

Jacques Fellay

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

194 papers	13,623 citations	50 h-index	115 g-index
246 ext. papers	16,830 ext. citations	11.1 avg, IF	5.52 L-index

#	Paper	IF	Citations
194	Genetic variation in IL28B predicts hepatitis C treatment-induced viral clearance. <i>Nature</i> , 2009 , 461, 399-401	50.4	2992
193	A whole-genome association study of major determinants for host control of HIV-1. <i>Science</i> , 2007 , 317, 944-7	33.3	999
192	Inborn errors of type I IFN immunity in patients with life-threatening COVID-19. <i>Science</i> , 2020 , 370,	33.3	994
191	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, 120-9.e18	13.3	582
190	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, 30-6	40	575
189	ITPA gene variants protect against anaemia in patients treated for chronic hepatitis C. <i>Nature</i> , 2010 , 464, 405-8	50.4	380
188	Common genetic variation and the control of HIV-1 in humans. <i>PLoS Genetics</i> , 2009 , 5, e1000791	6	310
187	IL28B genotype is associated with differential expression of intrahepatic interferon-stimulated genes in patients with chronic hepatitis C. <i>Hepatology</i> , 2010 , 52, 1888-96	11.2	310
186	Prevalence of adverse events associated with potent antiretroviral treatment: Swiss HIV Cohort Study. <i>Lancet, The</i> , 2001 , 358, 1322-7	40	280
185	Influence of HLA-C expression level on HIV control. <i>Science</i> , 2013 , 340, 87-91	33.3	277
184	HLA-C cell surface expression and control of HIV/AIDS correlate with a variant upstream of HLA-C. <i>Nature Genetics</i> , 2009 , 41, 1290-4	36.3	230
183	Population pharmacokinetics and effects of efavirenz in patients with human immunodeficiency virus infection. <i>Clinical Pharmacology and Therapeutics</i> , 2003 , 73, 20-30	6.1	200
182	A global scientific strategy to cure hepatitis B. <i>The Lancet Gastroenterology and Hepatology</i> , 2019 , 4, 545-558	18.8	187
181	Variants in the ITPA gene protect against ribavirin-induced hemolytic anemia and decrease the need for ribavirin dose reduction. <i>Gastroenterology</i> , 2010 , 139, 1181-9	13.3	156
180	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, 2391-400	15.9	144
179	WGAVIEWER: software for genomic annotation of whole genome association studies. <i>Genome Research</i> , 2008 , 18, 640-3	9.7	138
178	Evidence of dysregulation of dendritic cells in primary HIV infection. <i>Blood</i> , 2010 , 116, 3839-52	2.2	137

177	Genome-wide mRNA expression correlates of viral control in CD4+ T-cells from HIV-1-infected individuals. <i>PLoS Pathogens</i> , 2010 , 6, e1000781	7.6	135
176	Privacy in the Genomic Era. <i>ACM Computing Surveys</i> , 2015 , 48,	13.4	133
175	The characterization of twenty sequenced human genomes. <i>PLoS Genetics</i> , 2010 , 6, e1001111	6	133
174	Host determinants of HIV-1 control in African Americans. <i>Journal of Infectious Diseases</i> , 2010 , 201, 1141-9		125
173	Hepatitis C pharmacogenetics: state of the art in 2010. <i>Hepatology</i> , 2011 , 53, 336-45	11.2	120
172	A Global Effort to Define the Human Genetics of Protective Immunity to SARS-CoV-2 Infection. <i>Cell</i> , 2020 , 181, 1194-1199	56.2	113
171	Natural variation in the parameters of innate immune cells is preferentially driven by genetic factors. <i>Nature Immunology</i> , 2018 , 19, 302-314	19.1	112
170	Copy number variation of KIR genes influences HIV-1 control. <i>PLoS Biology</i> , 2011 , 9, e1001208	9.7	111
169	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, 14658-63	11.5	108
168	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	11.5	107
167	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, 3035-40	11.5	107
166	Inosine triphosphate protects against ribavirin-induced adenosine triphosphate loss by adenylosuccinate synthase function. <i>Gastroenterology</i> , 2011 , 140, 1314-21	13.3	103
165	Determinants of HIV-1 broadly neutralizing antibody induction. <i>Nature Medicine</i> , 2016 , 22, 1260-1267	50.5	99
164	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,	28	91
163	Elevated expression impairs HIV control through inhibition of NKG2A-expressing cells. <i>Science</i> , 2018 , 359, 86-90	33.3	89
162	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	7.6	86
161	The HCP5 single-nucleotide polymorphism: a simple screening tool for prediction of hypersensitivity reaction to abacavir. <i>Journal of Infectious Diseases</i> , 2008 , 198, 864-7	7	85
160	A genome-to-genome analysis of associations between human genetic variation, HIV-1 sequence diversity, and viral control. <i>ELife</i> , 2013 , 2, e01123	8.9	85

