

Andrea Califano

List of Publications by Year in descending order

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Version: 2024-02-01

228
papers

34,622
citations

8755

77
h-index

4853

174
g-index

264
all docs

264
docs citations

264
times ranked

51537
citing authors

#	ARTICLE	IF	CITATIONS
1	The Immune Landscape of Cancer. <i>Immunity</i> , 2018, 48, 812-830.e14.	6.6	3,706
2	ARACNE: An Algorithm for the Reconstruction of Gene Regulatory Networks in a Mammalian Cellular Context. <i>BMC Bioinformatics</i> , 2006, 7, S7.	1.2	2,218
3	Prediction of central nervous system embryonal tumour outcome based on gene expression. <i>Nature</i> , 2002, 415, 436-442.	13.7	2,154
4	A promoter-level mammalian expression atlas. <i>Nature</i> , 2014, 507, 462-470.	13.7	1,838
5	Reverse engineering of regulatory networks in human B cells. <i>Nature Genetics</i> , 2005, 37, 382-390.	9.4	1,268
6	Cross-Species Single-Cell Analysis of Pancreatic Ductal Adenocarcinoma Reveals Antigen-Presenting Cancer-Associated Fibroblasts. <i>Cancer Discovery</i> , 2019, 9, 1102-1123.	7.7	1,120
7	The transcriptional network for mesenchymal transformation of brain tumours. <i>Nature</i> , 2010, 463, 318-325.	13.7	1,114
8	Mutations of multiple genes cause deregulation of NF- κ B in diffuse large B-cell lymphoma. <i>Nature</i> , 2009, 459, 717-721.	13.7	969
9	Gene Expression Profiling of B Cell Chronic Lymphocytic Leukemia Reveals a Homogeneous Phenotype Related to Memory B Cells. <i>Journal of Experimental Medicine</i> , 2001, 194, 1625-1638.	4.2	823
10	The DLEU2/miR-15a/16-1 Cluster Controls B Cell Proliferation and Its Deletion Leads to Chronic Lymphocytic Leukemia. <i>Cancer Cell</i> , 2010, 17, 28-40.	7.7	753
11	NOTCH1 directly regulates c-MYC and activates a feed-forward-loop transcriptional network promoting leukemic cell growth. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 18261-18266.	3.3	745
12	Functional characterization of somatic mutations in cancer using network-based inference of protein activity. <i>Nature Genetics</i> , 2016, 48, 838-847.	9.4	703
13	An Extensive MicroRNA-Mediated Network of RNA-RNA Interactions Regulates Established Oncogenic Pathways in Glioblastoma. <i>Cell</i> , 2011, 147, 370-381.	13.5	671
14	Structure-based prediction of protein-protein interactions on a genome-wide scale. <i>Nature</i> , 2012, 490, 556-560.	13.7	652
15	Toward understanding and exploiting tumor heterogeneity. <i>Nature Medicine</i> , 2015, 21, 846-853.	15.2	604
16	tRNA-derived microRNA modulates proliferation and the DNA damage response and is down-regulated in B cell lymphoma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 1404-1409.	3.3	487
17	Transcriptional analysis of the B cell germinal center reaction. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 2639-2644.	3.3	370
18	Reverse engineering cellular networks. <i>Nature Protocols</i> , 2006, 1, 662-671.	5.5	345

