 11, e1003973.	3.2	51
106	Virus-Specific CD8 ⁺ T-Cell Responses Better Define HIV Disease Progression than HLA Genotype. Journal of Virology, 2010, 84, 4461-4468.	3.4	50
107	HIV-1 Conserved-Element Vaccines: Relationship between Sequence Conservation and Replicative Capacity. Journal of Virology, 2013, 87, 5461-5467.	3.4	50
108	HIV-1 infections with multiple founders are associated with higher viral loads than infections with single founders. Nature Medicine, 2015, 21, 1139-1141.	30.7	50

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109	Monotypic Human Immunodeficiency Virus Type 1 Genotypes across the Uterine Cervix and in Blood Suggest Proliferation of Cells with Provirus. Journal of Virology, 2009, 83, 6020-6028.	3.4	49
110	Altered Response Hierarchy and Increased T-Cell Breadth upon HIV-1 Conserved Element DNA Vaccination in Macaques. PLoS ONE, 2014, 9, e86254.	2.5	47
111	Importance and detection of virus reservoirs and compartments of HIV infection. Current Opinion in Microbiology, 2003, 6, 410-416.	5.1	46
112	Enhanced Detection of Human Immunodeficiency Virus Type 1 (HIV-1) Nef-Specific T Cells Recognizing Multiple Variants in Early HIV-1 Infection. Journal of Virology, 2007, 81, 5225-5237.	3.4	45
113	Emerging genetic diversity of HIV-1 in South America. Aids, 2000, 14, 1785-1791.	2.2	44
114	HIV-1 p24gag Derived Conserved Element DNA Vaccine Increases the Breadth of Immune Response in Mice. PLoS ONE, 2013, 8, e60245.	2.5	44
115	In-depth single-cell analysis of translation-competent HIV-1 reservoirs identifies cellular sources of plasma viremia. Nature Communications, 2021, 12, 3727.	12.8	43
116	Cytopathicity of Human Immunodeficiency Virus Type 1 Primary Isolates Depends on Coreceptor Usage and Not Patient Disease Status. Journal of Virology, 2001, 75, 8842-8847.	3.4	42
117	Genetic Characterization of Rebounding Human Immunodeficiency Virus Type 1 in Plasma during Multiple Interruptions of Highly Active Antiretroviral Therapy. Journal of Virology, 2003, 77, 3229-3237.	3.4	42
118	Immunogen sequence: the fourth tier of AIDS vaccine design. Expert Review of Vaccines, 2004, 3, \$151-\$159.	4.4	42
119	HIV-1 Superinfection in the Antiretroviral Therapy Era: Are Seroconcordant Sexual Partners at Risk?. PLoS ONE, 2009, 4, e5690.	2.5	39
120	Complex Patterns of Protease Inhibitor Resistance among Antiretroviral Treatment-Experienced HIV-2 Patients from Senegal: Implications for Second-Line Therapy. Antimicrobial Agents and Chemotherapy, 2013, 57, 2751-2760.	3.2	39
121	Human Immunodeficiency Virus Type 1 Molecular Evolution and the Measure of Selection. AIDS Research and Human Retroviruses, 1996, 12, 1681-1685.	1.1	37
122	Evolution of a Simian Immunodeficiency Virus Pathogen. Journal of Virology, 1998, 72, 405-414.	3.4	37
123	HIV-1 Conserved Elements p24CE DNA Vaccine Induces Humoral Immune Responses with Broad Epitope Recognition in Macaques. PLoS ONE, 2014, 9, e111085.	2.5	37
124	Human Immunodeficiency Virus Type 1 Bound to B Cells: Relationship to Virus Replicating in CD4+ T Cells and Circulating in Plasma. Journal of Virology, 2002, 76, 8855-8863.	3.4	36
125	HIV Type 1 Superinfection with a Dual-Tropic Virus and Rapid Progression to AIDS: A Case Report. Clinical Infectious Diseases, 2007, 45, 501-509.	5.8	35
126	Restriction of HIV-1 Genotypes in Breast Milk Does Not Account for the Population Transmission Genetic Bottleneck That Occurs following Transmission. PLoS ONE, 2010, 5, e10213.	2.5	35

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127	Molecular Epidemiology of Dual HIV-1/HIV-2 Seropositive Adults from Senegal, West Africa. AIDS Research and Human Retroviruses, 2003, 19, 575-584.	1.1	34
