

Chanson J Brumme

List of Publications by Year in descending order

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124
papers

7,557
citations

70961

41
h-index

56606

83
g-index

144
all docs

144
docs citations

144
times ranked

8424
citing authors

#	ARTICLE	IF	CITATIONS
1	People With Human Immunodeficiency Virus Receiving Suppressive Antiretroviral Therapy Show Typical Antibody Durability After Dual Coronavirus Disease 2019 Vaccination and Strong Third Dose Responses. <i>Journal of Infectious Diseases</i> , 2023, 227, 838-849.	1.9	31
2	Impact of combinations of clinically observed HIV integrase mutations on phenotypic resistance to integrase strand transfer inhibitors (INSTIs): a molecular study. <i>Journal of Antimicrobial Chemotherapy</i> , 2022, 77, 979-988.	1.3	7
3	Reduced Magnitude and Durability of Humoral Immune Responses to COVID-19 mRNA Vaccines Among Older Adults. <i>Journal of Infectious Diseases</i> , 2022, 225, 1129-1140.	1.9	65
4	Humoral immune responses to COVID-19 vaccination in people living with HIV receiving suppressive antiretroviral therapy. <i>Npj Vaccines</i> , 2022, 7, 28.	2.9	64
5	A participant-derived xenograft model of HIV enables long-term evaluation of autologous immunotherapies. <i>Journal of Experimental Medicine</i> , 2021, 218, .	4.2	9
6	Intra-host evolutionary dynamics of the hepatitis C virus among people who inject drugs. <i>Scientific Reports</i> , 2021, 11, 9986.	1.6	1
7	Rapid Detection of SARS-CoV-2 Variants of Concern, Including B.1.1.28/P.1, British Columbia, Canada. <i>Emerging Infectious Diseases</i> , 2021, 27, 1673-1676.	2.0	38
8	Proviral Turnover During Untreated HIV Infection Is Dynamic and Variable Between Hosts, Impacting Reservoir Composition on ART. <i>Frontiers in Microbiology</i> , 2021, 12, 719153.	1.5	8
9	Validation of a Genotype-Independent Hepatitis C Virus Near-Whole Genome Sequencing Assay. <i>Viruses</i> , 2021, 13, 1721.	1.5	1
10	SARS-CoV-2 RNA Quantification Using Droplet Digital RT-PCR. <i>Journal of Molecular Diagnostics</i> , 2021, 23, 907-919.	1.2	17
11	Understanding patterns of HIV multi-drug resistance through models of temporal and spatial drug heterogeneity. <i>ELife</i> , 2021, 10, .	2.8	27
12	Concordance of HIV transmission risk factors elucidated using viral diversification rate and phylogenetic clustering. <i>Evolution, Medicine and Public Health</i> , 2021, 9, 338-348.	1.1	5
13	Untimed Efavirenz Drug Levels After Switching From Brand to Generic Formulations: A Short Communication. <i>Therapeutic Drug Monitoring</i> , 2021, 43, 701-705.	1.0	1
14	HIV-1 diversity considerations in the application of the Intact Proviral DNA Assay (IPDA). <i>Nature Communications</i> , 2021, 12, 165.	5.8	60
15	HIV Proviral Burden, Genetic Diversity, and Dynamics in Viremic Controllers Who Subsequently Initiated Suppressive Antiretroviral Therapy. <i>MBio</i> , 2021, 12, e0249021.	1.8	14
16	Variation in HIV-1 Nef function within and among viral subtypes reveals genetically separable antagonism of SERINC3 and SERINC5. <i>PLoS Pathogens</i> , 2020, 16, e1008813.	2.1	20
17	Genetic Diversity, Compartmentalization, and Age of HIV Proviruses Persisting in CD4 ⁺ T Cell Subsets during Long-Term Combination Antiretroviral Therapy. <i>Journal of Virology</i> , 2020, 94, .	1.5	21
18	Discordance between Etravirine Phenotype and Genotype-Based Predicted Phenotype for Subtype C HIV-1 from First-Line Antiretroviral Therapy Failures in South Africa. <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 64, .	1.4	1

