Casey S. Greene

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/1779523/publications.pdf

Version: 2024-02-01

176	12,825	44066	32838
papers	citations	48 h-index	100 g-index

254	254	254	23456
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Oncogenic Signaling Pathways in The Cancer Genome Atlas. Cell, 2018, 173, 321-337.e10.	28.9	2,111
2	Opportunities and obstacles for deep learning in biology and medicine. Journal of the Royal Society Interface, 2018, 15, 20170387.	3.4	1,282
3	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. Cell Reports, 2018, 23, 239-254.e6.	6.4	801
4	Understanding multicellular function and disease with human tissue-specific networks. Nature Genetics, 2015, 47, 569-576.	21.4	738
5	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. Genome Biology, 2016, 17, 184.	8.8	308
6	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. Genome Biology, 2019, 20, 244.	8.8	261
7	International genome-wide meta-analysis identifies new primary biliary cirrhosis risk loci and targetable pathogenic pathways. Nature Communications, 2015, 6, 8019.	12.8	245
8	Genome-wide association study implicates novel loci and reveals candidate effector genes for longitudinal pediatric bone accrual. Genome Biology, 2021, 22, 1.	8.8	239
9	Transparency and reproducibility in artificial intelligence. Nature, 2020, 586, E14-E16.	27.8	233
10	Failure to Replicate a Genetic Association May Provide Important Clues About Genetic Architecture. PLoS ONE, 2009, 4, e5639.	2.5	227
11	The antimicrobial potential of Streptomyces from insect microbiomes. Nature Communications, 2019, 10, 516.	12.8	222
12	Defining cell-type specificity at the transcriptional level in human disease. Genome Research, 2013, 23, 1862-1873.	5.5	196
13	Enter the Matrix: Factorization Uncovers Knowledge from Omics. Trends in Genetics, 2018, 34, 790-805.	6.7	181
14	Privacy-Preserving Generative Deep Neural Networks Support Clinical Data Sharing. Circulation: Cardiovascular Quality and Outcomes, 2019, 12, e005122.	2.2	172
15	Big Data Bioinformatics. Journal of Cellular Physiology, 2014, 229, 1896-1900.	4.1	161
16	Targeted exploration and analysis of large cross-platform human transcriptomic compendia. Nature Methods, 2015, 12, 211-214.	19.0	137
17	Semi-supervised learning of the electronic health record for phenotype stratification. Journal of Biomedical Informatics, 2016, 64, 168-178.	4.3	135
18	Constructing knowledge graphs and their biomedical applications. Computational and Structural Biotechnology Journal, 2020, 18, 1414-1428.	4.1	132

#	Article	IF	Citations
19	Recent Advances and Emerging Applications in Text and Data Mining for Biomedical Discovery. Briefings in Bioinformatics, 2016, 17, 33-42.	6.5	131
20	Spatially Uniform ReliefF (SURF) for computationally-efficient filtering of gene-gene interactions. BioData Mining, 2009, 2, 5.	4.0	129
21	Characterizing Long COVID: Deep Phenotype of a Complex Condition. EBioMedicine, 2021, 74, 103722.	6.1	127
22	Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. Cell Reports, 2018, 23, 172-180.e3.	6.4	119
23	ADAGE-Based Integration of Publicly Available Pseudomonas aeruginosa Gene Expression Data with Denoising Autoencoders Illuminates Microbe-Host Interactions. MSystems, 2016, 1, .	3.8	116
24	Systems Level Analysis of Systemic Sclerosis Shows a Network of Immune and Profibrotic Pathways Connected with Genetic Polymorphisms. PLoS Computational Biology, 2015, 11, e1004005.	3.2	115
25	Immune landscapes associated with different glioblastoma molecular subtypes. Acta Neuropathologica Communications, 2019, 7, 203.	5.2	112
26	Reproducibility of computational workflows is automated using continuous analysis. Nature Biotechnology, 2017, 35, 342-346.	17.5	111
27	Aerobic deconstruction of cellulosic biomass by an insect-associated Streptomyces. Scientific Reports, 2013, 3, 1030.	3.3	107
28	IMP: a multi-species functional genomics portal for integration, visualization and prediction of protein functions and networks. Nucleic Acids Research, 2012, 40, W484-W490.	14.5	105
29	Genomic Profiling of Childhood Tumor Patient-Derived Xenograft Models to Enable Rational Clinical Trial Design. Cell Reports, 2019, 29, 1675-1689.e9.	6.4	103
30	Extracting a biologically relevant latent space from cancer transcriptomes with variational autoencoders. , 2018, , .		101
31	Metabolic pathways and immunometabolism in rare kidney diseases. Annals of the Rheumatic Diseases, 2018, 77, annrheumdis-2017-212935.	0.9	101
32	Reproducibility standards for machine learning in the life sciences. Nature Methods, 2021, 18, 1132-1135.	19.0	96
33	Population-scale longitudinal mapping of COVID-19 symptoms, behaviour and testing. Nature Human Behaviour, 2020, 4, 972-982.	12.0	93
34	A novel multi-network approach reveals tissue-specific cellular modulators of fibrosis in systemic sclerosis. Genome Medicine, 2017, 9, 27.	8.2	92
35	MultiPLIER: A Transfer Learning Framework for Transcriptomics Reveals Systemic Features of Rare Disease. Cell Systems, 2019, 8, 380-394.e4.	6.2	92
36	Sci-Hub provides access to nearly all scholarly literature. ELife, 2018, 7, .	6.0	89

