

Jacques Fellay

List of Publications by Year in descending order

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Version: 2024-02-01

195
papers

18,919
citations

28190

55
h-index

13338

130
g-index

246
all docs

246
docs citations

246
times ranked

23594
citing authors

#	ARTICLE	IF	CITATIONS
1	Genetic variation in IL28B predicts hepatitis C treatment-induced viral clearance. <i>Nature</i> , 2009, 461, 399-401.	13.7	3,394
2	Inborn errors of type I IFN immunity in patients with life-threatening COVID-19. <i>Science</i> , 2020, 370, .	6.0	1,749
3	A Whole-Genome Association Study of Major Determinants for Host Control of HIV-1. <i>Science</i> , 2007, 317, 944-947.	6.0	1,136
4	Response to antiretroviral treatment in HIV-1-infected individuals with allelic variants of the multidrug resistance transporter 1: a pharmacogenetics study. <i>Lancet, The</i> , 2002, 359, 30-36.	6.3	635
5	Interleukin-28B Polymorphism Improves Viral Kinetics and Is the Strongest Pretreatment Predictor of Sustained Virologic Response in Genotype 1 Hepatitis C Virus. <i>Gastroenterology</i> , 2010, 139, 120-129.e18.	0.6	633
6	ITPA gene variants protect against anaemia in patients treated for chronic hepatitis C. <i>Nature</i> , 2010, 464, 405-408.	13.7	430
7	Common Genetic Variation and the Control of HIV-1 in Humans. <i>PLoS Genetics</i> , 2009, 5, e1000791.	1.5	377
8	Autoantibodies neutralizing type I IFNs are present in ~4% of uninfected individuals over 70 years old and account for ~20% of COVID-19 deaths. <i>Science Immunology</i> , 2021, 6, .	5.6	357
9	Influence of HLA-C Expression Level on HIV Control. <i>Science</i> , 2013, 340, 87-91.	6.0	352
10	A global scientific strategy to cure hepatitis B. <i>The Lancet Gastroenterology and Hepatology</i> , 2019, 4, 545-558.	3.7	342
11	IL28B genotype is associated with differential expression of intrahepatic interferon-stimulated genes in patients with chronic hepatitis C. <i>Hepatology</i> , 2010, 52, 1888-1896.	3.6	332
12	Prevalence of adverse events associated with potent antiretroviral treatment: Swiss HIV Cohort Study. <i>Lancet, The</i> , 2001, 358, 1322-1327.	6.3	317
13	X-linked recessive TLR7 deficiency in ~1% of men under 60 years old with life-threatening COVID-19. <i>Science Immunology</i> , 2021, 6, .	5.6	267
14	HLA-C cell surface expression and control of HIV/AIDS correlate with a variant upstream of HLA-C. <i>Nature Genetics</i> , 2009, 41, 1290-1294.	9.4	265
15	Population pharmacokinetics and effects of efavirenz in patients with human immunodeficiency virus infection. <i>Clinical Pharmacology and Therapeutics</i> , 2003, 73, 20-30.	2.3	231
16	Human genetic and immunological determinants of critical COVID-19 pneumonia. <i>Nature</i> , 2022, 603, 587-598.	13.7	216
17	Natural variation in the parameters of innate immune cells is preferentially driven by genetic factors. <i>Nature Immunology</i> , 2018, 19, 302-314.	7.0	205
18	Privacy in the Genomic Era. <i>ACM Computing Surveys</i> , 2015, 48, 1-44.	16.1	197

