

# David Amar

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7046168/publications.pdf>

Version: 2024-02-01

17  
papers

1,368  
citations

759233

12  
h-index

839539

18  
g-index

22  
all docs

22  
docs citations

22  
times ranked

2785  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genetics of 35 blood and urine biomarkers in the UK Biobank. <i>Nature Genetics</i> , 2021, 53, 185-194.	21.4	377
2	Graphical analysis for phenome-wide causal discovery in genotyped population-scale biobanks. <i>Nature Communications</i> , 2021, 12, 350.	12.8	13
3	Time trajectories in the transcriptomic response to exercise - a meta-analysis. <i>Nature Communications</i> , 2021, 12, 3471.	12.8	48
4	Molecular Transducers of Physical Activity Consortium (MoTrPAC): Mapping the Dynamic Responses to Exercise. <i>Cell</i> , 2020, 181, 1464-1474.	28.9	147
5	ADEPTUS: a discovery tool for disease prediction, enrichment and network analysis based on profiles from many diseases. <i>Bioinformatics</i> , 2018, 34, 1959-1961.	4.1	7
6	FOCS: a novel method for analyzing enhancer and gene activity patterns infers an extensive enhancer-promoter map. <i>Genome Biology</i> , 2018, 19, 56.	8.8	63
7	Analysis of blood-based gene expression in idiopathic Parkinson disease. <i>Neurology</i> , 2017, 89, 1676-1683.	1.1	112
8	Extracting replicable associations across multiple studies: Empirical Bayes algorithms for controlling the false discovery rate. <i>PLoS Computational Biology</i> , 2017, 13, e1005700.	3.2	14
9	A machine learning approach for predicting CRISPR-Cas9 cleavage efficiencies and patterns underlying its mechanism of action. <i>PLoS Computational Biology</i> , 2017, 13, e1005807.	3.2	147
10	Enhancer methylation dynamics contribute to cancer plasticity and patient mortality. <i>Genome Research</i> , 2016, 26, 601-611.	5.5	88
11	RichMind: A Tool for Improved Inference from Large-Scale Neuroimaging Results. <i>PLoS ONE</i> , 2016, 11, e0159643.	2.5	4
12	A hierarchical Bayesian model for flexible module discovery in three-way time-series data. <i>Bioinformatics</i> , 2015, 31, i17-i26.	4.1	19
13	The MORPH web server and software tool for predicting missing genes in biological pathways. <i>Physiologia Plantarum</i> , 2015, 155, 12-20.	5.2	3
14	Integrated analysis of numerous heterogeneous gene expression profiles for detecting robust disease-specific biomarkers and proposing drug targets. <i>Nucleic Acids Research</i> , 2015, 43, 7779-7789.	14.5	30
15	Evaluation and integration of functional annotation pipelines for newly sequenced organisms: the potato genome as a test case. <i>BMC Plant Biology</i> , 2014, 14, 329.	3.6	42
16	Constructing module maps for integrated analysis of heterogeneous biological networks. <i>Nucleic Acids Research</i> , 2014, 42, 4208-4219.	14.5	29
17	Dissection of Regulatory Networks that Are Altered in Disease via Differential Co-expression. <i>PLoS Computational Biology</i> , 2013, 9, e1002955.	3.2	164