

Daniel S Himmelstein

List of Publications by Year in Descending Order

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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	PMLB v1.0: An open-source dataset collection for benchmarking machine learning methods. <i>Bioinformatics</i> , 2021 ,	7.2	3
96	Is authorship sufficient for today's collaborative research? A call for contributor roles. <i>Accountability in Research</i> , 2021 , 28, 23-43	1.9	17
95	Analysis of scientific society honors reveals disparities. <i>Cell Systems</i> , 2021 , 12, 900-906.e5	10.6	2
94	An Open-Publishing Response to the COVID-19 Infodemic.. <i>CEUR Workshop Proceedings</i> , 2021 , 2976, 29-38	0.2	
93	Compressing gene expression data using multiple latent space dimensionalities learns complementary biological representations. <i>Genome Biology</i> , 2020 , 21, 109	18.3	20
92	Open collaborative writing with Manubot. <i>PLoS Computational Biology</i> , 2019 , 15, e1007128	5	24
91	Opportunities and obstacles for deep learning in biology and medicine. <i>Journal of the Royal Society Interface</i> , 2018 , 15,	4.1	780
90	Sci-Hub provides access to nearly all scholarly literature. <i>ELife</i> , 2018 , 7,	8.9	59
89	Precision annotation of digital samples in NCBI's gene expression omnibus. <i>Scientific Data</i> , 2017 , 4, 170125	12.5	19
88	Systematic integration of biomedical knowledge prioritizes drugs for repurposing. <i>ELife</i> , 2017 , 6,	8.9	151
87	Visualizing the top epilepsy predictions in Cytoscape 2017 ,		2
86	Why we predicted ictogenic tricyclic compounds treat epilepsy? 2017 ,		2
85	Association of HLA Genetic Risk Burden With Disease Phenotypes in Multiple Sclerosis. <i>JAMA Neurology</i> , 2016 , 73, 795-802	17.2	43
84	Data nomenclature: naming and abbreviating our network types 2016 ,		2
83	Positive correlations between knockdown and overexpression profiles from LINCS L1000 2016 ,		2
82	Assessing the effectiveness of our hetnet permutations 2016 ,		2
81	Workshop to analyze LINCS data for the Systems Pharmacology course at UCSF 2016 ,		2

80	Announcing PharmacotherapyDB: the Open Catalog of Drug Therapies for Disease 2016 ,	2
79	Assessing the imputation quality of gene expression in LINCS L1000 2016 ,	3
78	Incorporating DrugCentral data in our network 2016 ,	2
77	Estimating the complexity of hetnet traversal 2016 ,	2
76	Transforming DWPCs for hetnet edge prediction 2016 ,	2
75	Network Edge Prediction: how to deal with self-testing 2016 ,	2
74	Measuring user contribution and content creation 2016 ,	2
73	Network Edge Prediction: Estimating the prior 2016 ,	2
72	Predictions of whether a compound treats a disease 2016 ,	2
71	Computing standardized logistic regression coefficients 2016 ,	3
70	Our hetnet edge prediction methodology: the modeling framework for Project Rephetio 2016 ,	2
69	Cataloging drug-disease therapies in the ClinicalTrials.gov database 2016 ,	2
68	Sounding the alarm on DrugBank's new license and terms of use 2016 ,	2
67	Edge dropout contamination in hetnet edge prediction 2016 ,	2
66	Hosting Hetionet in the cloud: creating a public Neo4j instance 2016 ,	2
65	Exploring the power of Hetionet: a Cypher query depot 2016 ,	2
64	Prediction in epilepsy 2016 ,	2
63	Brainstorming future directions for Hetionet 2016 ,	2

