

Oscar FranzÃ©n

List of Publications by Year in descending order

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Version: 2024-02-01

38
papers

3,607
citations

304743

22
h-index

315739

38
g-index

41
all docs

41
docs citations

41
times ranked

7480
citing authors

#	ARTICLE	IF	CITATIONS
1	PanglaoDB: a web server for exploration of mouse and human single-cell RNA sequencing data. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	3.0	762
2	Assembly and diploid architecture of an individual human genome via single-molecule technologies. Nature Methods, 2015, 12, 780-786.	19.0	465
3	Cardiometabolic risk loci share downstream cis- and trans-gene regulation across tissues and diseases. Science, 2016, 353, 827-830.	12.6	241
4	Draft Genome Sequencing of Giardia intestinalis Assemblage B Isolate GS: Is Human Giardiasis Caused by Two Different Species?. PLoS Pathogens, 2009, 5, e1000560.	4.7	236
5	Systematic Evaluation of Pleiotropy Identifies 6 Further Loci Associated WithÂCoronary ArteryÂDisease. Journal of the American College of Cardiology, 2017, 69, 823-836.	2.8	214
6	Meta-Analysis of Genome-Wide Association Studies for Abdominal Aortic Aneurysm Identifies Four New Disease-Specific Risk Loci. Circulation Research, 2017, 120, 341-353.	4.5	166
7	Shotgun Sequencing Analysis of Trypanosoma cruzi I Sylvio X10/1 and Comparison with T. cruzi VI CL Brener. PLoS Neglected Tropical Diseases, 2011, 5, e984.	3.0	129
8	Genome analysis and comparative genomics of a Giardia intestinalis assemblage E isolate. BMC Genomics, 2010, 11, 543.	2.8	125
9	Integrative functional genomics identifies regulatory mechanisms at coronary artery disease loci. Nature Communications, 2016, 7, 12092.	12.8	123
10	Cross-Tissue Regulatory Gene Networks in Coronary Artery Disease. Cell Systems, 2016, 2, 196-208.	6.2	120
11	Multiple Mitochondrial Introgression Events and Heteroplasmy in Trypanosoma cruzi Revealed by Maxicircle MLST and Next Generation Sequencing. PLoS Neglected Tropical Diseases, 2012, 6, e1584.	3.0	104
12	Large-Scale Identification of Common Trait and Disease Variants Affecting Gene Expression. American Journal of Human Genetics, 2017, 100, 885-894.	6.2	91
13	Improved OTU-picking using long-read 16S rRNA gene amplicon sequencing and generic hierarchical clustering. Microbiome, 2015, 3, 43.	11.1	77
14	Comparative genomic analysis of human infective Trypanosoma cruzi lineages with the bat-restricted subspecies T. cruzi marinkellei. BMC Genomics, 2012, 13, 531.	2.8	57
15	Transcriptome Profiling of Giardia intestinalis Using Strand-specific RNA-Seq. PLoS Computational Biology, 2013, 9, e1003000.	3.2	56
16	Comparative genomic analyses of freshly isolated Giardia intestinalis assemblage A isolates. BMC Genomics, 2015, 16, 697.	2.8	55
17	A mechanistic framework for cardiometabolic and coronary artery diseases. , 2022, 1, 85-100.		51
18	Plasmidome-Analysis of ESBL-Producing Escherichia coli Using Conventional Typing and High-Throughput Sequencing. PLoS ONE, 2013, 8, e65793.	2.5	44

#	ARTICLE	IF	CITATIONS
19	Network analysis of coronary artery disease risk genes elucidates disease mechanisms and druggable targets. <i>Scientific Reports</i> , 2018, 8, 3434.	3.3	43
20	A novel high-resolution multilocus sequence typing of <i>Giardia intestinalis</i> Assemblage A isolates reveals zoonotic transmission, clonal outbreaks and recombination. <i>Infection, Genetics and Evolution</i> , 2018, 60, 7-16.	2.3	42
21	An integrative multiomic network model links lipid metabolism to glucose regulation in coronary artery disease. <i>Nature Communications</i> , 2021, 12, 547.	12.8	35
22	The Short Non-Coding Transcriptome of the Protozoan Parasite <i>Trypanosoma cruzi</i> . <i>PLoS Neglected Tropical Diseases</i> , 2011, 5, e1283.	3.0	35
23	alona: a web server for single-cell RNA-seq analysis. <i>Bioinformatics</i> , 2020, 36, 3910-3912.	4.1	33
24	Single-cell analysis of mosquito hemocytes identifies signatures of immune cell subtypes and cell differentiation. <i>ELife</i> , 2021, 10, .	6.0	31
25	Functional regulatory mechanism of smooth muscle cell-restricted LMOD1 coronary artery disease locus. <i>PLoS Genetics</i> , 2018, 14, e1007755.	3.5	30
26	Transcription Factor MAFF (MAF Basic Leucine Zipper Transcription Factor F) Regulates an Atherosclerosis Relevant Network Connecting Inflammation and Cholesterol Metabolism. <i>Circulation</i> , 2021, 143, 1809-1823.	1.6	28
27	CD90 Identifies Adventitial Mesenchymal Progenitor Cells in Adult Human Medium- and Large-Sized Arteries. <i>Stem Cell Reports</i> , 2018, 11, 242-257.	4.8	26
28	Complex Polymorphisms in the <i>Plasmodium falciparum</i> Multidrug Resistance Protein 2 Gene and Its Contribution to Antimalarial Response. <i>Antimicrobial Agents and Chemotherapy</i> , 2014, 58, 7390-7397.	3.2	25
29	Regulation of PfEMP1â€™VAR2CSA translation by a <i>Plasmodium</i> translation-enhancing factor. <i>Nature Microbiology</i> , 2017, 2, 17068.	13.3	25
30	Poliovirus Receptorâ€™Related 2. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2017, 37, 534-542.	2.4	23
31	A particular set of small non-coding RNAs is bound to the distinctive Argonaute protein of <i>Trypanosoma cruzi</i> : Insights from RNA-interference deficient organisms. <i>Gene</i> , 2014, 538, 379-384.	2.2	21
32	Global analysis of A-to-I RNA editing reveals association with common disease variants. <i>PeerJ</i> , 2018, 6, e4466.	2.0	21
33	Preservation Analysis of Macrophage Gene Coexpression Between Human and Mouse Identifies PARK2 as a Genetically Controlled Master Regulator of Oxidative Phosphorylation in Humans. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 3361-3371.	1.8	15
34	EnsembleCNV: an ensemble machine learning algorithm to identify and genotype copy number variation using SNP array data. <i>Nucleic Acids Research</i> , 2019, 47, e39-e39.	14.5	15
35	<i>Cis</i>-epistasis at the <i>LPA</i> locus and risk of cardiovascular diseases. <i>Cardiovascular Research</i> , 2022, 118, 1088-1102.	3.8	14
36	Integrative Prioritization of Causal Genes for Coronary Artery Disease. <i>Circulation Genomic and Precision Medicine</i> , 2022, 15, CIRCGEN121003365.	3.6	11

#	ARTICLE	IF	CITATIONS
37	Integrative analysis of loss-of-function variants in clinical and genomic data reveals novel genes associated with cardiovascular traits. <i>BMC Medical Genomics</i> , 2019, 12, 108.	1.5	8
38	Characterization of Evolutionarily Conserved <i>Trypanosoma cruzi</i> NatC and NatA-N-Terminal Acetyltransferase Complexes. <i>Journal of Parasitology Research</i> , 2019, 2019, 1-11.	1.2	3