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19	A Global Effort to Define the Human Genetics of Protective Immunity to SARS-CoV-2 Infection. <i>Cell</i> , 2020, 181, 1194-1199.	13.5	185
20	Distinctive roles of age, sex, and genetics in shaping transcriptional variation of human immune responses to microbial challenges. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E488-E497.	3.3	181
21	Variants in the ITPA Gene Protect Against Ribavirin-Induced Hemolytic Anemia and Decrease the Need for Ribavirin Dose Reduction. <i>Gastroenterology</i> , 2010, 139, 1181-1189.e2.	0.6	171
22	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.	3.9	168
23	Evidence of dysregulation of dendritic cells in primary HIV infection. <i>Blood</i> , 2010, 116, 3839-3852.	0.6	159
24	Genome-Wide mRNA Expression Correlates of Viral Control in CD4+ T-Cells from HIV-1-Infected Individuals. <i>PLoS Pathogens</i> , 2010, 6, e1000781.	2.1	158
25	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.	3.3	154
26	WGAVIEWER: Software for genomic annotation of whole genome association studies: Figure 1.. <i>Genome Research</i> , 2008, 18, 640-643.	2.4	147
27	Host Determinants of HIV-1 Control in African Americans. <i>Journal of Infectious Diseases</i> , 2010, 201, 1141-1149.	1.9	145
28	The Characterization of Twenty Sequenced Human Genomes. <i>PLoS Genetics</i> , 2010, 6, e1001111.	1.5	144
29	Elevated HLA-A expression impairs HIV control through inhibition of NKG2A-expressing cells. <i>Science</i> , 2018, 359, 86-90.	6.0	135
30	Determinants of HIV-1 broadly neutralizing antibody induction. <i>Nature Medicine</i> , 2016, 22, 1260-1267.	15.2	133
31	Copy Number Variation of KIR Genes Influences HIV-1 Control. <i>PLoS Biology</i> , 2011, 9, e1001208.	2.6	132
32	Hepatitis C pharmacogenetics: State of the art in 2010. <i>Hepatology</i> , 2011, 53, 336-345.	3.6	131
33	Role of retroviral restriction factors in the interferon- γ -mediated suppression of HIV-1 in vivo. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 3035-3040.	3.3	129
34	Genome-to-genome analysis highlights the effect of the human innate and adaptive immune systems on the hepatitis C virus. <i>Nature Genetics</i> , 2017, 49, 666-673.	9.4	129
35	A genome-to-genome analysis of associations between human genetic variation, HIV-1 sequence diversity, and viral control. <i>ELife</i> , 2013, 2, e01123.	2.8	126
36	Gender medicine and oncology: report and consensus of an ESMO workshop. <i>Annals of Oncology</i> , 2019, 30, 1914-1924.	0.6	120

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37	Genetics of human susceptibility to active and latent tuberculosis: present knowledge and future perspectives. <i>Lancet Infectious Diseases</i> , The, 2018, 18, e64-e75.	4.6	119
38	Human genetic variants and age are the strongest predictors of humoral immune responses to common pathogens and vaccines. <i>Genome Medicine</i> , 2018, 10, 59.	3.6	113
39	Determinants of HIV-1 reservoir size and long-term dynamics during suppressive ART. <i>Nature Communications</i> , 2019, 10, 3193.	5.8	112
40	Inosine Triphosphate Protects Against Ribavirin-Induced Adenosine Triphosphate Loss by Adenylosuccinate Synthase Function. <i>Gastroenterology</i> , 2011, 140, 1314-1321.	0.6	111
41	Severe viral respiratory infections in children with <i>IFIH1</i> loss-of-function mutations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 8342-8347.	3.3	111
42	The risk of COVID-19 death is much greater and age dependent with type I IFN autoantibodies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2200413119.	3.3	110
43	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.	2.1	109
44	Genetic interplay between <i>HLA-C</i> and <i>MIR148A</i> in HIV control and Crohn disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 20705-20710.	3.3	109
45	A comprehensive assessment of demographic, environmental, and host genetic associations with gut microbiome diversity in healthy individuals. <i>Microbiome</i> , 2019, 7, 130.	4.9	101
46	SARS-CoV-2-related MIS-C: A key to the viral and genetic causes of Kawasaki disease?. <i>Journal of Experimental Medicine</i> , 2021, 218, .	4.2	100
47	The HCP5 Single Nucleotide Polymorphism: A Simple Screening Tool for Prediction of Hypersensitivity Reaction to Abacavir. <i>Journal of Infectious Diseases</i> , 2008, 198, 864-867.	1.9	90
48	Standardized Whole-Blood Transcriptional Profiling Enables the Deconvolution of Complex Induced Immune Responses. <i>Cell Reports</i> , 2016, 16, 2777-2791.	2.9	84
49	LILRB2 Interaction with HLA Class I Correlates with Control of HIV-1 Infection. <i>PLoS Genetics</i> , 2014, 10, e1004196.	1.5	83
50	Genomewide Association Study for Determinants of HIV-1 Acquisition and Viral Set Point in HIV-1 Serodiscordant Couples with Quantified Virus Exposure. <i>PLoS ONE</i> , 2011, 6, e28632.	1.1	80
51	Common human genetic variants and HIV-1 susceptibility: a genome-wide survey in a homogeneous African population. <i>Aids</i> , 2011, 25, 513-518.	1.0	77
52	Treatment-Naive Individuals Are the Major Source of Transmitted HIV-1 Drug Resistance in Men Who Have Sex With Men in the Swiss HIV Cohort Study. <i>Clinical Infectious Diseases</i> , 2014, 58, 285-294.	2.9	75
53	Variations of CYP3A activity induced by antiretroviral treatment in HIV-1 infected patients. <i>European Journal of Clinical Pharmacology</i> , 2005, 60, 865-873.	0.8	70
54	CCL3L1 and HIV/AIDS susceptibility. <i>Nature Medicine</i> , 2009, 15, 1110-1112.	15.2	70

