Julie G Hussin

List of Publications by Year in Descending Order

29 papers	927 citations	15 h-index	30 g-index
46 ext. papers	1,155 ext. citations	10.8 avg, IF	3.25 L-index

#	Paper	IF	Citations
29	Population Genomics Approaches for Genetic Characterization of SARS-CoV-2 Lineages.. *Frontiers in Medicine*, **2022**, 9, 826746	4.9	1
28	deepSimDEF: deep neural embeddings of gene products and Gene Ontology terms for functional analysis of genes.. *Bioinformatics*, **2022**,	7.2	1
27	The mutational landscape of SARS-CoV-2 variants diversifies T cell targets in an HLA-supertype-dependent manner. *Cell Systems*, **2021**,	10.6	6
26	Long-Chain Acylcarnitines and Monounsaturated Fatty Acids Discriminate Heart Failure Patients According to Pulmonary Hypertension Status. *Metabolites*, **2021**, 11,	5.6	1
25	Genetics of symptom remission in outpatients with COVID-19. *Scientific Reports*, **2021**, 11, 10847	4.9	1
24	Genomic epidemiology and associated clinical outcomes of a SARS-CoV-2 outbreak in a general adult hospital in Quebec **2021**,		1
23	Differential modulation of polyunsaturated fatty acids in patients with myocardial infarction treated with ticagrelor or clopidogrel. *Cell Reports Medicine*, **2021**, 2, 100299	18	
22	Polygenic risk scores predict diabetes complications and their response to intensive blood pressure and glucose control. *Diabetologia*, **2021**, 64, 2012-2025	10.3	6
21	SARS-CoV-2 Receptor ACE2 Gene Is Associated with Hypertension and Severity of COVID 19: Interaction with Sex, Obesity, and Smoking. *American Journal of Hypertension*, **2021**, 34, 367-376	2.3	16
20	Implementing Machine Learning in Interventional Cardiology: The Benefits Are Worth the Trouble.. *Frontiers in Cardiovascular Medicine*, **2021**, 8, 711401	5.4	3
19	Insights into Platypus Population Structure and History from Whole-Genome Sequencing. *Molecular Biology and Evolution*, **2018**, 35, 1238-1252	8.3	15
18	The impact of recombination on human mutation load and disease. *Philosophical Transactions of the Royal Society B: Biological Sciences*, **2017**, 372,	5.8	16
17	Re-engineering the zinc fingers of PRDM9 reverses hybrid sterility in mice. *Nature*, **2016**, 530, 171-176	50.4	135
16	Multicohort analysis of the maternal age effect on recombination. *Nature Communications*, **2015**, 6, 7846	17.4	21
15	Recombination affects accumulation of damaging and disease-associated mutations in human populations. *Nature Genetics*, **2015**, 47, 400-4	36.3	63
14	Rare allelic forms of PRDM9 associated with childhood leukemogenesis. *Genome Research*, **2013**, 23, 419-30	9.7	37
13	Whole-exome sequencing reveals a rapid change in the frequency of rare functional variants in a founding population of humans. *PLoS Genetics*, **2013**, 9, e1003815	6	52

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12	Next-generation sequencing approaches for genetic mapping of complex diseases. *Journal of Neuroimmunology*, **2012**, 248, 10-22	3.5	15
11	Rare copy number variants contribute to congenital left-sided heart disease. *PLoS Genetics*, **2012**, 8, e1002903	6	102
10	A family-based probabilistic method for capturing de novo mutations from high-throughput short-read sequencing data. *Statistical Applications in Genetics and Molecular Biology*, **2012**, 11,	1.2	12
9	Plasmodium falciparum genetic diversity maintained and amplified over 5 years of a low transmission endemic in the Peruvian Amazon. *Molecular Biology and Evolution*, **2011**, 28, 1973-86	8.3	44
8	A population genetic approach to mapping neurological disorder genes using deep resequencing. *PLoS Genetics*, **2011**, 7, e1001318	6	72
7	Age-dependent recombination rates in human pedigrees. *PLoS Genetics*, **2011**, 7, e1002251	6	37
6	Mutations in centrosomal protein CEP152 in primary microcephaly families linked to MCPH4. *American Journal of Human Genetics*, **2010**, 87, 40-51	11	163
5	Haplotype allelic classes for detecting ongoing positive selection. *BMC Bioinformatics*, **2010**, 11, 65	3.6	13
4	Comparison of polygenic risk scores for heart disease highlights obstacles to overcome for clinical use		3
3	Multiscale PHATE Exploration of SARS-CoV-2 Data Reveals Multimodal Signatures of Disease		1
2	Single-cell RNA-sequencing reveals pervasive but highly cell type-specific genetic ancestry effects on the response to viral infection		3
1	ImputeCoVNet: 2D ResNet Autoencoder for Imputation of SARS-CoV-2 Sequences		3