

Soumya Raychaudhuri

List of Publications by Year in descending order

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Version: 2024-02-01

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 | Multimodal platform for assessing drug distribution and response in clinical trials. <i>Neuro-Oncology</i> , 2022, 24, 64-77. | 1.2 | 4 |
| 2 | Co-varying neighborhood analysis identifies cell populations associated with phenotypes of interest from single-cell transcriptomics. <i>Nature Biotechnology</i> , 2022, 40, 355-363. | 17.5 | 30 |
| 3 | Association with HLA-DR ¹ position 37 distinguishes juvenile dermatomyositis from adult-onset myositis. <i>Human Molecular Genetics</i> , 2022, 31, 2471-2481. | 2.9 | 9 |
| 4 | Rheumatoid Arthritis Synovial Inflammation Quantification Using Computer Vision. <i>ACR Open Rheumatology</i> , 2022, 4, 322-331. | 2.1 | 4 |
| 5 | A framework for employing longitudinally collected multicenter electronic health records to stratify heterogeneous patient populations on disease history. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2022, 29, 761-769. | 4.4 | 6 |
| 6 | TCR-sequencing in cancer and autoimmunity: barcodes and beyond. <i>Trends in Immunology</i> , 2022, 43, 180-194. | 6.8 | 20 |
| 7 | Urine Proteomics and Renal <i>Single-Cell</i> Transcriptomics Implicate Interleukin-16 in Lupus Nephritis. <i>Arthritis and Rheumatology</i> , 2022, 74, 829-839. | 5.6 | 38 |
| 8 | Repertoire analyses reveal T cell antigen receptor sequence features that influence T cell fate. <i>Nature Immunology</i> , 2022, 23, 446-457. | 14.5 | 37 |
| 9 | HLA autoimmune risk alleles restrict the hypervariable region of T cell receptors. <i>Nature Genetics</i> , 2022, 54, 393-402. | 21.4 | 40 |
| 10 | Monocytes transition to macrophages within the inflamed vasculature via monocyte CCR2 and endothelial TNFR2. <i>Journal of Experimental Medicine</i> , 2022, 219, . | 8.5 | 25 |
| 11 | P190 <i>Unsupervised automated clustering of mass cytometry data identifies unique CD4+ T cell subsets in rheumatoid arthritis.</i> <i>Rheumatology</i> , 2022, 61, . | 1.9 | 0 |
| 12 | Single-cell eQTL models reveal dynamic T cell state dependence of disease loci. <i>Nature</i> , 2022, 606, 120-128. | 27.8 | 75 |
| 13 | Cross-tissue, single-cell stromal atlas identifies shared pathological fibroblast phenotypes in four chronic inflammatory diseases. <i>Med</i> , 2022, 3, 481-518.e14. | 4.4 | 51 |
| 14 | Genetics are not likely to offer clinically useful predictions for elevated liver enzyme levels in patients using low dose methotrexate. <i>Seminars in Arthritis and Rheumatism</i> , 2022, 55, 152036. | 3.4 | 1 |
| 15 | Granzyme K ⁺ CD8 T cells form a core population in inflamed human tissue. <i>Science Translational Medicine</i> , 2022, 14, . | 12.4 | 74 |
| 16 | Orgo-Seq integrates single-cell and bulk transcriptomic data to identify cell type specific-driver genes associated with autism spectrum disorder. <i>Nature Communications</i> , 2022, 13, . | 12.8 | 11 |
| 17 | Higher native Peruvian genetic ancestry proportion is associated with tuberculosis progression risk. <i>Cell Genomics</i> , 2022, 2, 100151. | 6.5 | 5 |
| 18 | HATK: HLA analysis toolkit. <i>Bioinformatics</i> , 2021, 37, 416-418. | 4.1 | 13 |

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|----|---|------|-----------|