#	Article	IF	Citations
37	Unsupervised Extraction of Stable Expression Signatures from Public Compendia with an Ensemble of Neural Networks. Cell Systems, 2017, 5, 63-71.e6.	6.2	84
38	Recommendations to enhance rigor and reproducibility in biomedical research. GigaScience, 2020, 9, .	6.4	83
39	UNSUPERVISED FEATURE CONSTRUCTION AND KNOWLEDGE EXTRACTION FROM GENOME-WIDE ASSAYS OF BREAST CANCER WITH DENOISING AUTOENCODERS. , 2014, , .		79
40	Cross-platform normalization of microarray and RNA-seq data for machine learning applications. PeerJ, 2016, 4, e1621.	2.0	78
41	Multifactor dimensionality reduction for graphics processing units enables genome-wide testing of epistasis in sporadic ALS. Bioinformatics, 2010, 26, 694-695.	4.1	76
42	Cellulolytic Streptomyces Strains Associated with Herbivorous Insects Share a Phylogenetically Linked Capacity To Degrade Lignocellulose. Applied and Environmental Microbiology, 2014, 80, 4692-4701.	3.1	70
43	A Pilot Characterization of the Human Chronobiome. Scientific Reports, 2017, 7, 17141.	3.3	70
44	Evolution of substrate specificity in bacterial AA10 lytic polysaccharide monooxygenases. Biotechnology for Biofuels, 2014, 7, 109.	6.2	69
45	Dietary Supplements and Nutraceuticals under Investigation for COVID-19 Prevention and Treatment. MSystems, 2021, 6, .	3.8	68
46	Evolution of High Cellulolytic Activity in Symbiotic Streptomyces through Selection of Expanded Gene Content and Coordinated Gene Expression. PLoS Biology, 2016, 14, e1002475.	5.6	68
47	Responsible, practical genomic data sharing that accelerates research. Nature Reviews Genetics, 2020, 21, 615-629.	16.3	66
48	Extracting a biologically relevant latent space from cancer transcriptomes with variational autoencoders. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2018, 23, 80-91.	0.7	66
49	Functional Knowledge Transfer for High-accuracy Prediction of Under-studied Biological Processes. PLoS Computational Biology, 2013, 9, e1002957.	3.2	62
50	Inclusion of Unstructured Clinical Text Improves Early Prediction of Death or Prolonged ICU Stay*. Critical Care Medicine, 2018, 46, 1125-1132.	0.9	61
51	The Pediatric Cell Atlas: Defining the Growth Phase of Human Development at Single-Cell Resolution. Developmental Cell, 2019, 49, 10-29.	7.0	57
52	Challenges and Opportunities in Studying the Epidemiology of Ovarian Cancer Subtypes. Current Epidemiology Reports, 2017, 4, 211-220.	2.4	56
53	A Multimodal Strategy Used by a Large c-di-GMP Network. Journal of Bacteriology, 2018, 200, .	2.2	52
54	Open collaborative writing with Manubot. PLoS Computational Biology, 2019, 15, e1007128.	3.2	51

