

Amalio Telenti

List of Publications by Year in descending order

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Version: 2024-02-01

268
papers

34,096
citations

4658

85
h-index

4645

170
g-index

298
all docs

298
docs citations

298
times ranked

38446
citing authors

#	ARTICLE	IF	CITATIONS
1	<scp>MP–NeRF</scp>: A massively parallel method for accelerating protein structure reconstruction from internal coordinates. Journal of Computational Chemistry, 2022, 43, 74-78.	3.3	1
2	Predicting the mutational drivers of future SARS-CoV-2 variants of concern. Science Translational Medicine, 2022, 14, eabk3445.	12.4	101
3	Broadly neutralizing antibodies overcome SARS-CoV-2 Omicron antigenic shift. Nature, 2022, 602, 664-670.	27.8	917
4	The Evolution and Biology of SARS-CoV-2 Variants. Cold Spring Harbor Perspectives in Medicine, 2022, 12, a041390.	6.2	110
5	Structure, receptor recognition, and antigenicity of the human coronavirus CCoV-HuPn-2018 spike glycoprotein. Cell, 2022, 185, 2279-2291.e17.	28.9	25
6	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.	12.2	9
7	Circulating SARS-CoV-2 spike N439K variants maintain fitness while evading antibody-mediated immunity. Cell, 2021, 184, 1171-1187.e20.	28.9	541
8	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.	6.5	4
9	N-terminal domain antigenic mapping reveals a site of vulnerability for SARS-CoV-2. Cell, 2021, 184, 2332-2347.e16.	28.9	784
10	Transfer transcriptomic signatures for infectious diseases. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	8
11	SARS-CoV-2 immune evasion by the B.1.427/B.1.429 variant of concern. Science, 2021, 373, 648-654.	12.6	385
12	After the pandemic: perspectives on the future trajectory of COVID-19. Nature, 2021, 596, 495-504.	27.8	260
13	Broad sarbecovirus neutralization by a human monoclonal antibody. Nature, 2021, 597, 103-108.	27.8	220
14	SARS-CoV-2 RBD antibodies that maximize breadth and resistance to escape. Nature, 2021, 597, 97-102.	27.8	385
15	Lectins enhance SARS-CoV-2 infection and influence neutralizing antibodies. Nature, 2021, 598, 342-347.	27.8	230
16	Broad betacoronavirus neutralization by a stem helix–specific human antibody. Science, 2021, 373, 1109-1116.	12.6	262
17	SARS-CoV-2 interaction with Siglec-1 mediates trans-infection by dendritic cells. Cellular and Molecular Immunology, 2021, 18, 2676-2678.	10.5	36
18	Machine Learning to Decode Genomics. Clinical Chemistry, 2020, 66, 45-47.	3.2	6

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19	Regulatory genome variants in human susceptibility to infection. Human Genetics, 2020, 139, 759-768.	3.8	14
20	Advances in Genomics for Drug Development. Genes, 2020, 11, 942.	2.4	22
21	Treating medical data as a durable asset. Nature Genetics, 2020, 52, 1005-1010.	21.4	25
22	Cross-neutralization of SARS-CoV-2 by a human monoclonal SARS-CoV antibody. Nature, 2020, 583, 290-295.	27.8	1,695
23	Simulating patient matching to clinical trials using a property rights blockchain. Digital Medicine, 2020, 6, 44.	0.1	2
24	Transcription Factor-Directed Re-wiring of Chromatin Architecture for Somatic Cell Nuclear Reprogramming toward trans-Differentiation. Molecular Cell, 2019, 76, 453-472.e8.	9.7	67
25	Proteo-Transcriptomic Dynamics of Cellular Response to HIV-1 Infection. Scientific Reports, 2019, 9, 213.	3.3	24
26	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.	7.1	33
27	Entry of Polarized Effector Cells into Quiescence Forces HIV Latency. MBio, 2019, 10, .	4.1	41
28	Ranking of non-coding pathogenic variants and putative essential regions of the human genome. Nature Communications, 2019, 10, 5241.	12.8	65
29	A primer on deep learning in genomics. Nature Genetics, 2019, 51, 12-18.	21.4	542
30	Response to Whiffin etÂal.. American Journal of Human Genetics, 2019, 104, 186.	6.2	1
31	Profound Perturbation of the Metabolome in Obesity Is Associated with Health Risk. Cell Metabolism, 2019, 29, 488-500.e2.	16.2	235
32	Novel insight into the genetic basis of high-altitude pulmonary hypertension in Kyrgyz highlanders. European Journal of Human Genetics, 2019, 27, 150-159.	2.8	14
33	Acetaminophen (Paracetamol) Use Modifies the Sulfation of Sex Hormones. EBioMedicine, 2018, 28, 316-323.	6.1	28
34	The human noncoding genome defined by genetic diversity. Nature Genetics, 2018, 50, 333-337.	21.4	137
35	Paternally inherited cis-regulatory structural variants are associated with autism. Science, 2018, 360, 327-331.	12.6	174
36	Identification of Misclassified ClinVar Variants via Disease Population Prevalence. American Journal of Human Genetics, 2018, 102, 609-619.	6.2	117

