Soumya Raychaudhuri

List of Publications by Year
in descending order

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236 papers	61,596 citations	3159 92 h-index	1190 228 g-index
301 all docs	301 docs citations	301 times ranked	71890 citing authors

#	Article	IF	Citations
1	Hostâ€“microbe interactions have shaped the genetic architecture of inflammatory bowel disease. Nature, 2012, 491, 119-124.	27.8	4,038
2	Fast, sensitive and accurate integration of single-cell data with Harmony. Nature Methods, 2019, 16, 1289-1296.	19.0	3,494
3	The landscape of somatic copy-number alteration across human cancers. Nature, 2010, 463, 899-905.	27.8	3,331
4	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. Nature Genetics, 2010, 42, 937-948.	21.4	2,634
5	Genome-wide meta-analysis increases to 71 the number of confirmed Crohn's disease susceptibility loci. Nature Genetics, 2010, 42, 1118-1125.	21.4	2,284
6	Genetic relationship between five psychiatric disorders estimated from genome-wide SNPs. Nature Genetics, 2013, 45, 984-994.	21.4	2,067
7	Partitioning heritability by functional annotation using genome-wide association summary statistics. Nature Genetics, 2015, 47, 1228-1235.	21.4	2,045
8	Genetics of rheumatoid arthritis contributes to biology and drug discovery. Nature, 2014, 506, 376-381.	27.8	1,974
9	Hundreds of variants clustered in genomic loci and biological pathways affect human height. Nature, 2010, 467, 832-838.	27.8	1,789
10	Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. Nature Genetics, 2012, 44, 981-990.	21.4	1,748
11	Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. Nature Genetics, 2010, 42, 579-589.	21.4	1,631
12	Large-scale genome-wide association analysis of bipolar disorder identifies a new susceptibility locus near ODZ4. Nature Genetics, 2011, 43, 977-983.	21.4	1,283
13	Genome-wide association study meta-analysis identifies seven new rheumatoid arthritis risk loci. Nature Genetics, 2010, 42, 508-514.	21.4	1,132
14	Genome-wide meta-analysis identifies 56 bone mineral density loci and reveals 14 loci associated with risk of fracture. Nature Genetics, 2012, 44, 491-501.	21.4	1,100
15	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. Nature Genetics, 2014, 46, 234-244.	21.4	959
16	Heritability enrichment of specifically expressed genes identifies disease-relevant tissues and cell types. Nature Genetics, 2018, 50, 621-629.	21.4	807
17	Five amino acids in three HLA proteins explain most of the association between MHC and seropositive rheumatoid arthritis. Nature Genetics, 2012, 44, 291-296.	21.4	768
18	Pathologically expanded peripheral T helper cell subset drives B cells in rheumatoid arthritis. Nature, 2017, 542, 110-114.	27.8	767

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19	Defining inflammatory cell states in rheumatoid arthritis joint synovial tissues by integrating single-cell transcriptomics and mass cytometry. Nature Immunology, 2019, 20, 928-942.	14.5	760
20	Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. Nature Genetics, 2012, 44, 991-1005.	21.4	746
21	Meta-analysis of genome scans and replication identify CD6, IRF8 and TNFRSF1A as new multiple sclerosis susceptibility loci. Nature Genetics, 2009, 41, 776-782.	21.4	729
22	Biological interpretation of genome-wide association studies using predicted gene functions. Nature Communications, 2015, 6, 5890.	12.8	706
23	Psychiatric genome-wide association study analyses implicate neuronal, immune and histone pathways. Nature Neuroscience, 2015, 18, 199-209.	14.8	701
24	Analysis of five chronic inflammatory diseases identifies 27 new associations and highlights disease-specific patterns at shared loci. Nature Genetics, 2016, 48, 510-518.	21.4	617
25	Partitioning Heritability of Regulatory and Cell-Type-Specific Variants across 11 Common Diseases. American Journal of Human Genetics, 2014, 95, 535-552.	6.2	569
26	High-density genetic mapping identifies new susceptibility loci for rheumatoid arthritis. Nature Genetics, 2012, 44, 1336-1340.	21.4	558
