

George Nicholson

List of Publications by Year in descending order

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Version: 2024-02-01

28
papers

8,919
citations

304368

22
h-index

454577

30
g-index

32
all docs

32
docs citations

32
times ranked

17549
citing authors

#	ARTICLE	IF	CITATIONS
1	The COVID-19 Pandemic Is Associated with Reduced Survival after Pancreatic Ductal Adenocarcinoma Diagnosis: A Single-Centre Retrospective Analysis. <i>Journal of Clinical Medicine</i> , 2022, 11, 2574.	1.0	6
2	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. <i>Nature Communications</i> , 2021, 12, 24.	5.8	87
3	Tumour-infiltrating CD8+ lymphocytes and colorectal cancer recurrence by tumour and nodal stage. <i>British Journal of Cancer</i> , 2019, 121, 474-482.	2.9	41
4	Transcript Analysis Reveals a Hypoxic Inflammatory Environment in Human Chronic Otitis Media With Effusion. <i>Frontiers in Genetics</i> , 2019, 10, 1327.	1.1	12
5	Reproducibility of Molecular Phenotypes after Long-Term Differentiation to Human iPSC-Derived Neurons: A Multi-Site Omics Study. <i>Stem Cell Reports</i> , 2018, 11, 897-911.	2.3	135
6	Reproducibility and replicability of rodent phenotyping in preclinical studies. <i>Neuroscience and Biobehavioral Reviews</i> , 2018, 87, 218-232.	2.9	153
7	Tumour-infiltrating CD8+ lymphocytes as a prognostic marker in colorectal cancer: A retrospective, pooled analysis of the QUASAR2 and VICTOR trials. <i>Journal of Clinical Oncology</i> , 2018, 36, 3515-3515.	0.8	4
8	A note on statistical repeatability and study design for high-throughput assays. <i>Statistics in Medicine</i> , 2017, 36, 790-798.	0.8	9
9	Genome-to-genome analysis highlights the effect of the human innate and adaptive immune systems on the hepatitis C virus. <i>Nature Genetics</i> , 2017, 49, 666-673.	9.4	129
10	Variability of genome-wide DNA methylation and mRNA expression profiles in reproductive and endocrine disease related tissues. <i>Epigenetics</i> , 2017, 12, 897-908.	1.3	33
11	The <i>goya</i> mutation identifies distinct novel roles for MAP3K1 in cochlear sensory hair cell development and survival. <i>DMM Disease Models and Mechanisms</i> , 2015, 8, 1555-68.	1.2	12
12	New genetic loci link adipose and insulin biology to body fat distribution. <i>Nature</i> , 2015, 518, 187-196.	13.7	1,328
13	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015, 518, 197-206.	13.7	3,823
14	Analysis of mammalian gene function through broad-based phenotypic screens across a consortium of mouse clinics. <i>Nature Genetics</i> , 2015, 47, 969-978.	9.4	137
15	Distinct Developmental Profile of Lower-Body Adipose Tissue Defines Resistance Against Obesity-Associated Metabolic Complications. <i>Diabetes</i> , 2014, 63, 3785-3797.	0.3	148
16	Meta-analysis of Gene-Level Associations for Rare Variants Based on Single-Variant Statistics. <i>American Journal of Human Genetics</i> , 2013, 93, 236-248.	2.6	60
17	A comparative phenotypic and genomic analysis of C57BL/6J and C57BL/6N mouse strains. <i>Genome Biology</i> , 2013, 14, R82.	13.9	403
18	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. <i>Nature Genetics</i> , 2013, 45, 501-512.	9.4	578

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19	Sex-stratified Genome-wide Association Studies Including 270,000 Individuals Show Sexual Dimorphism in Genetic Loci for Anthropometric Traits. <i>PLoS Genetics</i> , 2013, 9, e1003500.	1.5	371
20	The Presence of Methylation Quantitative Trait Loci Indicates a Direct Genetic Influence on the Level of DNA Methylation in Adipose Tissue. <i>PLoS ONE</i> , 2013, 8, e55923.	1.1	83
21	Coexpression Network Analysis in Abdominal and Gluteal Adipose Tissue Reveals Regulatory Genetic Loci for Metabolic Syndrome and Related Phenotypes. <i>PLoS Genetics</i> , 2012, 8, e1002505.	1.5	57
22	Functional Inactivation of the Genome-Wide Association Study Obesity Gene Neuronal Growth Regulator 1 in Mice Causes a Body Mass Phenotype. <i>PLoS ONE</i> , 2012, 7, e41537.	1.1	66
23	MicroRNA Expression in Abdominal and Gluteal Adipose Tissue Is Associated with mRNA Expression Levels and Partly Genetically Driven. <i>PLoS ONE</i> , 2011, 6, e27338.	1.1	46
24	Variance decomposition of protein profiles from antibody arrays using a longitudinal twin model. <i>Proteome Science</i> , 2011, 9, 73.	0.7	19
25	Human metabolic profiles are stably controlled by genetic and environmental variation. <i>Molecular Systems Biology</i> , 2011, 7, 525.	3.2	158
26	A Genome-Wide Metabolic QTL Analysis in Europeans Implicates Two Loci Shaped by Recent Positive Selection. <i>PLoS Genetics</i> , 2011, 7, e1002270.	1.5	132
27	Meta-analysis identifies 13 new loci associated with waist-hip ratio and reveals sexual dimorphism in the genetic basis of fat distribution. <i>Nature Genetics</i> , 2010, 42, 949-960.	9.4	836
28	Microsatellite Mutations and Inferences About Human Demography. <i>Genetics</i> , 2000, 154, 1793-1807.	1.2	39