

Casey S. Greene

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.

184
papers

7,291
citations

41
h-index

82
g-index

254
ext. papers

10,432
ext. citations

9.7
avg, IF

5.99
L-index

#	Paper	IF	Citations
184	Correction for Rando et al., "Pathogenesis, Symptomatology, and Transmission of SARS-CoV-2 through Analysis of Viral Genomics and Structure".. <i>MSystems</i> , 2022 , e0144721	7.6	2
183	Computational audits combat disparities in recognition.. <i>Nature Human Behaviour</i> , 2022 ,	12.8	0
182	Examining linguistic shifts between preprints and publications.. <i>PLoS Biology</i> , 2022 , 20, e3001470	9.7	1
181	Ten quick tips for deep learning in biology.. <i>PLoS Computational Biology</i> , 2022 , 18, e1009803	5	1
180	Long-Term Cellulose Enrichment Selects for Highly Cellulolytic Consortia and Competition for Public Goods.. <i>MSystems</i> , 2022 , e0151921	7.6	0
179	Identification and Development of Therapeutics for COVID-19. <i>MSystems</i> , 2021 , e0023321	7.6	5
178	Characterizing Long COVID: Deep Phenotype of a Complex Condition. <i>EBioMedicine</i> , 2021 , 74, 103722	8.8	25
177	A field guide to cultivating computational biology. <i>PLoS Biology</i> , 2021 , 19, e3001419	9.7	2
176	Pathogenesis, Symptomatology, and Transmission of SARS-CoV-2 through Analysis of Viral Genomics and Structure. <i>MSystems</i> , 2021 , 6, e0009521	7.6	8
175	Macrophages in SHH subgroup medulloblastoma display dynamic heterogeneity that varies with treatment modality. <i>Cell Reports</i> , 2021 , 34, 108917	10.6	7
174	Dietary Supplements and Nutraceuticals under Investigation for COVID-19 Prevention and Treatment. <i>MSystems</i> , 2021 , 6,	7.6	25
173	Expanding and Remixing the Metadata Landscape. <i>Trends in Cancer</i> , 2021 , 7, 276-278	12.5	2
172	Genome-wide association study implicates novel loci and reveals candidate effector genes for longitudinal pediatric bone accrual. <i>Genome Biology</i> , 2021 , 22, 1	18.3	58
171	Parameterized algorithms for identifying gene co-expression modules via weighted clique decomposition. 2021 , 2021, 111-122		1
170	Induction of ADAM10 by Radiation Therapy Drives Fibrosis, Resistance, and Epithelial-to-Mesenchymal Transition in Pancreatic Cancer. <i>Cancer Research</i> , 2021 , 81, 3255-3269	10.1	9
169	Reproducibility standards for machine learning in the life sciences. <i>Nature Methods</i> , 2021 , 18, 1132-1135	21.6	14
168	Community-wide hackathons to identify central themes in single-cell multi-omics. <i>Genome Biology</i> , 2021 , 22, 220	18.3	2

