Steven J Schrodi

List of Publications by Year
in descending order

63 papers	6,631 citations	201674 27 h-index	149698 56 g-index
68 all docs	68 docs citations	68 times ranked	9024 citing authors

#	Article	IF	Citations
1	A Missense Single-Nucleotide Polymorphism in a Gene Encoding a Protein Tyrosine Phosphatase (PTPN22) Is Associated with Rheumatoid Arthritis. American Journal of Human Genetics, 2004, 75, 330-337.	6.2	1,313
2	Genome-wide scan reveals association of psoriasis with IL-23 and NF-ÎºB pathways. Nature Genetics, 2009, 41, 199-204.	21.4	1,229
3	A Large-Scale Genetic Association Study Confirms IL12B and Leads to the Identification of IL23R as Psoriasis-Risk Genes. American Journal of Human Genetics, 2007, 80, 273-290.	6.2	988
4	Identification of 15 new psoriasis susceptibility loci highlights the role of innate immunity. Nature Genetics, 2012, 44, 1341-1348.	21.4	848
5	A Candidate Gene Approach Identifies the TRAF1/C5 Region as a Risk Factor for Rheumatoid Arthritis. PLoS Medicine, 2007, 4, e278.	8.4	232
6	PTPN22 Genetic Variation: Evidence for Multiple Variants Associated with Rheumatoid Arthritis. American Journal of Human Genetics, 2005, 77, 567-581.	6.2	215
7	Multiple Loci within the Major Histocompatibility Complex Confer Risk of Psoriasis. PLoS Genetics, 2009, 5, e1000606.	3.5	141
8	Association of late-onset Alzheimer's disease with genetic variation in multiple members of the GAPD gene family. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 15688-15693.	7.1	134
9	Identification of Two Gene Variants Associated With Risk of Advanced Fibrosis in Patients With Chronic Hepatitis C. Gastroenterology, 2006, 130, 1679-1687.	1.3	113
10	Changes in Gut and Plasma Microbiome following Exercise Challenge in Myalgic Encephalomyelitis/Chronic Fatigue Syndrome (ME/CFS). PLoS ONE, 2015, 10, e0145453.	2.5	96
11	Apoptosis, Autophagy, NETosis, Necroptosis, and Pyroptosis Mediated Programmed Cell Death as Targets for Innovative Therapy in Rheumatoid Arthritis. Frontiers in Immunology, 2021, 12, 809806.	4.8	87
12	A PheWAS approach in studying HLA-DRB1*1501. Genes and Immunity, 2013, 14, 187-191.	4.1	86
13	A Large-Scale Rheumatoid Arthritis Genetic Study Identifies Association at Chromosome 9q33.2. PLoS Genetics, 2008, 4, e1000107.	3.5	75
14	Association between IL13 Polymorphisms and Psoriatic Arthritis Is Modified by Smoking. Journal of Investigative Dermatology, 2009, 129, 2777-2783.	0.7	70
15	Further Genetic Evidence for Three Psoriasis-Risk Genes: ADAM33, CDKAL1, and PTPN22. Journal of Investigative Dermatology, 2009, 129, 629-634.	0.7	67
16	Mining Retrospective Data for Virtual Prospective Drug Repurposing: L-DOPA and Age-related Macular Degeneration. American Journal of Medicine, 2016, 129, 292-298.	1.5	66
17	Variants in the 5q31 cytokine gene cluster are associated with psoriasis. Genes and Immunity, 2008, 9, 176-181.	4.1	64
18	Association of ABCA1 with late-onset Alzheimerâ€™s disease is not observed in a case-control study. Neuroscience Letters, 2004, 366, 268-271.	2.1	58

