# Asif Javed

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/5719949/publications.pdf

Version: 2024-02-01

| 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 | Phen-Gen: combining phenotype and genotype to analyze rare disorders. Nature Methods, 2014, 11, 935-937. | 9.0 | 130 |
| 2 | Large-Scale Whole-Genome Sequencing of Three Diverse Asian Populations in Singapore. Cell, 2019, 179, 736-749.e15. | 13.5 | 126 |
| 3 | 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 |
| 4 | De novo mutations in SMCHD1 cause Bosma arhinia microphthalmia syndrome and abrogate nasal development. Nature Genetics, 2017, 49, 249-255. | 9.4 | 88 |
| 5 | Frequent Pattern Mining on Message Passing Multiprocessor Systems. Distributed and Parallel Databases, 2004, 16, 321-334. | 1.0 | 69 |
| 6 | Isolation and 3D expansion of multipotent Sox9+ mouse lung progenitors. Nature Methods, 2017, 14, 1205-1212. | 9.0 | 66 |
| 7 | Ancestry informative markers for fine-scale individual assignment to worldwide populations. Journal of Medical Genetics, 2010, 47, 835-847. | 1.5 | 65 |
| 8 | 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 |
| 9 | An integrative model of pathway convergence in genetically heterogeneous blast crisis chronic myeloid leukemia. Blood, 2020, 135, 2337-2353. | 0.6 | 49 |
| 10 | Aboriginal Australian mitochondrial genome variation â€“ an increased understanding of population antiquity and diversity. Scientific Reports, 2017, 7, 43041. | 1.6 | 39 |
| 11 | Intra- and interpopulation genotype reconstruction from tagging SNPs. Genome Research, 2006, 17, 96-107. | 2.4 | 35 |
| 12 | 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 |
| 13 | 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 |
| 14 | 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 |
| 15 | Incidentalome from Genomic Sequencing: A Barrier to Personalized Medicine?. EBioMedicine, 2016, 5, 211-216. | 2.7 | 23 |
| 16 | A New Method to Reconstruct Recombination Events at a Genomic Scale. PLoS Computational Biology, 2010, 6, e1001010. | 1.5 | 14 |
| 17 | IRiS: Construction of ARG networks at genomic scales. Bioinformatics, 2011, 27, 2448-2450. | 1.8 | 14 |
| 18 | Minimizing recombinations in consensus networks for phylogeographic studies. BMC Bioinformatics, 2009, 10, S72. | 1.2 | 12 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | Cancerâ€associated missense mutations enhance the pluripotency reprogramming activity of OCT4 and SOX17. FEBS Journal, 2020, 287, 122-144. | 2.2 | 11 |
| 20 | Novel SOX10 Mutations in Waardenburg Syndrome: Functional Characterization and Genotype-Phenotype Analysis. Frontiers in Genetics, 2020, 11, 589784. | 1.1 | 10 |
| 21 | MITF variants cause nonsyndromic sensorineural hearing loss with autosomal recessive inheritance. Scientific Reports, 2020, 10, 12712. | 1.6 | 9 |
| 22 | A minimal descriptor of an ancestral recombinations graph. BMC Bioinformatics, 2011, 12, S6. | 1.2 | 7 |
| 23 | Recombination networks as genetic markers in a human variation study of the Old World. Human Genetics, 2012, 131, 601-613. | 1.8 | 7 |
| 24 | Redefining prognostication of de novo cytogenetically normal acute myeloid leukemia in young adults. Blood Cancer Journal, 2020, 10, 104. | 2.8 | 7 |
| 25 | Efficient Genomewide Selection of PCA-Correlated tSNPs for Genotype Imputation. Annals of Human Genetics, 2011, 75, 707-722. | 0.3 | 3 |
| 26 | Experimental and bioinformatics considerations in cancer application of single cell genomics. Computational and Structural Biotechnology Journal, 2021, 19, 343-354. | 1.9 | 3 |
| 27 | 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 |
| 28 | NSIT: Novel Sequence Identification Tool. PLoS ONE, 2014, 9, e108011. | 1.1 | 1 |
| 29 | 3D culture of multipotent Sox9+ mouse embryonic lung progenitors: Isolation, Expansion and Cryopreservation. Protocol Exchange, 0, , . | 0.3 | 1 |
| 30 | Recombinomics. , 2010, , . | | 0 |