

# Dimitris Anastassiou

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8358787/publications.pdf>

Version: 2024-02-01

19  
papers

4,705  
citations

840776

11  
h-index

839539

18  
g-index

22  
all docs

22  
docs citations

22  
times ranked

8518  
citing authors

#	ARTICLE	IF	CITATIONS
1	The Immune Landscape of Cancer. <i>Immunity</i> , 2018, 48, 812-830.e14.	14.3	3,706
2	Multi-cancer computational analysis reveals invasion-associated variant of desmoplastic reaction involving INHBA, THBS2 and COL11A1. <i>BMC Medical Genomics</i> , 2010, 3, 51.	1.5	156
3	Computational analysis of the synergy among multiple interacting genes. <i>Molecular Systems Biology</i> , 2007, 3, 83.	7.2	142
4	Development of a Prognostic Model for Breast Cancer Survival in an Open Challenge Environment. <i>Science Translational Medicine</i> , 2013, 5, 181ra50.	12.4	110
5	Biomolecular Events in Cancer Revealed by Attractor Metagenes. <i>PLoS Computational Biology</i> , 2013, 9, e1002920.	3.2	94
6	A community effort to create standards for evaluating tumor subclonal reconstruction. <i>Nature Biotechnology</i> , 2020, 38, 97-107.	17.5	58
7	Variable window binding for mutually exclusive alternative splicing. <i>Genome Biology</i> , 2006, 7, R2.	9.6	46
8	Single-cell analysis reveals the pan-cancer invasiveness-associated transition of adipose-derived stromal cells into COL11A1-expressing cancer-associated fibroblasts. <i>PLoS Computational Biology</i> , 2021, 17, e1009228.	3.2	30
9	Breast Cancer Prognostic Biomarker Using Attractor Metagenes and the <i>FGD3</i> Metagene. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2014, 23, 2850-2856.	2.5	18
10	2DImpute: imputation in single-cell RNA-seq data from correlations in two dimensions. <i>Bioinformatics</i> , 2020, 36, 3588-3589.	4.1	13
11	Columbia's VoD and Multimedia Research Testbed with Heterogeneous Network Support. <i>Multimedia Tools and Applications</i> , 1997, 5, 171-184.	3.9	12
12	Meta-analysis of expression and methylation signatures indicates a stress-related epigenetic mechanism in multiple neuropsychiatric disorders. <i>Translational Psychiatry</i> , 2019, 9, 32.	4.8	11
13	Discovering Genome-Wide Tag SNPs Based on the Mutual Information of the Variants. <i>PLoS ONE</i> , 2016, 11, e0167994.	2.5	6
14	Pan-cancer driver copy number alterations identified by joint expression/CNA data analysis. <i>Scientific Reports</i> , 2020, 10, 17199.	3.3	6
15	Silence detection for multimedia communication systems. <i>Multimedia Systems</i> , 1999, 7, 157-164.	4.7	4
16	A sequential Monte Carlo algorithm for inference of subclonal structure in cancer. <i>PLoS ONE</i> , 2019, 14, e0211213.	2.5	2
17	Bayesian Basecalling for DNA Sequence Analysis using Hidden Markov Models. , 2006, , .		1
18	Comment on "A COL11A1-correlated pan-cancer gene signature of activated fibroblasts for the prioritization of therapeutic targets," <i>Cancer Lett.</i> 2016 Nov 28; 382 (2): 203-214. <i>Cancer Letters</i> , 2017, 393, 125-126.	7.2	1

#	ARTICLE	IF	CITATIONS
19	Characterizing intra-tumor heterogeneity from somatic mutations without copy-neutral assumption. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 18, 1-1.	3.0	0