Andrea Califano

List of Publications by Year
in descending order

228 papers	34,622 citations	7568 77 h-index	4228 174 g-index
264 all docs	264 docs citations	264 times ranked	46652 citing authors

#	Article	IF	Citations
1	The Immune Landscape of Cancer. Immunity, 2018, 48, 812-830.e14.	14.3	3,706
2	ARACNE: An Algorithm for the Reconstruction of Gene Regulatory Networks in a Mammalian Cellular Context. BMC Bioinformatics, 2006, 7, S7.	2.6	2,218
3	Prediction of central nervous system embryonal tumour outcome based on gene expression. Nature, 2002, 415, 436-442.	27.8	2,154
4	A promoter-level mammalian expression atlas. Nature, 2014, 507, 462-470.	27.8	1,838
5	Reverse engineering of regulatory networks in human B cells. Nature Genetics, 2005, 37, 382-390.	21.4	1,268
6	Cross-Species Single-Cell Analysis of Pancreatic Ductal Adenocarcinoma Reveals Antigen-Presenting Cancer-Associated Fibroblasts. Cancer Discovery, 2019, 9, 1102-1123.	9.4	1,120
7	The transcriptional network for mesenchymal transformation of brain tumours. Nature, 2010, 463, 318-325.	27.8	1,114
8	Mutations of multiple genes cause deregulation of NF-ÎºB in diffuse large B-cell lymphoma. Nature, 2009, 459, 717-721.	27.8	969
9	Gene Expression Profiling of B Cell Chronic Lymphocytic Leukemia Reveals a Homogeneous Phenotype Related to Memory B Cells. Journal of Experimental Medicine, 2001, 194, 1625-1638.	8.5	823
10	The DLEU2/miR-15a/16-1 Cluster Controls B Cell Proliferation and Its Deletion Leads to Chronic Lymphocytic Leukemia. Cancer Cell, 2010, 17, 28-40.	16.8	753
11	NOTCH1 directly regulates c-MYC and activates a feed-forward-loop transcriptional network promoting leukemic cell growth. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 18261-18266.	7.1	745
12	Functional characterization of somatic mutations in cancer using network-based inference of protein activity. Nature Genetics, 2016, 48, 838-847.	21.4	703
13	An Extensive MicroRNA-Mediated Network of RNA-RNA Interactions Regulates Established Oncogenic Pathways in Glioblastoma. Cell, 2011, 147, 370-381.	28.9	671
14	Structure-based prediction of proteinâ€"protein interactions on a genome-wide scale. Nature, 2012, 490, 556-560.	27.8	652
15	Toward understanding and exploiting tumor heterogeneity. Nature Medicine, 2015, 21, 846-853.	30.7	604
16	tRNA-derived microRNA modulates proliferation and the DNA damage response and is down-regulated in B cell lymphoma. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 1404-1409.	7.1	487
17	Transcriptional analysis of the B cell germinal center reaction. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 2639-2644.	7.1	370
18	Reverse engineering cellular networks. Nature Protocols, 2006, 1, 662-671.	12.0	345

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19	A human Bâ€cell interactome identifies MYB and FOXM1 as master regulators of proliferation in germinal centers. Molecular Systems Biology, 2010, 6, 377.	7.2	336
20	Dialogue on Reverseâ€Engineering Assessment and Methods. Annals of the New York Academy of Sciences, 2007, 1115, 1-22.	3.8	318
21	ARACNe-AP: gene network reverse engineering through adaptive partitioning inference of mutual information. Bioinformatics, 2016, 32, 2233-2235.	4.1	305
22	Cross-Species Regulatory Network Analysis Identifies a Synergistic Interaction between FOXM1 and CENPF that Drives Prostate Cancer Malignancy. Cancer Cell, 2014, 25, 638-651.	16.8	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. Circulation, 2020, 142, 2060-2075.	1.6	292
24	Elucidating Compound Mechanism of Action by Network Perturbation Analysis. Cell, 2015, 162, 441-451.	28.9	278