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19	A human B-cell interactome identifies MYB and FOXM1 as master regulators of proliferation in germinal centers. <i>Molecular Systems Biology</i> , 2010, 6, 377.	3.2	336
20	Dialogue on Reverse-Engineering Assessment and Methods. <i>Annals of the New York Academy of Sciences</i> , 2007, 1115, 1-22.	1.8	318
21	ARACNe-AP: gene network reverse engineering through adaptive partitioning inference of mutual information. <i>Bioinformatics</i> , 2016, 32, 2233-2235.	1.8	305
22	Cross-Species Regulatory Network Analysis Identifies a Synergistic Interaction between FOXM1 and CENPF that Drives Prostate Cancer Malignancy. <i>Cancer Cell</i> , 2014, 25, 638-651.	7.7	293
23	Single-Cell Genomics Reveals a Novel Cell State During Smooth Muscle Cell Phenotypic Switching and Potential Therapeutic Targets for Atherosclerosis in Mouse and Human. <i>Circulation</i> , 2020, 142, 2060-2075.	1.6	292
24	Elucidating Compound Mechanism of Action by Network Perturbation Analysis. <i>Cell</i> , 2015, 162, 441-451.	13.5	278
25	Transdifferentiation as a Mechanism of Treatment Resistance in a Mouse Model of Castration-Resistant Prostate Cancer. <i>Cancer Discovery</i> , 2017, 7, 736-749.	7.7	275
26	Gene expression analysis of peripheral T cell lymphoma, unspecified, reveals distinct profiles and new potential therapeutic targets. <i>Journal of Clinical Investigation</i> , 2007, 117, 823-834.	3.9	272
27	A community computational challenge to predict the activity of pairs of compounds. <i>Nature Biotechnology</i> , 2014, 32, 1213-1222.	9.4	264
28	Lineage analysis of basal epithelial cells reveals their unexpected plasticity and supports a cell-of-origin model for prostate cancer heterogeneity. <i>Nature Cell Biology</i> , 2013, 15, 274-283.	4.6	261
29	Leveraging models of cell regulation and GWAS data in integrative network-based association studies. <i>Nature Genetics</i> , 2012, 44, 841-847.	9.4	252
30	Genome-wide identification of post-translational modulators of transcription factor activity in human B cells. <i>Nature Biotechnology</i> , 2009, 27, 829-837.	9.4	226
31	Gene Expression Analysis of Angioimmunoblastic Lymphoma Indicates Derivation from T Follicular Helper Cells and Vascular Endothelial Growth Factor Deregulation. <i>Cancer Research</i> , 2007, 67, 10703-10710.	0.4	220
32	Direct Reversal of Glucocorticoid Resistance by AKT Inhibition in Acute Lymphoblastic Leukemia. <i>Cancer Cell</i> , 2013, 24, 766-776.	7.7	220
33	Integrated biochemical and computational approach identifies BCL6 direct target genes controlling multiple pathways in normal germinal center B cells. <i>Blood</i> , 2010, 115, 975-984.	0.6	216
34	Fingerprint matching using transformation parameter clustering. <i>IEEE Computational Science and Engineering</i> , 1997, 4, 42-49.	0.6	201
35	Dclk1 Defines Quiescent Pancreatic Progenitors that Promote Injury-Induced Regeneration and Tumorigenesis. <i>Cell Stem Cell</i> , 2016, 18, 441-455.	5.2	196
36	Resistance to neoadjuvant chemotherapy in triple-negative breast cancer mediated by a reversible drug-tolerant state. <i>Science Translational Medicine</i> , 2019, 11, .	5.8	192