| 19 | How COVID-19 is changing rheumatology clinical practice. <i>Nature Reviews Rheumatology</i> , 2021, 17, 11-15. | 8.0 | 25 |
| 20 | OUP accepted manuscript. <i>Human Molecular Genetics</i> , 2021, 30, 1521-1534. | 2.9 | 32 |
| 21 | Population-specific causal disease effect sizes in functionally important regions impacted by selection. <i>Nature Communications</i> , 2021, 12, 1098. | 12.8 | 68 |
| 22 | Transethnic analysis of the human leukocyte antigen region for ulcerative colitis reveals not only shared but also ethnicity-specific disease associations. <i>Human Molecular Genetics</i> , 2021, 30, 356-369. | 2.9 | 19 |
| 23 | Accurate imputation of human leukocyte antigens with CookHLA. <i>Nature Communications</i> , 2021, 12, 1264. | 12.8 | 21 |
| 24 | IFN- γ and TNF- α drive a CXCL10 ⁺ CCL2 ⁺ macrophage phenotype expanded in severe COVID-19 lungs and inflammatory diseases with tissue inflammation. <i>Genome Medicine</i> , 2021, 13, 64. | 8.2 | 128 |
| 25 | Multimodally profiling memory T cells from a tuberculosis cohort identifies cell state associations with demographics, environment and disease. <i>Nature Immunology</i> , 2021, 22, 781-793. | 14.5 | 52 |
| 26 | Medical Records-Based Genetic Studies of the Complement System. <i>Journal of the American Society of Nephrology: JASN</i> , 2021, 32, 2031-2047. | 6.1 | 10 |
| 27 | Genome editing to define the function of risk loci and variants in rheumatic disease. <i>Nature Reviews Rheumatology</i> , 2021, 17, 462-474. | 8.0 | 9 |
| 28 | The Power of Systems Biology. <i>Rheumatic Disease Clinics of North America</i> , 2021, 47, 335-350. | 1.9 | 9 |
| 29 | Fc γ R engagement reprograms neutrophils into antigen cross-presenting cells that elicit acquired anti-tumor immunity. <i>Nature Communications</i> , 2021, 12, 4791. | 12.8 | 55 |
| 30 | A sex-specific evolutionary interaction between ADCY9 and CETP. <i>ELife</i> , 2021, 10, . | 6.0 | 8 |
| 31 | IL-1-driven stromal-neutrophil interactions define a subset of patients with inflammatory bowel disease that does not respond to therapies. <i>Nature Medicine</i> , 2021, 27, 1970-1981. | 30.7 | 117 |
| 32 | 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. | 21.4 | 69 |
| 33 | Efficient and precise single-cell reference atlas mapping with Symphony. <i>Nature Communications</i> , 2021, 12, 5890. | 12.8 | 100 |
| 34 | Maximizing statistical power to detect differentially abundant cell states with scPOST. <i>Cell Reports Methods</i> , 2021, 1, 100120. | 2.9 | 2 |
| 35 | Advances in genetics toward identifying pathogenic cell states of rheumatoid arthritis. <i>Immunological Reviews</i> , 2020, 294, 188-204. | 6.0 | 23 |
| 36 | RNA Identification of PRIME Cells Predicting Rheumatoid Arthritis Flares. <i>New England Journal of Medicine</i> , 2020, 383, 218-228. | 27.0 | 111 |

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|----|---|------|-----------|
| 37 | Improving the trans-ancestry portability of polygenic risk scores by prioritizing variants in predicted cell-type-specific regulatory elements. <i>Nature Genetics</i> , 2020, 52, 1346-1354. | 21.4 | 126 |
| 38 | Interactions Between Genome-wide Genetic Factors and Smoking Influencing Risk of Systemic Lupus Erythematosus. <i>Arthritis and Rheumatology</i> , 2020, 72, 1863-1871. | 5.6 | 13 |
