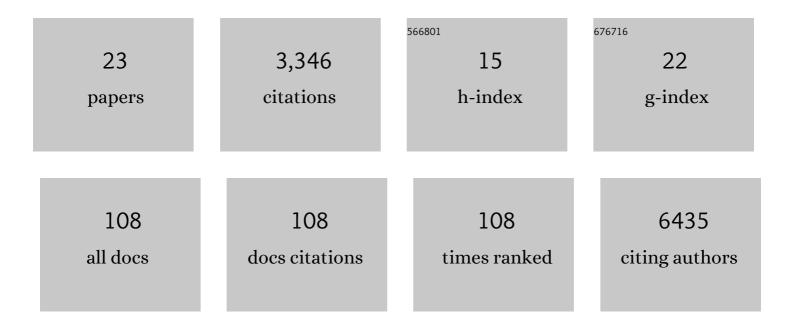
## Daniel S Himmelstein

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/3838324/publications.pdf Version: 2024-02-01



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

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#	Article	IF	CITATIONS
19	Analysis of scientific society honors reveals disparities. Cell Systems, 2021, 12, 900-906.e5.	2.9	10
20	Genetic Association–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