David Amar

List of Publications by Year in Descending Order

21 papers	591 citations	11 h-index	22 g-index
22 ext. papers	1,028 ext. citations	13.9 avg, IF	3.93 L-index

#	Paper	IF	Citations
21	Time trajectories in the transcriptomic response to exercise - a meta-analysis. *Nature Communications*, **2021**, 12, 3471	17.4	8
20	Genetics of 35 blood and urine biomarkers in the UK Biobank. *Nature Genetics*, **2021**, 53, 185-194	36.3	78
19	Graphical analysis for phenome-wide causal discovery in genotyped population-scale biobanks. *Nature Communications*, **2021**, 12, 350	17.4	1
18	Molecular Transducers of Physical Activity Consortium (MoTrPAC): Mapping the Dynamic Responses to Exercise. *Cell*, **2020**, 181, 1464-1474	56.2	51
17	High-throughput SARS-CoV-2 and host genome sequencing from single nasopharyngeal swabs **2020**,		4
16	ADEPTUS: a discovery tool for disease prediction, enrichment and network analysis based on profiles from many diseases. *Bioinformatics*, **2018**, 34, 1959-1961	7.2	6
15	FOCS: a novel method for analyzing enhancer and gene activity patterns infers an extensive enhancer-promoter map. *Genome Biology*, **2018**, 19, 56	18.3	32
14	Analysis of blood-based gene expression in idiopathic Parkinson disease. *Neurology*, **2017**, 89, 1676-1683	6.5	59
13	Extracting replicable associations across multiple studies: Empirical Bayes algorithms for controlling the false discovery rate. *PLoS Computational Biology*, **2017**, 13, e1005700	5	7
12	A machine learning approach for predicting CRISPR-Cas9 cleavage efficiencies and patterns underlying its mechanism of action. *PLoS Computational Biology*, **2017**, 13, e1005807	5	73
11	Enhancer methylation dynamics contribute to cancer plasticity and patient mortality. *Genome Research*, **2016**, 26, 601-11	9.7	67
10	RichMind: A Tool for Improved Inference from Large-Scale Neuroimaging Results. *PLoS ONE*, **2016**, 11, e0159643	3.7	3
9	Integrated analysis of numerous heterogeneous gene expression profiles for detecting robust disease-specific biomarkers and proposing drug targets. *Nucleic Acids Research*, **2015**, 43, 7779-89	20.1	20
8	A hierarchical Bayesian model for flexible module discovery in three-way time-series data. *Bioinformatics*, **2015**, 31, i17-26	7.2	8
7	The MORPH-R web server and software tool for predicting missing genes in biological pathways. *Physiologia Plantarum*, **2015**, 155, 12-20	4.6	1
6	Evaluation and integration of functional annotation pipelines for newly sequenced organisms: the potato genome as a test case. *BMC Plant Biology*, **2014**, 14, 329	5.3	17
5	Constructing module maps for integrated analysis of heterogeneous biological networks. *Nucleic Acids Research*, **2014**, 42, 4208-19	20.1	23

LIST OF PUBLICATIONS

4	Dissection of regulatory networks that are altered in disease via differential co-expression. *PLoS Computational Biology*, **2013**, 9, e1002955	5	104
3	Mono- and bi-allelic protein truncating variants in alpha-actinin 2 cause cardiomyopathy through distinct mechanisms		1
2	Constraint-based analysis for causal discovery in population-based biobanks		2
1	Genetics of 38 blood and urine biomarkers in the UK Biobank		25