62	Decomposing the DWPC to assess intermediate node or edge contributions 2016 ,		2
61	Decomposing predictions into their network support 2016 ,		2
60	Genetic Association-Guided Analysis of Gene Networks for the Study of Complex Traits. <i>Circulation: Cardiovascular Genetics</i> , 2016 , 9, 179-84		7
59	Meta-analysis of genome-wide association studies reveals genetic overlap between Hodgkin lymphoma and multiple sclerosis. <i>International Journal of Epidemiology</i> , 2016 , 45, 728-40	7.8	16
58	Understanding multicellular function and disease with human tissue-specific networks. <i>Nature Genetics</i> , 2015 , 47, 569-76	36.3	473
57	iCTNet2: integrating heterogeneous biological interactions to understand complex traits. <i>F1000Research</i> , 2015 , 4, 485	3.6	7
56	iCTNet2: integrating heterogeneous biological interactions to understand complex traits. <i>F1000Research</i> , 2015 , 4, 485	3.6	6
55	Heterogeneous Network Edge Prediction: A Data Integration Approach to Prioritize Disease-Associated Genes. <i>PLoS Computational Biology</i> , 2015 , 11, e1004259	5	69
54	One network to rule them all 2015 ,		2
53	Renaming heterogeneous networks to a more concise and catchy term 2015 ,		2
52	Processing DisGeNET for disease-gene relationships 2015 ,		2
51	Processing the DISEASES resource for disease-gene relationships 2015 ,		2
50	Integrating resources with disparate licensing into an open network 2015 ,		4
49	MSigDB licensing 2015 ,		2
48	LINCS L1000 licensing 2015 ,		2
47	Incomplete Interactome licensing 2015 ,		2
46	Using the neo4j graph database for hetnets 2015 ,		2
45	Assessing the informativeness of features 2015 ,		2

44	Processing Bgee for tissue-specific gene presence and over/under-expression 2015,	2
43	Permuting hetnets and implementing randomized edge swaps in cypher 2015,	2
42	How should we construct a catalog of drug indications? 2015,	2
41	Enabling reproducibility and reuse 2015,	2
40	Using Entrez Gene as our gene vocabulary 2015,	2
39	Compiling Gene Ontology annotations into an easy-to-use format 2015,	2
38	Unifying drug vocabularies 2015,	2
37	Tissue Node 2015,	2
36	Computing consensus transcriptional profiles for LINCS L1000 perturbations 2015,	2
35	Unifying disease vocabularies 2015,	2
34	Processing LabeledIn to extract indications 2015,	2
33	Integrating drug target information from BindingDB 2015,	2
32	Selecting informative ERC (evolutionary rate covariation) values between genes 2015,	2
31	Extracting indications from the ehrlink resource 2015,	2
30	Protein (target, carrier, transporter, and enzyme) interactions in DrugBank 2015,	2
29	Mining knowledge from MEDLINE articles and their indexed MeSH terms 2015,	5
28	Disease Ontology feature requests 2015,	2
27	Calculating molecular similarities between DrugBank compounds 2015,	2

26	Calculating genomic windows for GWAS lead SNPs 2015 ,		2
25	Adding pathway resources to your network 2015 ,		2
24	Extracting disease-gene associations from the GWAS Catalog 2015 ,		5
23	Tissue-specific gene expression resources 2015 ,		2
22	Creating a catalog of protein interactions 2015 ,		2
21	The TISSUES resource for the tissue-specificity of genes 2015 ,		2
20	Disease similarity from MEDLINE topic cooccurrence 2015 ,		2
19	Functional disease annotations for genes using DOAF 2015 ,		2
18	Expert curation of our indication catalog for disease-modifying treatments 2015 ,		2
17	STARGEO: expression signatures for disease using crowdsourced GEO annotation 2015 ,		2
16	Extracting side effects from SIDER 4 2015 ,		2
15	Lung cancer incidence decreases with elevation: evidence for oxygen as an inhaled carcinogen. <i>PeerJ</i> , 2015 , 3, e705	3.1	19
14	Evolving hard problems: Generating human genetics datasets with a complex etiology. <i>BioData Mining</i> , 2011 , 4, 21	4.3	12
13	Multifactor dimensionality reduction for graphics processing units enables genome-wide testing of epistasis in sporadic ALS. <i>Bioinformatics</i> , 2010 , 26, 694-5	7.2	60
12	Enabling personal genomics with an explicit test of epistasis. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2010 , 327-36	1.3	31
11	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	0.9	16
10	A Model Free Method to Generate Human Genetics Datasets with Complex Gene-Disease Relationships. <i>Lecture Notes in Computer Science</i> , 2010 , 74-85	0.9	2
9	Rephetio: Repurposing drugs on a hetnet [project]		3

8	Rephetio: Repurposing drugs on a hetnet [proposal]	2
7	Sci-Hub provides access to nearly all scholarly literature	10
6	Sci-Hub provides access to nearly all scholarly literature	5
5	Systematic integration of biomedical knowledge prioritizes drugs for repurposing	1
4	Opportunities and obstacles for deep learning in biology and medicine	45
3	Analysis of ISCB honorees and keynotes reveals disparities	7
2	Sequential compression of gene expression across dimensionalities and methods reveals no single best method or dimensionality	3
1	Expanding a Database-derived Biomedical Knowledge Graph via Multi-relation Extraction from Biomedical Abstracts	1