25	Transdifferentiation as a Mechanism of Treatment Resistance in a Mouse Model of Castration-Resistant Prostate Cancer. Cancer Discovery, 2017, 7, 736-749.	9.4	275
26	Gene expression analysis of peripheral T cell lymphoma, unspecified, reveals distinct profiles and new potential therapeutic targets. Journal of Clinical Investigation, 2007, 117, 823-834.	8.2	272
27	A community computational challenge to predict the activity of pairs of compounds. Nature Biotechnology, 2014, 32, 1213-1222.	17.5	264
28	Lineage analysis of basal epithelial cells reveals their unexpected plasticity and supports a cell-of-origin model for prostate cancer heterogeneity. Nature Cell Biology, 2013, 15, 274-283.	10.3	261
29	Leveraging models of cell regulation and GWAS data in integrative network-based association studies. Nature Genetics, 2012, 44, 841-847.	21.4	252
30	Genome-wide identification of post-translational modulators of transcription factor activity in human B cells. Nature Biotechnology, 2009, 27, 829-837.	17.5	226
31	Gene Expression Analysis of Angioimmunoblastic Lymphoma Indicates Derivation from T Follicular Helper Cells and Vascular Endothelial Growth Factor Deregulation. Cancer Research, 2007, 67, 10703-10710.	0.9	220
32	Direct Reversal of Glucocorticoid Resistance by AKT Inhibition in Acute Lymphoblastic Leukemia. Cancer Cell, 2013, 24, 766-776.	16.8	220
33	Integrated biochemical and computational approach identifies BCL6 direct target genes controlling multiple pathways in normal germinal center B cells. Blood, 2010, 115, 975-984.	1.4	216
34	Fingerprint matching using transformation parameter clustering. IEEE Computational Science and Engineering, 1997, 4, 42-49.	0.6	201
35	Dclk1 Defines Quiescent Pancreatic Progenitors that Promote Injury-Induced Regeneration and Tumorigenesis. Cell Stem Cell, 2016, 18, 441-455.	11.1	196
36	Resistance to neoadjuvant chemotherapy in triple-negative breast cancer mediated by a reversible drug-tolerant state. Science Translational Medicine, 2019, 11, .	12.4	192

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37	Identification of Hodgkin and Reed-Sternberg cell-specific genes by gene expression profiling. Journal of Clinical Investigation, 2003, 111, 529-537.	8.2	192
38	A systems biology approach to prediction of oncogenes and molecular perturbation targets in Bâ€cell lymphomas. Molecular Systems Biology, 2008, 4, 169.	7.2	191
39	Identification of Causal Genetic Drivers of Human Disease through Systems-Level Analysis of Regulatory Networks. Cell, 2014, 159, 402-414.	28.9	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. Journal of Experimental Medicine, 2004, 199, 59-68.	8.5	181
41	Lessons from the DREAM2 Challenges. Annals of the New York Academy of Sciences, 2009, 1158, 159-195.	3.8	173
42	BCL6 suppression of BCL2 via Miz1 and its disruption in diffuse large B cell lymphoma. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 11294-11299.	7.1	170
43	The recurrent architecture of tumour initiation, progression and drug sensitivity. Nature Reviews Cancer, 2017, 17, 116-130.	28.4	170
44	A precision oncology approach to the pharmacological targeting of mechanistic dependencies in neuroendocrine tumors. Nature Genetics, 2018, 50, 979-989.	21.4	168
45	Single-cell protein activity analysis identifies recurrence-associated renal tumor macrophages. Cell, 2021, 184, 2988-3005.e16.	28.9	166
46	Comparative analysis of microarray normalization procedures: effects on reverse engineering gene networks. Bioinformatics, 2007, 23, i282-i288.	4.1	163
47	A multi-organ chip with matured tissue niches linked by vascular flow. Nature Biomedical Engineering, 2022, 6, 351-371.	22.5	162
