

# Chanson J Brumme

## List of Publications by Citations

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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	The major genetic determinants of HIV-1 control affect HLA class I peptide presentation. <i>Science</i> , <b>2010</b> , 330, 1551-7	33.3	884
124	Adaptation of HIV-1 to human leukocyte antigen class I. <i>Nature</i> , <b>2009</b> , 458, 641-5	50.4	361
123	Predictors of HIV drug-resistance mutations in a large antiretroviral-naive cohort initiating triple antiretroviral therapy. <i>Journal of Infectious Diseases</i> , <b>2005</b> , 191, 339-47	7	349
122	Influence of HLA-C expression level on HIV control. <i>Science</i> , <b>2013</b> , 340, 87-91	33.3	277
121	Whole genome deep sequencing of HIV-1 reveals the impact of early minor variants upon immune recognition during acute infection. <i>PLoS Pathogens</i> , <b>2012</b> , 8, e1002529	7.6	270
120	Molecular and clinical epidemiology of CXCR4-using HIV-1 in a large population of antiretroviral-naive individuals. <i>Journal of Infectious Diseases</i> , <b>2005</b> , 192, 466-74	7	237
119	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> , <b>2009</b> , 83, 2743-55	6.6	225
118	Antigen load and viral sequence diversification determine the functional profile of HIV-1-specific CD8+ T cells. <i>PLoS Medicine</i> , <b>2008</b> , 5, e100	11.6	181
117	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> , <b>2009</b> , 83, 7641-8	6.6	153
116	Marked epitope- and allele-specific differences in rates of mutation in human immunodeficiency virus type 1 (HIV-1) Gag, Pol, and Nef cytotoxic T-lymphocyte epitopes in acute/early HIV-1 infection. <i>Journal of Virology</i> , <b>2008</b> , 82, 9216-27	6.6	152
115	Evidence of differential HLA class I-mediated viral evolution in functional and accessory/regulatory genes of HIV-1. <i>PLoS Pathogens</i> , <b>2007</b> , 3, e94	7.6	139
114	HLA-associated immune escape pathways in HIV-1 subtype B Gag, Pol and Nef proteins. <i>PLoS ONE</i> , <b>2009</b> , 4, e6687	3.7	131
113	Automating HIV drug resistance genotyping with RECall, a freely accessible sequence analysis tool. <i>Journal of Clinical Microbiology</i> , <b>2012</b> , 50, 1936-42	9.7	126
112	Definition of the viral targets of protective HIV-1-specific T cell responses. <i>Journal of Translational Medicine</i> , <b>2011</b> , 9, 208	8.5	124
111	Impaired replication capacity of acute/early viruses in persons who become HIV controllers. <i>Journal of Virology</i> , <b>2010</b> , 84, 7581-91	6.6	107
110	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> , <b>2008</b> , 82, 8422-30	6.6	107
109	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> , <b>2009</b> , 83, 140-9	6.6	103