| 39 | A positively selected FBN1 missense variant reduces height in Peruvian individuals. <i>Nature</i> , 2020, 582, 234-239. | 27.8 | 39 |
| 40 | Using genetics to prioritize diagnoses for rheumatology outpatients with inflammatory arthritis. <i>Science Translational Medicine</i> , 2020, 12, . | 12.4 | 31 |
| 41 | Large-scale genome-wide association study in a Japanese population identifies novel susceptibility loci across different diseases. <i>Nature Genetics</i> , 2020, 52, 669-679. | 21.4 | 304 |
| 42 | Synoviocyte-targeted therapy synergizes with TNF inhibition in arthritis reversal. <i>Science Advances</i> , 2020, 6, eaba4353. | 10.3 | 43 |
| 43 | Allele-specific expression changes dynamically during T cell activation in HLA and other autoimmune loci. <i>Nature Genetics</i> , 2020, 52, 247-253. | 21.4 | 85 |
| 44 | CUX1 and IRF1 (NFKBIZ) mediate the synergistic inflammatory response to TNF and IL-17A in stromal fibroblasts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 5532-5541. | 7.1 | 44 |
| 45 | Notch signalling drives synovial fibroblast identity and arthritis pathology. <i>Nature</i> , 2020, 582, 259-264. | 27.8 | 267 |
| 46 | Disruptive innovation in rheumatology: new networks of global public-private partnerships are needed to take advantage of scientific progress. <i>Annals of the Rheumatic Diseases</i> , 2020, 79, 553-555. | 0.9 | 1 |
| 47 | Genome-wide Study Identifies Association between HLA-B*55:01 and Self-Reported Penicillin Allergy. <i>American Journal of Human Genetics</i> , 2020, 107, 612-621. | 6.2 | 34 |
| 48 | Integrated urine proteomics and renal single-cell genomics identify an IFN- γ response gradient in lupus nephritis. <i>JCI Insight</i> , 2020, 5, . | 5.0 | 57 |
| 49 | Multimodal single-cell approaches shed light on T cell heterogeneity. <i>Current Opinion in Immunology</i> , 2019, 61, 17-25. | 5.5 | 13 |
| 50 | Early progression to active tuberculosis is a highly heritable trait driven by 3q23 in Peruvians. <i>Nature Communications</i> , 2019, 10, 3765. | 12.8 | 43 |
| 51 | Distinct HLA Associations with Rheumatoid Arthritis Subsets Defined by Serological Subphenotype. <i>American Journal of Human Genetics</i> , 2019, 105, 616-624. | 6.2 | 27 |
| 52 | Harmonizing Clinical Sequencing and Interpretation for the eMERGE III Network. <i>American Journal of Human Genetics</i> , 2019, 105, 588-605. | 6.2 | 99 |
| 53 | The immune cell landscape in kidneys of patients with lupus nephritis. <i>Nature Immunology</i> , 2019, 20, 902-914. | 14.5 | 501 |
| 54 | Cross-disorder analysis of schizophrenia and 19 immune-mediated diseases identifies shared genetic risk. <i>Human Molecular Genetics</i> , 2019, 28, 3498-3513. | 2.9 | 65 |

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|----|---|------|-----------|
| 55 | Distinct fibroblast subsets drive inflammation and damage in arthritis. <i>Nature</i> , 2019, 570, 246-251. | 27.8 | 550 |
| 56 | HBEGF ⁺ macrophages in rheumatoid arthritis induce fibroblast invasiveness. <i>Science Translational Medicine</i> , 2019, 11, . | 12.4 | 143 |
| 57 | Tubular cell and keratinocyte single-cell transcriptomics applied to lupus nephritis reveal type I IFN and fibrosis relevant pathways. <i>Nature Immunology</i> , 2019, 20, 915-927. | 14.5 | 275 |
