Julian Knight

List of Publications by Year
in descending order

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202 papers	34,276 citations	8732 75 h-index	4978 167 g-index
241 all docs	241 docs citations	241 times ranked	58514 citing authors

#	Article	IF	Citations
1	Blood leukocyte transcriptomes in Gram-positive and Gram-negative community-acquired pneumonia. European Respiratory Journal, 2022, 59, 2101856.	3.1	3
2	Priority index: database of genetic targets in immune-mediated disease. Nucleic Acids Research, 2022, 50, D1358-D1367.	6.5	16
3	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
4	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
5	Response to Letter to the Editor by Ish et al. entitled â€˜COVID-19 vaccine equityâ€”the need of the hourâ€™. QJM - Monthly Journal of the Association of Physicians, 2022, , .	0.2	0
6	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
7	A blood atlas of COVID-19 defines hallmarks of disease severity and specificity. Cell, 2022, 185, 916-938.e58.	13.5	164
8	Fine-Scale Genetic Structure in the United Arab Emirates Reflects Endogamous and Consanguineous Culture, Population History, and Geography. Molecular Biology and Evolution, 2022, 39, .	3.5	3
9	Common, low-frequency, rare, and ultra-rare coding variants contribute to COVID-19 severity. Human Genetics, 2022, 141, 147-173.	1.8	22
10	Implementation and Extended Evaluation of the Euroimmun Anti-SARS-CoV-2 IgG Assay and Its Contribution to the United Kingdomâ€™s COVID-19 Public Health Response. Microbiology Spectrum, 2022, 10, e0228921.	1.2	2
11	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
12	Whole-genome sequencing reveals host factors underlying critical COVID-19. Nature, 2022, 607, 97-103.	13.7	174
13	Divergent trajectories of antiviral memory after SARS-CoV-2 infection. Nature Communications, 2022, 13, 1251.	5.8	20
14	Identification of hostâ€“pathogen-disease relationships using a scalable multiplex serology platform in UK Biobank. Nature Communications, 2022, 13, 1818.	5.8	28
15	Why do breakthrough COVID-19 infections occur in the vaccinated?. QJM - Monthly Journal of the Association of Physicians, 2022, 115, 67-68.	0.2	2
16	Redefining critical illness. Nature Medicine, 2022, 28, 1141-1148.	15.2	136
17	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
18	Natural Killer cells demonstrate distinct eQTL and transcriptome-wide disease associations, highlighting their role in autoimmunity. Nature Communications, 2022, 13, .	5.8	10