167	Cancer Informatics for Cancer Centers: Scientific Drivers for Informatics, Data Science, and Care in Pediatric, Adolescent, and Young Adult Cancer. <i>JCO Clinical Cancer Informatics</i> , 2021 , 5, 881-896	5.2	1
166	miQC: An adaptive probabilistic framework for quality control of single-cell RNA-sequencing data. <i>PLoS Computational Biology</i> , 2021 , 17, e1009290	5	4
165	Analysis of scientific society honors reveals disparities. <i>Cell Systems</i> , 2021 , 12, 900-906.e5	10.6	2
164	Genetic demultiplexing of pooled single-cell RNA-sequencing samples in cancer facilitates effective experimental design. <i>GigaScience</i> , 2021 , 10,	7.6	3
163	An Open-Publishing Response to the COVID-19 Infodemic.. <i>CEUR Workshop Proceedings</i> , 2021 , 2976, 29-38	0.2	
162	Compressing gene expression data using multiple latent space dimensionalities learns complementary biological representations. <i>Genome Biology</i> , 2020 , 21, 109	18.3	20
161	Recommendations to enhance rigor and reproducibility in biomedical research. <i>GigaScience</i> , 2020 , 9,	7.6	20
160	Building an international consortium for tracking coronavirus health status. <i>Nature Medicine</i> , 2020 , 26, 1161-1165	50.5	16
159	Development and Validation of the Gene Expression Predictor of High-grade Serous Ovarian Carcinoma Molecular SubTYPE (PrOTYPE). <i>Clinical Cancer Research</i> , 2020 , 26, 5411-5423	12.9	21
158	Constructing knowledge graphs and their biomedical applications. <i>Computational and Structural Biotechnology Journal</i> , 2020 , 18, 1414-1428	6.8	36
157	Integrative Analysis Identifies Candidate Tumor Microenvironment and Intracellular Signaling Pathways that Define Tumor Heterogeneity in NF1. <i>Genes</i> , 2020 , 11,	4.2	4
156	mutant fitness in microoxia is supported by an Anr-regulated oxygen-binding hemerythrin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 3167-3173	11.5	12
155	Incorporating biological structure into machine learning models in biomedicine. <i>Current Opinion in Biotechnology</i> , 2020 , 63, 126-134	11.4	15
154	Specific histone modifications associate with alternative exon selection during mammalian development. <i>Nucleic Acids Research</i> , 2020 , 48, 4709-4724	20.1	7
153	Correcting for experiment-specific variability in expression compendia can remove underlying signals. <i>GigaScience</i> , 2020 , 9,	7.6	4
152	Embracing study heterogeneity for finding genetic interactions in large-scale research consortia. <i>Genetic Epidemiology</i> , 2020 , 44, 52-66	2.6	1
151	Biologically Informed Neural Networks Predict Drug Responses. <i>Cancer Cell</i> , 2020 , 38, 613-615	24.3	3
150	Transparency and reproducibility in artificial intelligence. <i>Nature</i> , 2020 , 586, E14-E16	50.4	85

149	Responsible, practical genomic data sharing that accelerates research. <i>Nature Reviews Genetics</i> , 2020 , 21, 615-629	30.1	20
148	Bacteria Contribute to Plant Secondary Compound Degradation in a Generalist Herbivore System. <i>MBio</i> , 2020 , 11,	7.8	9
147	Population-scale longitudinal mapping of COVID-19 symptoms, behaviour and testing. <i>Nature Human Behaviour</i> , 2020 , 4, 972-982	12.8	51
146	The antimicrobial potential of Streptomyces from insect microbiomes. <i>Nature Communications</i> , 2019 , 10, 516	17.4	110
145	MultiPLIER: A Transfer Learning Framework for Transcriptomics Reveals Systemic Features of Rare Disease. <i>Cell Systems</i> , 2019 , 8, 380-394.e4	10.6	38
144	Open collaborative writing with Manubot. <i>PLoS Computational Biology</i> , 2019 , 15, e1007128	5	24
143	Show me the models. <i>Nature Biotechnology</i> , 2019 , 37, 623-625	44.5	
142	The Pediatric Cell Atlas: Defining the Growth Phase of Human Development at Single-Cell Resolution. <i>Developmental Cell</i> , 2019 , 49, 10-29	10.2	39
141	Privacy-Preserving Generative Deep Neural Networks Support Clinical Data Sharing. <i>Circulation: Cardiovascular Quality and Outcomes</i> , 2019 , 12, e005122	5.8	79
140	Discovering Pathway and Cell Type Signatures in Transcriptomic Compendia with Machine Learning. <i>Annual Review of Biomedical Data Science</i> , 2019 , 2, 1-17	5.6	7
139	Genomic Profiling of Childhood Tumor Patient-Derived Xenograft Models to Enable Rational Clinical Trial Design. <i>Cell Reports</i> , 2019 , 29, 1675-1689.e9	10.6	51
138	Parameter tuning is a key part of dimensionality reduction via deep variational autoencoders for single cell RNA transcriptomics. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2019 , 24, 362-373	1.3	22
137	Integrated phosphoproteomics and transcriptional classifiers reveal hidden RAS signaling dynamics in multiple myeloma. <i>Blood Advances</i> , 2019 , 3, 3214-3227	7.8	9
136	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. <i>Genome Biology</i> , 2019 , 20, 244	18.3	111
135	Immune landscapes associated with different glioblastoma molecular subtypes. <i>Acta Neuropathologica Communications</i> , 2019 , 7, 203	7.3	56
134	New Long-Term Memory Genes Revealed by Assessing Computational Function Prediction Methods. <i>G3: Genes, Genomes, Genetics</i> , 2019 , 9, 251-267	3.2	11
133	Learning and Imputation for Mass-spec Bias Reduction (LIMBR). <i>Bioinformatics</i> , 2019 , 35, 1518-1526	7.2	9
132	Opportunities and obstacles for deep learning in biology and medicine. <i>Journal of the Royal Society Interface</i> , 2018 , 15,	4.1	780

