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List of Publications by Year in Descending Order

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Version: 2024-04-10

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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.

49 papers	4,088 citations	32 h-index	52 g-index
52 ext. papers	4,739 ext. citations	10.5 avg, IF	4.05 L-index

#	Paper	IF	Citations
49	HLA-associated preadaptation in HIV Vif is associated with higher set point viral load and faster CD4+ decline in Zambian transmission pairs. <i>Aids</i> , 2021 , 35, 1157-1165	3.5	
48	Elevated HIV Infection of CD4 T Cells in MRKAd5 Vaccine Recipients Due to CD8 T Cells Targeting Adapted Epitopes. <i>Journal of Virology</i> , 2021 , 95, e0016021	6.6	1
47	A large-scale database of T-cell receptor beta (TCR) sequences and binding associations from natural and synthetic exposure to SARS-CoV-2 2020 ,		30
46	Magnitude and Dynamics of the T-Cell Response to SARS-CoV-2 Infection at Both Individual and Population Levels 2020 ,		64
45	CD8 T cells targeting adapted epitopes in chronic HIV infection promote dendritic cell maturation and CD4 T cell trans-infection. <i>PLoS Pathogens</i> , 2019 , 15, e1007970	7.6	12
44	Clinical and evolutionary consequences of HIV adaptation to HLA: implications for vaccine and cure. <i>Current Opinion in HIV and AIDS</i> , 2019 , 14, 194-204	4.2	5
43	Elevated expression impairs HIV control through inhibition of NKG2A-expressing cells. <i>Science</i> , 2018 , 359, 86-90	33.3	89
42	Antisense-Derived HIV-1 Cryptic Epitopes Are Not Major Drivers of Viral Evolution during the Acute Phase of Infection. <i>Journal of Virology</i> , 2018 , 92,	6.6	1
41	Killer cell immunoglobulin-like receptor 3DL1 variation modifies HLA-B*57 protection against HIV-1. <i>Journal of Clinical Investigation</i> , 2018 , 128, 1903-1912	15.9	30
40	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
39	Brief Report: Selection of HIV-1 Variants With Higher Transmission Potential by 1% Tenofovir Gel Microbicide. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2017 , 76, 43-47	3.1	4
38	Differences in the Selection Bottleneck between Modes of Sexual Transmission Influence the Genetic Composition of the HIV-1 Founder Virus. <i>PLoS Pathogens</i> , 2016 , 12, e1005619	7.6	70
37	HIV-1-Specific CD8 T Cells Exhibit Limited Cross-Reactivity during Acute Infection. <i>Journal of Immunology</i> , 2016 , 196, 3276-86	5.3	20
36	Impact of pre-adapted HIV transmission. <i>Nature Medicine</i> , 2016 , 22, 606-13	50.5	66
35	CD8+ TCR Bias and Immunodominance in HIV-1 Infection. <i>Journal of Immunology</i> , 2015 , 194, 5329-45	5.3	25
34	HIV-1 adaptation to HLA: a window into virus-host immune interactions. <i>Trends in Microbiology</i> , 2015 , 23, 212-24	12.4	66
33	HIV transmission. Selection bias at the heterosexual HIV-1 transmission bottleneck. <i>Science</i> , 2014 , 345, 1254031	33.3	177

32	HIV control is mediated in part by CD8+ T-cell targeting of specific epitopes. <i>Journal of Virology</i> , 2014 , 88, 12937-48	6.6	61
31	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
30	Impact of HLA-driven HIV adaptation on virulence in populations of high HIV seroprevalence. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, E5393-400	11.5	65
29	Influence of HLA-C expression level on HIV control. <i>Science</i> , 2013 , 340, 87-91	33.3	277
28	HIV escape mutations occur preferentially at HLA-binding sites of CD8 T-cell epitopes. <i>Aids</i> , 2013 , 27, 899-905	3.5	30
27	Role of transmitted Gag CTL polymorphisms in defining replicative capacity and early HIV-1 pathogenesis. <i>PLoS Pathogens</i> , 2012 , 8, e1003041	7.6	70
26	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
25	Widespread impact of HLA restriction on immune control and escape pathways of HIV-1. <i>Journal of Virology</i> , 2012 , 86, 5230-43	6.6	90
24	High-avidity, high-IFN γ -producing CD8 T-cell responses following immune selection during HIV-1 infection. <i>Immunology and Cell Biology</i> , 2012 , 90, 224-34	5	32
23	Differential clade-specific HLA-B*3501 association with HIV-1 disease outcome is linked to immunogenicity of a single Gag epitope. <i>Journal of Virology</i> , 2012 , 86, 12643-54	6.6	42
22	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
21	HLA-A*7401-mediated control of HIV viremia is independent of its linkage disequilibrium with HLA-B*5703. <i>Journal of Immunology</i> , 2011 , 186, 5675-86	5.3	45
20	Translation of HLA-HIV associations to the cellular level: HIV adapts to inflate CD8 T cell responses against Nef and HLA-adapted variant epitopes. <i>Journal of Immunology</i> , 2011 , 187, 2502-13	5.3	24
19	Progression to AIDS in South Africa is associated with both reverting and compensatory viral mutations. <i>PLoS ONE</i> , 2011 , 6, e19018	3.7	50
18	CD8 T cell response and evolutionary pressure to HIV-1 cryptic epitopes derived from antisense transcription. <i>Journal of Experimental Medicine</i> , 2010 , 207, 51-9	16.6	60
17	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
16	Adaptive interactions between HLA and HIV-1: highly divergent selection imposed by HLA class I molecules with common supertype motifs. <i>Journal of Immunology</i> , 2010 , 184, 4368-77	5.3	38
15	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

14	The major genetic determinants of HIV-1 control affect HLA class I peptide presentation. <i>Science</i> , 2010 , 330, 1551-7	33.3	884
13	Protective HLA class I alleles that restrict acute-phase CD8+ T-cell responses are associated with viral escape mutations located in highly conserved regions of human immunodeficiency virus type 1. <i>Journal of Virology</i> , 2009 , 83, 1845-55	6.6	99
12	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
11	Transmission of HIV-1 Gag immune escape mutations is associated with reduced viral load in linked recipients. <i>Journal of Experimental Medicine</i> , 2008 , 205, 1009-17	16.6	187
10	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
9	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
8	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
7	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
6	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
5	SCOPE: a web server for practical de novo motif discovery. <i>Nucleic Acids Research</i> , 2007 , 35, W259-64	20.1	85
4	Founder effects in the assessment of HIV polymorphisms and HLA allele associations. <i>Science</i> , 2007 , 315, 1583-6	33.3	213
3	Leveraging hierarchical population structure in discrete association studies. <i>PLoS ONE</i> , 2007 , 2, e591	3.7	30
2	Bounded search for de novo identification of degenerate cis-regulatory elements. <i>BMC Bioinformatics</i> , 2006 , 7, 254	3.6	18
1	Diagnosis and Tracking of SARS-CoV-2 Infection By T-Cell Receptor Sequencing		8