Gabriel Cuellar-Partida

List of Publications by Year
in descending order

55 papers	5,014 citations	186265 28 h-index	149698 56 g-index
76 all docs	76 docs citations	76 times ranked	11192 citing authors

#	Article	IF	Citations
1	Genomics-driven screening for causal determinants of suicide attempt. Australian and New Zealand Journal of Psychiatry, 2023, 57, 423-431.	2.3	3
2	Shared Genetic Etiology between Cortical Brain Morphology and Tobacco, Alcohol, and Cannabis Use. Cerebral Cortex, 2022, 32, 796-807.	2.9	9
3	Phenome-wide screening of the putative causal determinants of depression using genetic data. Human Molecular Genetics, 2022, 31, 2887-2898.	2.9	4
4	DNA methylation in peripheral tissues and left-handedness. Scientific Reports, 2022, 12, 5606.	3.3	12
5	Assessment and visualization of phenome-wide causal relationships using genetic data: an application to dental caries and periodontitis. European Journal of Human Genetics, 2021, 29, 300-308.	2.8	23
6	Genome-wide association study identifies 48 common genetic variants associated with handedness. Nature Human Behaviour, 2021, 5, 59-70.	12.0	79
7	Inference of causal relationships between sleep-related traits and 1,527 phenotypes using genetic data. Sleep, 2021, 44, .	1.1	16
8	Genetic basis to structural grey matter associations with chronic pain. Brain, 2021, 144, 3611-3622.	7.6	10
9	Evidence of Genetic Overlap Between Circadian Preference and Brain White Matter Microstructure. Twin Research and Human Genetics, 2021, 24, 1-6.	0.6	2
10	Abstract PR003: Multi-tissue transcriptome-wide association study identifies genetic mechanisms underlying endometrial cancer susceptibility. , 2021, , .		0
11	Utilising multi-large omics data to elucidate biological mechanisms within multiple sclerosis genetic susceptibility loci. Multiple Sclerosis Journal, 2021, 27, 2141-2149.	3.0	3
12	Comorbid Chronic Pain and Depression: Shared Risk Factors and Differential Antidepressant Effectiveness. Frontiers in Psychiatry, 2021, 12, 643609.	2.6	55
13	Phenome-wide screening of GWAS data reveals the complex causal architecture of obesity. Human Genetics, 2021, 140, 1253-1265.	3.8	11
14	The relationship between adrenocortical candidate gene expression and clinical response to hydrocortisone in patients with septic shock. Intensive Care Medicine, 2021, 47, 974-983.	8.2	12
15	Genetic Susceptibility to Pneumonia: A GWAS Meta-Analysis Between the UK Biobank and FinnGen. Twin Research and Human Genetics, 2021, 24, 145-154.	0.6	10
16	Phenome-wide analysis highlights putative causal relationships between self-reported migraine and other complex traits. Journal of Headache and Pain, 2021, 22, 66.	6.0	12
17	The Genetic Architecture of Depression in Individuals of East Asian Ancestry. JAMA Psychiatry, 2021, 78, 1258.	11.0	88
18	Therapeutic Inhibition of Acid-Sensing Ion Channel 1a Recovers Heart Function After Ischemiaâ€“Reperfusion Injury. Circulation, 2021, 144, 947-960.	1.6	40

