Kristen M Naegle

List of Publications by Year
in descending order

24 papers	878 citations	623734 14 h-index	580821 25 g-index
31 all docs	31 docs citations	31 times ranked	1676 citing authors

#	Article	IF	Citations
1	Injury-Induced HDAC5 Nuclear Export Is Essential for Axon Regeneration. Cell, 2013, 155, 894-908.	28.9	270
2	Avoiding common pitfalls when clustering biological data. Science Signaling, 2016, 9, re6.	3.6	118
3	Phosphoproteomics of collagen receptor networks reveals SHP-2 phosphorylation downstream of wild-type DDR2 and its lung cancer mutants. Biochemical Journal, 2013, 454, 501-513.	3.7	68
4	Predicting Patient Response to the Antiarrhythmic Mexiletine Based on Genetic Variation. Circulation Research, 2019, 124, 539-552.	4.5	48
5	Different Epidermal Growth Factor Receptor (EGFR) Agonists Produce Unique Signatures for the Recruitment of Downstream Signaling Proteins. Journal of Biological Chemistry, 2016, 291, 5528-5540.	3.4	46
6	ProteomeScout: a repository and analysis resource for post-translational modifications and proteins. Nucleic Acids Research, 2015, 43, D521-D530.	14.5	42
7	PTMScout, a Web Resource for Analysis of High Throughput Post-translational Proteomics Studies. Molecular and Cellular Proteomics, 2010, 9, 2558-2570.	3.8	39
8	MCAM: Multiple Clustering Analysis Methodology for Deriving Hypotheses and Insights from High-Throughput Proteomic Datasets. PLoS Computational Biology, 2011, 7, e1002119.	3.2	28
9	A Crowdsourcing Approach to Developing and Assessing Prediction Algorithms for AML Prognosis. PLoS Computational Biology, 2016, 12, e1004890.	3.2	28
10	An integrated comparative phosphoproteomic and bioinformatic approach reveals a novel class of MPM-2 motifs upregulated in EGFRvIII-expressing glioblastoma cells. Molecular BioSystems, 2009, 5, 59-67.	2.9	27
11	Accounting for noise when clustering biological data. Briefings in Bioinformatics, 2013, 14, 423-436.	6.5	24
12	Criteria for biological reproducibility: What does â€œ <i>n</i> â€•mean?. Science Signaling, 2015, 8, fs7.	3.6	22
13	Robust co-regulation of tyrosine phosphorylation sites on proteins reveals novel protein interactions. Molecular BioSystems, 2012, 8, 2771.	2.9	19
14	ProteoClade: AÂ taxonomic toolkit for multi-species and metaproteomic analysis. PLoS Computational Biology, 2020, 16, e1007741.	3.2	12
15	KinPred: A unified and sustainable approach for harnessing proteome-level human kinase-substrate predictions. PLoS Computational Biology, 2021, 17, e1008681.	3.2	10
16	Defining phenotypic and functional heterogeneity of glioblastoma stem cells by mass cytometry. JCI Insight, 2021, 6, .	5.0	10
17	Reproducible Analysis of Post-Translational Modifications in Proteomesâ€"Application to Human Mutations. PLoS ONE, 2015, 10, e0144692.	2.5	9
18	High-Resolution Identification of Specificity Determining Positions in the LacI Protein Family Using Ensembles of Sub-Sampled Alignments. PLoS ONE, 2016, 11, e0162579.	2.5	9

#	Article	IF	Citations
19	Proteome-Level Analysis Indicates Global Mechanisms for Post-Translational Regulation of RRM Domains. Journal of Molecular Biology, 2018, 430, 41-44.	4.2	7
20	Using ProteomeScout: A Resource of Post–Translational Modifications, Their Experiments, and the Proteins That They Annotate. Current Protocols in Bioinformatics, 2017, 59, 13.32.1-13.32.27.	25.8	6
21	Ten simple rules for effective presentation slides. PLoS Computational Biology, 2021, 17, e1009554.	3.2	5
22	ASPEN, a methodology for reconstructing protein evolution with improved accuracy using ensemble models. ELife, 2019, 8, .	6.0	4
23	New analysis pipeline for high-throughput domain–peptide affinity experiments improves SH2 interaction data. Journal of Biological Chemistry, 2020, 295, 11346-11363.	3.4	2
24	Ensemble clustering of phosphoproteomic data identifies differences in protein interactions and cell–cell junction integrity of HER2-overexpressing cells. Integrative Biology (United Kingdom), 2017, 9, 539-547.	1.3	1