Julian Knight

List of Publications by Year
in descending order

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		8749	4988
202	34,276	75	167
papers	citations	h-index	g-index

241	241	241	58514
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Safety and efficacy of the ChAdOx1 nCoV-19 vaccine (AZD1222) against SARS-CoV-2: an interim analysis of four randomised controlled trials in Brazil, South Africa, and the UK. Lancet, The, 2021, 397, 99-111.	6.3	3,887
2	Safety and immunogenicity of the ChAdOx1 nCoV-19 vaccine against SARS-CoV-2: a preliminary report of a phase 1/2, single-blind, randomised controlled trial. Lancet, The, 2020, 396, 467-478.	6.3	2,080
3	Systematic identification of trans eQTLs as putative drivers of known disease associations. Nature Genetics, 2013, 45, 1238-1243.	9.4	1,544
4	Safety and immunogenicity of ChAdOx1 nCoV-19 vaccine administered in a prime-boost regimen in young and old adults (COV002): a single-blind, randomised, controlled, phase 2/3 trial. Lancet, The, 2020, 396, 1979-1993.	6.3	1,196
5	Broad and strong memory CD4+ and CD8+ T cells induced by SARS-CoV-2 in UK convalescent individuals following COVID-19. Nature Immunology, 2020, 21, 1336-1345.	7.0	1,066
6	Genetic mechanisms of critical illness in COVID-19. Nature, 2021, 591, 92-98.	13.7	1,014
7	Single-dose administration and the influence of the timing of the booster dose on immunogenicity and efficacy of ChAdOx1 nCoV-19 (AZD1222) vaccine: a pooled analysis of four randomised trials. Lancet, The, 2021, 397, 881-891.	6.3	979
8	Integrating mapping-, assembly- and haplotype-based approaches for calling variants in clinical sequencing applications. Nature Genetics, 2014, 46, 912-918.	9.4	937
9	Evidence of escape of SARS-CoV-2 variant B.1.351 from natural and vaccine-induced sera. Cell, 2021, 184, 2348-2361.e6.	13.5	936
10	Germline mutations affecting the proofreading domains of POLE and POLD1 predispose to colorectal adenomas and carcinomas. Nature Genetics, 2013, 45, 136-144.	9.4	851
11	A ChIP-seq defined genome-wide map of vitamin D receptor binding: Associations with disease and evolution. Genome Research, 2010, 20, 1352-1360.	2.4	737
12	Genetic association analyses implicate aberrant regulation of innate and adaptive immunity genes in the pathogenesis of systemic lupus erythematosus. Nature Genetics, 2015, 47, 1457-1464.	9.4	730
13	Innate Immune Activity Conditions the Effect of Regulatory Variants upon Monocyte Gene Expression. Science, 2014, 343, 1246949.	6.0	706
14	Reduced neutralization of SARS-CoV-2 B.1.617 by vaccine and convalescent serum. Cell, 2021, 184, 4220-4236.e13.	13.5	630
15	Large-scale cis- and trans-eQTL analyses identify thousands of genetic loci and polygenic scores that regulate blood gene expression. Nature Genetics, 2021, 53, 1300-1310.	9.4	590
16	Major Histocompatibility Complex Genomics and Human Disease. Annual Review of Genomics and Human Genetics, 2013, 14, 301-323.	2.5	580
17	Genomic landscape of the individual host response and outcomes in sepsis: a prospective cohort study. Lancet Respiratory Medicine,the, 2016, 4, 259-271.	5.2	536
18	Antibody evasion by the P.1 strain of SARS-CoV-2. Cell, 2021, 184, 2939-2954.e9.	13.5	519

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19	Genetics of gene expression in primary immune cells identifies cell typeâ€“specific master regulators and roles of HLA alleles. Nature Genetics, 2012, 44, 502-510.	9.4	445
20	A polymorphism that affects OCT-1 binding to the TNF promoter region is associated with severe malaria. Nature Genetics, 1999, 22, 145-150.	9.4	442
