Michael E March

List of Publications by Year
in descending order

65	3,975	279798 23	123424 61
papers	citations	h-index	g-index

67	67	67	6658
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Treatment of severe Kaposiform lymphangiomatosis positive for NRAS mutation by MEK inhibition. Pediatric Research, 2023, 94, 1911-1915.	2.3	16
2	A genome-wide association meta-analysis identifies new eosinophilic esophagitis loci. Journal of Allergy and Clinical Immunology, 2022, 149, 988-998.	2.9	19
3	A novel <scp>MBTPS2</scp> variant associated with <scp>BRESHECK</scp> syndrome impairs <scp>sterolâ€regulated</scp> transcription and the endoplasmic reticulum stress response. American Journal of Medical Genetics, Part A, 2022, 188, 463-472.	1.2	4
4	Improved genetic risk scoring algorithm for type 1 diabetes prediction. Pediatric Diabetes, 2022, 23, 320-323.	2.9	11
5	Genetic analysis for type 1 diabetes genes in juvenile dermatomyositis unveils genetic disease overlap. Rheumatology, 2022, , .	1.9	2
6	Identification of Novel Loci Shared by Juvenile Idiopathic Arthritis Subtypes Through Integrative Genetic Analysis. Arthritis and Rheumatology, 2022, 74, 1420-1429.	5.6	4
7	Exome and <scp>RNAâ€Seq</scp> analyses of an incomplete penetrance variant in <scp> USP9X </scp> in femaleâ€specific syndromic intellectual disability. American Journal of Medical Genetics, Part A, 2022, , .	1.2	1
8	Association of DLL1 with type 1 diabetes in patients characterized by low polygenic risk score. Metabolism: Clinical and Experimental, 2021, 114, 154418.	3.4	6
9	Unsupervised modeling and genome-wide association identify novel features of allergic march trajectories. Journal of Allergy and Clinical Immunology, 2021, 147, 677-685.e10.	2.9	19
10	Association of novel rare coding variants with juvenile idiopathic arthritis. Annals of the Rheumatic Diseases, 2021, 80, 626-631.	0.9	6
11	Integrative analysis of genome-wide association studies identifies novel loci associated with neuropsychiatric disorders. Translational Psychiatry, 2021, 11, 69.	4.8	39
12	NAC blocks Cystatin C amyloid complex aggregation in a cell system and in skin of HCCAA patients. Nature Communications, 2021, 12, 1827.	12.8	5
13	The Role of Autophagy in Skeletal Muscle Diseases. Frontiers in Physiology, 2021, 12, 638983.	2.8	52
14	Pathogenic variants in CDH11 impair cell adhesion and cause Teebi hypertelorism syndrome. Human Genetics, 2021, 140, 1061-1076.	3.8	4
15	Pathogenic variants in SMARCA5 , a chromatin remodeler, cause a range of syndromic neurodevelopmental features. Science Advances, 2021, 7, .	10.3	17
16	Combined application of genetic and polygenic risk scores for type 1 diabetes risk prediction. Diabetes, Obesity and Metabolism, 2021, 23, 2001-2003.	4.4	2
17	Bi-allelic variants in the ER quality-control mannosidase gene EDEM3 cause a congenital disorder of glycosylation. American Journal of Human Genetics, 2021, 108, 1342-1349.	6.2	9
18	Genetic architecture of type 1 diabetes with low genetic risk score informed by 41 unreported loci. Communications Biology, 2021, 4, 908.	4.4	9