| 58 | Defining inflammatory cell states in rheumatoid arthritis joint synovial tissues by integrating single-cell transcriptomics and mass cytometry. <i>Nature Immunology</i> , 2019, 20, 928-942. | 14.5 | 760 |
| 59 | Association of response to TNF inhibitors in rheumatoid arthritis with quantitative trait loci for <i>CD40</i> and <i>CD39</i> . <i>Annals of the Rheumatic Diseases</i> , 2019, 78, 1055-1061. | 0.9 | 25 |
| 60 | Genes with High Network Connectivity Are Enriched for Disease Heritability. <i>American Journal of Human Genetics</i> , 2019, 104, 896-913. | 6.2 | 46 |
| 61 | Benchmark: An Unbiased, Association-Data-Driven Strategy to Evaluate Gene Prioritization Algorithms. <i>American Journal of Human Genetics</i> , 2019, 104, 1025-1039. | 6.2 | 16 |
| 62 | IMPACT: Genomic Annotation of Cell-State-Specific Regulatory Elements Inferred from the Epigenome of Bound Transcription Factors. <i>American Journal of Human Genetics</i> , 2019, 104, 879-895. | 6.2 | 49 |
| 63 | Immunoprofiling comes of age. <i>Nature Medicine</i> , 2019, 25, 362-364. | 30.7 | 3 |
| 64 | Lymphocyte innateness defined by transcriptional states reflects a balance between proliferation and effector functions. <i>Nature Communications</i> , 2019, 10, 687. | 12.8 | 136 |
| 65 | SAT0062...STRATIFIED MEDICINE FOR RHEUMATOID ARTHRITIS: PREDICTING RESPONSE TO BIOLOGIC THERAPY USING IMMUNE CELL SIGNATURES. , 2019, , . | | 0 |
| 66 | OP0190...META-ANALYSIS OF IMMUNOCHIP DATA OF FOUR AUTOIMMUNE DISEASES REVEALS NOVEL SINGLE-DISEASE AND CROSS-PHENOTYPE ASSOCIATIONS. , 2019, , . | | 0 |
| 67 | AB1282...A BIG-DATA APPROACH TO ELECTRONIC HEALTH RECORD DATA " USING DIMENSIONALITY REDUCTION AND CLUSTERING TECHNIQUES TO STUDY LONGITUDINAL RELATIONSHIPS BETWEEN DISEASES. , 2019, , . | | 1 |
| 68 | Fast, sensitive and accurate integration of single-cell data with Harmony. <i>Nature Methods</i> , 2019, 16, 1289-1296. | 19.0 | 3,494 |
| 69 | The eMERGE genotype set of 83,717 subjects imputed to ~40% million variants genome wide and association with the herpes zoster medical record phenotype. <i>Genetic Epidemiology</i> , 2019, 43, 63-81. | 1.3 | 63 |
| 70 | Functionally distinct disease-associated fibroblast subsets in rheumatoid arthritis. <i>Nature Communications</i> , 2018, 9, 789. | 12.8 | 368 |
| 71 | Heritability enrichment of specifically expressed genes identifies disease-relevant tissues and cell types. <i>Nature Genetics</i> , 2018, 50, 621-629. | 21.4 | 807 |
| 72 | Imputation-based analysis of MICA alleles in the susceptibility to ankylosing spondylitis. <i>Annals of the Rheumatic Diseases</i> , 2018, 77, 1691-1692. | 0.9 | 14 |

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|----|--|------|-----------|
| 73 | Review: Genetics and the Classification of Arthritis in Adults and Children. <i>Arthritis and Rheumatology</i> , 2018, 70, 7-17. | 5.6 | 100 |
| 74 | Functional genomics of stromal cells in chronic inflammatory diseases. <i>Current Opinion in Rheumatology</i> , 2018, 30, 65-71. | 4.3 | 10 |
| 75 | Meta-analysis of ImmunoChip data of four autoimmune diseases reveals novel single-disease and cross-phenotype associations. <i>Genome Medicine</i> , 2018, 10, 97. | 8.2 | 73 |
| 76 | Mixed-effects association of single cells identifies an expanded effector CD4 ⁺ T cell subset in rheumatoid arthritis. <i>Science Translational Medicine</i> , 2018, 10, . | 12.4 | 119 |