108	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> , <b>2010</b> , 84, 11937-49	6.6	101
107	Phylogenetic dependency networks: inferring patterns of CTL escape and codon covariation in HIV-1 Gag. <i>PLoS Computational Biology</i> , <b>2008</b> , 4, e1000225	5	98
106	A genome-to-genome analysis of associations between human genetic variation, HIV-1 sequence diversity, and viral control. <i>ELife</i> , <b>2013</b> , 2, e01123	8.9	85
105	Correlates of protective cellular immunity revealed by analysis of population-level immune escape pathways in HIV-1. <i>Journal of Virology</i> , <b>2012</b> , 86, 13202-16	6.6	81
104	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> , <b>2015</b> , 211, 926-35	7	73
103	Efficacious early antiviral activity of HIV Gag- and Pol-specific HLA-B 2705-restricted CD8+ T cells. <i>Journal of Virology</i> , <b>2010</b> , 84, 10543-57	6.6	72
102	Gag-protease-mediated replication capacity in HIV-1 subtype C chronic infection: associations with HLA type and clinical parameters. <i>Journal of Virology</i> , <b>2010</b> , 84, 10820-31	6.6	71
101	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> , <b>2010</b> , 86, 88-92	11	71
100	Impact of pre-adapted HIV transmission. <i>Nature Medicine</i> , <b>2016</b> , 22, 606-13	50.5	66
99	HLA-associated viral mutations are common in human immunodeficiency virus type 1 elite controllers. <i>Journal of Virology</i> , <b>2009</b> , 83, 3407-12	6.6	62
98	Human leukocyte antigen-specific polymorphisms in HIV-1 Gag and their association with viral load in chronic untreated infection. <i>Aids</i> , <b>2008</b> , 22, 1277-86	3.5	60
97	Ability of HIV-1 Nef to downregulate CD4 and HLA class I differs among viral subtypes. <i>Retrovirology</i> , <b>2013</b> , 10, 100	3.6	56
96	Suboptimal Biological Sampling as a Probable Cause of False-Negative COVID-19 Diagnostic Test Results. <i>Journal of Infectious Diseases</i> , <b>2020</b> , 222, 899-902	7	54
95	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> , <b>2011</b> , 56, 100-8	3.1	52
94	Transmission and long-term stability of compensated CD8 escape mutations. <i>Journal of Virology</i> , <b>2009</b> , 83, 3993-7	6.6	52
93	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> , <b>2008</b> , 49, 266-71	3.1	46
92	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> , <b>2010</b> , 207, 61-75	16.6	43
91	Influence of Gag-protease-mediated replication capacity on disease progression in individuals recently infected with HIV-1 subtype C. <i>Journal of Virology</i> , <b>2011</b> , 85, 3996-4006	6.6	42

90	HIV drug resistance testing by high-multiplex "wide" sequencing on the MiSeq instrument. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2015</b> , 59, 6824-33	5.9	41
89	Rates of antiretroviral resistance among HIV-infected patients with and without a history of injection drug use. <i>Aids</i> , <b>2005</b> , 19, 1189-95	3.5	39
88	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> , <b>2012</b> , 61, 279-86	3.1	38
87	HIV-1 drug resistance: degree of underestimation by a cross-sectional versus a longitudinal testing approach. <i>Journal of Infectious Diseases</i> , <b>2005</b> , 191, 1325-30	7	38
86	Genotypic and functional impact of HIV-1 adaptation to its host population during the North American epidemic. <i>PLoS Genetics</i> , <b>2014</b> , 10, e1004295	6	34
85	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> , <b>2007</b> , 44, 1503-8	11.6	31
84	Uncommon pathways of immune escape attenuate HIV-1 integrase replication capacity. <i>Journal of Virology</i> , <b>2012</b> , 86, 6913-23	6.6	28
83	Theoretical and experimental assessment of degenerate primer tagging in ultra-deep applications of next-generation sequencing. <i>Nucleic Acids Research</i> , <b>2014</b> , 42, e98	20.1	27
82	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> , <b>2011</b> , 203, 976-83	7	27
81	Aminopeptidase substrate preference affects HIV epitope presentation and predicts immune escape patterns in HIV-infected individuals. <i>Journal of Immunology</i> , <b>2012</b> , 188, 5924-34	5.3	26
80	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> , <b>2007</b> , 195, 1694-704 <sup>7</sup>		26
79	Structure of TCR and antigen complexes at an immunodominant CTL epitope in HIV-1 infection. <i>Scientific Reports</i> , <b>2013</b> , 3, 3097	4.9	25
78	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> , <b>2018</b> , 21, e25193	5.4	24
77	Prevalence and virologic consequences of transmitted HIV-1 drug resistance in Uganda. <i>AIDS Research and Human Retroviruses</i> , <b>2014</b> , 30, 896-906	1.6	23
76	Direct non-productive HIV-1 infection in a T-cell line is driven by cellular activation state and NFB. <i>Retrovirology</i> , <b>2014</b> , 11, 17	3.6	23
75	Performance comparison of next generation sequencing analysis pipelines for HIV-1 drug resistance testing. <i>Scientific Reports</i> , <b>2020</b> , 10, 1634	4.9	21
74	CD4-dependent characteristics of coreceptor use and HIV type 1 V3 sequence in a large population of therapy-naïve individuals. <i>AIDS Research and Human Retroviruses</i> , <b>2008</b> , 24, 219-28	1.6	21
73	Rapid Detection of SARS-CoV-2 Variants of Concern, Including B.1.1.28/P.1, British Columbia, Canada. <i>Emerging Infectious Diseases</i> , <b>2021</b> , 27, 1673-1676	10.2	20