159	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	36.3	81
158	Genetics of human susceptibility to active and latent tuberculosis: present knowledge and future perspectives. <i>Lancet Infectious Diseases</i> , 2018 , 18, e64-e75	25.5	74
157	Severe viral respiratory infections in children with loss-of-function mutations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, 8342-8347	11.5	74
156	Genetic interplay between HLA-C and MIR148A in HIV control and Crohn disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 20705-10	11.5	74
155	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	3.7	68
154	Treatment-naïve 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, 285-94	11.6	67
153	Common human genetic variants and HIV-1 susceptibility: a genome-wide survey in a homogeneous African population. <i>Aids</i> , 2011 , 25, 513-8	3.5	67
152	X-linked recessive TLR7 deficiency in ~1% of men under 60 years old with life-threatening COVID-19. <i>Science Immunology</i> , 2021 , 6,	28	67
151	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	14.4	64
150	CCL3L1 and HIV/AIDS susceptibility. <i>Nature Medicine</i> , 2009 , 15, 1110-2	50.5	60
149	Variations of CYP3A activity induced by antiretroviral treatment in HIV-1 infected patients. <i>European Journal of Clinical Pharmacology</i> , 2005 , 60, 865-73	2.8	56
148	Dynamics of HIV latency and reactivation in a primary CD4+ T cell model. <i>PLoS Pathogens</i> , 2014 , 10, e1004156	14.56	54
147	Estimating the net contribution of interleukin-28B variation to spontaneous hepatitis C virus clearance. <i>Hepatology</i> , 2011 , 53, 1446-54	11.2	53
146	A comprehensive assessment of demographic, environmental, and host genetic associations with gut microbiome diversity in healthy individuals. <i>Microbiome</i> , 2019 , 7, 130	16.6	52
145	Determinants of HIV-1 reservoir size and long-term dynamics during suppressive ART. <i>Nature Communications</i> , 2019 , 10, 3193	17.4	50
144	LILRB2 interaction with HLA class I correlates with control of HIV-1 infection. <i>PLoS Genetics</i> , 2014 , 10, e1004196	6	49
143	Gender medicine and oncology: report and consensus of an ESMO workshop. <i>Annals of Oncology</i> , 2019 , 30, 1914-1924	10.3	47
142	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, 112-21	11.6	45