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37	Deep learning of genomic variation and regulatory network data. Human Molecular Genetics, 2018, 27, R63-R71.	2.9	64
38	Genetic risk, dysbiosis, and treatment stratification using host genome and gut microbiome in inflammatory bowel disease. Clinical and Translational Gastroenterology, 2018, 9, e132.	2.5	97
39	Rethinking the medical record. Lancet, The, 2018, 391, 1013.	13.7	6
40	Microbial metagenome of urinary tract infection. Scientific Reports, 2018, 8, 4333.	3.3	93
41	Human gene essentiality. Nature Reviews Genetics, 2018, 19, 51-62.	16.3	213
42	Hepatitis E virus as a cause of acute hepatitis acquired in Switzerland. Liver International, 2018, 38, 619-626.	3.9	25
43	Integrating metabolomics with genomics. Pharmacogenomics, 2018, 19, 1377-1381.	1.3	5
44	Chromosome Yâ€‘encoded antigens associate with acute graft-versus-host disease in sex-mismatched stem cell transplant. Blood Advances, 2018, 2, 2419-2429.	5.2	11
45	The fecal metabolome as a functional readout of the gut microbiome. Nature Genetics, 2018, 50, 790-795.	21.4	482
46	Comparison of phasing strategies for whole human genomes. PLoS Genetics, 2018, 14, e1007308.	3.5	118
47	IFT88 mutations identified in individuals with non-syndromic recessive retinal degeneration result in abnormal ciliogenesis. Human Genetics, 2018, 137, 447-458.	3.8	11
48	The Human Microbiome and Cancer. Cancer Prevention Research, 2017, 10, 226-234.	1.5	230
49	Whole-genome sequencing identifies common-to-rare variants associated with human blood metabolites. Nature Genetics, 2017, 49, 568-578.	21.4	341
50	Profiling of Short-Tandem-Repeat Disease Alleles in 12,632 Human Whole Genomes. American Journal of Human Genetics, 2017, 101, 700-715.	6.2	142
51	Fine population structure analysis method for genomes of many. Scientific Reports, 2017, 7, 12608.	3.3	1
52	New Insights into the Genetic Basis of Mongeâ€™s Disease and Adaptation to High-Altitude. Molecular Biology and Evolution, 2017, 34, 3154-3168.	8.9	31
53	Identification of individuals by trait prediction using whole-genome sequencing data. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 10166-10171.	7.1	118
54	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.	7.1	111

