Cathy C Laurie

List of Publications by Year
in descending order

112 papers	14,411 citations	28274 55 h-index	24258 110 g-index
120 all docs	120 docs citations	120 times ranked	24898 citing authors

#	Article	IF	Citations
1	Genetic determinants of telomere length from 109,122 ancestrally diverse whole-genome sequences in TOPMed. Cell Genomics, 2022, 2, 100084.	6.5	29
2	Assessing the contribution of rare variants to complex trait heritability from whole-genome sequence data. Nature Genetics, 2022, 54, 263-273.	21.4	156
3	Insights From a Large-Scale Whole-Genome Sequencing Study of Systolic Blood Pressure, Diastolic Blood Pressure, and Hypertension. Hypertension, 2022, 79, 1656-1667.	2.7	12
4	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 2021, 590, 290-299.	27.8	1,069
5	Chromosome Xq23 is associated with lower atherogenic lipid concentrations and favorable cardiometabolic indices. Nature Communications, 2021, 12, 2182.	12.8	17
6	A System for Phenotype Harmonization in the National Heart, Lung, and Blood Institute Trans-Omics for Precision Medicine (TOPMed) Program. American Journal of Epidemiology, 2021, 190, 1977-1992.	3.4	29
7	Whole-genome sequencing association analysis of quantitative red blood cell phenotypes: The NHLBI TOPMed program. American Journal of Human Genetics, 2021, 108, 874-893.	6.2	28
8	Genome sequencing unveils a regulatory landscape of platelet reactivity. Nature Communications, 2021, 12, 3626.	12.8	29
9	Variant-specific inflation factors for assessing population stratification at the phenotypic variance level. Nature Communications, 2021, 12, 3506.	12.8	1
10	Whole-genome association analyses of sleep-disordered breathing phenotypes in the NHLBI TOPMed program. Genome Medicine, 2021, 13, 136.	8.2	16
11	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
12	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. Nature, 2020, 586, 763-768.	27.8	376
13	A Genome-wide Association Study Discovers 46 Loci of the Human Metabolome in the Hispanic Community Health Study/Study of Latinos. American Journal of Human Genetics, 2020, 107, 849-863.	6.2	48
14	Genome-wide association study of cognitive function in diverse Hispanics/Latinos: results from the Hispanic Community Health Study/Study of Latinos. Translational Psychiatry, 2020, 10, 245.	4.8	9
15	Dynamic incorporation of multiple in silico functional annotations empowers rare variant association analysis of large whole-genome sequencing studies at scale. Nature Genetics, 2020, 52, 969-983.	21.4	146
16	GWAS of QRS duration identifies new loci specific to Hispanic/Latino populations. PLoS ONE, 2019, 14, e0217796.	2.5	8
17	Variants Associated with the Ankle Brachial Index Differ by Hispanic/Latino Ethnic Group: a genome-wide association study in the Hispanic Community Health Study/Study of Latinos. Scientific Reports, 2019, 9, 11410.	3.3	10
18	Whole Genome Sequencing Identifies CRISPLD2 as a Lung Function Gene in Children With Asthma. Chest, 2019, 156, 1068-1079.	0.8	5

