

# David J Martino

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/872452/publications.pdf>

Version: 2024-02-01

64  
papers

2,580  
citations

172386

29  
h-index

197736

49  
g-index

67  
all docs

67  
docs citations

67  
times ranked

4229  
citing authors

#	ARTICLE	IF	CITATIONS
1	Epigenetics and Prenatal Influences on Asthma and Allergic Airways Disease. <i>Chest</i> , 2011, 139, 640-647.	0.4	206
2	Longitudinal, genome-scale analysis of DNA methylation in twins from birth to 18 months of age reveals rapid epigenetic change in early life and pair-specific effects of discordance. <i>Genome Biology</i> , 2013, 14, R42.	13.9	172
3	Silent mysteries: epigenetic paradigms could hold the key to conquering the epidemic of allergy and immune disease. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2010, 65, 7-15.	2.7	148
4	Evidence for age-related and individual-specific changes in DNA methylation profile of mononuclear cells during early immune development in humans. <i>Epigenetics</i> , 2011, 6, 1085-1094.	1.3	120
5	Postnatal Fish Oil Supplementation in High-Risk Infants to Prevent Allergy: Randomized Controlled Trial. <i>Pediatrics</i> , 2012, 130, 674-682.	1.0	117
6	Epigenome-wide association study reveals longitudinally stable DNA methylation differences in CD4+ T cells from children with IgE-mediated food allergy. <i>Epigenetics</i> , 2014, 9, 998-1006.	1.3	106
7	Analysis of epigenetic changes in survivors of preterm birth reveals the effect of gestational age and evidence for a long term legacy. <i>Genome Medicine</i> , 2013, 5, 96.	3.6	101
8	Blood DNA methylation biomarkers predict clinical reactivity in food-sensitized infants. <i>Journal of Allergy and Clinical Immunology</i> , 2015, 135, 1319-1328.e12.	1.5	86
9	Gestational diabetes and maternal obesity are associated with epigenome-wide methylation changes in children. <i>JCI Insight</i> , 2018, 3, .	2.3	83
10	Cohort Profile: The HealthNuts Study: Population prevalence and environmental/genetic predictors of food allergy. <i>International Journal of Epidemiology</i> , 2015, 44, 1161-1171.	0.9	80
11	Genome-wide DNA methylation profiling identifies a folate-sensitive region of differential methylation upstream of <i>ZFP57</i> imprinting regulator in humans. <i>FASEB Journal</i> , 2014, 28, 4068-4076.	0.2	75
12	Epigenetic dysregulation of naive CD4+ T-cell activation genes in childhood food allergy. <i>Nature Communications</i> , 2018, 9, 3308.	5.8	71
13	Egg allergen specific IgE diversity predicts resolution of egg allergy in the population cohort HealthNuts. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2019, 74, 318-326.	2.7	66
14	Genome-wide association study and meta-analysis in multiple populations identifies new loci for peanut allergy and establishes C11orf30/EMSY as a genetic risk factor for food allergy. <i>Journal of Allergy and Clinical Immunology</i> , 2018, 141, 991-1001.	1.5	57
15	The skin barrier function gene <i>SPINK5</i> is associated with challenge-proven IgE-mediated food allergy in infants. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2017, 72, 1356-1364.	2.7	56
16	Early life innate immune signatures of persistent food allergy. <i>Journal of Allergy and Clinical Immunology</i> , 2018, 142, 857-864.e3.	1.5	55
17	Polymorphisms affecting vitamin D binding protein modify the relationship between serum vitamin D (25[OH]D3) and food allergy. <i>Journal of Allergy and Clinical Immunology</i> , 2016, 137, 500-506.e4.	1.5	52
18	T-cell activation genes differentially expressed at birth in CD4+ T cells from children who develop IgE food allergy. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2012, 67, 191-200.	2.7	47