21	Expression of the Multiple Sclerosis-Associated MHC Class II Allele HLA-DRB1*1501 Is Regulated by Vitamin D. PLoS Genetics, 2009, 5, e1000369.	1.5	442
22	Reduced neutralization of SARS-CoV-2 B.1.1.7 variant by convalescent and vaccine sera. Cell, 2021, 184, 2201-2211.e7.	13.5	442
23	The Polygenic and Monogenic Basis of Blood Traits and Diseases. Cell, 2020, 182, 1214-1231.e11.	13.5	388
24	Classification of patients with sepsis according to blood genomic endotype: a prospective cohort study. Lancet Respiratory Medicine,the, 2017, 5, 816-826.	5.2	381
25	Performance characteristics of five immunoassays for SARS-CoV-2: a head-to-head benchmark comparison. Lancet Infectious Diseases, The, 2020, 20, 1390-1400.	4.6	336
26	The antigenic anatomy of SARS-CoV-2 receptor binding domain. Cell, 2021, 184, 2183-2200.e22.	13.5	331
27	Factors influencing success of clinical genome sequencing across a broad spectrum of disorders. Nature Genetics, 2015, 47, 717-726.	9.4	310
28	Longitudinal COVID-19 profiling associates IL-1RA and IL-10 with disease severity and RANTES with mild disease. JCI Insight, 2020, 5, .	2.3	310
29	Phase 1/2 trial of SARS-CoV-2 vaccine ChAdOx1 nCoV-19 with a booster dose induces multifunctional antibody responses. Nature Medicine, 2021, 27, 279-288.	15.2	265
30	The chromosome 6p22 haplotype associated with dyslexia reduces the expression of KIAA0319 , a novel gene involved in neuronal migration. Human Molecular Genetics, 2006, 15, 1659-1666.	1.4	240
31	Severe Malarial Anemia and Cerebral Malaria Are Associated with Different Tumor Necrosis Factor Promoter Alleles. Journal of Infectious Diseases, 1999, 179, 287-290.	1.9	231
32	In vivo characterization of regulatory polymorphisms by allele-specific quantification of RNA polymerase loading. Nature Genetics, 2003, 33, 469-475.	9.4	231
33	Clinical whole-genome sequencing in severe early-onset epilepsy reveals new genes and improves molecular diagnosis. Human Molecular Genetics, 2014, 23, 3200-3211.	1.4	222
34	Meta-analysis of genome-wide association studies identifies ten loci influencing allergic sensitization. Nature Genetics, 2013, 45, 902-906.	9.4	221
35	Regulatory polymorphisms underlying complex disease traits. Journal of Molecular Medicine, 2005, 83, 97-109.	1.7	217
36	Peripheral CD8+ T cell characteristics associated with durable responses to immune checkpoint blockade in patients with metastatic melanoma. Nature Medicine, 2020, 26, 193-199.	15.2	211

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37	Allele-specific gene expression uncovered. Trends in Genetics, 2004, 20, 113-116.	2.9	189
38	The association between endometriosis and autoimmune diseases: a systematic review and meta-analysis. Human Reproduction Update, 2019, 25, 486-503.	5.2	179
39	Antibody testing for COVID-19: A report from theÂNational COVID Scientific Advisory Panel. Wellcome Open Research, 2020, 5, 139.	0.9	179
40	Shared and Distinct Aspects of the Sepsis Transcriptomic Response to Fecal Peritonitis and Pneumonia. American Journal of Respiratory and Critical Care Medicine, 2017, 196, 328-339.	2.5	178
41	A community approach to mortality prediction in sepsis via gene expression analysis. Nature Communications, 2018, 9, 694.	5.8	178
42	Transcriptomic Signatures in Sepsis and a Differential Response to Steroids. From the VANISH Randomized Trial. American Journal of Respiratory and Critical Care Medicine, 2019, 199, 980-986.	2.5	178
43	Whole-genome sequencing reveals host factors underlying critical COVID-19. Nature, 2022, 607, 97-103.	13.7	174