| 77 | Discovering in vivo cytokine-eQTL interactions from a lupus clinical trial. <i>Genome Biology</i> , 2018, 19, 168. | 8.8 | 36 |
| 78 | Fine-mapping and functional studies highlight potential causal variants for rheumatoid arthritis and type 1 diabetes. <i>Nature Genetics</i> , 2018, 50, 1366-1374. | 21.4 | 122 |
| 79 | Methods for high-dimensional analysis of cells dissociated from cryopreserved synovial tissue. <i>Arthritis Research and Therapy</i> , 2018, 20, 139. | 3.5 | 93 |
| 80 | High-throughput identification of noncoding functional SNPs via type IIS enzyme restriction. <i>Nature Genetics</i> , 2018, 50, 1180-1188. | 21.4 | 31 |
| 81 | An integrated clinical program and crowdsourcing strategy for genomic sequencing and Mendelian disease gene discovery. <i>Npj Genomic Medicine</i> , 2018, 3, 21. | 3.8 | 24 |
| 82 | Pathologically expanded peripheral T helper cell subset drives B cells in rheumatoid arthritis. <i>Nature</i> , 2017, 542, 110-114. | 27.8 | 767 |
| 83 | Investigating methotrexate toxicity within a randomized double-blinded, placebo-controlled trial: Rationale and design of the Cardiovascular Inflammation Reduction Trial-Adverse Events (CIRT-AE) Study. <i>Seminars in Arthritis and Rheumatism</i> , 2017, 47, 133-142. | 3.4 | 26 |
| 84 | A rare coding allele in <i>IFIH1</i> is protective for psoriatic arthritis. <i>Annals of the Rheumatic Diseases</i> , 2017, 76, 1321-1324. | 0.9 | 22 |
| 85 | Phenome-wide scanning identifies multiple diseases and disease severity phenotypes associated with HLA variants. <i>Science Translational Medicine</i> , 2017, 9, . | 12.4 | 105 |
| 86 | Genetic association study of exfoliation syndrome identifies a protective rare variant at <i>LOXL1</i> and five new susceptibility loci. <i>Nature Genetics</i> , 2017, 49, 993-1004. | 21.4 | 114 |
| 87 | Transethnic meta-analysis identifies <i>GSDMA</i> and <i>PRDM1</i> as susceptibility genes to systemic sclerosis. <i>Annals of the Rheumatic Diseases</i> , 2017, 76, 1150-1158. | 0.9 | 77 |
| 88 | Genetic landscape of interactive effects of <i>HLA-DRB1</i> alleles on susceptibility to ACPA(+) rheumatoid arthritis and ACPA levels in Japanese population. <i>Journal of Medical Genetics</i> , 2017, 54, 853-858. | 3.2 | 3 |
| 89 | Leveraging blood and tissue CD4 ⁺ T cell heterogeneity at the single cell level to identify mechanisms of disease in rheumatoid arthritis. <i>Current Opinion in Immunology</i> , 2017, 49, 27-36. | 5.5 | 15 |
| 90 | Molecular basis for increased susceptibility of Indigenous North Americans to seropositive rheumatoid arthritis. <i>Annals of the Rheumatic Diseases</i> , 2017, 76, 1915-1923. | 0.9 | 36 |

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|-----|--|------|-----------|
| 91 | Brief Report: The Role of Rare Protein-Coding Variants in Anti-Tumor Necrosis Factor Treatment Response in Rheumatoid Arthritis. <i>Arthritis and Rheumatology</i> , 2017, 69, 735-741. | 5.6 | 8 |
| 92 | An argument for early genomic sequencing in atypical cases: a <i>WISP3</i> variant leads to diagnosis of progressive pseudorheumatoid arthropathy of childhood. <i>Rheumatology</i> , 2016, 55, kev367. | 1.9 | 6 |
| 93 | Mapping rare, deleterious mutations in Factor H: Association with early onset, drusen burden and lower antigenic levels in familial AMD. <i>Scientific Reports</i> , 2016, 6, 31531. | 3.3 | 48 |