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19	Molecular and Cellular Heterogeneity in Rheumatoid Arthritis: Mechanisms and Clinical Implications. Frontiers in Immunology, 2021, 12, 790122.	4.8	58
20	Genetic evidence for ubiquitin-specific proteasesUSP24andUSP40as candidate genes for late-onset Parkinson disease. Human Mutation, 2006, 27, 1017-1023.	2.5	53
21	Genetic-based prediction of disease traits: prediction is very difficult, especially about the futureÃ¢â‚¬Â. Frontiers in Genetics, 2014, 5, 162.	2.3	53
22	The inflammatory diseaseâ€“associated variants in IL12B and IL23R are not associated with rheumatoid arthritis. Arthritis and Rheumatism, 2008, 58, 1877-1881.	6.7	41
23	A Case-Control Association Study of the 12 Single-Nucleotide Polymorphisms Implicated in Parkinson Disease by a Recent Genome Scan. American Journal of Human Genetics, 2006, 78, 1090-1092.	6.2	38
24	Genome wide association study of SNP-, gene-, and pathway-based approaches to identify genes influencing susceptibility to Staphylococcus aureus infections. Frontiers in Genetics, 2014, 5, 125.	2.3	38
25	Phenome-wide association studies (PheWASs) for functional variants. European Journal of Human Genetics, 2015, 23, 523-529.	2.8	38
26	Metaâ€‰analysis evidence of a differential risk of the FCRL3 â˜…169Tâ†’C polymorphism in white and East Asian rheumatoid arthritis patients. Arthritis and Rheumatism, 2007, 56, 3168-3171.	6.7	31
27	Complex host genetic susceptibility to Staphylococcus aureus infections. Trends in Microbiology, 2015, 23, 529-536.	7.7	29
28	The 5q31 variants associated with psoriasis and Crohn's disease are distinct. Human Molecular Genetics, 2008, 17, 2978-2985.	2.9	27
29	Prevalence estimation for monogenic autosomal recessive diseases using population-based genetic data. Human Genetics, 2015, 134, 659-669.	3.8	27
30	Validation of a metabolite panel for early diagnosis of type 2 diabetes. Metabolism: Clinical and Experimental, 2016, 65, 1399-1408.	3.4	25
31	Hypomethylation in HBV integration regions aids non-invasive surveillance to hepatocellular carcinoma by low-pass genome-wide bisulfite sequencing. BMC Medicine, 2020, 18, 200.	5.5	25
32	Selecting Tagging SNPs for Association Studies Using Power Calculations from Genotype Data. Human Heredity, 2004, 57, 156-170.	0.8	24
33	Detailed genetic characterization of the interleukin-23 receptor in psoriasis. Genes and Immunity, 2008, 9, 546-555.	4.1	24
34	SeqHBase: a big data toolset for family based sequencing data analysis. Journal of Medical Genetics, 2015, 52, 282-288.	3.2	17
35	Neither Replication nor Simulation Supports a Role for the Axon Guidance Pathway in the Genetics of Parkinson's Disease. PLoS ONE, 2008, 3, e2707.	2.5	17
36	(5R)-5-Hydroxytriptolide (LLDT-8) induces substantial epigenetic mediated immune response network changes in fibroblast-like synoviocytes from rheumatoid arthritis patients. Scientific Reports, 2019, 9, 11155.	3.3	16