44	Genome-wide association study of survival from sepsis due to pneumonia: an observational cohort study. Lancet Respiratory Medicine,the, 2015, 3, 53-60.	5.2	166
45	A blood atlas of COVID-19 defines hallmarks of disease severity and specificity. Cell, 2022, 185, 916-938.e58.	13.5	164
46	Choice of transcripts and software has a large effect on variant annotation. Genome Medicine, 2014, 6, 26.	3.6	158
47	A genetics-led approach defines the drug target landscape of 30 immune-related traits. Nature Genetics, 2019, 51, 1082-1091.	9.4	157
48	Two doses of SARS-CoV-2 vaccination induce robust immune responses to emerging SARS-CoV-2 variants of concern. Nature Communications, 2021, 12, 5061.	5.8	150
49	Tensor decomposition for multiple-tissue gene expression experiments. Nature Genetics, 2016, 48, 1094-1100.	9.4	142
50	Interferon-Induced Transmembrane Protein 3 Genetic Variant rs12252-C Associated With Disease Severity in Coronavirus Disease 2019. Journal of Infectious Diseases, 2020, 222, 34-37.	1.9	140
51	Identification of Common Genetic Variation That Modulates Alternative Splicing. PLoS Genetics, 2007, 3, e99.	1.5	139
52	Leprosy and the Adaptation of Human Toll-Like Receptor 1. PLoS Pathogens, 2010, 6, e1000979.	2.1	139
53	XGR software for enhanced interpretation of genomic summary data, illustrated by application to immunological traits. Genome Medicine, 2016, 8, 129.	3.6	137
54	Redefining critical illness. Nature Medicine, 2022, 28, 1141-1148.	15.2	136

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55	Increased in vivo transcription of an IL-8 haplotype associated with respiratory syncytial virus disease-susceptibility. Genes and Immunity, 2004, 5, 274-282.	2.2	127
56	Regulation of major histocompatibility complex class II gene expression, genetic variation and disease. Genes and Immunity, 2010, 11, 99-112.	2.2	122
57	SARS-CoV-2 RNA detected in blood products from patients with COVID-19 is not associated with infectious virus. Wellcome Open Research, 2020, 5, 181.	0.9	122
58	Genomic modulators of gene expression in human neutrophils. Nature Communications, 2015, 6, 7545.	5.8	120
59	Unique transcriptome signatures and GM-CSF expression in lymphocytes from patients with spondyloarthritis. Nature Communications, 2017, 8, 1510.	5.8	118
60	Congenital myasthenic syndromes due to mutations inALG2andALG14. Brain, 2013, 136, 944-956.	3.7	117
61	Complex NF-ÎºB Interactions at the Distal Tumor Necrosis Factor Promoter Region in Human Monocytes. Journal of Biological Chemistry, 1998, 273, 21178-21186.	1.6	115
62	Cell Specific eQTL Analysis without Sorting Cells. PLoS Genetics, 2015, 11, e1005223.	1.5	115
63	Pathogenic implications for autoimmune mechanisms derived by comparative eQTL analysis of CD4+ versus CD8+ T cells. PLoS Genetics, 2017, 13, e1006643.	1.5	110
64	An immunodominant NP105â€“113-B*07:02 cytotoxic T cell response controls viral replication and is associated with less severe COVID-19 disease. Nature Immunology, 2022, 23, 50-61.	7.0	110
65	SARS-CoV-2-specific antibody and T-cell responses 1 year after infection in people recovered from COVID-19: a longitudinal cohort study. Lancet Microbe, The, 2022, 3, e348-e356.	3.4	107
66	Allele-specific repression of lymphotoxin-Î± by activated B cell factor-1. Nature Genetics, 2004, 36, 394-399.	9.4	105
67	Inherited Variability of Tumor Necrosis Factor Production and Susceptibility to Infectious Disease. Proceedings of the Association of American Physicians, 1999, 111, 290-298.	2.1	105