48	Promotion of cholangiocarcinoma growth by diverse cancer-associated fibroblast subpopulations. Cancer Cell, 2021, 39, 866-882.e11.	16.8	159
49	HAUSP deubiquitinates and stabilizes N-Myc in neuroblastoma. Nature Medicine, 2016, 22, 1180-1186.	30.7	158
50	Tracking CD40 signaling during germinal center development. Blood, 2004, 104, 4088-4096.	1.4	154
51	MEF2B mutations lead to deregulated expression of the oncogene BCL6 in diffuse large B cell lymphoma. Nature Immunology, 2013, 14, 1084-1092.	14.5	153
52	Experimental microdissection enables functional harmonisation of pancreatic cancer subtypes. Gut, 2019, 68, 1034-1043.	12.1	147
53	The TLX1 oncogene drives aneuploidy in T cell transformation. Nature Medicine, 2010, 16, 1321-1327.	30.7	139
54	Reverse engineering of TLX oncogenic transcriptional networks identifies RUNX1 as tumor suppressor in T-ALL. Nature Medicine, 2012, 18, 436-440.	30.7	138

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55	Differentiation-state plasticity is a targetable resistance mechanism in basal-like breast cancer. Nature Communications, 2018, 9, 3815.	12.8	137
56	The N-Myc-DLL3 Cascade Is Suppressed by the Ubiquitin Ligase Huwe1 to Inhibit Proliferation and Promote Neurogenesis in the Developing Brain. Developmental Cell, 2009, 17, 210-221.	7.0	135
57	An expanded universe of cancer targets. Cell, 2021, 184, 1142-1155.	28.9	135
58	Gene expression analysis uncovers similarity and differences among Burkitt lymphoma subtypes. Blood, 2011, 117, 3596-3608.	1.4	128
59	Identification of the Human Mature B Cell miRNome. Immunity, 2009, 30, 744-752.	14.3	124
60	Genomic and Phenotypic Characterization of a Broad Panel of Patient-Derived Xenografts Reflects the Diversity of Glioblastoma. Clinical Cancer Research, 2020, 26, 1094-1104.	7.0	124
61	Cross-Cohort Analysis Identifies a TEAD4â€"MYCN Positive Feedback Loop as the Core Regulatory Element of High-Risk Neuroblastoma. Cancer Discovery, 2018, 8, 582-599.	9.4	119
62	Multidimensional indexing for recognizing visual shapes. IEEE Transactions on Pattern Analysis and Machine Intelligence, 1994, 16, 373-392.	13.9	117
63	A Molecular Signature Predictive of Indolent Prostate Cancer. Science Translational Medicine, 2013, 5, 202ra122.	12.4	114
64	PFT1, the MED25 subunit of the plant Mediator complex, promotes flowering through CONSTANS dependent and independent mechanisms in Arabidopsis. Plant Journal, 2012, 69, 601-612.	5.7	113
65	ETV4 promotes metastasis in response to activation of PI3-kinase and Ras signaling in a mouse model of advanced prostate cancer. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E3506-15.	7.1	113
66	Identification of neurodegenerative factors using translatomeâ€"regulatory network analysis. Nature Neuroscience, 2015, 18, 1325-1333.	14.8	113
67	PLATE-Seq for genome-wide regulatory network analysis of high-throughput screens. Nature Communications, 2017, 8, 105.	12.8	109
68	An ID2-dependent mechanism for VHL inactivation in cancer. Nature, 2016, 529, 172-177.	27.8	108
69	ZFHX4 Interacts with the NuRD Core Member CHD4 and Regulates the Glioblastoma Tumor-Initiating Cell State. Cell Reports, 2014, 6, 313-324.	6.4	106
70	An Integrated Systems Biology Approach Identifies TRIM25 as a Key Determinant of Breast Cancer Metastasis. Cell Reports, 2017, 20, 1623-1640.	6.4	96
71	Quantitative assessment of protein activity in orphan tissues and single cells using the metaVIPER algorithm. Nature Communications, 2018, 9, 1471.	12.8	95
72	Inhibition of the autocrine IL-6â€"JAK2â€"STAT3â€"calprotectin axis as targeted therapy for HR^{â^'}/HER2⁺ breast cancers. Genes and Development, 2015, 29, 1631-1648.	5.9	94

