

Gregory P Way

List of Publications by Year in descending order

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Version: 2024-02-01

30
papers

5,632
citations

471061

17
h-index

525886

27
g-index

47
all docs

47
docs citations

47
times ranked

11817
citing authors

#	ARTICLE	IF	CITATIONS
1	Oncogenic Signaling Pathways in The Cancer Genome Atlas. <i>Cell</i> , 2018, 173, 321-337.e10.	13.5	2,111
2	Opportunities and obstacles for deep learning in biology and medicine. <i>Journal of the Royal Society Interface</i> , 2018, 15, 20170387.	1.5	1,282
3	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. <i>Cell Reports</i> , 2018, 23, 239-254.e6.	2.9	801
4	Genome-wide association study implicates novel loci and reveals candidate effector genes for longitudinal pediatric bone accrual. <i>Genome Biology</i> , 2021, 22, 1.	3.8	239
5	Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. <i>Cell Reports</i> , 2018, 23, 172-180.e3.	2.9	119
6	Immune landscapes associated with different glioblastoma molecular subtypes. <i>Acta Neuropathologica Communications</i> , 2019, 7, 203.	2.4	112
7	Genomic Profiling of Childhood Tumor Patient-Derived Xenograft Models to Enable Rational Clinical Trial Design. <i>Cell Reports</i> , 2019, 29, 1675-1689.e9.	2.9	103
8	Extracting a biologically relevant latent space from cancer transcriptomes with variational autoencoders. , 2018, , .		101
9	A Comparison of Methodologies to Test Aggression in Zebrafish. <i>Zebrafish</i> , 2015, 12, 144-151.	0.5	83
10	Predicting cell health phenotypes using image-based morphology profiling. <i>Molecular Biology of the Cell</i> , 2021, 32, 995-1005.	0.9	71
11	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.	0.7	66
12	Challenges and Opportunities in Studying the Epidemiology of Ovarian Cancer Subtypes. <i>Current Epidemiology Reports</i> , 2017, 4, 211-220.	1.1	56
13	Compressing gene expression data using multiple latent space dimensionalities learns complementary biological representations. <i>Genome Biology</i> , 2020, 21, 109.	3.8	43
14	Epigenomic profiling of neuroblastoma cell lines. <i>Scientific Data</i> , 2020, 7, 116.	2.4	32
15	Sex differences in a shoaling-boldness behavioral syndrome, but no link with aggression. <i>Behavioural Processes</i> , 2015, 113, 7-12.	0.5	31
16	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.	0.8	31
17	A machine learning classifier trained on cancer transcriptomes detects NF1 inactivation signal in glioblastoma. <i>BMC Genomics</i> , 2017, 18, 127.	1.2	30
18	Sharing biological data: why, when, and how. <i>FEBS Letters</i> , 2021, 595, 847-863.	1.3	26

#	ARTICLE	IF	CITATIONS
19	Bayesian deep learning for single-cell analysis. <i>Nature Methods</i> , 2018, 15, 1009-1010.	9.0	21
20	Deconvolution of DNA methylation identifies differentially methylated gene regions on 1p36 across breast cancer subtypes. <i>Scientific Reports</i> , 2017, 7, 11594.	1.6	20
21	Integrated phosphoproteomics and transcriptional classifiers reveal hidden RAS signaling dynamics in multiple myeloma. <i>Blood Advances</i> , 2019, 3, 3214-3227.	2.5	19
22	Implicating candidate genes at GWAS signals by leveraging topologically associating domains. <i>European Journal of Human Genetics</i> , 2017, 25, 1286-1289.	1.4	18
23	Predicting drug polypharmacology from cell morphology readouts using variational autoencoder latent space arithmetic. <i>PLoS Computational Biology</i> , 2022, 18, e1009888.	1.5	17
24	PathCORE-T: identifying and visualizing globally co-occurring pathways in large transcriptomic compendia. <i>BioData Mining</i> , 2018, 11, 14.	2.2	14
25	Interactions between aggression, boldness and shoaling within a brood of convict cichlids (<i>Amatitlania nigrofasciatus</i>). <i>Behavioural Processes</i> , 2015, 121, 63-69.	0.5	11
26	Discovering Pathway and Cell Type Signatures in Transcriptomic Compendia with Machine Learning. <i>Annual Review of Biomedical Data Science</i> , 2019, 2, 1-17.	2.8	11
27	Boldness, Aggression, and Shoaling Assays for Zebrafish Behavioral Syndromes. <i>Journal of Visualized Experiments</i> , 2016, , .	0.2	8
28	A field guide to cultivating computational biology. <i>PLoS Biology</i> , 2021, 19, e3001419.	2.6	6
29	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.	0.7	0
30	Image-based profiling: a powerful and challenging new data type. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2022, 27, 407-411.	0.7	0