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19	Differential Vpu-Mediated CD4 and Tetherin Downregulation Functions among Major HIV-1 Group M Subtypes. <i>Journal of Virology</i> , 2020, 94, .	1.5	6
20	Are We Ready for NGS HIV Drug Resistance Testing? The Second "Winnipeg Consensus" Symposium. <i>Viruses</i> , 2020, 12, 586.	1.5	18
21	The Impact of Treatment as Prevention on the HIV Epidemic in British Columbia, Canada. <i>Current HIV/AIDS Reports</i> , 2020, 17, 77-87.	1.1	16
22	Suboptimal Biological Sampling as a Probable Cause of False-Negative COVID-19 Diagnostic Test Results. <i>Journal of Infectious Diseases</i> , 2020, 222, 899-902.	1.9	75
23	Multi-Laboratory Comparison of Next-Generation to Sanger-Based Sequencing for HIV-1 Drug Resistance Genotyping. <i>Viruses</i> , 2020, 12, 694.	1.5	34
24	Longitudinal within-host evolution of HIV Nef-mediated CD4, HLA and SERINC5 downregulation activity: a case study. <i>Retrovirology</i> , 2020, 17, 3.	0.9	10
25	Performance comparison of next generation sequencing analysis pipelines for HIV-1 drug resistance testing. <i>Scientific Reports</i> , 2020, 10, 1634.	1.6	45
26	Evaluation of Nasopharyngeal Swab Collection Techniques for Nucleic Acid Recovery and Participant Experience: Recommendations for COVID-19 Diagnostics. <i>Open Forum Infectious Diseases</i> , 2020, 7, ofaa488.	0.4	21
27	T-cell responses to sequentially emerging viral escape mutants shape long-term HIV-1 population dynamics. <i>PLoS Pathogens</i> , 2020, 16, e1009177.	2.1	4
28	Title is missing!. , 2020, 16, e1009177.		0
29	Title is missing!. , 2020, 16, e1009177.		0
30	Title is missing!. , 2020, 16, e1009177.		0
31	Title is missing!. , 2020, 16, e1009177.		0
32	Detection of HIV transmission hotspots in British Columbia, Canada: A novel framework for the prioritization and allocation of treatment and prevention resources. <i>EBioMedicine</i> , 2019, 48, 405-413.	2.7	8
33	Rates and Correlates of Short Term Virologic Response among Treatment-Naïve HIV-Infected Children Initiating Antiretroviral Therapy in Ethiopia: A Multi-Center Prospective Cohort Study. <i>Pathogens</i> , 2019, 8, 161.	1.2	4
34	Prevalence and Correlates of Pre-Treatment HIV Drug Resistance among HIV-Infected Children in Ethiopia. <i>Viruses</i> , 2019, 11, 877.	1.5	9
35	Intra- and inter-individual HIV diversity limits the application of the intact proviral detection assay (IPDA). <i>Journal of Virus Eradication</i> , 2019, 5, 9.	0.3	0
36	HIV Subtype and Nef-Mediated Immune Evasion Function Correlate with Viral Reservoir Size in Early-Treated Individuals. <i>Journal of Virology</i> , 2019, 93, .	1.5	32

