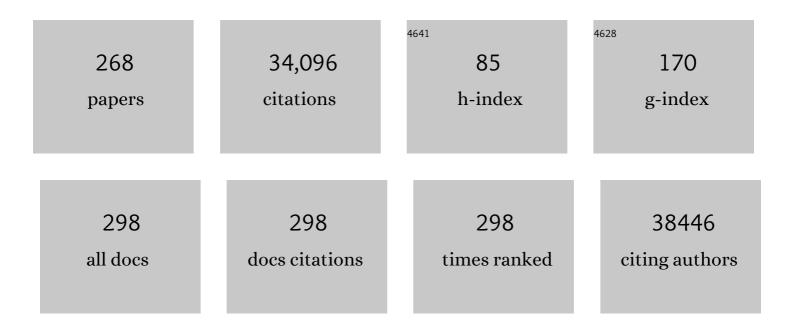
List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Cross-neutralization of SARS-CoV-2 by a human monoclonal SARS-CoV antibody. Nature, 2020, 583, 290-295.	13.7	1,695
2	Antiretroviral Treatment of Adult HIV Infection. JAMA - Journal of the American Medical Association, 2012, 308, 387-402.	3.8	1,239
3	A Whole-Genome Association Study of Major Determinants for Host Control of HIV-1. Science, 2007, 317, 944-947.	6.0	1,136
4	The Major Genetic Determinants of HIV-1 Control Affect HLA Class I Peptide Presentation. Science, 2010, 330, 1551-1557.	6.0	1,054
5	Broadly neutralizing antibodies overcome SARS-CoV-2 Omicron antigenic shift. Nature, 2022, 602, 664-670.	13.7	917
6	Clinical progression and virological failure on highly active antiretroviral therapy in HIV-1 patients: a prospective cohort study. Lancet, The, 1999, 353, 863-868.	6.3	894
7	N-terminal domain antigenic mapping reveals a site of vulnerability for SARS-CoV-2. Cell, 2021, 184, 2332-2347.e16.	13.5	784
8	Efavirenz plasma levels can predict treatment failure and central nervous system side effects in HIV-1-infected patients. Aids, 2001, 15, 71-75.	1.0	743
9	Antiretroviral Treatment of Adult HIV Infection. JAMA - Journal of the American Medical Association, 2010, 304, 321.	3.8	732
10	Innate partnership of HLA-B and KIR3DL1 subtypes against HIV-1. Nature Genetics, 2007, 39, 733-740.	9.4	691
11	Critical role for the chemokine receptor CXCR6 in NK cell–mediated antigen-specific memory of haptens and viruses. Nature Immunology, 2010, 11, 1127-1135.	7.0	644
12	Response to antiretroviral treatment in HIV-1-infected individuals with allelic variants of the multidrug resistance transporter 1: a pharmacogenetics study. Lancet, The, 2002, 359, 30-36.	6.3	635
13	Atherogenic Dyslipidemia in HIV-Infected Individuals Treated With Protease Inhibitors. Circulation, 1999, 100, 700-705.	1.6	592
14	A primer on deep learning in genomics. Nature Genetics, 2019, 51, 12-18.	9.4	542
15	Circulating SARS-CoV-2 spike N439K variants maintain fitness while evading antibody-mediated immunity. Cell, 2021, 184, 1171-1187.e20.	13.5	541
16	Towards an HIV cure: a global scientific strategy. Nature Reviews Immunology, 2012, 12, 607-614.	10.6	485
17	The fecal metabolome as a functional readout of the gut microbiome. Nature Genetics, 2018, 50, 790-795.	9.4	482
18	Antiretroviral Treatment of Adult HIV Infection. JAMA - Journal of the American Medical Association, 2014, 312, 410.	3.8	428

#	Article	IF	CITATIONS
19	AIDS-Related Opportunistic Illnesses Occurring After Initiation of Potent Antiretroviral Therapy. JAMA - Journal of the American Medical Association, 1999, 282, 2220.	3.8	416
20	The emb operon, a gene cluster of Mycobacterium tuberculosis involved in resistance to ethambutol. Nature Medicine, 1997, 3, 567-570.	15.2	405
21	Molecular beacon sequence analysis for detecting drug resistance in Mycobacterium tuberculosis. Nature Biotechnology, 1998, 16, 359-363.	9.4	393
22	SARS-CoV-2 immune evasion by the B.1.427/B.1.429 variant of concern. Science, 2021, 373, 648-654.	6.0	385
23	SARS-CoV-2 RBD antibodies that maximize breadth and resistance to escape. Nature, 2021, 597, 97-102.	13.7	385
24	Common Genetic Variation and the Control of HIV-1 in Humans. PLoS Genetics, 2009, 5, e1000791.	1.5	377
25	Whole-genome sequencing identifies common-to-rare variants associated with human blood metabolites. Nature Genetics, 2017, 49, 568-578.	9.4	341
26	Differential microRNA regulation of HLA-C expression and its association with HIV control. Nature, 2011, 472, 495-498.	13.7	328
27	Cohort Profile: The Swiss HIV Cohort Study. International Journal of Epidemiology, 2010, 39, 1179-1189.	0.9	322
28	Prevalence of adverse events associated with potent antiretroviral treatment: Swiss HIV Cohort Study. Lancet, The, 2001, 358, 1322-1327.	6.3	317
29	Deep sequencing of 10,000 human genomes. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 11901-11906.	3.3	315
30	Discontinuation of Primary Prophylaxis againstPneumocystis cariniiPneumonia in HIV-1–Infected Adults Treated with Combination Antiretroviral Therapy. New England Journal of Medicine, 1999, 340, 1301-1306.	13.9	271
31	HLA-C cell surface expression and control of HIV/AIDS correlate with a variant upstream of HLA-C. Nature Genetics, 2009, 41, 1290-1294.	9.4	265
32	HIV entry inhibitors. Lancet, The, 2007, 370, 81-88.	6.3	264
33	Broad betacoronavirus neutralization by a stem helix–specific human antibody. Science, 2021, 373, 1109-1116.	6.0	262
34	After the pandemic: perspectives on the future trajectory of COVID-19. Nature, 2021, 596, 495-504.	13.7	260
35	The blood DNA virome in 8,000 humans. PLoS Pathogens, 2017, 13, e1006292.	2.1	259
36	Long-Term Antiretroviral Treatment Initiated at Primary HIV-1 Infection Affects the Size, Composition, and Decay Kinetics of the Reservoir of HIV-1-Infected CD4 T Cells. Journal of Virology, 2014, 88, 10056-10065.	1.5	242

