

Oscar FranzÃ©n

List of Publications by Year in descending order

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38
papers

3,607
citations

304743

22
h-index

315739

38
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41
all docs

41
docs citations

41
times ranked

7480
citing authors

#	ARTICLE	IF	CITATIONS
1	<i>Cis</i>-epistasis at the <i>LPA</i> locus and risk of cardiovascular diseases. Cardiovascular Research, 2022, 118, 1088-1102.	3.8	14
2	A mechanistic framework for cardiometabolic and coronary artery diseases. , 2022, 1, 85-100.		51
3	Integrative Prioritization of Causal Genes for Coronary Artery Disease. Circulation Genomic and Precision Medicine, 2022, 15, CIRCGEN121003365.	3.6	11
4	An integrative multiomic network model links lipid metabolism to glucose regulation in coronary artery disease. Nature Communications, 2021, 12, 547.	12.8	35
5	Transcription Factor MAFF (MAF Basic Leucine Zipper Transcription Factor F) Regulates an Atherosclerosis Relevant Network Connecting Inflammation and Cholesterol Metabolism. Circulation, 2021, 143, 1809-1823.	1.6	28
6	Single-cell analysis of mosquito hemocytes identifies signatures of immune cell subtypes and cell differentiation. ELife, 2021, 10, .	6.0	31
7	alona: a web server for single-cell RNA-seq analysis. Bioinformatics, 2020, 36, 3910-3912.	4.1	33
8	Integrative analysis of loss-of-function variants in clinical and genomic data reveals novel genes associated with cardiovascular traits. BMC Medical Genomics, 2019, 12, 108.	1.5	8
9	Characterization of Evolutionarily Conserved <i>Trypanosoma cruzi</i> NatC and NatA-N-Terminal Acetyltransferase Complexes. Journal of Parasitology Research, 2019, 2019, 1-11.	1.2	3
10	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
11	EnsembleCNV: an ensemble machine learning algorithm to identify and genotype copy number variation using SNP array data. Nucleic Acids Research, 2019, 47, e39-e39.	14.5	15
12	Network analysis of coronary artery disease risk genes elucidates disease mechanisms and druggable targets. Scientific Reports, 2018, 8, 3434.	3.3	43
13	A novel high-resolution multilocus sequence typing of Giardia intestinalis Assemblage A isolates reveals zoonotic transmission, clonal outbreaks and recombination. Infection, Genetics and Evolution, 2018, 60, 7-16.	2.3	42
14	Functional regulatory mechanism of smooth muscle cell-restricted LMOD1 coronary artery disease locus. PLoS Genetics, 2018, 14, e1007755.	3.5	30
15	CD90 Identifies Adventitial Mesenchymal Progenitor Cells in Adult Human Medium- and Large-Sized Arteries. Stem Cell Reports, 2018, 11, 242-257.	4.8	26
16	Global analysis of A-to-I RNA editing reveals association with common disease variants. PeerJ, 2018, 6, e4466.	2.0	21
17	Poliovirus Receptor-Related 2. Arteriosclerosis, Thrombosis, and Vascular Biology, 2017, 37, 534-542.	2.4	23
18	Systematic Evaluation of Pleiotropy Identifies 6 Further Loci Associated With Coronary Artery Disease. Journal of the American College of Cardiology, 2017, 69, 823-836.	2.8	214

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19	Regulation of PfEMP1â€™VAR2CSA translation by a Plasmodium translation-enhancing factor. <i>Nature Microbiology</i> , 2017, 2, 17068.	13.3	25
20	Meta-Analysis of Genome-Wide Association Studies for Abdominal Aortic Aneurysm Identifies Four New Disease-Specific Risk Loci. <i>Circulation Research</i> , 2017, 120, 341-353.	4.5	166
21	Large-Scale Identification of Common Trait and Disease Variants Affecting Gene Expression. <i>American Journal of Human Genetics</i> , 2017, 100, 885-894.	6.2	91
22	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
23	Cardiometabolic risk loci share downstream cis- and trans-gene regulation across tissues and diseases. <i>Science</i> , 2016, 353, 827-830.	12.6	241
24	Integrative functional genomics identifies regulatory mechanisms at coronary artery disease loci. <i>Nature Communications</i> , 2016, 7, 12092.	12.8	123
25	Cross-Tissue Regulatory Gene Networks in Coronary Artery Disease. <i>Cell Systems</i> , 2016, 2, 196-208.	6.2	120
26	Comparative genomic analyses of freshly isolated <i>Giardia intestinalis</i> assemblage A isolates. <i>BMC Genomics</i> , 2015, 16, 697.	2.8	55
27	Assembly and diploid architecture of an individual human genome via single-molecule technologies. <i>Nature Methods</i> , 2015, 12, 780-786.	19.0	465
28	Improved OTU-picking using long-read 16S rRNA gene amplicon sequencing and generic hierarchical clustering. <i>Microbiome</i> , 2015, 3, 43.	11.1	77
29	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
30	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
31	Transcriptome Profiling of <i>Giardia intestinalis</i> Using Strand-specific RNA-Seq. <i>PLoS Computational Biology</i> , 2013, 9, e1003000.	3.2	56
32	Plasmidome-Analysis of ESBL-Producing <i>Escherichia coli</i> Using Conventional Typing and High-Throughput Sequencing. <i>PLoS ONE</i> , 2013, 8, e65793.	2.5	44
33	Multiple Mitochondrial Introgression Events and Heteroplasmy in <i>Trypanosoma cruzi</i> Revealed by Maxicircle MLST and Next Generation Sequencing. <i>PLoS Neglected Tropical Diseases</i> , 2012, 6, e1584.	3.0	104
34	Comparative genomic analysis of human infective <i>Trypanosoma cruzi</i> lineages with the bat-restricted subspecies <i>T. cruzi marinkellei</i> . <i>BMC Genomics</i> , 2012, 13, 531.	2.8	57
35	Shotgun Sequencing Analysis of <i>Trypanosoma cruzi</i> I Sylvio X10/1 and Comparison with <i>T. cruzi</i> VI CL Brener. <i>PLoS Neglected Tropical Diseases</i> , 2011, 5, e984.	3.0	129
36	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

#	ARTICLE	IF	CITATIONS
37	Genome analysis and comparative genomics of a Giardia intestinalis assemblage E isolate. BMC Genomics, 2010, 11, 543.	2.8	125
38	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