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19	Discovery of Novel Host Molecular Factors Underlying HBV/HCV Infection. Frontiers in Cell and Developmental Biology, 2021, 9, 690882.	3.7	0
20	Insights into non-autoimmune type 1 diabetes with 13 novel loci in low polygenic risk score patients. Scientific Reports, 2021, 11, 16013.	3.3	7
21	HIF-1Î± Pulmonary Phenotype Wide Association Study Unveils a Link to Inflammatory Airway Conditions. Frontiers in Genetics, 2021, 12, 756645.	2.3	6
22	Genetic Underpinnings of Asthma and Related Traits. , 2020, , 341-360.		0
23	Severe Lymphatic Disorder Resolved With MEK Inhibition in a Patient With Noonan Syndrome and SOS1 Mutation. Pediatrics, 2020, 146, .	2.1	56
24	Histone H3.3 beyond cancer: Germline mutations in Histone 3 Family 3A and 3B cause a previously unidentified neurodegenerative disorder in 46 patients. Science Advances, 2020, 6, .	10.3	43
25	Rare copy number variants in over 100,000 European ancestry subjects reveal multiple disease associations. Nature Communications, 2020, 11, 255.	12.8	48
26	Regulation of Janus Kinase 2 by an Inflammatory Bowel Disease Causal Non-coding Single Nucleotide Polymorphism. Journal of Crohn's and Colitis, 2020, 14, 646-653.	1.3	5
27	Kaposiform lymphangiomatosis effectively treated with <scp>MEK</scp> inhibition. EMBO Molecular Medicine, 2020, 12, e12324.	6.9	51
28	Intragenic Deletions of GNAS in Pseudohypoparathyroidism Type 1A Identify a New Region Affecting Methylation of Exon A/B. Journal of Clinical Endocrinology and Metabolism, 2020, 105, e3197-e3206.	3.6	6
29	ARAF recurrent mutation causes central conducting lymphatic anomaly treatable with a MEK inhibitor. Nature Medicine, 2019, 25, 1116-1122.	30.7	136
30	Detecting multiple differentially methylated CpG sites and regions related to dimensional psychopathology in youths. Clinical Epigenetics, 2019, 11, 146.	4.1	13
31	Target Genes of Autism Risk Loci in Brain Frontal Cortex. Frontiers in Genetics, 2019, 10, 707.	2.3	16
32	Identification of Target Genes at Juvenile Idiopathic Arthritis GWAS Loci in Human Neutrophils. Frontiers in Genetics, 2019, 10, 181.	2.3	6
33	Novel locus for atopic dermatitis in African Americans and replication in European Americans. Journal of Allergy and Clinical Immunology, 2019, 143, 1229-1231.	2.9	7
34	Heterozygous Deletion Impacting SMARCAD1 in the Original Kindred with Absent Dermatoglyphs and Associated Features (Baird, 1964). Journal of Pediatrics, 2018, 194, 248-252.e2.	1.8	6
35	Common variants at 5q33.1 predispose to migraine in African-American children. Journal of Medical Genetics, 2018, 55, 831-836.	3.2	15
36	Phenome-wide association studies across large population cohorts support drug target validation. Nature Communications, 2018, 9, 4285.	12.8	134