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37	Premature atherosclerosis in HIV-infected individuals – focus on protease inhibitor therapy. Aids, 2001, 15, 329-334.	1.0	241
38	Profound Perturbation of the Metabolome in Obesity Is Associated with Health Risk. Cell Metabolism, 2019, 29, 488-500.e2.	7.2	235
39	Population pharmacokinetics and effects of efavirenz in patients with human immunodeficiency virus infection. Clinical Pharmacology and Therapeutics, 2003, 73, 20-30.	2.3	231
40	The Human Microbiome and Cancer. Cancer Prevention Research, 2017, 10, 226-234.	0.7	230
41	Lectins enhance SARS-CoV-2 infection and influence neutralizing antibodies. Nature, 2021, 598, 342-347.	13.7	230
42	Broad sarbecovirus neutralization by a human monoclonal antibody. Nature, 2021, 597, 103-108.	13.7	220
43	Crystal structure of GyrA intein from Mycobacterium xenopi reveals structural basis of protein splicing. Nature Structural Biology, 1998, 5, 31-36.	9.7	217
44	Human gene essentiality. Nature Reviews Genetics, 2018, 19, 51-62.	7.7	213
45	Guanylate Binding Protein (GBP) 5 Is an Interferon-Inducible Inhibitor of HIV-1 Infectivity. Cell Host and Microbe, 2016, 19, 504-514.	5.1	211
46	Risk of HIV related Kaposi's sarcoma and non-Hodgkin's lymphoma with potent antiretroviral therapy: prospective cohort study. BMJ: British Medical Journal, 1999, 319, 23-24.	2.4	208
47	Siglec-1 Is a Novel Dendritic Cell Receptor That Mediates HIV-1 Trans-Infection Through Recognition of Viral Membrane Gangliosides. PLoS Biology, 2012, 10, e1001448.	2.6	208
48	SAMHD1 is mutated recurrently in chronic lymphocytic leukemia and is involved in response to DNA damage. Blood, 2014, 123, 1021-1031.	0.6	205
49	Genotypic Analysis of <i>Mycobacterium tuberculosis</i> in Two Distinct Populations Using Molecular Beacons: Implications for Rapid Susceptibility Testing. Antimicrobial Agents and Chemotherapy, 2000, 44, 103-110.	1.4	195
50	HIV Treatment Failure: Testing for HIV Resistance in Clinical Practice. Science, 1998, 280, 1871-1873.	6.0	187
51	APOBEC3G Genetic Variants and Their Influence on the Progression to AIDS. Journal of Virology, 2004, 78, 11070-11076.	1.5	178
52	Paternally inherited cis-regulatory structural variants are associated with autism. Science, 2018, 360, 327-331.	6.0	174
53	Evolutionary and Functional Analyses of the Interaction between the Myeloid Restriction Factor SAMHD1 and the Lentiviral Vpx Protein. Cell Host and Microbe, 2012, 11, 205-217.	5.1	169
54	Comparative transcriptomics of extreme phenotypes of human HIV-1 infection and SIV infection in sooty mangabey and rhesus macaque. Journal of Clinical Investigation, 2011, 121, 2391-2400.	3.9	168

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55	Lausannevirus, a giant amoebal virus encoding histone doublets. Environmental Microbiology, 2011, 13, 1454-1466.	1.8	164
56	Genome-Wide mRNA Expression Correlates of Viral Control in CD4+ T-Cells from HIV-1-Infected Individuals. PLoS Pathogens, 2010, 6, e1000781.	2.1	158
57	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.	3.3	154
58	WGAViewer: Software for genomic annotation of whole genome association studies: Figure 1 Genome Research, 2008, 18, 640-643.	2.4	147
59	Profiling of Short-Tandem-Repeat Disease Alleles in 12,632 Human Whole Genomes. American Journal of Human Genetics, 2017, 101, 700-715.	2.6	142
60	Polymorphisms in Toll-like receptor 9 influence the clinical course of HIV-1 infection. Aids, 2007, 21, 441-446.	1.0	139
61	Mutation position and type of substitution in the β-subunit of the RNA polymerase influence in-vitro activity of rifamycins in rifampicin-resistant Mycobacterium tuberculosis. Journal of Antimicrobial Chemotherapy, 1995, 35, 345-348.	1.3	138
62	The human noncoding genome defined by genetic diversity. Nature Genetics, 2018, 50, 333-337.	9.4	137
63	24 Hours in the Life of HIV-1 in a T Cell Line. PLoS Pathogens, 2013, 9, e1003161.	2.1	134
64	Hepatic Cyst Infection in Autosomal Dominant Polycystic Kidney Disease. Mayo Clinic Proceedings, 1990, 65, 933-942.	1.4	132
65	Copy Number Variation of KIR Genes Influences HIV-1 Control. PLoS Biology, 2011, 9, e1001208.	2.6	132
66	A genome-to-genome analysis of associations between human genetic variation, HIV-1 sequence diversity, and viral control. ELife, 2013, 2, e01123.	2.8	126
67	Identification of individuals by trait prediction using whole-genome sequencing data. Proceedings of the United States of America, 2017, 114, 10166-10171.	3.3	118
68	Fast and accurate HLA typing from short-read next-generation sequence data with xHLA. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 8059-8064.	3.3	118
69	Comparison of phasing strategies for whole human genomes. PLoS Genetics, 2018, 14, e1007308.	1.5	118