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19	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
20	Host genetics and infectious disease: new tools, insights and translational opportunities. Nature Reviews Genetics, 2021, 22, 137-153.	7.7	98
21	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
22	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
23	Early childhood epilepsies: epidemiology, classification, aetiology, and socio-economic determinants. Brain, 2021, 144, 2879-2891.	3.7	64
24	Sepsis Subclasses: A Framework for Development and Interpretation*. Critical Care Medicine, 2021, 49, 748-759.	0.4	81
25	Genome-wide CRISPR/Cas9-knockout in human induced Pluripotent Stem Cell (iPSC)-derived macrophages. Scientific Reports, 2021, 11, 4245.	1.6	25
26	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
27	A haemagglutination test for rapid detection of antibodies to SARS-CoV-2. Nature Communications, 2021, 12, 1951.	5.8	54
28	Transcriptomic Analysis of Inflammatory Cardiomyopathy Identifies Molecular Signatures of Disease and Informs in silico Prediction of a Network-Based Rationale for Therapy. Frontiers in Immunology, 2021, 12, 640837.	2.2	3
29	The antigenic anatomy of SARS-CoV-2 receptor binding domain. Cell, 2021, 184, 2183-2200.e22.	13.5	331
30	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
31	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
32	Functional Genomic Analysis of a RUNX3 Polymorphism Associated With Ankylosing Spondylitis. Arthritis and Rheumatology, 2021, 73, 980-990.	2.9	10
33	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
34	Antibody evasion by the P.1 strain of SARS-CoV-2. Cell, 2021, 184, 2939-2954.e9.	13.5	519
35	Pre-existing asthma as a comorbidity does not modify cytokine responses and severity of COVID-19. Allergy, Asthma and Clinical Immunology, 2021, 17, 67.	0.9	3
36	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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37	Using de novo assembly to identify structural variation of eight complex immune system gene regions. PLoS Computational Biology, 2021, 17, e1009254.	1.5	22
38	Reduced neutralization of SARS-CoV-2 B.1.617 by vaccine and convalescent serum. Cell, 2021, 184, 4220-4236.e13.	13.5	630
39	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
40	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
41	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
42	Genetic mechanisms of critical illness in COVID-19. Nature, 2021, 591, 92-98.	13.7	1,014
43	The impact of viral mutations on recognition by SARS-CoV-2 specific TÂcells. IScience, 2021, 24, 103353.	1.9	57
44	Identification of LZTFL1 as a candidate effector gene at a COVID-19 risk locus. Nature Genetics, 2021, 53, 1606-1615.	9.4	93
45	Maternal immune activation downregulates schizophrenia genes in the foetal mouse brain. Brain Communications, 2021, 3, fcab275.	1.5	10
46	Musical Activities, Prosocial Behaviors, and Executive Function Skills of Kindergarten Children. Music & Science, 2021, 4, 205920432110548.	0.6	4
47	Disruption of c-MYC Binding and Chromosomal Looping Involving Genetic Variants Associated With Ankylosing Spondylitis Upstream of the RUNX3 Promoter. Frontiers in Genetics, 2021, 12, 741867.	1.1	3
48	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
49	From genome-wide association studies to rational drug target prioritisation in inflammatory arthritis. Lancet Rheumatology, The, 2020, 2, e50-e62.	2.2	17
50	The Polygenic and Monogenic Basis of Blood Traits and Diseases. Cell, 2020, 182, 1214-1231.e11.	13.5	388
51	Early-onset autoimmunity associated with SOCS1 haploinsufficiency. Nature Communications, 2020, 11, 5341.	5.8	74
52	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
53	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
54	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

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55	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
56	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
57	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
58	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
59	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
60	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
61	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
62	Antibody testing for COVID-19: A report from theÂNational COVID Scientific Advisory Panel. Wellcome Open Research, 2020, 5, 139.	0.9	179
63	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
64	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
65	Defective tubulin detyrosination causes structural brain abnormalities with cognitive deficiency in humans and mice. Human Molecular Genetics, 2019, 28, 3391-3405.	1.4	43
66	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
67	A genetics-led approach defines the drug target landscape of 30 immune-related traits. Nature Genetics, 2019, 51, 1082-1091.	9.4	157
68	Context-specific regulation of surface and soluble IL7R expression by an autoimmune risk allele. Nature Communications, 2019, 10, 4575.	5.8	37
69	O32â€ƒAnkylosing spondylitis associated polymorphism of the IL7R controls expression surface and soluble IL7R-alpha during in inflammation. Rheumatology, 2019, 58, .	0.9	0
70	The association between endometriosis and autoimmune diseases: a systematic review and meta-analysis. Human Reproduction Update, 2019, 25, 486-503.	5.2	179
71	I089â€ƒNovel ways to identify new treatment targets for inflammatory arthritis. Rheumatology, 2019, 58, .	0.9	0
72	Joint sequencing of human and pathogen genomes reveals the genetics of pneumococcal meningitis. Nature Communications, 2019, 10, 2176.	5.8	83

