

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	Control of tissue development and cell diversity by cell cycle-dependent transcriptional filtering. <i>ELife</i> , 2021, 10, .	6.0	7
2	Dynamics of the cell-free DNA methylome of metastatic prostate cancer during androgen-targeting treatment. <i>Epigenomics</i> , 2020, 12, 1317-1332.	2.1	15
3	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
4	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
5	Pathway enrichment analysis and visualization of omics data using g:Profiler, GSEA, Cytoscape and EnrichmentMap. <i>Nature Protocols</i> , 2019, 14, 482-517.	12.0	1,172
6	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
7	netDx: interpretable patient classification using integrated patient similarity networks. <i>Molecular Systems Biology</i> , 2019, 15, e8497.	7.2	65
8	Single-cell transcriptomic profiling of the aging mouse brain. <i>Nature Neuroscience</i> , 2019, 22, 1696-1708.	14.8	432
9	The Relative Contributions of Cell-Dependent Cortical Microcircuit Aging to Cognition and Anxiety. <i>Biological Psychiatry</i> , 2019, 85, 257-267.	1.3	28
10	RCy3: Network biology using Cytoscape from within R. <i>F1000Research</i> , 2019, 8, 1774.	1.6	39
11	RCy3: Network biology using Cytoscape from within R. <i>F1000Research</i> , 2019, 8, 1774.	1.6	80
12	Mammary molecular portraits reveal lineage-specific features and progenitor cell vulnerabilities. <i>Journal of Cell Biology</i> , 2018, 217, 2951-2974.	5.2	35
13	Integrative Cancer Pharmacogenomics to Infer Large-Scale Drug Taxonomy. <i>Cancer Research</i> , 2017, 77, 3057-3069.	0.9	33
14	Exercise-responsive phosphoproteins in the heart. <i>Journal of Molecular and Cellular Cardiology</i> , 2017, 111, 61-68.	1.9	13
15	Global neuroscience and mental health research: a bibliometrics case study. <i>Scientometrics</i> , 2016, 109, 515-531.	3.0	26
16	Ectopic miR-125a Expression Induces Long-Term Repopulating Stem Cell Capacity in Mouse and Human Hematopoietic Progenitors. <i>Cell Stem Cell</i> , 2016, 19, 383-396.	11.1	52
17	Global phosphoproteomic profiling reveals perturbed signaling in a mouse model of dilated cardiomyopathy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 12592-12597.	7.1	35
18	Dynamic interplay between locus-specific DNA methylation and hydroxymethylation regulates distinct biological pathways in prostate carcinogenesis. <i>Clinical Epigenetics</i> , 2016, 8, 32.	4.1	20

#	ARTICLE	IF	CITATIONS
19	miR-126 Regulates Distinct Self-Renewal Outcomes in Normal and Malignant Hematopoietic Stem Cells. <i>Cancer Cell</i> , 2016, 29, 214-228.	16.8	216
20	AutoAnnotate: A Cytoscape app for summarizing networks with semantic annotations. <i>F1000Research</i> , 2016, 5, 1717.	1.6	249
21	Phosphoproteomic network analysis in the sea urchin <i>Strongylocentrotus purpuratus</i> reveals new candidates in egg activation. <i>Proteomics</i> , 2015, 15, 4080-4095.	2.2	24
22	Cardioprotective Signature of Short-Term Caloric Restriction. <i>PLoS ONE</i> , 2015, 10, e0130658.	2.5	47
23	Metabolomic profiling in liver of adiponectin-knockout mice uncovers lysophospholipid metabolism as an important target of adiponectin action. <i>Biochemical Journal</i> , 2015, 469, 71-82.	3.7	20
24	A Call for Systematic Research on Solute Carriers. <i>Cell</i> , 2015, 162, 478-487.	28.9	457
25	Unbiased phosphoproteomic method identifies the initial effects of a methacrylic acid copolymer on macrophages. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 10673-10678.	7.1	16
26	Systems analysis reveals down-regulation of a network of pro-survival miRNAs drives the apoptotic response in dilated cardiomyopathy. <i>Molecular BioSystems</i> , 2015, 11, 239-251.	2.9	23
27	Social Network: a Cytoscape app for visualizing co-authorship networks. <i>F1000Research</i> , 2015, 4, 481.	1.6	12
28	Social Network: a Cytoscape app for visualizing co-publication networks. <i>F1000Research</i> , 2015, 4, 481.	1.6	6
29	Enrichment Map – a Cytoscape app to visualize and explore OMICs pathway enrichment results. <i>F1000Research</i> , 2014, 3, 141.	1.6	128
30	Large-scale label-free phosphoproteomics: from technology to data interpretation. <i>Bioanalysis</i> , 2014, 6, 2403-2420.	1.5	8
31	A draft map of the human proteome. <i>Nature</i> , 2014, 509, 575-581.	27.8	1,948
32	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
33	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. <i>Proteomics</i> , 2013, 13, 1325-1333.	2.2	14
34	PSICQUIC and PSISCORE: accessing and scoring molecular interactions. <i>Nature Methods</i> , 2011, 8, 528-529.	19.0	274
35	Too many roads not taken. <i>Nature</i> , 2011, 470, 163-165.	27.8	341
36	Delineation of Two Clinically and Molecularly Distinct Subgroups of Posterior Fossa Ependymoma. <i>Cancer Cell</i> , 2011, 20, 143-157.	16.8	494

#	ARTICLE	IF	CITATIONS
37	WordCloud: a Cytoscape plugin to create a visual semantic summary of networks. Source Code for Biology and Medicine, 2011, 6, 7.	1.7	120
38	Pathway analysis of dilated cardiomyopathy using global proteomic profiling and enrichment maps. Proteomics, 2010, 10, 1316-1327.	2.2	55
39	Enrichment Map: A Network-Based Method for Gene-Set Enrichment Visualization and Interpretation. PLoS ONE, 2010, 5, e13984.	2.5	1,883
40	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
41	Constitutively active calcineurin induces cardiac endoplasmic reticulum stress and protects against apoptosis that is mediated by I χ -crystallin-B. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 18481-18486.	7.1	56
42	Large-Scale Characterization and Analysis of the Murine Cardiac Proteome. Journal of Proteome Research, 2009, 8, 1887-1901.	3.7	45
43	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
44	Interpretation of large-scale quantitative shotgun proteomic profiles for biomarker discovery. Current Opinion in Molecular Therapeutics, 2008, 10, 231-42.	2.8	8
45	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. Proteomics - Clinical Applications, 2007, 1, 1156-1168.	1.6	6
46	Integration of biological networks and gene expression data using Cytoscape. Nature Protocols, 2007, 2, 2366-2382.	12.0	2,275
47	RCy3: Network biology using Cytoscape from within R. F1000Research, 0, 8, 1774.	1.6	101