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55	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.	7.1	118
56	Exploring viral infection using single-cell sequencing. Virus Research, 2017, 239, 55-68.	2.2	23
57	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.	2.4	14
58	Retroviruses As Myeloid Cell Riders: What Natural Human Siglec-1 "Knockouts" Tell Us About Pathogenesis. Frontiers in Immunology, 2017, 8, 1593.	4.8	14
59	Estimating the Respective Contributions of Human and Viral Genetic Variation to HIV Control. PLoS Computational Biology, 2017, 13, e1005339.	3.2	28
60	The blood DNA virome in 8,000 humans. PLoS Pathogens, 2017, 13, e1006292.	4.7	259
61	Single-cell analysis identifies cellular markers of the HIV permissive cell. PLoS Pathogens, 2017, 13, e1006678.	4.7	44
62	Single-Cell Genomics for Virology. Viruses, 2016, 8, 123.	3.3	32
63	Innate immune defects in HIV permissive cell lines. Retrovirology, 2016, 13, 43.	2.0	17
64	Establishing the involvement of the novel gene <i>AGBL5</i> in retinitis pigmentosa by whole genome sequencing. Physiological Genomics, 2016, 48, 922-927.	2.3	29
65	Privacy-preserving genomic testing in the clinic: a model using HIV treatment. Genetics in Medicine, 2016, 18, 814-822.	2.4	36
66	Deep sequencing of 10,000 human genomes. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 11901-11906.	7.1	315
67	Identification of Siglec-1 null individuals infected with HIV-1. Nature Communications, 2016, 7, 12412.	12.8	38
68	Dynamics of an Aging Genome. Cell Metabolism, 2016, 23, 949-950.	16.2	9
69	Guanylate Binding Protein (GBP) 5 Is an Interferon-Inducible Inhibitor of HIV-1 Infectivity. Cell Host and Microbe, 2016, 19, 504-514.	11.0	211
70	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.	1.0	5
71	The Characteristics of Heterozygous Protein Truncating Variants in the Human Genome. PLoS Computational Biology, 2015, 11, e1004647.	3.2	34
72	Genomics of HIV infection. Current Opinion in HIV and AIDS, 2015, 10, 77-78.	3.8	1

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73	HIV-1 immune activation induces Siglec-1 expression and enhances viral trans-infection in blood and tissue myeloid cells. <i>Retrovirology</i> , 2015, 12, 37.	2.0	85
74	Identification of potential HIV restriction factors by combining evolutionary genomic signatures with functional analyses. <i>Retrovirology</i> , 2015, 12, 41.	2.0	78
75	In Vivo Profiling and Distribution of Known and Novel Phase I and Phase II Metabolites of Efavirenz in Plasma, Urine, and Cerebrospinal Fluid. <i>Drug Metabolism and Disposition</i> , 2015, 44, 151-161.	3.3	27
76	Polymorphisms of large effect explain the majority of the host genetic contribution to variation of HIV-1 virus load. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 14658-14663.	7.1	154
77	<i>scell</i> : an R/Bioconductor package for statistical assessment of cell-state hierarchies from single-cell RNA-seq. <i>Bioinformatics</i> , 2015, 31, 3380-3382.	4.1	61
78	Bioinformatics and HIV Latency. <i>Current HIV/AIDS Reports</i> , 2015, 12, 97-106.	3.1	12
79	The Interplay Between Host Genetic Variation, Viral Replication, and Microbial Translocation in Untreated HIV-Infected Individuals. <i>Journal of Infectious Diseases</i> , 2015, 212, 578-584.	4.0	20
80	Evolutionary genomics and HIV restriction factors. <i>Current Opinion in HIV and AIDS</i> , 2015, 10, 79-83.	3.8	13
81	Investigation of Efavirenz Discontinuation in Multi-ethnic Populations of HIV-positive Individuals by Genetic Analysis. <i>EBioMedicine</i> , 2015, 2, 706-712.	6.1	20
82	Identifying Adverse Effects of HIV Drug Treatment and Associated Sentiments Using Twitter. <i>JMIR Public Health and Surveillance</i> , 2015, 1, e7.	2.6	53
83	Disentangling Human Tolerance and Resistance Against HIV. <i>PLoS Biology</i> , 2014, 12, e1001951.	5.6	53
84	Dynamics of HIV Latency and Reactivation in a Primary CD4+ T Cell Model. <i>PLoS Pathogens</i> , 2014, 10, e1004156.	4.7	70
85	LILRB2 Interaction with HLA Class I Correlates with Control of HIV-1 Infection. <i>PLoS Genetics</i> , 2014, 10, e1004196.	3.5	83
86	HIV-1 Capture and Transmission by Dendritic Cells: The Role of Viral Glycolipids and the Cellular Receptor Siglec-1. <i>PLoS Pathogens</i> , 2014, 10, e1004146.	4.7	108
87	Analysis of Stop-Gain and Frameshift Variants in Human Innate Immunity Genes. <i>PLoS Computational Biology</i> , 2014, 10, e1003757.	3.2	32
88	Reconciling Utility with Privacy in Genomics. , 2014, , .		24
89	Highly pathogenic adapted HIV-1 strains limit host immunity and dictate rapid disease progression. <i>Aids</i> , 2014, 28, 1261-1272.	2.2	18
90	Antiretroviral Treatment of Adult HIV Infection. <i>JAMA - Journal of the American Medical Association</i> , 2014, 312, 410.	7.4	428

