Juan L Rodriguez-Flores

List of Publications by Year
in descending order

42 papers	23,314 citations	279487 23 h-index	264894 42 g-index
47 all docs	47 docs citations	47 times ranked	47367 citing authors

#	Article	IF	Citations
1	A global reference for human genetic variation. Nature, 2015, 526, 68-74.	13.7	13,998
2	An integrated map of genetic variation from 1,092 human genomes. Nature, 2012, 491, 56-65.	13.7	7,199
3	Integrative Annotation of Variants from 1092 Humans: Application to Cancer Genomics. Science, 2013, 342, 1235587.	6.0	341
4	Punctuated bursts in human male demography inferred from 1,244 worldwide Y-chromosome sequences. Nature Genetics, 2016, 48, 593-599.	9.4	273
5	Reconstructing Native American Migrations from Whole-Genome and Whole-Exome Data. PLoS Genetics, 2013, 9, e1004023.	1.5	185
6	RNA-Seq quantification of the human small airway epithelium transcriptome. BMC Genomics, 2012, 13, 82.	1.2	107
7	Point-of-care whole-exome sequencing of idiopathic male infertility. Genetics in Medicine, 2018, 20, 1365-1373.	1.1	105
8	The Qatar genome: a population-specific tool for precision medicine in the Middle East. Human Genome Variation, 2016, 3, 16016.	0.4	103
9	Tyrosine Hydroxylase, the Rate-Limiting Enzyme in Catecholamine Biosynthesis. Circulation, 2007, 116, 993-1006.	1.6	89
10	Indigenous Arabs are descendants of the earliest split from ancient Eurasian populations. Genome Research, 2016, 26, 151-162.	2.4	89
11	Discovery of common human genetic variants of GTP cyclohydrolase 1 (GCH1) governing nitric oxide, autonomic activity, and cardiovascular risk. Journal of Clinical Investigation, 2007, 117, 2658-2671.	3.9	87
12	Cathepsin L Colocalizes with Chromogranin A in Chromaffin Vesicles to Generate Active Peptides. Endocrinology, 2009, 150, 3547-3557.	1.4	67
13	Whole-exome sequencing identifies common and rare variant metabolic QTLs in a Middle Eastern population. Nature Communications, 2018, 9, 333.	5.8	63
14	Inferring genome-wide patterns of admixture in Qataris using fifty-five ancestral populations. BMC Genetics, 2012, 13, 49.	2.7	55
15	Human dopamine beta-hydroxylase (DBH) regulatory polymorphism that influences enzymatic activity, autonomic function, and blood pressure. Journal of Hypertension, 2010, 28, 76-86.	0.3	48
16	Naturally Occurring Human Genetic Variation in the 3â€²-Untranslated Region of the Secretory Protein Chromogranin A Is Associated With Autonomic Blood Pressure Regulation and Hypertension in a Sex-Dependent Fashion. Journal of the American College of Cardiology, 2008, 52, 1468-1481.	1.2	44
17	Exome Sequencing Identifies Potential Risk Variants for Mendelian Disorders at High Prevalence in Qatar. Human Mutation, 2014, 35, 105-116.	1.1	43
18	Pro-hormone Secretogranin II Regulates Dense Core Secretory Granule Biogenesis in Catecholaminergic Cells. Journal of Biological Chemistry, 2010, 285, 10030-10043.	1.6	38

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19	Type 2 Diabetes Risk Allele Loci in the Qatari Population. PLoS ONE, 2016, 11, e0156834.	1.1	30
20	Neuropeptide Y1Receptor NPY1R. Journal of the American College of Cardiology, 2009, 54, 944-954.	1.2	28
21	Human Tyrosine Hydroxylase Natural Genetic Variation. Circulation: Cardiovascular Genetics, 2010, 3, 187-198.	5.1	28
22	Common genetic variants in the chromogranin A promoter alter autonomic activity and blood pressure. Kidney International, 2008, 74, 115-125.	2.6	27
23	Autonomic Function in Hypertension. Circulation: Cardiovascular Genetics, 2009, 2, 46-56.	5.1	26
24	Rare Synaptogenesis-Impairing Mutations in SLITRK5 Are Associated with Obsessive Compulsive Disorder. PLoS ONE, 2017, 12, e0169994.	1.1	25
25	Large-scale Identification of Clonal Hematopoiesis and Mutations Recurrent in Blood Cancers. Blood Cancer Discovery, 2021, 2, 226-237.	2.6	22
26	Human Dopamine Â-Hydroxylase Promoter Variant Alters Transcription in Chromaffin Cells, Enzyme Secretion, and Blood Pressure. American Journal of Hypertension, 2011, 24, 24-32.	1.0	21
27	Common Functional Genetic Variants in Catecholamine Storage Vesicle Protein Promoter Motifs Interact to Trigger Systemic Hypertension. Journal of the American College of Cardiology, 2010, 55, 1463-1475.	1.2	20
28	Adrenergic Polymorphism and the Human Stress Response. Annals of the New York Academy of Sciences, 2008, 1148, 282-296.	1.8	18
29	Thousands of Qatari genomes inform human migration history and improve imputation of Arab haplotypes. Nature Communications, 2021, 12, 5929.	5.8	18
30	Human Tyrosine Hydroxylase Natural Allelic Variation: Influence on Autonomic Function and Hypertension. Cellular and Molecular Neurobiology, 2010, 30, 1391-1394.	1.7	16
31	Exome Sequencing of Only Seven Qataris Identifies Potentially Deleterious Variants in the Qatari Population. PLoS ONE, 2012, 7, e47614.	1.1	16
32	Prevalence of the Apolipoprotein E Arg145Cys Dyslipidemia At-Risk Polymorphism in African-Derived Populations. American Journal of Cardiology, 2014, 113, 302-308.	0.7	13
33	Copy number variations in the genome of the Qatari population. BMC Genomics, 2015, 16, 834.	1.2	9
34	Genome diversity in Ukraine. GigaScience, 2021, 10, .	3.3	9
35	Genomes of Three Closely Related Caribbean Amazons Provide Insight for Species History and Conservation. Genes, 2019, 10, 54.	1.0	8
36	Whole-methylome analysis of circulating monocytes in acute diabetic Charcot foot reveals differentially methylated genes involved in the formation of osteoclasts. Epigenomics, 2019, 11, 281-296.	1.0	8

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37	Exome sequencing-based identification of novel type 2 diabetes risk allele loci in the Qatari population. PLoS ONE, 2018, 13, e0199837.	1.1	7
38	Conserved regulatory motifs at phenylethanolamine N-methyltransferase (PNMT) are disrupted by common functional genetic variation: an integrated computational/experimental approach. Mammalian Genome, 2010, 21, 195-204.	1.0	6
39	Mitochondrial haplogroup J associated with higher risk of obesity in the Qatari population. Scientific Reports, 2021, 11, 1091.	1.6	5
40	The QChip1 knowledgebase and microarray for precision medicine in Qatar. Npj Genomic Medicine, 2022, 7, 3.	1.7	4
41	Genetic Evaluation of Male Infertility. , 2020, , 95-118.		2
42	Qatari Genotype May Contribute to Complications in Type 2 Diabetes. Journal of Diabetes Research, 2020, 2020, 1-6.	1.0	1