#	ARTICLE	IF	CITATIONS
19	Epigenome-wide analysis of neonatal CD4 <sup>+</sup> T-cell DNA methylation sites potentially affected by maternal fish oil supplementation. <i>Epigenetics</i> , 2014, 9, 1570-1576.	1.3	46
20	Relationship between early intestinal colonization, mucosal immunoglobulin A production and systemic immune development. <i>Clinical and Experimental Allergy</i> , 2008, 38, 69-78.	1.4	40
21	Persistent Food Allergy and Food Allergy Coexistent with Eczema Is Associated with Reduced Growth in the First 4 Years of Life. <i>Journal of Allergy and Clinical Immunology: in Practice</i> , 2016, 4, 248-256.e3.	2.0	40
22	Genomewide association study of peanut allergy reproduces association with amino acid polymorphisms in <i>HLA-DRB1</i> . <i>Clinical and Experimental Allergy</i> , 2017, 47, 217-223.	1.4	40
23	Identification and analysis of peanut-specific effector T and regulatory T cells in children allergic and tolerant to peanut. <i>Journal of Allergy and Clinical Immunology</i> , 2018, 141, 1699-1710.e7.	1.5	37
24	Genetic determinants of paediatric food allergy: A systematic review. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2019, 74, 1631-1648.	2.7	37
25	Oral immunotherapy and tolerance induction in childhood. <i>Pediatric Allergy and Immunology</i> , 2013, 24, 512-520.	1.1	35
26	Epigenetics in immune development and in allergic and autoimmune diseases. <i>Journal of Reproductive Immunology</i> , 2014, 104-105, 43-48.	0.8	34
27	The ontogeny of naïve and regulatory CD4 <sup>+</sup> T cell subsets during the first postnatal year: a cohort study. <i>Clinical and Translational Immunology</i> , 2015, 4, e34.	1.7	34
28	Genome-scale profiling reveals a subset of genes regulated by DNA methylation that program somatic T-cell phenotypes in humans. <i>Genes and Immunity</i> , 2012, 13, 388-398.	2.2	33
29	Variable promoter methylation contributes to differential expression of key genes in human placenta-derived venous and arterial endothelial cells. <i>BMC Genomics</i> , 2013, 14, 475.	1.2	32
30	Food-allergic infants have impaired regulatory T cell responses following <i>in vivo</i> allergen exposure. <i>Pediatric Allergy and Immunology</i> , 2016, 27, 35-43.	1.1	32
31	Epigenetic Regulation in Early Childhood: A Miniaturized and Validated Method to Assess Histone Acetylation. <i>International Archives of Allergy and Immunology</i> , 2015, 168, 173-181.	0.9	31
32	Genetic variation at the Th2 immune gene <i>IL13</i> is associated with IgE-mediated paediatric food allergy. <i>Clinical and Experimental Allergy</i> , 2017, 47, 1032-1037.	1.4	29
33	Progress in Understanding the Epigenetic Basis for Immune Development, Immune Function, and the Rising Incidence of Allergic Disease. <i>Current Allergy and Asthma Reports</i> , 2013, 13, 85-92.	2.4	25
34	Risk Factors for Gut Dysbiosis in Early Life. <i>Microorganisms</i> , 2021, 9, 2066.	1.6	25
35	Children of Asian ethnicity in Australia have higher risk of food allergy and early-onset eczema than those in Singapore. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2021, 76, 3171-3182.	2.7	24
36	Genetic Variations in IL28B and Allergic Disease in Children. <i>PLoS ONE</i> , 2012, 7, e30607.	1.1	23

