Fabio Vandin

List of Publications by Year
in descending order

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52	15,013	394390	289230
papers	citations	19 h-index	40 g-index

54	54	54	26239
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Genomic and Epigenomic Landscapes of Adult De Novo Acute Myeloid Leukemia. New England Journal of Medicine, 2013, 368, 2059-2074.	27.0	4,139
2	Mutational landscape and significance across 12 major cancer types. Nature, 2013, 502, 333-339.	27.8	3,695
3	Integrated Genomic Characterization of Papillary Thyroid Carcinoma. Cell, 2014, 159, 676-690.	28.9	2,318
4	The mutational landscape of lethal castration-resistant prostate cancer. Nature, 2012, 487, 239-243.	27.8	2,128
5	Pan-cancer network analysis identifies combinations of rare somatic mutations across pathways and protein complexes. Nature Genetics, 2015, 47, 106-114.	21.4	830
6	Algorithms for Detecting Significantly Mutated Pathways in Cancer. Journal of Computational Biology, 2011, 18, 507-522.	1.6	434
7	De novo discovery of mutated driver pathways in cancer. Genome Research, 2012, 22, 375-385.	5.5	391
8	Identifying driver mutations in sequenced cancer genomes: computational approaches to enable precision medicine. Genome Medicine, 2014, 6, 5.	8.2	186
9	CoMEt: a statistical approach to identify combinations of mutually exclusive alterations in cancer. Genome Biology, 2015, 16, 160.	8.8	182
10	HIT'nDRIVE: patient-specific multidriver gene prioritization for precision oncology. Genome Research, 2017, 27, 1573-1588.	5.5	78
11	Discovery of mutated subnetworks associated with clinical data in cancer. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2012, , 55-66.	0.7	60
12	DISCOVERY OF MUTATED SUBNETWORKS ASSOCIATED WITH CLINICAL DATA IN CANCER. , 2011, , .		59
13	De novo pathway-based biomarker identification. Nucleic Acids Research, 2017, 45, e151-e151.	14.5	48
14	Diseaseâ€Concordant Twins Empower Genetic Association Studies. Annals of Human Genetics, 2017, 81, 20-26.	0.8	46
15	Mining top-K frequent itemsets through progressive sampling. Data Mining and Knowledge Discovery, 2010, 21, 310-326.	3.7	33
16	Clustering uncertain graphs. Proceedings of the VLDB Endowment, 2017, 11, 472-484.	3.8	30
17	Attention-Based Deep Learning Framework for Human Activity Recognition With User Adaptation. IEEE Sensors Journal, 2021, 21, 13474-13483.	4.7	30
18	Simultaneous Inference of Cancer Pathways and Tumor Progression from Cross-Sectional Mutation Data. Journal of Computational Biology, 2015, 22, 510-527.	1.6	28

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19	Computational Methods for Characterizing Cancer Mutational Heterogeneity. Frontiers in Genetics, 2017, 8, 83.	2.3	27
20	Accurate Computation of Survival Statistics in Genome-Wide Studies. PLoS Computational Biology, 2015, 11, e1004071.	3.2	24
21	Differentially Methylated Genomic Regions in Birthâ€Weight Discordant Twin Pairs. Annals of Human Genetics, 2016, 80, 81-87.	0.8	19
22	SPuManTE. , 2019, , .		19
23	Comparison of microbiome samples: methods and computational challenges. Briefings in Bioinformatics, 2021, 22, 88-95.	6.5	17
24	Hypothesis Testing and Statistically-sound Pattern Mining. , 2019, , .		16
25	Efficient Mining of the Most Significant Patterns with Permutation Testing. , 2018, , .		15
26	Efficient mining of the most significant patterns with permutation testing. Data Mining and Knowledge Discovery, 2020, 34, 1201-1234.	3.7	15
27	MADMX: A Strategy for Maximal Dense Motif Extraction. Journal of Computational Biology, 2011, 18, 535-545.	1.6	14
28	Permutation Strategies for Mining Significant Sequential Patterns. , 2019, , .		14
29	Efficient Incremental Mining of Top-K Frequent Closed Itemsets. , 2007, , 275-280.		13
30	Algorithms and Genome Sequencing: Identifying Driver Pathways in Cancer. Computer, 2012, 45, 39-46.	1.1	10
31	Efficient detection of differentially methylated regions using DiMmeR. Bioinformatics, 2017, 33, 549-551.	4.1	9
32	CoExpresso: assess the quantitative behavior of protein complexes in human cells. BMC Bioinformatics, 2019, 20, 17.	2.6	9
33	Efficient algorithms to discover alterations with complementary functional association in cancer. PLoS Computational Biology, 2019, 15, e1006802.	3.2	9
34	NoMAS: A Computational Approach to Find Mutated Subnetworks Associated With Survival in Genome-Wide Cancer Studies. Frontiers in Genetics, 2019, 10, 265.	2.3	8
35	Mining Sequential Patterns with VC-Dimension and Rademacher Complexity. Algorithms, 2020, 13, 123.	2.1	8
36	Differentially mutated subnetworks discovery. Algorithms for Molecular Biology, 2019, 14, 10.	1.2	7

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37	MCRapper: Monte-Carlo Rademacher Averages for Poset Families and Approximate Pattern Mining. , 2020, , .		7
38	On the Sample Complexity of Cancer Pathways Identification. Journal of Computational Biology, 2016, 23, 30-41.	1.6	6
39	Fast Approximation of Frequent k-Mers and Applications to Metagenomics. Journal of Computational Biology, 2020, 27, 534-549.	1.6	5
40	Identifying Drug Sensitivity Subnetworks with NETPHIX. IScience, 2020, 23, 101619.	4.1	5
41	<scp>Ballast</scp>: A Ball-based Algorithm for Structural Motifs. Journal of Computational Biology, 2013, 20, 137-151.	1.6	4
42	Enriched power of disease-concordant twin-case-only design in detecting interactions in genome-wide association studies. European Journal of Human Genetics, 2019, 27, 631-636.	2.8	4
43	MCRapper: Monte-Carlo Rademacher Averages for Poset Families and Approximate Pattern Mining. ACM Transactions on Knowledge Discovery From Data, 2022, 16, 1-29.	3.5	3
44	Jllumina - A comprehensive Java-based API for statistical Illumina Infinium HumanMethylation450 and Infinium MethylationEPIC BeadChip data processing. Journal of Integrative Bioinformatics, 2016, 13, 24-32.	1.5	2
45	Reply: Co-occurrence of MYC amplification and TP53 mutations in human cancer. Nature Genetics, 2016, 48, 106-108.	21.4	2
46	The Impact of Global Structural Information in Graph Neural Networks Applications. Data, 2022, 7, 10.	2.3	2
47	CASPITA: Mining Statistically Significant Paths in Time Series Data from an Unknown Network. , 2021, , .		2
48	SPRISS: approximating frequentk-mers by sampling reads, and applications. Bioinformatics, 2022, 38, 3343-3350.	4.1	2
49	gRosSo: Mining Statistically Robust Patterns from a Sequence of Datasets. , 2020, , .		1
50	Workshop: Algorithms for discovery of mutated pathways in cancer. , 2012, , .		0
51	Identifying significant mutations in large cohorts of cancer genomes. , 2013, , .		0
52	Principles of Systems Biology, No. 31. Cell Systems, 2018, 7, 133-135.	6.2	0