70	Contribution of <i>kasA</i> Analysis to Detection of Isoniazid-Resistant <i>Mycobacterium tuberculosis</i> in Singapore. Antimicrobial Agents and Chemotherapy, 1999, 43, 2087-2089.	1.4	117
71	Polymorphism of HIV Type 1 Gag p7/p1 and p1/p6 Cleavage Sites: Clinical Significance and Implications for Resistance to Protease Inhibitors. AIDS Research and Human Retroviruses, 2000, 16, 1209-1213.	0.5	117
72	Clinical Implications of Mycobacterium kansasii Species Heterogeneity: Swiss National Survey. Journal of Clinical Microbiology, 2003, 41, 1240-1244.	1.8	117

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73	Identification of Misclassified ClinVar Variants via Disease Population Prevalence. American Journal of Human Genetics, 2018, 102, 609-619.	2.6	117
74	Severe viral respiratory infections in children with <i>IFIH1</i> loss-of-function mutations. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 8342-8347.	3.3	111
75	The Evolution and Biology of SARS-CoV-2 Variants. Cold Spring Harbor Perspectives in Medicine, 2022, 12, a041390.	2.9	110
76	Association Study of Common Genetic Variants and HIV-1 Acquisition in 6,300 Infected Cases and 7,200 Controls. PLoS Pathogens, 2013, 9, e1003515.	2.1	109
77	Phylogenetic Approach Reveals That Virus Genotype Largely Determines HIV Set-Point Viral Load. PLoS Pathogens, 2010, 6, e1001123.	2.1	108
78	HIV-1 Capture and Transmission by Dendritic Cells: The Role of Viral Glycolipids and the Cellular Receptor Siglec-1. PLoS Pathogens, 2014, 10, e1004146.	2.1	108
79	HIV-Protease Inhibitors Reduce Cell Adherence of Candida Albicans Strains by Inhibition of Yeast Secreted Aspartic Proteases. Journal of Investigative Dermatology, 1999, 113, 747-751.	0.3	107
80	Intermittent and sustained low-level HIV viral rebound in patients receiving potent antiretroviral therapy. Aids, 2002, 16, 1967-1969.	1.0	107
81	Evidence of Viral Adaptation to HLA Class I-Restricted Immune Pressure in Chronic Hepatitis C Virus Infection. Journal of Virology, 2006, 80, 11094-11104.	1.5	103
82	Transplacental passage of protease inhibitors at delivery. Aids, 2002, 16, 889-893.	1.0	102
83	Mortality in the Swiss HIV Cohort Study (SHCS) and the Swiss general population. Lancet, The, 2003, 362, 877-878.	6.3	101
84	Predicting the mutational drivers of future SARS-CoV-2 variants of concern. Science Translational Medicine, 2022, 14, eabk3445.	5.8	101
85	Broadly neutralizing antibodies overcome SARS-CoV-2 Omicron antigenic shift. Nature, 0, , .	13.7	101
86	Analysis of HIV-1–  and CMV-specific memory CD4 T-cell responses during primary and chronic infection. Blood, 2002, 100, 1381-1387.	0.6	97
87	Genetic risk, dysbiosis, and treatment stratification using host genome and gut microbiome in inflammatory bowel disease. Clinical and Translational Gastroenterology, 2018, 9, e132.	1.3	97
88	Microbial metagenome of urinary tract infection. Scientific Reports, 2018, 8, 4333.	1.6	93
89	Oral administration of a low dose of midazolam (75�?g) as an in vivo probe for CYP3A activity. European Journal of Clinical Pharmacology, 2004, 60, 237-46.	0.8	89
90	Association of Pharmacogenetic Markers with Premature Discontinuation of First-line Anti-HIV Therapy: An Observational Cohort Study. Journal of Infectious Diseases, 2011, 203, 246-257.	1.9	89

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91	HIV-1 immune activation induces Siglec-1 expression and enhances viral trans-infection in blood and tissue myeloid cells. Retrovirology, 2015, 12, 37.	0.9	85
92	LILRB2 Interaction with HLA Class I Correlates with Control of HIV-1 Infection. PLoS Genetics, 2014, 10, e1004196.	1.5	83
93	Pharmacokinetics of midazolam in CYP3A4- and CYP3A5-genotyped subjects. European Journal of Clinical Pharmacology, 2004, 60, 231-6.	0.8	82
94	Population Pharmacokinetics of Atazanavir in Patients with Human Immunodeficiency Virus Infection. Antimicrobial Agents and Chemotherapy, 2006, 50, 3801-3808.	1.4	82
95	Individual Contributions of Mutant Protease and Reverse Transcriptase to Viral Infectivity, Replication, and Protein Maturation of Antiretroviral Drug-Resistant Human Immunodeficiency Virus Type 1. Journal of Virology, 2001, 75, 3291-3300.	1.5	79
96	Host and Viral Genetic Correlates of Clinical Definitions of HIV-1 Disease Progression. PLoS ONE, 2010, 5, e11079.	1.1	78
97	Identification of potential HIV restriction factors by combining evolutionary genomic signatures with functional analyses. Retrovirology, 2015, 12, 41.	0.9	78
98	Innate immunogenetics: a tool for exploring new frontiers of host defence. Lancet Infectious Diseases, The, 2007, 7, 531-542.	4.6	76
99	Resistance to Nucleoside Analog Reverse Transcriptase Inhibitors Mediated by Human Immunodeficiency Virus Type 1 p6 Protein. Journal of Virology, 2001, 75, 9644-9653.	1.5	73
100	Changes in renal function associated with indinavir. Aids, 1998, 12, F249-F254.	1.0	72