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19	A fully adjusted twoâ€stage procedure for rankâ€normalization in genetic association studies. Genetic Epidemiology, 2019, 43, 263-275.	1.3	60
20	Genetic analyses of diverse populations improves discovery for complex traits. Nature, 2019, 570, 514-518.	27.8	679
21	Associations of variants In the hexokinase 1 and interleukin 18 receptor regions with oxyhemoglobin saturation during sleep. PLoS Genetics, 2019, 15, e1007739.	3.5	28
22	A multi-ancestry genome-wide study incorporating geneâ€“smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. Human Molecular Genetics, 2019, 28, 2615-2633.	2.9	31
23	Multi-ancestry genome-wide geneâ€“smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. Nature Genetics, 2019, 51, 636-648.	21.4	112
24	Associations between SLC16A11 variants and diabetes in the Hispanic Community Health Study/Study of Latinos (HCHS/SOL). Scientific Reports, 2019, 9, 843.	3.3	9
25	Genome-wide association reveals contribution of MRAS to painful temporomandibular disorder in males. Pain, 2019, 160, 579-591.	4.2	37
26	Admixture mapping identifies novel loci for obstructive sleep apnea in Hispanic/Latino Americans. Human Molecular Genetics, 2019, 28, 675-687.	2.9	41
27	Genomic analyses in African populations identify novel risk loci for cleft palate. Human Molecular Genetics, 2019, 28, 1038-1051.	2.9	61
28	Efficient Variant Set Mixed Model Association Tests for Continuous and Binary Traits in Large-Scale Whole-Genome Sequencing Studies. American Journal of Human Genetics, 2019, 104, 260-274.	6.2	103
29	A Genome-Wide Association Study in Hispanics/Latinos Identifies Novel Signals for Lung Function. The Hispanic Community Health Study/Study of Latinos. American Journal of Respiratory and Critical Care Medicine, 2018, 198, 208-219.	5.6	37
30	Genome-Wide Association Study of Heavy Smoking and Daily/Nondaily Smoking in the Hispanic Community Health Study/Study of Latinos (HCHS/SOL). Nicotine and Tobacco Research, 2018, 20, 448-457.	2.6	21
31	Multiethnic Meta-Analysis Identifies RAI1 as a Possible Obstructive Sleep Apneaâ€“related Quantitative Trait Locus in Men. American Journal of Respiratory Cell and Molecular Biology, 2018, 58, 391-401.	2.9	65
32	Complex patterns of direct and indirect association between the transcription Factor-7 like 2 gene, body mass index and type 2 diabetes diagnosis in adulthood in the Hispanic Community Health Study/Study of Latinos. BMC Obesity, 2018, 5, 26.	3.1	6
33	Ancestry-specific recent effective population size in the Americas. PLoS Genetics, 2018, 14, e1007385.	3.5	87
34	Identification of paternal uniparental disomy on chromosome 22 and a de novo deletion on chromosome 18 in individuals with orofacial clefts. Molecular Genetics & Genomic Medicine, 2018, 6, 924-932.	1.2	4
35	Multi-Omics Analysis Reveals a HIF Network and Hub Gene EPAS1 Associated with Lung Adenocarcinoma. EBioMedicine, 2018, 32, 93-101.	6.1	35
36	Common Î±-globin variants modify hematologic and other clinical phenotypes in sickle cell trait and disease. PLoS Genetics, 2018, 14, e1007293.	3.5	45

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37	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. PLoS ONE, 2018, 13, e0198166.	2.5	94
38	Genome-wide association study of familial lung cancer. Carcinogenesis, 2018, 39, 1135-1140.	2.8	42
39	Genomeâ€Wide Association Analysis Reveals Genetic Heterogeneity of SjÃ¶gren's Syndrome According to Ancestry. Arthritis and Rheumatology, 2017, 69, 1294-1305.	5.6	80
40	A powerful statistical framework for generalization testing in GWAS, with application to the HCHS/SOL. Genetic Epidemiology, 2017, 41, 251-258.	1.3	41
41	A genome-wide interaction analysis of tricyclic/tetracyclic antidepressants and RR and QT intervals: a pharmacogenomics study from the Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) consortium. Journal of Medical Genetics, 2017, 54, 313-323.	3.2	9
42	Admixture Mapping Identifies an Amerindian Ancestry Locus Associated with Albuminuria in Hispanics in the United States. Journal of the American Society of Nephrology: JASN, 2017, 28, 2211-2220.	6.1	33
43	Genetics of Type 2 Diabetes in U.S. Hispanic/Latino Individuals: Results From the Hispanic Community Health Study/Study of Latinos (HCHS/SOL). Diabetes, 2017, 66, 1419-1425.	0.6	60
44	A meta-analysis of genome-wide association studies of asthma in PuertoÂRicans. European Respiratory Journal, 2017, 49, 1601505.	6.7	51
45	Genetic loci associated with heart rate variability and their effects on cardiac disease risk. Nature Communications, 2017, 8, 15805.	12.8	95
46	Genome-wide association of white blood cell counts in Hispanic/Latino Americans: the Hispanic Community Health Study/Study of Latinos. Human Molecular Genetics, 2017, 26, 1193-1204.	2.9	38
47	Genome-wide association study of heart rate and its variability in Hispanic/Latino cohorts. Heart Rhythm, 2017, 14, 1675-1684.	0.7	18
48	Genome-wide association study of iron traits and relation to diabetes in the Hispanic Community Health Study/Study of Latinos (HCHS/SOL): potential genomic intersection of iron and glucose regulation?. Human Molecular Genetics, 2017, 26, 1966-1978.	2.9	31
49	Analysis commons, a team approach to discovery in a big-data environment for genetic epidemiology. Nature Genetics, 2017, 49, 1560-1563.	21.4	93
50	African Ancestryâ€“Specific Alleles and Kidney Disease Risk in Hispanics/Latinos. Journal of the American Society of Nephrology: JASN, 2017, 28, 915-922.	6.1	57
51	GWAS of the electrocardiographic QT interval in Hispanics/Latinos generalizes previously identified loci and identifies population-specific signals. Scientific Reports, 2017, 7, 17075.	3.3	23
52	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
53	Single-trait and multi-trait genome-wide association analyses identify novel loci for blood pressure in African-ancestry populations. PLoS Genetics, 2017, 13, e1006728.	3.5	88
54	Genome-wide association study of red blood cell traits in Hispanics/Latinos: The Hispanic Community Health Study/Study of Latinos. PLoS Genetics, 2017, 13, e1006760.	3.5	53