128	Evolution of CCR5 Use before and during Coreceptor Switching. Journal of Virology, 2008, 82, 11758-11766.	3.4	34
129	Selective Induction of CTL Helper Rather Than Killer Activity by Natural Epitope Variants Promotes Dendritic Cell–Mediated HIV-1 Dissemination. Journal of Immunology, 2013, 191, 2570-2580.	0.8	34
130	Lack of Evidence for Changing Virulence of HIV-1 in North America. PLoS ONE, 2008, 3, e1525.	2.5	34
131	Evidence for Limited Genetic Compartmentalization of HIV-1 between Lung and Blood. PLoS ONE, 2009, 4, e6949.	2.5	34
132	Genetic Analysis of Viral Variants Selected in Transmission of Human Immunodeficiency Viruses to Newborns. AIDS Research and Human Retroviruses, 2000, 16, 1223-1233.	1.1	33
133	Feline Immunodeficiency Virus Cell Entry. Journal of Virology, 2001, 75, 5433-5440.	3.4	33
134	DNA Prime-Boost Vaccine Regimen To Increase Breadth, Magnitude, and Cytotoxicity of the Cellular Immune Responses to Subdominant Gag Epitopes of Simian Immunodeficiency Virus and HIV. Journal of Immunology, 2016, 197, 3999-4013.	0.8	33
135	Fidelity of SNP Array Genotyping Using Epstein Barr Virus-Transformed B-Lymphocyte Cell Lines: Implications for Genome-Wide Association Studies. PLoS ONE, 2009, 4, e6915.	2.5	32
136	Genetic Analyses of HIV-1 <i>env</i> Sequences Demonstrate Limited Compartmentalization in Breast Milk and Suggest Viral Replication within the Breast That Increases with Mastitis. Journal of Virology, 2010, 84, 10812-10819.	3.4	32
137	Fitness-Balanced Escape Determines Resolution of Dynamic Founder Virus Escape Processes in HIV-1 Infection. Journal of Virology, 2015, 89, 10303-10318.	3.4	31
138	Cloned genomic segments of Zea mays homologous to zein mRNAs. Gene, 1981, 14, 205-215.	2.2	29
139	Increased detection of HIV-specific T cell responses by combination of central sequences with comparable immunogenicity. Aids, 2008, 22, 447-456.	2.2	29
140	Amino-Acid Co-Variation in HIV-1 Gag Subtype C: HLA-Mediated Selection Pressure and Compensatory Dynamics. PLoS ONE, 2010, 5, e12463.	2.5	29
141	Anti-HIV Type 1 Memory Cytotoxic T Lymphocyte Responses Associated with Changes in CD4 ⁺ T Cell Numbers in Progression of HIV Type 1 Infection. AIDS Research and Human Retroviruses, 1998, 14, 1423-1433.	1.1	28
142	EVOLUTION OF INTRAHOST HIV - 1 GENETIC DIVERSITY DURING CHRONIC INFECTION. Evolution; International Journal of Organic Evolution, 2006, 60, 1165-1176.	2.3	28
143	Early therapy of feline leukemia virus infection (FeLV-FAIDS) with 9-(2-phosphonyl-methoxyethyl)adenine (PMEA). Antiviral Research, 1991, 16, 77-92.	4.1	27
144	An HIV Epidemic Model Based on Viral Load Dynamics: Value in Assessing Empirical Trends in HIV Virulence and Community Viral Load. PLoS Computational Biology, 2014, 10, e1003673.	3.2	27

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145	How often does treatment of primary HIV lead to post-treatment control?. Antiviral Therapy, 2015, 20, 855-863.	1.0	27
146	Sieve analysis of breakthrough HIV-1 sequences in HVTN 505 identifies vaccine pressure targeting the CD4 binding site of Env-gp120. PLoS ONE, 2017, 12, e0185959.	2.5	27
147	Induction of aplastic anemia by intra-bone marrow inoculation of a molecularly cloned feline retrovirus. Leukemia Research, 1989, 13, 745-755.	0.8	26
148	HIV-2 Integrase Variation in Integrase Inhibitor-NaÃ-ve Adults in Senegal, West Africa. PLoS ONE, 2011, 6, e22204.	2.5	26
149	Fitness Costs of Mutations at the HIV-1 Capsid Hexamerization Interface. PLoS ONE, 2013, 8, e66065.	2.5	26
