

# Juan L Rodriguez-Flores

## List of Publications by Year in descending order

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Version: 2024-02-01

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	The QChip1 knowledgebase and microarray for precision medicine in Qatar. <i>Npj Genomic Medicine</i> , 2022, 7, 3.	1.7	4
2	Genome diversity in Ukraine. <i>GigaScience</i> , 2021, 10, .	3.3	9
3	Mitochondrial haplogroup J associated with higher risk of obesity in the Qatari population. <i>Scientific Reports</i> , 2021, 11, 1091.	1.6	5
4	Large-scale Identification of Clonal Hematopoiesis and Mutations Recurrent in Blood Cancers. <i>Blood Cancer Discovery</i> , 2021, 2, 226-237.	2.6	22
5	Thousands of Qatari genomes inform human migration history and improve imputation of Arab haplotypes. <i>Nature Communications</i> , 2021, 12, 5929.	5.8	18
6	Qatari Genotype May Contribute to Complications in Type 2 Diabetes. <i>Journal of Diabetes Research</i> , 2020, 2020, 1-6.	1.0	1
7	Genetic Evaluation of Male Infertility. , 2020, , 95-118.		2
8	Genomes of Three Closely Related Caribbean Amazons Provide Insight for Species History and Conservation. <i>Genes</i> , 2019, 10, 54.	1.0	8
9	Whole-methylome analysis of circulating monocytes in acute diabetic Charcot foot reveals differentially methylated genes involved in the formation of osteoclasts. <i>Epigenomics</i> , 2019, 11, 281-296.	1.0	8
10	Point-of-care whole-exome sequencing of idiopathic male infertility. <i>Genetics in Medicine</i> , 2018, 20, 1365-1373.	1.1	105
11	Whole-exome sequencing identifies common and rare variant metabolic QTLs in a Middle Eastern population. <i>Nature Communications</i> , 2018, 9, 333.	5.8	63
12	Exome sequencing-based identification of novel type 2 diabetes risk allele loci in the Qatari population. <i>PLoS ONE</i> , 2018, 13, e0199837.	1.1	7
13	Rare Synaptogenesis-Impairing Mutations in SLITRK5 Are Associated with Obsessive Compulsive Disorder. <i>PLoS ONE</i> , 2017, 12, e0169994.	1.1	25
14	Punctuated bursts in human male demography inferred from 1,244 worldwide Y-chromosome sequences. <i>Nature Genetics</i> , 2016, 48, 593-599.	9.4	273
15	The Qatar genome: a population-specific tool for precision medicine in the Middle East. <i>Human Genome Variation</i> , 2016, 3, 16016.	0.4	103
16	Indigenous Arabs are descendants of the earliest split from ancient Eurasian populations. <i>Genome Research</i> , 2016, 26, 151-162.	2.4	89
17	Type 2 Diabetes Risk Allele Loci in the Qatari Population. <i>PLoS ONE</i> , 2016, 11, e0156834.	1.1	30
18	Copy number variations in the genome of the Qatari population. <i>BMC Genomics</i> , 2015, 16, 834.	1.2	9

#	ARTICLE	IF	CITATIONS
19	A global reference for human genetic variation. <i>Nature</i> , 2015, 526, 68-74.	13.7	13,998
20	Exome Sequencing Identifies Potential Risk Variants for Mendelian Disorders at High Prevalence in Qatar. <i>Human Mutation</i> , 2014, 35, 105-116.	1.1	43
21	Prevalence of the Apolipoprotein E Arg145Cys Dyslipidemia At-Risk Polymorphism in African-Derived Populations. <i>American Journal of Cardiology</i> , 2014, 113, 302-308.	0.7	13
22	Integrative Annotation of Variants from 1092 Humans: Application to Cancer Genomics. <i>Science</i> , 2013, 342, 1235587.	6.0	341
23	Reconstructing Native American Migrations from Whole-Genome and Whole-Exome Data. <i>PLoS Genetics</i> , 2013, 9, e1004023.	1.5	185
24	Inferring genome-wide patterns of admixture in Qataris using fifty-five ancestral populations. <i>BMC Genetics</i> , 2012, 13, 49.	2.7	55
25	An integrated map of genetic variation from 1,092 human genomes. <i>Nature</i> , 2012, 491, 56-65.	13.7	7,199
26	Exome Sequencing of Only Seven Qataris Identifies Potentially Deleterious Variants in the Qatari Population. <i>PLoS ONE</i> , 2012, 7, e47614.	1.1	16
27	RNA-Seq quantification of the human small airway epithelium transcriptome. <i>BMC Genomics</i> , 2012, 13, 82.	1.2	107
28	Human Dopamine $\alpha$ -Hydroxylase Promoter Variant Alters Transcription in Chromaffin Cells, Enzyme Secretion, and Blood Pressure. <i>American Journal of Hypertension</i> , 2011, 24, 24-32.	1.0	21
29	Human dopamine beta-hydroxylase (DBH) regulatory polymorphism that influences enzymatic activity, autonomic function, and blood pressure. <i>Journal of Hypertension</i> , 2010, 28, 76-86.	0.3	48
30	Conserved regulatory motifs at phenylethanolamine N-methyltransferase (PNMT) are disrupted by common functional genetic variation: an integrated computational/experimental approach. <i>Mammalian Genome</i> , 2010, 21, 195-204.	1.0	6
31	Human Tyrosine Hydroxylase Natural Allelic Variation: Influence on Autonomic Function and Hypertension. <i>Cellular and Molecular Neurobiology</i> , 2010, 30, 1391-1394.	1.7	16
32	Human Tyrosine Hydroxylase Natural Genetic Variation. <i>Circulation: Cardiovascular Genetics</i> , 2010, 3, 187-198.	5.1	28
33	Pro-hormone Secretogranin II Regulates Dense Core Secretory Granule Biogenesis in Catecholaminergic Cells. <i>Journal of Biological Chemistry</i> , 2010, 285, 10030-10043.	1.6	38
34	Common Functional Genetic Variants in Catecholamine Storage Vesicle Protein Promoter Motifs Interact to Trigger Systemic Hypertension. <i>Journal of the American College of Cardiology</i> , 2010, 55, 1463-1475.	1.2	20
35	Autonomic Function in Hypertension. <i>Circulation: Cardiovascular Genetics</i> , 2009, 2, 46-56.	5.1	26
36	Cathepsin L Colocalizes with Chromogranin A in Chromaffin Vesicles to Generate Active Peptides. <i>Endocrinology</i> , 2009, 150, 3547-3557.	1.4	67

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37	Neuropeptide Y1 Receptor NPY1R. Journal of the American College of Cardiology, 2009, 54, 944-954.	1.2	28
38	Adrenergic Polymorphism and the Human Stress Response. Annals of the New York Academy of Sciences, 2008, 1148, 282-296.	1.8	18
39	Naturally Occurring Human Genetic Variation in the 3' 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
40	Common genetic variants in the chromogranin A promoter alter autonomic activity and blood pressure. Kidney International, 2008, 74, 115-125.	2.6	27
41	Tyrosine Hydroxylase, the Rate-Limiting Enzyme in Catecholamine Biosynthesis. Circulation, 2007, 116, 993-1006.	1.6	89
42	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