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37	Identification of Hodgkin and Reed-Sternberg cell-specific genes by gene expression profiling. <i>Journal of Clinical Investigation</i> , 2003, 111, 529-537.	3.9	192
38	A systems biology approach to prediction of oncogenes and molecular perturbation targets in B-cell lymphomas. <i>Molecular Systems Biology</i> , 2008, 4, 169.	3.2	191
39	Identification of Causal Genetic Drivers of Human Disease through Systems-Level Analysis of Regulatory Networks. <i>Cell</i> , 2014, 159, 402-414.	13.5	185
40	Gene Expression Profiling of Hairy Cell Leukemia Reveals a Phenotype Related to Memory B Cells with Altered Expression of Chemokine and Adhesion Receptors. <i>Journal of Experimental Medicine</i> , 2004, 199, 59-68.	4.2	181
41	Lessons from the DREAM2 Challenges. <i>Annals of the New York Academy of Sciences</i> , 2009, 1158, 159-195.	1.8	173
42	BCL6 suppression of BCL2 via Miz1 and its disruption in diffuse large B cell lymphoma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 11294-11299.	3.3	170
43	The recurrent architecture of tumour initiation, progression and drug sensitivity. <i>Nature Reviews Cancer</i> , 2017, 17, 116-130.	12.8	170
44	A precision oncology approach to the pharmacological targeting of mechanistic dependencies in neuroendocrine tumors. <i>Nature Genetics</i> , 2018, 50, 979-989.	9.4	168
45	Single-cell protein activity analysis identifies recurrence-associated renal tumor macrophages. <i>Cell</i> , 2021, 184, 2988-3005.e16.	13.5	166
46	Comparative analysis of microarray normalization procedures: effects on reverse engineering gene networks. <i>Bioinformatics</i> , 2007, 23, i282-i288.	1.8	163
47	A multi-organ chip with matured tissue niches linked by vascular flow. <i>Nature Biomedical Engineering</i> , 2022, 6, 351-371.	11.6	162
48	Promotion of cholangiocarcinoma growth by diverse cancer-associated fibroblast subpopulations. <i>Cancer Cell</i> , 2021, 39, 866-882.e11.	7.7	159
49	HAUSP deubiquitinates and stabilizes N-Myc in neuroblastoma. <i>Nature Medicine</i> , 2016, 22, 1180-1186.	15.2	158
50	Tracking CD40 signaling during germinal center development. <i>Blood</i> , 2004, 104, 4088-4096.	0.6	154
51	MEF2B mutations lead to deregulated expression of the oncogene BCL6 in diffuse large B cell lymphoma. <i>Nature Immunology</i> , 2013, 14, 1084-1092.	7.0	153
52	Experimental microdissection enables functional harmonisation of pancreatic cancer subtypes. <i>Gut</i> , 2019, 68, 1034-1043.	6.1	147
53	The TLX1 oncogene drives aneuploidy in T cell transformation. <i>Nature Medicine</i> , 2010, 16, 1321-1327.	15.2	139
54	Reverse engineering of TLX oncogenic transcriptional networks identifies RUNX1 as tumor suppressor in T-ALL. <i>Nature Medicine</i> , 2012, 18, 436-440.	15.2	138

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55	Differentiation-state plasticity is a targetable resistance mechanism in basal-like breast cancer. <i>Nature Communications</i> , 2018, 9, 3815.	5.8	137
56	The N-Myc-DLL3 Cascade Is Suppressed by the Ubiquitin Ligase Huwe1 to Inhibit Proliferation and Promote Neurogenesis in the Developing Brain. <i>Developmental Cell</i> , 2009, 17, 210-221.	3.1	135
57	An expanded universe of cancer targets. <i>Cell</i> , 2021, 184, 1142-1155.	13.5	135
58	Gene expression analysis uncovers similarity and differences among Burkitt lymphoma subtypes. <i>Blood</i> , 2011, 117, 3596-3608.	0.6	128
59	Identification of the Human Mature B Cell miRNome. <i>Immunity</i> , 2009, 30, 744-752.	6.6	124
60	Genomic and Phenotypic Characterization of a Broad Panel of Patient-Derived Xenografts Reflects the Diversity of Glioblastoma. <i>Clinical Cancer Research</i> , 2020, 26, 1094-1104.	3.2	124
61	Cross-Cohort Analysis Identifies a TEAD4-MYCN Positive Feedback Loop as the Core Regulatory Element of High-Risk Neuroblastoma. <i>Cancer Discovery</i> , 2018, 8, 582-599.	7.7	119
62	Multidimensional indexing for recognizing visual shapes. <i>IEEE Transactions on Pattern Analysis and Machine Intelligence</i> , 1994, 16, 373-392.	9.7	117
63	A Molecular Signature Predictive of Indolent Prostate Cancer. <i>Science Translational Medicine</i> , 2013, 5, 202ra122.	5.8	114
64	PFT1, the MED25 subunit of the plant Mediator complex, promotes flowering through CONSTANS dependent and independent mechanisms in Arabidopsis. <i>Plant Journal</i> , 2012, 69, 601-612.	2.8	113
65	ETV4 promotes metastasis in response to activation of PI3-kinase and Ras signaling in a mouse model of advanced prostate cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E3506-15.	3.3	113
66	Identification of neurodegenerative factors using translational regulatory network analysis. <i>Nature Neuroscience</i> , 2015, 18, 1325-1333.	7.1	113
67	PLATE-Seq for genome-wide regulatory network analysis of high-throughput screens. <i>Nature Communications</i> , 2017, 8, 105.	5.8	109
68	An ID2-dependent mechanism for VHL inactivation in cancer. <i>Nature</i> , 2016, 529, 172-177.	13.7	108
69	ZFH4 Interacts with the NuRD Core Member CHD4 and Regulates the Glioblastoma Tumor-Initiating Cell State. <i>Cell Reports</i> , 2014, 6, 313-324.	2.9	106
70	An Integrated Systems Biology Approach Identifies TRIM25 as a Key Determinant of Breast Cancer Metastasis. <i>Cell Reports</i> , 2017, 20, 1623-1640.	2.9	96
71	Quantitative assessment of protein activity in orphan tissues and single cells using the metaVIPER algorithm. <i>Nature Communications</i> , 2018, 9, 1471.	5.8	95
72	Inhibition of the autocrine IL-6/JAK2-STAT3/calprotectin axis as targeted therapy for HR ⁺ /HER2 ⁺ breast cancers. <i>Genes and Development</i> , 2015, 29, 1631-1648.	2.7	94