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91	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. <i>Journal of Virology</i> , 2014, 88, 10056-10065.	3.4	242
92	The mixed blessing of interferon. <i>Nature</i> , 2014, 511, 537-538.	27.8	10
93	Genomics of host–pathogen interactions. <i>Current Opinion in Immunology</i> , 2014, 30, 32-38.	5.5	30
94	SAMHD1 is mutated recurrently in chronic lymphocytic leukemia and is involved in response to DNA damage. <i>Blood</i> , 2014, 123, 1021-1031.	1.4	205
95	On genomics, kin, and privacy. <i>F1000Research</i> , 2014, 3, 80.	1.6	8
96	Free and Total Plasma Levels of Lopinavir during Pregnancy, at Delivery and Postpartum: Implications for Dosage Adjustments in Pregnant Women. <i>Antiviral Therapy</i> , 2013, 18, 171-182.	1.0	31
97	Contribution of Genetic Background, Traditional Risk Factors, and HIV-Related Factors to Coronary Artery Disease Events in HIV-Positive Persons. <i>Clinical Infectious Diseases</i> , 2013, 57, 112-121.	5.8	56
98	Multiplex Liquid Chromatography-Tandem Mass Spectrometry Assay for Simultaneous Therapeutic Drug Monitoring of Ribavirin, Boceprevir, and Telaprevir. <i>Antimicrobial Agents and Chemotherapy</i> , 2013, 57, 3147-3158.	3.2	22
99	24 Hours in the Life of HIV-1 in a T Cell Line. <i>PLoS Pathogens</i> , 2013, 9, e1003161.	4.7	134
100	Association Study of Common Genetic Variants and HIV-1 Acquisition in 6,300 Infected Cases and 7,200 Controls. <i>PLoS Pathogens</i> , 2013, 9, e1003515.	4.7	109
101	State of genomics and epigenomics research in the perspective of HIV cure. <i>Current Opinion in HIV and AIDS</i> , 2013, 8, 176-181.	3.8	5
102	A genome-wide association study of resistance to HIV infection in highly exposed uninfected individuals with hemophilia A. <i>Human Molecular Genetics</i> , 2013, 22, 1903-1910.	2.9	38
103	A validated assay by liquid chromatography–tandem mass spectrometry for the simultaneous quantification of elvitegravir and rilpivirine in HIV positive patients. <i>Journal of Mass Spectrometry</i> , 2013, 48, 616-625.	1.6	45
104	Efavirenz intoxication due to a new CYP2B6 constellation. <i>Antiviral Therapy</i> , 2013, 18, 735-738.	1.0	6
105	European Genetic Diversity and Susceptibility to Pathogens. <i>Human Heredity</i> , 2013, 76, 187-193.	0.8	3
106	A genome-to-genome analysis of associations between human genetic variation, HIV-1 sequence diversity, and viral control. <i>ELife</i> , 2013, 2, e01123.	6.0	126
107	Siglec-1 Is a Novel Dendritic Cell Receptor That Mediates HIV-1 Trans-Infection Through Recognition of Viral Membrane Gangliosides. <i>PLoS Biology</i> , 2012, 10, e1001448.	5.6	208
108	The role of tripartite motif family members in mediating susceptibility to HIV-1 infection. <i>Current Opinion in HIV and AIDS</i> , 2012, 7, 180-186.	3.8	16