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55	Dynamics of HIV Latency and Reactivation in a Primary CD4+ T Cell Model. <i>PLoS Pathogens</i> , 2014, 10, e1004156.	2.1	70
56	Cohort Profile Update: The Swiss HIV Cohort Study (SHCS). <i>International Journal of Epidemiology</i> , 2022, 51, 33-34j.	0.9	69
57	A high-resolution HLA reference panel capturing global population diversity enables multi-ancestry fine-mapping in HIV host response. <i>Nature Genetics</i> , 2021, 53, 1504-1516.	9.4	69
58	Easy and accurate reconstruction of whole HIV genomes from short-read sequence data with shiver. <i>Virus Evolution</i> , 2018, 4, vey007.	2.2	64
59	Truly privacy-preserving federated analytics for precision medicine with multiparty homomorphic encryption. <i>Nature Communications</i> , 2021, 12, 5910.	5.8	64
60	Amino Acid Variation in HLA Class II Proteins Is a Major Determinant of Humoral Response to Common Viruses. <i>American Journal of Human Genetics</i> , 2015, 97, 738-743.	2.6	63
61	Assessing the impact of non-pharmaceutical interventions on SARS-CoV-2 transmission in Switzerland. <i>Swiss Medical Weekly</i> , 2020, 150, w20295.	0.8	61
62	HLA Heterozygote Advantage against HIV-1 Is Driven by Quantitative and Qualitative Differences in HLA Allele-Specific Peptide Presentation. <i>Molecular Biology and Evolution</i> , 2020, 37, 639-650.	3.5	60
63	Associations between consumption of dietary fibers and the risk of cardiovascular diseases, cancers, type 2 diabetes, and mortality in the prospective NutriNet-Sant� cohort. <i>American Journal of Clinical Nutrition</i> , 2020, 112, 195-207.	2.2	60
64	Recessive inborn errors of type I IFN immunity in children with COVID-19 pneumonia. <i>Journal of Experimental Medicine</i> , 2022, 219, .	4.2	59
65	Estimating the net contribution of interleukin�28B variation to spontaneous hepatitis C virus clearance. <i>Hepatology</i> , 2011, 53, 1446-1454.	3.6	56
66	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.	2.9	56
67	Revolutionizing Medical Data Sharing Using Advanced Privacy-Enhancing Technologies: Technical, Legal, and Ethical Synthesis. <i>Journal of Medical Internet Research</i> , 2021, 23, e25120.	2.1	54
68	Disentangling Human Tolerance and Resistance Against HIV. <i>PLoS Biology</i> , 2014, 12, e1001951.	2.6	53
69	HIV-1 Vpu is a potent transcriptional suppressor of NF-�B-elicited antiviral immune responses. <i>ELife</i> , 2019, 8, .	2.8	53
70	Blacklisting variants common in private cohorts but not in public databases optimizes human exome analysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 950-959.	3.3	52
71	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.	3.9	52
72	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.	0.9	51

