Anil K Giri

List of Publications by Year in descending order

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36 36 36 3766
all docs docs citations times ranked citing authors

#	Article	IF	CITATIONS
1	Fully-automated and ultra-fast cell-type identification using specific marker combinations from single-cell transcriptomic data. Nature Communications, 2022, 13, 1246.	12.8	163
2	SynergyFinder 3.0: an interactive analysis and consensus interpretation of multi-drug synergies across multiple samples. Nucleic Acids Research, 2022, 50, W739-W743.	14.5	139
3	Patient-tailored design for selective co-inhibition of leukemic cell subpopulations. Science Advances, 2021, 7, .	10.3	28
4	High-throughput screening for drug discovery targeting the cancer cell-microenvironment interactions in hematological cancers. Expert Opinion on Drug Discovery, 2021, , 1-10.	5.0	4
5	Multifaceted genome-wide study identifies novel regulatory loci in SLC22A11 and ZNF45 for body mass index in Indians. Molecular Genetics and Genomics, 2020, 295, 1013-1026.	2.1	8
6	SynToxProfiler: An interactive analysis of drug combination synergy, toxicity and efficacy. PLoS Computational Biology, 2020, 16, e1007604.	3.2	43
7	SynergyFinder 2.0: visual analytics of multi-drug combination synergies. Nucleic Acids Research, 2020, 48, W488-W493.	14.5	545
8	Higher ETV5 Expression Associates With Poor 5-Florouracil-Based Adjuvant Therapy Response in Colon Cancer. Frontiers in Pharmacology, 2020, 11, 620811.	3.5	4
9	SynToxProfiler: An interactive analysis of drug combination synergy, toxicity and efficacy. , 2020, 16, e1007604.		O
10	SynToxProfiler: An interactive analysis of drug combination synergy, toxicity and efficacy., 2020, 16, e1007604.		0
11	SynToxProfiler: An interactive analysis of drug combination synergy, toxicity and efficacy. , 2020, 16, e1007604.		O
12	SynToxProfiler: An interactive analysis of drug combination synergy, toxicity and efficacy., 2020, 16, e1007604.		0
13	Genome-Wide Association Study of Metabolic Syndrome Reveals Primary Genetic Variants at CETP Locus in Indians. Biomolecules, 2019, 9, 321.	4.0	16
14	Genome-wide off-targets of drugs: risks and opportunities. Cell Biology and Toxicology, 2019, 35, 485-487.	5. 3	16
15	DNMT Inhibitors Increase Methylation in the Cancer Genome. Frontiers in Pharmacology, 2019, 10, 385.	3 . 5	67
16	Normative range of blood biochemical parameters in urban Indian school-going adolescents. PLoS ONE, 2019, 14, e0213255.	2.5	5
17	Genome-wide association study of blood lipids in Indians confirms universality of established variants. Journal of Human Genetics, 2019, 64, 573-587.	2.3	22
18	Genomewide association study for C-reactive protein in Indians replicates known associations of common variants. Journal of Genetics, 2019, 98, 1.	0.7	9

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19	JAK/STAT-Activating Genomic Alterations Are a Hallmark of T-PLL. Cancers, 2019, 11, 1833.	3.7	38
20	Prediction of drug combination effects with a minimal set of experiments. Nature Machine Intelligence, 2019, 1, 568-577.	16.0	99
21	Genomewide association study for C-reactive protein in Indians replicates known associations of common variants. Journal of Genetics, 2019, 98, .	0.7	6
22	Common variants of ARID1A and KAT2B are associated with obesity in Indian adolescents. Scientific Reports, 2018, 8, 3964.	3.3	3
23	Pharmacogenetic landscape of <i>DPYD</i> variants in south Asian populations by integration of genome-scale data. Pharmacogenomics, 2018, 19, 227-241.	1.3	25
24	DNA methylation profiling reveals the presence of population-specific signatures correlating with phenotypic characteristics. Molecular Genetics and Genomics, 2017, 292, 655-662.	2.1	29
25	Common Variants in CLDN2 and MORC4 Genes Confer Disease Susceptibility in Patients with Chronic Pancreatitis. PLoS ONE, 2016, 11, e0147345.	2.5	34
26	Genome wide association study of uric acid in Indian population and interaction of identified variants with Type 2 diabetes. Scientific Reports, 2016, 6, 21440.	3.3	36
27	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	27.8	173
28	Genetic epidemiology of pharmacogenetic variations in <i>CYP2C9</i> , <i>CYP4F2</i> and <i>VKORC1</i> genes associated with warfarin dosage in the Indian population. Pharmacogenomics, 2014, 15, 1337-1354.	1.3	35
29	Pharmacogenetic landscape of clopidogrel in north Indians suggest distinct interpopulation differences in allele frequencies. Pharmacogenomics, 2014, 15, 643-653.	1.3	18