

Chanson J Brumme

List of Publications by Year in Descending Order

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Version: 2024-04-25

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

125
papers

6,058
citations

38
h-index

76
g-index

144
ext. papers

6,982
ext. citations

7.1
avg, IF

4.66
L-index

#	Paper	IF	Citations
125	Humoral immune responses to COVID-19 vaccination in people living with HIV receiving suppressive antiretroviral therapy.. <i>Npj Vaccines</i> , 2022 , 7, 28	9.5	4
124	Reduced magnitude and durability of humoral immune responses to COVID-19 mRNA vaccines among older adults. <i>Journal of Infectious Diseases</i> , 2021 ,	7	12
123	HIV Proviral Burden, Genetic Diversity, and Dynamics in Viremic Controllers Who Subsequently Initiated Suppressive Antiretroviral Therapy. <i>MBio</i> , 2021 , e0249021	7.8	0
122	Humoral immune responses to COVID-19 vaccination in people living with HIV receiving suppressive antiretroviral therapy 2021 ,		2
121	Weak humoral immune reactivity among residents of long-term care facilities following one dose of the BNT162b2 mRNA COVID-19 vaccine 2021 ,		11
120	A participant-derived xenograft model of HIV enables long-term evaluation of autologous immunotherapies. <i>Journal of Experimental Medicine</i> , 2021 , 218,	16.6	2
119	Intra-host evolutionary dynamics of the hepatitis C virus among people who inject drugs. <i>Scientific Reports</i> , 2021 , 11, 9986	4.9	1
118	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	10.2	20
117	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	5.7	2
116	SARS-CoV-2 RNA Quantification Using Droplet Digital RT-PCR. <i>Journal of Molecular Diagnostics</i> , 2021 , 23, 907-919	5.1	6
115	Understanding patterns of HIV multi-drug resistance through models of temporal and spatial drug heterogeneity. <i>ELife</i> , 2021 , 10,	8.9	4
114	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	3	1
113	Untimed Efavirenz Drug Levels After Switching From Brand to Generic Formulations: A Short Communication. <i>Therapeutic Drug Monitoring</i> , 2021 , 43, 701-705	3.2	
112	HIV-1 diversity considerations in the application of the Intact Proviral DNA Assay (IPDA). <i>Nature Communications</i> , 2021 , 12, 165	17.4	12
111	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,	6.6	9
110	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,	5.9	1
109	Differential Vpu-Mediated CD4 and Tetherin Downregulation Functions among Major HIV-1 Group M Subtypes. <i>Journal of Virology</i> , 2020 , 94,	6.6	4

108	Are We Ready for NGS HIV Drug Resistance Testing? The Second "Winnipeg Consensus" Symposium. <i>Viruses</i> , 2020 , 12,	6.2	6
107	The Impact of Treatment as Prevention on the HIV Epidemic in British Columbia, Canada. <i>Current HIV/AIDS Reports</i> , 2020 , 17, 77-87	5.9	8
106	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	7	54
105	Multi-Laboratory Comparison of Next-Generation to Sanger-Based Sequencing for HIV-1 Drug Resistance Genotyping. <i>Viruses</i> , 2020 , 12,	6.2	10
104	Longitudinal within-host evolution of HIV Nef-mediated CD4, HLA and SERINC5 downregulation activity: a case study. <i>Retrovirology</i> , 2020 , 17, 3	3.6	5
103	Performance comparison of next generation sequencing analysis pipelines for HIV-1 drug resistance testing. <i>Scientific Reports</i> , 2020 , 10, 1634	4.9	21
102	T-cell responses to sequentially emerging viral escape mutants shape long-term HIV-1 population dynamics. <i>PLoS Pathogens</i> , 2020 , 16, e1009177	7.6	2
101	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	1	11
100	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	7.6	6
99	T-cell responses to sequentially emerging viral escape mutants shape long-term HIV-1 population dynamics 2020 , 16, e1009177		
98	T-cell responses to sequentially emerging viral escape mutants shape long-term HIV-1 population dynamics 2020 , 16, e1009177		
97	T-cell responses to sequentially emerging viral escape mutants shape long-term HIV-1 population dynamics 2020 , 16, e1009177		
96	T-cell responses to sequentially emerging viral escape mutants shape long-term HIV-1 population dynamics 2020 , 16, e1009177		
95	Prevalence and Correlates of Pre-Treatment HIV Drug Resistance among HIV-Infected Children in Ethiopia. <i>Viruses</i> , 2019 , 11,	6.2	4
94	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	8.8	3
93	HIV Subtype and Nef-Mediated Immune Evasion Function Correlate with Viral Reservoir Size in Early-Treated Individuals. <i>Journal of Virology</i> , 2019 , 93,	6.6	18
92	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	4.5	5
91	Genotypic and Mechanistic Characterization of Subtype-Specific HIV Adaptation to Host Cellular Immunity. <i>Journal of Virology</i> , 2019 , 93,	6.6	11

