Michael R Erdos

List of Publications by Year
in descending order

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Version: 2024-02-01

84 papers	30,625 citations	19657 61 h-index	54911 84 g-index
89 all docs	89 docs citations	89 times ranked	31873 citing authors

#	Article	IF	Citations
1	Genome-wide association studies of metabolites in Finnish men identify disease-relevant loci. Nature Communications, 2022, 13, 1644.	12.8	63
2	In vivo base editing rescues Hutchinsonâ€“Gilford progeria syndrome in mice. Nature, 2021, 589, 608-614.	27.8	275
3	A targeted antisense therapeutic approach for Hutchinsonâ€“Gilford progeria syndrome. Nature Medicine, 2021, 27, 536-545.	30.7	55
4	A Transcription Start Site Map in Human Pancreatic Islets Reveals Functional Regulatory Signatures. Diabetes, 2021, 70, 1581-1591.	0.6	7
5	Base editor treats progeria in mice. Nature, 2021, , .	27.8	4
6	Genetic effects on liver chromatin accessibility identify disease regulatory variants. American Journal of Human Genetics, 2021, 108, 1169-1189.	6.2	22
7	Genetic reduction of mTOR extends lifespan in a mouse model of Hutchinsonâ€Gilford Progeria syndrome. Aging Cell, 2021, 20, e13457.	6.7	27
8	Single-cell ATAC-Seq in human pancreatic islets and deep learning upscaling of rare cells reveals cell-specific type 2 diabetes regulatory signatures. Molecular Metabolism, 2020, 32, 109-121.	6.5	103
9	Evaluation of musculoskeletal phenotype of the G608G progeria mouse model with lonafarnib, pravastatin, and zoledronic acid as treatment groups. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 12029-12040.	7.1	20
10	Genetic variant effects on gene expression in human pancreatic islets and their implications for T2D. Nature Communications, 2020, 11, 4912.	12.8	89
11	Analysis of somatic mutations identifies signs of selection during in vitro aging of primary dermal fibroblasts. Aging Cell, 2019, 18, e13010.	6.7	6
12	Integrative analysis of gene expression, DNA methylation, physiological traits, and genetic variation in human skeletal muscle. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 10883-10888.	7.1	114
13	Single-cell transcriptomics from human pancreatic islets: sample preparation matters. Biology Methods and Protocols, 2019, 4, bpz019.	2.2	15
14	Multiomic Profiling Identifies cis-Regulatory Networks Underlying Human Pancreatic Î² Cell Identity and Function. Cell Reports, 2019, 26, 788-801.e6.	6.4	68
15	Biotinylation by antibody recognitionâ€”a method for proximity labeling. Nature Methods, 2018, 15, 127-133.	19.0	107
16	Everolimus rescues multiple cellular defects in laminopathy-patient fibroblasts. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 4206-4211.	7.1	43
17	Interactions between genetic variation and cellular environment in skeletal muscle gene expression. PLoS ONE, 2018, 13, e0195788.	2.5	18
18	Addendum: Biotinylation by antibody recognitionâ€”a method for proximity labeling. Nature Methods, 2018, 15, 749-749.	19.0	6

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19	Genetic regulatory signatures underlying islet gene expression and type 2 diabetes. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 2301-2306.	7.1	189
20	A Type 2 Diabetesâ€“Associated Functional Regulatory Variant in a Pancreatic Islet Enhancer at the ADCY5 Locus. Diabetes, 2017, 66, 2521-2530.	0.6	54
21	The genetic regulatory signature of type 2 diabetes in human skeletal muscle. Nature Communications, 2016, 7, 11764.	12.8	114
22	Global genome splicing analysis reveals an increased number of alternatively spliced genes with aging. Aging Cell, 2016, 15, 267-278.	6.7	79
23	Motif signatures in stretch enhancers are enriched for disease-associated genetic variants. Epigenetics and Chromatin, 2015, 8, 23.	3.9	28
24	Addressing Bias in Small RNA Library Preparation for Sequencing: A New Protocol Recovers MicroRNAs that Evade Capture by Current Methods. Frontiers in Genetics, 2015, 6, 352.	2.3	106
25	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	27.8	1,328
26	Super-enhancers delineate disease-associated regulatory nodes in T cells. Nature, 2015, 520, 558-562.	27.8	323
27	Impact of Type 2 Diabetes Susceptibility Variants on Quantitative Glycemic Traits Reveals Mechanistic Heterogeneity. Diabetes, 2014, 63, 2158-2171.	0.6	297
28	Loss of lamin B1 results in prolongation of S phase and decondensation of chromosome territories. FASEB Journal, 2014, 28, 3423-3434.	0.5	53
29	Correlated alterations in genome organization, histone methylation, and DNAâ€“lamin A/C interactions in Hutchinson-Gilford progeria syndrome. Genome Research, 2013, 23, 260-269.	5.5	282
30	Chromatin stretch enhancer states drive cell-specific gene regulation and harbor human disease risk variants. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 17921-17926.	7.1	606
31	C-reactive protein (CRP) promoter polymorphisms influence circulating CRP levels in a genome-wide association study of African Americans. Human Molecular Genetics, 2012, 21, 3063-3072.	2.9	32
32	UGT1A1 is a major locus influencing bilirubin levels in African Americans. European Journal of Human Genetics, 2012, 20, 463-468.	2.8	63
33	No Interactions Between Previously Associated 2-Hour Glucose Gene Variants and Physical Activity or BMI on 2-Hour Glucose Levels. Diabetes, 2012, 61, 1291-1296.	0.6	23
34	Genome-wide association study identifies novel loci association with fasting insulin and insulin resistance in African Americans. Human Molecular Genetics, 2012, 21, 4530-4536.	2.9	80
35	Human longevity and common variations in the LMNA gene: a metaâ€analysis. Aging Cell, 2012, 11, 475-481.	6.7	40
36	A genome-wide approach accounting for body mass index identifies genetic variants influencing fasting glycemic traits and insulin resistance. Nature Genetics, 2012, 44, 659-669.	21.4	762