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73	Cupid: simultaneous reconstruction of microRNA-target and ceRNA networks. Genome Research, 2015, 25, 257-267.	5.5	94
74	B-Raf Activation Cooperates with PTEN Loss to Drive c-Myc Expression in Advanced Prostate Cancer. Cancer Research, 2012, 72, 4765-4776.	0.9	87
75	Assembly and Interrogation of Alzheimerâ€™s Disease Genetic Networks Reveal Novel Regulators of Progression. PLoS ONE, 2015, 10, e0120352.	2.5	87
76	Verification of systems biology research in the age of collaborative competition. Nature Biotechnology, 2011, 29, 811-815.	17.5	83
77	geWorkbench: an open source platform for integrative genomics. Bioinformatics, 2010, 26, 1779-1780.	4.1	82
78	Identification of Hodgkin and Reed-Sternberg cell-specific genes by gene expression profiling. Journal of Clinical Investigation, 2003, 111, 529-537.	8.2	82
79	Novel Hybrid Phenotype Revealed in Small Cell Lung Cancer by a Transcription Factor Network Model That Can Explain Tumor Heterogeneity. Cancer Research, 2017, 77, 1063-1074.	0.9	81
80	Identification of an NKX3.1-G9a-UTY transcriptional regulatory network that controls prostate differentiation. Science, 2016, 352, 1576-1580.	12.6	80
81	Dual Targeting of the Akt/mTOR Signaling Pathway Inhibits Castration-Resistant Prostate Cancer in a Genetically Engineered Mouse Model. Cancer Research, 2012, 72, 4483-4493.	0.9	79
82	A modular master regulator landscape controls cancer transcriptional identity. Cell, 2021, 184, 334-351.e20.	28.9	78
83	Theory and Limitations of Genetic Network Inference from Microarray Data. Annals of the New York Academy of Sciences, 2007, 1115, 51-72.	3.8	77
84	Improving Breast Cancer Survival Analysis through Competition-Based Multidimensional Modeling. PLoS Computational Biology, 2013, 9, e1003047.	3.2	76
85	A CRISPR/Cas9-Engineered ARID1A-Deficient Human Gastric Cancer Organoid Model Reveals Essential and Nonessential Modes of Oncogenic Transformation. Cancer Discovery, 2021, 11, 1562-1581.	9.4	75
86	ChIP-on-chip significance analysis reveals large-scale binding and regulation by human transcription factor oncogenes. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 244-249.	7.1	74
87	Gene expression analysis provides a potential rationale for revising the histological grading of follicular lymphomas. Haematologica, 2008, 93, 1033-1038.	3.5	73
88	A complementary role for ELF3 and TFL1 in the regulation of flowering time by ambient temperature. Plant Journal, 2009, 58, 629-640.	5.7	73
89	Bone Marrow Myeloid Cells Regulate Myeloid-Biased Hematopoietic Stem Cells via a Histamine-Dependent Feedback Loop. Cell Stem Cell, 2017, 21, 747-760.e7.	11.1	68
90	The miR-424(322)/503 cluster orchestrates remodeling of the epithelium in the involuting mammary gland. Genes and Development, 2014, 28, 765-782.	5.9	66

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91	NSD2 is a conserved driver of metastatic prostate cancer progression. Nature Communications, 2018, 9, 5201.	12.8	66
92	Towards patient-based cancer therapeutics. Nature Biotechnology, 2010, 28, 904-906.	17.5	65
93	Immunostimulatory Cancer-Associated Fibroblast Subpopulations Can Predict Immunotherapy Response in Head and Neck Cancer. Clinical Cancer Research, 2022, 28, 2094-2109.	7.0	60
94	STK38 is a critical upstream regulator of MYCâ€™s oncogenic activity in human B-cell lymphoma. Oncogene, 2013, 32, 5283-5291.	5.9	58
95	Gene expression changes consistent with neuroAIDS and impaired working memory in HIV-1 transgenic rats. Molecular Neurodegeneration, 2014, 9, 26.	10.8	58
96	Rewiring makes the difference. Molecular Systems Biology, 2011, 7, 463.	7.2	57