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55	Genome-Wide Association Study Reveals Multiple Loci Influencing Normal Human Facial Morphology. PLoS Genetics, 2016, 12, e1006149.	3.5	140
56	Metaâ€Analysis of Genomeâ€Wide Association Studies with Correlated Individuals: Application to the Hispanic Community Health Study/Study of Latinos (HCHS/SOL). Genetic Epidemiology, 2016, 40, 492-501.	1.3	16
57	Local Ancestry Inference in a Large US-Based Hispanic/Latino Study: Hispanic Community Health Study/Study of Latinos (HCHS/SOL). G3: Genes, Genomes, Genetics, 2016, 6, 1525-1534.	1.8	51
58	Control for Population Structure and Relatedness for Binary Traits in Genetic Association Studies via Logistic Mixed Models. American Journal of Human Genetics, 2016, 98, 653-666.	6.2	347
59	A multi-ethnic genome-wide association study identifies novel loci for non-syndromic cleft lip with or without cleft palate on 2p24.2, 17q23 and 19q13. Human Molecular Genetics, 2016, 25, ddw104.	2.9	163
60	Trans-ethnic Fine Mapping Highlights Kidney-Function Genes Linked to Salt Sensitivity. American Journal of Human Genetics, 2016, 99, 636-646.	6.2	67
61	Genetic variation near <scp>IRS</scp>1 is associated with adiposity and a favorable metabolic profile in <scp>U</scp>.<scp>S.</scp><scp>H</scp>ispanics/<scp>L</scp>atinos. Obesity, 2016, 24, 2407-2413.	3.0	5
62	Genome-wide association of familial prostate cancer cases identifies evidence for a rare segregating haplotype at 8q24.21. Human Genetics, 2016, 135, 923-938.	3.8	37
63	Improved imputation accuracy in Hispanic/Latino populations with larger and more diverse reference panels: applications in the Hispanic Community Health Study/Study of Latinos (HCHS/SOL). Human Molecular Genetics, 2016, 25, 3245-3254.	2.9	23
64	Genome-Wide Association Analysis of Young-Onset Stroke Identifies a Locus on Chromosome 10q25 Near HABP2. Stroke, 2016, 47, 307-316.	2.0	54
65	Loci associated with ischaemic stroke and its subtypes (SiGN): a genome-wide association study. Lancet Neurology, The, 2016, 15, 174-184.	10.2	217
66	Genetic Associations with Obstructive Sleep Apnea Traits in Hispanic/Latino Americans. American Journal of Respiratory and Critical Care Medicine, 2016, 194, 886-897.	5.6	107
67	A Genome-wide Association Study of Nonsyndromic Cleft Palate Identifies an Etiologic Missense Variant in GRHL3. American Journal of Human Genetics, 2016, 98, 744-754.	6.2	146
68	Genome-wide association study of dental caries in the Hispanic Communities Health Study/Study of Latinos (HCHS/SOL). Human Molecular Genetics, 2016, 25, 807-816.	2.9	29
69	Genome-wide Association Study of Platelet Count Identifies Ancestry-Specific Loci in Hispanic/Latino Americans. American Journal of Human Genetics, 2016, 98, 229-242.	6.2	71
70	Genetic Diversity and Association Studies in US Hispanic/Latino Populations: Applications in the Hispanic Community Health Study/Study of Latinos. American Journal of Human Genetics, 2016, 98, 165-184.	6.2	266
71	Characterization of Large Structural Genetic Mosaicism in Human Autosomes. American Journal of Human Genetics, 2015, 96, 487-497.	6.2	101
72	Genetic Associations with Plasma B12, B6, and Folate Levels in an Ischemic Stroke Population from the Vitamin Intervention for Stroke Prevention (VISP) Trial. Frontiers in Public Health, 2014, 2, 112.	2.7	23