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73	Use of gene expression studies to investigate the human immunological response to malaria infection. Malaria Journal, 2019, 18, 418.	0.8	11
74	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
75	Assessment of an Antibody-in-Lymphocyte Supernatant Assay for the Etiological Diagnosis of Pneumococcal Pneumonia in Children. Frontiers in Cellular and Infection Microbiology, 2019, 9, 459.	1.8	3
76	AltHapAlignR: improved accuracy of RNA-seq analyses through the use of alternative haplotypes. Bioinformatics, 2018, 34, 2401-2408.	1.8	27
77	Genomic Response to Vitamin D Supplementation in the Setting of a Randomized, Placebo-Controlled Trial. EBioMedicine, 2018, 31, 133-142.	2.7	29
78	A community approach to mortality prediction in sepsis via gene expression analysis. Nature Communications, 2018, 9, 694.	5.8	178
79	NOX1 loss-of-function genetic variants in patients with inflammatory bowel disease. Mucosal Immunology, 2018, 11, 562-574.	2.7	71
80	Evidence for a second ankylosing spondylitis-associated RUNX3 regulatory polymorphism. RMD Open, 2018, 4, e000628.	1.8	16
81	Risk of nontyphoidal Salmonella bacteraemia in African children is modified by STAT4. Nature Communications, 2018, 9, 1014.	5.8	29
82	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
83	Microvesicle Subsets in Sepsis Due to Community Acquired Pneumonia Compared to Faecal Peritonitis. Shock, 2018, 49, 393-401.	1.0	25
84	Investigating the Impact of a Musical Intervention on Preschool Childrenâ€™s Executive Function. Frontiers in Psychology, 2018, 9, 2389.	1.1	25
85	Distinct HLA associations of LGI1 and CASPR2-antibody diseases. Brain, 2018, 141, 2263-2271.	3.7	100
86	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
87	MicroRNA profiles are associated with lymphocyte count after a major traumatic injury: a potential role for immunometabolism?. British Journal of Anaesthesia, 2018, 121, e23-e24.	1.5	0
88	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
89	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
90	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

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91	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
92	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
93	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
94	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
95	Unique transcriptome signatures and GM-CSF expression in lymphocytes from patients with spondyloarthritis. Nature Communications, 2017, 8, 1510.	5.8	118
96	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
97	ReliableGenome: annotation of genomic regions with high/low variant calling concordance. Bioinformatics, 2017, 33, 155-160.	1.8	7
98	Pathogenic implications for autoimmune mechanisms derived by comparative eQTL analysis of CD4+ versus CD8+ T cells. PLoS Genetics, 2017, 13, e1006643.	1.5	110
99	High resolution HLA haplotyping by imputation for a British population bioresource. Human Immunology, 2017, 78, 242-251.	1.2	31
100	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
101	Characterisation of the global transcriptional response to heat shock and the impact of individual genetic variation. Genome Medicine, 2016, 8, 87.	3.6	4
102	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
103	Tensor decomposition for multiple-tissue gene expression experiments. Nature Genetics, 2016, 48, 1094-1100.	9.4	142
104	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
105	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
106	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
107	XGR software for enhanced interpretation of genomic summary data, illustrated by application to immunological traits. Genome Medicine, 2016, 8, 129.	3.6	137
108	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

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109	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
110	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
111	The Role of Micrornas in The Development of Hospital Acquired Infection in Polytrauma Patients. Intensive Care Medicine Experimental, 2015, 3, .	0.9	1
112	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
113	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
114	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
115	Reply to Pembrey et al: â€˜ZNF277 microdeletions, specific language impairment and the meiotic mismatch methylation (3M) hypothesisâ€™. European Journal of Human Genetics, 2015, 23, 1113-1115.	1.4	2
116	Preclinical target validation using patient-derived cells. Nature Reviews Drug Discovery, 2015, 14, 149-150.	21.5	46
117	Cell Specific eQTL Analysis without Sorting Cells. PLoS Genetics, 2015, 11, e1005223.	1.5	115
118	Genomic modulators of gene expression in human neutrophils. Nature Communications, 2015, 6, 7545.	5.8	120
119	Transcriptomic profiling facilitates classification of response to influenza challenge. Journal of Molecular Medicine, 2015, 93, 105-114.	1.7	38
120	Factors influencing success of clinical genome sequencing across a broad spectrum of disorders. Nature Genetics, 2015, 47, 717-726.	9.4	310
121	Genetic variants associated with non-typhoidal Salmonella bacteraemia in African children. Lancet, The, 2015, 385, S13.	6.3	5
122	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
123	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
124	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
125	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
126	Genomic mapping of the MHC transactivator CIITA using an integrated ChIP-seq and genetical genomics approach. Genome Biology, 2014, 15, 494.	3.8	32