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73	Cupid: simultaneous reconstruction of microRNA-target and ceRNA networks. <i>Genome Research</i> , 2015, 25, 257-267.	2.4	94
74	B-Raf Activation Cooperates with PTEN Loss to Drive c-Myc Expression in Advanced Prostate Cancer. <i>Cancer Research</i> , 2012, 72, 4765-4776.	0.4	87
75	Assembly and Interrogation of Alzheimer's Disease Genetic Networks Reveal Novel Regulators of Progression. <i>PLoS ONE</i> , 2015, 10, e0120352.	1.1	87
76	Verification of systems biology research in the age of collaborative competition. <i>Nature Biotechnology</i> , 2011, 29, 811-815.	9.4	83
77	geWorkbench: an open source platform for integrative genomics. <i>Bioinformatics</i> , 2010, 26, 1779-1780.	1.8	82
78	Identification of Hodgkin and Reed-Sternberg cell-specific genes by gene expression profiling. <i>Journal of Clinical Investigation</i> , 2003, 111, 529-537.	3.9	82
79	Novel Hybrid Phenotype Revealed in Small Cell Lung Cancer by a Transcription Factor Network Model That Can Explain Tumor Heterogeneity. <i>Cancer Research</i> , 2017, 77, 1063-1074.	0.4	81
80	Identification of an NKX3.1-G9a-UTY transcriptional regulatory network that controls prostate differentiation. <i>Science</i> , 2016, 352, 1576-1580.	6.0	80
81	Dual Targeting of the Akt/mTOR Signaling Pathway Inhibits Castration-Resistant Prostate Cancer in a Genetically Engineered Mouse Model. <i>Cancer Research</i> , 2012, 72, 4483-4493.	0.4	79
82	A modular master regulator landscape controls cancer transcriptional identity. <i>Cell</i> , 2021, 184, 334-351.e20.	13.5	78
83	Theory and Limitations of Genetic Network Inference from Microarray Data. <i>Annals of the New York Academy of Sciences</i> , 2007, 1115, 51-72.	1.8	77
84	Improving Breast Cancer Survival Analysis through Competition-Based Multidimensional Modeling. <i>PLoS Computational Biology</i> , 2013, 9, e1003047.	1.5	76
85	A CRISPR/Cas9-Engineered ARID1A-Deficient Human Gastric Cancer Organoid Model Reveals Essential and Nonessential Modes of Oncogenic Transformation. <i>Cancer Discovery</i> , 2021, 11, 1562-1581.	7.7	75
86	ChIP-on-chip significance analysis reveals large-scale binding and regulation by human transcription factor oncogenes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 244-249.	3.3	74
87	Gene expression analysis provides a potential rationale for revising the histological grading of follicular lymphomas. <i>Haematologica</i> , 2008, 93, 1033-1038.	1.7	73
88	A complementary role for ELF3 and TFL1 in the regulation of flowering time by ambient temperature. <i>Plant Journal</i> , 2009, 58, 629-640.	2.8	73
89	Bone Marrow Myeloid Cells Regulate Myeloid-Biased Hematopoietic Stem Cells via a Histamine-Dependent Feedback Loop. <i>Cell Stem Cell</i> , 2017, 21, 747-760.e7.	5.2	68
90	The miR-424(322)/503 cluster orchestrates remodeling of the epithelium in the involuting mammary gland. <i>Genes and Development</i> , 2014, 28, 765-782.	2.7	66