68	Application of whole genome and RNA sequencing to investigate the genomic landscape of common variable immunodeficiency disorders. Clinical Immunology, 2015, 160, 301-314.	1.4	100
69	Distinct HLA associations of LGI1 and CASPR2-antibody diseases. Brain, 2018, 141, 2263-2271.	3.7	100
70	Host genetics and infectious disease: new tools, insights and translational opportunities. Nature Reviews Genetics, 2021, 22, 137-153.	7.7	98
71	Identification of LZTFL1 as a candidate effector gene at a COVID-19 risk locus. Nature Genetics, 2021, 53, 1606-1615.	9.4	93
72	A Common Variant Associated with Dyslexia Reduces Expression of the KIAA0319 Gene. PLoS Genetics, 2009, 5, e1000436.	1.5	92

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73	Mutations in CDC45 , Encoding an Essential Component of the Pre-initiation Complex, Cause Meier-Gorlin Syndrome and Craniosynostosis. American Journal of Human Genetics, 2016, 99, 125-138.	2.6	92
74	HLA class I alleles tag HLA-DRB1 * 1501 haplotypes for differential risk in multiple sclerosis susceptibility. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 13069-13074.	3.3	86
75	The human Major Histocompatibility Complex as a paradigm in genomics research. Briefings in Functional Genomics & Proteomics, 2009, 8, 379-394.	3.8	85
76	Joint sequencing of human and pathogen genomes reveals the genetics of pneumococcal meningitis. Nature Communications, 2019, 10, 2176.	5.8	83
77	Gene-centric meta-analyses of 108 912 individuals confirm known body mass index loci and reveal three novel signals. Human Molecular Genetics, 2013, 22, 184-201.	1.4	82
78	Whole-genome sequencing of bladder cancers reveals somatic CDKN1A mutations and clinicopathological associations with mutation burden. Nature Communications, 2014, 5, 3756.	5.8	81
79	Sepsis Subclasses: A Framework for Development and Interpretation*. Critical Care Medicine, 2021, 49, 748-759.	0.4	81
80	SARS-CoV-2 RNA detected in blood products from patients with COVID-19 is not associated with infectious virus. Wellcome Open Research, 2020, 5, 181.	0.9	81
81	Multiple sclerosis and the major histocompatibility complex. Current Opinion in Neurology, 2009, 22, 219-225.	1.8	77
82	Early-onset autoimmunity associated with SOCS1 haploinsufficiency. Nature Communications, 2020, 11, 5341.	5.8	74
83	Vitamin D receptor gene methylation is associated with ethnicity, tuberculosis, and TaqI polymorphism. Human Immunology, 2011, 72, 262-268.	1.2	72
84	Functional implications of genetic variation in non-coding DNA for disease susceptibility and gene regulation. Clinical Science, 2003, 104, 493-501.	1.8	71
85	Homozygous mutations in a predicted endonuclease are a novel cause of congenital dyserythropoietic anemia type I. Haematologica, 2013, 98, 1383-1387.	1.7	71
86	NOX1 loss-of-function genetic variants in patients with inflammatory bowel disease. Mucosal Immunology, 2018, 11, 562-574.	2.7	71
87	Associations of HLA alleles with specific language impairment. Journal of Neurodevelopmental Disorders, 2014, 6, 1.	1.5	67
88	Gene panel sequencing improves the diagnostic work-up of patients with idiopathic erythrocytosis and identifies new mutations. Haematologica, 2016, 101, 1306-1318.	1.7	66
89	Early childhood epilepsies: epidemiology, classification, aetiology, and socio-economic determinants. Brain, 2021, 144, 2879-2891.	3.7	64
90	Pervasive haplotypic variation in the spliceo-transcriptome of the human major histocompatibility complex. Genome Research, 2011, 21, 1042-1054.	2.4	63