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73	HLA tapasin independence: broader peptide repertoire and HIV control. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 28232-28238.	3.3	51
74	Host Genetics and HIV-1: The Final Phase?. PLoS Pathogens, 2010, 6, e1001033.	2.1	44
75	The Duffy Antigen Receptor for Chemokines Null Promoter Variant Does Not Influence HIV-1 Acquisition or Disease Progression. Cell Host and Microbe, 2009, 5, 408-410.	5.1	43
76	X Chromosomal Variation Is Associated with Slow Progression to AIDS in HIV-1-Infected Women. American Journal of Human Genetics, 2009, 85, 228-239.	2.6	41
77	A global effort to dissect the human genetic basis of resistance to SARS-CoV-2 infection. Nature Immunology, 2022, 23, 159-164.	7.0	41
78	Host Genetic Determinants of T Cell Responses to the MRKAd5 HIV-1 gag/pol/nef Vaccine in the Step Trial. Journal of Infectious Diseases, 2011, 203, 773-779.	1.9	40
79	GenoGuard: Protecting Genomic Data against Brute-Force Attacks. , 2015, , .		40
80	Genome-wide association study of interferon-related cytopenia in chronic hepatitis C patients. Journal of Hepatology, 2012, 56, 313-319.	1.8	39
81	HIV-1 and human genetic variation. Nature Reviews Genetics, 2021, 22, 645-657.	7.7	39
82	Harnessing Type I IFN Immunity Against SARS-CoV-2 with Early Administration of IFN-Î². Journal of Clinical Immunology, 2021, 41, 1425-1442.	2.0	39
83	A highly virulent variant of HIV-1 circulating in the Netherlands. Science, 2022, 375, 540-545.	6.0	39
84	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
85	Identification of Siglec-1 null individuals infected with HIV-1. Nature Communications, 2016, 7, 12412.	5.8	38
86	Viral genetic variation accounts for a third of variability in HIV-1 set-point viral load in Europe. PLoS Biology, 2017, 15, e2001855.	2.6	38
87	Dissecting HIV Virulence: Heritability of Setpoint Viral Load, CD4+ T-Cell Decline, and Per-Parasite Pathogenicity. Molecular Biology and Evolution, 2018, 35, 27-37.	3.5	37
88	Privacy-preserving genomic testing in the clinic: a model using HIV treatment. Genetics in Medicine, 2016, 18, 814-822.	1.1	36
89	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
90	Vaccine breakthrough hypoxemic COVID-19 pneumonia in patients with auto-Abs neutralizing type I IFNs. Science Immunology, 2023, 8, .	5.6	35

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91	Interleukin 28B polymorphisms are the only common genetic variants associated with low-density lipoprotein cholesterol (LDL) in genotype-1 chronic hepatitis C and determine the association between LDL and treatment response. <i>Journal of Viral Hepatitis</i> , 2012, 19, 332-340.	1.0	34
92	Co-Trimoxazole Prophylaxis Is Associated with Reduced Risk of Incident Tuberculosis in Participants in the Swiss HIV Cohort Study. <i>Antimicrobial Agents and Chemotherapy</i> , 2014, 58, 2363-2368.	1.4	34
93	The Characteristics of Heterozygous Protein Truncating Variants in the Human Genome. <i>PLoS Computational Biology</i> , 2015, 11, e1004647.	1.5	34
94	Viral Metagenomics in the Clinical Realm: Lessons Learned from a Swiss-Wide Ring Trial. <i>Genes</i> , 2019, 10, 655.	1.0	34
95	Analysis of Stop-Gain and Frameshift Variants in Human Innate Immunity Genes. <i>PLoS Computational Biology</i> , 2014, 10, e1003757.	1.5	32
96	Genome-Wide Association Study Identifies Single Nucleotide Polymorphism in DYRK1A Associated with Replication of HIV-1 in Monocyte-Derived Macrophages. <i>PLoS ONE</i> , 2011, 6, e17190.	1.1	31
97	CYP3A activity measured by the midazolam test is not related to 3435 C>T polymorphism in the multiple drug resistance transporter gene. <i>Pharmacogenetics and Genomics</i> , 2004, 14, 255-260.	5.7	30
98	Treatment of Cytomegalovirus Infection or Disease in Solid Organ Transplant Recipients With Valganciclovir. <i>Transplantation Proceedings</i> , 2005, 37, 949-951.	0.3	29
99	Hepatitis C trials that combine investigational agents with pegylated interferon should be stratified by interleukin-28B genotype. <i>Hepatology</i> , 2010, 52, 2243-2244.	3.6	28
100	Estimating the Respective Contributions of Human and Viral Genetic Variation to HIV Control. <i>PLoS Computational Biology</i> , 2017, 13, e1005339.	1.5	28
101	Increased prevalence of clonal hematopoiesis of indeterminate potential amongst people living with HIV. <i>Scientific Reports</i> , 2022, 12, 577.	1.6	27
102	A privacy-preserving solution for compressed storage and selective retrieval of genomic data. <i>Genome Research</i> , 2016, 26, 1687-1696.	2.4	26
103	HIV peptidome-wide association study reveals patient-specific epitope repertoires associated with HIV control. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 944-949.	3.3	26
104	Data protection and ethics requirements for multisite research with health data: a comparative examination of legislative governance frameworks and the role of data protection technologies. <i>Journal of Law and the Biosciences</i> , 2020, 7, lsa010.	0.8	26
105	The Association of Genetic Variants with Hepatic Steatosis in Patients with Genotype 1 Chronic Hepatitis C Infection. <i>Digestive Diseases and Sciences</i> , 2012, 57, 2213-2221.	1.1	25
106	Host genetics influences on HIV type-1 disease. <i>Antiviral Therapy</i> , 2009, 14, 731-738.	0.6	24
107	Counteraction of HLA-C-Mediated Immune Control of HIV-1 by Nef. <i>Journal of Virology</i> , 2010, 84, 7300-7311.	1.5	23
108	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.	1.6	23

