

Hana Lango Allen

List of Publications by Year in descending order

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Version: 2024-02-01

53
papers

30,262
citations

81839

39
h-index

149623

56
g-index

59
all docs

59
docs citations

59
times ranked

36645
citing authors

#	ARTICLE	IF	CITATIONS
1	Whole-genome sequencing of a sporadic primary immunodeficiency cohort. <i>Nature</i> , 2020, 583, 90-95.	13.7	148
2	ADA2 deficiency complicated by EBV-driven lymphoproliferative disease. <i>Clinical Immunology</i> , 2020, 215, 108443.	1.4	9
3	Whole-genome sequencing of patients with rare diseases in a national health system. <i>Nature</i> , 2020, 583, 96-102.	13.7	338
4	Characterization of the clinical and immunologic phenotype and management of 157 individuals with 56 distinct heterozygous NFKB1 mutations. <i>Journal of Allergy and Clinical Immunology</i> , 2020, 146, 901-911.	1.5	78
5	Thousands of missing variants in the UK Biobank are recoverable by genome realignment. <i>Annals of Human Genetics</i> , 2020, 84, 214-220.	0.3	20
6	Predicting the Occurrence of Variants in RAG1 and RAG2. <i>Journal of Clinical Immunology</i> , 2019, 39, 688-701.	2.0	3
7	Loss of the interleukin-6 receptor causes immunodeficiency, atopy, and abnormal inflammatory responses. <i>Journal of Experimental Medicine</i> , 2019, 216, 1986-1998.	4.2	153
8	A Specific CNOT1 Mutation Results in a Novel Syndrome of Pancreatic Agenesis and Holoprosencephaly through Impaired Pancreatic and Neurological Development. <i>American Journal of Human Genetics</i> , 2019, 104, 985-989.	2.6	43
9	Copy number variation of <i>LINGO1</i> in familial dystonic tremor. <i>Neurology: Genetics</i> , 2019, 5, e307.	0.9	8
10	Pathogenic NFKB2 variant in the ankyrin repeat domain (R635X) causes a variable antibody deficiency. <i>Clinical Immunology</i> , 2019, 203, 23-27.	1.4	5
11	Prevalence and clinical challenges among adults with primary immunodeficiency and recombination-activating gene deficiency. <i>Journal of Allergy and Clinical Immunology</i> , 2018, 141, 2303-2306.	1.5	40
12	Loss-of-function nuclear factor κ B subunit 1 (NFKB1) variants are the most common monogenic cause of common variable immunodeficiency in Europeans. <i>Journal of Allergy and Clinical Immunology</i> , 2018, 142, 1285-1296.	1.5	185
13	Diagnosis of lethal or prenatal-onset autosomal recessive disorders by parental exome sequencing. <i>Prenatal Diagnosis</i> , 2018, 38, 33-43.	1.1	64
14	De Novo Truncating Mutations in WASF1 Cause Intellectual Disability with Seizures. <i>American Journal of Human Genetics</i> , 2018, 103, 144-153.	2.6	36
15	Comprehensive Cancer-Predisposition Gene Testing in an Adult Multiple Primary Tumor Series Shows a Broad Range of Deleterious Variants and Atypical Tumor Phenotypes. <i>American Journal of Human Genetics</i> , 2018, 103, 3-18.	2.6	46
16	Biallelic Mutation of ARHGEF18, Involved in the Determination of Epithelial Apicobasal Polarity, Causes Adult-Onset Retinal Degeneration. <i>American Journal of Human Genetics</i> , 2017, 100, 334-342.	2.6	26
17	Recessively Inherited <i>LRBA</i> Mutations Cause Autoimmunity Presenting as Neonatal Diabetes. <i>Diabetes</i> , 2017, 66, 2316-2322.	0.3	59
18	Polycystic Kidney Disease with Hyperinsulinemic Hypoglycemia Caused by a Promoter Mutation in Phosphomannomutase 2. <i>Journal of the American Society of Nephrology: JASN</i> , 2017, 28, 2529-2539.	3.0	99

