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List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/2890340/publications.pdf

Version: 2024-02-01

24	5,737	623574	610775
papers	citations	14 h-index	24 g-index

26	26	26	12908
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Mutational landscape and significance across 12 major cancer types. Nature, 2013, 502, 333-339.	13.7	3,695
2	Pan-cancer network analysis identifies combinations of rare somatic mutations across pathways and protein complexes. Nature Genetics, 2015, 47, 106-114.	9.4	830
3	Integrated analysis of germline and somatic variants in ovarian cancer. Nature Communications, 2014, 5, 3156.	5.8	253
4	Patterns and functional implications of rare germline variants across 12 cancer types. Nature Communications, 2015, 6, 10086.	5.8	243
5	CoMEt: a statistical approach to identify combinations of mutually exclusive alterations in cancer. Genome Biology, 2015, 16, 160.	3.8	182
6	Precision Oncology: The Road Ahead. Trends in Molecular Medicine, 2017, 23, 874-898.	3.5	131
7	Hierarchical HotNet: identifying hierarchies of altered subnetworks. Bioinformatics, 2018, 34, i972-i980.	1.8	102
8	Network analysis of GWAS data. Current Opinion in Genetics and Development, 2013, 23, 602-610.	1.5	95
9	MAGI: visualization and collaborative annotation of genomic aberrations. Nature Methods, 2015, 12, 483-484.	9.0	25
10	A systematic genome-wide mapping of oncogenic mutation selection during CRISPR-Cas9 genome editing. Nature Communications, 2021, 12, 6512.	5.8	24
11	Criticality in tumor evolution and clinical outcome. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E11101-E11110.	3.3	23
12	Functional protein representations from biological networks enable diverse cross-species inference. Nucleic Acids Research, 2019, 47, e51-e51.	6.5	23
13	Hidden Markov models lead to higher resolution maps of mutation signature activity in cancer. Genome Medicine, 2019, 11, 49.	3.6	22
14	Network-based approaches elucidate differences within APOBEC and clock-like signatures in breast cancer. Genome Medicine, 2020, 12, 52.	3.6	20
15	Mutational Signatures: From Methods to Mechanisms. Annual Review of Biomedical Data Science, 2021, 4, 189-206.	2.8	19
16	Modeling clinical and molecular covariates of mutational process activity in cancer. Bioinformatics, 2019, 35, i492-i500.	1.8	15
17	A multifactorial model of T cell expansion and durable clinical benefit in response to a PD-L1 inhibitor. PLoS ONE, 2018, 13, e0208422.	1.1	14
18	A mixture model for signature discovery from sparse mutation data. Genome Medicine, 2021, 13, 173.	3.6	8

#	Article	IF	Citations
19	A Sticky Multinomial Mixture Model of Strand-Coordinated Mutational Processes in Cancer. IScience, 2020, 23, 100900.	1.9	5
20	Reply: Co-occurrence of MYC amplification and TP53 mutations in human cancer. Nature Genetics, 2016, 48, 106-108.	9.4	2
21	SuperDendrix algorithm integrates genetic dependencies and genomic alterations across pathways and cancer types. Cell Genomics, 2022, 2, 100099.	3.0	2
22	A data-driven approach for constructing mutation categories for mutational signature analysis. PLoS Computational Biology, 2021, 17, e1009542.	1.5	1
23	Matrix (factorization) reloaded: flexible methods for imputing genetic interactions with cross-species and side information. Bioinformatics, 2020, 36, i866-i874.	1.8	1
24	<scp>ScalpelSig</scp> Designs Targeted Genomic Panels from Data to Detect Activity of Mutational Signatures. Journal of Computational Biology, 2022, 29, 56-73.	0.8	1