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109	Population Pharmacokinetic Analysis and Pharmacogenetics of Raltegravir in HIV-Positive and Healthy Individuals. <i>Antimicrobial Agents and Chemotherapy</i> , 2012, 56, 2959-2966.	3.2	39
110	Dosage Optimization of Treatments Using Population Pharmacokinetic Modeling and Simulation. <i>Chimia</i> , 2012, 66, 291-295.	0.6	8
111	Evolutionary and Functional Analyses of the Interaction between the Myeloid Restriction Factor SAMHD1 and the Lentiviral Vpx Protein. <i>Cell Host and Microbe</i> , 2012, 11, 205-217.	11.0	169
112	Host Genes Important to HIV Replication and Evolution. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2012, 2, a007203-a007203.	6.2	23
113	Towards an HIV cure: a global scientific strategy. <i>Nature Reviews Immunology</i> , 2012, 12, 607-614.	22.7	485
114	Antiretroviral Treatment of Adult HIV Infection. <i>JAMA - Journal of the American Medical Association</i> , 2012, 308, 387-402.	7.4	1,239
115	Determinants of Sustained Viral Suppression in HIV-Infected Patients with Self-Reported Poor Adherence to Antiretroviral Therapy. <i>PLoS ONE</i> , 2012, 7, e29186.	2.5	21
116	Low-Replicating Viruses and Strong Anti-Viral Immune Response Associated with Prolonged Disease Control in a Superinfected HIV-1 LTNP Elite Controller. <i>PLoS ONE</i> , 2012, 7, e31928.	2.5	21
117	Genetic Diversity of EBV-Encoded LMP1 in the Swiss HIV Cohort Study and Implication for NF- κ B Activation. <i>PLoS ONE</i> , 2012, 7, e32168.	2.5	20
118	Antiretroviral drug toxicity in relation to pharmacokinetics, metabolic profile and pharmacogenetics. <i>Expert Opinion on Drug Metabolism and Toxicology</i> , 2011, 7, 609-622.	3.3	15
119	A polymorphism in the leptin gene promoter is associated with anemia in patients with HIV disease. <i>Blood</i> , 2011, 118, 5401-5408.	1.4	7
120	Copy Number Variation of KIR Genes Influences HIV-1 Control. <i>PLoS Biology</i> , 2011, 9, e1001208.	5.6	132
121	Development and Validation of Decision Rules to Guide Frequency of Monitoring CD4 Cell Count in HIV-1 Infection before Starting Antiretroviral Therapy. <i>PLoS ONE</i> , 2011, 6, e18578.	2.5	16
122	Successful Efavirenz Dose Reduction Guided by Therapeutic Drug Monitoring. <i>Antiviral Therapy</i> , 2011, 16, 189-197.	1.0	38
123	Lausannevirus, a giant amoebal virus encoding histone doublets. <i>Environmental Microbiology</i> , 2011, 13, 1454-1466.	3.8	164
124	Differential microRNA regulation of HLA-C expression and its association with HIV control. <i>Nature</i> , 2011, 472, 495-498.	27.8	328
125	Mapping of positive selection sites in the HIV-1 genome in the context of RNA and protein structural constraints. <i>Retrovirology</i> , 2011, 8, 87.	2.0	51
126	Estimating the net contribution of interleukin-28B variation to spontaneous hepatitis C virus clearance. <i>Hepatology</i> , 2011, 53, 1446-1454.	7.3	56

