

Ruth Isserlin

List of Publications by Year in descending order

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Version: 2024-02-01

47
papers

11,097
citations

236925

25
h-index

223800

46
g-index

52
all docs

52
docs citations

52
times ranked

24554
citing authors

#	ARTICLE	IF	CITATIONS
1	Integration of biological networks and gene expression data using Cytoscape. Nature Protocols, 2007, 2, 2366-2382.	12.0	2,275
2	A draft map of the human proteome. Nature, 2014, 509, 575-581.	27.8	1,948
3	Enrichment Map: A Network-Based Method for Gene-Set Enrichment Visualization and Interpretation. PLoS ONE, 2010, 5, e13984.	2.5	1,883
4	Pathway enrichment analysis and visualization of omics data using g:Profiler, GSEA, Cytoscape and EnrichmentMap. Nature Protocols, 2019, 14, 482-517.	12.0	1,172
5	Delineation of Two Clinically and Molecularly Distinct Subgroups of Posterior Fossa Ependymoma. Cancer Cell, 2011, 20, 143-157.	16.8	494
6	A Call for Systematic Research on Solute Carriers. Cell, 2015, 162, 478-487.	28.9	457
7	Single-cell transcriptomic profiling of the aging mouse brain. Nature Neuroscience, 2019, 22, 1696-1708.	14.8	432
8	Too many roads not taken. Nature, 2011, 470, 163-165.	27.8	341
9	PSICQUIC and PSISCORE: accessing and scoring molecular interactions. Nature Methods, 2011, 8, 528-529.	19.0	274
10	AutoAnnotate: A Cytoscape app for summarizing networks with semantic annotations. F1000Research, 2016, 5, 1717.	1.6	249
11	miR-126 Regulates Distinct Self-Renewal Outcomes in Normal and Malignant Hematopoietic Stem Cells. Cancer Cell, 2016, 29, 214-228.	16.8	216
12	Enrichment Map "a Cytoscape app to visualize and explore OMICs pathway enrichment results. F1000Research, 2014, 3, 141.	1.6	128
13	WordCloud: a Cytoscape plugin to create a visual semantic summary of networks. Source Code for Biology and Medicine, 2011, 6, 7.	1.7	120
14	RCy3: Network biology using Cytoscape from within R. F1000Research, 0, 8, 1774.	1.6	101
15	Comparative Proteomics Profiling of a Phospholamban Mutant Mouse Model of Dilated Cardiomyopathy Reveals Progressive Intracellular Stress Responses. Molecular and Cellular Proteomics, 2008, 7, 519-533.	3.8	91
16	A Lentiviral Functional Proteomics Approach Identifies Chromatin Remodeling Complexes Important for the Induction of Pluripotency. Molecular and Cellular Proteomics, 2010, 9, 811-823.	3.8	83
17	RCy3: Network biology using Cytoscape from within R. F1000Research, 2019, 8, 1774.	1.6	80
18	netDx: interpretable patient classification using integrated patient similarity networks. Molecular Systems Biology, 2019, 15, e8497.	7.2	65