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109	Efficacy and safety of universal valganciclovir prophylaxis combined with a tacrolimus/mycophenolate-based regimen in kidney transplantation. <i>Swiss Medical Weekly</i> , 2007, 137, 669-76.	0.8	22
110	Exome Sequencing Reveals Primary Immunodeficiencies in Children with Community-Acquired <i>Pseudomonas aeruginosa</i> Sepsis. <i>Frontiers in Immunology</i> , 2016, 7, 357.	2.2	21
111	From Your Nose to Your Toes: A Review of Severe Acute Respiratory Syndrome Coronavirus 2 Pandemic-Associated Pernio. <i>Journal of Investigative Dermatology</i> , 2021, 141, 2791-2796.	0.3	21
112	Respiratory viral infections in otherwise healthy humans with inherited IRF7 deficiency. <i>Journal of Experimental Medicine</i> , 2022, 219, .	4.2	21
113	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.	1.9	20
114	Evaluating the Impact of Functional Genetic Variation on HIV-1 Control. <i>Journal of Infectious Diseases</i> , 2017, 216, 1063-1069.	1.9	20
115	Adverse events to antiretrovirals in the Swiss HIV Cohort Study: effect on mortality and treatment modification. <i>Antiviral Therapy</i> , 2007, 12, 1157-64.	0.6	20
116	Quantifying Genomic Privacy via Inference Attack with High-Order SNV Correlations. , 2015, , .		19
117	Immune Profiling Enables Stratification of Patients With Active Tuberculosis Disease or <i>Mycobacterium tuberculosis</i> Infection. <i>Clinical Infectious Diseases</i> , 2021, 73, e3398-e3408.	2.9	18
118	A Novel Acute Retroviral Syndrome Severity Score Predicts the Key Surrogate Markers for HIV-1 Disease Progression. <i>PLoS ONE</i> , 2014, 9, e114111.	1.1	17
119	Role of APOBEC3F Gene Variation in HIV-1 Disease Progression and Pneumocystis Pneumonia. <i>PLoS Genetics</i> , 2016, 12, e1005921.	1.5	17
120	Treatment of Cytomegalovirus Infection or Disease in Solid Organ Transplant Recipients with Valganciclovir. <i>American Journal of Transplantation</i> , 2005, 5, 1781-1782.	2.6	16
121	HLA Class I and KIR Genes Do Not Protect Against HIV Type 1 Infection in Highly Exposed Uninfected Individuals With Hemophilia A. <i>Journal of Infectious Diseases</i> , 2014, 210, 1047-1051.	1.9	16
122	Neonatal Group B Streptococcal Disease in Otherwise Healthy Infants: Failure of Specific Neonatal Immune Responses. <i>Frontiers in Immunology</i> , 2017, 8, 215.	2.2	15
123	Adaptation of hepatitis C virus to interferon lambda polymorphism across multiple viral genotypes. <i>ELife</i> , 2019, 8, .	2.8	15
124	HLA-B*14:02-Restricted Env-Specific CD8 + T-Cell Activity Has Highly Potent Antiviral Efficacy Associated with Immune Control of HIV Infection. <i>Journal of Virology</i> , 2017, 91, .	1.5	14
125	Differential Immunodominance Hierarchy of CD8 ⁺ T-Cell Responses in HLA-B*27:05- and -B*27:02-Mediated Control of HIV-1 Infection. <i>Journal of Virology</i> , 2018, 92, .	1.5	14
126	Correcting for Population Stratification Reduces False Positive and False Negative Results in Joint Analyses of Host and Pathogen Genomes. <i>Frontiers in Genetics</i> , 2018, 9, 266.	1.1	14