101	Variations of CYP3A activity induced by antiretroviral treatment in HIV-1 infected patients. European Journal of Clinical Pharmacology, 2005, 60, 865-873.	0.8	70
102	CCL3L1 and HIV/AIDS susceptibility. Nature Medicine, 2009, 15, 1110-1112.	15.2	70
103	Dynamics of HIV Latency and Reactivation in a Primary CD4+ T Cell Model. PLoS Pathogens, 2014, 10, e1004156.	2.1	70
104	Transcriptional Profiling of CD4 T Cells Identifies Distinct Subgroups of HIV-1 Elite Controllers. Journal of Virology, 2011, 85, 3015-3019.	1.5	69
105	Stopping primary prophylaxis in HIV-1-infected patients at high risk of toxoplasma encephalitis. Lancet, The, 2000, 355, 2217-2218.	6.3	67
106	Structure-Function Analyses Point to a Polynucleotide-Accommodating Groove Essential for APOBEC3A Restriction Activities. Journal of Virology, 2011, 85, 1765-1776.	1.5	67
107	Transcription Factor-Directed Re-wiring of Chromatin Architecture for Somatic Cell Nuclear Reprogramming toward trans-Differentiation. Molecular Cell, 2019, 76, 453-472.e8.	4.5	67
108	Orosomucoid (α1-acid glycoprotein) plasma concentration and genetic variants: Effects on human immunodeficiency virus protease inhibitor clearance and cellular accumulation. Clinical Pharmacology and Therapeutics, 2006, 80, 307-318.	2.3	66

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109	Ranking of non-coding pathogenic variants and putative essential regions of the human genome. Nature Communications, 2019, 10, 5241.	5.8	65
110	Deep learning of genomic variation and regulatory network data. Human Molecular Genetics, 2018, 27, R63-R71.	1.4	64
111	In Vitro Whole-Genome Analysis Identifies a Susceptibility Locus for HIV-1. PLoS Biology, 2008, 6, e32.	2.6	63
112	Quantitative Blood Cultures in Candidemia. Mayo Clinic Proceedings, 1991, 66, 1120-1123.	1.4	62
113	HIV-1 co/super-infection in intravenous drug users. Aids, 2004, 18, 1413-1421.	1.0	62
114	Genomics meets HIV-1. Nature Reviews Microbiology, 2006, 4, 865-873.	13.6	62
115	Analysis of HIV-1 Expression Level and Sense of Transcription by High-Throughput Sequencing of the Infected Cell. Journal of Virology, 2011, 85, 6205-6211.	1.5	62
116	<i>Sincell</i> : an R/Bioconductor package for statistical assessment of cell-state hierarchies from single-cell RNA-seq. Bioinformatics, 2015, 31, 3380-3382.	1.8	61
117	Infrequent Transmission of HIV-1 Drug-Resistant Variants. Antiviral Therapy, 2004, 9, 375-384.	0.6	59
118	Use of a Combined Ex Vivo/In Vivo Population Approach for Screening of Human Genes Involved in the Human Immunodeficiency Virus Type 1 Life Cycle for Variants Influencing Disease Progression. Journal of Virology, 2005, 79, 12674-12680.	1.5	56
119	Estimating the net contribution of interleukinâ€⊋8B variation to spontaneous hepatitis C virus clearance. Hepatology, 2011, 53, 1446-1454.	3.6	56
120	Contribution of Genetic Background, Traditional Risk Factors, and HIV-Related Factors to Coronary Artery Disease Events in HIV-Positive Persons. Clinical Infectious Diseases, 2013, 57, 112-121.	2.9	56
121	HumanImmunodeficiency Virus Type 1 Fitness Is a Determining Factor in ViralRebound and Set Point in ChronicInfection. Journal of Virology, 2003, 77, 13146-13155.	1.5	54
122	Model Structure of Human APOBEC3G. PLoS ONE, 2007, 2, e378.	1.1	53
123	Disentangling Human Tolerance and Resistance Against HIV. PLoS Biology, 2014, 12, e1001951.	2.6	53
124	Identifying Adverse Effects of HIV Drug Treatment and Associated Sentiments Using Twitter. JMIR Public Health and Surveillance, 2015, 1, e7.	1.2	53
125	Nelfinavir Plasma Levels Under Twice-Daily and Three-Times-Daily Regimens: High Interpatient and Low Intrapatient Variability. Therapeutic Drug Monitoring, 2001, 23, 394-398.	1.0	52
126	Stable virulence levels in the HIV epidemic of Switzerland over two decades. Aids, 2006, 20, 889-894.	1.0	52

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127	Analysis of Natural Variants of the Human Immunodeficiency Virus Type 1 gag-pol Frameshift Stem-Loop Structure. Journal of Virology, 2002, 76, 7868-7873.	1.5	51
128	Mapping of positive selection sites in the HIV-1 genome in the context of RNA and protein structural constraints. Retrovirology, 2011, 8, 87.	0.9	51
129	Evolutionary Trajectories of Primate Genes Involved in HIV Pathogenesis. Molecular Biology and Evolution, 2009, 26, 2865-2875.	3.5	50
130	Efavirenz decreases methadone blood concentrations. Aids, 2000, 14, 1291.	1.0	50
131	GENETICS OF DRUG RESISTANCE IN TUBERCULOSIS. Clinics in Chest Medicine, 1997, 18, 55-64.	0.8	49
132	Drug-Resistant Tuberculosis. Drugs, 2000, 59, 171-179.	4.9	48
133	Determination of Unbound Antiretroviral Drug Concentrations by a Modified Ultrafiltration Method Reveals High Variability in the Free Fraction. Therapeutic Drug Monitoring, 2008, 30, 511-522.	1.0	47
