

Noam Auslander

List of Publications by Citations

Source: <https://exaly.com/author-pdf/3316835/noam-auslander-publications-by-citations.pdf>

Version: 2024-04-28

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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

24
papers

802
citations

12
h-index

25
g-index

25
ext. papers

1,201
ext. citations

14.8
avg, IF

4.34
L-index

#	Paper	IF	Citations
24	Robust prediction of response to immune checkpoint blockade therapy in metastatic melanoma. <i>Nature Medicine</i> , 2018 , 24, 1545-1549	50.5	230
23	Genomic determinants of pathogenicity in SARS-CoV-2 and other human coronaviruses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 15193-15199	11.5	120
22	Urea Cycle Dysregulation Generates Clinically Relevant Genomic and Biochemical Signatures. <i>Cell</i> , 2018 , 174, 1559-1570.e22	56.2	102
21	Chemoradiotherapy Resistance in Colorectal Cancer Cells is Mediated by Wnt/βcatenin Signaling. <i>Molecular Cancer Research</i> , 2017 , 15, 1481-1490	6.6	71
20	Harnessing synthetic lethality to predict the response to cancer treatment. <i>Nature Communications</i> , 2018 , 9, 2546	17.4	44
19	Co-targeting the tumor endothelium and P-selectin-expressing glioblastoma cells leads to a remarkable therapeutic outcome. <i>ELife</i> , 2017 , 6,	8.9	32
18	A joint analysis of transcriptomic and metabolomic data uncovers enhanced enzyme-metabolite coupling in breast cancer. <i>Scientific Reports</i> , 2016 , 6, 29662	4.9	30
17	An integrated computational and experimental study uncovers FUT9 as a metabolic driver of colorectal cancer. <i>Molecular Systems Biology</i> , 2017 , 13, 956	12.2	28
16	Seeker: alignment-free identification of bacteriophage genomes by deep learning. <i>Nucleic Acids Research</i> , 2020 , 48, e121	20.1	19
15	Predicting Complete Remission of Acute Myeloid Leukemia: Machine Learning Applied to Gene Expression. <i>Cancer Informatics</i> , 2019 , 18, 1176935119835544	2.4	14
14	A unique insert in the genomes of high-risk human papillomaviruses with a predicted dual role in conferring oncogenic risk. <i>F1000Research</i> , 2019 , 8, 1000	3.6	13
13	Pyruvium Pamoate Induces Death of Triple-Negative Breast Cancer Stem-Like Cells and Reduces Metastases through Effects on Lipid Anabolism. <i>Cancer Research</i> , 2020 , 80, 4087-4102	10.1	13
12	In silico learning of tumor evolution through mutational time series. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 9501-9510	11.5	11
11	Interplay between DNA damage repair and apoptosis shapes cancer evolution through aneuploidy and microsatellite instability. <i>Nature Communications</i> , 2020 , 11, 1234	17.4	11
10	Genomic determinants of pathogenicity in SARS-CoV-2 and other human coronaviruses 2020 ,		10
9	Prediction of the incubation period for COVID-19 and future virus disease outbreaks. <i>BMC Biology</i> , 2020 , 18, 186	7.3	10
8	Incorporating Machine Learning into Established Bioinformatics Frameworks. <i>International Journal of Molecular Sciences</i> , 2021 , 22,	6.3	9

7	A unique insert in the genomes of high-risk human papillomaviruses with a predicted dual role in conferring oncogenic risk. <i>F1000Research</i> , 2019 , 8, 1000	3.6	7
6	Data-Driven Metabolic Pathway Compositions Enhance Cancer Survival Prediction. <i>PLoS Computational Biology</i> , 2016 , 12, e1005125	5	6
5	Reply to: bMPRES does not reproducibly predict response to immune checkpoint blockade therapy in metastatic melanoma <i>Nature Medicine</i> , 2019 , 25, 1836-1838	50.5	5
4	Single-Cell-Derived Primary Rectal Carcinoma Cell Lines Reflect Intratumor Heterogeneity Associated with Treatment Response. <i>Clinical Cancer Research</i> , 2020 , 26, 3468-3480	12.9	5
3	Hard wiring of normal tissue-specific chromosome-wide gene expression levels is an additional factor driving cancer type-specific aneuploidies. <i>Genome Medicine</i> , 2021 , 13, 93	14.4	3
2	The GENDULF algorithm: mining transcriptomics to uncover modifier genes for monogenic diseases. <i>Molecular Systems Biology</i> , 2020 , 16, e9701	12.2	1
1	Identification of combinations of somatic mutations that predict cancer survival and immunotherapy benefit. <i>NAR Cancer</i> , 2021 , 3, zcab017	5.2	1