

Assaf Gottlieb

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9529189/publications.pdf>

Version: 2024-02-01

34
papers

1,985
citations

471371

17
h-index

414303

32
g-index

40
all docs

40
docs citations

40
times ranked

3052
citing authors

#	ARTICLE	IF	CITATIONS
1	PREDICT: a method for inferring novel drug indications with application to personalized medicine. <i>Molecular Systems Biology</i> , 2011, 7, 496.	3.2	655
2	INDI: a computational framework for inferring drug interactions and their associated recommendations. <i>Molecular Systems Biology</i> , 2012, 8, 592.	3.2	208
3	Combining Drug and Gene Similarity Measures for Drug-Target Elucidation. <i>Journal of Computational Biology</i> , 2011, 18, 133-145.	0.8	174
4	Novel Unsupervised Feature Filtering of Biological Data. <i>Bioinformatics</i> , 2006, 22, e507-e513.	1.8	149
5	Reconstruction of the Mouse Otocyst and Early Neuroblast Lineage at Single-Cell Resolution. <i>Cell</i> , 2014, 157, 964-978.	13.5	140
6	Algorithm for Data Clustering in Pattern Recognition Problems Based on Quantum Mechanics. <i>Physical Review Letters</i> , 2001, 88, 018702.	2.9	132
7	Environmental Stresses Disrupt Telomere Length Homeostasis. <i>PLoS Genetics</i> , 2013, 9, e1003721.	1.5	89
8	A method for inferring medical diagnoses from patient similarities. <i>BMC Medicine</i> , 2013, 11, 194.	2.3	57
9	PRINCIPLE: a tool for associating genes with diseases via network propagation. <i>Bioinformatics</i> , 2011, 27, 3325-3326.	1.8	42
10	Ranking Adverse Drug Reactions With Crowdsourcing. <i>Journal of Medical Internet Research</i> , 2015, 17, e80.	2.1	35
11	Human brain transcriptome analysis finds region- and subject-specific expression signatures of GABAAR subunits. <i>Communications Biology</i> , 2019, 2, 153.	2.0	34
12	Large-Scale Elucidation of Drug Response Pathways in Humans. <i>Journal of Computational Biology</i> , 2012, 19, 163-174.	0.8	31
13	SCOR: A secure international informatics infrastructure to investigate COVID-19. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2020, 27, 1721-1726.	2.2	31
14	Unsupervised feature selection under perturbations: meeting the challenges of biological data. <i>Bioinformatics</i> , 2007, 23, 3343-3349.	1.8	22
15	Integrating Systems Biology Sources Illuminates Drug Action. <i>Clinical Pharmacology and Therapeutics</i> , 2014, 95, 663-669.	2.3	20
16	3D computational reconstruction of tissues with hollow spherical morphologies using single-cell gene expression data. <i>Nature Protocols</i> , 2015, 10, 459-474.	5.5	20
17	High-resolution and differential analysis of rat microglial markers in traumatic brain injury: conventional flow cytometric and bioinformatics analysis. <i>Scientific Reports</i> , 2020, 10, 11991.	1.6	19
18	Comparing diagnostic accuracy of current practice guidelines in predicting choledocholithiasis: outcomes from a large healthcare system comprising both academic and community settings. <i>Gastrointestinal Endoscopy</i> , 2021, 93, 1351-1359.	0.5	17

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19	Explainable drug sensitivity prediction through cancer pathway enrichment. <i>Scientific Reports</i> , 2021, 11, 3128.	1.6	17
20	Estimating the effects of second-line therapy for type 2 diabetes mellitus: retrospective cohort study. <i>BMJ Open Diabetes Research and Care</i> , 2017, 5, e000435.	1.2	13
21	SynPathy: Predicting Drug Synergy through Drug-Associated Pathways Using Deep Learning. <i>Molecular Cancer Research</i> , 2022, 20, 762-769.	1.5	13
22	Cohort-specific imputation of gene expression improves prediction of warfarin dose for African Americans. <i>Genome Medicine</i> , 2017, 9, 98.	3.6	11
23	Fast and Efficient Feature Engineering for Multi-Cohort Analysis of EHR Data. <i>Studies in Health Technology and Informatics</i> , 2017, 235, 181-185.	0.2	9
24	Stratification of co-evolving genomic groups using ranked phylogenetic profiles. <i>BMC Bioinformatics</i> , 2009, 10, 355.	1.2	8
25	Common peptides shed light on evolution of Olfactory Receptors. <i>BMC Evolutionary Biology</i> , 2009, 9, 91.	3.2	7
26	Time dependent analysis of rat microglial surface markers in traumatic brain injury reveals dynamics of distinct cell subpopulations. <i>Scientific Reports</i> , 2022, 12, 6289.	1.6	7
27	Population stratification enables modeling effects of reopening policies on mortality and hospitalization rates. <i>Journal of Biomedical Informatics</i> , 2021, 119, 103818.	2.5	5
28	Common Peptides Study of Aminoacyl-tRNA Synthetases. <i>PLoS ONE</i> , 2011, 6, e20361.	1.1	4
29	A Phenotyping Algorithm to Identify People With HIV in Electronic Health Record Data (HIV-Phen): Development and Evaluation Study. <i>JMIR Formative Research</i> , 2021, 5, e28620.	0.7	4
30	UFFizi: a generic platform for ranking informative features. <i>BMC Bioinformatics</i> , 2010, 11, 300.	1.2	2
31	Data mining of protein families using common peptides. <i>Nature Precedings</i> , 2008, , .	0.1	1
32	Translational Bioinformatics Curricula in Graduate Biomedical Informatics Programs. <i>Computers in Health Care</i> , 2020, , 59-74.	0.2	0
33	Tissue-Specific Variations in Transcription Factors Elucidate Complex Immune System Regulation. <i>Genes</i> , 2022, 13, 929.	1.0	0
34	A Method for Bridging Population-Specific Genotypes to Detect Gene Modules Associated with Alzheimer's Disease. <i>Cells</i> , 2022, 11, 2219.	1.8	0