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19	Multi-tissue transcriptome-wide association study identifies eight candidate genes and tissue-specific gene expression underlying endometrial cancer susceptibility. Communications Biology, 2021, 4, 1211.	4.4	11
20	Large-scale genetic investigation reveals genetic liability to multiple complex traits influencing a higher risk of ADHD. Scientific Reports, 2021, 11, 22628.	3.3	8
21	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	27.8	353
22	Identification of susceptibility variants to benign childhood epilepsy with centro-temporal spikes (BECTS) in Chinese Han population. EBioMedicine, 2020, 57, 102840.	6.1	8
23	Educational attainment polygenic scores are associated with cortical total surface area and regions important for language and memory. NeuroImage, 2020, 212, 116691.	4.2	29
24	Insights into the aetiology of snoring from observational and genetic investigations in the UK Biobank. Nature Communications, 2020, 11, 817.	12.8	74
25	Estimating indirect parental genetic effects on offspring phenotypes using virtual parental genotypes derived from sibling and half sibling pairs. PLoS Genetics, 2020, 16, e1009154.	3.5	22
26	New insight into human sweet taste: a genome-wide association study of the perception and intake of sweet substances. American Journal of Clinical Nutrition, 2019, 109, 1724-1737.	4.7	53
27	Genetic architecture of subcortical brain structures in 38,851 individuals. Nature Genetics, 2019, 51, 1624-1636.	21.4	192
28	Partitioning Phenotypic Variance Due to Parent-of-Origin Effects Using Genomic Relatedness Matrices. Behavior Genetics, 2018, 48, 67-79.	2.1	7
29	Assessment of moderate coffee consumption and risk of epithelial ovarian cancer: a Mendelian randomization study. International Journal of Epidemiology, 2018, 47, 450-459.	1.9	15
30	Genome-wide association meta-analysis highlights light-induced signaling as a driver for refractive error. Nature Genetics, 2018, 50, 834-848.	21.4	239
31	Cross-ancestry genome-wide association analysis of corneal thickness strengthens link between complex and Mendelian eye diseases. Nature Communications, 2018, 9, 1864.	12.8	63
32	Genome-wide survey of parent-of-origin effects on DNA methylation identifies candidate imprinted loci in humans. Human Molecular Genetics, 2018, 27, 2927-2939.	2.9	22
33	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
34	Novel genetic loci associated with hippocampal volume. Nature Communications, 2017, 8, 13624.	12.8	250
35	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	27.8	544
36	New insights into the genetics of primary open-angle glaucoma based on meta-analyses of intraocular pressure and optic disc characteristics.. Human Molecular Genetics, 2017, 26, ddw399.	2.9	120

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37	Genetically low vitamin D concentrations and myopic refractive error: a Mendelian randomization study. International Journal of Epidemiology, 2017, 46, 1882-1890.	1.9	47
38	Assessing the genetic architecture of epithelial ovarian cancer histological subtypes. Human Genetics, 2016, 135, 741-756.	3.8	19
39	Association of vitamin D levels and risk of ovarian cancer: a Mendelian randomization study. International Journal of Epidemiology, 2016, 45, 1619-1630.	1.9	111
40	Novel genetic loci underlying human intracranial volume identified through genome-wide association. Nature Neuroscience, 2016, 19, 1569-1582.	14.8	213
41	Sweet Taste Perception is Associated with Body Mass Index at the Phenotypic and Genotypic Level. Twin Research and Human Genetics, 2016, 19, 465-471.	0.6	13
42	Assessing the Genetic Predisposition of Education on Myopia: A Mendelian Randomization Study. Genetic Epidemiology, 2016, 40, 66-72.	1.3	56
43	Assessment of polygenic effects links primary open-angle glaucoma and age-related macular degeneration. Scientific Reports, 2016, 6, 26885.	3.3	21
44	Genetic influences on schizophrenia and subcortical brain volumes: large-scale proof of concept. Nature Neuroscience, 2016, 19, 420-431.	14.8	204
45	Genetic and Environmental Factors in Conjunctival UV Autofluorescence. JAMA Ophthalmology, 2015, 133, 406.	2.5	30
46	ARHGEF12 influences the risk of glaucoma by increasing intraocular pressure. Human Molecular Genetics, 2015, 24, 2689-2699.	2.9	79
47	Common genetic variants influence human subcortical brain structures. Nature, 2015, 520, 224-229.	27.8	772
48	Genetics and Brain Morphology. Neuropsychology Review, 2015, 25, 63-96.	4.9	49
49	LocusTrack: Integrated visualization of GWAS results and genomic annotation. Source Code for Biology and Medicine, 2015, 10, 1.	1.7	31
50	Identification of myopia-associated WNT7B polymorphisms provides insights into the mechanism underlying the development of myopia. Nature Communications, 2015, 6, 6689.	12.8	70
51	Shared genetics underlying epidemiological association between endometriosis and ovarian cancer. Human Molecular Genetics, 2015, 24, 5955-5964.	2.9	68
52	WNT10A exonic variant increases the risk of keratoconus by decreasing corneal thickness. Human Molecular Genetics, 2015, 24, 5060-5068.	2.9	58
53	Genome-wide analysis of multi-ancestry cohorts identifies new loci influencing intraocular pressure and susceptibility to glaucoma. Nature Genetics, 2014, 46, 1126-1130.	21.4	212
54	Epigenetic priors for identifying active transcription factor binding sites. Bioinformatics, 2012, 28, 56-62.	4.1	103

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55	Genome-wide in silico prediction of gene expression. Bioinformatics, 2012, 28, 2789-2796.	4.1	50