Asif Javed

List of Publications by Year
in descending order

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30	1,043	567144 15	501076 28
papers	citations	h-index	g-index

30	30	30	2522
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Validation and refinement of a RUNX1 mutation-associated gene expression signature in blast crisis chronic myeloid leukemia. Leukemia, 2022, 36, 892-896.	3.3	2
2	Experimental and bioinformatics considerations in cancer application of single cell genomics. Computational and Structural Biotechnology Journal, 2021, 19, 343-354.	1.9	3
3	Cancerâ€associated missense mutations enhance the pluripotency reprogramming activity of OCT4 and SOX17. FEBS Journal, 2020, 287, 122-144.	2.2	11
4	Redefining prognostication of de novo cytogenetically normal acute myeloid leukemia in young adults. Blood Cancer Journal, 2020, 10, 104.	2.8	7
5	Novel SOX10 Mutations in Waardenburg Syndrome: Functional Characterization and Genotype-Phenotype Analysis. Frontiers in Genetics, 2020, 11, 589784.	1.1	10
6	MITF variants cause nonsyndromic sensorineural hearing loss with autosomal recessive inheritance. Scientific Reports, 2020, 10, 12712.	1.6	9
7	An integrative model of pathway convergence in genetically heterogeneous blast crisis chronic myeloid leukemia. Blood, 2020, 135, 2337-2353.	0.6	49
8	Large-Scale Whole-Genome Sequencing of Three Diverse Asian Populations in Singapore. Cell, 2019, 179, 736-749.e15.	13.5	126
9	ALPK1 missense pathogenic variant in five families leads to ROSAH syndrome, an ocular multisystem autosomal dominant disorder. Genetics in Medicine, 2019, 21, 2103-2115.	1.1	28
10	De novo mutations in SMCHD1 cause Bosma arhinia microphthalmia syndrome and abrogate nasal development. Nature Genetics, 2017, 49, 249-255.	9.4	88
11	Meta-analysis identifies novel risk loci and yields systematic insights into the biology of male-pattern baldness. Nature Communications, 2017, 8, 14694.	5.8	58
12	Aboriginal Australian mitochondrial genome variation â€“ an increased understanding of population antiquity and diversity. Scientific Reports, 2017, 7, 43041.	1.6	39
13	Isolation and 3D expansion of multipotent Sox9+ mouse lung progenitors. Nature Methods, 2017, 14, 1205-1212.	9.0	66
14	Incidentalome from Genomic Sequencing: A Barrier to Personalized Medicine?. EBioMedicine, 2016, 5, 211-216.	2.7	23
15	NSIT: Novel Sequence Identification Tool. PLoS ONE, 2014, 9, e108011.	1.1	1
16	An international effort towards developing standards for best practices in analysis, interpretation and reporting of clinical genome sequencing results in the CLARITY Challenge. Genome Biology, 2014, 15, R53.	13.9	101
17	Genetic diversity in <scp>P</scp>uerto <scp>R</scp>ico and its implications for the peopling of the <scp>I</scp>sland and the <scp>W</scp>est <scp>I</scp>ndies. American Journal of Physical Anthropology, 2014, 155, 352-368.	2.1	34
18	Phen-Gen: combining phenotype and genotype to analyze rare disorders. Nature Methods, 2014, 11, 935-937.	9.0	130

#	Article	IF	Citations
19	Recombination Gives a New Insight in the Effective Population Size and the History of the Old World Human Populations. Molecular Biology and Evolution, 2012, 29, 25-30.	3.5	31
20	Recombination networks as genetic markers in a human variation study of the Old World. Human Genetics, 2012, 131, 601-613.	1.8	7
21	Efficient Genomewide Selection of PCA-Correlated tSNPs for Genotype Imputation. Annals of Human Genetics, 2011, 75, 707-722.	0.3	3
22	A minimal descriptor of an ancestral recombinations graph. BMC Bioinformatics, 2011, 12, S6.	1.2	7
23	IRiS: Construction of ARG networks at genomic scales. Bioinformatics, 2011, 27, 2448-2450.	1.8	14
24	A New Method to Reconstruct Recombination Events at a Genomic Scale. PLoS Computational Biology, 2010, 6, e1001010.	1.5	14
25	Recombinomics. , 2010, , .		0
26	Ancestry informative markers for fine-scale individual assignment to worldwide populations. Journal of Medical Genetics, 2010, 47, 835-847.	1.5	65
27	Minimizing recombinations in consensus networks for phylogeographic studies. BMC Bioinformatics, 2009, 10, S72.	1.2	12
28	Intra- and interpopulation genotype reconstruction from tagging SNPs. Genome Research, 2006, 17, 96-107.	2.4	35
29	Frequent Pattern Mining on Message Passing Multiprocessor Systems. Distributed and Parallel Databases, 2004, 16, 321-334.	1.0	69
30	3D culture of multipotent Sox9+ mouse embryonic lung progenitors: Isolation, Expansion and Cryopreservation. Protocol Exchange, 0, , .	0.3	1