Eimear E Kenny

List of Publications by Year
in descending order

104	26,852	66343	37204
papers	citations	42	96
		h-index	g-index

129	129	129	44692
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	A global reference for human genetic variation. Nature, 2015, 526, 68-74.	27.8	13,998
2	Evolution and Functional Impact of Rare Coding Variation from Deep Sequencing of Human Exomes. Science, 2012, 337, 64-69.	12.6	1,535
3	Human Demographic History Impacts Genetic Risk Prediction across Diverse Populations. American Journal of Human Genetics, 2017, 100, 635-649.	6.2	1,120
4	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. American Journal of Human Genetics, 2015, 97, 576-592.	6.2	1,098
5	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 2021, 590, 290-299.	27.8	1,069
6	RFMix: A Discriminative Modeling Approach for Rapid and Robust Local-Ancestry Inference. American Journal of Human Genetics, 2013, 93, 278-288.	6.2	686
7	Genetic analyses of diverse populations improves discovery for complex traits. Nature, 2019, 570, 514-518.	27.8	679
8	Textpresso: An Ontology-Based Information Retrieval and Extraction System for Biological Literature. PLoS Biology, 2004, 2, e309.	5.6	504
9	A brief history of human disease genetics. Nature, 2020, 577, 179-189.	27.8	441
10	The genetics of Mexico recapitulates Native American substructure and affects biomedical traits. Science, 2014, 344, 1280-1285.	12.6	420
11	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. Nature, 2020, 586, 763-768.	27.8	376
12	ImmunoChip Study Implicates Antigen Presentation to T Cells in Narcolepsy. PLoS Genetics, 2013, 9, e1003270.	3.5	206
13	Genomeâ€wide association study of schizophrenia in Ashkenazi Jews. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2015, 168, 649-659.	1.7	203
14	Personalized Medicine and the Power of Electronic Health Records. Cell, 2019, 177, 58-69.	28.9	197
15	The Human Pangenome Project: a global resource to map genomic diversity. Nature, 2022, 604, 437-446.	27.8	192
16	Reconstructing Native American Migrations from Whole-Genome and Whole-Exome Data. PLoS Genetics, 2013, 9, e1004023.	3.5	185
17	The Great Migration and African-American Genomic Diversity. PLoS Genetics, 2016, 12, e1006059.	3.5	166
18	Assessing the contribution of rare variants to complex trait heritability from whole-genome sequence data. Nature Genetics, 2022, 54, 263-273.	21.4	156

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19	WormBase: a comprehensive data resource for Caenorhabditis biology and genomics. Nucleic Acids Research, 2004, 33, D383-D389.	14.5	155
20	A Genome-Wide Scan of Ashkenazi Jewish Crohn's Disease Suggests Novel Susceptibility Loci. PLoS Genetics, 2012, 8, e1002559.	3.5	144
21	A continuum of admixture in the Western Hemisphere revealed by the African Diaspora genome. Nature Communications, 2016, 7, 12522.	12.8	136
22	The Clinical Sequencing Evidence-Generating Research Consortium: Integrating Genomic Sequencing in Diverse and Medically Underserved Populations. American Journal of Human Genetics, 2018, 103, 319-327.	6.2	122
23	Common SNPs in HMGCR in Micronesians and Whites Associated With LDL-Cholesterol Levels Affect Alternative Splicing of Exon13. Arteriosclerosis, Thrombosis, and Vascular Biology, 2008, 28, 2078-2084.	2.4	120
24	The genetic architecture of membranous nephropathy and its potential to improve non-invasive diagnosis. Nature Communications, 2020, 11, 1600.	12.8	120
25	WormBase: a cross-species database for comparative genomics. Nucleic Acids Research, 2003, 31, 133-137.	14.5	107
26	Melanesian Blond Hair Is Caused by an Amino Acid Change in TYRP1. Science, 2012, 336, 554-554.	12.6	104
27	Harmonizing Clinical Sequencing and Interpretation for the eMERGE III Network. American Journal of Human Genetics, 2019, 105, 588-605.	6.2	99
28	Multiscale causal networks identify VGF as a key regulator of Alzheimerâ€™s disease. Nature Communications, 2020, 11, 3942.	12.8	94
29	Association of the V122I Hereditary Transthyretin Amyloidosis Genetic Variant With Heart Failure Among Individuals of African or Hispanic/Latino Ancestry. JAMA - Journal of the American Medical Association, 2019, 322, 2191.	7.4	93
30	Getting genetic ancestry right for science and society. Science, 2022, 376, 250-252.	12.6	93
31	Genome-Wide Association Studies in an Isolated Founder Population from the Pacific Island of Kosrae. PLoS Genetics, 2009, 5, e1000365.	3.5	89
32	Toward a fine-scale population health monitoring system. Cell, 2021, 184, 2068-2083.e11.	28.9	78
33	DASH: A Method for Identical-by-Descent Haplotype Mapping Uncovers Association with Recent Variation. American Journal of Human Genetics, 2011, 88, 706-717.	6.2	77
34	Effect of Genetic African Ancestry on eGFR and Kidney Disease. Journal of the American Society of Nephrology: JASN, 2015, 26, 1682-1692.	6.1	75
35	WormBase: better software, richer content. Nucleic Acids Research, 2006, 34, D475-D478.	14.5	74
36	Strategies for Enriching Variant Coverage in Candidate Disease Loci on a Multiethnic Genotyping Array. PLoS ONE, 2016, 11, e0167758.	2.5	72