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19	Constitutively active calcineurin induces cardiac endoplasmic reticulum stress and protects against apoptosis that is mediated by α -crystallin-B. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 18481-18486.	7.1	56
20	Pathway analysis of dilated cardiomyopathy using global proteomic profiling and enrichment maps. Proteomics, 2010, 10, 1316-1327.	2.2	55
21	Ectopic miR-125a Expression Induces Long-Term Repopulating Stem Cell Capacity in Mouse and Human Hematopoietic Progenitors. Cell Stem Cell, 2016, 19, 383-396.	11.1	52
22	Cardioprotective Signature of Short-Term Caloric Restriction. PLoS ONE, 2015, 10, e0130658.	2.5	47
23	Large-Scale Characterization and Analysis of the Murine Cardiac Proteome. Journal of Proteome Research, 2009, 8, 1887-1901.	3.7	45
24	RCy3: Network biology using Cytoscape from within R. F1000Research, 2019, 8, 1774.	1.6	39
25	Global phosphoproteomic profiling reveals perturbed signaling in a mouse model of dilated cardiomyopathy. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 12592-12597.	7.1	35
26	Mammary molecular portraits reveal lineage-specific features and progenitor cell vulnerabilities. Journal of Cell Biology, 2018, 217, 2951-2974.	5.2	35
27	Integrative Cancer Pharmacogenomics to Infer Large-Scale Drug Taxonomy. Cancer Research, 2017, 77, 3057-3069.	0.9	33
28	The Relative Contributions of Cell-Dependent Cortical Microcircuit Aging to Cognition and Anxiety. Biological Psychiatry, 2019, 85, 257-267.	1.3	28
29	Global neuroscience and mental health research: a bibliometrics case study. Scientometrics, 2016, 109, 515-531.	3.0	26
30	Phosphoproteomic network analysis in the sea urchin <i>Strongylocentrotus purpuratus</i> reveals new candidates in egg activation. Proteomics, 2015, 15, 4080-4095.	2.2	24
31	Systems analysis reveals down-regulation of a network of pro-survival miRNAs drives the apoptotic response in dilated cardiomyopathy. Molecular BioSystems, 2015, 11, 239-251.	2.9	23
32	Metabolomic profiling in liver of adiponectin-knockout mice uncovers lysophospholipid metabolism as an important target of adiponectin action. Biochemical Journal, 2015, 469, 71-82.	3.7	20
33	Dynamic interplay between locus-specific DNA methylation and hydroxymethylation regulates distinct biological pathways in prostate carcinogenesis. Clinical Epigenetics, 2016, 8, 32.	4.1	20
34	Unbiased phosphoproteomic method identifies the initial effects of a methacrylic acid copolymer on macrophages. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 10673-10678.	7.1	16
35	Dynamics of the cell-free DNA methylome of metastatic prostate cancer during androgen-targeting treatment. Epigenomics, 2020, 12, 1317-1332.	2.1	15
36	Integrative network analysis of signaling in human CD34 ⁺ hematopoietic progenitor cells by global phosphoproteomic profiling using TiO ₂ enrichment combined with 2D LC-MS/MS and pathway mapping. Proteomics, 2013, 13, 1325-1333.	2.2	14

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37	Exercise-responsive phosphoproteins in the heart. <i>Journal of Molecular and Cellular Cardiology</i> , 2017, 111, 61-68.	1.9	13
38	Bmi1 regulates human glioblastoma stem cells through activation of differential gene networks in CD133+ brain tumor initiating cells. <i>Journal of Neuro-Oncology</i> , 2019, 143, 417-428.	2.9	13
39	Social Network: a Cytoscape app for visualizing co-authorship networks. <i>F1000Research</i> , 2015, 4, 481.	1.6	12
40	Discovery of Novel Disease-specific and Membrane-associated Candidate Markers in a Mouse Model of Multiple Sclerosis. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 679-700.	3.8	10
41	Large-scale label-free phosphoproteomics: from technology to data interpretation. <i>Bioanalysis</i> , 2014, 6, 2403-2420.	1.5	8
42	Interpretation of large-scale quantitative shotgun proteomic profiles for biomarker discovery. <i>Current Opinion in Molecular Therapeutics</i> , 2008, 10, 231-42.	2.8	8
43	Control of tissue development and cell diversity by cell cycle-dependent transcriptional filtering. <i>ELife</i> , 2021, 10, .	6.0	7
44	Nine steps to proteomic wisdom: A practical guide to using protein-protein interaction networks and molecular pathways as a framework for interpreting disease proteomic profiles. <i>Proteomics - Clinical Applications</i> , 2007, 1, 1156-1168.	1.6	6
45	Social Network: a Cytoscape app for visualizing co-publication networks. <i>F1000Research</i> , 2015, 4, 481.	1.6	6
46	netDx: Software for building interpretable patient classifiers by multi-'omic data integration using patient similarity networks. <i>F1000Research</i> , 2020, 9, 1239.	1.6	2
47	netDx: Software for building interpretable patient classifiers by multi-'omic data integration using patient similarity networks. <i>F1000Research</i> , 2020, 9, 1239.	1.6	2