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91	NSD2 is a conserved driver of metastatic prostate cancer progression. Nature Communications, 2018, 9, 5201.	5.8	66
92	Towards patient-based cancer therapeutics. Nature Biotechnology, 2010, 28, 904-906.	9.4	65
93	Immunostimulatory Cancer-Associated Fibroblast Subpopulations Can Predict Immunotherapy Response in Head and Neck Cancer. Clinical Cancer Research, 2022, 28, 2094-2109.	3.2	60
94	STK38 is a critical upstream regulator of MYC's oncogenic activity in human B-cell lymphoma. Oncogene, 2013, 32, 5283-5291.	2.6	58
95	Gene expression changes consistent with neuroAIDS and impaired working memory in HIV-1 transgenic rats. Molecular Neurodegeneration, 2014, 9, 26.	4.4	58
96	Rewiring makes the difference. Molecular Systems Biology, 2011, 7, 463.	3.2	57
97	Regulation of extra-embryonic endoderm stem cell differentiation by Nodal and Cripto signaling. Development (Cambridge), 2011, 138, 3885-3895.	1.2	53
98	Motif-based construction of a functional map for mammalian olfactory receptors. Genomics, 2003, 81, 443-456.	1.3	51
99	High-definition CpG methylation of novel genes in gastric carcinogenesis identified by next-generation sequencing. Modern Pathology, 2016, 29, 182-193.	2.9	50
100	Synergistic antileukemic therapies in NOTCH1-induced T-ALL. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 2006-2011.	3.3	50
101	The Transcriptional Regulatory Network of Proneural Glioma Determines the Genetic Alterations Selected during Tumor Progression. Cancer Research, 2014, 74, 1440-1451.	0.4	48
102	Identifying candidate drivers of alcohol dependence-induced excessive drinking by assembly and interrogation of brain-specific regulatory networks. Genome Biology, 2015, 16, 68.	3.8	47
103	Elucidation and Pharmacological Targeting of Novel Molecular Drivers of Follicular Lymphoma Progression. Cancer Research, 2016, 76, 664-674.	0.4	47
104	Master regulators used as breast cancer metastasis classifier. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2009, , 504-15.	0.7	47
105	High-throughput validation of ceRNA regulatory networks. BMC Genomics, 2017, 18, 418.	1.2	46
106	T-cell lymphoblastic lymphoma shows differences and similarities with T-cell acute lymphoblastic leukemia by genomic and gene expression analyses. Genes Chromosomes and Cancer, 2011, 50, 1063-1075.	1.5	44
107	Reverse-engineering human regulatory networks. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2012, 4, 311-325.	6.6	44
108	BACH2 inhibition reverses β^2 cell failure in type 2 diabetes models. Journal of Clinical Investigation, 2021, 131, .	3.9	43