72	Longitudinal trends of HIV drug resistance in a large Canadian cohort, 1996-2016. <i>Clinical Microbiology and Infection</i> , <b>2018</b> , 24, 185-191	9.5	19
71	Promises and pitfalls of Illumina sequencing for HIV resistance genotyping. <i>Virus Research</i> , <b>2017</b> , 239, 97-105	6.4	18
70	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> , <b>2009</b> , 49, 956-64	11.6	18
69	HIV Subtype and Nef-Mediated Immune Evasion Function Correlate with Viral Reservoir Size in Early-Treated Individuals. <i>Journal of Virology</i> , <b>2019</b> , 93,	6.6	18
68	Novel HLA class I associations with HIV-1 control in a unique genetically admixed population. <i>Scientific Reports</i> , <b>2018</b> , 8, 6111	4.9	17
67	Estimating the Respective Contributions of Human and Viral Genetic Variation to HIV Control. <i>PLoS Computational Biology</i> , <b>2017</b> , 13, e1005339	5	16
66	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> , <b>2013</b> , 57, 6122-30	5.9	16
65	Prevalence and clinical impacts of HIV-1 intersubtype recombinants in Uganda revealed by near-full-genome population and deep sequencing approaches. <i>Aids</i> , <b>2017</b> , 31, 2345-2354	3.5	14
64	Trends in plasma HIV-RNA suppression and antiretroviral resistance in British Columbia, 1997-2010. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , <b>2014</b> , 65, 107-14	3.1	13
63	Reduced magnitude and durability of humoral immune responses to COVID-19 mRNA vaccines among older adults. <i>Journal of Infectious Diseases</i> , <b>2021</b> ,	7	12
62	HIV-1 diversity considerations in the application of the Intact Proviral DNA Assay (IPDA). <i>Nature Communications</i> , <b>2021</b> , 12, 165	17.4	12
61	Technical and regulatory shortcomings of the TaqMan version 1 HIV viral load assay. <i>PLoS ONE</i> , <b>2012</b> , 7, e43882	3.7	11
60	Evaluation of Nasopharyngeal Swab Collection Techniques for Nucleic Acid Recovery and Participant Experience: Recommendations for COVID-19 Diagnostics. <i>Open Forum Infectious Diseases</i> , <b>2020</b> , 7, ofaa488	1	11
59	Weak humoral immune reactivity among residents of long-term care facilities following one dose of the BNT162b2 mRNA COVID-19 vaccine <b>2021</b> ,		11
58	Genotypic and Mechanistic Characterization of Subtype-Specific HIV Adaptation to Host Cellular Immunity. <i>Journal of Virology</i> , <b>2019</b> , 93,	6.6	11
57	Multi-Laboratory Comparison of Next-Generation to Sanger-Based Sequencing for HIV-1 Drug Resistance Genotyping. <i>Viruses</i> , <b>2020</b> , 12,	6.2	10
56	HIV VprR77Q mutation does not influence clinical response of individuals initiating highly active antiretroviral therapy. <i>AIDS Research and Human Retroviruses</i> , <b>2006</b> , 22, 615-8	1.6	10
55	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> , <b>2017</b> , 61,	5.9	9

