

Kristen M Naegle

List of Publications by Year in descending order

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Version: 2024-02-01

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	KinPred: A unified and sustainable approach for harnessing proteome-level human kinase-substrate predictions. <i>PLoS Computational Biology</i> , 2021, 17, e1008681.	3.2	10
2	Defining phenotypic and functional heterogeneity of glioblastoma stem cells by mass cytometry. <i>JCI Insight</i> , 2021, 6, .	5.0	10
3	Ten simple rules for effective presentation slides. <i>PLoS Computational Biology</i> , 2021, 17, e1009554.	3.2	5
4	ProteoClade: A taxonomic toolkit for multi-species and metaproteomic analysis. <i>PLoS Computational Biology</i> , 2020, 16, e1007741.	3.2	12
5	New analysis pipeline for high-throughput domain peptide affinity experiments improves SH2 interaction data. <i>Journal of Biological Chemistry</i> , 2020, 295, 11346-11363.	3.4	2
6	Predicting Patient Response to the Antiarrhythmic Mexiletine Based on Genetic Variation. <i>Circulation Research</i> , 2019, 124, 539-552.	4.5	48
7	ASPEN, a methodology for reconstructing protein evolution with improved accuracy using ensemble models. <i>ELife</i> , 2019, 8, .	6.0	4
8	Proteome-Level Analysis Indicates Global Mechanisms for Post-Translational Regulation of RRM Domains. <i>Journal of Molecular Biology</i> , 2018, 430, 41-44.	4.2	7
9	Ensemble clustering of phosphoproteomic data identifies differences in protein interactions and cell-cell junction integrity of HER2-overexpressing cells. <i>Integrative Biology (United Kingdom)</i> , 2017, 9, 539-547.	1.3	1
10	Using ProteomeScout: A Resource of Post-Translational Modifications, Their Experiments, and the Proteins That They Annotate. <i>Current Protocols in Bioinformatics</i> , 2017, 59, 13.32.1-13.32.27.	25.8	6
11	High-Resolution Identification of Specificity Determining Positions in the LacI Protein Family Using Ensembles of Sub-Sampled Alignments. <i>PLoS ONE</i> , 2016, 11, e0162579.	2.5	9
12	Avoiding common pitfalls when clustering biological data. <i>Science Signaling</i> , 2016, 9, re6.	3.6	118
13	Different Epidermal Growth Factor Receptor (EGFR) Agonists Produce Unique Signatures for the Recruitment of Downstream Signaling Proteins. <i>Journal of Biological Chemistry</i> , 2016, 291, 5528-5540.	3.4	46
14	A Crowdsourcing Approach to Developing and Assessing Prediction Algorithms for AML Prognosis. <i>PLoS Computational Biology</i> , 2016, 12, e1004890.	3.2	28
15	Reproducible Analysis of Post-Translational Modifications in Proteomes Application to Human Mutations. <i>PLoS ONE</i> , 2015, 10, e0144692.	2.5	9
16	ProteomeScout: a repository and analysis resource for post-translational modifications and proteins. <i>Nucleic Acids Research</i> , 2015, 43, D521-D530.	14.5	42
17	Criteria for biological reproducibility: What does it mean?. <i>Science Signaling</i> , 2015, 8, fs7.	3.6	22
18	Injury-Induced HDAC5 Nuclear Export Is Essential for Axon Regeneration. <i>Cell</i> , 2013, 155, 894-908.	28.9	270

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19	Accounting for noise when clustering biological data. <i>Briefings in Bioinformatics</i> , 2013, 14, 423-436.	6.5	24
20	Phosphoproteomics of collagen receptor networks reveals SHP-2 phosphorylation downstream of wild-type DDR2 and its lung cancer mutants. <i>Biochemical Journal</i> , 2013, 454, 501-513.	3.7	68
21	Robust co-regulation of tyrosine phosphorylation sites on proteins reveals novel protein interactions. <i>Molecular BioSystems</i> , 2012, 8, 2771.	2.9	19
22	MCAM: Multiple Clustering Analysis Methodology for Deriving Hypotheses and Insights from High-Throughput Proteomic Datasets. <i>PLoS Computational Biology</i> , 2011, 7, e1002119.	3.2	28
23	PTMScout, a Web Resource for Analysis of High Throughput Post-translational Proteomics Studies. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 2558-2570.	3.8	39
24	An integrated comparative phosphoproteomic and bioinformatic approach reveals a novel class of MPM-2 motifs upregulated in EGFRvIII-expressing glioblastoma cells. <i>Molecular BioSystems</i> , 2009, 5, 59-67.	2.9	27