131	Oncogenic Signaling Pathways in The Cancer Genome Atlas. <i>Cell</i> , 2018 , 173, 321-337.e10	56.2	1124
130	Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. <i>Cell Reports</i> , 2018 , 23, 172-180.e3	10.6	66
129	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. <i>Cell Reports</i> , 2018 , 23, 239-254.e6	10.6	405
128	Inclusion of Unstructured Clinical Text Improves Early Prediction of Death or Prolonged ICU Stay. <i>Critical Care Medicine</i> , 2018 , 46, 1125-1132	1.4	37
127	A Multimodal Strategy Used by a Large c-di-GMP Network. <i>Journal of Bacteriology</i> , 2018 , 200,	3.5	29
126	Extracting a biologically relevant latent space from cancer transcriptomes with variational autoencoders 2018 ,		20
125	PathCORE-T: identifying and visualizing globally co-occurring pathways in large transcriptomic compendia. <i>BioData Mining</i> , 2018 , 11, 14	4.3	6
124	Metabolic pathways and immunometabolism in rare kidney diseases. <i>Annals of the Rheumatic Diseases</i> , 2018 , 77, 1226-1233	2.4	41
123	Enter the Matrix: Factorization Uncovers Knowledge from Omics. <i>Trends in Genetics</i> , 2018 , 34, 790-805	8.5	84
122	Extracting a biologically relevant latent space from cancer transcriptomes with variational autoencoders. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2018 , 23, 80-91	1.3	57
121	Functional network community detection can disaggregate and filter multiple underlying pathways in enrichment analyses. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2018 , 23, 157-167	1.3	
120	Integrating Phosphoproteomics and Transcriptional Classifiers Reveals "Hidden Signaling" in Multiple Myeloma Including Differential KRAS and NRAS Mutant Effects. <i>Blood</i> , 2018 , 132, 469-469	2.2	
119	Parameter tuning is a key part of dimensionality reduction via deep variational autoencoders for single cell RNA transcriptomics 2018 ,		7
118	A parasite's perspective on data sharing. <i>GigaScience</i> , 2018 , 7,	7.6	4
117	Bayesian deep learning for single-cell analysis. <i>Nature Methods</i> , 2018 , 15, 1009-1010	21.6	14
116	Sci-Hub provides access to nearly all scholarly literature. <i>ELife</i> , 2018 , 7,	8.9	59
115	Data-Sharing Models. <i>New England Journal of Medicine</i> , 2017 , 376, 2305-2306	59.2	10
114	Tissue-specific network-based genome wide study of amygdala imaging phenotypes to identify functional interaction modules. <i>Bioinformatics</i> , 2017 , 33, 3250-3257	7.2	18