141	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,	16.6	45
140	Standardized Whole-Blood Transcriptional Profiling Enables the Deconvolution of Complex Induced Immune Responses. <i>Cell Reports</i> , 2016 , 16, 2777-2791	10.6	43
139	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	3.6	42
138	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, 738-43	11	40
137	X chromosomal variation is associated with slow progression to AIDS in HIV-1-infected women. <i>American Journal of Human Genetics</i> , 2009 , 85, 228-39	11	39
136	Host genetics and HIV-1: the final phase?. <i>PLoS Pathogens</i> , 2010 , 6, e1001033	7.6	38
135	Easy and accurate reconstruction of whole HIV genomes from short-read sequence data with shiver. <i>Virus Evolution</i> , 2018 , 4, vey007	3.7	38
134	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, 1903-10	5.6	37
133	Disentangling human tolerance and resistance against HIV. <i>PLoS Biology</i> , 2014 , 12, e1001951	9.7	36
132	Genome-wide association study of interferon-related cytopenia in chronic hepatitis C patients. <i>Journal of Hepatology</i> , 2012 , 56, 313-9	13.4	34
131	The Duffy antigen receptor for chemokines null promoter variant does not influence HIV-1 acquisition or disease progression. <i>Cell Host and Microbe</i> , 2009 , 5, 408-10; author reply 418-9	23.4	33
130	Assessing the impact of non-pharmaceutical interventions on SARS-CoV-2 transmission in Switzerland. <i>Swiss Medical Weekly</i> , 2020 , 150, w20295	3.1	33
129	Host genetic determinants of T cell responses to the MRKAd5 HIV-1 gag/pol/nef vaccine in the step trial. <i>Journal of Infectious Diseases</i> , 2011 , 203, 773-9	7	31
128	HIV-1 Vpu is a potent transcriptional suppressor of NF- κ B-elicited antiviral immune responses. <i>ELife</i> , 2019 , 8,	8.9	30
127	Killer cell immunoglobulin-like receptor 3DL1 variation modifies HLA-B*57 protection against HIV-1. <i>Journal of Clinical Investigation</i> , 2018 , 128, 1903-1912	15.9	30
126	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	3.7	30
125	Interleukin 28B polymorphisms are the only common genetic variants associated with low-density lipoprotein cholesterol (LDL-C) in genotype-1 chronic hepatitis C and determine the association between LDL-C and treatment response. <i>Journal of Viral Hepatitis</i> , 2012 , 19, 332-40	3.4	29
124	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, 255-60		27

123	GenoGuard: Protecting Genomic Data against Brute-Force Attacks 2015 ,		26
122	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, 2363-8	5.9	26
121	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	8.3	26
120	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	11.5	26
119	Treatment of cytomegalovirus infection or disease in solid organ transplant recipients with valganciclovir. <i>Transplantation Proceedings</i> , 2005 , 37, 949-51	1.1	25
118	Privacy-preserving genomic testing in the clinic: a model using HIV treatment. <i>Genetics in Medicine</i> , 2016 , 18, 814-22	8.1	25
117	Adverse Events to Antiretrovirals in the Swiss HIV Cohort Study: Effect on Mortality and Treatment Modification. <i>Antiviral Therapy</i> , 2007 , 12, 1157-1164	1.6	24
116	The Characteristics of Heterozygous Protein Truncating Variants in the Human Genome. <i>PLoS Computational Biology</i> , 2015 , 11, e1004647	5	23
115	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, 2213-21	4	23
114	Counteraction of HLA-C-mediated immune control of HIV-1 by Nef. <i>Journal of Virology</i> , 2010 , 84, 7300-16.6	16.6	23
113	Hepatitis C trials that combine investigational agents with pegylated interferon should be stratified by interleukin-28B genotype. <i>Hepatology</i> , 2010 , 52, 2243-4	11.2	23
112	Human genetic and immunological determinants of critical COVID-19 pneumonia.. <i>Nature</i> , 2022 ,	50.4	23
111	Associations between consumption of dietary fibers and the risk of cardiovascular diseases, cancers, type 2 diabetes, and mortality in the prospective NutriNet-Santé cohort. <i>American Journal of Clinical Nutrition</i> , 2020 , 112, 195-207	7	21
110	Analysis of stop-gain and frameshift variants in human innate immunity genes. <i>PLoS Computational Biology</i> , 2014 , 10, e1003757	5	21
109	Viral genetic variation accounts for a third of variability in HIV-1 set-point viral load in Europe. <i>PLoS Biology</i> , 2017 , 15, e2001855	9.7	21
108	Viral Metagenomics in the Clinical Realm: Lessons Learned from a Swiss-Wide Ring Trial. <i>Genes</i> , 2019 , 10,	4.2	20
107	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	3.1	20
106	Dissecting HIV Virulence: Heritability of Setpoint Viral Load, CD4+ T-Cell Decline, and Per-Parasite Pathogenicity. <i>Molecular Biology and Evolution</i> , 2018 , 35, 27-37	8.3	19