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91	Distinct Transcriptional and Anti-Mycobacterial Profiles of Peripheral Blood Monocytes Dependent on the Ratio of Monocytes: Lymphocytes. EBioMedicine, 2015, 2, 1619-1626.	2.7	61
92	miR-10b-5p is a novel Th17 regulator present in Th17 cells from ankylosing spondylitis. Annals of the Rheumatic Diseases, 2017, 76, 620-625.	0.5	61
93	The impact of viral mutations on recognition by SARS-CoV-2 specific TÂcells. IScience, 2021, 24, 103353.	1.9	57
94	Gain-of-Function Mutations in ZIC1 Are Associated with Coronal Craniosynostosis and Learning Disability. American Journal of Human Genetics, 2015, 97, 378-388.	2.6	56
95	â€œNot pathogenic until proven otherwiseâ€: perspectives of UK clinical genomics professionals toward secondary findings in context of a Genomic Medicine Multidisciplinary Team and the 100,000 Genomes Project. Genetics in Medicine, 2018, 20, 320-328.	1.1	56
96	Genetics of gene expression in immunity to infection. Current Opinion in Immunology, 2014, 30, 63-71.	2.4	54
97	A haemagglutination test for rapid detection of antibodies to SARS-CoV-2. Nature Communications, 2021, 12, 1951.	5.8	54
98	Genomic modulators of the immune response. Trends in Genetics, 2013, 29, 74-83.	2.9	52
99	HLA-C Level Is Regulated by a Polymorphic Oct1 Binding Site in the HLA-C Promoter Region. American Journal of Human Genetics, 2016, 99, 1353-1358.	2.6	49
100	The genetic association ofRUNX3with ankylosing spondylitis can be explained by allele-specific effects on IRF4 recruitment that alter gene expression. Annals of the Rheumatic Diseases, 2016, 75, 1534-1540.	0.5	48
101	Preclinical target validation using patient-derived cells. Nature Reviews Drug Discovery, 2015, 14, 149-150.	21.5	46
102	Genome-wide analysis identifies a role for common copy number variants in specific language impairment. European Journal of Human Genetics, 2015, 23, 1370-1377.	1.4	46
103	An ankylosing spondylitis-associated genetic variant in theIL23R-IL12RB2intergenic region modulates enhancer activity and is associated with increased Th1-cell differentiation. Annals of the Rheumatic Diseases, 2016, 75, 2150-2156.	0.5	45
104	Identifying collagen VI as a target of fibrotic diseases regulated by CREBBP/EP300. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 20753-20763.	3.3	45
105	Defective tubulin detyrosination causes structural brain abnormalities with cognitive deficiency in humans and mice. Human Molecular Genetics, 2019, 28, 3391-3405.	1.4	43
106	Increased prevalence of sex chromosome aneuploidies in specific language impairment and dyslexia. Developmental Medicine and Child Neurology, 2014, 56, 346-353.	1.1	42
107	Transcriptomic profiling facilitates classification of response to influenza challenge. Journal of Molecular Medicine, 2015, 93, 105-114.	1.7	38
108	Context-specific regulation of surface and soluble IL7R expression by an autoimmune risk allele. Nature Communications, 2019, 10, 4575.	5.8	37

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109	Whole-genome sequencing of spermatocytic tumors provides insights into the mutational processes operating in the male germline. PLoS ONE, 2017, 12, e0178169.	1.1	36
110	Erythrocytosis associated with a novel missense mutation in the BPGM gene. Haematologica, 2014, 99, e201-e204.	1.7	35
111	A point mutation in the ion conduction pore of AMPA receptor GRIA3 causes dramatically perturbed sleep patterns as well as intellectual disability. Human Molecular Genetics, 2017, 26, 3869-3882.	1.4	35