150	Efficacy of an Inactivated Feline Leukemia Virus Vaccine. AIDS Research and Human Retroviruses, 1996, 12, 379-383.	1.1	25
151	Therapeutic conserved elements (CE) DNA vaccine induces strong T-cell responses against highly conserved viral sequences during simian-human immunodeficiency virus infection. Human Vaccines and Immunotherapeutics, 2018, 14, 1820-1831.	3.3	25
152	Cells producing residual viremia during antiretroviral treatment appear to contribute to rebound viremia following interruption of treatment. PLoS Pathogens, 2020, 16, e1008791.	4.7	25
153	Recognition of HIV-1 Peptides by Host CTL Is Related to HIV-1 Similarity to Human Proteins. PLoS ONE, 2007, 2, e823.	2.5	24
154	Molecular cloning and characterization of Antheraea mylitta cytoplasmic polyhedrosis virus genome segment 9. Journal of General Virology, 2002, 83, 1483-1491.	2.9	23
155	Host Genetic and Viral Determinants of HIV-1 RNA Set Point among HIV-1 Seroconverters from Sub-Saharan Africa. Journal of Virology, 2015, 89, 2104-2111.	3.4	22
156	Conserved V3 Loop Sequences and Transmission of Human Immunodeficiency Virus Type 1. AIDS Research and Human Retroviruses, 1994, 10, 1679-1684.	1.1	21
157	Should Patients with Drug-Resistant HIV-1 Continue to Receive Antiretroviral Therapy?. New England Journal of Medicine, 2001, 344, 520-522.	27.0	21
158	Partner Characteristics Predicting HIV-1 Set Point in Sexually Acquired HIV-1 Among African Seroconverters. AIDS Research and Human Retroviruses, 2013, 29, 164-171.	1.1	21
159	Clonal Expansion of Human Immunodeficiency Virus–Infected Cells and Human Immunodeficiency Virus Persistence During Antiretroviral Therapy. Journal of Infectious Diseases, 2017, 215, S119-S127.	4.0	21
160	Droplet-microfluidics-assisted sequencing of HIV proviruses and their integration sites in cells from people on antiretroviral therapy. Nature Biomedical Engineering, 2022, 6, 1004-1012.	22.5	21
161	Increased Breadth and Depth of Cytotoxic T Lymphocytes Responses against HIV-1-B Nef by Inclusion of Epitope Variant Sequences. PLoS ONE, 2011, 6, e17969.	2,5	20
162	Comparison of Major and Minor Viral SNPs Identified through Single Template Sequencing and Pyrosequencing in Acute HIV-1 Infection. PLoS ONE, 2015, 10, e0135903.	2.5	20

#	Article	IF	CITATIONS
163	Efficient amplification of HIV half-genomes from tissue DNA. Nucleic Acids Research, 1992, 20, 4933-4933.	14.5	19
164	FeLV-FAIDS-induced immunodeficiency syndrome in cats. Veterinary Immunology and Immunopathology, 1989, 21, 25-37.	1.2	18
165	Site-Directed Mutagenesis Using Uracil-Containing Double-Stranded DNA Templates and DpnI Digestion. BioTechniques, 1999, 27, 734-738.	1.8	18
166	Prevalence and Genetic Diversity of HIV Type 1 Subtypes A and D in Women Attending Antenatal Clinics in Uganda. AIDS Research and Human Retroviruses, 2007, 23, 755-760.	1.1	18
167	Increased Sequence Coverage through Combined Targeting of Variant and Conserved Epitopes Correlates with Control of HIV Replication. Journal of Virology, 2014, 88, 1354-1365.	3.4	18
168	Impact of Mutations in Highly Conserved Amino Acids of the HIV-1 Gag-p24 and Env-gp120 Proteins on Viral Replication in Different Genetic Backgrounds. PLoS ONE, 2014, 9, e94240.	2.5	18
169	Molecular Clones from a Non-Acutely Pathogenic Derivative of SIV _{smmPBj14} : Characterization and Comparison to Acutely Pathogenic Clones. AIDS Research and Human Retroviruses, 1992, 8, 1179-1187.	1.1	17
170	Validation of an Oligonucleotide Ligation Assay for Quantification of Human Immunodeficiency Virus Type 1 Drug-Resistant Mutants by Use of Massively Parallel Sequencing. Journal of Clinical Microbiology, 2014, 52, 2320-2327.	3.9	17