54	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> , <b>2015</b> , 53, 2942-50	9.7	9
53	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> , <b>2020</b> , 94,	6.6	9
52	The Impact of Treatment as Prevention on the HIV Epidemic in British Columbia, Canada. <i>Current HIV/AIDS Reports</i> , <b>2020</b> , 17, 77-87	5.9	8
51	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> , <b>2013</b> , 87, 8805-7	6.6	8
50	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> , <b>2012</b> , 54, 1652-9	11.6	8
49	Limited evolution of inferred HIV-1 tropism while viremia is undetectable during standard HAART therapy. <i>PLoS ONE</i> , <b>2014</b> , 9, e99000	3.7	7
48	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> , <b>2012</b> , 421, 291-5	3.4	7
47	Are We Ready for NGS HIV Drug Resistance Testing? The Second "Winnipeg Consensus" Symposium. <i>Viruses</i> , <b>2020</b> , 12,	6.2	6
46	High Levels of Dual-Class Drug Resistance in HIV-Infected Children Failing First-Line Antiretroviral Therapy in Southern Ethiopia. <i>Viruses</i> , <b>2018</b> , 10,	6.2	6
45	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> , <b>2014</b> , 58, 2430-3	5.9	6
44	Variation in HIV-1 Nef function within and among viral subtypes reveals genetically separable antagonism of SERINC3 and SERINC5. <i>PLoS Pathogens</i> , <b>2020</b> , 16, e1008813	7.6	6
43	SARS-CoV-2 RNA Quantification Using Droplet Digital RT-PCR. <i>Journal of Molecular Diagnostics</i> , <b>2021</b> , 23, 907-919	5.1	6
42	Longitudinal within-host evolution of HIV Nef-mediated CD4, HLA and SERINC5 downregulation activity: a case study. <i>Retrovirology</i> , <b>2020</b> , 17, 3	3.6	5
41	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> , <b>2018</b> , 26, 2040206618762985	3.5	5
40	Characteristics and outcomes of initial virologic suppressors during analytic treatment interruption in a therapeutic HIV-1 gag vaccine trial. <i>PLoS ONE</i> , <b>2012</b> , 7, e34134	3.7	5
39	A systematic, deep sequencing-based methodology for identification of mixed-genotype hepatitis C virus infections. <i>Infection, Genetics and Evolution</i> , <b>2019</b> , 69, 76-84	4.5	5
38	Mother-to-Child HIV Transmission Bottleneck Selects for Consensus Virus with Lower Gag-Protease-Driven Replication Capacity. <i>Journal of Virology</i> , <b>2017</b> , 91,	6.6	4
37	Prevalence and Correlates of Pre-Treatment HIV Drug Resistance among HIV-Infected Children in Ethiopia. <i>Viruses</i> , <b>2019</b> , 11,	6.2	4

36	Differential Vpu-Mediated CD4 and Tetherin Downregulation Functions among Major HIV-1 Group M Subtypes. <i>Journal of Virology</i> , <b>2020</b> , 94,	6.6	4
35	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> , <b>2005</b> , 191, 1778-9; author reply 1779-80	7	4
34	Sociodemographic correlates of HIV drug resistance and access to drug resistance testing in British Columbia, Canada. <i>PLoS ONE</i> , <b>2017</b> , 12, e0184848	3.7	4
33	Suboptimal biological sampling as a probable cause of false-negative COVID-19 diagnostic test results		4
32	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
31	Understanding patterns of HIV multi-drug resistance through models of temporal and spatial drug heterogeneity. <i>ELife</i> , <b>2021</b> , 10,	8.9	4
30	Humoral immune responses to COVID-19 vaccination in people living with HIV receiving suppressive antiretroviral therapy.. <i>Npj Vaccines</i> , <b>2022</b> , 7, 28	9.5	4
29	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> , <b>2019</b> , 48, 405-413	8.8	3
28	"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> , <b>2013</b> , 57, 478-9	11.6	3
27	Estimation of measurement error in plasma HIV-1 RNA assays near their limit of quantification. <i>PLoS ONE</i> , <b>2017</b> , 12, e0171155	3.7	3
26	Weaker HLA Footprints on HIV in the Unique and Highly Genetically Admixed Host Population of Mexico. <i>Journal of Virology</i> , <b>2018</b> , 92,	6.6	3
25	Reduced magnitude and durability of humoral immune responses by COVID-19 mRNA vaccines among older adults		3
24	Genotypic susceptibility score (GSS) and CD4+ T cell recovery in HIV-1 patients with suppressed viral load. <i>Journal of Antimicrobial Chemotherapy</i> , <b>2017</b> , 72, 496-503	5.1	2
23	Lack of a significant impact of Gag-Protease-mediated HIV-1 replication capacity on clinical parameters in treatment-naïve Japanese individuals. <i>Retrovirology</i> , <b>2015</b> , 12, 98	3.6	2
22	T-cell responses to sequentially emerging viral escape mutants shape long-term HIV-1 population dynamics. <i>PLoS Pathogens</i> , <b>2020</b> , 16, e1009177	7.6	2
21	Humoral immune responses to COVID-19 vaccination in people living with HIV receiving suppressive antiretroviral therapy <b>2021</b> ,		2
20	Estimating the respective contributions of human and viral genetic variation to HIV control		2
19	A participant-derived xenograft model of HIV enables long-term evaluation of autologous immunotherapies. <i>Journal of Experimental Medicine</i> , <b>2021</b> , 218,	16.6	2



