

Daniel S Himmelstein

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3838324/publications.pdf>

Version: 2024-02-01

23
papers

3,346
citations

566801

15
h-index

676716

22
g-index

108
all docs

108
docs citations

108
times ranked

6435
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 1 | Opportunities and obstacles for deep learning in biology and medicine. <i>Journal of the Royal Society Interface</i> , 2018, 15, 20170387. | 1.5 | 1,282 |
| 2 | Understanding multicellular function and disease with human tissue-specific networks. <i>Nature Genetics</i> , 2015, 47, 569-576. | 9.4 | 738 |
| 3 | Systematic integration of biomedical knowledge prioritizes drugs for repurposing. <i>ELife</i> , 2017, 6, . | 2.8 | 333 |
| 4 | Heterogeneous Network Edge Prediction: A Data Integration Approach to Prioritize Disease-Associated Genes. <i>PLoS Computational Biology</i> , 2015, 11, e1004259. | 1.5 | 120 |
| 5 | Sci-Hub provides access to nearly all scholarly literature. <i>ELife</i> , 2018, 7, . | 2.8 | 89 |
| 6 | Multifactor dimensionality reduction for graphics processing units enables genome-wide testing of epistasis in sporadic ALS. <i>Bioinformatics</i> , 2010, 26, 694-695. | 1.8 | 76 |
| 7 | Association of HLA Genetic Risk Burden With Disease Phenotypes in Multiple Sclerosis. <i>JAMA Neurology</i> , 2016, 73, 795. | 4.5 | 64 |
| 8 | Open collaborative writing with Manubot. <i>PLoS Computational Biology</i> , 2019, 15, e1007128. | 1.5 | 51 |
| 9 | Precision annotation of digital samples in NCBI's gene expression omnibus. <i>Scientific Data</i> , 2017, 4, 170125. | 2.4 | 44 |
| 10 | Compressing gene expression data using multiple latent space dimensionalities learns complementary biological representations. <i>Genome Biology</i> , 2020, 21, 109. | 3.8 | 43 |
| 11 | Is authorship sufficient for today's collaborative research? A call for contributor roles. <i>Accountability in Research</i> , 2021, 28, 23-43. | 1.6 | 40 |
| 12 | ENABLING PERSONAL GENOMICS WITH AN EXPLICIT TEST OF EPISTASIS. , 2009, , 327-336. | | 35 |
| 13 | Lung cancer incidence decreases with elevation: evidence for oxygen as an inhaled carcinogen. <i>PeerJ</i> , 2015, 3, e705. | 0.9 | 26 |
| 14 | The Informative Extremes: Using Both Nearest and Farthest Individuals Can Improve Relief Algorithms in the Domain of Human Genetics. <i>Lecture Notes in Computer Science</i> , 2010, , 182-193. | 1.0 | 24 |
| 15 | Meta-analysis of genome-wide association studies reveals genetic overlap between Hodgkin lymphoma and multiple sclerosis. <i>International Journal of Epidemiology</i> , 2016, 45, 728-740. | 0.9 | 20 |
| 16 | Evolving hard problems: Generating human genetics datasets with a complex etiology. <i>BioData Mining</i> , 2011, 4, 21. | 2.2 | 19 |
| 17 | PMLB v1.0: an open-source dataset collection for benchmarking machine learning methods. <i>Bioinformatics</i> , 2022, 38, 878-880. | 1.8 | 15 |
| 18 | iCTNet2: integrating heterogeneous biological interactions to understand complex traits. <i>F1000Research</i> , 2015, 4, 485. | 0.8 | 11 |

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|----|--|-----|-----------|
| 19 | Analysis of scientific society honors reveals disparities. Cell Systems, 2021, 12, 900-906.e5. | 2.9 | 10 |
| 20 | Genetic Associationâ€“Guided Analysis of Gene Networks for the Study of Complex Traits. Circulation: Cardiovascular Genetics, 2016, 9, 179-184. | 5.1 | 9 |
| 21 | iCTNet2: integrating heterogeneous biological interactions to understand complex traits. F1000Research, 2015, 4, 485. | 0.8 | 8 |
| 22 | A Model Free Method to Generate Human Genetics Datasets with Complex Gene-Disease Relationships. Lecture Notes in Computer Science, 2010, , 74-85. | 1.0 | 2 |
| 23 | An Open-Publishing Response to the COVID-19 Infodemic.. CEUR Workshop Proceedings, 2021, 2976, 29-38. | 2.3 | 2 |