171	Dendritic Cells Restore CD8 ⁺ T Cell Reactivity to Autologous HIV-1. Journal of Virology, 2014, 88, 9976-9990.	3.4	17
172	HIV Env conserved element DNA vaccine alters immunodominance in macaques. Human Vaccines and Immunotherapeutics, 2017, 13, 2859-2871.	3.3	17
173	Novel Cytotoxic T-Lymphocyte Escape Mutation by a Three-Amino-Acid Insertion in the Human Immunodeficiency Virus Type 1 p6 ^{Pol} and p6 ^{Gag} Late Domain Associated with Drug Resistance. Journal of Virology, 2008, 82, 495-502.	3.4	16
174	Effective Cytotoxic T Lymphocyte Targeting of Persistent HIV-1 during Antiretroviral Therapy Requires Priming of Naive CD8 + T Cells. MBio, 2016, 7, .	4.1	16
175	Patterns and rates of viral evolution in HIV-1 subtype B infected females and males. PLoS ONE, 2017, 12, e0182443.	2.5	16
176	Whole genome sequencing of extreme phenotypes identifies variants in CD101 and UBE2V1 associated with increased risk of sexually acquired HIV-1. PLoS Pathogens, 2017, 13, e1006703.	4.7	16
177	HIV population-level adaptation can rapidly diminish the impact of a partially effective vaccine. Vaccine, 2018, 36, 514-520.	3.8	15
178	Satellite Ic: a possible link between the satellite DNAs of D. virilis and D. melanogaster. Cell, 1979, 17, 615-621.	28.9	14
179	Treatment of FeLV-induced immunodeficiency syndrome (FeLV-FAIDS) with controlled release capsular implantation of 2′,3′-dideoxycytidine. Antiviral Research, 1989, 11, 147-160.	4.1	14
180	Substitution Model of Sequence Evolution for the Human Immunodeficiency Virus Type 1 Subtype B gp120 Gene over the C2-V5 Region. Journal of Molecular Evolution, 2001, 53, 55-62.	1.8	14

#	Article	IF	CITATIONS
181	Differences in the Expressed HLA Class I Alleles Effect the Differential Clustering of HIV Type 1-Specific T Cell Responses in Infected Chinese and Caucasians. AIDS Research and Human Retroviruses, 2004, 20, 557-564.	1.1	14
182	Dendritic Cells Reveal a Broad Range of MHC Class I Epitopes for HIV-1 in Persons with Suppressed Viral Load on Antiretroviral Therapy. PLoS ONE, 2010, 5, e12936.	2.5	14
183	Gag and env conserved element CE DNA vaccines elicit broad cytotoxic T cell responses targeting subdominant epitopes of HIV and SIV Able to recognize virus-infected cells in macaques. Human Vaccines and Immunotherapeutics, 2018, 14, 2163-2177.	3.3	14
184	Comparison of Immunogen Designs That Optimize Peptide Coverage: Reply to Fischer et al PLoS Computational Biology, 2008, 4, e25.	3.2	13
185	A sensitive real-time PCR based assay to estimate the impact of amino acid substitutions on the competitive replication fitness of human immunodeficiency virus type 1 in cell culture. Journal of Virological Methods, 2013, 189, 157-166.	2.1	13
186	Spontaneous control of HIV-1 viremia in a subject with protective HLA-B plus HLA-C alleles and HLA-C associated single nucleotide polymorphisms. Journal of Translational Medicine, 2014, 12, 335.	4.4	13
187	DNA Vaccine–Induced Long-Lasting Cytotoxic T Cells Targeting Conserved Elements of Human Immunodeficiency Virus Gag Are Boosted Upon DNA or Recombinant Modified Vaccinia Ankara Vaccination. Human Gene Therapy, 2018, 29, 1029-1043.	2.7	12
188	Control of SARS-CoV-2 infection after Spike DNA or Spike DNA+Protein co-immunization in rhesus macaques. PLoS Pathogens, 2021, 17, e1009701.	4.7	12
189	Improved Detection of Rare HIV-1 Variants using 454 Pyrosequencing. PLoS ONE, 2013, 8, e76502.	2.5	12
190	Preinfection Human Immunodeficiency Virus (HIV)-Specific Cytotoxic T Lymphocytes Failed To Prevent HIV Type 1 Infection from Strains Genetically Unrelated to Viruses in Long-Term Exposed Partners. Journal of Virology, 2009, 83, 10821-10829.	3.4	11