113	A novel multi-network approach reveals tissue-specific cellular modulators of fibrosis in systemic sclerosis. <i>Genome Medicine</i> , 2017 , 9, 27	14.4	60
112	Celebrating parasites. <i>Nature Genetics</i> , 2017 , 49, 483-484	36.3	19
111	Reproducibility of computational workflows is automated using continuous analysis. <i>Nature Biotechnology</i> , 2017 , 35, 342-346	44.5	73
110	ADAGE signature analysis: differential expression analysis with data-defined gene sets. <i>BMC Bioinformatics</i> , 2017 , 18, 512	3.6	7
109	Machine Learning Analysis Identifies as an Important Learning and Memory Gene Required for Memory Retention and Social Learning. <i>G3: Genes, Genomes, Genetics</i> , 2017 , 7, 3705-3718	3.2	6
108	Unsupervised Extraction of Stable Expression Signatures from Public Compendia with an Ensemble of Neural Networks. <i>Cell Systems</i> , 2017 , 5, 63-71.e6	10.6	50
107	Implicating candidate genes at GWAS signals by leveraging topologically associating domains. <i>European Journal of Human Genetics</i> , 2017 , 25, 1286-1289	5.3	15
106	Challenges and Opportunities in Studying the Epidemiology of Ovarian Cancer Subtypes. <i>Current Epidemiology Reports</i> , 2017 , 4, 211-220	2.9	33
105	A Pilot Characterization of the Human Chronobiome. <i>Scientific Reports</i> , 2017 , 7, 17141	4.9	48
104	A machine learning classifier trained on cancer transcriptomes detects NF1 inactivation signal in glioblastoma. <i>BMC Genomics</i> , 2017 , 18, 127	4.5	23
103	NO-BOUNDARY THINKING IN BIOINFORMATICS. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2017 , 22, 646-648	1.3	1
102	Tell me your neighbors, and I will tell you what you are. <i>Science Translational Medicine</i> , 2017 , 9,	17.5	1
101	Adapting bioinformatics curricula for big data. <i>Briefings in Bioinformatics</i> , 2016 , 17, 43-50	13.4	37
100	Semi-supervised learning of the electronic health record for phenotype stratification. <i>Journal of Biomedical Informatics</i> , 2016 , 64, 168-178	10.2	92
99	Pathway and network-based strategies to translate genetic discoveries into effective therapies. <i>Human Molecular Genetics</i> , 2016 , 25, R94-R98	5.6	22
98	Network-based analysis of genetic variants associated with hippocampal volume in Alzheimer's disease: a study of ADNI cohorts. <i>BioData Mining</i> , 2016 , 9, 3	4.3	21
97	ADAGE-Based Integration of Publicly Available Gene Expression Data with Denoising Autoencoders Illuminates Microbe-Host Interactions. <i>MSystems</i> , 2016 , 1,	7.6	70
96	Recent Advances and Emerging Applications in Text and Data Mining for Biomedical Discovery. <i>Briefings in Bioinformatics</i> , 2016 , 17, 33-42	13.4	89