#	Article	IF	Citations
55	Unsupervised feature construction and knowledge extraction from genome-wide assays of breast cancer with denoising autoencoders. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2015, , 132-43.	0.7	45
56	Adapting bioinformatics curricula for big data. Briefings in Bioinformatics, 2016, 17, 43-50.	6.5	44
57	Pseudomonas aeruginosa lasR mutant fitness in microoxia is supported by an Anr-regulated oxygen-binding hemerythrin. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 3167-3173.	7.1	44
58	Compressing gene expression data using multiple latent space dimensionalities learns complementary biological representations. Genome Biology, 2020, 21, 109.	8.8	43
59	Development and Validation of the Gene Expression Predictor of High-grade Serous Ovarian Carcinoma Molecular SubTYPE (PrOTYPE). Clinical Cancer Research, 2020, 26, 5411-5423.	7.0	43
60	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. Oncotarget, 2016, 7, 17087-17102.	1.8	40
61	miQC: An adaptive probabilistic framework for quality control of single-cell RNA-sequencing data. PLoS Computational Biology, 2021, 17, e1009290.	3.2	38
62	Ant Colony Optimization for Genome-Wide Genetic Analysis. Lecture Notes in Computer Science, 2008, , 37-47.	1.3	38
63	Induction of ADAM10 by Radiation Therapy Drives Fibrosis, Resistance, and Epithelial-to-Mesenchyal Transition in Pancreatic Cancer. Cancer Research, 2021, 81, 3255-3269.	0.9	37
64	Accelerating epistasis analysis in human genetics with consumer graphics hardware. BMC Research Notes, 2009, 2, 149.	1.4	36
65	Ability of epistatic interactions of cytokine singleâ€nucleotide polymorphisms to predict susceptibility to disease subsets in systemic sclerosis patients. Arthritis and Rheumatism, 2008, 59, 974-983.	6.7	35
66	ENABLING PERSONAL GENOMICS WITH AN EXPLICIT TEST OF EPISTASIS. , 2009, , 327-336.		35
67	Pathway and network-based strategies to translate genetic discoveries into effective therapies. Human Molecular Genetics, 2016, 25, R94-R98.	2.9	33
68	Comprehensive Cross-Population Analysis of High-Grade Serous Ovarian Cancer Supports No More Than Three Subtypes. G3: Genes, Genomes, Genetics, 2016, 6, 4097-4103.	1.8	31
69	A machine learning classifier trained on cancer transcriptomes detects NF1 inactivation signal in glioblastoma. BMC Genomics, 2017, 18, 127.	2.8	30
70	Bacteria Contribute to Plant Secondary Compound Degradation in a Generalist Herbivore System. MBio, 2020, 11, .	4.1	30
71	Cellulose-Enriched Microbial Communities from Leaf-Cutter Ant (Atta colombica) Refuse Dumps Vary in Taxonomic Composition and Degradation Ability. PLoS ONE, 2016, 11, e0151840.	2.5	29
72	Network-based analysis of genetic variants associated with hippocampal volume in Alzheimerâ€™s disease: a study of ADNI cohorts. BioData Mining, 2016, 9, 3.	4.0	28

#	Article	IF	Citations
73	PILGRM: an interactive data-driven discovery platform for expert biologists. Nucleic Acids Research, 2011, 39, W368-W374.	14.5	27
74	Macrophages in SHH subgroup medulloblastoma display dynamic heterogeneity that varies with treatment modality. Cell Reports, 2021, 34, 108917.	6.4	27
75	Incorporating biological structure into machine learning models in biomedicine. Current Opinion in Biotechnology, 2020, 63, 126-134.	6.6	26
76	Pathogenesis, Symptomatology, and Transmission of SARS-CoV-2 through Analysis of Viral Genomics and Structure. MSystems, 2021, 6, e0009521.	3.8	26
77	Celebrating parasites. Nature Genetics, 2017, 49, 483-484.	21.4	25
78	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.	1.3	24
79	Tissue-specific network-based genome wide study of amygdala imaging phenotypes to identify functional interaction modules. Bioinformatics, 2017, 33, 3250-3257.	4.1	23
80	Building an international consortium for tracking coronavirus health status. Nature Medicine, 2020, 26, 1161-1165.	30.7	23
81	Parameter tuning is a key part of dimensionality reduction via deep variational autoencoders for single cell RNA transcriptomics. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2019, 24, 362-373.	0.7	23
82	Parameter tuning is a key part of dimensionality reduction via deep variational autoencoders for single cell RNA transcriptomics. , 2018, , .		22
83	LTR Retrotransposon-Gene Associations in Drosophila melanogaster. Journal of Molecular Evolution, 2006, 62, 111-120.	1.8	21
84	Bayesian deep learning for single-cell analysis. Nature Methods, 2018, 15, 1009-1010.	19.0	21
85	Optimal Use of Expert Knowledge in Ant Colony Optimization for the Analysis of Epistasis in Human Disease. Lecture Notes in Computer Science, 2009, , 92-103.	1.3	21
86	Integrative Systems Biology for Data-Driven Knowledge Discovery. Seminars in Nephrology, 2010, 30, 443-454.	1.6	20
87	Accurate evaluation and analysis of functional genomics data and methods. Annals of the New York Academy of Sciences, 2012, 1260, 95-100.	3.8	20
88	Identification and Development of Therapeutics for COVID-19. MSystems, 2021, 6, e0023321.	3.8	20
89	Evolving hard problems: Generating human genetics datasets with a complex etiology. BioData Mining, 2011, 4, 21.	4.0	19
90	Integrated phosphoproteomics and transcriptional classifiers reveal hidden RAS signaling dynamics in multiple myeloma. Blood Advances, 2019, 3, 3214-3227.	5.2	19