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127	Exploring the interactions between the human and viral genomes. <i>Human Genetics</i> , 2020, 139, 777-781.	1.8	14
128	GuavaH: a compendium of host genomic data in HIV biology and disease. <i>Retrovirology</i> , 2014, 11, 6.	0.9	13
129	A polymorphism in the HCP5 gene associated with HLA-B*5701 does not restrict HIV-1 in vitro. <i>Aids</i> , 2010, 24, 155-157.	1.0	12
130	Detection of novel astroviruses MLB1 and MLB2 in the sera of febrile Tanzanian children. <i>Emerging Microbes and Infections</i> , 2018, 7, 1-3.	3.0	12
131	Whole-exome Sequencing for the Identification of Rare Variants in Primary Immunodeficiency Genes in Children With Sepsis: A Prospective, Population-based Cohort Study. <i>Clinical Infectious Diseases</i> , 2020, 71, e614-e623.	2.9	12
132	Anti-apolipoprotein A-1 autoantibodies are associated with immunodeficiency and systemic inflammation in HIV patients. <i>Journal of Infection</i> , 2018, 76, 186-195.	1.7	12
133	Viral genome wide association study identifies novel hepatitis C virus polymorphisms associated with sofosbuvir treatment failure. <i>Nature Communications</i> , 2021, 12, 6105.	5.8	11
134	Effect of Fc Receptor Genetic Diversity on HIV-1 Disease Pathogenesis. <i>Frontiers in Immunology</i> , 2019, 10, 970.	2.2	10
135	Citizen-centered, auditable and privacy-preserving population genomics. <i>Nature Computational Science</i> , 2021, 1, 192-198.	3.8	10
136	Host genomics of SARS-CoV-2 infection. <i>European Journal of Human Genetics</i> , 0, , .	1.4	10
137	Human genetic variation in HIV disease. <i>Current Opinion in HIV and AIDS</i> , 2015, 10, 110-115.	1.5	9
138	Virosaurus A Reference to Explore and Capture Virus Genetic Diversity. <i>Viruses</i> , 2020, 12, 1248.	1.5	9
139	Dissemination of <i>Mycobacterium tuberculosis</i> is associated to a <i>SIGLEC1</i> null variant that limits antigen exchange via trafficking extracellular vesicles. <i>Journal of Extracellular Vesicles</i> , 2021, 10, e12046.	5.5	9
140	Blood virosphere in febrile Tanzanian children. <i>Emerging Microbes and Infections</i> , 2021, 10, 982-993.	3.0	9
141	Human genomics of the humoral immune response against polyomaviruses. <i>Virus Evolution</i> , 2021, 7, veab058.	2.2	9
142	SQC: secure quality control for meta-analysis of genome-wide association studies. <i>Bioinformatics</i> , 2017, 33, 2273-2280.	1.8	8
143	Susceptibility to infection in early life: a growing role for human genetics. <i>Human Genetics</i> , 2020, 139, 733-743.	1.8	8
144	The influence of human genetic variation on Epstein-Barr virus sequence diversity. <i>Scientific Reports</i> , 2021, 11, 4586.	1.6	8