95	Evolution of High Cellulolytic Activity in Symbiotic Streptomyces through Selection of Expanded Gene Content and Coordinated Gene Expression. <i>PLoS Biology</i> , 2016 , 14, e1002475	9.7	46
94	Cellulose-Enriched Microbial Communities from Leaf-Cutter Ant (<i>Atta colombica</i>) Refuse Dumps Vary in Taxonomic Composition and Degradation Ability. <i>PLoS ONE</i> , 2016 , 11, e0151840	3.7	17
93	Genomic characterization of patient-derived xenograft models established from fine needle aspirate biopsies of a primary pancreatic ductal adenocarcinoma and from patient-matched metastatic sites. <i>Oncotarget</i> , 2016 , 7, 17087-102	3.3	30
92	Cross-platform normalization of microarray and RNA-seq data for machine learning applications. <i>PeerJ</i> , 2016 , 4, e1621	3.1	45
91	Cheap-seq. <i>Science Translational Medicine</i> , 2016 , 8, 370ec203	17.5	
90	Comprehensive Cross-Population Analysis of High-Grade Serous Ovarian Cancer Supports No More Than Three Subtypes. <i>G3: Genes, Genomes, Genetics</i> , 2016 , 6, 4097-4103	3.2	18
89	COMPUTATIONAL APPROACHES TO STUDY MICROBES AND MICROBIOMES 2016 ,		3
88	Genetic Association-Guided Analysis of Gene Networks for the Study of Complex Traits. <i>Circulation: Cardiovascular Genetics</i> , 2016 , 9, 179-84		7
87	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. <i>Genome Biology</i> , 2016 , 17, 184	18.3	218
86	Integrative Networks Illuminate Biological Factors Underlying GeneDisease Associations. <i>Current Genetic Medicine Reports</i> , 2016 , 4, 155-162	2.2	6
85	Targeted exploration and analysis of large cross-platform human transcriptomic compendia. <i>Nature Methods</i> , 2015 , 12, 211-4, 3 p following 214	21.6	92
84	Systems level analysis of systemic sclerosis shows a network of immune and profibrotic pathways connected with genetic polymorphisms. <i>PLoS Computational Biology</i> , 2015 , 11, e1004005	5	78
83	Understanding multicellular function and disease with human tissue-specific networks. <i>Nature Genetics</i> , 2015 , 47, 569-76	36.3	473
82	International genome-wide meta-analysis identifies new primary biliary cirrhosis risk loci and targetable pathogenic pathways. <i>Nature Communications</i> , 2015 , 6, 8019	17.4	185
81	Identification of shared and unique susceptibility pathways among cancers of the lung, breast, and prostate from genome-wide association studies and tissue-specific protein interactions. <i>Human Molecular Genetics</i> , 2015 , 24, 7406-20	5.6	11
80	Identification of Novel Genetic Models of Glaucoma Using the EMERGENT Genetic Programming-Based Artificial Intelligence System. <i>Genetic and Evolutionary Computation</i> , 2015 , 17-35	0.8	4
79	Leveraging global gene expression patterns to predict expression of unmeasured genes. <i>BMC Genomics</i> , 2015 , 16, 1065	4.5	2
78	Testing multiple hypotheses through IMP weighted FDR based on a genetic functional network with application to a new zebrafish transcriptome study. <i>BioData Mining</i> , 2015 , 8, 17	4.3	2

77	Unsupervised feature construction and knowledge extraction from genome-wide assays of breast cancer with denoising autoencoders. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2015 , 132-43	1.3	43
76	Cellulolytic <i>Streptomyces</i> strains associated with herbivorous insects share a phylogenetically linked capacity to degrade lignocellulose. <i>Applied and Environmental Microbiology</i> , 2014 , 80, 4692-701	4.8	49
75	Computational genetics analysis of grey matter density in Alzheimer's disease. <i>BioData Mining</i> , 2014 , 7, 17	4.3	5
74	Big data bioinformatics. <i>Journal of Cellular Physiology</i> , 2014 , 229, 1896-900	7	109
73	UNSUPERVISED FEATURE CONSTRUCTION AND KNOWLEDGE EXTRACTION FROM GENOME-WIDE ASSAYS OF BREAST CANCER WITH DENOISING AUTOENCODERS 2014 ,		27
72	Evolution of substrate specificity in bacterial AA10 lytic polysaccharide monooxygenases. <i>Biotechnology for Biofuels</i> , 2014 , 7, 109	7.8	59
71	Predicting targeted drug combinations based on Pareto optimal patterns of coexpression network connectivity. <i>Genome Medicine</i> , 2014 , 6, 33	14.4	9
70	Biochemical properties and atomic resolution structure of a proteolytically processed β mannanase from cellulolytic <i>Streptomyces</i> sp. SirexAA-E. <i>PLoS ONE</i> , 2014 , 9, e94166	3.7	12
69	Aerobic deconstruction of cellulosic biomass by an insect-associated <i>Streptomyces</i> . <i>Scientific Reports</i> , 2013 , 3, 1030	4.9	93
68	Defining cell-type specificity at the transcriptional level in human disease. <i>Genome Research</i> , 2013 , 23, 1862-73	9.7	139
67	Functional knowledge transfer for high-accuracy prediction of under-studied biological processes. <i>PLoS Computational Biology</i> , 2013 , 9, e1002957	5	44
66	LT-IIb(T13I), a non-toxic type II heat-labile enterotoxin, augments the capacity of a ricin toxin subunit vaccine to evoke neutralizing antibodies and protective immunity. <i>PLoS ONE</i> , 2013 , 8, e69678	3.7	14
65	Time-Point Specific Weighting Improves Coexpression Networks from Time-Course Experiments. <i>Lecture Notes in Computer Science</i> , 2013 , 11-22	0.9	1
64	Pharmacological Validation Of Potentiating Targets From SAHA RNA-Interference Modifier Screens In Acute Myeloid Leukemia. <i>Blood</i> , 2013 , 122, 3832-3832	2.2	
63	Accurate evaluation and analysis of functional genomics data and methods. <i>Annals of the New York Academy of Sciences</i> , 2012 , 1260, 95-100	6.5	19
62	TEXT AND DATA MINING FOR BIOMEDICAL DISCOVERY 2012 ,		1
61	Chapter 2: Data-driven view of disease biology. <i>PLoS Computational Biology</i> , 2012 , 8, e1002816	5	11
60	IMP: a multi-species functional genomics portal for integration, visualization and prediction of protein functions and networks. <i>Nucleic Acids Research</i> , 2012 , 40, W484-90	20.1	76