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37	Pathogenic variant in EPHB4 results in central conducting lymphatic anomaly. Human Molecular Genetics, 2018, 27, 3233-3245.	2.9	73
38	Loss-of-Function Mutations in KIF15 Underlying a Braddock-Carey Genocopy. Human Mutation, 2017, 38, 507-510.	2.5	8
39	Copy number variation meta-analysis reveals a novel duplication at 9p24 associated with multiple neurodevelopmental disorders. Genome Medicine, 2017, 9, 106.	8.2	41
40	Genome-wide association study identifies novel type II diabetes risk loci in Jordan subpopulations. PeerJ, 2017, 5, e3618.	2.0	9
41	Association of a rare NOTCH4 coding variant with systemic sclerosis: a family-based whole exome sequencing study. BMC Musculoskeletal Disorders, 2016, 17, 462.	1.9	12
42	Genome-wide association study for acute otitis media in children identifies FNDC1 as disease contributing gene. Nature Communications, 2016, 7, 12792.	12.8	50
43	Systematic data-querying of large pediatric biorepository identifies novel Ehlers-Danlos Syndrome variant. BMC Musculoskeletal Disorders, 2016, 17, 80.	1.9	5
44	Stress and Bronchodilator Response in Children with Asthma. American Journal of Respiratory and Critical Care Medicine, 2015, 192, 47-56.	5.6	99
45	Genome-wide association studies in asthma: progress and pitfalls. Advances in Genomics and Genetics, 2015, , 107.	0.8	2
46	Copy number variation in CEP57L1 predisposes to congenital absence of bilateral ACL and PCL ligaments. Human Genomics, 2015, 9, 31.	2.9	9
47	The genetic basis of eosinophilic esophagitis. Bailliere's Best Practice and Research in Clinical Gastroenterology, 2015, 29, 701-707.	2.4	13
48	Application of Whole Exome Sequencing in Six Families with an Initial Diagnosis of Autosomal Dominant Retinitis Pigmentosa: Lessons Learned. PLoS ONE, 2015, 10, e0133624.	2.5	19
49	A signaling network stimulated by Î² ₂ integrin promotes the polarization of lytic granules in cytotoxic cells. Science Signaling, 2014, 7, ra96.	3.6	59
50	A genome-wide association study identifies CDHR3 as a susceptibility locus for early childhood asthma with severe exacerbations. Nature Genetics, 2014, 46, 51-55.	21.4	497
51	Genetic Underpinnings of Asthma and Related Traits. , 2013, , 1-17.		1
52	Genetic polymorphisms and associated susceptibility to asthma. International Journal of General Medicine, 2013, 6, 253.	1.8	50
53	Meta-analysis of genome-wide association studies identifies three new risk loci for atopic dermatitis. Nature Genetics, 2012, 44, 187-192.	21.4	311
54	Î²2 Integrin Induces TCRÎ¶â€“Sykâ€“Phospholipase C-Î³ Phosphorylation and Paxillin-Dependent Granule Polarization in Human NK Cells. Journal of Immunology, 2011, 186, 2998-3005.	0.8	51

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55	The genetics of asthma and allergic disorders. Discovery Medicine, 2011, 11, 35-45.	0.5	21
56	Use of Transfected Drosophila S2 Cells to Study NK Cell Activation. Methods in Molecular Biology, 2010, 612, 67-88.	0.9	7
57	Recruitment of Activation Receptors at Inhibitory NK Cell Immune Synapses. PLoS ONE, 2008, 3, e3278.	2.5	36
58	Synergy among receptors on resting NK cells for the activation of natural cytotoxicity and cytokine secretion. Blood, 2006, 107, 159-166.	1.4	697
59	Activation, coactivation, and costimulation of resting human natural killer cells. Immunological Reviews, 2006, 214, 73-91.	6.0	531
60	Cytolytic granule polarization and degranulation controlled by different receptors in resting NK cells. Journal of Experimental Medicine, 2005, 202, 1001-1012.	8.5	409
61	Regulation of the immune response by SHIP. Seminars in Immunology, 2002, 14, 37-47.	5.6	57
62	p135 Src Homology 2 Domain-containing Inositol 5â€²-Phosphatase (SHIPÎ²) Isoform Can Substitute for p145 SHIP in FcÎ³RIIB1-mediated Inhibitory Signaling in B Cells. Journal of Biological Chemistry, 2000, 275, 29960-29967.	3.4	6
63	Essential Role for the C-Terminal Noncatalytic Region of SHIP in FcÎ³RIIB1-Mediated Inhibitory Signaling. Molecular and Cellular Biology, 2000, 20, 3576-3589.	2.3	56
64	Roles of Lck, Syk and ZAP-70 tyrosine kinases in TCR-mediated phosphorylation of the adapter protein Shc. European Journal of Immunology, 1998, 28, 2265-2275.	2.9	63
65	Genome-wide association study (GWAS) approaches to sleep phenotypes. , 0, , 22-32.		0