27	Chromatin marks identify critical cell types for fine mapping complex trait variants. Nature Genetics, 2013, 45, 124-130.	21.4	553
28	Distinct fibroblast subsets drive inflammation and damage in arthritis. Nature, 2019, 570, 246-251.	27.8	550
29	Imputing Amino Acid Polymorphisms in Human Leukocyte Antigens. PLoS ONE, 2013, 8, e64683.	2.5	538
30	The immune cell landscape in kidneys of patients with lupus nephritis. Nature Immunology, 2019, 20, 902-914.	14.5	501
31	Polarization of the Effects of Autoimmune and Neurodegenerative Risk Alleles in Leukocytes. Science, 2014, 344, 519-523.	12.6	480
32	Common variants at CD40 and other loci confer risk of rheumatoid arthritis. Nature Genetics, 2008, 40, 1216-1223.	21.4	476
33	Practical aspects of imputation-driven meta-analysis of genome-wide association studies. Human Molecular Genetics, 2008, 17, R122-R128.	2.9	475
34	Proteins Encoded in Genomic Regions Associated with Immune-Mediated Disease Physically Interact and Suggest Underlying Biology. PLoS Genetics, 2011, 7, e1001273.	3.5	450
35	Novel Loci for Adiponectin Levels and Their Influence on Type 2 Diabetes and Metabolic Traits: A Multi-Ethnic Meta-Analysis of 45,891 Individuals. PLoS Genetics, 2012, 8, e1002607.	3.5	419
36	Genome-wide association study of advanced age-related macular degeneration identifies a role of the hepatic lipase gene (LIPC). Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 7395-7400.	7.1	406

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37	Bayesian inference analyses of the polygenic architecture of rheumatoid arthritis. Nature Genetics, 2012, 44, 483-489.	21.4	402
38	Common Genetic Variants Modulate Pathogen-Sensing Responses in Human Dendritic Cells. Science, 2014, 343, 1246980.	12.6	391
39	Identifying Relationships among Genomic Disease Regions: Predicting Genes at Pathogenic SNP Associations and Rare Deletions. PLoS Genetics, 2009, 5, e1000534.	3.5	371
40	Functionally distinct disease-associated fibroblast subsets in rheumatoid arthritis. Nature Communications, 2018, 9, 789.	12.8	368
41	PRINCIPAL COMPONENTS ANALYSIS TO SUMMARIZE MICROARRAY EXPERIMENTS: APPLICATION TO SPORULATION TIME SERIES. , 1999, , 455-66.		359
42	Genetics and epigenetics of rheumatoid arthritis. Nature Reviews Rheumatology, 2013, 9, 141-153.	8.0	325
43	Rare variants in CFI, C3 and C9 are associated with high risk of advanced age-related macular degeneration. Nature Genetics, 2013, 45, 1366-1370.	21.4	311
44	Meta-Analysis of Genome-Wide Association Studies in Celiac Disease and Rheumatoid Arthritis Identifies Fourteen Non-HLA Shared Loci. PLoS Genetics, 2011, 7, e1002004.	3.5	307
45	Genetic variants at CD28, PRDM1 and CD2/CD58 are associated with rheumatoid arthritis risk. Nature Genetics, 2009, 41, 1313-1318.	21.4	306
46	Large-scale genome-wide association study in a Japanese population identifies novel susceptibility loci across different diseases. Nature Genetics, 2020, 52, 669-679.	21.4	304
47	A rare penetrant mutation in CFH confers high risk of age-related macular degeneration. Nature Genetics, 2011, 43, 1232-1236.	21.4	291
48	Investigating hypoxic tumor physiology through gene expression patterns. Oncogene, 2003, 22, 5907-5914.	5.9	283
49	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. Nature Genetics, 2014, 46, 826-836.	21.4	281
50	Tubular cell and keratinocyte single-cell transcriptomics applied to lupus nephritis reveal type I IFN and fibrosis relevant pathways. Nature Immunology, 2019, 20, 915-927.	14.5	275
51	Electronic medical records for discovery research in rheumatoid arthritis. Arthritis Care and Research, 2010, 62, 1120-1127.	3.4	272
52	Notch signalling drives synovial fibroblast identity and arthritis pathology. Nature, 2020, 582, 259-264.	27.8	267
53	Rare Complete Knockouts in Humans: Population Distribution and Significant Role in Autism Spectrum Disorders. Neuron, 2013, 77, 235-242.	8.1	242
54	Additive and interaction effects at three amino acid positions in HLA-DQ and HLA-DR molecules drive type 1 diabetes risk. Nature Genetics, 2015, 47, 898-905.	21.4	235