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37	A systematic, deep sequencing-based methodology for identification of mixed-genotype hepatitis C virus infections. <i>Infection, Genetics and Evolution</i> , 2019, 69, 76-84.	1.0	6
38	Genotypic and Mechanistic Characterization of Subtype-Specific HIV Adaptation to Host Cellular Immunity. <i>Journal of Virology</i> , 2019, 93, .	1.5	17
39	Novel HLA class I associations with HIV-1 control in a unique genetically admixed population. <i>Scientific Reports</i> , 2018, 8, 6111.	1.6	32
40	Frequent cross-resistance to rilpivirine among subtype C HIV-1 from first-line antiretroviral therapy failures in South Africa. <i>Antiviral Chemistry and Chemotherapy</i> , 2018, 26, 204020661876298.	0.3	6
41	Longitudinal trends of HIV drug resistance in a large Canadian cohort, 1996â€“2016. <i>Clinical Microbiology and Infection</i> , 2018, 24, 185-191.	2.8	33
42	Weaker HLA Footprints on HIV in the Unique and Highly Genetically Admixed Host Population of Mexico. <i>Journal of Virology</i> , 2018, 92, .	1.5	5
43	Bioinformatic data processing pipelines in support of nextâ€“generation sequencingâ€“based <scp>HIV</scp> drug resistance testing: the Winnipeg Consensus. <i>Journal of the International AIDS Society</i> , 2018, 21, e25193.	1.2	34
44	High Levels of Dual-Class Drug Resistance in HIV-Infected Children Failing First-Line Antiretroviral Therapy in Southern Ethiopia. <i>Viruses</i> , 2018, 10, 60.	1.5	11
45	Frequent Cross-Resistance to Dapivirine in HIV-1 Subtype C-Infected Individuals after First-Line Antiretroviral Therapy Failure in South Africa. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	1.4	12
46	Mother-to-Child HIV Transmission Bottleneck Selects for Consensus Virus with Lower Gag-Protease-Driven Replication Capacity. <i>Journal of Virology</i> , 2017, 91, .	1.5	13
47	Genotypic susceptibility score (GSS) and CD4+ T cell recovery in HIV-1 patients with suppressed viral load. <i>Journal of Antimicrobial Chemotherapy</i> , 2017, 72, 496-503.	1.3	5
48	Promises and pitfalls of Illumina sequencing for HIV resistance genotyping. <i>Virus Research</i> , 2017, 239, 97-105.	1.1	27
49	Prevalence and clinical impacts of HIV-1 intersubtype recombinants in Uganda revealed by near-full-genome population and deep sequencing approaches. <i>Aids</i> , 2017, 31, 2345-2354.	1.0	23
50	Estimating the Respective Contributions of Human and Viral Genetic Variation to HIV Control. <i>PLoS Computational Biology</i> , 2017, 13, e1005339.	1.5	28
51	Estimation of measurement error in plasma HIV-1 RNA assays near their limit of quantification. <i>PLoS ONE</i> , 2017, 12, e0171155.	1.1	7
52	Sociodemographic correlates of HIV drug resistance and access to drug resistance testing in British Columbia, Canada. <i>PLoS ONE</i> , 2017, 12, e0184848.	1.1	5
53	Impact of pre-adapted HIV transmission. <i>Nature Medicine</i> , 2016, 22, 606-613.	15.2	87
54	Increasing prevalence of K65K and K66K in HIV-1 subtype B reverse transcriptase. <i>Aids</i> , 2016, 30, 2787-2793.	1.0	1

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55	Lack of a significant impact of Gag-Protease-mediated HIV-1 replication capacity on clinical parameters in treatment-naïve Japanese individuals. <i>Retrovirology</i> , 2015, 12, 98.	0.9	4
56	Development and Validation of Two Screening Assays for the Hepatitis C Virus NS3 Q80K Polymorphism Associated with Reduced Response to Combination Treatment Regimens Containing Simeprevir. <i>Journal of Clinical Microbiology</i> , 2015, 53, 2942-2950.	1.8	11
57	The Impact of Clinical, Demographic and Risk Factors on Rates of HIV Transmission: A Population-based Phylogenetic Analysis in British Columbia, Canada. <i>Journal of Infectious Diseases</i> , 2015, 211, 926-935.	1.9	89
58	HIV Drug Resistance Testing by High-Multiplex "Wide" Sequencing on the MiSeq Instrument. <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 6824-6833.	1.4	50
59	Limited Evolution of Inferred HIV-1 Tropism while Viremia Is Undetectable during Standard HAART Therapy. <i>PLoS ONE</i> , 2014, 9, e99000.	1.1	7
60	Competitive Fitness Assays Indicate that the E138A Substitution in HIV-1 Reverse Transcriptase Decreases In Vitro Susceptibility to Emtricitabine. <i>Antimicrobial Agents and Chemotherapy</i> , 2014, 58, 2430-2433.	1.4	8
61	Genotypic and Functional Impact of HIV-1 Adaptation to Its Host Population during the North American Epidemic. <i>PLoS Genetics</i> , 2014, 10, e1004295.	1.5	45
62	Theoretical and experimental assessment of degenerate primer tagging in ultra-deep applications of next-generation sequencing. <i>Nucleic Acids Research</i> , 2014, 42, e98-e98.	6.5	29
63	Direct non-productive HIV-1 infection in a T-cell line is driven by cellular activation state and NF- κ B. <i>Retrovirology</i> , 2014, 11, 17.	0.9	37
64	Prevalence and Virologic Consequences of Transmitted HIV-1 Drug Resistance in Uganda. <i>AIDS Research and Human Retroviruses</i> , 2014, 30, 896-906.	0.5	26
65	Subtype-Specific HIV-1 Adaptation to Host HLA. <i>AIDS Research and Human Retroviruses</i> , 2014, 30, A218-A218.	0.5	0
66	Transmitted Escape Mutations Lead to Accelerated HIV-1 Disease Progression and Largely Define the Relative Contribution of HLA Alleles to Control. <i>AIDS Research and Human Retroviruses</i> , 2014, 30, A40-A40.	0.5	0
67	Trends in Plasma HIV-RNA Suppression and Antiretroviral Resistance in British Columbia, 1997-2010. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2014, 65, 107-114.	0.9	14
68	Ability of HIV-1 Nef to downregulate CD4 and HLA class I differs among viral subtypes. <i>Retrovirology</i> , 2013, 10, 100.	0.9	68
69	Influence of HLA-C Expression Level on HIV Control. <i>Science</i> , 2013, 340, 87-91.	6.0	352
70	"Test-and-Treat" Strategy for Control of HIV and AIDS Can Lead to a Decrease, Not an Increase, of Multidrug-Resistant Viruses. <i>Clinical Infectious Diseases</i> , 2013, 57, 478-479.	2.9	3
71	Structure of TCR and antigen complexes at an immunodominant CTL epitope in HIV-1 infection. <i>Scientific Reports</i> , 2013, 3, 3097.	1.6	35
72	Replication Fitness of Multiple Nonnucleoside Reverse Transcriptase-Resistant HIV-1 Variants in the Presence of Etravirine Measured by 454 Deep Sequencing. <i>Journal of Virology</i> , 2013, 87, 8805-8807.	1.5	9

