Daniel S Himmelstein

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

97 papers	2,057 citations	16 h-index	45 g-index
108 ext. papers	2,831 ext. citations	7 avg, IF	4.74 L-index

#	Paper	IF	Citations
97	Opportunities and obstacles for deep learning in biology and medicine. *Journal of the Royal Society Interface*, **2018**, 15,	4.1	780
96	Understanding multicellular function and disease with human tissue-specific networks. *Nature Genetics*, **2015**, 47, 569-76	36.3	473
95	Systematic integration of biomedical knowledge prioritizes drugs for repurposing. *ELife*, **2017**, 6,	8.9	151
94	Heterogeneous Network Edge Prediction: A Data Integration Approach to Prioritize Disease-Associated Genes. *PLoS Computational Biology*, **2015**, 11, e1004259	5	69
93	Multifactor dimensionality reduction for graphics processing units enables genome-wide testing of epistasis in sporadic ALS. *Bioinformatics*, **2010**, 26, 694-5	7.2	60
92	Sci-Hub provides access to nearly all scholarly literature. *ELife*, **2018**, 7,	8.9	59
91	Opportunities and obstacles for deep learning in biology and medicine		45
90	Association of HLA Genetic Risk Burden With Disease Phenotypes in Multiple Sclerosis. *JAMA Neurology*, **2016**, 73, 795-802	17.2	43
89	Enabling personal genomics with an explicit test of epistasis. *Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing*, **2010**, 327-36	1.3	31
88	Open collaborative writing with Manubot. *PLoS Computational Biology*, **2019**, 15, e1007128	5	24
87	Compressing gene expression data using multiple latent space dimensionalities learns complementary biological representations. *Genome Biology*, **2020**, 21, 109	18.3	20
86	Precision annotation of digital samples in NCBI's gene expression omnibus. *Scientific Data*, **2017**, 4, 170125	8.1	19
85	Lung cancer incidence decreases with elevation: evidence for oxygen as an inhaled carcinogen. *PeerJ*, **2015**, 3, e705	3.1	19
84	Is authorship sufficient for today's collaborative research? A call for contributor roles. *Accountability in Research*, **2021**, 28, 23-43	1.9	17
83	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	0.9	16
82	Meta-analysis of genome-wide association studies reveals genetic overlap between Hodgkin lymphoma and multiple sclerosis. *International Journal of Epidemiology*, **2016**, 45, 728-40	7.8	16
81	Evolving hard problems: Generating human genetics datasets with a complex etiology. *BioData Mining*, **2011**, 4, 21	4.3	12

80	Sci-Hub provides access to nearly all scholarly literature		10
79	iCTNet2: integrating heterogeneous biological interactions to understand complex traits. *F1000Research*, **2015**, 4, 485	3.6	7
78	Analysis of ISCB honorees and keynotes reveals disparities		7
77	Genetic Association-Guided Analysis of Gene Networks for the Study of Complex Traits. *Circulation: Cardiovascular Genetics*, **2016**, 9, 179-84		7
76	iCTNet2: integrating heterogeneous biological interactions to understand complex traits. *F1000Research*, **2015**, 4, 485	3.6	6
75	Mining knowledge from MEDLINE articles and their indexed MeSH terms **2015**,		5
74	Extracting disease-gene associations from the GWAS Catalog **2015**,		5
73	Sci-Hub provides access to nearly all scholarly literature		5
72	Integrating resources with disparate licensing into an open network **2015**,		4
71	Rephetio: Repurposing drugs on a hetnet [project]		3
70	Assessing the imputation quality of gene expression in LINCS L1000 **2016**,		3
69	Computing standardized logistic regression coefficients **2016**,		3
68	PMLB v1.0: An open-source dataset collection for benchmarking machine learning methods. *Bioinformatics*, **2021**,	7.2	3
67	Sequential compression of gene expression across dimensionalities and methods reveals no single best method or dimensionality		3
66	Rephetio: Repurposing drugs on a hetnet [proposal]		2
65	One network to rule them all **2015**,		2
64	Renaming "heterogeneous networks" to a more concise and catchy term **2015**,		2
63	Processing DisGeNET for disease-gene relationships **2015**,		2