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37	Genome-wide associated loci influencing interleukin (IL)-10, IL-1Ra, and IL-6 levels in African Americans. Immunogenetics, 2012, 64, 351-359.	2.4	31
38	Rapamycin Reverses Cellular Phenotypes and Enhances Mutant Protein Clearance in Hutchinson-Gilford Progeria Syndrome Cells. Science Translational Medicine, 2011, 3, 89ra58.	12.4	294
39	Progerin and telomere dysfunction collaborate to trigger cellular senescence in normal human fibroblasts. Journal of Clinical Investigation, 2011, 121, 2833-2844.	8.2	252
40	Heritable Individual-Specific and Allele-Specific Chromatin Signatures in Humans. Science, 2010, 328, 235-239.	12.6	304
41	Genetic variation in GIPR influences the glucose and insulin responses to an oral glucose challenge. Nature Genetics, 2010, 42, 142-148.	21.4	591
42	Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. Nature Genetics, 2010, 42, 579-589.	21.4	1,631
43	Meta-analysis identifies 13 new loci associated with waist-hip ratio and reveals sexual dimorphism in the genetic basis of fat distribution. Nature Genetics, 2010, 42, 949-960.	21.4	836
44	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. Nature Genetics, 2010, 42, 937-948.	21.4	2,634
45	Detailed Physiologic Characterization Reveals Diverse Mechanisms for Novel Genetic Loci Regulating Glucose and Insulin Metabolism in Humans. Diabetes, 2010, 59, 1266-1275.	0.6	237
46	Global Epigenomic Analysis of Primary Human Pancreatic Islets Provides Insights into Type 2 Diabetes Susceptibility Loci. Cell Metabolism, 2010, 12, 443-455.	16.2	190
47	New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. Nature Genetics, 2010, 42, 105-116.	21.4	1,982
48	Cardiovascular Pathology in Hutchinson-Gilford Progeria: Correlation With the Vascular Pathology of Aging. Arteriosclerosis, Thrombosis, and Vascular Biology, 2010, 30, 2301-2309.	2.4	332
49	Genome-Wide Association Scan Meta-Analysis Identifies Three Loci Influencing Adiposity and Fat Distribution. PLoS Genetics, 2009, 5, e1000508.	3.5	453
50	Six new loci associated with body mass index highlight a neuronal influence on body weight regulation. Nature Genetics, 2009, 41, 25-34.	21.4	1,572
51	Common variant in MTNR1B associated with increased risk of type 2 diabetes and impaired early insulin secretion. Nature Genetics, 2009, 41, 82-88.	21.4	642
52	Variants in MTNR1B influence fasting glucose levels. Nature Genetics, 2009, 41, 77-81.	21.4	662
53	A progeria mutation reveals functions for lamin A in nuclear assembly, architecture, and chromosome organization. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 20788-20793.	7.1	185
54	Tissue-specific alternative splicing of TCF7L2. Human Molecular Genetics, 2009, 18, 3795-3804.	2.9	100

