

# Anna Ritz

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6188256/publications.pdf>

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	Graphery: interactive tutorials for biological network algorithms. <i>Nucleic Acids Research</i> , 2021, 49, W257-W262.	14.5	0
2	Cabozantinib and dasatinib synergize to induce tumor regression in non-clear cell renal cell carcinoma. <i>Cell Reports Medicine</i> , 2021, 2, 100267.	6.5	4
3	Ten simple rules for attending your first conference. <i>PLoS Computational Biology</i> , 2021, 17, e1009133.	3.2	1
4	Reconciling Signaling Pathway Databases with Network Topologies. , 2021, , .		1
5	MsPAC: a tool for haplotype-phased structural variant detection. <i>Bioinformatics</i> , 2020, 36, 922-924.	4.1	23
6	Distance measures for tumor evolutionary trees. <i>Bioinformatics</i> , 2020, 36, 2090-2097.	4.1	26
7	The <i>Drosophila melanogaster</i> Rab GAP RN-tre cross-talks with the Rho1 signaling pathway to regulate nonmuscle myosin II localization and function. <i>Molecular Biology of the Cell</i> , 2020, 31, 2379-2397.	2.1	1
8	Augmenting Signaling Pathway Reconstructions. , 2020, , .		4
9	A Protein-Protein Interactome for an African Cichlid. , 2020, , .		0
10	Hypergraph-based connectivity measures for signaling pathway topologies. <i>PLoS Computational Biology</i> , 2019, 15, e1007384.	3.2	19
11	Network-based prediction of polygenic disease genes involved in cell motility. <i>BMC Bioinformatics</i> , 2019, 20, 313.	2.6	6
12	Factors Affecting Network-Based Gene Prediction Across Diverse Diseases. , 2019, , .		0
13	Integrating protein localization with automated signaling pathway reconstruction. <i>BMC Bioinformatics</i> , 2019, 20, 505.	2.6	4
14	Improved Differentially Private Analysis of Variance. <i>Proceedings on Privacy Enhancing Technologies</i> , 2019, 2019, 310-330.	2.8	6
15	Hypergraph-based connectivity measures for signaling pathway topologies. , 2019, 15, e1007384.		0
16	Hypergraph-based connectivity measures for signaling pathway topologies. , 2019, 15, e1007384.		0
17	Hypergraph-based connectivity measures for signaling pathway topologies. , 2019, 15, e1007384.		0
18	Hypergraph-based connectivity measures for signaling pathway topologies. , 2019, 15, e1007384.		0

#	ARTICLE	IF	CITATIONS
19	Integrating Protein Localization with Automated Signaling Pathway Reconstruction. , 2018, , .		1
20	A Cell-based Assay to Investigate Non-muscle Myosin II Contractility <em>via</em> the Folded-gastrulation Signaling Pathway in <em>Drosophila</em> S2R+ Cells. Journal of Visualized Experiments, 2018, , .	0.3	4
21	Differentially Private ANOVA Testing. , 2018, , .		8
22	Pathway Analysis with Signaling Hypergraphs. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2017, 14, 1042-1055.	3.0	13
23	GraphSpace: stimulating interdisciplinary collaborations in network biology. Bioinformatics, 2017, 33, 3134-3136.	4.1	23
24	Metabolic reprogramming ensures cancer cell survival despite oncogenic signaling blockade. Genes and Development, 2017, 31, 2067-2084.	5.9	57
25	Pathways on demand: automated reconstruction of human signaling networks. Npj Systems Biology and Applications, 2016, 2, 16002.	3.0	55
26	Copy Number Variation and Adaptive Evolutionary Radiations across the African Cichlid phylogeny. , 2016, , .		0
27	Pathway analysis with signaling hypergraphs. , 2014, , .		8
28	Characterization of structural variants with single molecule and hybrid sequencing approaches. Bioinformatics, 2014, 30, 3458-3466.	4.1	56
29	Signaling hypergraphs. Trends in Biotechnology, 2014, 32, 356-362.	9.3	39
30	Quantitative Phosphoproteomics Reveals SLP-76 Dependent Regulation of PAG and Src Family Kinases in T Cells. PLoS ONE, 2012, 7, e46725.	2.5	22
31	Detection of recurrent rearrangement breakpoints from copy number data. BMC Bioinformatics, 2011, 12, 114.	2.6	21
32	Environmental chemistry through intelligent atmospheric data analysis. Environmental Modelling and Software, 2010, 25, 760-769.	4.5	48
33	Structural variation analysis with strobe reads. Bioinformatics, 2010, 26, 1291-1298.	4.1	33
34	Gremlin: An Interactive Visualization Model for Analyzing Genomic Rearrangements. IEEE Transactions on Visualization and Computer Graphics, 2010, 16, 918-926.	4.4	24
35	A New Approach for Quantitative Phosphoproteomic Dissection of Signaling Pathways Applied to T Cell Receptor Activation. Molecular and Cellular Proteomics, 2009, 8, 2418-2431.	3.8	66
36	Discovery of phosphorylation motif mixtures in phosphoproteomics data. Bioinformatics, 2009, 25, 14-21.	4.1	42

#	ARTICLE	IF	CITATIONS
37	Quantitative Time-Resolved Phosphoproteomic Analysis of Mast Cell Signaling. Journal of Immunology, 2007, 179, 5864-5876.	0.8	66