#	Article	IF	Citations
91	Specific histone modifications associate with alternative exon selection during mammalian development. Nucleic Acids Research, 2020, 48, 4709-4724.	14.5	19
92	Implicating candidate genes at GWAS signals by leveraging topologically associating domains. European Journal of Human Genetics, 2017, 25, 1286-1289.	2.8	18
93	Biochemical Properties and Atomic Resolution Structure of a Proteolytically Processed Î²-Mannanase from Cellulolytic Streptomyces sp. SirexAA-E. PLoS ONE, 2014, 9, e94166.	2.5	18
94	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. Human Molecular Genetics, 2015, 24, 7406-7420.	2.9	17
95	ADAGE signature analysis: differential expression analysis with data-defined gene sets. BMC Bioinformatics, 2017, 18, 512.	2.6	17
96	Genetic demultiplexing of pooled single-cell RNA-sequencing samples in cancer facilitates effective experimental design. GigaScience, 2021, 10, .	6.4	17
97	An Expert Knowledge-Guided Mutation Operator for Genome-Wide Genetic Analysis Using Genetic Programming. Lecture Notes in Computer Science, 2007, , 30-40.	1.3	17
98	Correcting for experiment-specific variability in expression compendia can remove underlying signals. GigaScience, 2020, 9, .	6.4	17
99	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. PLoS ONE, 2013, 8, e69678.	2.5	16
100	Chapter 2: Data-Driven View of Disease Biology. PLoS Computational Biology, 2012, 8, e1002816.	3.2	15
101	NewDrosophilaLong-Term Memory Genes Revealed by Assessing Computational Function Prediction Methods. G3: Genes, Genomes, Genetics, 2019, 9, 251-267.	1.8	15
102	Learning and Imputation for Mass-spec Bias Reduction (LIMBR). Bioinformatics, 2019, 35, 1518-1526.	4.1	15
103	Sensible initialization using expert knowledge for genome-wide analysis of epistasis using genetic programming. , 2009, 2009, 1289-1296.		14
104	PathCORE-T: identifying and visualizing globally co-occurring pathways in large transcriptomic compendia. BioData Mining, 2018, 11, 14.	4.0	14
105	Ten quick tips for deep learning in biology. PLoS Computational Biology, 2022, 18, e1009803.	3.2	14
106	Examining linguistic shifts between preprints and publications. PLoS Biology, 2022, 20, e3001470.	5.6	12
107	Data-Sharing Models. New England Journal of Medicine, 2017, 376, 2305-2306.	27.0	11
108	Discovering Pathway and Cell Type Signatures in Transcriptomic Compendia with Machine Learning. Annual Review of Biomedical Data Science, 2019, 2, 1-17.	6.5	11