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55	Meta-analysis of genome-wide association data and large-scale replication identifies additional susceptibility loci for type 2 diabetes. Nature Genetics, 2008, 40, 638-645.	21.4	1,683
56	A farnesyltransferase inhibitor prevents both the onset and late progression of cardiovascular disease in a progeria mouse model. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 15902-15907.	7.1	181
57	Targeted transgenic expression of the mutation causing Hutchinson-Gilford progeria syndrome leads to proliferative and degenerative epidermal disease. Journal of Cell Science, 2008, 121, 969-978.	2.0	76
58	Variations in the G6PC2/ABCB11 genomic region are associated with fasting glucose levels. Journal of Clinical Investigation, 2008, 118, 2620-8.	8.2	146
59	A lamin A protein isoform overexpressed in Hutchinsonâ€“Gilford progeria syndrome interferes with mitosis in progeria and normal cells. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 4949-4954.	7.1	235
60	Screening of 134 Single Nucleotide Polymorphisms (SNPs) Previously Associated With Type 2 Diabetes Replicates Association With 12 SNPs in Nine Genes. Diabetes, 2007, 56, 256-264.	0.6	109
61	A Genome-Wide Association Study of Type 2 Diabetes in Finns Detects Multiple Susceptibility Variants. Science, 2007, 316, 1341-1345.	12.6	2,534
62	DNase-chip: a high-resolution method to identify DNase I hypersensitive sites using tiled microarrays. Nature Methods, 2006, 3, 503-509.	19.0	222
63	Progressive vascular smooth muscle cell defects in a mouse model of Hutchinson-Gilford progeria syndrome. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 3250-3255.	7.1	255
64	Mutant nuclear lamin A leads to progressive alterations of epigenetic control in premature aging. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 8703-8708.	7.1	685
65	Common Variants in Maturity-Onset Diabetes of the Young Genes Contribute to Risk of Type 2 Diabetes in Finns. Diabetes, 2006, 55, 2534-2540.	0.6	69
66	Association of Transcription Factor 7-Like 2 (TCF7L2) Variants With Type 2 Diabetes in a Finnish Sample. Diabetes, 2006, 55, 2649-2653.	0.6	224
67	Mitochondrial polymorphisms and susceptibility to type 2 diabetes-related traits in Finns. Human Genetics, 2005, 118, 245-254.	3.8	73
68	Inhibiting farnesylation of progerin prevents the characteristic nuclear blebbing of Hutchinson-Gilford progeria syndrome. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 12879-12884.	7.1	334
69	Accumulation of mutant lamin A causes progressive changes in nuclear architecture in Hutchinsonâ€“Gilford progeria syndrome. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 8963-8968.	7.1	988
70	Genetic Variation Near the Hepatocyte Nuclear Factor-4Î± Gene Predicts Susceptibility to Type 2 Diabetes. Diabetes, 2004, 53, 1141-1149.	0.6	255
71	A Large Set of Finnish Affected Sibling Pair Families With Type 2 Diabetes Suggests Susceptibility Loci on Chromosomes 6, 11, and 14. Diabetes, 2004, 53, 821-829.	0.6	73
72	Recurrent de novo point mutations in lamin A cause Hutchinsonâ€“Gilford progeria syndrome. Nature, 2003, 423, 293-298.	27.8	1,925

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73	High-throughput screening for evidence of association by using mass spectrometry genotyping on DNA pools. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 16928-16933.	7.1	117
74	Variation in Three Single Nucleotide Polymorphisms in the Calpain-10 Gene Not Associated With Type 2 Diabetes in a Large Finnish Cohort. Diabetes, 2002, 51, 1644-1648.	0.6	67
75	p300 Modulates the BRCA1 inhibition of estrogen receptor activity. Cancer Research, 2002, 62, 141-51.	0.9	119
76	Role of direct interaction in BRCA1 inhibition of estrogen receptor activity. Oncogene, 2001, 20, 77-87.	5.9	243
77	Disruption of BRCA1 LXCXE motif alters BRCA1 functional activity and regulation of RB family but not RB protein binding. Oncogene, 2001, 20, 4827-4841.	5.9	40
78	Menin Interacts with the AP1 Transcription Factor JunD and Represses JunD-Activated Transcription. Cell, 1999, 96, 143-152.	28.9	569
79	BRCA1 as a potential human prostate tumor suppressor: modulation of proliferation, damage responses and expression of cell regulatory proteins. Oncogene, 1998, 16, 3069-3082.	5.9	95
80	Evolutionary sequence comparisons using high-density oligonucleotide arrays. Nature Genetics, 1998, 18, 155-158.	21.4	95
81	Characterization ofEZH1,a Human Homolog ofDrosophila Enhancer of zestenearBRCA1. Genomics, 1996, 37, 161-171.	2.9	49
82	The murine homolog of the human breast and ovarian cancer susceptibility geneBrca1 maps to mouse chromosome 11D. Human Genetics, 1996, 97, 256-259.	3.8	14
83	Mutations in the BRCA1 gene in families with early-onset breast and ovarian cancer. Nature Genetics, 1994, 8, 387-391.	21.4	384
84	Heterodimerization of the IL-2 receptor Î²- and Î³-chain cytoplasmic domains is required for signalling. Nature, 1994, 369, 330-333.	27.8	320