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109	Survival factor NFIL3 restricts FOXO-induced gene expression in cancer. <i>Genes and Development</i> , 2013, 27, 916-927.	2.7	42
110	HDAC6 activity is a non-oncogene addiction hub for inflammatory breast cancers. <i>Breast Cancer Research</i> , 2015, 17, 149.	2.2	42
111	The Regulatory Machinery of Neurodegeneration in InÂVitro Models of Amyotrophic Lateral Sclerosis. <i>Cell Reports</i> , 2015, 12, 335-345.	2.9	42
112	Quantitative Tyrosine Phosphoproteomics of Epidermal Growth Factor Receptor (EGFR) Tyrosine Kinase Inhibitor-treated Lung Adenocarcinoma Cells Reveals Potential Novel Biomarkers of Therapeutic Response. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 891-910.	2.5	42
113	ScreenBEAM: a novel meta-analysis algorithm for functional genomics screens via Bayesian hierarchical modeling. <i>Bioinformatics</i> , 2016, 32, 260-267.	1.8	40
114	A CLK3-HMGA2 Alternative Splicing Axis Impacts Human Hematopoietic Stem Cell Molecular Identity throughout Development. <i>Cell Stem Cell</i> , 2018, 22, 575-588.e7.	5.2	40
115	Toward better benchmarking: challenge-based methods assessment in cancer genomics. <i>Genome Biology</i> , 2014, 15, 462.	3.8	38
116	Quantitative modeling of the terminal differentiation of B cells and mechanisms of lymphomagenesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 2672-2677.	3.3	37
117	SJARACNe: a scalable software tool for gene network reverse engineering from big data. <i>Bioinformatics</i> , 2019, 35, 2165-2166.	1.8	36
118	Convection-enhanced delivery of etoposide is effective against murine proneural glioblastoma. <i>Neuro-Oncology</i> , 2014, 16, 1210-1219.	0.6	34
119	Predicting Drug Response in Human Prostate Cancer from Preclinical Analysis of InÂVivo Mouse Models. <i>Cell Reports</i> , 2015, 12, 2060-2071.	2.9	34
120	A community challenge for a pancancer drug mechanism of action inference from perturbational profile data. <i>Cell Reports Medicine</i> , 2022, 3, 100492.	3.3	33
121	Interrogation of a Context-Specific Transcription Factor Network Identifies Novel Regulators of Pluripotency. <i>Stem Cells</i> , 2015, 33, 367-377.	1.4	32
122	The number of titrated microRNA species dictates ceRNA regulation. <i>Nucleic Acids Research</i> , 2018, 46, 4354-4369.	6.5	32
123	Discovering transcriptional regulatory regions in <i>Drosophila</i> by a nonalignment method for phylogenetic footprinting. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 6305-6310.	3.3	31
124	Gene Expression Dynamics during Germinal Center Transit in B Cells. <i>Annals of the New York Academy of Sciences</i> , 2003, 987, 166-172.	1.8	30
125	A computational systems approach identifies synergistic specification genes that facilitate lineage conversion to prostate tissue. <i>Nature Communications</i> , 2017, 8, 14662.	5.8	30
126	Epigenetic Regulation of ZBTB18 Promotes Glioblastoma Progression. <i>Molecular Cancer Research</i> , 2017, 15, 998-1011.	1.5	30

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127	Cooperation of loss of <i>NKX3.1</i> and inflammation in prostate cancer initiation. <i>DMM Disease Models and Mechanisms</i> , 2018, 11, .	1.2	30
128	A Phase II Study of the Efficacy and Safety of Oral Selinexor in Recurrent Glioblastoma. <i>Clinical Cancer Research</i> , 2022, 28, 452-460.	3.2	29
129	Systematic elucidation of neuron-astrocyte interaction in models of amyotrophic lateral sclerosis using multi-modal integrated bioinformatics workflow. <i>Nature Communications</i> , 2020, 11, 5579.	5.8	28
130	iTools: A Framework for Classification, Categorization and Integration of Computational Biology Resources. <i>PLoS ONE</i> , 2008, 3, e2265.	1.1	27
131	Hypothalamic proteoglycan syndecan-3 is a novel cocaine addiction resilience factor. <i>Nature Communications</i> , 2013, 4, 1955.	5.8	26
132	SECAT: Quantifying Protein Complex Dynamics across Cell States by Network-Centric Analysis of SEC-SWATH-MS Profiles. <i>Cell Systems</i> , 2020, 11, 589-607.e8.	2.9	26
133	HER3 Is an Actionable Target in Advanced Prostate Cancer. <i>Cancer Research</i> , 2021, 81, 6207-6218.	0.4	25
134	hARACNe: improving the accuracy of regulatory model reverse engineering via higher-order data processing inequality tests. <i>Interface Focus</i> , 2013, 3, 20130011.	1.5	24
135	Systematic and Fully Automated Identification of Protein Sequence Patterns. <i>Journal of Computational Biology</i> , 2000, 7, 585-600.	0.8	23
136	Genome-Wide Discovery of Modulators of Transcriptional Interactions in Human B Lymphocytes. <i>Lecture Notes in Computer Science</i> , 2006, , 348-362.	1.0	23
137	CTD2 Dashboard: a searchable web interface to connect validated results from the Cancer Target Discovery and Development Network. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	1.4	23
138	Systematic, network-based characterization of therapeutic target inhibitors. <i>PLoS Computational Biology</i> , 2017, 13, e1005599.	1.5	23
139	Transcription factor activating protein 4 is synthetically lethal and a master regulator of MYCN-amplified neuroblastoma. <i>Oncogene</i> , 2018, 37, 5451-5465.	2.6	22
140	Oncoprotein-specific molecular interaction maps (SigMaps) for cancer network analyses. <i>Nature Biotechnology</i> , 2021, 39, 215-224.	9.4	21
141	Inferring Protein Modulation from Gene Expression Data Using Conditional Mutual Information. <i>PLoS ONE</i> , 2014, 9, e109569.	1.1	21
142	The transcriptomic response of cells to a drug combination is more than the sum of the responses to the monotherapies. <i>ELife</i> , 2020, 9, .	2.8	21
143	Report: workshop on mediastinal grey zone lymphoma. <i>European Journal of Haematology</i> , 2005, 75, 45-52.	1.1	19
144	The Master Regulator Protein BAZ2B Can Reprogram Human Hematopoietic Lineage-Committed Progenitors into a Multipotent State. <i>Cell Reports</i> , 2020, 33, 108474.	2.9	19