112	Identification of a Novel Î²-Cell Glucokinase (GCK) Promoter Mutation (âˆ'71G>C) That ModulatesGCKGene Expression Through Loss of Allele-Specific Sp1 Binding Causing Mild Fasting Hyperglycemia in Humans. Diabetes, 2009, 58, 1929-1935.	0.3	34
113	Approaches for establishing the function of regulatory genetic variants involved in disease. Genome Medicine, 2014, 6, 92.	3.6	34
114	Enhanced understanding of the hostâ€"pathogen interaction in sepsis: new opportunities for omic approaches. Lancet Respiratory Medicine,the, 2017, 5, 212-223.	5.2	33
115	Genomic mapping of the MHC transactivator CIITA using an integrated ChIP-seq and genetical genomics approach. Genome Biology, 2014, 15, 494.	3.8	32
116	High resolution HLA haplotyping by imputation for a British population bioresource. Human Immunology, 2017, 78, 242-251.	1.2	31
117	A functional SNP associated with atopic dermatitis controls cell type-specific methylation of the VSTM1 gene locus. Genome Medicine, 2017, 9, 18.	3.6	30
118	The suboptimal fibrinolytic response in COVIDâ€19 is dictated by high PAIâ€1. Journal of Thrombosis and Haemostasis, 2022, 20, 2394-2406.	1.9	30
119	Polymorphisms in tumor necrosis factor and other cytokines as risks for infectious diseases and the septic syndrome. Current Infectious Disease Reports, 2001, 3, 427-439.	1.3	29
120	Genomic Response to Vitamin D Supplementation in the Setting of a Randomized, Placebo-Controlled Trial. EBioMedicine, 2018, 31, 133-142.	2.7	29
121	Risk of nontyphoidal Salmonella bacteraemia in African children is modified by STAT4. Nature Communications, 2018, 9, 1014.	5.8	29
122	Identification of hostâ€"pathogen-disease relationships using a scalable multiplex serology platform in UK Biobank. Nature Communications, 2022, 13, 1818.	5.8	28
123	Homozygous microdeletion of exon 5 in ZNF277 in a girl with specific language impairment. European Journal of Human Genetics, 2014, 22, 1165-1171.	1.4	27
124	AltHapAlignR: improved accuracy of RNA-seq analyses through the use of alternative haplotypes. Bioinformatics, 2018, 34, 2401-2408.	1.8	27
125	The malarial fever response - pathogenesis, polymorphism and prospects for intervention. Annals of Tropical Medicine and Parasitology, 1997, 91, 533-542.	1.6	26
126	Post-operative pain in children after day case surgery. Paediatric Anaesthesia, 1994, 4, 45-51.	0.6	25

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127	Chronic mucocutaneous candidiasis: characterization of a family with STAT-1 gain-of-function and development of an ex-vivo assay for Th17 deficiency of diagnostic utility. Clinical and Experimental Immunology, 2016, 184, 216-227.	1.1	25
128	Microvesicle Subsets in Sepsis Due to Community Acquired Pneumonia Compared to Faecal Peritonitis. Shock, 2018, 49, 393-401.	1.0	25
129	Investigating the Impact of a Musical Intervention on Preschool Childrenâ€™s Executive Function. Frontiers in Psychology, 2018, 9, 2389.	1.1	25
130	ImplementationÂof a genomic medicine multi-disciplinary team approach for rare diseaseÂin the clinical setting: a prospective exome sequencingÂcase series. Genome Medicine, 2019, 11, 46.	3.6	25
131	Genome-wide CRISPR/Cas9-knockout in human induced Pluripotent Stem Cell (iPSC)-derived macrophages. Scientific Reports, 2021, 11, 4245.	1.6	25
132	Insights from early experience of a Rare Disease Genomic Medicine Multidisciplinary Team: a qualitative study. European Journal of Human Genetics, 2017, 25, 680-686.	1.4	24
133	Chromatin profiling across the human tumour necrosis factor gene locus reveals a complex, cell type-specific landscape with novel regulatory elements. Nucleic Acids Research, 2008, 36, 4845-4862.	6.5	23