191	No Time to Delay! Fiebig Stages and Referral in Acute HIV infection: Seattle Primary Infection Program Experience. AIDS Research and Human Retroviruses, 2018, 34, 657-666.	1.1	11
192	Therapy of Presymptomatic FeLV-Induced Immunodeficiency Syndrome with AZT in Combination with Alpha Interferon. Annals of the New York Academy of Sciences, 1990, 616, 258-269.	3.8	10
193	Preferential detection of HIV subtype $C\hat{a} \in \mathbb{R}^2$ over subtype A in cervical cells from a dually infected woman. Aids, 2005, 19, 990-993.	2.2	10
194	Rare HLA Drive Additional HIV Evolution Compared to More Frequent Alleles. AIDS Research and Human Retroviruses, 2009, 25, 297-303.	1.1	10
195	The impact of viral evolution and frequency of variant epitopes on primary and memory human immunodeficiency virus type 1-specific CD8+ T cell responses. Virology, 2014, 450-451, 34-48.	2.4	10
196	Performance of commonly used genotypic assays and comparison with phenotypic assays of HIV-1 coreceptor tropism in acutely HIV-1-infected patients. Journal of Antimicrobial Chemotherapy, 2015, 70, 1391-1395.	3.0	10
197	Breast milk and in utero transmission of HIV-1 select for envelope variants with unique molecular signatures. Retrovirology, 2017, 14, 6.	2.0	10
198	Mucosal T Helper 17 and T Regulatory Cell Homeostasis Correlate with Acute Simian Immunodeficiency Virus Viremia and Responsiveness to Antiretroviral Therapy in Macaques. AIDS Research and Human Retroviruses, 2019, 35, 295-305.	1.1	10

#	Article	IF	CITATIONS
199	Transmission of HIV-1 drug resistance mutations within partner-pairs: A cross-sectional study of a primary HIV infection cohort. PLoS Medicine, 2018, 15, e1002537.	8.4	10
200	Mammalian cell/vaccinia virus expression vectors with increased stability of retroviral sequences in Escherichia coli: production of feline immunodeficiency virus envelope protein. Gene, 1995, 153, 197-202.	2.2	9
201	Quality Score Based Identification and Correction of Pyrosequencing Errors. PLoS ONE, 2013, 8, e73015.	2.5	9
202	Intra-host changes in Kaposi sarcoma-associated herpesvirus genomes in Ugandan adults with Kaposi sarcoma. PLoS Pathogens, 2021, 17, e1008594.	4.7	9
203	CD8 and CD4 Epitope Predictions in RV144: No Strong Evidence of a T-Cell Driven Sieve Effect in HIV-1 Breakthrough Sequences from Trial Participants. PLoS ONE, 2014, 9, e111334.	2.5	9
204	Selective impairment of humoral immunity in feline leukemia virus-induced immunodeficiency. Veterinary Immunology and Immunopathology, 1991, 28, 183-200.	1.2	8
205	Viral evolution and escape during primary human immunodeficiency virus-1 infection: implications for vaccine design. Current Opinion in HIV and AIDS, 2008, 3, 60-66.	3.8	8
206	Sequence Note: Human Immunodeficiency Virus Type 1 Subtypes B and C Detected in New Zealand. AIDS Research and Human Retroviruses, 1998, 14, 1105-1108.	1.1	7
207	Composite Sequence–Structure Stability Models as Screening Tools for Identifying Vulnerable Targets for HIV Drug and Vaccine Development. Viruses, 2015, 7, 5718-5735.	3.3	7
208	ISDB: a database toolkit for storing and analyzing viral integration site data. Bioinformatics, 2019, 35, 1073-1075.	4.1	6
209	Natural history of SIVmac BK28 and H824 infection in <i>Macaca nemestrina</i> Primatology, 1998, 27, 87-93.	0.6	5
210	Antigenâ€specific cytokine responses in vaccinated Macaca nemestrina. Journal of Medical Primatology, 1999, 28, 181-189.	0.6	5