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19	A <i>CACNA1D</i> mutation in a patient with persistent hyperinsulinaemic hypoglycaemia, heart defects, and severe hypotonia. <i>Pediatric Diabetes</i> , 2017, 18, 320-323.	1.2	67
20	Comprehensive Rare Variant Analysis via Whole-Genome Sequencing to Determine the Molecular Pathology of Inherited Retinal Disease. <i>American Journal of Human Genetics</i> , 2017, 100, 75-90.	2.6	343
21	<i>SOS1</i> frameshift mutations cause pure mucosal neuroma syndrome, a clinical phenotype distinct from multiple endocrine neoplasia type 2B. <i>Clinical Endocrinology</i> , 2016, 84, 715-719.	1.2	11
22	A Method to Exploit the Structure of Genetic Ancestry Space to Enhance Case-Control Studies. <i>American Journal of Human Genetics</i> , 2016, 98, 857-868.	2.6	21
23	An exome sequencing strategy to diagnose lethal autosomal recessive disorders. <i>European Journal of Human Genetics</i> , 2015, 23, 401-404.	1.4	51
24	The effect of early, comprehensive genomic testing on clinical care in neonatal diabetes: an international cohort study. <i>Lancet</i> , 2015, 386, 957-963.	6.3	250
25	Biallelic <i>RFX6</i> mutations can cause childhood as well as neonatal onset diabetes mellitus. <i>European Journal of Human Genetics</i> , 2015, 23, 1744-1748.	1.4	34
26	<i>GATA4</i> Mutations Are a Cause of Neonatal and Childhood-Onset Diabetes. <i>Diabetes</i> , 2014, 63, 2888-2894.	0.3	108
27	A rare SNP in pre-miR-34a is associated with increased levels of miR-34a in pancreatic beta cells. <i>Acta Diabetologica</i> , 2014, 51, 325-329.	1.2	30
28	Recessive mutations in a distal <i>PTF1A</i> enhancer cause isolated pancreatic agenesis. <i>Nature Genetics</i> , 2014, 46, 61-64.	9.4	255
29	Activating germline mutations in <i>STAT3</i> cause early-onset multi-organ autoimmune disease. <i>Nature Genetics</i> , 2014, 46, 812-814.	9.4	411
30	Analysis of Transcription Factors Key for Mouse Pancreatic Development Establishes <i>NKX2-2</i> and <i>MNX1</i> Mutations as Causes of Neonatal Diabetes in Man. <i>Cell Metabolism</i> , 2014, 19, 146-154.	7.2	123
31	Next generation sequencing of chromosomal rearrangements in patients with split-hand/split-foot malformation provides evidence for <i>DYNC111</i> exonic enhancers of <i>DLX5/6</i> expression in humans. <i>Journal of Medical Genetics</i> , 2014, 51, 264-267.	1.5	43
32	Improved genetic testing for monogenic diabetes using targeted next-generation sequencing. <i>Diabetologia</i> , 2013, 56, 1958-1963.	2.9	248
33	An in-frame deletion at the polymerase active site of <i>POLD1</i> causes a multisystem disorder with lipodystrophy. <i>Nature Genetics</i> , 2013, 45, 947-950.	9.4	151
34	<i>GATA6</i> haploinsufficiency causes pancreatic agenesis in humans. <i>Nature Genetics</i> , 2012, 44, 20-22.	9.4	249
35	Genome-wide association study of CNVs in 16,000 cases of eight common diseases and 3,000 shared controls. <i>Nature</i> , 2010, 464, 713-720.	13.7	737
36	Hundreds of variants clustered in genomic loci and biological pathways affect human height. <i>Nature</i> , 2010, 467, 832-838.	13.7	1,789

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37	Meta-analysis identifies 13 new loci associated with waist-hip ratio and reveals sexual dimorphism in the genetic basis of fat distribution. <i>Nature Genetics</i> , 2010, 42, 949-960.	9.4	836
38	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. <i>Nature Genetics</i> , 2010, 42, 937-948.	9.4	2,634
39	Polygenic Risk Variants for Type 2 Diabetes Susceptibility Modify Age at Diagnosis in Monogenic <i><i>HNF1A</i></i> Diabetes. <i>Diabetes</i> , 2010, 59, 266-271.	0.3	37
40	Type 2 Diabetes Risk Alleles Are Associated With Reduced Size at Birth. <i>Diabetes</i> , 2009, 58, 1428-1433.	0.3	135
41	What will whole genome searches for susceptibility genes for common complex disease offer to clinical practice?. <i>Journal of Internal Medicine</i> , 2008, 263, 16-27.	2.7	49
42	Gene variants influencing measures of inflammation or predisposing to autoimmune and inflammatory diseases are not associated with the risk of type 2 diabetes. <i>Diabetologia</i> , 2008, 51, 2205-2213.	2.9	41
43	A Genome-Wide Association Study Identifies Protein Quantitative Trait Loci (pQTLs). <i>PLoS Genetics</i> , 2008, 4, e1000072.	1.5	415
44	Genome-wide association analysis identifies 20 loci that influence adult height. <i>Nature Genetics</i> , 2008, 40, 575-583.	9.4	742
45	Assessing the Combined Impact of 18 Common Genetic Variants of Modest Effect Sizes on Type 2 Diabetes Risk. <i>Diabetes</i> , 2008, 57, 3129-3135.	0.3	279
46	Meta-analysis of genome-wide association data and large-scale replication identifies additional susceptibility loci for type 2 diabetes. <i>Nature Genetics</i> , 2008, 40, 638-645.	9.4	1,683
47	Common Variation in the <i><i>FTO</i></i> Gene Alters Diabetes-Related Metabolic Traits to the Extent Expected Given Its Effect on BMI. <i>Diabetes</i> , 2008, 57, 1419-1426.	0.3	277
48	A Common Variant in the <i>FTO</i> Gene Is Associated with Body Mass Index and Predisposes to Childhood and Adult Obesity. <i>Science</i> , 2007, 316, 889-894.	6.0	3,884
49	Replication of Genome-Wide Association Signals in UK Samples Reveals Risk Loci for Type 2 Diabetes. <i>Science</i> , 2007, 316, 1336-1341.	6.0	2,040
50	Association scan of 14,500 nonsynonymous SNPs in four diseases identifies autoimmunity variants. <i>Nature Genetics</i> , 2007, 39, 1329-1337.	9.4	1,298
51	Common variants in <i>WFS1</i> confer risk of type 2 diabetes. <i>Nature Genetics</i> , 2007, 39, 951-953.	9.4	333
52	A common variant of <i>HMGA2</i> is associated with adult and childhood height in the general population. <i>Nature Genetics</i> , 2007, 39, 1245-1250.	9.4	373
53	Genome-wide association study of 14,000 cases of seven common diseases and 3,000 shared controls. <i>Nature</i> , 2007, 447, 661-678.	13.7	8,895