105	Evaluating the Impact of Functional Genetic Variation on HIV-1 Control. <i>Journal of Infectious Diseases</i> , 2017 , 216, 1063-1069	7	18
104	Identification of Siglec-1 null individuals infected with HIV-1. <i>Nature Communications</i> , 2016 , 7, 12412	17.4	18
103	A privacy-preserving solution for compressed storage and selective retrieval of genomic data. <i>Genome Research</i> , 2016 , 26, 1687-1696	9.7	18
102	Host genetics influences on HIV type-1 disease. <i>Antiviral Therapy</i> , 2009 , 14, 731-8	1.6	18
101	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, 1336-42	3.8	18
100	HLA tapasin independence: broader peptide repertoire and HIV control. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 28232-28238	11.5	18
99	Adverse events to antiretrovirals in the Swiss HIV Cohort Study: effect on mortality and treatment modification. <i>Antiviral Therapy</i> , 2007 , 12, 1157-64	1.6	18
98	The Interplay Between Host Genetic Variation, Viral Replication, and Microbial Translocation in Untreated HIV-Infected Individuals. <i>Journal of Infectious Diseases</i> , 2015 , 212, 578-84	7	17
97	Estimating the Respective Contributions of Human and Viral Genetic Variation to HIV Control. <i>PLoS Computational Biology</i> , 2017 , 13, e1005339	5	16
96	Role of APOBEC3F Gene Variation in HIV-1 Disease Progression and Pneumocystis Pneumonia. <i>PLoS Genetics</i> , 2016 , 12, e1005921	6	16
95	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, 1047-51	7	15
94	Treatment of cytomegalovirus infection or disease in solid organ transplant recipients with valganciclovir. <i>American Journal of Transplantation</i> , 2005 , 5, 1781-2; author reply 1783	8.7	14
93	Exome Sequencing Reveals Primary Immunodeficiencies in Children with Community-Acquired Sepsis. <i>Frontiers in Immunology</i> , 2016 , 7, 357	8.4	14
92	Revolutionizing Medical Data Sharing Using Advanced Privacy-Enhancing Technologies: Technical, Legal, and Ethical Synthesis. <i>Journal of Medical Internet Research</i> , 2021 , 23, e25120	7.6	13
91	A novel Acute Retroviral Syndrome Severity Score predicts the key surrogate markers for HIV-1 disease progression. <i>PLoS ONE</i> , 2014 , 9, e114111	3.7	12
90	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	11.5	12
89	GuavaH: a compendium of host genomic data in HIV biology and disease. <i>Retrovirology</i> , 2014 , 11, 6	3.6	11
88	A polymorphism in the HCP5 gene associated with HLA-B*5701 does not restrict HIV-1 in vitro. <i>Aids</i> , 2010 , 24, 155-7	3.5	11

87	Neonatal Group B Streptococcal Disease in Otherwise Healthy Infants: Failure of Specific Neonatal Immune Responses. <i>Frontiers in Immunology</i> , 2017 , 8, 215	8.4	10
86	Human genetic variation in HIV disease: beyond genome-wide association studies. <i>Current Opinion in HIV and AIDS</i> , 2015 , 10, 110-5	4.2	9
85	Detection of novel astroviruses MLB1 and MLB2 in the sera of febrile Tanzanian children. <i>Emerging Microbes and Infections</i> , 2018 , 7, 27	18.9	9
84	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,	6.6	9
83	Quantifying Genomic Privacy via Inference Attack with High-Order SNV Correlations 2015 ,		9
82	Adaptation of hepatitis C virus to interferon lambda polymorphism across multiple viral genotypes. <i>ELife</i> , 2019 , 8,	8.9	9
81	Anti-apolipoprotein A-1 autoantibodies are associated with immunodeficiency and systemic inflammation in HIV patients. <i>Journal of Infection</i> , 2018 , 76, 186-195	18.9	9
80	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,	6.6	9
79	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	36.3	7
78	A global effort to dissect the human genetic basis of resistance to SARS-CoV-2 infection. <i>Nature Immunology</i> , 2021 ,	19.1	7
77	HIV and solid organ transplantation: the Swiss experience. <i>Swiss Medical Weekly</i> , 2006 , 136, 194-6	3.1	7
76	SQC: secure quality control for meta-analysis of genome-wide association studies. <i>Bioinformatics</i> , 2017 , 33, 2273-2280	7.2	6
75	Role of human leukocyte antigen class I alleles in progressive multifocal leukoencephalopathy. <i>Journal of NeuroVirology</i> , 2010 , 16, 41-7	3.9	6
74	Opportunistic testing for urogenital infection with Chlamydia trachomatis in south-western Switzerland, 2012: a feasibility study. <i>Eurosurveillance</i> , 2015 , 20,	19.8	6
73	Truly privacy-preserving federated analytics for precision medicine with multiparty homomorphic encryption. <i>Nature Communications</i> , 2021 , 12, 5910	17.4	6
72	A high-resolution HLA reference panel capturing global population diversity enables multi-ethnic fine-mapping in HIV host response		6
71	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	4.3	6
70	Cohort Profile Update: The Swiss HIV Cohort Study (SHCS). <i>International Journal of Epidemiology</i> , 2021 ,	7.8	6