| 94 | Protective coding variants in <i>CFH</i> and <i>PELI3</i> and a variant near <i>CTRB1</i> are associated with age-related macular degeneration. <i>Human Molecular Genetics</i> , 2016, 25, ddw336. | 2.9 | 16 |
| 95 | A method to decipher pleiotropy by detecting underlying heterogeneity driven by hidden subgroups applied to autoimmune and neuropsychiatric diseases. <i>Nature Genetics</i> , 2016, 48, 803-810. | 21.4 | 62 |
| 96 | A general framework for meta-analyzing dependent studies with overlapping subjects in association mapping. <i>Human Molecular Genetics</i> , 2016, 25, 1857-1866. | 2.9 | 42 |
| 97 | Contribution of a Non-classical HLA Gene, HLA-DOA, to the Risk of Rheumatoid Arthritis. <i>American Journal of Human Genetics</i> , 2016, 99, 366-374. | 6.2 | 68 |
| 98 | Genetic risk of extranodal natural killer T-cell lymphoma: a genome-wide association study. <i>Lancet Oncology</i> , The, 2016, 17, 1240-1247. | 10.7 | 84 |
| 99 | 52 Genetic Loci Influencing Myocardial Mass. <i>Journal of the American College of Cardiology</i> , 2016, 68, 1435-1448. | 2.8 | 113 |
| 100 | Atlas of prostate cancer heritability in European and African-American men pinpoints tissue-specific regulation. <i>Nature Communications</i> , 2016, 7, 10979. | 12.8 | 50 |
| 101 | Recent Advances in Defining the Genetic Basis of Rheumatoid Arthritis. <i>Annual Review of Genomics and Human Genetics</i> , 2016, 17, 273-301. | 6.2 | 44 |
| 102 | Genome-Wide Association Studies Suggest Limited Immune Gene Enrichment in Schizophrenia Compared to 5 Autoimmune Diseases. <i>Schizophrenia Bulletin</i> , 2016, 42, 1176-1184. | 4.3 | 62 |
| 103 | Familial aggregation of arthritis-related diseases in seropositive and seronegative rheumatoid arthritis: a register-based case-control study in Sweden. <i>Annals of the Rheumatic Diseases</i> , 2016, 75, 183-189. | 0.9 | 36 |
| 104 | Analysis of five chronic inflammatory diseases identifies 27 new associations and highlights disease-specific patterns at shared loci. <i>Nature Genetics</i> , 2016, 48, 510-518. | 21.4 | 617 |
| 105 | Autoimmune diseases "connecting" risk alleles with molecular traits of the immune system. <i>Nature Reviews Genetics</i> , 2016, 17, 160-174. | 16.3 | 173 |
| 106 | Functional implications of disease-specific variants in loci jointly associated with coeliac disease and rheumatoid arthritis. <i>Human Molecular Genetics</i> , 2016, 25, 180-190. | 2.9 | 29 |
| 107 | Loci associated with N-glycosylation of human IgG are not associated with rheumatoid arthritis: a Mendelian randomisation study. <i>Annals of the Rheumatic Diseases</i> , 2016, 75, 317-320. | 0.9 | 19 |
| 108 | Investigating the Causal Relationship of C-Reactive Protein with 32 Complex Somatic and Psychiatric Outcomes: A Large-Scale Cross-Consortium Mendelian Randomization Study. <i>PLoS Medicine</i> , 2016, 13, e1001976. | 8.4 | 150 |

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|-----|--|------|-----------|
| 109 | Disentangling the Effects of Colocalizing Genomic Annotations to Functionally Prioritize Non-coding Variants within Complex-Trait Loci. <i>American Journal of Human Genetics</i> , 2015, 97, 139-152. | 6.2 | 122 |