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55	Common variants near FRK/COL10A1 and VEGFA are associated with advanced age-related macular degeneration. Human Molecular Genetics, 2011, 20, 3699-3709.	2.9	232
56	Insights into the local residual entropy of proteins provided by NMR relaxation. Protein Science, 1996, 5, 2647-2650.	7.6	225
57	A Role for Noncoding Variation in Schizophrenia. Cell Reports, 2014, 9, 1417-1429.	6.4	225
58	Joint Analysis of Psychiatric Disorders Increases Accuracy of Risk Prediction for Schizophrenia, Bipolar Disorder, and Major Depressive Disorder. American Journal of Human Genetics, 2015, 96, 283-294.	6.2	225
59	A Genome-Wide Association Search for Type 2 Diabetes Genes in African Americans. PLoS ONE, 2012, 7, e29202.	2.5	197
60	Fine Mapping Major Histocompatibility Complex Associations in Psoriasis and Its Clinical Subtypes. American Journal of Human Genetics, 2014, 95, 162-172.	6.2	182
61	Autoimmune diseases â€" connecting risk alleles with molecular traits of the immune system. Nature Reviews Genetics, 2016, 17, 160-174.	16.3	173
62	Widespread non-additive and interaction effects within HLA loci modulate the risk of autoimmune diseases. Nature Genetics, 2015, 47, 1085-1090.	21.4	164
63	Identification of osteopontin as a prognostic plasma marker for head and neck squamous cell carcinomas. Clinical Cancer Research, 2003, 9, 59-67.	7.0	162
64	Associating Genes with Gene Ontology Codes Using a Maximum Entropy Analysis of Biomedical Literature. Genome Research, 2002, 12, 203-214.	5.5	161
65	Integrating Autoimmune Risk Loci with Gene-Expression Data Identifies Specific Pathogenic Immune Cell Subsets. American Journal of Human Genetics, 2011, 89, 496-506.	6.2	159
66	Fine Mapping Seronegative and Seropositive Rheumatoid Arthritis to Shared and Distinct HLA Alleles by Adjusting for the Effects of Heterogeneity. American Journal of Human Genetics, 2014, 94, 522-532.	6.2	156
67	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.	7.1	154
68	Investigating the Causal Relationship of C-Reactive Protein with 32 Complex Somatic and Psychiatric Outcomes: A Large-Scale Cross-Consortium Mendelian Randomization Study. PLoS Medicine, 2016, 13, e1001976.	8.4	150
69	Genome-Wide Association Study and Gene Expression Analysis Identifies CD84 as a Predictor of Response to Etanercept Therapy in Rheumatoid Arthritis. PLoS Genetics, 2013, 9, e1003394.	3.5	146
70	HBEGF ⁺ macrophages in rheumatoid arthritis induce fibroblast invasiveness. Science Translational Medicine, 2019, 11, .	12.4	143
71	HLA-DRB1*11and variants of the MHC class II locus are strong risk factors for systemic juvenile idiopathic arthritis. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 15970-15975.	7.1	139
72	Association of Granulomatosis With Polyangiitis (Wegener's) With HLAâ€"DPB1*04 and SEMA6A Gene Variants: Evidence From Genomeâ€Wide Analysis. Arthritis and Rheumatism, 2013, 65, 2457-2468.	6.7	138

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73	Risk for myasthenia gravis maps to a ¹⁵¹Proâ†'Ala change in TNIP1 and to human leukocyte antigenâ€B*08. Annals of Neurology, 2012, 72, 927-935.	5.3	137
74	Lymphocyte innateness defined by transcriptional states reflects a balance between proliferation and effector functions. Nature Communications, 2019, 10, 687.	12.8	136
75	Risk for ACPA-positive rheumatoid arthritis is driven by shared HLA amino acid polymorphisms in Asian and European populations. Human Molecular Genetics, 2014, 23, 6916-6926.	2.9	135
76	Accurately Assessing the Risk of Schizophrenia Conferred by Rare Copy-Number Variation Affecting Genes with Brain Function. PLoS Genetics, 2010, 6, e1001097.	3.5	134
77	Whole-genome expression analysis: challenges beyond clustering. Current Opinion in Structural Biology, 2001, 11, 340-347.	5.7	130
78	IFN-Î³ and TNF-Î± drive a CXCL10+ CCL2+ macrophage phenotype expanded in severe COVID-19 lungs and inflammatory diseases with tissue inflammation. Genome Medicine, 2021, 13, 64.	8.2	128
