

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	Vaccine breakthrough hypoxemic COVID-19 pneumonia in patients with auto-Abs neutralizing type I IFNs. <i>Science Immunology</i> , 2023, 8, .	5.6	35
2	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
3	Cohort Profile Update: The Swiss HIV Cohort Study (SHCS). <i>International Journal of Epidemiology</i> , 2022, 51, 33-34j.	0.9	69
4	A global effort to dissect the human genetic basis of resistance to SARS-CoV-2 infection. <i>Nature Immunology</i> , 2022, 23, 159-164.	7.0	41
5	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
6	Human genetic and immunological determinants of critical COVID-19 pneumonia. <i>Nature</i> , 2022, 603, 587-598.	13.7	216
7	Using population-specific add-on polymorphisms to improve genotype imputation in underrepresented populations. <i>PLoS Computational Biology</i> , 2022, 18, e1009628.	1.5	5
8	Increased prevalence of clonal hematopoiesis of indeterminate potential amongst people living with HIV. <i>Scientific Reports</i> , 2022, 12, 577.	1.6	27
9	A highly virulent variant of HIV-1 circulating in the Netherlands. <i>Science</i> , 2022, 375, 540-545.	6.0	39
10	Phylogenetic estimation of the viral fitness landscape of HIV-1 set-point viral load. <i>Virus Evolution</i> , 2022, 8, veac022.	2.2	1
11	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
12	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
13	Rhesus negative males have an enhanced IFN γ -mediated immune response to influenza A virus. <i>Genes and Immunity</i> , 2022, 23, 93-98.	2.2	2
14	Improving polygenic prediction with genetically inferred ancestry. <i>Human Genetics and Genomics Advances</i> , 2022, 3, 100109.	1.0	1
15	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
16	Respiratory viral infections in otherwise healthy humans with inherited IRF7 deficiency. <i>Journal of Experimental Medicine</i> , 2022, 219, .	4.2	21
17	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
18	Early IFN γ secretion determines variable downstream IL-12p70 responses upon TLR4 activation. <i>Cell Reports</i> , 2022, 39, 110989.	2.9	4

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19	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
20	Genetic variation near CXCL12 is associated with susceptibility to HIV-related non-Hodgkin lymphoma. <i>Haematologica</i> , 2021, 106, 2233-2241.	1.7	4
21	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
22	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
23	Blood virosphere in febrile Tanzanian children. <i>Emerging Microbes and Infections</i> , 2021, 10, 982-993.	3.0	9
24	The influence of human genetic variation on Epstein-Barr virus sequence diversity. <i>Scientific Reports</i> , 2021, 11, 4586.	1.6	8
25	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
26	Citizen-centered, auditable and privacy-preserving population genomics. <i>Nature Computational Science</i> , 2021, 1, 192-198.	3.8	10
27	Impact of Delaying Antiretroviral Treatment During Primary Human Immunodeficiency Virus Infection on Telomere Length. <i>Journal of Infectious Diseases</i> , 2021, , .	1.9	2
28	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
29	Systematic screening of viral and human genetic variation identifies antiretroviral resistance and immune escape link. <i>ELife</i> , 2021, 10, .	2.8	3
30	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
31	Human genomics of the humoral immune response against polyomaviruses. <i>Virus Evolution</i> , 2021, 7, veab058.	2.2	9
32	HIV-1 and human genetic variation. <i>Nature Reviews Genetics</i> , 2021, 22, 645-657.	7.7	39
33	Harnessing Type I IFN Immunity Against SARS-CoV-2 with Early Administration of IFN- β . <i>Journal of Clinical Immunology</i> , 2021, 41, 1425-1442.	2.0	39
34	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
35	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
36	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