134	Entry and Transcription as Key Determinants of Differences in CD4 T-Cell Permissiveness to Human Immunodeficiency Virus Type 1 Infection. Journal of Virology, 2004, 78, 10747-10754.	1.5	46
135	Cellular immune responses to HCV core increase and HCV RNA levels decrease during successful antiretroviral therapy. Gut, 2010, 59, 1252-1258.	6.1	46
136	Safety concerns about CCR5 as an antiviral target. Current Opinion in HIV and AIDS, 2009, 4, 131-135.	1.5	45
137	A validated assay by liquid chromatography–tandem mass spectrometry for the simultaneous quantification of elvitegravir and rilpivirine in HIV positive patients. Journal of Mass Spectrometry, 2013, 48, 616-625.	0.7	45
138	Host Genetics and HIV-1: The Final Phase?. PLoS Pathogens, 2010, 6, e1001033.	2.1	44
139	Single-cell analysis identifies cellular markers of the HIV permissive cell. PLoS Pathogens, 2017, 13, e1006678.	2.1	44
140	ZNRD1 (Zinc Ribbon Domain–Containing 1) Is a Host Cellular Factor That Influences HIVâ€1 Replication and Disease Progression. Clinical Infectious Diseases, 2010, 50, 1022-1032.	2.9	42
141	Entry of Polarized Effector Cells into Quiescence Forces HIV Latency. MBio, 2019, 10, .	1.8	41
142	Homocysteinaemia in HIV-infected patients treated with highly active antiretroviral therapy. Aids, 2001, 15, 1081-1082.	1.0	41
143	Response to first protease inhibitor- and efavirenz-containing antiretroviral combination therapy The Swiss HIV Cohort Study. Aids, 2001, 15, 1793-1800.	1.0	39
144	Population Pharmacokinetic Analysis and Pharmacogenetics of Raltegravir in HIV-Positive and Healthy Individuals. Antimicrobial Agents and Chemotherapy, 2012, 56, 2959-2966.	1.4	39

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145	Protection from HIV-1 Infection of Primary Cd4 T Cells by Ccr5 Silencing is Effective for the Full Spectrum of Ccr5 Expression. Antiviral Therapy, 2003, 8, 373-377.	0.6	39
146	Contribution of Genome-Wide Significant Single-Nucleotide Polymorphisms and Antiretroviral Therapy to Dyslipidemia in HIV-Infected Individuals. Circulation: Cardiovascular Genetics, 2009, 2, 621-628.	5.1	38
147	Successful Efavirenz Dose Reduction Guided by Therapeutic Drug Monitoring. Antiviral Therapy, 2011, 16, 189-197.	0.6	38
148	A genome-wide association study of resistance to HIV infection in highly exposed uninfected individuals with hemophilia A. Human Molecular Genetics, 2013, 22, 1903-1910.	1.4	38
149	Identification of Siglec-1 null individuals infected with HIV-1. Nature Communications, 2016, 7, 12412.	5.8	38
150	Genetic, ethnic, and gender differences in the pharmacokinetics of antiretroviral agents. Current HIV/AIDS Reports, 2006, 3, 118-125.	1.1	37
151	Salvage therapy with abacavir plus a non-nucleoside reverse transcriptase inhibitor and a protease inhibitor in heavily pre-treated HIV-1 infected patients. Aids, 2000, 14, 791-799.	1.0	36
152	Population Pharmacokinetics of Indinavir in Patients Infected with Human Immunodeficiency Virus. Antimicrobial Agents and Chemotherapy, 2004, 48, 3226-3232.	1.4	36
153	Privacy-preserving genomic testing in the clinic: a model using HIV treatment. Genetics in Medicine, 2016, 18, 814-822.	1.1	36
154	SARS-CoV-2 interaction with Siglec-1 mediates trans-infection by dendritic cells. Cellular and Molecular Immunology, 2021, 18, 2676-2678.	4.8	36
155	Individualising HIV treatment—pharmacogenetics and immunogenetics. Lancet, The, 2002, 359, 722-723.	6.3	35
156	Adverse Events to Antiretrovirals in the Swiss HIV Cohort Study: Effect on Mortality and Treatment Modification. Antiviral Therapy, 2007, 12, 1157-1164.	0.6	35
157	Polymorphisms, Resistance and Drug Response: Beyond Subtype-B HIV-1. Antiviral Therapy, 2004, 9, 1-1.	0.6	35
158	The Characteristics of Heterozygous Protein Truncating Variants in the Human Genome. PLoS Computational Biology, 2015, 11, e1004647.	1.5	34
159	Silencing of both β-TrCP1 and HOS (β-TrCP2) Is Required To Suppress Human Immunodeficiency Virus Type 1 Vpu-Mediated CD4 Down-Modulation. Journal of Virology, 2007, 81, 1502-1505.	1.5	33
160	Functional characterization of 3D protein structures informed by human genetic diversity. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 8960-8965.	3.3	33
161	HIV-1 elite controllers: Beware of super-infections. Journal of Clinical Virology, 2010, 47, 376-378.	1.6	32
162	Analysis of Stop-Gain and Frameshift Variants in Human Innate Immunity Genes. PLoS Computational Biology, 2014, 10, e1003757.	1.5	32

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163	Single-Cell Genomics for Virology. Viruses, 2016, 8, 123.	1.5	32
164	Switching from protease inhibitors to efavirenz: differences in efficacy and tolerance among risk groups: a case–control study from the Swiss HIV Cohort. Aids, 2002, 16, 381-385.	1.0	31
165	Free and Total Plasma Levels of Lopinavir during Pregnancy, at Delivery and Postpartum: Implications for Dosage Adjustments in Pregnant Women. Antiviral Therapy, 2013, 18, 171-182.	0.6	31