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127	Transcriptional Profiling of CD4 T Cells Identifies Distinct Subgroups of HIV-1 Elite Controllers. <i>Journal of Virology</i> , 2011, 85, 3015-3019.	3.4	69
128	Impact of Phenotype Definition on Genome-Wide Association Signals: Empirical Evaluation in Human Immunodeficiency Virus Type 1 Infection. <i>American Journal of Epidemiology</i> , 2011, 173, 1336-1342.	3.4	23
129	Cell disposition of raltegravir and newer antiretrovirals in HIV-infected patients: high inter-individual variability in raltegravir cellular penetration. <i>Journal of Antimicrobial Chemotherapy</i> , 2011, 66, 1573-1581.	3.0	25
130	No Longitudinal Mitochondrial DNA Sequence Changes in HIV-infected Individuals With and Without Lipotrophy. <i>Journal of Infectious Diseases</i> , 2011, 203, 620-624.	4.0	11
131	Structure-Function Analyses Point to a Polynucleotide-Accommodating Groove Essential for APOBEC3A Restriction Activities. <i>Journal of Virology</i> , 2011, 85, 1765-1776.	3.4	67
132	Analysis of HIV-1 Expression Level and Sense of Transcription by High-Throughput Sequencing of the Infected Cell. <i>Journal of Virology</i> , 2011, 85, 6205-6211.	3.4	62
133	Unique Spectrum of Activity of Prosimian TRIM5 α against Exogenous and Endogenous Retroviruses. <i>Journal of Virology</i> , 2011, 85, 4173-4183.	3.4	25
134	Association of Pharmacogenetic Markers with Premature Discontinuation of First-line Anti-HIV Therapy: An Observational Cohort Study. <i>Journal of Infectious Diseases</i> , 2011, 203, 246-257.	4.0	89
135	Comparative transcriptomics of extreme phenotypes of human HIV-1 infection and SIV infection in sooty mangabey and rhesus macaque. <i>Journal of Clinical Investigation</i> , 2011, 121, 2391-2400.	8.2	168
136	Infectious diseases not immune to genome-wide association. <i>Nature Genetics</i> , 2010, 42, 731-732.	21.4	23
137	Critical role for the chemokine receptor CXCR6 in NK cell-mediated antigen-specific memory of haptens and viruses. <i>Nature Immunology</i> , 2010, 11, 1127-1135.	14.5	644
138	Host and Viral Genetic Correlates of Clinical Definitions of HIV-1 Disease Progression. <i>PLoS ONE</i> , 2010, 5, e11079.	2.5	78
139	Dyslipidemia in HIV-infected individuals: from pharmacogenetics to pharmacogenomics. <i>Pharmacogenomics</i> , 2010, 11, 587-594.	1.3	22
140	Impact of Single Nucleotide Polymorphisms and of Clinical Risk Factors on New-Onset Diabetes Mellitus in HIV-Infected Individuals. <i>Clinical Infectious Diseases</i> , 2010, 51, 1090-1098.	5.8	26
141	ZNRD1 (Zinc Ribbon Domain-Containing 1) Is a Host Cellular Factor That Influences HIV-1 Replication and Disease Progression. <i>Clinical Infectious Diseases</i> , 2010, 50, 1022-1032.	5.8	42
142	Cellular immune responses to HCV core increase and HCV RNA levels decrease during successful antiretroviral therapy. <i>Gut</i> , 2010, 59, 1252-1258.	12.1	46
143	Counteraction of HLA-C-Mediated Immune Control of HIV-1 by Nef. <i>Journal of Virology</i> , 2010, 84, 7300-7311.	3.4	23
144	Genomic Approaches to the Study of HIV-1 Acquisition. <i>Journal of Infectious Diseases</i> , 2010, 202, S382-S386.	4.0	17