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73	Genotypic Analysis of the V3 Region of HIV from Virologic Nonresponders to Maraviroc-Containing Regimens Reveals Distinct Patterns of Failure. <i>Antimicrobial Agents and Chemotherapy</i> , 2013, 57, 6122-6130.	1.4	17
74	A genome-to-genome analysis of associations between human genetic variation, HIV-1 sequence diversity, and viral control. <i>ELife</i> , 2013, 2, e01123.	2.8	126
75	Whole Genome Deep Sequencing of HIV-1 Reveals the Impact of Early Minor Variants Upon Immune Recognition During Acute Infection. <i>PLoS Pathogens</i> , 2012, 8, e1002529.	2.1	306
76	Automating HIV Drug Resistance Genotyping with RECall, a Freely Accessible Sequence Analysis Tool. <i>Journal of Clinical Microbiology</i> , 2012, 50, 1936-1942.	1.8	156
77	Correlates of Protective Cellular Immunity Revealed by Analysis of Population-Level Immune Escape Pathways in HIV-1. <i>Journal of Virology</i> , 2012, 86, 13202-13216.	1.5	99
78	Aminopeptidase Substrate Preference Affects HIV Epitope Presentation and Predicts Immune Escape Patterns in HIV-Infected Individuals. <i>Journal of Immunology</i> , 2012, 188, 5924-5934.	0.4	30
79	Uncommon Pathways of Immune Escape Attenuate HIV-1 Integrase Replication Capacity. <i>Journal of Virology</i> , 2012, 86, 6913-6923.	1.5	33
80	Increasingly Successful Highly Active Antiretroviral Therapy Delays the Emergence of New HLA Class I-associated Escape Mutations in HIV-1. <i>Clinical Infectious Diseases</i> , 2012, 54, 1652-1659.	2.9	11
81	Population-Based Sequencing of the V3-loop Can Predict the Virological Response to Maraviroc in Treatment-Naive Patients of the MERIT Trial. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2012, 61, 279-286.	0.9	41
82	Minor contribution of HLA class I-associated selective pressure to the variability of HIV-1 accessory protein Vpu. <i>Biochemical and Biophysical Research Communications</i> , 2012, 421, 291-295.	1.0	9
83	Characteristics and Outcomes of Initial Virologic Suppressors during Analytic Treatment Interruption in a Therapeutic HIV-1 gag Vaccine Trial. <i>PLoS ONE</i> , 2012, 7, e34134.	1.1	5
84	Technical and Regulatory Shortcomings of the TaqMan Version 1 HIV Viral Load Assay. <i>PLoS ONE</i> , 2012, 7, e43882.	1.1	13
85	Reduced Replication Capacity of NL4-3 Recombinant Viruses Encoding Reverse Transcriptase-Integrase Sequences From HIV-1 Elite Controllers. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2011, 56, 100-108.	0.9	59
86	Definition of the viral targets of protective HIV-1-specific T cell responses. <i>Journal of Translational Medicine</i> , 2011, 9, 208.	1.8	143
87	Influence of Gag-Protease-Mediated Replication Capacity on Disease Progression in Individuals Recently Infected with HIV-1 Subtype C. <i>Journal of Virology</i> , 2011, 85, 3996-4006.	1.5	50
88	Factors Associated With Viral Rebound in HIV-1-Infected Individuals Enrolled in a Therapeutic HIV-1 gag Vaccine Trial. <i>Journal of Infectious Diseases</i> , 2011, 203, 976-983.	1.9	29
89	Quantitative Trait Loci for CD4:CD8 Lymphocyte Ratio Are Associated with Risk of Type 1 Diabetes and HIV-1 Immune Control. <i>American Journal of Human Genetics</i> , 2010, 86, 88-92.	2.6	80
90	Viral adaptation to immune selection pressure by HLA class I-restricted CTL responses targeting epitopes in HIV frameshift sequences. <i>Journal of Experimental Medicine</i> , 2010, 207, 61-75.	4.2	52