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145	Immunological lessons from genome-wide association studies of infections. <i>Current Opinion in Immunology</i> , 2021, 72, 87-93.	2.4	8
146	Integrative genetic and immune cell analysis of plasma proteins in healthy donors identifies novel associations involving primary immune deficiency genes. <i>Genome Medicine</i> , 2022, 14, 28.	3.6	8
147	Role of human leukocyte antigen class I alleles in progressive multifocal leukoencephalopathy. <i>Journal of NeuroVirology</i> , 2010, 16, 41-47.	1.0	7
148	A polymorphism in the leptin gene promoter is associated with anemia in patients with HIV disease. <i>Blood</i> , 2011, 118, 5401-5408.	0.6	7
149	Contribution of Genetic Background and Data Collection on Adverse Events of Anti-HIV Drugs (D:A:D) Clinical Risk Score to Chronic Kidney Disease in Swiss HIV-infected Persons With Normal Baseline Estimated Glomerular Filtration Rate. <i>Clinical Infectious Diseases</i> , 2019, 70, 890-897.	2.9	7
150	Telomere Length, Traditional Risk Factors, Factors Related to Human Immunodeficiency Virus (HIV) and Coronary Artery Disease Events in Swiss Persons Living With HIV. <i>Clinical Infectious Diseases</i> , 2021, 73, e2070-e2076.	2.9	7
151	Host Genomics of the HIV-1 Reservoir Size and Its Decay Rate During Suppressive Antiretroviral Treatment. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2020, 85, 517-524.	0.9	7
152	Rapid Progression of Kidney Dysfunction in People Living With HIV: Use of Polygenic and Data Collection on Adverse Events of Anti-HIV Drugs (D:A:D) Risk Scores. <i>Journal of Infectious Diseases</i> , 2020, 223, 2145-2153.	1.9	7
153	Impact of Genetic and Nongenetic Factors on Body Mass Index and Waist-Hip Ratio Change in HIV-Infected Individuals Initiating Antiretroviral Therapy. <i>Open Forum Infectious Diseases</i> , 2020, 7, ofz464.	0.4	7
154	HIV and solid organ transplantation: the Swiss experience. <i>Swiss Medical Weekly</i> , 2006, 136, 194-6.	0.8	7
155	HIV Lipoatrophy and Mosquito Bites. <i>Clinical Infectious Diseases</i> , 2002, 34, 288-289.	2.9	6
156	2015 GENOME WIDE ANALYSIS OF PATIENTS FROM THE IDEAL STUDY IDENTIFIES A CAUSAL ROLE FOR ITPA GENETIC VARIATION IN RIBAVIRIN-INDUCED HEMOLYTIC ANEMIA. <i>Journal of Hepatology</i> , 2010, 52, S470.	1.8	6
157	Interferon lambda 3/4 polymorphisms are associated with AIDS-related Kaposi's sarcoma. <i>Aids</i> , 2018, 32, 2759-2765.	1.0	6
158	Sequence Alignment Through the Looking Glass. , 2018, , .		6
159	Opportunistic testing for urogenital infection with <i>Chlamydia trachomatis</i> in south-western Switzerland, 2012: a feasibility study. <i>Eurosurveillance</i> , 2015, 20, .	3.9	6
160	Familial segregation of group B streptococcal infection in a consanguineous kindred. <i>International Journal of Infectious Diseases</i> , 2016, 51, 22-24.	1.5	5
161	Contribution of Genetic Background and Clinical Risk Factors to Low-Trauma Fractures in Human Immunodeficiency Virus (HIV)-Positive Persons: The Swiss HIV Cohort Study. <i>Open Forum Infectious Diseases</i> , 2016, 3, ofw101.	0.4	5
162	Are privacy-enhancing technologies for genomic data ready for the clinic? A survey of medical experts of the Swiss HIV Cohort Study. <i>Journal of Biomedical Informatics</i> , 2018, 79, 1-6.	2.5	5

#	ARTICLE	IF	CITATIONS
163	Heritability of the HIV-1 reservoir size and decay under long-term suppressive ART. <i>Nature Communications</i> , 2020, 11, 5542.	5.8	5
164	Coronary Artery Disease-Associated and Longevity-Associated Polygenic Risk Scores for Prediction of Coronary Artery Disease Events in Persons Living With Human Immunodeficiency Virus: The Swiss HIV Cohort Study. <i>Clinical Infectious Diseases</i> , 2021, 73, 1597-1604.	2.9	5
165	Using population-specific add-on polymorphisms to improve genotype imputation in underrepresented populations. <i>PLoS Computational Biology</i> , 2022, 18, e1009628.	1.5	5
166	No Evidence for Association of ð²â€œDefensin Genomic Copy Number with HIV Susceptibility, HIV Load during Clinical Latency, or Progression to AIDS. <i>Annals of Human Genetics</i> , 2017, 81, 27-34.	0.3	4
167	Human genomics of acute liver failure due to hepatitis B virus infection: An exome sequencing study in liver transplant recipients. <i>Journal of Viral Hepatitis</i> , 2019, 26, 271-277.	1.0	4
168	Genetic variation near CXCL12 is associated with susceptibility to HIV-related non-Hodgkin lymphoma. <i>Haematologica</i> , 2021, 106, 2233-2241.	1.7	4
169	Early IFNÎ² secretion determines variable downstream IL-12p70 responses upon TLR4 activation. <i>Cell Reports</i> , 2022, 39, 110989.	2.9	4
170	P08-06 LB. A genome-wide association study of host genetic determinants of T cell responses to the MRKAd5 HIV-1 gag/pol/nef vaccine in the STEP trial. <i>Retrovirology</i> , 2009, 6, .	0.9	3
171	European Genetic Diversity and Susceptibility to Pathogens. <i>Human Heredity</i> , 2013, 76, 187-193.	0.4	3
172	Predicting the Occurrence of Variants in RAG1 and RAG2. <i>Journal of Clinical Immunology</i> , 2019, 39, 688-701.	2.0	3
173	Systematic screening of viral and human genetic variation identifies antiretroviral resistance and immune escape link. <i>ELife</i> , 2021, 10, .	2.8	3
174	Identifying and Characterizing Trans Women in the Swiss HIV Cohort Study as an Epidemiologically Distinct Risk Group. <i>Clinical Infectious Diseases</i> , 2022, 74, 1468-1475.	2.9	3
175	Telomere Length Declines in Persons With Human Immunodeficiency Virus Before Antiretroviral Therapy Start but Not After Viral Suppression: A Longitudinal Study Over >17 Years. <i>Journal of Infectious Diseases</i> , 2022, 225, 1581-1591.	1.9	3
176	GenoShare: Supporting Privacy-Informed Decisions for Sharing Individual-Level Genetic Data. <i>Studies in Health Technology and Informatics</i> , 2020, 270, 238-241.	0.2	3
177	Multidrug resistance and response to antiretroviral treatment. <i>Lancet, The</i> , 2002, 359, 2114-2115.	6.3	2
178	How the Human Genome Can Predict Response to Hepatitis C Therapy. <i>Current Hepatitis Reports</i> , 2010, 9, 1-8.	0.3	2
179	Young and Early Career Investigators: Report from a Global HIV Vaccine Enterprise Working Group. <i>Nature Precedings</i> , 2010, , .	0.1	2
180	3 IL28B POLYMORPHISM IS ASSOCIATED WITH INTRAHEPATIC ISG EXPRESSION AND PEGINTERFERON-A/RIBAVIRIN RESPONSE RATE IN CHRONIC HCV INFECTION. <i>Journal of Hepatology</i> , 2010, 52, S2.	1.8	2