97	Regulation of extra-embryonic endoderm stem cell differentiation by Nodal and Cripto signaling. Development (Cambridge), 2011, 138, 3885-3895.	2.5	53
98	Motif-based construction of a functional map for mammalian olfactory receptors. Genomics, 2003, 81, 443-456.	2.9	51
99	High-definition CpG methylation of novel genes in gastric carcinogenesis identified by next-generation sequencing. Modern Pathology, 2016, 29, 182-193.	5.5	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.	7.1	50
101	The Transcriptional Regulatory Network of Proneural Glioma Determines the Genetic Alterations Selected during Tumor Progression. Cancer Research, 2014, 74, 1440-1451.	0.9	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.	8.8	47
103	Elucidation and Pharmacological Targeting of Novel Molecular Drivers of Follicular Lymphoma Progression. Cancer Research, 2016, 76, 664-674.	0.9	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.	2.8	46
106	Tâ€cell lymphoblastic lymphoma shows differences and similarities with Tâ€cell acute lymphoblastic leukemia by genomic and gene expression analyses. Genes Chromosomes and Cancer, 2011, 50, 1063-1075.	2.8	44
107	Reverseâ€engineering human regulatory networks. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2012, 4, 311-325.	6.6	44
108	BACH2 inhibition reverses Î² cell failure in type 2 diabetes models. Journal of Clinical Investigation, 2021, 131, .	8.2	43

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109	Survival factor NFIL3 restricts FOXO-induced gene expression in cancer. Genes and Development, 2013, 27, 916-927.	5.9	42
110	HDAC6 activity is a non-oncogene addiction hub for inflammatory breast cancers. Breast Cancer Research, 2015, 17, 149.	5.0	42
111	The Regulatory Machinery of Neurodegeneration in InÂVitro Models of Amyotrophic Lateral Sclerosis. Cell Reports, 2015, 12, 335-345.	6.4	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. Molecular and Cellular Proteomics, 2017, 16, 891-910.	3.8	42
113	ScreenBEAM: a novel meta-analysis algorithm for functional genomics screens via Bayesian hierarchical modeling. Bioinformatics, 2016, 32, 260-267.	4.1	40
114	A CLK3-HMGA2 Alternative Splicing Axis Impacts Human Hematopoietic Stem Cell Molecular Identity throughout Development. Cell Stem Cell, 2018, 22, 575-588.e7.	11.1	40
115	Toward better benchmarking: challenge-based methods assessment in cancer genomics. Genome Biology, 2014, 15, 462.	8.8	38
116	Quantitative modeling of the terminal differentiation of B cells and mechanisms of lymphomagenesis. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 2672-2677.	7.1	37
117	SJARACNe: a scalable software tool for gene network reverse engineering from big data. Bioinformatics, 2019, 35, 2165-2166.	4.1	36
118	Convection-enhanced delivery of etoposide is effective against murine proneural glioblastoma. Neuro-Oncology, 2014, 16, 1210-1219.	1.2	34
119	Predicting Drug Response in Human Prostate Cancer from Preclinical Analysis of InÂVivo Mouse Models. Cell Reports, 2015, 12, 2060-2071.	6.4	34
120	A community challenge for a pancancer drug mechanism of action inference from perturbational profile data. Cell Reports Medicine, 2022, 3, 100492.	6.5	33
121	Interrogation of a Context-Specific Transcription Factor Network Identifies Novel Regulators of Pluripotency. Stem Cells, 2015, 33, 367-377.	3.2	32
122	The number of titrated microRNA species dictates ceRNA regulation. Nucleic Acids Research, 2018, 46, 4354-4369.	14.5	32
123	Discovering transcriptional regulatory regions in Drosophila by a nonalignment method for phylogenetic footprinting. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 6305-6310.	7.1	31
