Klev Diamanti

List of Publications by Year in Descending Order

Source: https://exaly.com/author-pdf/4752275/klev-diamanti-publications-by-year.pdf

Version: 2024-04-09

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

25	1,376 citations	10	34
papers		h-index	g-index
34 ext. papers	2,377 ext. citations	11.4 avg, IF	7.03 L-index

#	Paper	IF	Citations
25	Interpretable machine learning identifies paediatric Systemic Lupus Erythematosus subtypes based on gene expression data <i>Scientific Reports</i> , 2022 , 12, 7433	4.9	O
24	R.ROSETTA: an interpretable machine learning framework. <i>BMC Bioinformatics</i> , 2021 , 22, 110	3.6	5
23	Mapping chromatin accessibility and active regulatory elements reveals pathological mechanisms in human gliomas. <i>Nature Communications</i> , 2021 , 12, 3621	17.4	2
22	Multifaceted regulation of hepatic lipid metabolism by YY1. Life Science Alliance, 2021, 4,	5.8	3
21	Nucleolar rDNA folds into condensed foci with a specific combination of epigenetic marks. <i>Plant Journal</i> , 2021 , 105, 1534-1548	6.9	O
20	Single nucleus transcriptomics data integration recapitulates the major cell types in human liver. <i>Hepatology Research</i> , 2021 , 51, 233-238	5.1	3
19	Interpretable Machine Learning Reveals Dissimilarities Between Subtypes of Autism Spectrum Disorder. <i>Frontiers in Genetics</i> , 2021 , 12, 618277	4.5	3
18	The Thioesterase as a Regulator of Lipid Metabolism in Type 2 Diabetes Detected in a Multi-Omics Study of Human Liver. <i>OMICS A Journal of Integrative Biology</i> , 2021 , 25, 652-659	3.8	0
17	Integration of whole-body [F]FDG PET/MRI with non-targeted metabolomics can provide new insights on tissue-specific insulin resistance in type 2 diabetes. <i>Scientific Reports</i> , 2020 , 10, 8343	4.9	2
16	A Multi-Omics Approach to Liver Diseases: Integration of Single Nuclei Transcriptomics with Proteomics and HiCap Bulk Data in Human Liver. <i>OMICS A Journal of Integrative Biology</i> , 2020 , 24, 180-7	1948	10
15	Combined burden and functional impact tests for cancer driver discovery using DriverPower. <i>Nature Communications</i> , 2020 , 11, 734	17.4	16
14	Integrative pathway enrichment analysis of multivariate omics data. <i>Nature Communications</i> , 2020 , 11, 735	17.4	53
13	Pathway and network analysis of more than 2500 whole cancer genomes. <i>Nature Communications</i> , 2020 , 11, 729	17.4	38
12	Analyses of non-coding somatic drivers in 2,658 Lancer whole genomes. <i>Nature</i> , 2020 , 578, 102-111	50.4	220
11	Pan-cancer analysis of whole genomes. <i>Nature</i> , 2020 , 578, 82-93	50.4	840
10	Cancer LncRNA Census reveals evidence for deep functional conservation of long noncoding RNAs in tumorigenesis. <i>Communications Biology</i> , 2020 , 3, 56	6.7	77
9	Sex differences in oncogenic mutational processes. <i>Nature Communications</i> , 2020 , 11, 4330	17.4	23

LIST OF PUBLICATIONS

8	Intra- and inter-individual metabolic profiling highlights carnitine and lysophosphatidylcholine pathways as key molecular defects in type 2 diabetes. <i>Scientific Reports</i> , 2019 , 9, 9653	4.9	18
7	Unveiling new interdependencies between significant DNA methylation sites, gene expression profiles and glioma patients survival. <i>Scientific Reports</i> , 2018 , 8, 4390	4.9	7
6	Discovering Networks of Interdependent Features in High-Dimensional Problems. <i>Studies in Big Data</i> , 2016 , 285-304	0.9	7
5	A Significant Regulatory Mutation Burden at a High-Affinity Position of the CTCF Motif in Gastrointestinal Cancers. <i>Human Mutation</i> , 2016 , 37, 904-13	4.7	28
4	Maps of context-dependent putative regulatory regions and genomic signal interactions. <i>Nucleic Acids Research</i> , 2016 , 44, 9110-9120	20.1	7
3	R.ROSETTA: an interpretable machine learning framework		1
2	Discovery and characterization of coding and non-coding driver mutations in more than 2,500 whole cancer genomes		12
1	Organ-specific metabolic pathways distinguish prediabetes, type 2 diabetes and normal tissues		1