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91	Impaired Replication Capacity of Acute/Early Viruses in Persons Who Become HIV Controllers. <i>Journal of Virology</i> , 2010, 84, 7581-7591.	1.5	118
92	Gag-Protease-Mediated Replication Capacity in HIV-1 Subtype C Chronic Infection: Associations with HLA Type and Clinical Parameters. <i>Journal of Virology</i> , 2010, 84, 10820-10831.	1.5	87
93	Early Selection in Gag by Protective HLA Alleles Contributes to Reduced HIV-1 Replication Capacity That May Be Largely Compensated for in Chronic Infection. <i>Journal of Virology</i> , 2010, 84, 11937-11949.	1.5	111
94	Efficacious Early Antiviral Activity of HIV Gag- and Pol-Specific HLA-B*2705-Restricted CD8 + T Cells. <i>Journal of Virology</i> , 2010, 84, 10543-10557.	1.5	84
95	The Major Genetic Determinants of HIV-1 Control Affect HLA Class I Peptide Presentation. <i>Science</i> , 2010, 330, 1551-1557.	6.0	1,054
96	HLA-Associated Viral Mutations Are Common in Human Immunodeficiency Virus Type 1 Elite Controllers. <i>Journal of Virology</i> , 2009, 83, 3407-3412.	1.5	67
97	Transmission and Long-Term Stability of Compensated CD8 Escape Mutations. <i>Journal of Virology</i> , 2009, 83, 3993-3997.	1.5	58
98	HLA-Associated Alterations in Replication Capacity of Chimeric NL4-3 Viruses Carrying gag-protease from Elite Controllers of Human Immunodeficiency Virus Type 1. <i>Journal of Virology</i> , 2009, 83, 140-149.	1.5	112
99	Human Immunodeficiency Virus Type 1-Specific CD8 ⁺ T-Cell Responses during Primary Infection Are Major Determinants of the Viral Set Point and Loss of CD4 ⁺ T Cells. <i>Journal of Virology</i> , 2009, 83, 7641-7648.	1.5	173
100	Impact of Select Immunologic and Virologic Biomarkers on CD4 Cell Count Decrease in Patients with Chronic HIV-1 Subtype C Infection: Results from Sinikithemba Cohort, Durban, South Africa. <i>Clinical Infectious Diseases</i> , 2009, 49, 956-964.	2.9	19
101	HLA-B57/B*5801 Human Immunodeficiency Virus Type 1 Elite Controllers Select for Rare Gag Variants Associated with Reduced Viral Replication Capacity and Strong Cytotoxic T-Lymphocyte Recognition. <i>Journal of Virology</i> , 2009, 83, 2743-2755.	1.5	261
102	Adaptation of HIV-1 to human leukocyte antigen class I. <i>Nature</i> , 2009, 458, 641-645.	13.7	408
103	HLA-Associated Immune Escape Pathways in HIV-1 Subtype B Gag, Pol and Nef Proteins. <i>PLoS ONE</i> , 2009, 4, e6687.	1.1	148
104	Marked Epitope- and Allele-Specific Differences in Rates of Mutation in Human Immunodeficiency Type 1 (HIV-1) Gag, Pol, and Nef Cytotoxic T-Lymphocyte Epitopes in Acute/Early HIV-1 Infection. <i>Journal of Virology</i> , 2008, 82, 9216-9227.	1.5	162
105	CD4-Dependent Characteristics of Coreceptor Use and HIV Type 1 V3 Sequence in a Large Population of Therapy-Naive Individuals. <i>AIDS Research and Human Retroviruses</i> , 2008, 24, 219-228.	0.5	23
106	Phylogenetic Dependency Networks: Inferring Patterns of CTL Escape and Codon Covariation in HIV-1 Gag. <i>PLoS Computational Biology</i> , 2008, 4, e1000225.	1.5	116
107	Genetic Characterization of Human Immunodeficiency Virus Type 1 in Elite Controllers: Lack of Gross Genetic Defects or Common Amino Acid Changes. <i>Journal of Virology</i> , 2008, 82, 8422-8430.	1.5	114
108	Human leukocyte antigen-specific polymorphisms in HIV-1 Gag and their association with viral load in chronic untreated infection. <i>Aids</i> , 2008, 22, 1277-1286.	1.0	67