211	Predicting Demographic Group Structures Based on DNA Sequence Data. Molecular Biology and Evolution, 2003, 20, 1168-1180.	8.9	5
212	Factors affecting relative fitness measurements in pairwise competition assays of human immunodeficiency viruses. Journal of Virological Methods, 2013, 194, 7-13.	2.1	5
213	A Pilot Study of Raltegravir Plus Combination Antiretroviral Therapy in Early Human Immunodeficiency Virus Infection: Challenges and Lessons Learned. BioResearch Open Access, 2016, 5, 15-21.	2.6	5
214	CD101 genetic variants modify regulatory and conventional TÂcell phenotypes and functions. Cell Reports Medicine, 2021, 2, 100322.	6.5	5
215	Comparisons of Human Immunodeficiency Virus Type 1 Envelope Variants in Blood and Genital Fluids near the Time of Male-to-Female Transmission. Journal of Virology, 2019, 93, .	3.4	4
216	CRISPR/Cas9-Mediated Insertion of HIV Long Terminal Repeat within∢i>BACH2⟨/i>Promotes Expansion of T Regulatory–like Cells. Journal of Immunology, 2022, 208, 1700-1710.	0.8	4

#	Article	IF	CITATIONS
217	Direct Amplification and Cloning of Up to 5-kb Lentivirus Genomes from Serum. BioTechniques, 1996, 21, 312-319.	1.8	3
218	HIV-1 superinfection with a triple-class drug-resistant strain in a patient successfully controlled with antiretroviral treatment. Aids, 2014, 28, 1840-1844.	2,2	3
219	Pairwise Growth Competition Assay for Determining the Replication Fitness of Human Immunodeficiency Viruses. Journal of Visualized Experiments, 2015, , e52610.	0.3	3
220	p21WAF1/CIP1 RNA Expression in Highly HIV-1 Exposed, Uninfected Individuals. PLoS ONE, 2015, 10, e0119218.	2.5	3
221	High-Sequence Diversity and Rapid Virus Turnover Contribute to Higher Rates of Coreceptor Switching in Treatment-Experienced Subjects with HIV-1 Viremia. AIDS Research and Human Retroviruses, 2017, 33, 234-245.	1.1	3
222	Phylogenetic Analyses Comparing HIV Sequences from Plasma at Virologic Failure to Cervix Versus Blood Sequences from Antecedent Antiretroviral Therapy Suppression. AIDS Research and Human Retroviruses, 2019, 35, 557-566.	1.1	3
223	HIV transmission patterns among transgender women, their cisgender male partners, and cisgender MSM in Lima, Peru: A molecular epidemiologic and phylodynamic analysis. The Lancet Regional Health Americas, 2022, 6, 100121.	2.6	3
224	Re: Follow-up Study of Intrahost HIV Type 2 Variability Reveals Discontinuous Evolution of C2V3 Sequences. AIDS Research and Human Retroviruses, 2001, 17, 1563-1567.	1.1	2
225	RV144 vaccine imprinting constrained HIV-1 evolution following breakthrough infection. Virus Evolution, 2021, 7, veab057.	4.9	2
226	Sources of Variation in Ancestral Sequence Reconstruction for HIV-1 Envelope Genes. Evolutionary Bioinformatics, 2006, 2, 117693430600200.	1.2	1
227	Inferring viral population structures using heteroduplex mobility and DNA sequence analyses. Journal of Virological Methods, 2013, 194, 169-177.	2.1	1
228	HIV Transmission During Condomless Sex With a Seropositive Partner With Suppressed Infection. JAMA - Journal of the American Medical Association, 2016, 316, 2044.	7.4	1
229	Passive Transfer of HIV-1 Antibodies and Drug Resistant Virus during a Health Care Worker Accident: Implications for HCW Post-Exposure Management. American Journal of Infectious Diseases, 2008, 4, 244-256.	0.2	1
230	Comprehensive Sieve Analysis of Breakthrough HIV-1 Sequences in the RV144 Vaccine Efficacy Trial. AIDS Research and Human Retroviruses, 2014, 30, A25-A26.	1.1	0
231	A Gut Reaction to SIV and SHIV Infection: Lower Dysregulation of Mucosal T Cells during Acute Infection Is Associated with Greater Viral Suppression during cART. Viruses, 2021, 13, 1609.	3.3	0