79	Basic microarray analysis: grouping and feature reduction. Trends in Biotechnology, 2001, 19, 189-193.	9.3	126
80	Improving the trans-ancestry portability of polygenic risk scores by prioritizing variants in predicted cell-type-specific regulatory elements. Nature Genetics, 2020, 52, 1346-1354.	21.4	126
81	Fine mapping in the MHC region accounts for 18% additional genetic risk for celiac disease. Nature Genetics, 2015, 47, 577-578.	21.4	123
82	Disentangling the Effects of Colocalizing Genomic Annotations to Functionally Prioritize Non-coding Variants within Complex-Trait Loci. American Journal of Human Genetics, 2015, 97, 139-152.	6.2	122
83	Fine-mapping and functional studies highlight potential causal variants for rheumatoid arthritis and type 1 diabetes. Nature Genetics, 2018, 50, 1366-1374.	21.4	122
84	TYK2 Protein-Coding Variants Protect against Rheumatoid Arthritis and Autoimmunity, with No Evidence of Major Pleiotropic Effects on Non-Autoimmune Complex Traits. PLoS ONE, 2015, 10, e0122271.	2.5	120
85	Association of HLA-DRB1 Haplotypes With Rheumatoid Arthritis Severity, Mortality, and Treatment Response. JAMA - Journal of the American Medical Association, 2015, 313, 1645.	7.4	119
86	Mixed-effects association of single cells identifies an expanded effector CD4 ⁺ T cell subset in rheumatoid arthritis. Science Translational Medicine, 2018, 10, .	12.4	119
87	IL-1-driven stromalâ€"neutrophil interactions define a subset of patients with inflammatory bowel disease that does not respond to therapies. Nature Medicine, 2021, 27, 1970-1981.	30.7	117
88	Quantifying Missing Heritability at Known GWAS Loci. PLoS Genetics, 2013, 9, e1003993.	3.5	115
89	Genetic association study of exfoliation syndrome identifies a protective rare variant at LOXL1 and five new susceptibility loci. Nature Genetics, 2017, 49, 993-1004.	21.4	114
90	Genetic variants in the complement system predisposing to age-related macular degeneration: A review. Molecular Immunology, 2014, 61, 118-125.	2.2	113

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91	Leveraging Cross-Species Transcription Factor Binding Site Patterns: From Diabetes Risk Loci to Disease Mechanisms. Cell, 2014, 156, 343-358.	28.9	113
92	52 Genetic Loci Influencing MyocardialÂMass. Journal of the American College of Cardiology, 2016, 68, 1435-1448.	2.8	113
93	Genetic Basis of Autoantibody Positive and Negative Rheumatoid Arthritis Risk in a Multi-ethnic Cohort Derived from Electronic Health Records. American Journal of Human Genetics, 2011, 88, 57-69.	6.2	112
94	RNA Identification of PRIME Cells Predicting Rheumatoid Arthritis Flares. New England Journal of Medicine, 2020, 383, 218-228.	27.0	111
95	Three ulcerative colitis susceptibility loci are associated with primary sclerosing cholangitis and indicate a role for IL2, REL , and CARD9. Hepatology, 2011, 53, 1977-1985.	7.3	110
96	Phenome-wide scanning identifies multiple diseases and disease severity phenotypes associated with HLA variants. Science Translational Medicine, 2017, 9, .	12.4	105
97	An international effort towards developing standards for best practices in analysis, interpretation and reporting of clinical genome sequencing results in the CLARITY Challenge. Genome Biology, 2014, 15, R53.	9.6	101
98	Mapping Rare and Common Causal Alleles for Complex Human Diseases. Cell, 2011, 147, 57-69.	28.9	100
99	Common Risk Alleles for Inflammatory Diseases Are Targets of Recent Positive Selection. American Journal of Human Genetics, 2013, 92, 517-529.	6.2	100
100	Rare genetic variants in the CFI gene are associated with advanced age-related macular degeneration and commonly result in reduced serum factor I levels. Human Molecular Genetics, 2015, 24, 3861-70.	2.9	100
101	High-density genotyping of immune loci in Koreans and Europeans identifies eight new rheumatoid arthritis risk loci. Annals of the Rheumatic Diseases, 2015, 74, e13-e13.	0.9	100
102	Review: Genetics and the Classification of Arthritis in Adults and Children. Arthritis and Rheumatology, 2018, 70, 7-17.	5.6	100