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145	Fimepinostat (CUDCâ€907) in patients with relapsed/refractory diffuse large B cell and highâ€grade Bâ€cell lymphoma: report of a phase 2 trial and exploratory biomarker analyses. <i>British Journal of Haematology</i> , 2021, 195, 201-209.	1.2	17
146	Gene Expression Profiles of Patients With Antibody-Mediated Rejection After Cardiac Transplantation. <i>Journal of Heart and Lung Transplantation</i> , 2008, 27, 932-934.	0.3	16
147	A case study of an integrative genomic and experimental therapeutic approach for rare tumors: identification of vulnerabilities in a pediatric poorly differentiated carcinoma. <i>Genome Medicine</i> , 2016, 8, 116.	3.6	15
148	Reply to â€H-STS, L-STS and KRJ-I are not authentic GEPNET cell linesâ€™. <i>Nature Genetics</i> , 2019, 51, 1427-1428.	9.4	15
149	Phase I/II trial of ruxolitinib in combination with trastuzumab in metastatic HER2 positive breast cancer. <i>Breast Cancer Research and Treatment</i> , 2021, 189, 177-185.	1.1	15
150	Genome-Wide Dissection of Posttranscriptional and Posttranslational Interactions. <i>Methods in Molecular Biology</i> , 2012, 786, 131-149.	0.4	15
151	Functional classification of proteins by pattern discovery and top-down clustering of primary sequences. <i>IBM Systems Journal</i> , 2001, 40, 379-393.	3.1	14
152	Correlating measurements across samples improves accuracy of large-scale expression profile experiments. <i>Genome Biology</i> , 2009, 10, R143.	13.9	14
153	Identification of immunotherapeutic targets by genomic profiling of rectal NET metastases. <i>Oncolmmunology</i> , 2016, 5, e1213931.	2.1	14
154	ZCCHC17 is a master regulator of synaptic gene expression in Alzheimerâ€™s disease. <i>Bioinformatics</i> , 2018, 34, 367-371.	1.8	14
155	Dissecting the interface between signaling and transcriptional regulation in human B cells. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2009, , 264-75.	0.7	14
156	Searching in parallel for similar strings [biological sequences]. <i>IEEE Computational Science and Engineering</i> , 1994, 1, 60-75.	0.6	13
157	Detection and removal of spatial bias in multiwell assays. <i>Bioinformatics</i> , 2016, 32, 1959-1965.	1.8	13
158	Accelerated parallel algorithm for gene network reverse engineering. <i>BMC Systems Biology</i> , 2017, 11, 83.	3.0	13
159	DIGGIT: a Bioconductor package to infer genetic variants driving cellular phenotypes. <i>Bioinformatics</i> , 2015, 31, btv499.	1.8	12
160	Gene Expression Analysis of Follicular Lymphoma Provides a Potential Rationale for Histological Grading Revision.. <i>Blood</i> , 2007, 110, 186-186.	0.6	12
161	A Systems Biology Approach to Transcription Factor Binding Site Prediction. <i>PLoS ONE</i> , 2010, 5, e9878.	1.1	11
162	Patient-Driven Discovery, Therapeutic Targeting, and Post-Clinical Validation of a Novel <i>AKT1</i> Fusionâ€Driven Cancer. <i>Cancer Discovery</i> , 2019, 9, 605-616.	7.7	11

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