90	Novel HLA class I associations with HIV-1 control in a unique genetically admixed population. <i>Scientific Reports</i> , 2018 , 8, 6111	4.9	17
89	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, 2040206618762985	3.5	5
88	Longitudinal trends of HIV drug resistance in a large Canadian cohort, 1996-2016. <i>Clinical Microbiology and Infection</i> , 2018 , 24, 185-191	9.5	19
87	High Levels of Dual-Class Drug Resistance in HIV-Infected Children Failing First-Line Antiretroviral Therapy in Southern Ethiopia. <i>Viruses</i> , 2018 , 10,	6.2	6
86	Weaker HLA Footprints on HIV in the Unique and Highly Genetically Admixed Host Population of Mexico. <i>Journal of Virology</i> , 2018 , 92,	6.6	3
85	Bioinformatic data processing pipelines in support of next-generation sequencing-based HIV drug resistance testing: the Winnipeg Consensus. <i>Journal of the International AIDS Society</i> , 2018 , 21, e25193	5.4	24
84	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,	5.9	9
83	Mother-to-Child HIV Transmission Bottleneck Selects for Consensus Virus with Lower Gag-Protease-Driven Replication Capacity. <i>Journal of Virology</i> , 2017 , 91,	6.6	4
82	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	5.1	2
81	Promises and pitfalls of Illumina sequencing for HIV resistance genotyping. <i>Virus Research</i> , 2017 , 239, 97-105	6.4	18
80	Estimating the Respective Contributions of Human and Viral Genetic Variation to HIV Control. <i>PLoS Computational Biology</i> , 2017 , 13, e1005339	5	16
79	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	3.5	14
78	Estimation of measurement error in plasma HIV-1 RNA assays near their limit of quantification. <i>PLoS ONE</i> , 2017 , 12, e0171155	3.7	3
77	Sociodemographic correlates of HIV drug resistance and access to drug resistance testing in British Columbia, Canada. <i>PLoS ONE</i> , 2017 , 12, e0184848	3.7	4
76	Increasing prevalence of K65K and K66K in HIV-1 subtype B reverse transcriptase. <i>Aids</i> , 2016 , 30, 2787-2793	3.9	3
75	Impact of pre-adapted HIV transmission. <i>Nature Medicine</i> , 2016 , 22, 606-13	50.5	66
74	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, 2942-50	9.7	9
73	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, 926-35	7	73