134	An integrated expression phenotype mapping approach defines common variants in LEP, ALOX15 and CAPNS1 associated with induction of IL-6. Human Molecular Genetics, 2010, 19, 720-730.	1.4	23
135	Using de novo assembly to identify structural variation of eight complex immune system gene regions. PLoS Computational Biology, 2021, 17, e1009254.	1.5	22
136	Common, low-frequency, rare, and ultra-rare coding variants contribute to COVID-19 severity. Human Genetics, 2022, 141, 147-173.	1.8	22
137	Genetic determinants of HSP70 gene expression following heat shock. Human Molecular Genetics, 2010, 19, 4939-4947.	1.4	21
138	Divergent trajectories of antiviral memory after SARS-CoV-2 infection. Nature Communications, 2022, 13, 1251.	5.8	20
139	Accuracy of Genotyping of Single-Nucleotide Polymorphisms by PCR-ELISA Allele-specific Oligonucleotide Hybridization Typing and by Amplification Refractory Mutation System. Clinical Chemistry, 1999, 45, 1860-1863.	1.5	19
140	The malarial fever responseâ€"pathogenesis, polymorphism and prospects for intervention. Annals of Tropical Medicine and Parasitology, 1997, 91, 533-542.	1.6	18
141	From genome-wide association studies to rational drug target prioritisation in inflammatory arthritis. Lancet Rheumatology, The, 2020, 2, e50-e62.	2.2	17
142	Fine mapping genetic determinants of the highly variably expressed MHC gene ZFP57. European Journal of Human Genetics, 2014, 22, 568-571.	1.4	16
143	Evidence for a second ankylosing spondylitis-associated RUNX3 regulatory polymorphism. RMD Open, 2018, 4, e000628.	1.8	16
144	Ex vivo mass cytometry analysis reveals a profound myeloid proinflammatory signature in psoriatic arthritis synovial fluid. Annals of the Rheumatic Diseases, 2021, 80, 1559-1567.	0.5	16

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145	Priority index: database of genetic targets in immune-mediated disease. Nucleic Acids Research, 2022, 50, D1358-D1367.	6.5	16
146	Allele-specific transcription of the asthma-associated PHD finger protein 11 gene (PHF11) modulated by octamer-binding transcription factor 1 (Oct-1). Journal of Allergy and Clinical Immunology, 2011, 127, 1054-1062.e2.	1.5	15
147	Resolving the variable genome and epigenome in human disease. Journal of Internal Medicine, 2012, 271, 379-391.	2.7	14
148	An Integrated Approach to Defining Genetic and Environmental Determinants for Major Clinical Outcomes Involving Vitamin D. Molecular Diagnosis and Therapy, 2014, 18, 261-272.	1.6	14
149	Transcriptional repression and DNA looping associated with a novel regulatory element in the final exon of the lymphotoxin-Î² gene. Genes and Immunity, 2011, 12, 126-135.	2.2	13
150	Epstein-Barr virus reactivation in sepsis due to community-acquired pneumonia is associated with increased morbidity and an immunosuppressed host transcriptomic endotype. Scientific Reports, 2020, 10, 9838.	1.6	13
151	Human Leukocyte Antigen Association Study Reveals DRB1*04:02 Effects Additional to DRB1*07:01 in Anti-LGI1 Encephalitis. Neurology: Neuroimmunology and NeuroInflammation, 2022, 9, .	3.1	13
152	A Common Haplotype of the TNF Receptor 2 Gene Modulates Endotoxin Tolerance. Journal of Immunology, 2011, 186, 3058-3065.	0.4	12
153	Polymorphisms in tumor necrosis factor and other cytokines as risks for infectious diseases and the septic syndrome. Current Infectious Disease Reports, 2007, 3, 427-439.	1.3	11
154	Genetics and the general physician: insights, applications and future challenges. QJM - Monthly Journal of the Association of Physicians, 2009, 102, 757-772.	0.2	11