59	Evolving hard problems: Generating human genetics datasets with a complex etiology. <i>BioData Mining</i> , 2011 , 4, 21	4.3	12
58	PILGRM: an interactive data-driven discovery platform for expert biologists. <i>Nucleic Acids Research</i> , 2011 , 39, W368-74	20.1	22
57	An Analysis of New Expert Knowledge Scaling Methods for Biologically Inspired Computing. <i>Lecture Notes in Computer Science</i> , 2011 , 286-293	0.9	1
56	An Open-Ended Computational Evolution Strategy for Evolving Parsimonious Solutions to Human Genetics Problems. <i>Lecture Notes in Computer Science</i> , 2011 , 313-320	0.9	1
55	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
54	Fast genome-wide epistasis analysis using ant colony optimization for multifactor dimensionality reduction analysis on graphics processing units 2010 ,		6
53	Integrative systems biology for data-driven knowledge discovery. <i>Seminars in Nephrology</i> , 2010 , 30, 443-448	4.4	11
52	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
51	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
50	Artificial Immune Systems for Epistasis Analysis in Human Genetics. <i>Lecture Notes in Computer Science</i> , 2010 , 194-204	0.9	3
49	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
48	Sensible Initialization of a Computational Evolution System Using Expert Knowledge for Epistasis Analysis in Human Genetics. <i>Adaptation, Learning, and Optimization</i> , 2010 , 215-226	0.7	8
47	Environmental Sensing of Expert Knowledge in a Computational Evolution System for Complex Problem Solving in Human Genetics. <i>Genetic and Evolutionary Computation</i> , 2010 , 19-36	0.8	8
46	Failure to replicate a genetic association may provide important clues about genetic architecture. <i>PLoS ONE</i> , 2009 , 4, e5639	3.7	198
45	Development and evaluation of an open-ended computational evolution system for the creation of digital organisms with complex genetic architecture 2009 ,		1
44	Sensible Initialization Using Expert Knowledge for Genome-Wide Analysis of Epistasis Using Genetic Programming 2009 , 2009, 1289-1296		12
43	Environmental noise improves epistasis models of genetic data discovered using a computational evolution system 2009 ,		6
42	Accelerating epistasis analysis in human genetics with consumer graphics hardware. <i>BMC Research Notes</i> , 2009 , 2, 149	2.3	29