62	Processing the DISEASES resource for disease–gene relationships **2015**,	2
61	MSigDB licensing **2015**,	2
60	LINCS L1000 licensing **2015**,	2
59	Incomplete Interactome licensing **2015**,	2
58	Using the neo4j graph database for hetnets **2015**,	2
57	Assessing the informativeness of features **2015**,	2
56	Processing Bgee for tissue-specific gene presence and over/under-expression **2015**,	2
55	Permuting hetnets and implementing randomized edge swaps in cypher **2015**,	2
54	Data nomenclature: naming and abbreviating our network types **2016**,	2
53	Positive correlations between knockdown and overexpression profiles from LINCS L1000 **2016**,	2
52	Assessing the effectiveness of our hetnet permutations **2016**,	2
51	Workshop to analyze LINCS data for the Systems Pharmacology course at UCSF **2016**,	2
50	Announcing PharmacotherapyDB: the Open Catalog of Drug Therapies for Disease **2016**,	2
49	Incorporating DrugCentral data in our network **2016**,	2
48	Estimating the complexity of hetnet traversal **2016**,	2
47	Transforming DWPCs for hetnet edge prediction **2016**,	2
46	Network Edge Prediction: how to deal with self-testing **2016**,	2
45	Measuring user contribution and content creation **2016**,	2

44	Network Edge Prediction: Estimating the prior **2016**,	2
43	Predictions of whether a compound treats a disease **2016**,	2
42	How should we construct a catalog of drug indications? **2015**,	2
41	Our hetnet edge prediction methodology: the modeling framework for Project Rephetio **2016**,	2
40	Cataloging drug–disease therapies in the ClinicalTrials.gov database **2016**,	2
39	Sounding the alarm on DrugBank's new license and terms of use **2016**,	2
38	Edge dropout contamination in hetnet edge prediction **2016**,	2
37	Hosting Hetionet in the cloud: creating a public Neo4j instance **2016**,	2
36	Exploring the power of Hetionet: a Cypher query depot **2016**,	2
35	Prediction in epilepsy **2016**,	2
34	Brainstorming future directions for Hetionet **2016**,	2
33	Decomposing the DWPC to assess intermediate node or edge contributions **2016**,	2
32	Decomposing predictions into their network support **2016**,	2
31	Enabling reproducibility and reuse **2015**,	2
30	Visualizing the top epilepsy predictions in Cytoscape **2017**,	2
29	Why we predicted ictogenic tricyclic compounds treat epilepsy? **2017**,	2
28	Using Entrez Gene as our gene vocabulary **2015**,	2
27	Compiling Gene Ontology annotations into an easy-to-use format **2015**,	2

26	Unifying drug vocabularies **2015**,	2
25	Tissue Node **2015**,	2
24	Computing consensus transcriptional profiles for LINCS L1000 perturbations **2015**,	2
23	Unifying disease vocabularies **2015**,	2
22	Processing LabeledIn to extract indications **2015**,	2
21	Integrating drug target information from BindingDB **2015**,	2
20	Selecting informative ERC (evolutionary rate covariation) values between genes **2015**,	2
19	Extracting indications from the ehrlink resource **2015**,	2
18	Protein (target, carrier, transporter, and enzyme) interactions in DrugBank **2015**,	2
17	Disease Ontology feature requests **2015**,	2
16	Calculating molecular similarities between DrugBank compounds **2015**,	2
15	Calculating genomic windows for GWAS lead SNPs **2015**,	2
14	Adding pathway resources to your network **2015**,	2
13	Tissue-specific gene expression resources **2015**,	2
12	Creating a catalog of protein interactions **2015**,	2
11	The TISSUES resource for the tissue-specificity of genes **2015**,	2
10	Disease similarity from MEDLINE topic cooccurrence **2015**,	2
9	Functional disease annotations for genes using DOAF **2015**,	2

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8	Expert curation of our indication catalog for disease-modifying treatments **2015**,		2
7	STARGEO: expression signatures for disease using crowdsourced GEO annotation **2015**,		2
6	Extracting side effects from SIDER 4 **2015**,		2
5	A Model Free Method to Generate Human Genetics Datasets with Complex Gene-Disease Relationships. *Lecture Notes in Computer Science*, **2010**, 74-85	0.9	2
4	Analysis of scientific society honors reveals disparities. *Cell Systems*, **2021**, 12, 900-906.e5	10.6	2
3	Systematic integration of biomedical knowledge prioritizes drugs for repurposing		1
2	Expanding a Database-derived Biomedical Knowledge Graph via Multi-relation Extraction from Biomedical Abstracts		1
1	An Open-Publishing Response to the COVID-19 Infodemic.. *CEUR Workshop Proceedings*, **2021**, 2976, 29-38	0.2	