69	Virosaurus A Reference to Explore and Capture Virus Genetic Diversity. <i>Viruses</i> , 2020 , 12,	6.2	5
68	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 ¹		5
67	A polymorphism in the leptin gene promoter is associated with anemia in patients with HIV disease. <i>Blood</i> , 2011 , 118, 5401-8	2.2	5
66	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	13.4	5
65	A highly virulent variant of HIV-1 circulating in the Netherlands.. <i>Science</i> , 2022 , 375, 540-545	33.3	5
64	Increased CHIP Prevalence Amongst People Living with HIV 2020 ,		5
63	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, lsaa010	4.1	5
62	HIV-1 and human genetic variation. <i>Nature Reviews Genetics</i> , 2021 , 22, 645-657	30.1	5
61	Interferon lambda 3/4 polymorphisms are associated with AIDS-related Kaposi's sarcoma. <i>Aids</i> , 2018 , 32, 2759-2765	3.5	5
60	No Evidence for Association of β -Defensin 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	2.2	4
59	Effect of Fc Receptor Genetic Diversity on HIV-1 Disease Pathogenesis. <i>Frontiers in Immunology</i> , 2019 , 10, 970	8.4	4
58	Contribution of Genetic Background and Data Collection on Adverse Events of Anti-human Immunodeficiency Virus (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> , 2020 , 70, e222-e227	11.6	4
57	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	11.6	4
56	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	10.2	4
55	Easy and Accurate Reconstruction of Whole HIV Genomes from Short-Read Sequence Data		4
54	Immune Profiling Enables Stratification of Patients With Active Tuberculosis Disease or Mycobacterium tuberculosis Infection. <i>Clinical Infectious Diseases</i> , 2021 , 73, e3398-e3408	11.6	4
53	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	11.6	4
52	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	4.5	4

51	Sequence Alignment Through the Looking Glass 2018 ,		4
50	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> , 2021 , 223, 2145-2153	7	3
49	Susceptibility to infection in early life: a growing role for human genetics. <i>Human Genetics</i> , 2020 , 139, 733-743	6.3	3
48	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	1	3
47	European genetic diversity and susceptibility to pathogens. <i>Human Heredity</i> , 2013 , 76, 187-93	1.1	3
46	HIV lipoatrophy and mosquito bites. <i>Clinical Infectious Diseases</i> , 2002 , 34, 288-9	11.6	3
45	Increased prevalence of clonal hematopoiesis of indeterminate potential amongst people living with HIV.. <i>Scientific Reports</i> , 2022 , 12, 577	4.9	3
44	Viral genome wide association study identifies novel hepatitis C virus polymorphisms associated with sofosbuvir treatment failure. <i>Nature Communications</i> , 2021 , 12, 6105	17.4	3
43	Assessing the impact of non-pharmaceutical interventions on SARS-CoV-2 transmission in Switzerland		3
42	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	3.1	3
41	Citizen-centered, auditable and privacy-preserving population genomics. <i>Nature Computational Science</i> , 2021 , 1, 192-198		3
40	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 ^{11.5}		3
39	Heritability of the HIV-1 reservoir size and decay under long-term suppressive ART. <i>Nature Communications</i> , 2020 , 11, 5542	17.4	2
38	HLA-Bw4 identifies a population of HIV-infected patients with an increased capacity to control viral replication after structured treatment interruption. <i>HIV Medicine</i> , 2012 , 13, 589-95	2.7	2
37	Adaptation on a genomic scale. <i>ELife</i> , 2015 , 4, e06193	8.9	2
36	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	13.4	2
35	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,	3.6	2
34	How the Human Genome Can Predict Response to Hepatitis C Therapy. <i>Current Hepatitis Reports</i> , 2010 , 9, 1-8		2