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37	Immunological lessons from genome-wide association studies of infections. <i>Current Opinion in Immunology</i> , 2021, 72, 87-93.	2.4	8
38	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
39	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
40	Truly privacy-preserving federated analytics for precision medicine with multiparty homomorphic encryption. <i>Nature Communications</i> , 2021, 12, 5910.	5.8	64
41	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
42	Exploring the interactions between the human and viral genomes. <i>Human Genetics</i> , 2020, 139, 777-781.	1.8	14
43	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, 1-10.	0.8	26
44	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
45	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.	3.3	51
46	Inborn errors of type I IFN immunity in patients with life-threatening COVID-19. <i>Science</i> , 2020, 370, .	6.0	1,749
47	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
48	Virosaurus A Reference to Explore and Capture Virus Genetic Diversity. <i>Viruses</i> , 2020, 12, 1248.	1.5	9
49	Heritability of the HIV-1 reservoir size and decay under long-term suppressive ART. <i>Nature Communications</i> , 2020, 11, 5542.	5.8	5
50	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.	2.2	60
51	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
52	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
53	Susceptibility to infection in early life: a growing role for human genetics. <i>Human Genetics</i> , 2020, 139, 733-743.	1.8	8
54	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

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55	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
56	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
57	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
58	Predicting the Occurrence of Variants in RAG1 and RAG2. <i>Journal of Clinical Immunology</i> , 2019, 39, 688-701.	2.0	3
59	HIV-1 Vpu is a potent transcriptional suppressor of NF- κ B-elicited antiviral immune responses. <i>ELife</i> , 2019, 8, .	2.8	53
60	Determinants of HIV-1 reservoir size and long-term dynamics during suppressive ART. <i>Nature Communications</i> , 2019, 10, 3193.	5.8	112
61	Gender medicine and oncology: report and consensus of an ESMO workshop. <i>Annals of Oncology</i> , 2019, 30, 1914-1924.	0.6	120
62	Viral Metagenomics in the Clinical Realm: Lessons Learned from a Swiss-Wide Ring Trial. <i>Genes</i> , 2019, 10, 655.	1.0	34
63	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
64	Effect of Fc Receptor Genetic Diversity on HIV-1 Disease Pathogenesis. <i>Frontiers in Immunology</i> , 2019, 10, 970.	2.2	10
65	A global scientific strategy to cure hepatitis B. <i>The Lancet Gastroenterology and Hepatology</i> , 2019, 4, 545-558.	3.7	342
66	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> , 2019, 70, 890-897.	2.9	7
67	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
68	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
69	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
70	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
71	Adaptation of hepatitis C virus to interferon lambda polymorphism across multiple viral genotypes. <i>ELife</i> , 2019, 8, .	2.8	15
72	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

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73	Distinctive roles of age, sex, and genetics in shaping transcriptional variation of human immune responses to microbial challenges. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E488-E497.	3.3	181
74	Are privacy-enhancing technologies for genomic data ready for the clinic? A survey of medical experts of the Swiss HIV Cohort Study. Journal of Biomedical Informatics, 2018, 79, 1-6.	2.5	5
75	Elevated <i>HLA-A</i> expression impairs HIV control through inhibition of NKG2A-expressing cells. Science, 2018, 359, 86-90.	6.0	135
76	Detection of novel astroviruses MLB1 and MLB2 in the sera of febrile Tanzanian children. Emerging Microbes and Infections, 2018, 7, 1-3.	3.0	12
77	Genetics of human susceptibility to active and latent tuberculosis: present knowledge and future perspectives. Lancet Infectious Diseases, The, 2018, 18, e64-e75.	4.6	119
78	Differential Immunodominance Hierarchy of CD8 ⁺ T-Cell Responses in HLA-B*27:05- and -B*27:02-Mediated Control of HIV-1 Infection. Journal of Virology, 2018, 92, .	1.5	14
79	Correcting for Population Stratification Reduces False Positive and False Negative Results in Joint Analyses of Host and Pathogen Genomes. Frontiers in Genetics, 2018, 9, 266.	1.1	14
80	Interferon lambda 3/4 polymorphisms are associated with AIDS-related Kaposi's sarcoma. Aids, 2018, 32, 2759-2765.	1.0	6
81	Easy and accurate reconstruction of whole HIV genomes from short-read sequence data with shiver. Virus Evolution, 2018, 4, vey007.	2.2	64
82	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
83	Sequence Alignment Through the Looking Glass. , 2018, , .		6
84	Human genetic variants and age are the strongest predictors of humoral immune responses to common pathogens and vaccines. Genome Medicine, 2018, 10, 59.	3.6	113
85	Anti-apolipoprotein A-1 autoantibodies are associated with immunodeficiency and systemic inflammation in HIV patients. Journal of Infection, 2018, 76, 186-195.	1.7	12
86	Killer cell immunoglobulin-like receptor 3DL1 variation modifies HLA-B*57 protection against HIV-1. Journal of Clinical Investigation, 2018, 128, 1903-1912.	3.9	52
87	Host Genetics and Genomics. , 2018, , 1015-1022.		0
88	Genome-to-genome analysis highlights the effect of the human innate and adaptive immune systems on the hepatitis C virus. Nature Genetics, 2017, 49, 666-673.	9.4	129
89	SQC: secure quality control for meta-analysis of genome-wide association studies. Bioinformatics, 2017, 33, 2273-2280.	1.8	8
90	No Evidence for Association of β -Defensin Genomic Copy Number with HIV Susceptibility, HIV Load during Clinical Latency, or Progression to AIDS. Annals of Human Genetics, 2017, 81, 27-34.	0.3	4