72	HIV drug resistance testing by high-multiplex "wide" sequencing on the MiSeq instrument. <i>Antimicrobial Agents and Chemotherapy</i> , 2015 , 59, 6824-33	5.9	41
71	Lack of a significant impact of Gag-Protease-mediated HIV-1 replication capacity on clinical parameters in treatment-naive Japanese individuals. <i>Retrovirology</i> , 2015 , 12, 98	3.6	2
70	Prevalence and virologic consequences of transmitted HIV-1 drug resistance in Uganda. <i>AIDS Research and Human Retroviruses</i> , 2014 , 30, 896-906	1.6	23
69	Subtype-Specific HIV-1 Adaptation to Host HLA. <i>AIDS Research and Human Retroviruses</i> , 2014 , 30, A218-A218	1.6	8
68	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	1.6	
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, 107-14	3.1	13
66	Limited evolution of inferred HIV-1 tropism while viremia is undetectable during standard HAART therapy. <i>PLoS ONE</i> , 2014 , 9, e99000	3.7	7
65	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, 2430-3	5.9	6
64	Genotypic and functional impact of HIV-1 adaptation to its host population during the North American epidemic. <i>PLoS Genetics</i> , 2014 , 10, e1004295	6	34
63	Theoretical and experimental assessment of degenerate primer tagging in ultra-deep applications of next-generation sequencing. <i>Nucleic Acids Research</i> , 2014 , 42, e98	20.1	27
62	Direct non-productive HIV-1 infection in a T-cell line is driven by cellular activation state and NFB. <i>Retrovirology</i> , 2014 , 11, 17	3.6	23
61	Ability of HIV-1 Nef to downregulate CD4 and HLA class I differs among viral subtypes. <i>Retrovirology</i> , 2013 , 10, 100	3.6	56
60	Influence of HLA-C expression level on HIV control. <i>Science</i> , 2013 , 340, 87-91	33.3	277
59	"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, 478-9	11.6	3
58	Structure of TCR and antigen complexes at an immunodominant CTL epitope in HIV-1 infection. <i>Scientific Reports</i> , 2013 , 3, 3097	4.9	25
57	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, 8805-7	6.6	8
56	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, 6122-30	5.9	16
55	A genome-to-genome analysis of associations between human genetic variation, HIV-1 sequence diversity, and viral control. <i>ELife</i> , 2013 , 2, e01123	8.9	85

54	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, 291-5	3.4	7
53	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	3.7	5
52	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	7.6	270
51	Automating HIV drug resistance genotyping with RECall, a freely accessible sequence analysis tool. <i>Journal of Clinical Microbiology</i> , 2012 , 50, 1936-42	9.7	126
50	Correlates of protective cellular immunity revealed by analysis of population-level immune escape pathways in HIV-1. <i>Journal of Virology</i> , 2012 , 86, 13202-16	6.6	81
49	Aminopeptidase substrate preference affects HIV epitope presentation and predicts immune escape patterns in HIV-infected individuals. <i>Journal of Immunology</i> , 2012 , 188, 5924-34	5.3	26
48	Uncommon pathways of immune escape attenuate HIV-1 integrase replication capacity. <i>Journal of Virology</i> , 2012 , 86, 6913-23	6.6	28
47	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, 1652-9	11.6	8
46	Population-based sequencing of the V3-loop can predict the virological response to maraviroc in treatment-naïve patients of the MERIT trial. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2012 , 61, 279-86	3.1	38
45	Technical and regulatory shortcomings of the TaqMan version 1 HIV viral load assay. <i>PLoS ONE</i> , 2012 , 7, e43882	3.7	11
44	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, 100-8	3.1	52
43	Definition of the viral targets of protective HIV-1-specific T cell responses. <i>Journal of Translational Medicine</i> , 2011 , 9, 208	8.5	124
42	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	6.6	42
41	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, 976-83	7	27
40	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	16.6	43
39	Impaired replication capacity of acute/early viruses in persons who become HIV controllers. <i>Journal of Virology</i> , 2010 , 84, 7581-91	6.6	107
38	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, 10820-31	6.6	71
37	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, 11937-49	6.6	101