| 110 | Rheumatoid Factor Is Associated With the Distribution of Hand Joint Destruction in Rheumatoid Arthritis. <i>Arthritis and Rheumatology</i> , 2015, 67, 3113-3123. | 5.6 | 25 |
| 111 | Interactions Between Amino Acid-Defined Major Histocompatibility Complex Class II Variants and Smoking in Seropositive Rheumatoid Arthritis. <i>Arthritis and Rheumatology</i> , 2015, 67, 2611-2623. | 5.6 | 58 |
| 112 | Disproportionate Contributions of Select Genomic Compartments and Cell Types to Genetic Risk for Coronary Artery Disease. <i>PLoS Genetics</i> , 2015, 11, e1005622. | 3.5 | 70 |
| 113 | Rare Variants in the Functional Domains of Complement Factor H Are Associated With Age-Related Macular Degeneration. , 2015, 56, 6873. | | 60 |
| 114 | Immune cell profiling to guide therapeutic decisions in rheumatic diseases. <i>Nature Reviews Rheumatology</i> , 2015, 11, 541-551. | 8.0 | 62 |
| 115 | Accurate and Fast Multiple-Testing Correction in eQTL Studies. <i>American Journal of Human Genetics</i> , 2015, 96, 857-868. | 6.2 | 25 |
| 116 | Rare genetic variants in the CFI gene are associated with advanced age-related macular degeneration and commonly result in reduced serum factor I levels. <i>Human Molecular Genetics</i> , 2015, 24, 3861-70. | 2.9 | 100 |
| 117 | Polymorphisms of large effect explain the majority of the host genetic contribution to variation of HIV-1 virus load. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 14658-14663. | 7.1 | 154 |
| 118 | <i>HLA-DRB1*11</i> and variants of the MHC class II locus are strong risk factors for systemic juvenile idiopathic arthritis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 15970-15975. | 7.1 | 139 |
| 119 | Joint Analysis of Psychiatric Disorders Increases Accuracy of Risk Prediction for Schizophrenia, Bipolar Disorder, and Major Depressive Disorder. <i>American Journal of Human Genetics</i> , 2015, 96, 283-294. | 6.2 | 225 |
| 120 | Psychiatric genome-wide association study analyses implicate neuronal, immune and histone pathways. <i>Nature Neuroscience</i> , 2015, 18, 199-209. | 14.8 | 701 |
| 121 | High-density genotyping of immune loci in Koreans and Europeans identifies eight new rheumatoid arthritis risk loci. <i>Annals of the Rheumatic Diseases</i> , 2015, 74, e13-e13. | 0.9 | 100 |
| 122 | Biological interpretation of genome-wide association studies using predicted gene functions. <i>Nature Communications</i> , 2015, 6, 5890. | 12.8 | 706 |
| 123 | Do Genetic Susceptibility Variants Associate with Disease Severity in Early Active Rheumatoid Arthritis?. <i>Journal of Rheumatology</i> , 2015, 42, 1131-1140. | 2.0 | 18 |
| 124 | Additive and interaction effects at three amino acid positions in HLA-DQ and HLA-DR molecules drive type 1 diabetes risk. <i>Nature Genetics</i> , 2015, 47, 898-905. | 21.4 | 235 |
| 125 | Association of HLA-DRB1 Haplotypes With Rheumatoid Arthritis Severity, Mortality, and Treatment Response. <i>JAMA - Journal of the American Medical Association</i> , 2015, 313, 1645. | 7.4 | 119 |
| 126 | O49. Personalized Genetic Medicine: Amino Acid Positions 11, 71 and 74 in HLA-DRB1 Predict Disease Severity, Mortality and Treatment Response in Rheumatoid Arthritis Multi-Centre Prospective Cohort Studies. <i>Rheumatology</i> , 2015, , . | 1.9 | 0 |

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|-----|--|------|-----------|