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91	Evaluating the Impact of Functional Genetic Variation on HIV-1 Control. <i>Journal of Infectious Diseases</i> , 2017, 216, 1063-1069.	1.9	20
92	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
93	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
94	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
95	Estimating the Respective Contributions of Human and Viral Genetic Variation to HIV Control. <i>PLoS Computational Biology</i> , 2017, 13, e1005339.	1.5	28
96	Human exome sequencing to evaluate the impact of rare coding variation on HIV-1 control. <i>Virus Evolution</i> , 2017, 3, .	2.2	0
97	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.	2.6	38
98	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
99	Privacy-preserving genomic testing in the clinic: a model using HIV treatment. <i>Genetics in Medicine</i> , 2016, 18, 814-822.	1.1	36
100	Determinants of HIV-1 broadly neutralizing antibody induction. <i>Nature Medicine</i> , 2016, 22, 1260-1267.	15.2	133
101	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
102	Standardized Whole-Blood Transcriptional Profiling Enables the Deconvolution of Complex Induced Immune Responses. <i>Cell Reports</i> , 2016, 16, 2777-2791.	2.9	84
103	Identification of Siglec-1 null individuals infected with HIV-1. <i>Nature Communications</i> , 2016, 7, 12412.	5.8	38
104	A privacy-preserving solution for compressed storage and selective retrieval of genomic data. <i>Genome Research</i> , 2016, 26, 1687-1696.	2.4	26
105	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
106	Role of APOBEC3F Gene Variation in HIV-1 Disease Progression and Pneumocystis Pneumonia. <i>PLoS Genetics</i> , 2016, 12, e1005921.	1.5	17
107	The Characteristics of Heterozygous Protein Truncating Variants in the Human Genome. <i>PLoS Computational Biology</i> , 2015, 11, e1004647.	1.5	34
108	Adaptation on a genomic scale. <i>ELife</i> , 2015, 4, e06193.	2.8	2