36	Efficacious early antiviral activity of HIV Gag- and Pol-specific HLA-B 2705-restricted CD8+ T cells. <i>Journal of Virology</i> , 2010 , 84, 10543-57	6.6	72
35	The major genetic determinants of HIV-1 control affect HLA class I peptide presentation. <i>Science</i> , 2010 , 330, 1551-7	33.3	884
34	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	11	71
33	HLA-associated viral mutations are common in human immunodeficiency virus type 1 elite controllers. <i>Journal of Virology</i> , 2009 , 83, 3407-12	6.6	62
32	Transmission and long-term stability of compensated CD8 escape mutations. <i>Journal of Virology</i> , 2009 , 83, 3993-7	6.6	52
31	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, 140-9	6.6	103
30	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, 7641-8	6.6	153
29	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, 956-64	11.6	18
28	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 [corrected] recognition. <i>Journal of Virology</i> , 2009 , 83, 2743-55	6.6	225
27	Adaptation of HIV-1 to human leukocyte antigen class I. <i>Nature</i> , 2009 , 458, 641-5	50.4	361
26	HLA-associated immune escape pathways in HIV-1 subtype B Gag, Pol and Nef proteins. <i>PLoS ONE</i> , 2009 , 4, e6687	3.7	131
25	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, 9216-27	6.6	152
24	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, 219-28	1.6	21
23	Phylogenetic dependency networks: inferring patterns of CTL escape and codon covariation in HIV-1 Gag. <i>PLoS Computational Biology</i> , 2008 , 4, e1000225	5	98
22	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, 8422-30	6.6	107
21	Human leukocyte antigen-specific polymorphisms in HIV-1 Gag and their association with viral load in chronic untreated infection. <i>Aids</i> , 2008 , 22, 1277-86	3.5	60
20	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 (1999)</i> , 2008 , 49, 266-71	3.1	46
19	Antigen load and viral sequence diversification determine the functional profile of HIV-1-specific CD8+ T cells. <i>PLoS Medicine</i> , 2008 , 5, e100	11.6	181

18	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	7.6	139
17	Reply to Waters et al.. <i>Clinical Infectious Diseases</i> , 2007 , 45, 1244-1245	11.6	
16	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, 1503-8	11.6	31
15	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, 1694-704 ⁷		26
14	Transmission of drug-resistant HIV-1 from an infected individual to a caregiver. <i>Antiviral Therapy</i> , 2007 , 12, 1139-44	1.6	1
13	Transmission of Drug-Resistant HIV-1 from an Infected Individual to a Caregiver. <i>Antiviral Therapy</i> , 2007 , 12, 1139-1144	1.6	1
12	HIV VprR77Q mutation does not influence clinical response of individuals initiating highly active antiretroviral therapy. <i>AIDS Research and Human Retroviruses</i> , 2006 , 22, 615-8	1.6	10
11	HIV-1 drug resistance: degree of underestimation by a cross-sectional versus a longitudinal testing approach. <i>Journal of Infectious Diseases</i> , 2005 , 191, 1325-30	7	38
10	Rates of antiretroviral resistance among HIV-infected patients with and without a history of injection drug use. <i>Aids</i> , 2005 , 19, 1189-95	3.5	39
9	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, 466-74	7	237
8	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, 1778-9; author reply 1779-80	7	4
7	Predictors of HIV drug-resistance mutations in a large antiretroviral-naive cohort initiating triple antiretroviral therapy. <i>Journal of Infectious Diseases</i> , 2005 , 191, 339-47	7	349
6	Estimating the respective contributions of human and viral genetic variation to HIV control		2
5	Suboptimal biological sampling as a probable cause of false-negative COVID-19 diagnostic test results		4
4	HIV Diversity Considerations in the Application of the Intact Proviral DNA Assay (IPDA)		1
3	Understanding patterns of HIV multi-drug resistance through models of temporal and spatial drug heterogeneity		
2	Rapid detection of SARS-CoV-2 variants of concern identifying a cluster of B.1.1.28/P.1 variant in British Columbia, Canada		4
1	Reduced magnitude and durability of humoral immune responses by COVID-19 mRNA vaccines among older adults		3