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73	Using previously genotyped controls in genome-wide association studies (GWAS): application to the Stroke Genetics Network (SiGN). Frontiers in Genetics, 2014, 5, 95.	2.3	30
74	Acquired chromosomal anomalies in chronic lymphocytic leukemia patients compared with more than 50,000 quasi-normal participants. Cancer Genetics, 2014, 207, 19-30.	0.4	5
75	Stroke Genetics Network (SiGN) Study. Stroke, 2013, 44, 2694-2702.	2.0	62
76	The chromosome 3q25 genomic region is associated with measures of adiposity in newborns in a multi-ethnic genome-wide association study. Human Molecular Genetics, 2013, 22, 3583-3596.	2.9	35
77	Linkage analysis identifies a locus for plasma von Willebrand factor undetected by genome-wide association. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 588-593.	7.1	85
78	Genome-Wide Association Study Identifies Novel Loci Associated With Concentrations of Four Plasma Phospholipid Fatty Acids in the De Novo Lipogenesis Pathway. Circulation: Cardiovascular Genetics, 2013, 6, 171-183.	5.1	91
79	Common Variants at 9p21 and 8q22 Are Associated with Increased Susceptibility to Optic Nerve Degeneration in Glaucoma. PLoS Genetics, 2012, 8, e1002654.	3.5	276
80	Genome-Wide Joint Meta-Analysis of SNP and SNP-by-Smoking Interaction Identifies Novel Loci for Pulmonary Function. PLoS Genetics, 2012, 8, e1003098.	3.5	130
81	A high-performance computing toolset for relatedness and principal component analysis of SNP data. Bioinformatics, 2012, 28, 3326-3328.	4.1	1,939
82	GWASTools: an R/Bioconductor package for quality control and analysis of genome-wide association studies. Bioinformatics, 2012, 28, 3329-3331.	4.1	177
83	Evaluating Genetic Risk for Prostate Cancer among Japanese and Latinos. Cancer Epidemiology Biomarkers and Prevention, 2012, 21, 2048-2058.	2.5	51
84	Is â€˜forwardâ€™ the same as â€˜plusâ€™?â€¦ and other adventures in SNP allele nomenclature. Trends in Genetics, 2012, 28, 361-363.	6.7	21
85	Detectable clonal mosaicism from birth to old age and its relationship to cancer. Nature Genetics, 2012, 44, 642-650.	21.4	511
86	Using Family Data as a Verification Standard to Evaluate Copy Number Variation Calling Strategies for Genetic Association Studies. Genetic Epidemiology, 2012, 36, 253-262.	1.3	19
87	<scp>CHRNB</scp>3 is more strongly associated with <scp>F</scp>agerstrÃ¶m <scp>T</scp>est for <scp>C</scp>igarette <scp>D</scp>ependenceâ€based nicotine dependence than cigarettes per day: phenotype definition changes genomeâ€wide association studies results. Addiction, 2012, 107, 2019-2028.	3.3	67
88	Clonal Chromosomal Anomalies Similar to CLL and Other Hematologic Malignancies Can Be Found in â€œNormalâ€•Individuals. Blood, 2012, 120, 873-873.	1.4	0
89	Genome-wide association study identifies novel loci predisposing to cutaneous melanomaâ€. Human Molecular Genetics, 2011, 20, 5012-5023.	2.9	187
90	Common variants near CAV1 and CAV2 are associated with primary open-angle glaucoma in Caucasians from the USA. Human Molecular Genetics, 2011, 20, 4707-4713.	2.9	156