#	Article	IF	Citations
109	Integrative Analysis Identifies Candidate Tumor Microenvironment and Intracellular Signaling Pathways that Define Tumor Heterogeneity in NF1. Genes, 2020, 11, 226.	2.4	11
110	Environmental Sensing of Expert Knowledge in a Computational Evolution System for Complex Problem Solving in Human Genetics. Genetic and Evolutionary Computation, 2010, , 19-36.	1.0	11
111	Fast genome-wide epistasis analysis using ant colony optimization for multifactor dimensionality reduction analysis on graphics processing units. , 2010, , .		10
112	Predicting targeted drug combinations based on Pareto optimal patterns of coexpression network connectivity. Genome Medicine, 2014, 6, 33.	8.2	10
113	Analysis of scientific society honors reveals disparities. Cell Systems, 2021, 12, 900-906.e5.	6.2	10
114	Genetic Associationâ€“Guided Analysis of Gene Networks for the Study of Complex Traits. Circulation: Cardiovascular Genetics, 2016, 9, 179-184.	5.1	9
115	Community-wide hackathons to identify central themes in single-cell multi-omics. Genome Biology, 2021, 22, 220.	8.8	9
116	Sensible Initialization of a Computational Evolution System Using Expert Knowledge for Epistasis Analysis in Human Genetics. Adaptation, Learning, and Optimization, 2010, , 215-226.	0.6	9
117	Biologically Informed Neural Networks Predict Drug Responses. Cancer Cell, 2020, 38, 613-615.	16.8	8
118	Integrating Phosphoproteomics and Transcriptional Classifiers Reveals "Hidden Signaling" in Multiple Myeloma Including Differential KRAS and NRAS Mutant Effects. Blood, 2018, 132, 469-469.	1.4	8
119	COMPUTATIONAL APPROACHES TO STUDY MICROBES AND MICROBIOMES. , 2016, , .		7
120	Integrative Networks Illuminate Biological Factors Underlying Geneâ€“Disease Associations. Current Genetic Medicine Reports, 2016, 4, 155-162.	1.9	7
121	Machine Learning Analysis IdentifiesDrosophila Grunge/Atrophinas an Important Learning and Memory Gene Required for Memory Retention and Social Learning. G3: Genes, Genomes, Genetics, 2017, 7, 3705-3718.	1.8	7
122	Environmental noise improves epistasis models of genetic data discovered using a computational evolution system. , 2009, , .		6
123	Computational genetics analysis of grey matter density in Alzheimerâ€™s disease. BioData Mining, 2014, 7, 17.	4.0	6
124	A field guide to cultivating computational biology. PLoS Biology, 2021, 19, e3001419.	5.6	6
125	GenomicSuperSignature facilitates interpretation of RNA-seq experiments through robust, efficient comparison to public databases. Nature Communications, 2022, 13, .	12.8	6
126	Using expert knowledge in initialization for genome-wide analysis of epistasis using genetic programming. , 2008, , .		5

#	Article	IF	Citations
127	A parasite's perspective on data sharing. GigaScience, 2018, 7, .	6.4	5
128	Voices in methods development. Nature Methods, 2019, 16, 945-951.	19.0	5
129	Expanding and Remixing the Metadata Landscape. Trends in Cancer, 2021, 7, 276-278.	7.4	5
130	Long-Term Cellulose Enrichment Selects for Highly Cellulolytic Consortia and Competition for Public Goods. MSystems, 2022, 7, e0151921.	3.8	5
131	Widespread redundancy in -omics profiles of cancer mutation states. Genome Biology, 2022, 23, .	8.8	5
132	Solving complex problems in human genetics using GP. ACM SIGEVOlution, 2008, 3, 2-8.	0.5	4
133	APPLICATIONS OF BIOINFORMATICS TO NON-CODING RNAS IN THE ERA OF NEXT-GENERATION SEQUENCING. , 2013, , .		4
134	Identification of Novel Genetic Models of Glaucoma Using the â€œEMERGENTâ€•Genetic Programming-Based Artificial Intelligence System. Genetic and Evolutionary Computation, 2015, , 17-35.	1.0	4
135	Embracing study heterogeneity for finding genetic interactions in largeâ€scale research consortia. Genetic Epidemiology, 2020, 44, 52-66.	1.3	4
136	Leveraging global gene expression patterns to predict expression of unmeasured genes. BMC Genomics, 2015, 16, 1065.	2.8	3
137	Advances in Text Mining and Visualization for Precision Medicine. , 2018, , .		3
138	Cancer Informatics for Cancer Centers: Scientific Drivers for Informatics, Data Science, and Care in Pediatric, Adolescent, and Young Adult Cancer. JCO Clinical Cancer Informatics, 2021, 5, 881-896.	2.1	3
139	Artificial Immune Systems for Epistasis Analysis in Human Genetics. Lecture Notes in Computer Science, 2010, , 194-204.	1.3	3
140	Pharmacological Validation Of Potentiating Targets From SAHA RNA-Interference Modifier Screens In Acute Myeloid Leukemia. Blood, 2013, 122, 3832-3832.	1.4	3
141	TEXT AND DATA MINING FOR BIOMEDICAL DISCOVERY. , 2012, , .		2
142	Testing multiple hypotheses through IMP weighted FDR based on a genetic functional network with application to a new zebrafish transcriptome study. BioData Mining, 2015, 8, 17.	4.0	2
143	A Model Free Method to Generate Human Genetics Datasets with Complex Gene-Disease Relationships. Lecture Notes in Computer Science, 2010, , 74-85.	1.3	2
144	An Analysis of New Expert Knowledge Scaling Methods for Biologically Inspired Computing. Lecture Notes in Computer Science, 2011, , 286-293.	1.3	2