124	Gene Expression Dynamics during Germinal Center Transit in B Cells. Annals of the New York Academy of Sciences, 2003, 987, 166-172.	3.8	30
125	A computational systems approach identifies synergistic specification genes that facilitate lineage conversion to prostate tissue. Nature Communications, 2017, 8, 14662.	12.8	30
126	Epigenetic Regulation of ZBTB18 Promotes Glioblastoma Progression. Molecular Cancer Research, 2017, 15, 998-1011.	3.4	30

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127	Cooperation of loss of NKX3.1 and inflammation in prostate cancer initiation. DMM Disease Models and Mechanisms, 2018, 11, .	2.4	30
128	A Phase II Study of the Efficacy and Safety of Oral Selinexor in Recurrent Glioblastoma. Clinical Cancer Research, 2022, 28, 452-460.	7.0	29
129	Systematic elucidation of neuron-astrocyte interaction in models of amyotrophic lateral sclerosis using multi-modal integrated bioinformatics workflow. Nature Communications, 2020, 11, 5579.	12.8	28
130	iTools: A Framework for Classification, Categorization and Integration of Computational Biology Resources. PLoS ONE, 2008, 3, e2265.	2.5	27
131	Hypothalamic proteoglycan syndecan-3 is a novel cocaine addiction resilience factor. Nature Communications, 2013, 4, 1955.	12.8	26
132	SECAT: Quantifying Protein Complex Dynamics across Cell States by Network-Centric Analysis of SEC-SWATH-MS Profiles. Cell Systems, 2020, 11, 589-607.e8.	6.2	26
133	HER3 Is an Actionable Target in Advanced Prostate Cancer. Cancer Research, 2021, 81, 6207-6218.	0.9	25
134	hARACNe: improving the accuracy of regulatory model reverse engineering via higher-order data processing inequality tests. Interface Focus, 2013, 3, 20130011.	3.0	24
135	Systematic and Fully Automated Identification of Protein Sequence Patterns. Journal of Computational Biology, 2000, 7, 585-600.	1.6	23
136	Genome-Wide Discovery of Modulators of Transcriptional Interactions in Human B Lymphocytes. Lecture Notes in Computer Science, 2006, , 348-362.	1.3	23
137	CTD2 Dashboard: a searchable web interface to connect validated results from the Cancer Target Discovery and Development Network. Database: the Journal of Biological Databases and Curation, 2017, 2017, .	3.0	23
138	Systematic, network-based characterization of therapeutic target inhibitors. PLoS Computational Biology, 2017, 13, e1005599.	3.2	23
139	Transcription factor activating protein 4 is synthetically lethal and a master regulator of MYCN-amplified neuroblastoma. Oncogene, 2018, 37, 5451-5465.	5.9	22
140	Oncoprotein-specific molecular interaction maps (SigMaps) for cancer network analyses. Nature Biotechnology, 2021, 39, 215-224.	17.5	21
141	Inferring Protein Modulation from Gene Expression Data Using Conditional Mutual Information. PLoS ONE, 2014, 9, e109569.	2.5	21
142	The transcriptomic response of cells to a drug combination is more than the sum of the responses to the monotherapies. ELife, 2020, 9, .	6.0	21
143	Report: workshop on mediastinal grey zone lymphoma. European Journal of Haematology, 2005, 75, 45-52.	2.2	19
144	The Master Regulator Protein BAZ2B Can Reprogram Human Hematopoietic Lineage-Committed Progenitors into a Multipotent State. Cell Reports, 2020, 33, 108474.	6.4	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. British Journal of Haematology, 2021, 195, 201-209.	2.5	17
146	Gene Expression Profiles of Patients With Antibody-Mediated Rejection After Cardiac Transplantation. Journal of Heart and Lung Transplantation, 2008, 27, 932-934.	0.6	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. Genome Medicine, 2016, 8, 116.	8.2	15
148	Reply to â€˜H-STS, L-STS and KRJ-I are not authentic GEPNET cell linesâ€™. Nature Genetics, 2019, 51, 1427-1428.	21.4	15