103	Efficient and precise single-cell reference atlas mapping with Symphony. Nature Communications, 2021, 12, 5890.	12.8	100
104	Harmonizing Clinical Sequencing and Interpretation for the eMERGE III Network. American Journal of Human Genetics, 2019, 105, 588-605.	6.2	99
105	Recent advances in the genetics of rheumatoid arthritis. Current Opinion in Rheumatology, 2010, 22, 109-118.	4.3	95
106	Rheumatoid arthritis risk allele PTPRC is also associated with response to antiâ€“tumor necrosis factor Î± therapy. Arthritis and Rheumatism, 2010, 62, 1849-1861.	6.7	95
107	Whole-exome sequencing identifies rare, functional CFH variants in families with macular degeneration. Human Molecular Genetics, 2014, 23, 5283-5293.	2.9	95
108	Methods for high-dimensional analysis of cells dissociated from cryopreserved synovial tissue. Arthritis Research and Therapy, 2018, 20, 139.	3.5	93

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109	Association of a singleâ€nucleotide polymorphism in CD40 with the rate of joint destruction in rheumatoid arthritis. Arthritis and Rheumatism, 2009, 60, 2242-2247.	6.7	91
110	Interrogating the major histocompatibility complex with high-throughput genomics. Human Molecular Genetics, 2012, 21, R29-R36.	2.9	85
111	Variation at HLA-DRB1 is associated with resistance to enteric fever. Nature Genetics, 2014, 46, 1333-1336.	21.4	85
112	Allele-specific expression changes dynamically during T cell activation in HLA and other autoimmune loci. Nature Genetics, 2020, 52, 247-253.	21.4	85
113	Genetic risk of extranodal natural killer T-cell lymphoma: a genome-wide association study. Lancet Oncology, The, 2016, 17, 1240-1247.	10.7	84
114	Rare, Low-Frequency, and Common Variants in the Protein-Coding Sequence of Biological Candidate Genes from GWASs Contribute to Risk of Rheumatoid Arthritis. American Journal of Human Genetics, 2013, 92, 15-27.	6.2	83
115	Predicting HLA alleles from high-resolution SNP data in three Southeast Asian populations. Human Molecular Genetics, 2014, 23, 4443-4451.	2.9	80
116	Transethnic meta-analysis identifies GSDMA and PRDM1 as susceptibility genes to systemic sclerosis. Annals of the Rheumatic Diseases, 2017, 76, 1150-1158.	0.9	77
117	Single-cell eQTL models reveal dynamic T cell state dependence of disease loci. Nature, 2022, 606, 120-128.	27.8	75
118	Granzyme K ⁺ CD8 T cells form a core population in inflamed human tissue. Science Translational Medicine, 2022, 14, .	12.4	74
119	Heritability and Genome-Wide Association Study to Assess Genetic Differences between Advanced Age-related Macular Degeneration Subtypes. Ophthalmology, 2012, 119, 1874-1885.	5.2	73
120	Meta-analysis of Immunochip data of four autoimmune diseases reveals novel single-disease and cross-phenotype associations. Genome Medicine, 2018, 10, 97.	8.2	73
121	Disproportionate Contributions of Select Genomic Compartments and Cell Types to Genetic Risk for Coronary Artery Disease. PLoS Genetics, 2015, 11, e1005622.	3.5	70
122	Use of a Multiethnic Approach to Identify Rheumatoid- Arthritis-Susceptibility Loci, 1p36 and 17q12. American Journal of Human Genetics, 2012, 90, 524-532.	6.2	69
123	A high-resolution HLA reference panel capturing global population diversity enables multi-ancestry fine-mapping in HIV host response. Nature Genetics, 2021, 53, 1504-1516.	21.4	69
124	Contribution of a Non-classical HLA Gene, HLA-DOA, to the Risk of Rheumatoid Arthritis. American Journal of Human Genetics, 2016, 99, 366-374.	6.2	68
125	Population-specific causal disease effect sizes in functionally important regions impacted by selection. Nature Communications, 2021, 12, 1098.	12.8	68
126	Cross-disorder analysis of schizophrenia and 19 immune-mediated diseases identifies shared genetic risk. Human Molecular Genetics, 2019, 28, 3498-3513.	2.9	65

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127	Using Text Analysis to Identify Functionally Coherent Gene Groups. Genome Research, 2002, 12, 1582-1590.	5.5	63
