

Muhammad S Nawaz

List of Publications by Year in descending order

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Version: 2024-02-01

12
papers

486
citations

1307366

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1125617

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1502
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#	ARTICLE	IF	CITATIONS
1	Rare SLC13A1 variants associate with intervertebral disc disorder highlighting role of sulfate in disc pathology. <i>Nature Communications</i> , 2022, 13, 634.	5.8	21
2	A genome-wide meta-analysis identifies 50 genetic loci associated with carpal tunnel syndrome. <i>Nature Communications</i> , 2022, 13, 1598.	5.8	8
3	A meta-analysis uncovers the first sequence variant conferring risk of Bell's palsy. <i>Scientific Reports</i> , 2021, 11, 4188.	1.6	8
4	A genome-wide meta-analysis uncovers six sequence variants conferring risk of vertigo. <i>Communications Biology</i> , 2021, 4, 1148.	2.0	12
5	Large genome-wide association study identifies three novel risk variants for restless legs syndrome. <i>Communications Biology</i> , 2020, 3, 703.	2.0	40
6	Attention-deficit hyperactivity disorder shares copy number variant risk with schizophrenia and autism spectrum disorder. <i>Translational Psychiatry</i> , 2019, 9, 258.	2.4	75
7	Interrogating the Genetic Determinants of Tourette's Syndrome and Other Tic Disorders Through Genome-Wide Association Studies. <i>American Journal of Psychiatry</i> , 2019, 176, 217-227.	4.0	242
8	In Silico Structure Modeling and Molecular Docking Analysis of Phosphoribosyl Pyrophosphate Amidotransferase (PPAT) with Antifolate Inhibitors. <i>Current Cancer Drug Targets</i> , 2019, 19, 408-416.	0.8	7
9	MAP1B mutations cause intellectual disability and extensive white matter deficit. <i>Nature Communications</i> , 2018, 9, 3456.	5.8	21
10	In silico analysis of glycinamide ribonucleotide transformylase inhibition by PY873, PY899 and DIA. <i>Saudi Journal of Biological Sciences</i> , 2017, 24, 1155-1161.	1.8	6
11	Association of AADAC Deletion and Gilles de la Tourette Syndrome in a Large European Cohort. <i>Biological Psychiatry</i> , 2016, 79, 383-391.	0.7	41
12	MotViz: A Tool for Sequence Motif Prediction in Parallel to Structural Visualization and Analyses. <i>Genomics, Proteomics and Bioinformatics</i> , 2012, 10, 35-43.	3.0	1