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37	Mechanisms of DNA Methylation in Virus-Host Interaction in Hepatitis B Infection: Pathogenesis and Oncogenetic Properties. International Journal of Molecular Sciences, 2021, 22, 9858.	4.1	15
38	A gene-based recessive diplotype exome scan discovers FGF6, a novel hepcidin-regulating iron-metabolism gene. Blood, 2019, 133, 1888-1898.	1.4	14
39	MicroRNA Variants and HLA-miRNA Interactions are Novel Rheumatoid Arthritis Susceptibility Factors. Frontiers in Genetics, 2021, 12, 747274.	2.3	14
40	Reduced Anti-Histone Antibodies and Increased Risk of Rheumatoid Arthritis Associated with a Single Nucleotide Polymorphism in PADI4 in North Americans. International Journal of Molecular Sciences, 2019, 20, 3093.	4.1	13
41	Use of an Electronic Medical Record to Create the Marshfield Clinic Twin/Multiple Birth Cohort. Genetic Epidemiology, 2014, 38, 692-698.	1.3	11
42	Differential Lipid Response to Statins Is Associated With Variants in the BUD13â€“APOA5 Gene Region. Journal of Cardiovascular Pharmacology, 2015, 66, 183-188.	1.9	11
43	Pro-inflammatory immune responses are associated with clinical signs and symptoms of human anaplasmosis. PLoS ONE, 2017, 12, e0179655.	2.5	11
44	DNA Methylation of T Lymphocytes as a Therapeutic Target: Implications for Rheumatoid Arthritis Etiology. Frontiers in Immunology, 2022, 13, 863703.	4.8	11
45	Genetic evidence of PTPN22 effects on chronic lymphocytic leukemia. Blood, 2013, 121, 237-238.	1.4	10
46	Pairwise linkage disequilibrium under disease models. European Journal of Human Genetics, 2007, 15, 212-220.	2.8	9
47	Genome-wide association scan in psoriasis: new insights into chronic inflammatory disease. Expert Review of Clinical Immunology, 2008, 4, 565-571.	3.0	9
48	Genetic and Functional Associations with Decreased Anti-inflammatory Tumor Necrosis Factor Alpha Induced Protein 3 in Macrophages from Subjects with Axial Spondyloarthritis. Frontiers in Immunology, 2017, 8, 860.	4.8	9
49	The Use of Multiplicity Corrections, Order Statistics and Generalized Family-Wise Statistics with Application to Genome-Wide Studies. PLoS ONE, 2016, 11, e0154472.	2.5	6
50	Trends in the Contribution of Genetic Susceptibility Loci to Hyperuricemia and Gout and Associated Novel Mechanisms. Frontiers in Cell and Developmental Biology, 0, 10, .	3.7	4
51	A Probabilistic Approach to Large-Scale Association Scans: A Semi-Bayesian Method to Detect Disease-Predisposing Alleles. Statistical Applications in Genetics and Molecular Biology, 2005, 4, Article31.	0.6	3
52	Cell line donor genotype and its influence on experimental phenotype: Toll-like receptor SNPs and potential variability in innate immunity. Molecular Genetics and Metabolism, 2016, 118, 147-152.	1.1	3
53	The Impact of Diagnostic Code Misclassification on Optimizing the Experimental Design of Genetic Association Studies. Journal of Healthcare Engineering, 2017, 2017, 1-5.	1.9	3
54	RNA-seq and Network Analysis Reveal Unique Chemokine Activity Signatures in the Synovial Tissue of Patients With Rheumatoid Arthritis. Frontiers in Medicine, 2022, 9, .	2.6	3

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55	Reflections on the Field of Human Genetics: A Call for Increased Disease Genetics Theory. Frontiers in Genetics, 2016, 7, 106.	2.3	1
56	The Decay of Disease Association with Declining Linkage Disequilibrium: A Fine Mapping Theorem. Frontiers in Genetics, 2016, 7, 217.	2.3	1
57	Remediation of ABCG5-Linked Macrothrombocytopenia With Ezetimibe Therapy. Frontiers in Genetics, 2021, 12, 769699.	2.3	1
58	Characterization of the Psoriasis-associated IL12B and IL23R Genes. Clinical Immunology, 2007, 123, S126.	3.2	0
59	Postmortem Genetic Testing for Sudden Unexpected Death. JAMA - Journal of the American Medical Association, 2017, 317, 320.	7.4	0
60	Empirical Bayesian approach to testing multiple hypotheses with separate priors for left and right alternatives. Statistical Applications in Genetics and Molecular Biology, 2018, 17, .	0.6	0
61	Broader Considerations of Medical and Dental Data Integration. Computers in Health Care, 2012, , 167-298.	0.3	0
62	LYP's implications cause both increased or decreased susceptibility towards autoimmune and acquired diseases (LB96). FASEB Journal, 2014, 28, LB96.	0.5	0
63	Calculating Exact P-Values from the McNamara Transmission/Disequilibrium Test Statistic. Journal of Investigative Genomics, 2015, 2, .	0.2	0