128	The eMERGE genotype set of 83,717 subjects imputed to ~40â€‰million variants genome wide and association with the herpes zoster medical record phenotype. Genetic Epidemiology, 2019, 43, 63-81.	1.3	63
129	Immune cell profiling to guide therapeutic decisions in rheumatic diseases. Nature Reviews Rheumatology, 2015, 11, 541-551.	8.0	62
130	A method to decipher pleiotropy by detecting underlying heterogeneity driven by hidden subgroups applied to autoimmune and neuropsychiatric diseases. Nature Genetics, 2016, 48, 803-810.	21.4	62
131	Genome-Wide Association Studies Suggest Limited Immune Gene Enrichment in Schizophrenia Compared to 5 Autoimmune Diseases. Schizophrenia Bulletin, 2016, 42, 1176-1184.	4.3	62
132	SNPsea: an algorithm to identify cell types, tissues and pathways affected by risk loci. Bioinformatics, 2014, 30, 2496-2497.	4.1	60
133	Rare Variants in the Functional Domains of Complement Factor H Are Associated With Age-Related Macular Degeneration. , 2015, 56, 6873.		60
134	Interactions Between Amino Acidâ€“Defined Major Histocompatibility Complex Class II Variants and Smoking in Seropositive Rheumatoid Arthritis. Arthritis and Rheumatology, 2015, 67, 2611-2623.	5.6	58
135	Integrated urine proteomics and renal single-cell genomics identify an IFN-Î³ response gradient in lupus nephritis. JCI Insight, 2020, 5, .	5.0	57
136	Associations of CFHR1â€“CFHR3 deletion and a CFH SNP to age-related macular degeneration are not independent. Nature Genetics, 2010, 42, 553-555.	21.4	55
137	A weighted genetic risk score using all known susceptibility variants to estimate rheumatoid arthritis risk. Annals of the Rheumatic Diseases, 2015, 74, 170-176.	0.9	55
138	FcÎ³R engagement reprograms neutrophils into antigen cross-presenting cells that elicit acquired anti-tumor immunity. Nature Communications, 2021, 12, 4791.	12.8	55
139	New data and an old puzzle: the negative association between schizophrenia and rheumatoid arthritis. International Journal of Epidemiology, 2015, 44, 1706-1721.	1.9	53
140	Human Genetics in Rheumatoid Arthritis Guides a High-Throughput Drug Screen of the CD40 Signaling Pathway. PLoS Genetics, 2013, 9, e1003487.	3.5	52
141	Multimodally profiling memory T cells from a tuberculosis cohort identifies cell state associations with demographics, environment and disease. Nature Immunology, 2021, 22, 781-793.	14.5	52
142	Cross-tissue, single-cell stromal atlas identifies shared pathological fibroblast phenotypes in four chronic inflammatory diseases. Med, 2022, 3, 481-518.e14.	4.4	51
143	Atlas of prostate cancer heritability in European and African-American men pinpoints tissue-specific regulation. Nature Communications, 2016, 7, 10979.	12.8	50
144	A literature-based method for assessing the functional coherence of a gene group. Bioinformatics, 2003, 19, 396-401.	4.1	49

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145	IMPACT: Genomic Annotation of Cell-State-Specific Regulatory Elements Inferred from the Epigenome of Bound Transcription Factors. American Journal of Human Genetics, 2019, 104, 879-895.	6.2	49
146	Stabilized bubbles in the body: pressure-radius relationships and the limits to stabilization. Journal of Applied Physiology, 1997, 82, 2045-2053.	2.5	48
147	Mapping rare, deleterious mutations in Factor H: Association with early onset, drusen burden and lower antigenic levels in familial AMD. Scientific Reports, 2016, 6, 31531.	3.3	48
148	The computational analysis of scientific literature to define and recognize gene expression clusters. Nucleic Acids Research, 2003, 31, 4553-4560.	14.5	47
149	Regulation of Gene Expression in Autoimmune Disease Loci and the Genetic Basis of Proliferation in CD4+ Effector Memory T Cells. PLoS Genetics, 2014, 10, e1004404.	3.5	46
150	Genes with High Network Connectivity Are Enriched for Disease Heritability. American Journal of Human Genetics, 2019, 104, 896-913.	6.2	46
151	Recent Advances in Defining the Genetic Basis of Rheumatoid Arthritis. Annual Review of Genomics and Human Genetics, 2016, 17, 273-301.	6.2	44