| 127 | Fine mapping in the MHC region accounts for 18% additional genetic risk for celiac disease. <i>Nature Genetics</i> , 2015, 47, 577-578. | 21.4 | 123 |
| 128 | A weighted genetic risk score using all known susceptibility variants to estimate rheumatoid arthritis risk. <i>Annals of the Rheumatic Diseases</i> , 2015, 74, 170-176. | 0.9 | 55 |
| 129 | Partitioning heritability by functional annotation using genome-wide association summary statistics. <i>Nature Genetics</i> , 2015, 47, 1228-1235. | 21.4 | 2,045 |
| 130 | Widespread non-additive and interaction effects within HLA loci modulate the risk of autoimmune diseases. <i>Nature Genetics</i> , 2015, 47, 1085-1090. | 21.4 | 164 |
| 131 | New data and an old puzzle: the negative association between schizophrenia and rheumatoid arthritis. <i>International Journal of Epidemiology</i> , 2015, 44, 1706-1721. | 1.9 | 53 |
| 132 | TYK2 Protein-Coding Variants Protect against Rheumatoid Arthritis and Autoimmunity, with No Evidence of Major Pleiotropic Effects on Non-Autoimmune Complex Traits. <i>PLoS ONE</i> , 2015, 10, e0122271. | 2.5 | 120 |
| 133 | Tissue-Specific Enrichment of Lymphoma Risk Loci in Regulatory Elements. <i>PLoS ONE</i> , 2015, 10, e0139360. | 2.5 | 5 |
| 134 | Integration of Sequence Data from a Consanguineous Family with Genetic Data from an Outbred Population Identifies PLB1 as a Candidate Rheumatoid Arthritis Risk Gene. <i>PLoS ONE</i> , 2014, 9, e87645. | 2.5 | 34 |
| 135 | A Role for Noncoding Variation in Schizophrenia. <i>Cell Reports</i> , 2014, 9, 1417-1429. | 6.4 | 225 |
| 136 | Association between low density lipoprotein and rheumatoid arthritis genetic factors with low density lipoprotein levels in rheumatoid arthritis and non-rheumatoid arthritis controls. <i>Annals of the Rheumatic Diseases</i> , 2014, 73, 1170-1175. | 0.9 | 30 |
| 137 | An international effort towards developing standards for best practices in analysis, interpretation and reporting of clinical genome sequencing results in the CLARITY Challenge. <i>Genome Biology</i> , 2014, 15, R53. | 9.6 | 101 |
| 138 | Regulation of Gene Expression in Autoimmune Disease Loci and the Genetic Basis of Proliferation in CD4+ Effector Memory T Cells. <i>PLoS Genetics</i> , 2014, 10, e1004404. | 3.5 | 46 |
| 139 | SNPsea: an algorithm to identify cell types, tissues and pathways affected by risk loci. <i>Bioinformatics</i> , 2014, 30, 2496-2497. | 4.1 | 60 |
| 140 | Genetic variants in the complement system predisposing to age-related macular degeneration: A review. <i>Molecular Immunology</i> , 2014, 61, 118-125. | 2.2 | 113 |
| 141 | HLA-DRB1 Associated Rheumatoid Arthritis Risk at Multiple Levels in African Americans: Hierarchical Classification Systems, Amino Acid Positions, and Residues. <i>Arthritis and Rheumatology</i> , 2014, 66, 3274-3282. | 5.6 | 32 |
| 142 | Common Genetic Variants Modulate Pathogen-Sensing Responses in Human Dendritic Cells. <i>Science</i> , 2014, 343, 1246980. | 12.6 | 391 |
| 143 | Predicting HLA alleles from high-resolution SNP data in three Southeast Asian populations. <i>Human Molecular Genetics</i> , 2014, 23, 4443-4451. | 2.9 | 80 |
| 144 | Genetics of rheumatoid arthritis contributes to biology and drug discovery. <i>Nature</i> , 2014, 506, 376-381. | 27.8 | 1,974 |

| # | ARTICLE | IF | CITATIONS |
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