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109	The Relationship Between Resistance and Adherence in Drug-Naive Individuals Initiating HAART Is Specific to Individual Drug Classes. <i>Journal of Acquired Immune Deficiency Syndromes</i> (1999), 2008, 49, 266-271.	0.9	52
110	Antigen Load and Viral Sequence Diversification Determine the Functional Profile of HIV-1-Specific CD8+ T Cells. <i>PLoS Medicine</i> , 2008, 5, e100.	3.9	205
111	Evidence of Differential HLA Class I-Mediated Viral Evolution in Functional and Accessory/Regulatory Genes of HIV-1. <i>PLoS Pathogens</i> , 2007, 3, e94.	2.1	153
112	Reply to Waters et al.. <i>Clinical Infectious Diseases</i> , 2007, 45, 1244-1245.	2.9	0
113	A Simple Screening Approach to Reduce B*5701-Associated Abacavir Hypersensitivity on the Basis of Sequence Variation in HIV Reverse Transcriptase. <i>Clinical Infectious Diseases</i> , 2007, 44, 1503-1508.	2.9	35
114	Effects of Human Leukocyte Antigen Class I Genetic Parameters on Clinical Outcomes and Survival after Initiation of Highly Active Antiretroviral Therapy. <i>Journal of Infectious Diseases</i> , 2007, 195, 1694-1704.	1.9	31
115	Transmission of drug-resistant HIV-1 from an infected individual to a caregiver. <i>Antiviral Therapy</i> , 2007, 12, 1139-44.	0.6	1
116	Transmission of Drug-Resistant HIV-1 from an Infected Individual to a Caregiver. <i>Antiviral Therapy</i> , 2007, 12, 1139-1144.	0.6	3
117	Short Communication: HIV VprR77Q Mutation Does Not Influence Clinical Response of Individuals Initiating Highly Active Antiretroviral Therapy. <i>AIDS Research and Human Retroviruses</i> , 2006, 22, 615-618.	0.5	13
118	Rates of antiretroviral resistance among HIV-infected patients with and without a history of injection drug use. <i>Aids</i> , 2005, 19, 1189-1195.	1.0	42
119	Molecular and Clinical Epidemiology of CXCR4-Using HIV-1 in a Large Population of Antiretroviral-Naive Individuals. <i>Journal of Infectious Diseases</i> , 2005, 192, 466-474.	1.9	260
120	No Inherent Association between Minor Mutations in HIV Protease at Baseline and Selection of the L90M Mutation at the Time of the First Virological Failure. <i>Journal of Infectious Diseases</i> , 2005, 191, 1778-1779.	1.9	5
121	Predictors of HIV Drug-Resistance Mutations in a Large Antiretroviral-Naive Cohort Initiating Triple Antiretroviral Therapy. <i>Journal of Infectious Diseases</i> , 2005, 191, 339-347.	1.9	386
122	HIV-1 Drug Resistance: Degree of Underestimation by a Cross-Sectional versus a Longitudinal Testing Approach. <i>Journal of Infectious Diseases</i> , 2005, 191, 1325-1330.	1.9	42
123	Association of the CCR5 ^{Δ32} Mutation with Clinical Response and >5-year Survival following Initiation of First Triple Antiretroviral Regimen. <i>Antiviral Therapy</i> , 2005, 10, 849-853.	0.6	7
124	A Participant-Derived Xenograft Model of HIV Enables Long-Term Evaluation of Autologous Immunotherapies. <i>SSRN Electronic Journal</i> , 0, , .	0.4	1