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91	Genetic Loci Associated with Plasma Phospholipid n-3 Fatty Acids: A Meta-Analysis of Genome-Wide Association Studies from the CHARGE Consortium. PLoS Genetics, 2011, 7, e1002193.	3.5	324
92	The gene, environment association studies consortium (GENEVA): maximizing the knowledge obtained from GWAS by collaboration across studies of multiple conditions. Genetic Epidemiology, 2010, 34, 364-372.	1.3	139
93	Quality control and quality assurance in genotypic data for genomeâ€wide association studies. Genetic Epidemiology, 2010, 34, 591-602.	1.3	389
94	Genetic variants in ABO blood group region, plasma soluble E-selectin levels and risk of type 2 diabetes. Human Molecular Genetics, 2010, 19, 1856-1862.	2.9	165
95	Genome-Wide Association Study Identifies Variants at the IL18 -BCO2 Locus Associated With Interleukin-18 Levels. Arteriosclerosis, Thrombosis, and Vascular Biology, 2010, 30, 885-890.	2.4	74
96	Genome-wide association study identifies polymorphisms in LEPR as determinants of plasma soluble leptin receptor levels. Human Molecular Genetics, 2010, 19, 1846-1855.	2.9	74
97	Genetic variants at 2q24 are associated with susceptibility to type 2 diabetes. Human Molecular Genetics, 2010, 19, 2706-2715.	2.9	178
98	A genome-wide association study of alcohol dependence. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 5082-5087.	7.1	418
99	A Genome-wide Association Study of Lung Cancer Identifies a Region of Chromosome 5p15 Associated with Risk for Adenocarcinoma. American Journal of Human Genetics, 2009, 85, 679-691.	6.2	489
100	Linkage Disequilibrium in Wild Mice. PLoS Genetics, 2007, 3, e144.	3.5	108
101	Integrating QTL and high-density SNP analyses in mice to identify Insig2 as a susceptibility gene for plasma cholesterol levels. Genomics, 2005, 86, 505-517.	2.9	132
102	The Genetic Architecture of Response to Long-Term Artificial Selection for Oil Concentration in the Maize Kernel. Genetics, 2004, 168, 2141-2155.	2.9	245
103	Genetic Dissection of Hybrid Incompatibilities Between Drosophila simulans and D. mauritiana. I. Differential Accumulation of Hybrid Male Sterility Effects on the X and Autosomes. Genetics, 2003, 164, 1383-1398.	2.9	131
104	Genetic Dissection of Hybrid Incompatibilities Between Drosophila simulans and D. mauritiana. II. Mapping Hybrid Male Sterility Loci on the Third Chromosome. Genetics, 2003, 164, 1399-1418.	2.9	76
105	Genetic Architecture of a Morphological Shape Difference Between Two Drosophila Species. Genetics, 2000, 154, 299-310.	2.9	180
106	An Introgression Analysis of Quantitative Trait Loci That Contribute to a Morphological Difference Between Drosophila simulans and D. mauritiana. Genetics, 1997, 145, 339-348.	2.9	72
107	The Weaker Sex Is Heterogametic: 75 Years of H<scp>aldane</scp>'s Rule. Genetics, 1997, 147, 937-951.	2.9	180
108	Differences in Crossover Frequency and Distribution Among Three Sibling Species of Drosophila. Genetics, 1996, 142, 507-523.	2.9	225

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109	A Genome-Wide Survey of Hybrid Incompatibility Factors by the Introgression of Marked Segments of Drosophila mauritiana Chromosomes into Drosophila simulans. Genetics, 1996, 142, 819-837.	2.9	270
110	Genetic Analysis of a Morphological Shape Difference in the Male Genitalia of Drosophila simulans and D. mauritiana. Genetics, 1996, 142, 1129-1145.	2.9	209
111	Molecular Dissection of a Major Gene Effect on a Quantitative Trait: The Level of Alcohol Dehydrogenase Expression in Drosophila melanogaster. Genetics, 1996, 144, 1559-1564.	2.9	140
112	The Relationship Between Dipeptidase Activity Variation and Larval Viability in Drosophila melanogaster. Genetics, 1987, 117, 503-512.	2.9	6