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145	Cohort Profile: The Swiss HIV Cohort Study. International Journal of Epidemiology, 2010, 39, 1179-1189.	1.9	322
146	Phylogenetic Approach Reveals That Virus Genotype Largely Determines HIV Set-Point Viral Load. PLoS Pathogens, 2010, 6, e1001123.	4.7	108
147	Genome-Wide mRNA Expression Correlates of Viral Control in CD4+ T-Cells from HIV-1-Infected Individuals. PLoS Pathogens, 2010, 6, e1000781.	4.7	158
148	Host Genetics and HIV-1: The Final Phase?. PLoS Pathogens, 2010, 6, e1001033.	4.7	44
149	Antiretroviral Treatment of Adult HIV Infection. JAMA - Journal of the American Medical Association, 2010, 304, 321.	7.4	732
150	HIV-1 elite controllers: Beware of super-infections. Journal of Clinical Virology, 2010, 47, 376-378.	3.1	32
151	The Major Genetic Determinants of HIV-1 Control Affect HLA Class I Peptide Presentation. Science, 2010, 330, 1551-1557.	12.6	1,054
152	Evolutionary Trajectories of Primate Genes Involved in HIV Pathogenesis. Molecular Biology and Evolution, 2009, 26, 2865-2875.	8.9	50
153	Common Genetic Variation and the Control of HIV-1 in Humans. PLoS Genetics, 2009, 5, e1000791.	3.5	377
154	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
155	HLA-C cell surface expression and control of HIV/AIDS correlate with a variant upstream of HLA-C. Nature Genetics, 2009, 41, 1290-1294.	21.4	265
156	CCL3L1 and HIV/AIDS susceptibility. Nature Medicine, 2009, 15, 1110-1112.	30.7	70
157	Safety concerns about CCR5 as an antiviral target. Current Opinion in HIV and AIDS, 2009, 4, 131-135.	3.8	45
158	HIV-1 host interactions: integration of large-scale datasets. F1000 Biology Reports, 2009, 1, 71.	4.0	7
159	Optimizing efavirenz treatment: CYP2B6 genotyping or therapeutic drug monitoring?. European Journal of Clinical Pharmacology, 2008, 64, 335-336.	1.9	24
160	Genomic determinants of the efficiency of internal ribosomal entry sites of viral and cellular origin. Nucleic Acids Research, 2008, 36, 6918-6925.	14.5	13
161	HLA-B*47:01 Homozygosity Is Associated with an Impaired CD4 T Cell Recovery after Initiation of Antiretroviral Therapy. Clinical Infectious Diseases, 2008, 46, 1921-1925.	5.8	28
162	Antiretroviral Activity of Ancestral TRIM5 α . Journal of Virology, 2008, 82, 2089-2096.	3.4	27

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163	WGAVIEWER: Software for genomic annotation of whole genome association studies: Figure 1.. Genome Research, 2008, 18, 640-643.	5.5	147
164	In Vitro Whole-Genome Analysis Identifies a Susceptibility Locus for HIV-1. PLoS Biology, 2008, 6, e32.	5.6	63
165	Host factors associated with outcome from primary human immunodeficiency virus-1 infection. Current Opinion in HIV and AIDS, 2008, 3, 28-35.	3.8	7
166	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.	2.0	47
167	Polymorphisms in Toll-like receptor 9 influence the clinical course of HIV-1 infection. Aids, 2007, 21, 441-446.	2.2	139
168	Silencing of both β 2-TrCP1 and HOS (β 2-TrCP2) Is Required To Suppress Human Immunodeficiency Virus Type 1 Vpu-Mediated CD4 Down-Modulation. Journal of Virology, 2007, 81, 1502-1505.	3.4	33
169	HIV entry inhibitors. Lancet, The, 2007, 370, 81-88.	13.7	264
170	Innate immunogenetics: a tool for exploring new frontiers of host defence. Lancet Infectious Diseases, The, 2007, 7, 531-542.	9.1	76
171	A Whole-Genome Association Study of Major Determinants for Host Control of HIV-1. Science, 2007, 317, 944-947.	12.6	1,136
172	Model Structure of Human APOBEC3G. PLoS ONE, 2007, 2, e378.	2.5	53
173	Innate partnership of HLA-B and KIR3DL1 subtypes against HIV-1. Nature Genetics, 2007, 39, 733-740.	21.4	691
174	Does tenofovir influence efavirenz pharmacokinetics?. Antiviral Therapy, 2007, 12, 115-8.	1.0	8
175	Adverse events to antiretrovirals in the Swiss HIV Cohort Study: effect on mortality and treatment modification. Antiviral Therapy, 2007, 12, 1157-64.	1.0	20
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