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109	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
110	Quantifying Genomic Privacy via Inference Attack with High-Order SNV Correlations. , 2015, , .		19
111	Privacy in the Genomic Era. ACM Computing Surveys, 2015, 48, 1-44.	16.1	197
112	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
113	Human genetic variation in HIV disease. Current Opinion in HIV and AIDS, 2015, 10, 110-115.	1.5	9
114	Amino Acid Variation in HLA Class II Proteins Is a Major Determinant of Humoral Response to Common Viruses. American Journal of Human Genetics, 2015, 97, 738-743.	2.6	63
115	GenoGuard: Protecting Genomic Data against Brute-Force Attacks. , 2015, , .		40
116	Opportunistic testing for urogenital infection with Chlamydia trachomatis in south-western Switzerland, 2012: a feasibility study. Eurosurveillance, 2015, 20, .	3.9	6
117	A Novel Acute Retroviral Syndrome Severity Score Predicts the Key Surrogate Markers for HIV-1 Disease Progression. PLoS ONE, 2014, 9, e114111.	1.1	17
118	Disentangling Human Tolerance and Resistance Against HIV. PLoS Biology, 2014, 12, e1001951.	2.6	53
119	Dynamics of HIV Latency and Reactivation in a Primary CD4+ T Cell Model. PLoS Pathogens, 2014, 10, e1004156.	2.1	70
120	LILRB2 Interaction with HLA Class I Correlates with Control of HIV-1 Infection. PLoS Genetics, 2014, 10, e1004196.	1.5	83
121	Analysis of Stop-Gain and Frameshift Variants in Human Innate Immunity Genes. PLoS Computational Biology, 2014, 10, e1003757.	1.5	32
122	GuavaH: a compendium of host genomic data in HIV biology and disease. Retrovirology, 2014, 11, 6.	0.9	13
123	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. Clinical Infectious Diseases, 2014, 58, 285-294.	2.9	75
124	HLA Class I and KIR Genes Do Not Protect Against HIV Type 1 Infection in Highly Exposed Uninfected Individuals With Hemophilia A. Journal of Infectious Diseases, 2014, 210, 1047-1051.	1.9	16
125	Co-Trimoxazole Prophylaxis Is Associated with Reduced Risk of Incident Tuberculosis in Participants in the Swiss HIV Cohort Study. Antimicrobial Agents and Chemotherapy, 2014, 58, 2363-2368.	1.4	34
126	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

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127	Influence of HLA-C Expression Level on HIV Control. <i>Science</i> , 2013, 340, 87-91.	6.0	352
128	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
129	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.	1.4	38
130	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
131	European Genetic Diversity and Susceptibility to Pathogens. <i>Human Heredity</i> , 2013, 76, 187-193.	0.4	3
132	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
133	Role of retroviral restriction factors in the interferon- λ -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
134	Genetic Associations with Resistance to HIV-1 Infection, Viral Control and Protection Against Disease. <i>PLoS Pathogens</i> , 2012, 8, e1002334.		0
135	Genome-wide association study of interferon-related cytopenia in chronic hepatitis C patients. <i>Journal of Hepatology</i> , 2012, 56, 313-319.	1.8	39
136	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
137	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
138	<i>HLA-B*57:01</i> 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, 589-595.	1.0	2
139	Inosine Triphosphate Protects Against Ribavirin-Induced Adenosine Triphosphate Loss by Adenylosuccinate Synthase Function. <i>Gastroenterology</i> , 2011, 140, 1314-1321.	0.6	111
140	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
141	Copy Number Variation of KIR Genes Influences HIV-1 Control. <i>PLoS Biology</i> , 2011, 9, e1001208.	2.6	132
142	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
143	Hepatitis C pharmacogenetics: State of the art in 2010. <i>Hepatology</i> , 2011, 53, 336-345.	3.6	131
144	Estimating the net contribution of interleukin-28B variation to spontaneous hepatitis C virus clearance. <i>Hepatology</i> , 2011, 53, 1446-1454.	3.6	56

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145	Personalized hepatitis C therapy: opportunities and pitfalls. <i>Expert Review of Molecular Diagnostics</i> , 2011, 11, 127-129.	1.5	2
146	Joint analysis of host and pathogen genomes. , 2011, , .		0
147	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, 773-779.	1.9	40
148	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
149	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
150	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
151	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
152	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
153	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
154	Evidence of dysregulation of dendritic cells in primary HIV infection. <i>Blood</i> , 2010, 116, 3839-3852.	0.6	159
155	Role of human leukocyte antigen class I alleles in progressive multifocal leukoencephalopathy. <i>Journal of NeuroVirology</i> , 2010, 16, 41-47.	1.0	7
156	How the Human Genome Can Predict Response to Hepatitis C Therapy. <i>Current Hepatitis Reports</i> , 2010, 9, 1-8.	0.3	2
157	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
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