155	Use of gene expression studies to investigate the human immunological response to malaria infection. Malaria Journal, 2019, 18, 418.	0.8	11
156	The Impact of Viral Mutations on Recognition by SARS-CoV-2 Specific T-Cells. SSRN Electronic Journal, 0, , .	0.4	11
157	Functional Differences Exist between TNFÎ± Promoters Encoding the Common â^'237G SNP and the Rarer HLA-B*5701-Linked A Variant. PLoS ONE, 2012, 7, e40100.	1.1	11
158	Functional Genomic Analysis of a RUNX3 Polymorphism Associated With Ankylosing Spondylitis. Arthritis and Rheumatology, 2021, 73, 980-990.	2.9	10
159	Maternal immune activation downregulates schizophrenia genes in the foetal mouse brain. Brain Communications, 2021, 3, fcab275.	1.5	10
160	Natural Killer cells demonstrate distinct eQTL and transcriptome-wide disease associations, highlighting their role in autoimmunity. Nature Communications, 2022, 13, .	5.8	10
161	Two Cases of Pulmonary Complications Associated with a Recently Recognised Salmonella enteritidis Phage Type, 21b, Affecting Immunocompetent Adults. European Journal of Clinical Microbiology and Infectious Diseases, 2000, 19, 725-726.	1.3	9
162	Accuracy of genotyping of single-nucleotide polymorphisms by PCR-ELISA allele-specific oligonucleotide hybridization typing and by amplification refractory mutation system. Clinical Chemistry, 1999, 45, 1860-3.	1.5	9

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163	Epigenomic analysis reveals a dynamic and context-specific macrophage enhancer landscape associated with innate immune activation and tolerance. Genome Biology, 2022, 23, .	3.8	9
164	Investigation of a possible extended risk haplotype in the IL23R region associated with ankylosing spondylitis. Genes and Immunity, 2017, 18, 105-108.	2.2	8
165	Genomic Insights into Myasthenia Gravis Identify Distinct Immunological Mechanisms in Early and Late Onset Disease. Annals of Neurology, 2021, 90, 455-463.	2.8	8
166	Polymorphisms in Tumor Necrosis Factor and Other Cytokines As Risks for Infectious Diseases and the Septic Syndrome. Current Infectious Disease Reports, 2001, 3, 427-439.	1.3	8
167	ReliableGenome: annotation of genomic regions with high/low variant calling concordance. Bioinformatics, 2017, 33, 155-160.	1.8	7
168	Serum calprotectin is not an independent predictor of severe COVID-19 in ambulatory adult patients. Journal of Infection, 2022, 84, e27-e29.	1.7	7
169	A functional AT/G polymorphism in the 5â€²-untranslated region of SETDB2 in the IgE locus on human chromosome 13q14. Genes and Immunity, 2015, 16, 488-494.	2.2	6
170	Translating GWAS in rheumatic disease: approaches to establishing mechanism and function for genetic associations with ankylosing spondylitis. Briefings in Functional Genomics, 2018, 17, 308-318.	1.3	6
171	Multi-level evidence of an allelic hierarchy of USH2A variants in hearing, auditory processing and speech/language outcomes. Communications Biology, 2020, 3, 180.	2.0	6
172	Decreased ATM Function Causes Delayed DNA Repair and Apoptosis in Common Variable Immunodeficiency Disorders. Journal of Clinical Immunology, 2021, 41, 1315-1330.	2.0	6
173	Genetic variants associated with non-typhoidal Salmonella bacteraemia in African children. Lancet, The, 2015, 385, S13.	6.3	5
174	Elevated risk of invasive group A streptococcal disease and host genetic variation in the human leucocyte antigen locus. Genes and Immunity, 2020, 21, 63-70.	2.2	5
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