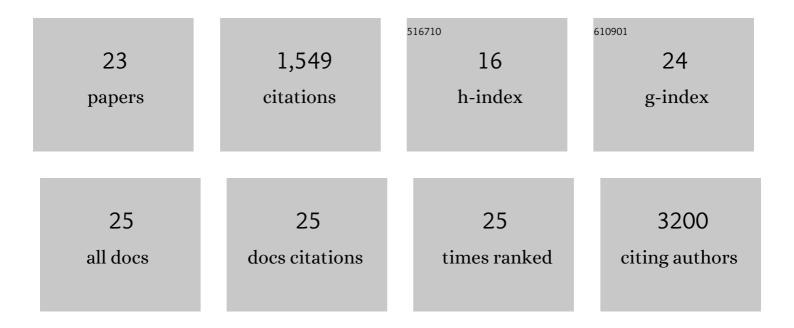
Noam Auslander

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/3316835/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Incorporating Machine Learning into Established Bioinformatics Frameworks. International Journal of Molecular Sciences, 2021, 22, 2903.	4.1	48
2	Identification of combinations of somatic mutations that predict cancer survival and immunotherapy benefit. NAR Cancer, 2021, 3, zcab017.	3.1	2
3	Hard wiring of normal tissue-specific chromosome-wide gene expression levels is an additional factor driving cancer type-specific aneuploidies. Genome Medicine, 2021, 13, 93.	8.2	10
4	Seeker: alignment-free identification of bacteriophage genomes by deep learning. Nucleic Acids Research, 2020, 48, e121-e121.	14.5	78
5	Prediction of the incubation period for COVID-19 and future virus disease outbreaks. BMC Biology, 2020, 18, 186.	3.8	16
6	Pyrvinium Pamoate Induces Death of Triple-Negative Breast Cancer Stem–Like Cells and Reduces Metastases through Effects on Lipid Anabolism. Cancer Research, 2020, 80, 4087-4102.	0.9	36
7	Genomic determinants of pathogenicity in SARS-CoV-2 and other human coronaviruses. Proceedings of the United States of America, 2020, 117, 15193-15199.	7.1	196
8	Interplay between DNA damage repair and apoptosis shapes cancer evolution through aneuploidy and microsatellite instability. Nature Communications, 2020, 11, 1234.	12.8	23
9	Single-Cell–Derived Primary Rectal Carcinoma Cell Lines Reflect Intratumor Heterogeneity Associated with Treatment Response. Clinical Cancer Research, 2020, 26, 3468-3480.	7.0	9
10	The GENDULF algorithm: mining transcriptomics to uncover modifier genes for monogenic diseases. Molecular Systems Biology, 2020, 16, e9701.	7.2	2
11	In silico learning of tumor evolution through mutational time series. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 9501-9510.	7.1	18
12	Predicting Complete Remission of Acute Myeloid Leukemia: Machine Learning Applied to Gene Expression. Cancer Informatics, 2019, 18, 117693511983554.	1.9	27
13	Reply to: â€~IMPRES does not reproducibly predict response to immune checkpoint blockade therapy in metastatic melanoma'. Nature Medicine, 2019, 25, 1836-1838.	30.7	10
14	A unique insert in the genomes of high-risk human papillomaviruses with a predicted dual role in conferring oncogenic risk. F1000Research, 2019, 8, 1000.	1.6	10
15	A unique insert in the genomes of high-risk human papillomaviruses with a predicted dual role in conferring oncogenic risk. F1000Research, 2019, 8, 1000.	1.6	27
16	Harnessing synthetic lethality to predict the response to cancer treatment. Nature Communications, 2018, 9, 2546.	12.8	97
17	Robust prediction of response to immune checkpoint blockade therapy in metastatic melanoma. Nature Medicine, 2018, 24, 1545-1549.	30.7	473
18	Urea Cycle Dysregulation Generates Clinically Relevant Genomic and Biochemical Signatures. Cell, 2018, 174, 1559-1570.e22.	28.9	183

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#	Article	IF	CITATIONS
19	Chemoradiotherapy Resistance in Colorectal Cancer Cells is Mediated by Wnt/β-catenin Signaling. Molecular Cancer Research, 2017, 15, 1481-1490.	3.4	105
20	An integrated computational and experimental study uncovers <scp>FUT</scp> 9 as a metabolic driver of colorectal cancer. Molecular Systems Biology, 2017, 13, 956.	7.2	38
21	Co-targeting the tumor endothelium and P-selectin-expressing glioblastoma cells leads to a remarkable therapeutic outcome. ELife, 2017, 6, .	6.0	50
22	A joint analysis of transcriptomic and metabolomic data uncovers enhanced enzyme-metabolite coupling in breast cancer. Scientific Reports, 2016, 6, 29662.	3.3	43
23	Data-Driven Metabolic Pathway Compositions Enhance Cancer Survival Prediction. PLoS Computational Biology, 2016, 12, e1005125.	3.2	8