152	CUX1 and IÎºBÎ¶ (NFKBIZ) mediate the synergistic inflammatory response to TNF and IL-17A in stromal fibroblasts. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 5532-5541.	7.1	44
153	Early progression to active tuberculosis is a highly heritable trait driven by 3q23 in Peruvians. Nature Communications, 2019, 10, 3765.	12.8	43
154	Synoviocyte-targeted therapy synergizes with TNF inhibition in arthritis reversal. Science Advances, 2020, 6, eaba4353.	10.3	43
155	A general framework for meta-analyzing dependent studies with overlapping subjects in association mapping. Human Molecular Genetics, 2016, 25, 1857-1866.	2.9	42
156	HLA autoimmune risk alleles restrict the hypervariable region of T cell receptors. Nature Genetics, 2022, 54, 393-402.	21.4	40
157	A positively selected FBN1 missense variant reduces height in Peruvian individuals. Nature, 2020, 582, 234-239.	27.8	39
158	Using chromatin marks to interpret and localize genetic associations to complex human traits and diseases. Current Opinion in Genetics and Development, 2013, 23, 635-641.	3.3	38
159	Urine Proteomics and Renal <scp>Singleâ€Cell</scp> Transcriptomics Implicate Interleukinâ€16 in Lupus Nephritis. Arthritis and Rheumatology, 2022, 74, 829-839.	5.6	38
160	Repertoire analyses reveal T cell antigen receptor sequence features that influence T cell fate. Nature Immunology, 2022, 23, 446-457.	14.5	37
161	Familial aggregation of arthritis-related diseases in seropositive and seronegative rheumatoid arthritis: a register-based case-control study in Sweden. Annals of the Rheumatic Diseases, 2016, 75, 183-189.	0.9	36
162	Molecular basis for increased susceptibility of Indigenous North Americans to seropositive rheumatoid arthritis. Annals of the Rheumatic Diseases, 2017, 76, 1915-1923.	0.9	36

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163	Discovering in vivo cytokine-eQTL interactions from a lupus clinical trial. Genome Biology, 2018, 19, 168.	8.8	36
164	Integration of Sequence Data from a Consanguineous Family with Genetic Data from an Outbred Population Identifies PLB1 as a Candidate Rheumatoid Arthritis Risk Gene. PLoS ONE, 2014, 9, e87645.	2.5	34
165	Genome-wide Study Identifies Association between HLA-Bâˆ—55:01 and Self-Reported Penicillin Allergy. American Journal of Human Genetics, 2020, 107, 612-621.	6.2	34
166	HLAâ€“DRB1â€“Associated Rheumatoid Arthritis Risk at Multiple Levels in African Americans: Hierarchical Classification Systems, Amino Acid Positions, and Residues. Arthritis and Rheumatology, 2014, 66, 3274-3282.	5.6	32
167	OUP accepted manuscript. Human Molecular Genetics, 2021, 30, 1521-1534.	2.9	32
168	High-throughput identification of noncoding functional SNPs via type IIS enzyme restriction. Nature Genetics, 2018, 50, 1180-1188.	21.4	31
169	Using genetics to prioritize diagnoses for rheumatology outpatients with inflammatory arthritis. Science Translational Medicine, 2020, 12, .	12.4	31
170	Meta-analysis identifies aMECOMgene as a novel predisposing factor of osteoporotic fracture. Journal of Medical Genetics, 2013, 50, 212-219.	3.2	30
171	Association between low density lipoprotein and rheumatoid arthritis genetic factors with low density lipoprotein levels in rheumatoid arthritis and non-rheumatoid arthritis controls. Annals of the Rheumatic Diseases, 2014, 73, 1170-1175.	0.9	30
172	Co-varying neighborhood analysis identifies cell populations associated with phenotypes of interest from single-cell transcriptomics. Nature Biotechnology, 2022, 40, 355-363.	17.5	30
173	A Novel Test for Recessive Contributions to Complex Diseases Implicates Bardet-Biedl Syndrome Gene BBS10 in Idiopathic Type 2 Diabetes and Obesity. American Journal of Human Genetics, 2014, 95, 509-520.	6.2	29
174	Functional implications of disease-specific variants in loci jointly associated with coeliac disease and rheumatoid arthritis. Human Molecular Genetics, 2016, 25, 180-190.	2.9	29
175	Complex Diseases, Complex Genes. Epidemiology, 2009, 20, 508-511.	2.7	27
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