166	New Insights into the Genetic Basis of Monge's Disease and Adaptation to High-Altitude. Molecular Biology and Evolution, 2017, 34, 3154-3168.	3.5	31
167	Long-term hydroxyurea in combination with didanosine and stavudine for the treatment of HIV-1 infection. Aids, 2000, 14, 2145-2151.	1.0	30
168	Genomics of host–pathogen interactions. Current Opinion in Immunology, 2014, 30, 32-38.	2.4	30
169	Toxicogenetics of Antiretroviral Therapy: Genetic Factors that Contribute to Metabolic Complications. Antiviral Therapy, 2007, 12, 999-1014.	0.6	30
170	The role of CFTR and SPINK-1 mutations in pancreatic disorders in HIV-positive patients. Aids, 2004, 18, 1521-1527.	1.0	29
171	Establishing the involvement of the novel gene <i>AGBL5</i> in retinitis pigmentosa by whole genome sequencing. Physiological Genomics, 2016, 48, 922-927.	1.0	29
172	Discontinuing or withholding primary prophylaxis against Mycobacterium avium in patients on successful antiretroviral combination therapy. The Swiss HIV Cohort Study. Aids, 2000, 14, 1409-1412.	1.0	28
173	<i>HLAâ€Bw4</i> Homozygosity Is Associated with an Impaired CD4 T Cell Recovery after Initiation of Antiretroviral Therapy. Clinical Infectious Diseases, 2008, 46, 1921-1925.	2.9	28
174	Estimating the Respective Contributions of Human and Viral Genetic Variation to HIV Control. PLoS Computational Biology, 2017, 13, e1005339.	1.5	28
175	Acetaminophen (Paracetamol) Use Modifies the Sulfation of Sex Hormones. EBioMedicine, 2018, 28, 316-323.	2.7	28
176	Efficacy and safety of fluvastatin in hyperlipidemic protease inhibitor-treated HIV-infected patients. Aids, 2002, 16, 1982-1983.	1.0	28
177	Ritonavir-Boosted Atazanavir-Lopinavir Combination: A Pharmacokinetic Interaction Study of Total, Unbound Plasma and Cellular Exposures. Antiviral Therapy, 2006, 11, 53-62.	0.6	28
178	Idiopathic Granulomatosis Manifesting as Fever of Unknown Origin. Mayo Clinic Proceedings, 1989, 64, 44-50.	1.4	27
179	Consistent Effects of TSG101 Genetic Variability on Multiple Outcomes of Exposure to Human Immunodeficiency Virus Type 1. Journal of Virology, 2006, 80, 6757-6763.	1.5	27
180	Antiretroviral Activity of Ancestral TRIM5α. Journal of Virology, 2008, 82, 2089-2096.	1.5	27

#	Article	IF	CITATIONS
181	In Vivo Profiling and Distribution of Known and Novel Phase I and Phase II Metabolites of Efavirenz in Plasma, Urine, and Cerebrospinal Fluid. Drug Metabolism and Disposition, 2015, 44, 151-161.	1.7	27
182	Virological and immunological characteristics of HIV treatment failure. Aids, 2000, 14, 1767-1774.	1.0	26
183	Discontinuation of primary prophylaxis in HIV-infected patients at high risk of Pneumocystis carinii pneumonia: prospective multicentre study. Aids, 2001, 15, 501-507.	1.0	26
184	Impact of Single Nucleotide Polymorphisms and of Clinical Risk Factors on Newâ€Onset Diabetes Mellitus in HIVâ€Infected Individuals. Clinical Infectious Diseases, 2010, 51, 1090-1098.	2.9	26
185	Cell disposition of raltegravir and newer antiretrovirals in HIV-infected patients: high inter-individual variability in raltegravir cellular penetration. Journal of Antimicrobial Chemotherapy, 2011, 66, 1573-1581.	1.3	25
186	Unique Spectrum of Activity of Prosimian TRIM5Â against Exogenous and Endogenous Retroviruses. Journal of Virology, 2011, 85, 4173-4183.	1.5	25
187	Hepatitis E virus as a cause of acute hepatitis acquired in Switzerland. Liver International, 2018, 38, 619-626.	1.9	25
188	Treating medical data as a durable asset. Nature Genetics, 2020, 52, 1005-1010.	9.4	25
189	Structure, receptor recognition, and antigenicity of the human coronavirus CCoV-HuPn-2018 spike glycoprotein. Cell, 2022, 185, 2279-2291.e17.	13.5	25
190	Optimizing efavirenz treatment: CYP2B6 genotyping or therapeutic drug monitoring?. European Journal of Clinical Pharmacology, 2008, 64, 335-336.	0.8	24
191	Reconciling Utility with Privacy in Genomics. , 2014, , .		24
192	Proteo-Transcriptomic Dynamics of Cellular Response to HIV-1 Infection. Scientific Reports, 2019, 9, 213.	1.6	24
193	Infectious diseases not immune to genome-wide association. Nature Genetics, 2010, 42, 731-732.	9.4	23
194	Counteraction of HLA-C-Mediated Immune Control of HIV-1 by Nef. Journal of Virology, 2010, 84, 7300-7311.	1.5	23
195	Impact of Phenotype Definition on Genome-Wide Association Signals: Empirical Evaluation in Human Immunodeficiency Virus Type 1 Infection. American Journal of Epidemiology, 2011, 173, 1336-1342.	1.6	23
196	Host Genes Important to HIV Replication and Evolution. Cold Spring Harbor Perspectives in Medicine, 2012, 2, a007203-a007203.	2.9	23
197	Exploring viral infection using single-cell sequencing. Virus Research, 2017, 239, 55-68.	1.1	23
198	MDR1Genetic Polymorphism Does Not Modify either Cell Permissiveness to HIVâ€l or Disease Progression before Treatment. Journal of Infectious Diseases, 2004, 189, 583-586.	1.9	22