18	Proviral Turnover During Untreated HIV Infection Is Dynamic and Variable Between Hosts, Impacting Reservoir Composition on ART. <i>Frontiers in Microbiology</i> , <b>2021</b> , 12, 719153	5.7	2
17	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> , <b>2020</b> , 64,	5.9	1
16	HIV Diversity Considerations in the Application of the Intact Proviral DNA Assay (IPDA)		1
15	Understanding patterns of HIV multi-drug resistance through models of temporal and spatial drug heterogeneity		
14	Intra-host evolutionary dynamics of the hepatitis C virus among people who inject drugs. <i>Scientific Reports</i> , <b>2021</b> , 11, 9986	4.9	1
13	Concordance of HIV transmission risk factors elucidated using viral diversification rate and phylogenetic clustering. <i>Evolution, Medicine and Public Health</i> , <b>2021</b> , 9, 338-348	3	1
12	Transmission of drug-resistant HIV-1 from an infected individual to a caregiver. <i>Antiviral Therapy</i> , <b>2007</b> , 12, 1139-44	1.6	1
11	Transmission of Drug-Resistant HIV-1 from an Infected Individual to a Caregiver. <i>Antiviral Therapy</i> , <b>2007</b> , 12, 1139-1144	1.6	1
10	HIV Proviral Burden, Genetic Diversity, and Dynamics in Viremic Controllers Who Subsequently Initiated Suppressive Antiretroviral Therapy. <i>MBio</i> , <b>2021</b> , e0249021	7.8	0
9	Increasing prevalence of K65K and K66K in HIV-1 subtype B reverse transcriptase. <i>Aids</i> , <b>2016</b> , 30, 2787-2793		
8	Subtype-Specific HIV-1 Adaptation to Host HLA. <i>AIDS Research and Human Retroviruses</i> , <b>2014</b> , 30, A218-A218		
7	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> , <b>2014</b> , 30, A40-A40	1.6	
6	Reply to Waters et al.. <i>Clinical Infectious Diseases</i> , <b>2007</b> , 45, 1244-1245		11.6
5	Untimed Efavirenz Drug Levels After Switching From Brand to Generic Formulations: A Short Communication. <i>Therapeutic Drug Monitoring</i> , <b>2021</b> , 43, 701-705		3.2
4	T-cell responses to sequentially emerging viral escape mutants shape long-term HIV-1 population dynamics <b>2020</b> , 16, e1009177		
3	T-cell responses to sequentially emerging viral escape mutants shape long-term HIV-1 population dynamics <b>2020</b> , 16, e1009177		
2	T-cell responses to sequentially emerging viral escape mutants shape long-term HIV-1 population dynamics <b>2020</b> , 16, e1009177		
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