

Karen Sachs

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/10797649/publications.pdf>

Version: 2024-02-01

26
papers

6,185
citations

516710

16
h-index

752698

20
g-index

29
all docs

29
docs citations

29
times ranked

10012
citing authors

#	ARTICLE	IF	CITATIONS
1	Answer ALS, a large-scale resource for sporadic and familial ALS combining clinical and multi-omics data from induced pluripotent cell lines. <i>Nature Neuroscience</i> , 2022, 25, 226-237.	14.8	66
2	Variation of Immune Cell Responses in Humans Reveals Sex-Specific Coordinated Signaling Across Cell Types. <i>Frontiers in Immunology</i> , 2022, 13, 867016.	4.8	4
3	High-grade serous ovarian tumor cells modulate NK cell function to create an immune-tolerant microenvironment. <i>Cell Reports</i> , 2021, 36, 109632.	6.4	26
4	An integrated multi-omic analysis of iPSC-derived motor neurons from C9ORF72 ALS patients. <i>IScience</i> , 2021, 24, 103221.	4.1	27
5	Single-Cell Gene Expression Analyses Reveal Distinct Self-Renewing and Proliferating Subsets in the Leukemia Stem Cell Compartment in Acute Myeloid Leukemia. <i>Cancer Research</i> , 2020, 80, 458-470.	0.9	46
6	The Library of Integrated Network-Based Cellular Signatures NIH Program: System-Level Cataloging of Human Cells Response to Perturbations. <i>Cell Systems</i> , 2018, 6, 13-24.	6.2	327
7	A Bayesian Active Learning Experimental Design for Inferring Signaling Networks. <i>Journal of Computational Biology</i> , 2018, 25, 709-725.	1.6	1
8	A Bayesian Active Learning Experimental Design for Inferring Signaling Networks. <i>Lecture Notes in Computer Science</i> , 2017, , 134-156.	1.3	6
9	Distinct signaling programs control human hematopoietic stem cell survival and proliferation. <i>Blood</i> , 2017, 129, 307-318.	1.4	35
10	From Correlation to Causality: Statistical Approaches to Learning Regulatory Relationships in Large-Scale Biomolecular Investigations. <i>Journal of Proteome Research</i> , 2016, 15, 683-690.	3.7	17
11	Big data comes in tiny packages. <i>Xrds</i> , 2015, 21, 54-59.	0.3	0
12	NRAS G12V oncogene facilitates self-renewal in a murine model of acute myelogenous leukemia. <i>Blood</i> , 2014, 124, 3274-3283.	1.4	24
13	Abstract B15: NRASG12V oncogene mediates self-renewal in a murine model of acute myelogenous leukemia. , 2014, , .		0
14	Normalization of mass cytometry data with bead standards. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2013, 83A, 483-494.	1.5	655
15	Ras-Pathway Inhibition With Targeted Therapies Abrogates Self-Renewal In Acute Myelogenous Leukemia. <i>Blood</i> , 2013, 122, 819-819.	1.4	0
16	Multiplexed mass cytometry profiling of cellular states perturbed by small-molecule regulators. <i>Nature Biotechnology</i> , 2012, 30, 858-867.	17.5	502
17	Network-Based Discovery of Prognostic Markers in Pediatric AML by Multi-Dimensional Single Cell Mass Cytometry. <i>Blood</i> , 2012, 120, 1411-1411.	1.4	0
18	Extracting a cellular hierarchy from high-dimensional cytometry data with SPADE. <i>Nature Biotechnology</i> , 2011, 29, 886-891.	17.5	905

#	ARTICLE	IF	CITATIONS
19	Single-Cell Mass Cytometry of Differential Immune and Drug Responses Across a Human Hematopoietic Continuum. <i>Science</i> , 2011, 332, 687-696.	12.6	2,097
20	Single-cell phospho-specific flow cytometric analysis demonstrates biochemical and functional heterogeneity in human hematopoietic stem and progenitor compartments. <i>Blood</i> , 2011, 117, 4226-4233.	1.4	48
21	Oncogene Withdrawal Selectively Alters Phosphoprotein States and Shifts Differentiation Status In Myeloid Leukemia Subpopulations. <i>Blood</i> , 2010, 116, 3160-3160.	1.4	0
22	Learning Signaling Network Structures with Sparsely Distributed Data. <i>Journal of Computational Biology</i> , 2009, 16, 201-212.	1.6	25
23	Characterization of patient specific signaling via augmentation of bayesian networks with disease and patient state nodes. , 2009, 2009, 6624-7.		9
24	Structure learning for biomolecular pathways containing cycles. , 2008, , .		0
25	Causal Protein-Signaling Networks Derived from Multiparameter Single-Cell Data. <i>Science</i> , 2005, 308, 523-529.	12.6	1,267
26	Bayesian Network Approach to Cell Signaling Pathway Modeling. <i>Science Signaling</i> , 2002, 2002, pe38-pe38.	3.6	88