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	Insights into the genetic architecture of haematological traits from deep phenotyping and whole-genome sequencing for two Mediterranean isolated populations. Scientific Reports, 2022, 12, 1131.	3.3	2
2	Using multivariable Mendelian randomization to estimate the causal effect of bone mineral density on osteoarthritis risk, independently of body mass index. International Journal of Epidemiology, 2022, 51, 1254-1267.	1.9	20
3	An epigenome-wide view of osteoarthritis in primary tissues. American Journal of Human Genetics, 2022, 109, 1255-1271.	6.2	13
4	Genome-wide association of phenotypes based on clustering patterns of hand osteoarthritis identifyWNT9Aas novel osteoarthritis gene. Annals of the Rheumatic Diseases, 2021, 80, 367-375.	0.9	26
5	A molecular quantitative trait locus map for osteoarthritis. Nature Communications, 2021, 12, 1309.	12.8	53
6	Linking chondrocyte and synovial transcriptional profile to clinical phenotype in osteoarthritis. Annals of the Rheumatic Diseases, 2021, 80, 1070-1074.	0.9	25
7	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	21.4	341
8	Deciphering osteoarthritis genetics across 826,690 individuals from 9 populations. Cell, 2021, 184, 4784-4818.e17.	28.9	188
9	Accelerating functional gene discovery in osteoarthritis. Nature Communications, 2021, 12, 467.	12.8	33
10	Whole-genome sequencing analysis of the cardiometabolic proteome. Nature Communications, 2020, 11, 6336.	12.8	38
11	The transferability of lipid loci across African, Asian and European cohorts. Nature Communications, 2019, 10, 4330.	12.8	75
12	Identification of new therapeutic targets for osteoarthritis through genome-wide analyses of UK Biobank data. Nature Genetics, 2019, 51, 230-236.	21.4	331
13	GWAS of bone size yields twelve loci that also affect height, BMD, osteoarthritis or fractures. Nature Communications, 2019, 10, 2054.	12.8	74
14	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	21.4	89
15	The 2018 Otto Aufranc Award: How Does Genome-wide Variation Affect Osteolysis Risk After THA?. Clinical Orthopaedics and Related Research, 2019, 477, 297-309.	1.5	8
16	Very low-depth whole-genome sequencing in complex trait association studies. Bioinformatics, 2019, 35, 2555-2561.	4.1	68
17	Genome-wide analyses using UK Biobank data provide insights into the genetic architecture of osteoarthritis. Nature Genetics, 2018, 50, 549-558.	21.4	223
18	Cohort-wide deep whole genome sequencing and the allelic architecture of complex traits. Nature Communications, 2018, 9, 4674.	12.8	33

#	Article	IF	Citations
19	Combination therapy as a potential risk factor for the development of type 2 diabetes in patients with schizophrenia: the GOMAP study. BMC Psychiatry, 2018, 18, 249.	2.6	5
20	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
21	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	27.8	544
22	Radiographic endophenotyping in hip osteoarthritis improves the precision of genetic association analysis. Annals of the Rheumatic Diseases, 2017, 76, 1199-1206.	0.9	29
23	Whole genome sequencing and imputation in isolated populations identify genetic associations with medically-relevant complex traits. Nature Communications, 2017, 8, 15606.	12.8	79
24	Whole-Genome Sequencing Coupled to Imputation Discovers Genetic Signals for Anthropometric Traits. American Journal of Human Genetics, 2017, 100, 865-884.	6.2	131
25	Exome-wide association study of plasma lipids in >300,000 individuals. Nature Genetics, 2017, 49, 1758-1766.	21.4	470
26	New Blood Pressureâ€“Associated Loci Identified in Meta-Analyses of 475â€‰000 Individuals. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	48
27	A Genome-wide Association Study of Dupuytren Disease Reveals 17 Additional Variants Implicated in Fibrosis. American Journal of Human Genetics, 2017, 101, 417-427.	6.2	67
28	Enrichment of low-frequency functional variants revealed by whole-genome sequencing of multiple isolated European populations. Nature Communications, 2017, 8, 15927.	12.8	64
29	Pathways to understanding the genomic aetiology of osteoarthritis. Human Molecular Genetics, 2017, 26, R193-R201.	2.9	38
30	Discovery and refinement of genetic loci associated with cardiometabolic risk using dense imputation maps. Nature Genetics, 2016, 48, 1303-1312.	21.4	66
31	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. Nature Communications, 2016, 7, 13357.	12.8	74
32	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. Nature Genetics, 2016, 48, 1151-1161.	21.4	261
33	Very low-depth sequencing in a founder population identifies a cardioprotectiveAPOC3signal missed by genome-wide imputation. Human Molecular Genetics, 2016, 25, 2360-2365.	2.9	21
34	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
35	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. Nature Communications, 2015, 6, 5897.	12.8	173
36	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	27.8	173

#	Article	IF	Citations
37	The UK10K project identifies rare variants in health and disease. Nature, 2015, 526, 82-90.	27.8	1,014
38	Genetic characterization of Greek population isolates reveals strong genetic drift at missense and trait-associated variants. Nature Communications, 2014, 5, 5345.	12.8	60
39	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
40	A rare variant in APOC3 is associated with plasma triglyceride and VLDL levels in Europeans. Nature Communications, 2014, 5, 4871.	12.8	62
41	A rare functional cardioprotective APOC3 variant has risen in frequency in distinct population isolates. Nature Communications, 2013, 4, 2872.	12.8	77
42	Identification of new susceptibility loci for osteoarthritis (arcOGEN): a genome-wide association study. Lancet, The, 2012, 380, 815-823.	13.7	373
43	An SNP in the 5â€²-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
44	Mutations in the hepatocyte nuclear factor-1Î± gene in maturity-onset diabetes of the young (MODY3). Nature, 1996, 384, 455-458.	27.8	1,240