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127	Approaches for establishing the function of regulatory genetic variants involved in disease. Genome Medicine, 2014, 6, 92.	3.6	34
128	Fine mapping genetic determinants of the highly variably expressed MHC gene ZFP57. European Journal of Human Genetics, 2014, 22, 568-571.	1.4	16
129	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
130	Increased prevalence of sex chromosome aneuploidies in specific language impairment and dyslexia. Developmental Medicine and Child Neurology, 2014, 56, 346-353.	1.1	42
131	Choice of transcripts and software has a large effect on variant annotation. Genome Medicine, 2014, 6, 26.	3.6	158
132	Whole-genome sequencing of bladder cancers reveals somatic CDKN1A mutations and clinicopathological associations with mutation burden. Nature Communications, 2014, 5, 3756.	5.8	81
133	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
134	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
135	Associations of HLA alleles with specific language impairment. Journal of Neurodevelopmental Disorders, 2014, 6, 1.	1.5	67
136	Innate Immune Activity Conditions the Effect of Regulatory Variants upon Monocyte Gene Expression. Science, 2014, 343, 1246949.	6.0	706
137	Genetics of gene expression in immunity to infection. Current Opinion in Immunology, 2014, 30, 63-71.	2.4	54
138	Integrating mapping-, assembly- and haplotype-based approaches for calling variants in clinical sequencing applications. Nature Genetics, 2014, 46, 912-918.	9.4	937
139	Erythrocytosis associated with a novel missense mutation in the BPGM gene. Haematologica, 2014, 99, e201-e204.	1.7	35
140	Meta-analysis of genome-wide association studies identifies ten loci influencing allergic sensitization. Nature Genetics, 2013, 45, 902-906.	9.4	221
141	Major Histocompatibility Complex Genomics and Human Disease. Annual Review of Genomics and Human Genetics, 2013, 14, 301-323.	2.5	580
142	Systematic identification of trans eQTLs as putative drivers of known disease associations. Nature Genetics, 2013, 45, 1238-1243.	9.4	1,544
143	Genomic modulators of the immune response. Trends in Genetics, 2013, 29, 74-83.	2.9	52
144	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

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145	Congenital myasthenic syndromes due to mutations inALG2andALG14. Brain, 2013, 136, 944-956.	3.7	117
146	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
147	Homozygous mutations in a predicted endonuclease are a novel cause of congenital dyserythropoietic anemia type I. Haematologica, 2013, 98, 1383-1387.	1.7	71
148	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
149	Resolving the variable genome and epigenome in human disease. Journal of Internal Medicine, 2012, 271, 379-391.	2.7	14
150	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
151	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
152	Pervasive haplotypic variation in the spliceo-transcriptome of the human major histocompatibility complex. Genome Research, 2011, 21, 1042-1054.	2.4	63
153	Vitamin D receptor gene methylation is associated with ethnicity, tuberculosis, and TaqI polymorphism. Human Immunology, 2011, 72, 262-268.	1.2	72
154	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
155	A Common Haplotype of the TNF Receptor 2 Gene Modulates Endotoxin Tolerance. Journal of Immunology, 2011, 186, 3058-3065.	0.4	12
156	Understanding human genetic variation in the era of highâ€throughput sequencing. EMBO Reports, 2010, 11, 650-652.	2.0	3
157	Regulation of major histocompatibility complex class II gene expression, genetic variation and disease. Genes and Immunity, 2010, 11, 99-112.	2.2	122
158	An Allele-specific Gene Expression Assay to Test the Functional Basis of Genetic Associations. Journal of Visualized Experiments, 2010, , .	0.2	2
159	Genetic determinants of HSP70 gene expression following heat shock. Human Molecular Genetics, 2010, 19, 4939-4947.	1.4	21
160	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
161	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
162	Leprosy and the Adaptation of Human Toll-Like Receptor 1. PLoS Pathogens, 2010, 6, e1000979.	2.1	139

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163	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
164	A Common Variant Associated with Dyslexia Reduces Expression of the KIAA0319 Gene. PLoS Genetics, 2009, 5, e1000436.	1.5	92
165	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
166	Insights into the nature and consequences of our variable genome. Briefings in Functional Genomics & Proteomics, 2009, 8, 343-344.	3.8	0
167	Identification of a Novel Î²-Cell Glucokinase (GCK) Promoter Mutation (â^'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
168	The human Major Histocompatibility Complex as a paradigm in genomics research. Briefings in Functional Genomics & Proteomics, 2009, 8, 379-394.	3.8	85
169	Multiple sclerosis and the major histocompatibility complex. Current Opinion in Neurology, 2009, 22, 219-225.	1.8	77
170	Submicroscopic structural variation and genomic disorders. , 2009, , 125-142.		0
171	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
172	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
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