

Gregory P Way

List of Publications by Citations

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Version: 2024-04-26

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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.

38
papers

2,989
citations

18
h-index

47
g-index

47
ext. papers

4,480
ext. citations

7.9
avg, IF

4.49
L-index

#	Paper	IF	Citations
38	Oncogenic Signaling Pathways in The Cancer Genome Atlas. <i>Cell</i> , 2018 , 173, 321-337.e10	56.2	1124
37	Opportunities and obstacles for deep learning in biology and medicine. <i>Journal of the Royal Society Interface</i> , 2018 , 15,	4.1	780
36	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
35	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
34	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
33	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
32	Immune landscapes associated with different glioblastoma molecular subtypes. <i>Acta Neuropathologica Communications</i> , 2019 , 7, 203	7.3	56
31	A comparison of methodologies to test aggression in zebrafish. <i>Zebrafish</i> , 2015 , 12, 144-51	2	52
30	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
29	Opportunities and obstacles for deep learning in biology and medicine		45
28	Challenges and Opportunities in Studying the Epidemiology of Ovarian Cancer Subtypes. <i>Current Epidemiology Reports</i> , 2017 , 4, 211-220	2.9	33
27	A machine learning classifier trained on cancer transcriptomes detects NF1 inactivation signal in glioblastoma. <i>BMC Genomics</i> , 2017 , 18, 127	4.5	23
26	Extracting a Biologically Relevant Latent Space from Cancer Transcriptomes with Variational Autoencoders		23
25	Compressing gene expression data using multiple latent space dimensionalities learns complementary biological representations. <i>Genome Biology</i> , 2020 , 21, 109	18.3	20
24	Extracting a biologically relevant latent space from cancer transcriptomes with variational autoencoders 2018 ,		20
23	Predicting cell health phenotypes using image-based morphology profiling. <i>Molecular Biology of the Cell</i> , 2021 , 32, 995-1005	3.5	20
22	Sex differences in a shoaling-boldness behavioral syndrome, but no link with aggression. <i>Behavioural Processes</i> , 2015 , 113, 7-12	1.6	18

21	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
20	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
19	Bayesian deep learning for single-cell analysis. <i>Nature Methods</i> , 2018 , 15, 1009-1010	21.6	14
18	Deconvolution of DNA methylation identifies differentially methylated gene regions on 1p36 across breast cancer subtypes. <i>Scientific Reports</i> , 2017 , 7, 11594	4.9	13
17	Interactions between aggression, boldness and shoaling within a brood of convict cichlids (<i>Amatitlania nigrofasciatus</i>). <i>Behavioural Processes</i> , 2015 , 121, 63-9	1.6	9
16	Integrated phosphoproteomics and transcriptional classifiers reveal hidden RAS signaling dynamics in multiple myeloma. <i>Blood Advances</i> , 2019 , 3, 3214-3227	7.8	9
15	Epigenomic profiling of neuroblastoma cell lines. <i>Scientific Data</i> , 2020 , 7, 116	8.2	9
14	Boldness, Aggression, and Shoaling Assays for Zebrafish Behavioral Syndromes. <i>Journal of Visualized Experiments</i> , 2016 ,	1.6	7
13	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
12	PathCORE-T: identifying and visualizing globally co-occurring pathways in large transcriptomic compendia. <i>BioData Mining</i> , 2018 , 11, 14	4.3	6
11	Predicting cell health phenotypes using image-based morphology profiling		6
10	Genome-wide association study implicates novel loci and reveals candidate effector genes for longitudinal pediatric bone accrual through variant-to-gene mapping		5
9	Morphology and gene expression profiling provide complementary information for mapping cell state		4
8	Sequential compression of gene expression across dimensionalities and methods reveals no single best method or dimensionality		3
7	A field guide to cultivating computational biology. <i>PLoS Biology</i> , 2021 , 19, e3001419	9.7	2
6	Comprehensive Cross-Population Analysis of High-Grade Serous Ovarian Cancer Supports No More Than Three Subtypes		2
5	Predicting drug polypharmacology from cell morphology readouts using variational autoencoder latent space arithmetic.. <i>PLoS Computational Biology</i> , 2022 , 18, e1009888	5	2
4	Integrated Phosphoproteomics and Transcriptional Classifiers Reveal Hidden RAS Signaling Dynamics in Multiple Myeloma		1

- 3 Epigenomic profiling of neuroblastoma cell lines 1
- 2 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* 1.3
- 1 Image-based profiling: a powerful and challenging new data type. *Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2022, 27, 407-411* 1.3