

Lorraine Southam

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6007007/publications.pdf>

Version: 2024-02-01

44
papers

7,654
citations

147801

31
h-index

223800

46
g-index

55
all docs

55
docs citations

55
times ranked

15001
citing authors

#	ARTICLE	IF	CITATIONS
1	Mutations in the hepatocyte nuclear factor-1 β gene in maturity-onset diabetes of the young (MODY3). Nature, 1996, 384, 455-458.	27.8	1,240
2	The UK10K project identifies rare variants in health and disease. Nature, 2015, 526, 82-90.	27.8	1,014
3	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	27.8	544
4	Exome-wide association study of plasma lipids in >300,000 individuals. Nature Genetics, 2017, 49, 1758-1766.	21.4	470
5	Identification of new susceptibility loci for osteoarthritis (arcOGEN): a genome-wide association study. Lancet, The, 2012, 380, 815-823.	13.7	373
6	The trans-ancestral genomic architecture of glyceic traits. Nature Genetics, 2021, 53, 840-860.	21.4	341
7	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. PLoS Genetics, 2015, 11, e1005378.	3.5	331
8	Identification of new therapeutic targets for osteoarthritis through genome-wide analyses of UK Biobank data. Nature Genetics, 2019, 51, 230-236.	21.4	331
9	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. Nature Genetics, 2018, 50, 26-41.	21.4	286
10	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. Nature Genetics, 2016, 48, 1151-1161.	21.4	261
11	Genome-wide analyses using UK Biobank data provide insights into the genetic architecture of osteoarthritis. Nature Genetics, 2018, 50, 549-558.	21.4	223
12	Deciphering osteoarthritis genetics across 826,690 individuals from 9 populations. Cell, 2021, 184, 4784-4818.e17.	28.9	188
13	An SNP in the 5'UTR of GDF5 is associated with osteoarthritis susceptibility in Europeans and with in vivo differences in allelic expression in articular cartilage. Human Molecular Genetics, 2007, 16, 2226-2232.	2.9	180
14	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. Nature Communications, 2015, 6, 5897.	12.8	173
15	Directional dominance on stature and cognition in diverse human populations. Nature, 2015, 523, 459-462.	27.8	173
16	Whole-Genome Sequencing Coupled to Imputation Discovers Genetic Signals for Anthropometric Traits. American Journal of Human Genetics, 2017, 100, 865-884.	6.2	131
17	A meta-analysis of genome-wide association studies identifies novel variants associated with osteoarthritis of the hip. Annals of the Rheumatic Diseases, 2014, 73, 2130-2136.	0.9	108
18	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	21.4	89

#	ARTICLE	IF	CITATIONS
19	Whole genome sequencing and imputation in isolated populations identify genetic associations with medically-relevant complex traits. <i>Nature Communications</i> , 2017, 8, 15606.	12.8	79
20	A rare functional cardioprotective APOC3 variant has risen in frequency in distinct population isolates. <i>Nature Communications</i> , 2013, 4, 2872.	12.8	77
21	The transferability of lipid loci across African, Asian and European cohorts. <i>Nature Communications</i> , 2019, 10, 4330.	12.8	75
22	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. <i>Nature Communications</i> , 2016, 7, 13357.	12.8	74
23	GWAS of bone size yields twelve loci that also affect height, BMD, osteoarthritis or fractures. <i>Nature Communications</i> , 2019, 10, 2054.	12.8	74
24	Very low-depth whole-genome sequencing in complex trait association studies. <i>Bioinformatics</i> , 2019, 35, 2555-2561.	4.1	68
25	A Genome-wide Association Study of Dupuytren Disease Reveals 17 Additional Variants Implicated in Fibrosis. <i>American Journal of Human Genetics</i> , 2017, 101, 417-427.	6.2	67
26	Discovery and refinement of genetic loci associated with cardiometabolic risk using dense imputation maps. <i>Nature Genetics</i> , 2016, 48, 1303-1312.	21.4	66
27	Enrichment of low-frequency functional variants revealed by whole-genome sequencing of multiple isolated European populations. <i>Nature Communications</i> , 2017, 8, 15927.	12.8	64
28	A rare variant in APOC3 is associated with plasma triglyceride and VLDL levels in Europeans. <i>Nature Communications</i> , 2014, 5, 4871.	12.8	62
29	Genetic characterization of Greek population isolates reveals strong genetic drift at missense and trait-associated variants. <i>Nature Communications</i> , 2014, 5, 5345.	12.8	60
30	A molecular quantitative trait locus map for osteoarthritis. <i>Nature Communications</i> , 2021, 12, 1309.	12.8	53
31	New Blood Pressure-associated Loci Identified in Meta-Analyses of 475,000 Individuals. <i>Circulation: Cardiovascular Genetics</i> , 2017, 10, .	5.1	48
32	Pathways to understanding the genomic aetiology of osteoarthritis. <i>Human Molecular Genetics</i> , 2017, 26, R193-R201.	2.9	38
33	Whole-genome sequencing analysis of the cardiometabolic proteome. <i>Nature Communications</i> , 2020, 11, 6336.	12.8	38
34	Cohort-wide deep whole genome sequencing and the allelic architecture of complex traits. <i>Nature Communications</i> , 2018, 9, 4674.	12.8	33
35	Accelerating functional gene discovery in osteoarthritis. <i>Nature Communications</i> , 2021, 12, 467.	12.8	33
36	Radiographic endophenotyping in hip osteoarthritis improves the precision of genetic association analysis. <i>Annals of the Rheumatic Diseases</i> , 2017, 76, 1199-1206.	0.9	29

#	ARTICLE	IF	CITATIONS
37	Genome-wide association of phenotypes based on clustering patterns of hand osteoarthritis identify <i>WNT9A</i> as novel osteoarthritis gene. <i>Annals of the Rheumatic Diseases</i> , 2021, 80, 367-375.	0.9	26
38	Linking chondrocyte and synovial transcriptional profile to clinical phenotype in osteoarthritis. <i>Annals of the Rheumatic Diseases</i> , 2021, 80, 1070-1074.	0.9	25
39	Very low-depth sequencing in a founder population identifies a cardioprotective <i>APOC3</i> signal missed by genome-wide imputation. <i>Human Molecular Genetics</i> , 2016, 25, 2360-2365.	2.9	21
40	Using multivariable Mendelian randomization to estimate the causal effect of bone mineral density on osteoarthritis risk, independently of body mass index. <i>International Journal of Epidemiology</i> , 2022, 51, 1254-1267.	1.9	20
41	An epigenome-wide view of osteoarthritis in primary tissues. <i>American Journal of Human Genetics</i> , 2022, 109, 1255-1271.	6.2	13
42	The 2018 Otto Aufranc Award: How Does Genome-wide Variation Affect Osteolysis Risk After THA?. <i>Clinical Orthopaedics and Related Research</i> , 2019, 477, 297-309.	1.5	8
43	Combination therapy as a potential risk factor for the development of type 2 diabetes in patients with schizophrenia: the GOMAP study. <i>BMC Psychiatry</i> , 2018, 18, 249.	2.6	5
44	Insights into the genetic architecture of haematological traits from deep phenotyping and whole-genome sequencing for two Mediterranean isolated populations. <i>Scientific Reports</i> , 2022, 12, 1131.	3.3	2