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37	Association study in African-admixed populations across the Americas recapitulates asthma risk loci in non-African populations. Nature Communications, 2019, 10, 880.	12.8	71
38	Worldwide Frequencies of APOL1 Renal Risk Variants. New England Journal of Medicine, 2018, 379, 2571-2572.	27.0	69
39	A high-resolution HLA reference panel capturing global population diversity enables multi-ancestry fine-mapping in HIV host response. Nature Genetics, 2021, 53, 1504-1516.	21.4	69
40	Exome sequencing reveals a high prevalence of BRCA1 and BRCA2 founder variants in a diverse population-based biobank. Genome Medicine, 2020, 12, 2.	8.2	68
41	Genetic identification of a common collagen disease in Puerto Ricans via identity-by-descent mapping in a health system. ELife, 2017, 6, .	6.0	65
42	Variant Classification Concordance using the ACMG-AMP Variant Interpretation Guidelines across Nine Genomic Implementation Research Studies. American Journal of Human Genetics, 2020, 107, 932-941.	6.2	51
43	Genome-wide mapping of IBD segments in an Ashkenazi PD cohort identifies associated haplotypes. Human Molecular Genetics, 2014, 23, 4693-4702.	2.9	49
44	COVID-19 outcomes and the human genome. Genetics in Medicine, 2020, 22, 1175-1177.	2.4	49
45	Genome-wide polygenic score to predict chronic kidney disease across ancestries. Nature Medicine, 2022, 28, 1412-1420.	30.7	48
46	Apolipoprotein L1 VariantsÂand Blood Pressure Traits inÂAfrican Americans. Journal of the American College of Cardiology, 2017, 69, 1564-1574.	2.8	46
47	Genome-wide association study of primary open-angle glaucoma in continental and admixed African populations. Human Genetics, 2018, 137, 847-862.	3.8	40
48	A multi-stage genome-wide association study of uterine fibroids in African Americans. Human Genetics, 2017, 136, 1363-1373.	3.8	39
49	A positively selected FBN1 missense variant reduces height in Peruvian individuals. Nature, 2020, 582, 234-239.	27.8	39
50	Implementing genomic screening in diverse populations. Genome Medicine, 2021, 13, 17.	8.2	38
51	Genetic diversity in populations across Latin America: implications for population and medical genetic studies. Current Opinion in Genetics and Development, 2018, 53, 98-104.	3.3	37
52	Anticodon Sequence Mutants ofEscherichia coliInitiator tRNA:Â Effects of Overproduction of Aminoacyl-tRNA Synthetases, Methionyl-tRNA Formyltransferase, and Initiation Factor 2 on Activity in Initiationâ€. Biochemistry, 2003, 42, 4787-4799.	2.5	36
53	Mapping the Human Reference Genomeâ€™s Missing Sequence by Three-Way Admixture in Latino Genomes. American Journal of Human Genetics, 2013, 93, 411-421.	6.2	36
54	Imputation-Aware Tag SNP Selection To Improve Power for Large-Scale, Multi-ethnic Association Studies. G3: Genes, Genomes, Genetics, 2018, 8, 3255-3267.	1.8	36