#	ARTICLE	IF	CITATIONS
181	Personalized hepatitis C therapy: opportunities and pitfalls. <i>Expert Review of Molecular Diagnostics</i> , 2011, 11, 127-129.	1.5	2
182	<scp>HLA</scp>â€œ<scp>Bw4</scp> identifies a population of <scp>HIV</scp>â€œinfected patients with an increased capacity to control viral replication after structured treatment interruption. <i>HIV Medicine</i> , 2012, 13, 589-595.	1.0	2
183	Adaptation on a genomic scale. <i>ELife</i> , 2015, 4, e06193.	2.8	2
184	Impact of Delaying Antiretroviral Treatment During Primary Human Immunodeficiency Virus Infection on Telomere Length. <i>Journal of Infectious Diseases</i> , 2021, , .	1.9	2
185	CD38 Expression by Antigen-Specific CD4 T Cells Is Significantly Restored 5 Months After Treatment Initiation Independently of Sputum Bacterial Load at the Time of Tuberculosis Diagnosis. <i>Frontiers in Medicine</i> , 2022, 9, 821776.	1.2	2
186	Rhesus negative males have an enhanced IFN ^{Î³} -mediated immune response to influenza A virus. <i>Genes and Immunity</i> , 2022, 23, 93-98.	2.2	2
187	Phylogenetic estimation of the viral fitness landscape of HIV-1 set-point viral load. <i>Virus Evolution</i> , 2022, 8, veac022.	2.2	1
188	Improving polygenic prediction with genetically inferred ancestry. <i>Human Genetics and Genomics Advances</i> , 2022, 3, 100109.	1.0	1
189	SPHN/PHRT - MedCo in Action: Empowering the Swiss Molecular Tumor Board with Privacy-Preserving and Real-Time Patient Discovery. <i>Studies in Health Technology and Informatics</i> , 2020, 270, 1161-1162.	0.2	1
190	Host Genetics: Fine-Tuning Innate Signaling. <i>Current Biology</i> , 2007, 17, R516-R518.	1.8	0
191	Joint analysis of host and pathogen genomes. , 2011, , .		0
192	Genetic Associations with Resistance to HIV-1 Infection, Viral Control and Protection Against Disease. , 2012, , 319-334.		0
193	A39â€œHuman exome sequencing to evaluate the impact of rare coding variation on HIV-1 control. <i>Virus Evolution</i> , 2017, 3, .	2.2	0
194	HIV Transmission Chains Exhibit Greater HLA-B Homogeneity Than Randomly Expected. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2019, 81, 508-515.	0.9	0
195	Host Genetics and Genomics. , 2018, , 1015-1022.		0