41	Spatially uniform relief (SURF) for computationally-efficient filtering of gene-gene interactions. <i>BioData Mining</i> , 2009 , 2, 5	4.3	105
40	Optimal Use of Expert Knowledge in Ant Colony Optimization for the Analysis of Epistasis in Human Disease. <i>Lecture Notes in Computer Science</i> , 2009 , 92-103	0.9	21
39	Using expert knowledge in initialization for genome-wide analysis of epistasis using genetic programming 2008 ,		3
38	Solving complex problems in human genetics using GP. <i>ACM SIGEVolution</i> , 2008 , 3, 2-8	0.1	3
37	Ability of epistatic interactions of cytokine single-nucleotide polymorphisms to predict susceptibility to disease subsets in systemic sclerosis patients. <i>Arthritis and Rheumatism</i> , 2008 , 59, 974-83		30
36	Ant Colony Optimization for Genome-Wide Genetic Analysis. <i>Lecture Notes in Computer Science</i> , 2008 , 37-47	0.9	27
35	An Expert Knowledge-Guided Mutation Operator for Genome-Wide Genetic Analysis Using Genetic Programming. <i>Lecture Notes in Computer Science</i> , 2007 , 30-40	0.9	12
34	LTR retrotransposon-gene associations in <i>Drosophila melanogaster</i> . <i>Journal of Molecular Evolution</i> , 2006 , 62, 111-20	3.1	20
33	Solving Complex Problems in Human Genetics Using Nature-Inspired Algorithms Requires Strategies which Exploit Domain-Specific Knowledge 1867-1881		
32	Sci-Hub provides access to nearly all scholarly literature		10
31	Sci-Hub provides access to nearly all scholarly literature		5
30	New <i>Drosophila</i> long-term memory genes revealed by assessing computational function prediction methods		3
29	Comprehensive Cross-Population Analysis of High-Grade Serous Ovarian Cancer Supports No More Than Three Subtypes		2
28	ADAGE analysis of publicly available gene expression data collections illuminates <i>Pseudomonas aeruginosa</i> -host interactions		5
27	Tribe: The collaborative platform for reproducible web-based analysis of gene sets		1
26	Reproducible Computational Workflows with Continuous Analysis		2
25	Cross-Platform Normalization Enables Machine Learning Model Training On Microarray And RNA-Seq Data Simultaneously		5
24	Opportunities and obstacles for deep learning in biology and medicine		45

23	Privacy-preserving generative deep neural networks support clinical data sharing	23
22	Extracting a Biologically Relevant Latent Space from Cancer Transcriptomes with Variational Autoencoders	23
21	Enter the matrix: factorization uncovers knowledge from omics Names/Affiliations	2
20	Single-cell transcriptomic profile reveals macrophage heterogeneity in medulloblastoma and their treatment-dependent recruitment	1
19	Genome-wide association study implicates novel loci and reveals candidate effector genes for longitudinal pediatric bone accrual through variant-to-gene mapping	5
18	Analysis of ISCB honorees and keynotes reveals disparities	7
17	Genetic demultiplexing of pooled single-cell RNA-sequencing samples in cancer facilitates effective experimental design	2
16	Specific histone modifications associate with alternative exon selection during mammalian development	2
15	Parameter tuning is a key part of dimensionality reduction via deep variational autoencoders for single cell RNA transcriptomics	13
14	MultiPLIER: a transfer learning framework for transcriptomics reveals systemic features of rare disease	4
13	Inflammatory and JAK-STAT Pathways as Shared Molecular Targets for ANCA-Associated Vasculitis and Nephrotic Syndrome	2
12	Integrated Phosphoproteomics and Transcriptional Classifiers Reveal Hidden RAS Signaling Dynamics in Multiple Myeloma	1
11	Sequential compression of gene expression across dimensionalities and methods reveals no single best method or dimensionality	3
10	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens	7
9	Expanding a Database-derived Biomedical Knowledge Graph via Multi-relation Extraction from Biomedical Abstracts	1
8	Semi-Supervised Learning of the Electronic Health Record for Phenotype Stratification	1
7	Unsupervised extraction of stable expression signatures from public compendia with eADAGE	1
6	Machine learning analysis identifies <i>Drosophila</i> Grunge/Atrophin as an important learning and memory gene required for memory retention and social learning	2

5	miQC: An adaptive probabilistic framework for quality control of single-cell RNA-sequencing data	3
4	Characterizing Long COVID: Deep Phenotype of a Complex Condition	1
3	Analysis of scientific journalism in Nature reveals gender and regional disparities in coverage	1
2	Linguistic Analysis of the bioRxiv Preprint Landscape	3
1	Solving Complex Problems in Human Genetics using Nature-Inspired Algorithms Requires Strategies which Exploit Domain-Specific Knowledge166-180	