Rowmika Ravi

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/1434562/publications.pdf

Version: 2024-02-01

10 papers	105 citations	1937685 4 h-index	1372567 10 g-index
10 all docs	10 docs citations	10 times ranked	201 citing authors

#	Article	IF	Citations
1	Understanding the complexity of epimorphic regeneration in zebrafish caudal fin tissue: A transcriptomic and proteomic approach. Genomics, 2022, 114, 110300.	2.9	5
2	Metabolite Signature in the Carriers of Pathogenic Genetic Variants for Cardiomyopathy: A Population-Based METSIM Study. Metabolites, 2022, 12, 437.	2.9	1
3	Saliva microbiome in primary SjÃ¶grenâ€™s syndrome reveals distinct set of diseaseâ€associated microbes. Oral Diseases, 2020, 26, 295-301.	3.0	39
4	Pharmacogenetic landscape of DPYD variants in south Asian populations by integration of genome-scale data. Pharmacogenomics, 2018, 19, 227-241.	1.3	25
5	SAGE: a comprehensive resource of genetic variants integrating South Asian whole genomes and exomes. Database: the Journal of Biological Databases and Curation, 2018, 2018, 1-10.	3.0	20
6	<scp>E</scp>gyptian tale from <scp>I</scp>ndia: application of wholeâ€exome sequencing in diagnosis of atypical familial <scp>M</scp>editerranean fever. International Journal of Rheumatic Diseases, 2017, 20, 1770-1775.	1.9	7
7	Case Report: Whole exome sequencing reveals a novel frameshift deletion mutation p.G2254fs in COL7A1 associated with autosomal recessive dystrophic epidermolysis bullosa. F1000Research, 2016, 5, 900.	1.6	3
8	Case Report: Whole exome sequencing reveals a novel frameshift deletion mutation p.G2254fs in COL7A1 associated with autosomal recessive dystrophic epidermolysis bullosa. F1000Research, 2016, 5, 900.	1.6	2
9	Case Report:ÂWhole exome sequencing identifies variation c.2308G>A p.E770K in RAG1 associated with B- T- NK+ severe combined immunodeficiency. F1000Research, 2016, 5, 2532.	1.6	2
10	Case Report: Whole exome sequencing identifies variation c.2308G>A p.E770K in RAG1 associated with B- T- NK+ severe combined immunodeficiency. F1000Research, 2016, 5, 2532.	1.6	1