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55	Population structure in Argentina. PLoS ONE, 2018, 13, e0196325.	2.5	36
56	Mendelian randomization supports bidirectional causality between telomere length and clonal hematopoiesis of indeterminate potential. Science Advances, 2022, 8, eabl6579.	10.3	36
57	The Genomic Medicine Integrative Research Framework: A Conceptual Framework for Conducting Genomic Medicine Research. American Journal of Human Genetics, 2019, 104, 1088-1096.	6.2	35
58	A common variant in PNPLA3 is associated with age at diagnosis of NAFLD in patients from a multi-ethnic biobank. Journal of Hepatology, 2020, 72, 1070-1081.	3.7	35
59	An integrative multiomic network model links lipid metabolism to glucose regulation in coronary artery disease. Nature Communications, 2021, 12, 547.	12.8	35
60	The Future of Genomic Studies Must Be Globally Representative: Perspectives from PAGE. Annual Review of Genomics and Human Genetics, 2019, 20, 181-200.	6.2	33
61	A Trans-Ethnic Genome-Wide Association Study of Uterine Fibroids. Frontiers in Genetics, 2019, 10, 511.	2.3	32
62	Prognostic value of polygenic risk scores for adults with psychosis. Nature Medicine, 2021, 27, 1576-1581.	30.7	31
63	GBStools: A Statistical Method for Estimating Allelic Dropout in Reduced Representation Sequencing Data. PLoS Genetics, 2016, 12, e1005631.	3.5	30
64	Genetic determinants of telomere length from 109,122 ancestrally diverse whole-genome sequences in TOPMed. Cell Genomics, 2022, 2, 100084.	6.5	29
65	Identifying tagging SNPs for African specific genetic variation from the African Diaspora Genome. Scientific Reports, 2017, 7, 46398.	3.3	26
66	TOP-LD: A tool to explore linkage disequilibrium with TOPMed whole-genome sequence data. American Journal of Human Genetics, 2022, 109, 1175-1181.	6.2	25
67	Increased power of mixed models facilitates association mapping of 10 loci for metabolic traits in an isolated population. Human Molecular Genetics, 2011, 20, 827-839.	2.9	24
68	Rare coding variants in 35 genes associate with circulating lipid levelsâ€"A multi-ancestry analysis of 170,000 exomes. American Journal of Human Genetics, 2022, 109, 81-96.	6.2	24
69	Systematic haplotype analysis resolves a complex plasma plant sterol locus on the Micronesian Island of Kosrae. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 13886-13891.	7.1	23
70	The NYCKidSeq project: study protocol for a randomized controlled trial incorporating genomics into the clinical care of diverse New York City children. Trials, 2021, 22, 56.	1.6	21
71	Institutional profile: translational pharmacogenomics at the Icahn School of Medicine at Mount Sinai. Pharmacogenomics, 2017, 18, 1381-1386.	1.3	20
72	GUÃA: a digital platform to facilitate result disclosure in genetic counseling. Genetics in Medicine, 2021, 23, 942-949.	2.4	20

