

Klev Diamanti

List of Publications by Citations

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

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

#	Paper	IF	Citations
25	Pan-cancer analysis of whole genomes. <i>Nature</i> , 2020 , 578, 82-93	50.4	840
24	Analyses of non-coding somatic drivers in 2,658 cancer whole genomes. <i>Nature</i> , 2020 , 578, 102-111	50.4	220
23	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
22	Integrative pathway enrichment analysis of multivariate omics data. <i>Nature Communications</i> , 2020 , 11, 735	17.4	53
21	Pathway and network analysis of more than 2500 whole cancer genomes. <i>Nature Communications</i> , 2020 , 11, 729	17.4	38
20	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
19	Sex differences in oncogenic mutational processes. <i>Nature Communications</i> , 2020 , 11, 4330	17.4	23
18	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
17	Combined burden and functional impact tests for cancer driver discovery using DriverPower. <i>Nature Communications</i> , 2020 , 11, 734	17.4	16
16	Discovery and characterization of coding and non-coding driver mutations in more than 2,500 whole cancer genomes		12
15	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, 180-194	3.8	10
14	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
13	Discovering Networks of Interdependent Features in High-Dimensional Problems. <i>Studies in Big Data</i> , 2016 , 285-304	0.9	7
12	Maps of context-dependent putative regulatory regions and genomic signal interactions. <i>Nucleic Acids Research</i> , 2016 , 44, 9110-9120	20.1	7
11	R.ROSETTA: an interpretable machine learning framework. <i>BMC Bioinformatics</i> , 2021 , 22, 110	3.6	5
10	Multifaceted regulation of hepatic lipid metabolism by YY1. <i>Life Science Alliance</i> , 2021 , 4,	5.8	3
9	Single nucleus transcriptomics data integration recapitulates the major cell types in human liver. <i>Hepatology Research</i> , 2021 , 51, 233-238	5.1	3

8	Interpretable Machine Learning Reveals Dissimilarities Between Subtypes of Autism Spectrum Disorder. <i>Frontiers in Genetics</i> , 2021 , 12, 618277	4.5	3
7	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
6	Mapping chromatin accessibility and active regulatory elements reveals pathological mechanisms in human gliomas. <i>Nature Communications</i> , 2021 , 12, 3621	17.4	2
5	R.ROSETTA: an interpretable machine learning framework		1
4	Organ-specific metabolic pathways distinguish prediabetes, type 2 diabetes and normal tissues		1
3	Nucleolar rDNA folds into condensed foci with a specific combination of epigenetic marks. <i>Plant Journal</i> , 2021 , 105, 1534-1548	6.9	0
2	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
1	Interpretable machine learning identifies paediatric Systemic Lupus Erythematosus subtypes based on gene expression data.. <i>Scientific Reports</i> , 2022 , 12, 7433	4.9	0