#	Article	IF	CITATIONS
199	Dyslipidemia in HIV-infected individuals: from pharmacogenetics to pharmacogenomics. Pharmacogenomics, 2010, 11, 587-594.	0.6	22
200	Multiplex Liquid Chromatography-Tandem Mass Spectrometry Assay for Simultaneous Therapeutic Drug Monitoring of Ribavirin, Boceprevir, and Telaprevir. Antimicrobial Agents and Chemotherapy, 2013, 57, 3147-3158.	1.4	22
201	Advances in Genomics for Drug Development. Genes, 2020, 11, 942.	1.0	22
202	Limits to potent antiretroviral therapy. Reviews in Medical Virology, 2000, 10, 385-393.	3.9	21
203	A controlled trial of granulocyte macrophage-colony stimulating factor during interruption of HAART. Aids, 2003, 17, 1487-1492.	1.0	21
204	Determinants of Sustained Viral Suppression in HIV-Infected Patients with Self-Reported Poor Adherence to Antiretroviral Therapy. PLoS ONE, 2012, 7, e29186.	1.1	21
205	Low-Replicating Viruses and Strong Anti-Viral Immune Response Associated with Prolonged Disease Control in a Superinfected HIV-1 LTNP Elite Controller. PLoS ONE, 2012, 7, e31928.	1.1	21
206	The Interplay Between Host Genetic Variation, Viral Replication, and Microbial Translocation in Untreated HIV-Infected Individuals. Journal of Infectious Diseases, 2015, 212, 578-584.	1.9	20
207	Investigation of Efavirenz Discontinuation in Multi-ethnic Populations of HIV-positive Individuals by Genetic Analysis. EBioMedicine, 2015, 2, 706-712.	2.7	20
208	Genetic Diversity of EBV-Encoded LMP1 in the Swiss HIV Cohort Study and Implication for NF-Κb Activation. PLoS ONE, 2012, 7, e32168.	1.1	20
209	Adverse events to antiretrovirals in the Swiss HIV Cohort Study: effect on mortality and treatment modification. Antiviral Therapy, 2007, 12, 1157-64.	0.6	20
210	Are Plasma Levels Valid Surrogates for Cellular Concentrations of Antiretroviral Drugs in HIV-infected Patients?. Therapeutic Drug Monitoring, 2006, 28, 332-338.	1.0	19
211	Highly pathogenic adapted HIV-1 strains limit host immunity and dictate rapid disease progression. Aids, 2014, 28, 1261-1272.	1.0	18
212	Spare non-occupational HIV post-exposure prophylaxis by active contacting and testing of the source person. Aids, 2002, 16, 1171-1176.	1.0	17
213	Genomic Approaches to the Study of HIVâ€1 Acquisition. Journal of Infectious Diseases, 2010, 202, S382-S386.	1.9	17
214	Innate immune defects in HIV permissive cell lines. Retrovirology, 2016, 13, 43.	0.9	17
215	Development and Validation of Decision Rules to Guide Frequency of Monitoring CD4 Cell Count in HIV-1 Infection before Starting Antiretroviral Therapy. PLoS ONE, 2011, 6, e18578.	1.1	16
216	The role of tripartite motif family members in mediating susceptibility to HIV-1 infection. Current Opinion in HIV and AIDS, 2012, 7, 180-186.	1.5	16

#	Article	IF	CITATIONS
217	Development of a Molecular Typing Method for Pneumocystis carinii sp.f. hominis. Journal of Eukaryotic Microbiology, 1996, 43, 34S-34S.	0.8	15
218	Inteins in mycobacterial GyrA are a taxonomic character. Microbiology (United Kingdom), 1998, 144, 589-591.	0.7	15
219	Adaptation, co-evolution, and human susceptibility to HIV-1 infection. Infection, Genetics and Evolution, 2005, 5, 327-334.	1.0	15
220	Antiretroviral drug toxicity in relation to pharmacokinetics, metabolic profile and pharmacogenetics. Expert Opinion on Drug Metabolism and Toxicology, 2011, 7, 609-622.	1.5	15
221	Low Incidence of Communityâ€Acquired Pneumonia among Human Immunodeficiency Virus–Infected Patients after Interruption ofPneumocystis cariniiPneumonia Prophylaxis. Clinical Infectious Diseases, 2003, 36, 917-921.	2.9	14
222	Whole Genome Sequencing Revealed Mutations in Two Independent Genes as the Underlying Cause of Retinal Degeneration in an Ashkenazi Jewish Pedigree. Genes, 2017, 8, 210.	1.0	14
223	Retroviruses As Myeloid Cell Riders: What Natural Human Siglec-1 "Knockouts―Tell Us About Pathogenesis. Frontiers in Immunology, 2017, 8, 1593.	2.2	14
224	Novel insight into the genetic basis of high-altitude pulmonary hypertension in Kyrgyz highlanders. European Journal of Human Genetics, 2019, 27, 150-159.	1.4	14
225	Regulatory genome variants in human susceptibility to infection. Human Genetics, 2020, 139, 759-768.	1.8	14
226	The central region of human immunodeficiency virus type 1 p6 protein (Gag residues S14–I31) is dispensable for the virus in vitro. Journal of General Virology, 2004, 85, 921-927.	1.3	13
227	Genomic determinants of the efficiency of internal ribosomal entry sites of viral and cellular origin. Nucleic Acids Research, 2008, 36, 6918-6925.	6.5	13
228	Evolutionary genomics and HIV restriction factors. Current Opinion in HIV and AIDS, 2015, 10, 79-83.	1.5	13
229	Mycobacterial genome structure (minireview). Electrophoresis, 1998, 19, 573-576.	1.3	12
230	Bioinformatics and HIV Latency. Current HIV/AIDS Reports, 2015, 12, 97-106.	1.1	12