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73	Rapid detection of identity-by-descent tracts for mega-scale datasets. Nature Communications, 2021, 12, 3546.	12.8	20
74	Genetic architecture of lipid traits in the Hispanic community health study/study of Latinos. Lipids in Health and Disease, 2017, 16, 200.	3.0	18
75	Copy Number Variant Analysis and Genome-wide Association Study Identify Loci with Large Effect for Vesicoureteral Reflux. Journal of the American Society of Nephrology: JASN, 2021, 32, 805-820.	6.1	17
76	The role of country of birth, and genetic and self-identified ancestry, in obesity susceptibility among African and Hispanic Americans. American Journal of Clinical Nutrition, 2019, 110, 16-23.	4.7	13
77	Hope versus reality: Parent expectations of genomic testing. Patient Education and Counseling, 2021, 104, 2073-2079.	2.2	10
78	Perspectives of diverse Spanish- and English-speaking patients on the clinical use of polygenic risk scores. Genetics in Medicine, 2022, 24, 1217-1226.	2.4	10
79	iGAS: A framework for using electronic intraoperative medical records for genomic discovery. Journal of Biomedical Informatics, 2017, 67, 80-89.	4.3	8
80	Integrative analysis of loss-of-function variants in clinical and genomic data reveals novel genes associated with cardiovascular traits. BMC Medical Genomics, 2019, 12, 108.	1.5	8
81	Genomic Screening Identifies Individuals at High Risk for Hereditary Transthyretin Amyloidosis. Journal of Personalized Medicine, 2021, 11, 49.	2.5	8
82	â€œIs that something that should concern me?â€• a qualitative exploration of parent understanding of their childâ€™s genomic test results. Human Genetics and Genomics Advances, 2021, 2, 100027.	1.7	8
83	Imputation-based assessment of next generation rare exome variant arrays. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2014, , 241-52.	0.7	7
84	IMPUTATION-BASED ASSESSMENT OF NEXT GENERATION RARE EXOME VARIANT ARRAYS. , 2013, , .		6
85	Enrichment analyses identify shared associations for 25 quantitative traits in over 600,000 individuals from seven diverse ancestries. American Journal of Human Genetics, 2022, 109, 871-884.	6.2	6
86	Whole Genome Sequencing Identifies CRISPLD2 as a Lung Function Gene in Children With Asthma. Chest, 2019, 156, 1068-1079.	0.8	5
87	Lynch Syndromeâ€“Associated Variants and Cancer Rates in an Ancestrally Diverse Biobank. JCO Precision Oncology, 2020, 4, 1429-1444.	3.0	5
88	CDH1 pathogenic variants and cancer risk in an unselected patient population. Familial Cancer, 2022, 21, 235-239.	1.9	5
89	Predicted gene expression in ancestrally diverse populations leads to discovery of susceptibility loci for lifestyle and cardiometabolic traits. American Journal of Human Genetics, 2022, 109, 669-679.	6.2	5
90	Multi-Ethnic Genome-Wide Association Study of Decomposed Cardioelectric Phenotypes Illustrates Strategies to Identify and Characterize Evidence of Shared Genetic Effects for Complex Traits. Circulation Genomic and Precision Medicine, 2020, 13, e002680.	3.6	4

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91	Leveraging health systems data to characterize a large effect variant conferring risk for liver disease in Puerto Ricans. American Journal of Human Genetics, 2021, 108, 2099-2111.	6.2	4
92	Boricua Founder Variant in FRRS1L Causes Epileptic Encephalopathy With Hyperkinetic Movements. Journal of Child Neurology, 2021, 36, 93-98.	1.4	3
93	GenomeDiver: a platform for phenotype-guided medical genomic diagnosis. Genetics in Medicine, 2021, 23, 1998-2002.	2.4	3
94	Rare coding variants in RCN3 are associated with blood pressure. BMC Genomics, 2022, 23, 148.	2.8	2
95	eP236: TeleKidSeq: Incorporating telehealth into clinical care of children from diverse backgrounds undergoing clinical genome sequencing. Genetics in Medicine, 2022, 24, S150.	2.4	2
96	Genomewide association studies and lipid risk factors. Current Cardiovascular Risk Reports, 2009, 3, 12-17.	2.0	0
97	SnapShot: Human Biomedical Genomics. Cell, 2011, 147, 248-248.e1.	28.9	0
98	Rapid response to the alpha-1 adrenergic agent phenylephrine in the perioperative period is impacted by genomics and ancestry. Pharmacogenomics Journal, 2021, 21, 174-189.	2.0	0
99	EPS: automated feature selection in caseâ€“control studies using extreme pseudo-sampling. Bioinformatics, 2021, 37, 3372-3373.	4.1	0
100	SUN-032 Exome Sequencing Reveals that Pathogenic RET Variants Occur at Higher Prevalence Than Previously Recognized: Data from a US Health System Biobank. Journal of the Endocrine Society, 2019, 3, .	0.2	0
101	Genetic identification and characterization of Lynch syndrome in a multi-ethnic biobank.. Journal of Clinical Oncology, 2019, 37, 1520-1520.	1.6	0
102	eP113: Prevalence and clinical consequences of genetic variants associated with familial hypercholesterolemia and LDL-C lowering in a diverse patient population. Genetics in Medicine, 2022, 24, S71.	2.4	0
103	eP061: Genetic risk for breast and ovarian cancer in a diverse and unselected population. Genetics in Medicine, 2022, 24, S39-S40.	2.4	0
104	eP067: Diagnostic yield of genome sequencing versus targeted gene panel testing in diverse pediatric patients in the NYCKidSeq study. Genetics in Medicine, 2022, 24, S45.	2.4	0