

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 | SynPathy: Predicting Drug Synergy through Drug-Associated Pathways Using Deep Learning. <i>Molecular Cancer Research</i> , 2022, 20, 762-769. | 1.5 | 13 |
| 2 | 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 |
| 3 | Tissue-Specific Variations in Transcription Factors Elucidate Complex Immune System Regulation. <i>Genes</i> , 2022, 13, 929. | 1.0 | 0 |
| 4 | 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 |
| 5 | 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 |
| 6 | Explainable drug sensitivity prediction through cancer pathway enrichment. <i>Scientific Reports</i> , 2021, 11, 3128. | 1.6 | 17 |
| 7 | 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 |
| 8 | 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 |
| 9 | 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 |
| 10 | 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 |
| 11 | Translational Bioinformatics Curricula in Graduate Biomedical Informatics Programs. <i>Computers in Health Care</i> , 2020, , 59-74. | 0.2 | 0 |
| 12 | Human brain transcriptome analysis finds region- and subject-specific expression signatures of GABAAR subunits. <i>Communications Biology</i> , 2019, 2, 153. | 2.0 | 34 |
| 13 | 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 |
| 14 | Cohort-specific imputation of gene expression improves prediction of warfarin dose for African Americans. <i>Genome Medicine</i> , 2017, 9, 98. | 3.6 | 11 |
| 15 | 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 |
| 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 | Ranking Adverse Drug Reactions With Crowdsourcing. <i>Journal of Medical Internet Research</i> , 2015, 17, e80. | 2.1 | 35 |
| 18 | Integrating Systems Biology Sources Illuminates Drug Action. <i>Clinical Pharmacology and Therapeutics</i> , 2014, 95, 663-669. | 2.3 | 20 |

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|----|--|------|-----------|
| 19 | Reconstruction of the Mouse Otocyst and Early Neuroblast Lineage at Single-Cell Resolution. <i>Cell</i> , 2014, 157, 964-978. | 13.5 | 140 |
| 20 | A method for inferring medical diagnoses from patient similarities. <i>BMC Medicine</i> , 2013, 11, 194. | 2.3 | 57 |
| 21 | Environmental Stresses Disrupt Telomere Length Homeostasis. <i>PLoS Genetics</i> , 2013, 9, e1003721. | 1.5 | 89 |
| 22 | Large-Scale Elucidation of Drug Response Pathways in Humans. <i>Journal of Computational Biology</i> , 2012, 19, 163-174. | 0.8 | 31 |
| 23 | INDI: a computational framework for inferring drug interactions and their associated recommendations. <i>Molecular Systems Biology</i> , 2012, 8, 592. | 3.2 | 208 |
| 24 | PREDICT: a method for inferring novel drug indications with application to personalized medicine. <i>Molecular Systems Biology</i> , 2011, 7, 496. | 3.2 | 655 |
| 25 | Common Peptides Study of Aminoacyl-tRNA Synthetases. <i>PLoS ONE</i> , 2011, 6, e20361. | 1.1 | 4 |
| 26 | Combining Drug and Gene Similarity Measures for Drug-Target Elucidation. <i>Journal of Computational Biology</i> , 2011, 18, 133-145. | 0.8 | 174 |
| 27 | PRINCIPLE: a tool for associating genes with diseases via network propagation. <i>Bioinformatics</i> , 2011, 27, 3325-3326. | 1.8 | 42 |
| 28 | UFFizi: a generic platform for ranking informative features. <i>BMC Bioinformatics</i> , 2010, 11, 300. | 1.2 | 2 |
| 29 | Stratification of co-evolving genomic groups using ranked phylogenetic profiles. <i>BMC Bioinformatics</i> , 2009, 10, 355. | 1.2 | 8 |
| 30 | Common peptides shed light on evolution of Olfactory Receptors. <i>BMC Evolutionary Biology</i> , 2009, 9, 91. | 3.2 | 7 |
| 31 | Data mining of protein families using common peptides. <i>Nature Precedings</i> , 2008, , . | 0.1 | 1 |
| 32 | Unsupervised feature selection under perturbations: meeting the challenges of biological data. <i>Bioinformatics</i> , 2007, 23, 3343-3349. | 1.8 | 22 |
| 33 | Novel Unsupervised Feature Filtering of Biological Data. <i>Bioinformatics</i> , 2006, 22, e507-e513. | 1.8 | 149 |
| 34 | Algorithm for Data Clustering in Pattern Recognition Problems Based on Quantum Mechanics. <i>Physical Review Letters</i> , 2001, 88, 018702. | 2.9 | 132 |