231	No Longitudinal Mitochondrial DNA Sequence Changes in HIV-infected Individuals With and Without Lipoatrophy. Journal of Infectious Diseases, 2011, 203, 620-624.	1.9	11
232	Chromosome Y–encoded antigens associate with acute graft-versus-host disease in sex-mismatched stem cell transplant. Blood Advances, 2018, 2, 2419-2429.	2.5	11
233	IFT88 mutations identified in individuals with non-syndromic recessive retinal degeneration result in abnormal ciliogenesis. Human Genetics, 2018, 137, 447-458.	1.8	11
234	Peripheral oedema and high arterial blood flow as a complication of antiretroviral therapy. Aids, 2004, 18, 356-358.	1.0	10

#	Article	IF	CITATIONS
235	The mixed blessing of interferon. Nature, 2014, 511, 537-538.	13.7	10
236	Dynamics of an Aging Genome. Cell Metabolism, 2016, 23, 949-950.	7.2	9
237	Dissemination of <i>Mycobacterium tuberculosis</i> is associated to a <i>SIGLEC1</i> null variant that limits antigen exchange via trafficking extracellular vesicles. Journal of Extracellular Vesicles, 2021, 10, e12046.	5.5	9
238	Spare post-exposure prophylaxis with round-the-clock HIV testing of the source patient. Aids, 2001, 15, 2451-2452.	1.0	9
239	Dosage Optimization of Treatments Using Population Pharmacokinetic Modeling and Simulation. Chimia, 2012, 66, 291-295.	0.3	8
240	Transfer transcriptomic signatures for infectious diseases. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	8
241	On genomics, kin, and privacy. F1000Research, 2014, 3, 80.	0.8	8
242	Does tenofovir influence efavirenz pharmacokinetics?. Antiviral Therapy, 2007, 12, 115-8.	0.6	8
243	Typing of Pneumocystis carinii sp.f. hominis by PCR-SSCP of Four Genomic Regions. Journal of Eukaryotic Microbiology, 1997, 44, 16s-16s.	0.8	7
244	Host factors associated with outcome from primary human immunodeficiency virus-1 infection. Current Opinion in HIV and AIDS, 2008, 3, 28-35.	1.5	7
245	A polymorphism in the leptin gene promoter is associated with anemia in patients with HIV disease. Blood, 2011, 118, 5401-5408.	0.6	7
246	HIV-1 host interactions: integration of large-scale datasets. F1000 Biology Reports, 2009, 1, 71.	4.0	7
247	HIV Lipoatrophy and Mosquito Bites. Clinical Infectious Diseases, 2002, 34, 288-289.	2.9	6
248	Interactions of Processed Nef (58-206) with Virion Proteins of HIV Type 1. AIDS Research and Human Retroviruses, 2004, 20, 399-407.	0.5	6
249	Efavirenz intoxication due to a new CYP2B6 constellation. Antiviral Therapy, 2013, 18, 735-738.	0.6	6
250	Rethinking the medical record. Lancet, The, 2018, 391, 1013.	6.3	6
251	Machine Learning to Decode Genomics. Clinical Chemistry, 2020, 66, 45-47.	1.5	6
252	State of genomics and epigenomics research in the perspective of HIV cure. Current Opinion in HIV and AIDS, 2013, 8, 176-181.	1.5	5

#	Article	IF	CITATIONS
253	Vitamin D Time Profile Based on the Contribution of Non-Genetic and Genetic Factors in HIV-Infected Individuals of European Ancestry. Antiviral Therapy, 2015, 20, 261-269.	0.6	5
254	Integrating metabolomics with genomics. Pharmacogenomics, 2018, 19, 1377-1381.	0.6	5
255	Impaired absorption of rifabutin by concomitant administration of didanosine. Aids, 2001, 15, 2203-2204.	1.0	5
256	Analysis of Brugada syndrome loci reveals that fine-mapping clustered GWAS hits enhances the annotation of disease-relevant variants. Cell Reports Medicine, 2021, 2, 100250.	3.3	4
257	Identifying Safety Concerns from Genetic Data: Lessons from the Development of CCR5 Inhibitors. Antiviral Therapy, 2007, 12, 147-148.	0.6	4
258	Host polymorphism in steps of the HIV-1 lifecycle after entry and other genetic variants influencing HIV-1 pathogenesis. Current Opinion in HIV and AIDS, 2006, 1, 232-240.	1.5	3
259	European Genetic Diversity and Susceptibility to Pathogens. Human Heredity, 2013, 76, 187-193.	0.4	3
260	Simulating patient matching to clinical trials using a property rights blockchain. Digital Medicine, 2020, 6, 44.	0.1	2
261	Genomics of HIV infection. Current Opinion in HIV and AIDS, 2015, 10, 77-78.	1.5	1
262	Fine population structure analysis method for genomes of many. Scientific Reports, 2017, 7, 12608.	1.6	1
263	Response to Whiffin etÂal American Journal of Human Genetics, 2019, 104, 186.	2.6	1
264	<scp>MPâ€NeRF</scp> : A massively parallel method for accelerating protein structure reconstruction from internal coordinates. Journal of Computational Chemistry, 2022, 43, 74-78.	1.5	1
265	HIV Susceptibility Testing – Time for Standards. Antiviral Therapy, 2004, 9, 463-464.	0.6	1
266	Resistance to New Anti-HIV Agents: Problems in the Pathway of Drug Registration. Antiviral Therapy, 2005, 10, 867-872.	0.6	1
267	Nucleic acid amplification methods in diagnostic virology. Journal of Microbiological Methods, 1995, 23, 31-39.	0.7	0
268	HIV epidemiology and treatment – 1999. Ocular Immunology and Inflammation, 1999, 7, 129-132.	1.0	0