

Zia-Ur-Rehman Tanoli

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8347245/publications.pdf>

Version: 2024-02-01

20
papers

1,153
citations

777949

13
h-index

843174

20
g-index

26
all docs

26
docs citations

26
times ranked

1434
citing authors

#	ARTICLE	IF	CITATIONS
1	Community assessment to advance computational prediction of cancer drug combinations in a pharmacogenomic screen. <i>Nature Communications</i> , 2019, 10, 2674.	5.8	240
2	SynergyFinder Plus: Toward Better Interpretation and Annotation of Drug Combination Screening Datasets. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 587-596.	3.0	159
3	DrugComb: an integrative cancer drug combination data portal. <i>Nucleic Acids Research</i> , 2019, 47, W43-W51.	6.5	153
4	Drug Target Commons: A Community Effort to Build a Consensus Knowledge Base for Drug-Target Interactions. <i>Cell Chemical Biology</i> , 2018, 25, 224-229.e2.	2.5	124
5	Identifying GPCRs and their Types with Chou's Pseudo Amino Acid Composition: An Approach from Multi-scale Energy Representation and Position Specific Scoring Matrix. <i>Protein and Peptide Letters</i> , 2012, 19, 890-903.	0.4	83
6	Artificial intelligence, machine learning, and drug repurposing in cancer. <i>Expert Opinion on Drug Discovery</i> , 2021, 16, 977-989.	2.5	68
7	Exploration of databases and methods supporting drug repurposing: a comprehensive survey. <i>Briefings in Bioinformatics</i> , 2021, 22, 1656-1678.	3.2	66
8	Crowdsourced mapping of unexplored target space of kinase inhibitors. <i>Nature Communications</i> , 2021, 12, 3307.	5.8	41
9	Drug Target Commons 2.0: a community platform for systematic analysis of drug-target interaction profiles. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, 1-13.	1.4	36
10	A community challenge for a pancancer drug mechanism of action inference from perturbational profile data. <i>Cell Reports Medicine</i> , 2022, 3, 100492.	3.3	33
11	Interactive visual analysis of drug-target interaction networks using Drug Target Profiler, with applications to precision medicine and drug repurposing. <i>Briefings in Bioinformatics</i> , 2018, . .	3.2	25
12	G-protein-coupled receptor prediction using pseudo-amino-acid composition and multiscale energy representation of different physiochemical properties. <i>Analytical Biochemistry</i> , 2011, 412, 173-182.	1.1	23
13	Predicting G-Protein-Coupled Receptors Families Using Different Physiochemical Properties and Pseudo Amino Acid Composition. <i>Methods in Enzymology</i> , 2013, 522, 61-79.	0.4	15
14	Prediction of GPCRs with Pseudo Amino Acid Composition: Employing Composite Features and Grey Incidence Degree Based Classification. <i>Protein and Peptide Letters</i> , 2011, 18, 872-878.	0.4	13
15	Cartography of rhodopsin-like G protein-coupled receptors across vertebrate genomes. <i>Scientific Reports</i> , 2019, 9, 7058.	1.6	9
16	Identification of Celecoxib-Targeted Proteins Using Label-Free Thermal Proteome Profiling on Rat Hippocampus. <i>Molecular Pharmacology</i> , 2021, 99, 308-318.	1.0	9
17	Multi-modal meta-analysis of cancer cell line omics profiles identifies ECHDC1 as a novel breast tumor suppressor. <i>Molecular Systems Biology</i> , 2021, 17, e9526.	3.2	8
18	Minimal information for chemosensitivity assays (MICHA): a next-generation pipeline to enable the FAIRification of drug screening experiments. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	7

#	ARTICLE	IF	CITATIONS
19	MediSyn: uncertainty-aware visualization of multiple biomedical datasets to support drug treatment selection. BMC Bioinformatics, 2017, 18, 393.	1.2	6
20	Using BERT to identify drug-target interactions from whole PubMed. BMC Bioinformatics, 2022, 23, .	1.2	6