

Anna Ritz

List of Publications by Year in descending order

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Version: 2024-02-01

37
papers

685
citations

623734

14
h-index

610901

24
g-index

42
all docs

42
docs citations

42
times ranked

1184
citing authors

#	ARTICLE	IF	CITATIONS
1	Quantitative Time-Resolved Phosphoproteomic Analysis of Mast Cell Signaling. <i>Journal of Immunology</i> , 2007, 179, 5864-5876.	0.8	66
2	A New Approach for Quantitative Phosphoproteomic Dissection of Signaling Pathways Applied to T Cell Receptor Activation. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 2418-2431.	3.8	66
3	Metabolic reprogramming ensures cancer cell survival despite oncogenic signaling blockade. <i>Genes and Development</i> , 2017, 31, 2067-2084.	5.9	57
4	Characterization of structural variants with single molecule and hybrid sequencing approaches. <i>Bioinformatics</i> , 2014, 30, 3458-3466.	4.1	56
5	Pathways on demand: automated reconstruction of human signaling networks. <i>Npj Systems Biology and Applications</i> , 2016, 2, 16002.	3.0	55
6	Environmental chemistry through intelligent atmospheric data analysis. <i>Environmental Modelling and Software</i> , 2010, 25, 760-769.	4.5	48
7	Discovery of phosphorylation motif mixtures in phosphoproteomics data. <i>Bioinformatics</i> , 2009, 25, 14-21.	4.1	42
8	Signaling hypergraphs. <i>Trends in Biotechnology</i> , 2014, 32, 356-362.	9.3	39
9	Structural variation analysis with strobe reads. <i>Bioinformatics</i> , 2010, 26, 1291-1298.	4.1	33
10	Distance measures for tumor evolutionary trees. <i>Bioinformatics</i> , 2020, 36, 2090-2097.	4.1	26
11	Gremlin: An Interactive Visualization Model for Analyzing Genomic Rearrangements. <i>IEEE Transactions on Visualization and Computer Graphics</i> , 2010, 16, 918-926.	4.4	24
12	GraphSpace: stimulating interdisciplinary collaborations in network biology. <i>Bioinformatics</i> , 2017, 33, 3134-3136.	4.1	23
13	MsPAC: a tool for haplotype-phased structural variant detection. <i>Bioinformatics</i> , 2020, 36, 922-924.	4.1	23
14	Quantitative Phosphoproteomics Reveals SLP-76 Dependent Regulation of PAC and Src Family Kinases in T Cells. <i>PLoS ONE</i> , 2012, 7, e46725.	2.5	22
15	Detection of recurrent rearrangement breakpoints from copy number data. <i>BMC Bioinformatics</i> , 2011, 12, 114.	2.6	21
16	Hypergraph-based connectivity measures for signaling pathway topologies. <i>PLoS Computational Biology</i> , 2019, 15, e1007384.	3.2	19
17	Pathway Analysis with Signaling Hypergraphs. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2017, 14, 1042-1055.	3.0	13
18	Pathway analysis with signaling hypergraphs. , 2014, , .		8

#	ARTICLE	IF	CITATIONS
19	Differentially Private ANOVA Testing. , 2018, , .		8
20	Network-based prediction of polygenic disease genes involved in cell motility. BMC Bioinformatics, 2019, 20, 313.	2.6	6
21	Improved Differentially Private Analysis of Variance. Proceedings on Privacy Enhancing Technologies, 2019, 2019, 310-330.	2.8	6
22	A Cell-based Assay to Investigate Non-muscle Myosin II Contractility <i>via</i> the Folded-gastrulation Signaling Pathway in <i>Drosophila</i> S2R+ Cells. Journal of Visualized Experiments, 2018, , .	0.3	4
23	Integrating protein localization with automated signaling pathway reconstruction. BMC Bioinformatics, 2019, 20, 505.	2.6	4
24	Cabozantinib and dasatinib synergize to induce tumor regression in non-clear cell renal cell carcinoma. Cell Reports Medicine, 2021, 2, 100267.	6.5	4
25	Augmenting Signaling Pathway Reconstructions. , 2020, , .		4
26	Integrating Protein Localization with Automated Signaling Pathway Reconstruction. , 2018, , .		1
27	The <i>Drosophila melanogaster</i> Rab GAP RN-tre cross-talks with the Rho1 signaling pathway to regulate nonmuscle myosin II localization and function. Molecular Biology of the Cell, 2020, 31, 2379-2397.	2.1	1
28	Ten simple rules for attending your first conference. PLoS Computational Biology, 2021, 17, e1009133.	3.2	1
29	Reconciling Signaling Pathway Databases with Network Topologies. , 2021, , .		1
30	Copy Number Variation and Adaptive Evolutionary Radiations across the African Cichlid phylogeny. , 2016, , .		0
31	Factors Affecting Network-Based Gene Prediction Across Diverse Diseases. , 2019, , .		0
32	Graphery: interactive tutorials for biological network algorithms. Nucleic Acids Research, 2021, 49, W257-W262.	14.5	0
33	A Protein-Protein Interactome for an African Cichlid. , 2020, , .		0
34	Hypergraph-based connectivity measures for signaling pathway topologies. , 2019, 15, e1007384.		0
35	Hypergraph-based connectivity measures for signaling pathway topologies. , 2019, 15, e1007384.		0
36	Hypergraph-based connectivity measures for signaling pathway topologies. , 2019, 15, e1007384.		0

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37	Hypergraph-based connectivity measures for signaling pathway topologies. , 2019, 15, e1007384.		0