33	A mitochondrial mutational signature of temperature in ectothermic and endothermic vertebrates	2	
32	Estimating the respective contributions of human and viral genetic variation to HIV control	2	
31	Citizen-Centered, Auditable, and Privacy-Preserving Population Genomics	2	
30	Exploring the interactions between the human and viral genomes. <i>Human Genetics</i> , 2020 , 139, 777-781	6.3	2
29	Familial segregation of group B streptococcal infection in a consanguineous kindred. <i>International Journal of Infectious Diseases</i> , 2016 , 51, 22-24	10.5	2
28	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	3.4	2
27	Dissemination of is associated to a null variant that limits antigen exchange via trafficking extracellular vesicles. <i>Journal of Extracellular Vesicles</i> , 2021 , 10, e12046	16.4	2
26	Truly Privacy-Preserving Federated Analytics for Precision Medicine with Multiparty Homomorphic Encryption	2	
25	The influence of human genetic variation on Epstein-Barr virus sequence diversity. <i>Scientific Reports</i> , 2021 , 11, 4586	4.9	2
24	Immunological lessons from genome-wide association studies of infections. <i>Current Opinion in Immunology</i> , 2021 , 72, 87-93	7.8	2
23	Predicting the Occurrence of Variants in RAG1 and RAG2. <i>Journal of Clinical Immunology</i> , 2019 , 39, 688-701	9.7	1
22	Multidrug resistance and response to antiretroviral treatment. <i>Lancet, The</i> , 2002 , 359, 2114-2115	40	1
21	A genome-wide polygenic approach to HIV acquisition uncovers link to inflammatory bowel disease and identifies potential novel genetic variants		1
20	Ongoing evolution of KRAB zinc finger protein-coding genes in modern humans		1
19	Correcting for population stratification reduces false positive and false negative results in joint analyses of host and pathogen genomes		1
18	HIV Peptidome-Wide Association Study Reveals Patient-Specific Epitope Repertoires Associated with HIV Control		1
17	Risk of mitochondrial deletions is affected by the global secondary structure of the mitochondrial genome		1
16	Genetic variation near CXCL12 is associated with susceptibility to HIV-related non-Hodgkin lymphoma. <i>Haematologica</i> , 2021 , 106, 2233-2241	6.6	1

15	Impact of Delaying Antiretroviral Treatment during Primary HIV Infection on Telomere Length. <i>Journal of Infectious Diseases</i> , 2021 ,	7	1
14	Human genomics of the humoral immune response against polyomaviruses. <i>Virus Evolution</i> , 2021 , 7, veab058	3.7	1
13	Identifying and Characterizing Trans women in the Swiss HIV Cohort Study as an Epidemiologically Distinct Risk Group. <i>Clinical Infectious Diseases</i> , 2021 ,	11.6	1
12	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	14.4	1
11	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	0.5	1
10	Using population-specific add-on polymorphisms to improve genotype imputation in underrepresented populations.. <i>PLoS Computational Biology</i> , 2022 , 18, e1009628	5	0
9	GenoShare: Supporting Privacy-Informed Decisions for Sharing Individual-Level Genetic Data. <i>Studies in Health Technology and Informatics</i> , 2020 , 270, 238-241	0.5	0
8	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	11.6	0
7	Blood virosphere in febrile Tanzanian children. <i>Emerging Microbes and Infections</i> , 2021 , 10, 982-993	18.9	0
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