#	Article	IF	Citations
145	Correction for Rando et al., â€œPathogenesis, Symptomatology, and Transmission of SARS-CoV-2 through Analysis of Viral Genomics and Structureâ€. MSystems, 2022, , e0144721.	3.8	2
146	Computational audits combat disparities in recognition. Nature Human Behaviour, 2022, 6, 473-474.	12.0	2
147	An Open-Publishing Response to the COVID-19 Infodemic.. CEUR Workshop Proceedings, 2021, 2976, 29-38.	2.3	2
148	Development and evaluation of an open-ended computational evolution system for the creation of digital organisms with complex genetic architecture. , 2009, , .		1
149	Nature-inspired algorithms for the genetic analysis of epistasis in common human diseases: Theoretical assessment of wrapper vs. filter approaches. , 2009, , .		1
150	NO-BOUNDARY THINKING IN BIOINFORMATICS. , 2017, 22, 646-648.		1
151	Parameterized algorithms for identifying gene co-expression modules via weighted clique decomposition. , 2021, 2021, 111-122.		1
152	Time-Point Specific Weighting Improves Coexpression Networks from Time-Course Experiments. Lecture Notes in Computer Science, 2013, , 11-22.	1.3	1
153	An Open-Ended Computational Evolution Strategy for Evolving Parsimonious Solutions to Human Genetics Problems. Lecture Notes in Computer Science, 2011, , 313-320.	1.3	1
154	Tell me your neighbors, and I will tell you what you are. Science Translational Medicine, 2017, 9, .	12.4	1
155	Ten simple rules for large-scale data processing. PLoS Computational Biology, 2022, 18, e1009757.	3.2	1
156	Testing multiple hypotheses through IMP weighted FDR based on a genetic functional network with application to a new zebrafish transcriptome study. , 2014, , .		0
157	Show me the models. Nature Biotechnology, 2019, 37, 623-625.	17.5	0
158	Back Cover Image. Genetic Epidemiology, 2020, 44, ii.	1.3	0
159	Abstract A28: Identification of HDAC inhibitor potentiating targets in acute myeloid leukemia cells by large-scale RNA-interference. , 2013, , .		0
160	Abstract 1928: High-grade serous ovarian cancer subtypes are similar across diverse populations. , 2015, , .		0
161	Abstract 2171: Leveraging global gene expression patterns to identify gene sets that predict expression of large numbers of unmeasured genes. , 2015, , .		0
162	CoINcIDE: All together now. Science Translational Medicine, 2016, 8, .	12.4	0

#	Article	IF	Citations
163	Nothing but a hound dog. Science Translational Medicine, 2016, 8, .	12.4	0
164	Abstract 3407: Gene expression subtypes of high grade serous ovarian cancer in African American women. , 2016, , .		0
165	Abstract 815: Patterns of metagene activation in ovarian cancer subtypes. , 2016, , .		0
166	The future is unsupervised. Science Translational Medicine, 2016, 8, .	12.4	0
167	Gut check. Science Translational Medicine, 2016, 8, .	12.4	0
168	A stromal focus reveals tumor immune signatures. Science Translational Medicine, 2016, 8, .	12.4	0
169	How to know what we donâ€™t. Science Translational Medicine, 2016, 8, .	12.4	0
170	Cheap-seq. Science Translational Medicine, 2016, 8, 370ec203.	12.4	0
171	Abstract 5318: High-grade serous ovarian cancer DNA methylation and survival in African-American women. , 2018, , .		0
172	PSB 2019 Workshop on Text Mining and Visualization for Precision Medicine. , 2018, , .		0
173	Solving Complex Problems in Human Genetics Using Nature-Inspired Algorithms Requires Strategies which Exploit Domain-Specific Knowledge. , 0, , 1867-1881.		0
174	Functional network community detection can disaggregate and filter multiple underlying pathways in enrichment analyses. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2018, 23, 157-167.	0.7	0
175	Human Intrigue: Meta-analysis approaches for big questions with big data while shaking up the peer review process. , 2021, , .		0
176	Solving Complex Problems in Human Genetics using Nature-Inspired Algorithms Requires Strategies which Exploit Domain-Specific Knowledge. , 0, , 166-180.		0