#	ARTICLE	IF	CITATIONS
37	Environmental and genetic determinants of vitamin D insufficiency in 12-month-old infants. <i>Journal of Steroid Biochemistry and Molecular Biology</i> , 2014, 144, 445-454.	1.2	23
38	Genome-wide identification of mononuclear cell DNA methylation sites potentially affected by fish oil supplementation in young infants: A pilot study. <i>Prostaglandins Leukotrienes and Essential Fatty Acids</i> , 2015, 101, 1-7.	1.0	22
39	A Canadian genome-wide association study and meta-analysis confirm HLA as a risk factor for peanut allergy independent of asthma. <i>Journal of Allergy and Clinical Immunology</i> , 2018, 141, 1513-1516.	1.5	21
40	Reduced placental FOXP3 associated with subsequent infant allergic disease. <i>Journal of Allergy and Clinical Immunology</i> , 2011, 128, 886-887.e5.	1.5	20
41	In vitro exposure of human blood mononuclear cells to active vitamin D does not induce substantial change to DNA methylation on a genome-scale. <i>Journal of Steroid Biochemistry and Molecular Biology</i> , 2014, 141, 144-149.	1.2	19
42	Food for thought. <i>Current Opinion in Allergy and Clinical Immunology</i> , 2015, 15, 237-242.	1.1	16
43	A novel role for interleukin-1 receptor signaling in the developmental regulation of immune responses to endotoxin. <i>Pediatric Allergy and Immunology</i> , 2012, 23, 567-572.	1.1	14
44	Epigenetic modifications: mechanisms of disease and biomarkers of food allergy. <i>Current Opinion in Immunology</i> , 2016, 42, 9-15.	2.4	14
45	The Effects of Chlorinated Drinking Water on the Assembly of the Intestinal Microbiome. <i>Challenges</i> , 2019, 10, 10.	0.9	14
46	Methylation of the filaggrin gene promoter does not affect gene expression and allergy. <i>Pediatric Allergy and Immunology</i> , 2014, 25, 608-610.	1.1	13
47	The DNA methylation landscape of CD4+ T cells in oligoarticular juvenile idiopathic arthritis. <i>Journal of Autoimmunity</i> , 2018, 86, 29-38.	3.0	13
48	Folate levels in pregnancy and offspring food allergy and eczema. <i>Pediatric Allergy and Immunology</i> , 2020, 31, 38-46.	1.1	12
49	Children with East Asian-Born Parents Have an Increased Risk of Allergy but May Not Have More Asthma in Early Childhood. <i>Journal of Allergy and Clinical Immunology: in Practice</i> , 2019, 7, 539-547.e3.	2.0	10
50	Mapping the landscape of chromatin dynamics during naïve CD4+ T-cell activation. <i>Scientific Reports</i> , 2021, 11, 14101.	1.6	10
51	The role of gene-environment interactions in the development of food allergy. <i>Expert Review of Gastroenterology and Hepatology</i> , 2015, 9, 1371-1378.	1.4	8
52	B-cell phenotype and function in infants with egg allergy. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2019, 74, 1022-1025.	2.7	8
53	The Potential Effects of Short-Chain Fatty Acids on the Epigenetic Regulation of Innate Immune Memory. <i>Challenges</i> , 2020, 11, 25.	0.9	8
54	Association of prenatal alcohol exposure with offspring DNA methylation in mammals: a systematic review of the evidence. <i>Clinical Epigenetics</i> , 2022, 14, 12.	1.8	7

#	ARTICLE	IF	CITATIONS
55	Meeting the challenges of measuring human immune regulation. Journal of Immunological Methods, 2015, 424, 1-6.	0.6	6
56	Phenotype consensus is required to enable large-scale genetic consortium studies of food allergy. Allergy: European Journal of Allergy and Clinical Immunology, 2020, 75, 2383-2387.	2.7	5
57	Multimics and Systems Biology Are Needed to Unravel the Complex Origins of Chronic Disease. Challenges, 2019, 10, 23.	0.9	3
58	Progress in Understanding Postnatal Immune Dysregulation in Allergic Disease. World Allergy Organization Journal, 2010, 3, 162-166.	1.6	2
59	Epigenetic Aberrations in Human Allergic Diseases. , 2012, , 369-385.		1
60	Candidate Gene Testing in Clinical Cohort Studies with Multiplexed Genotyping and Mass Spectrometry. Journal of Visualized Experiments, 2018, , .	0.2	1
61	Skin Barrier Function and Candidate Genes IL-13 & SPINK5 in Food Allergy. Journal of Allergy and Clinical Immunology, 2015, 135, AB384.	1.5	0
62	Epigenetic Mechanisms in Food Allergy. , 2019, , 1293-1306.		0
63	Role of Dietary Components in the Epidemic of Allergic Disease. , 2010, , 353-370.		0
64	Epigenetic Mechanisms in Food Allergy. , 2017, , 1-14.		0