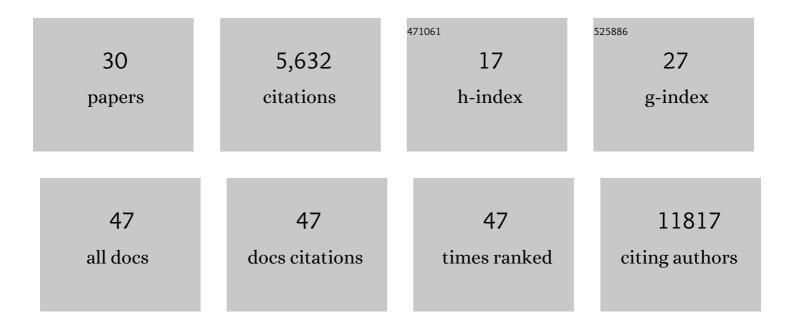
## Gregory P Way

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/2635721/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Oncogenic Signaling Pathways in The Cancer Genome Atlas. Cell, 2018, 173, 321-337.e10.	13.5	2,111
2	Opportunities and obstacles for deep learning in biology and medicine. Journal of the Royal Society Interface, 2018, 15, 20170387.	1.5	1,282
3	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. Cell Reports, 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. Genome Biology, 2021, 22, 1.	3.8	239
5	Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. Cell Reports, 2018, 23, 172-180.e3.	2.9	119
6	Immune landscapes associated with different glioblastoma molecular subtypes. Acta Neuropathologica Communications, 2019, 7, 203.	2.4	112
7	Genomic Profiling of Childhood Tumor Patient-Derived Xenograft Models to Enable Rational Clinical Trial Design. Cell Reports, 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. Zebrafish, 2015, 12, 144-151.	0.5	83
10	Predicting cell health phenotypes using image-based morphology profiling. Molecular Biology of the Cell, 2021, 32, 995-1005.	0.9	71
11	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
12	Challenges and Opportunities in Studying the Epidemiology of Ovarian Cancer Subtypes. Current Epidemiology Reports, 2017, 4, 211-220.	1.1	56
13	Compressing gene expression data using multiple latent space dimensionalities learns complementary biological representations. Genome Biology, 2020, 21, 109.	3.8	43
14	Epigenomic profiling of neuroblastoma cell lines. Scientific Data, 2020, 7, 116.	2.4	32
15	Sex differences in a shoaling-boldness behavioral syndrome, but no link with aggression. Behavioural Processes, 2015, 113, 7-12.	0.5	31
16	Comprehensive Cross-Population Analysis of High-Grade Serous Ovarian Cancer Supports No More Than Three Subtypes. G3: Genes, Genomes, Genetics, 2016, 6, 4097-4103.	0.8	31
17	A machine learning classifier trained on cancer transcriptomes detects NF1 inactivation signal in glioblastoma. BMC Genomics, 2017, 18, 127.	1.2	30
18	Sharing biological data: why, when, and how. FEBS Letters, 2021, 595, 847-863.	1.3	26

GREGORY P WAY

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