149	Phase I/II trial of ruxolitinib in combination with trastuzumab in metastatic HER2 positive breast cancer. Breast Cancer Research and Treatment, 2021, 189, 177-185.	2.5	15
150	Genome-Wide Dissection of Posttranscriptional and Posttranslational Interactions. Methods in Molecular Biology, 2012, 786, 131-149.	0.9	15
151	Functional classification of proteins by pattern discovery and top-down clustering of primary sequences. IBM Systems Journal, 2001, 40, 379-393.	3.0	14
152	Correlating measurements across samples improves accuracy of large-scale expression profile experiments. Genome Biology, 2009, 10, R143.	9.6	14
153	Identification of immunotherapeutic targets by genomic profiling of rectal NET metastases. OncoImmunology, 2016, 5, e1213931.	4.6	14
154	ZCCHC17 is a master regulator of synaptic gene expression in Alzheimerâ€™s disease. Bioinformatics, 2018, 34, 367-371.	4.1	14
155	Dissecting the interface between signaling and transcriptional regulation in human B cells. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2009, , 264-75.	0.7	14
156	Searching in parallel for similar strings [biological sequences]. IEEE Computational Science and Engineering, 1994, 1, 60-75.	0.6	13
157	Detection and removal of spatial bias in multiwell assays. Bioinformatics, 2016, 32, 1959-1965.	4.1	13
158	Accelerated parallel algorithm for gene network reverse engineering. BMC Systems Biology, 2017, 11, 83.	3.0	13
159	DIGGIT: a Bioconductor package to infer genetic variants driving cellular phenotypes. Bioinformatics, 2015, 31, btv499.	4.1	12
160	Gene Expression Analysis of Follicular Lymphoma Provides a Potential Rationale for Histological Grading Revision.. Blood, 2007, 110, 186-186.	1.4	12
161	A Systems Biology Approach to Transcription Factor Binding Site Prediction. PLoS ONE, 2010, 5, e9878.	2.5	11
162	Patient-Driven Discovery, Therapeutic Targeting, and Post-Clinical Validation of a Novel AKT1 Fusionâ€“Driven Cancer. Cancer Discovery, 2019, 9, 605-616.	9.4	11

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163	Longitudinal Immune Profiling Reveals Unique Myeloid and T-cell Phenotypes Associated with Spontaneous Immunoediting in a Prostate Tumor Model. Cancer Immunology Research, 2021, 9, 529-541.	3.4	11
164	Discovery of widespread transcription initiation at microsatellites predictable by sequence-based deep neural network. Nature Communications, 2021, 12, 3297.	12.8	11
165	Drawing networks of rejection - a systems biological approach to the identification of candidate genes in heart transplantation. Journal of Cellular and Molecular Medicine, 2011, 15, 949-956.	3.6	10
166	ABC Transporters and the Proteasome Complex Are Implicated in Susceptibility to Stevensâ€"Johnson Syndrome and Toxic Epidermal Necrolysis across Multiple Drugs. PLoS ONE, 2015, 10, e0131038.	2.5	9
167	The Cyni framework for network inference in Cytoscape. Bioinformatics, 2015, 31, 1499-1501.	4.1	9
168	iterClust: a statistical framework for iterative clustering analysis. Bioinformatics, 2018, 34, 2865-2866.	4.1	9
169	Prioritizing transcriptional factors in gene regulatory networks with PageRank. IScience, 2021, 24, 102017.	4.1	9
170	A 2:1 randomized, open-label, phase II study of selinexor vs. physicianâ€™s choice in older patients with relapsed or refractory acute myeloid leukemia. Leukemia and Lymphoma, 2021, 62, 1-12.	1.3	9
171	Direct ChIP-Seq significance analysis improves target prediction. BMC Genomics, 2015, 16, S4.	2.8	8
172	A Systems Approach to Drug Discovery in Alzheimer's Disease. Neurotherapeutics, 2015, 12, 126-131.	4.4	8
173	Mechanism and Role of SOX2 Repression in Seminoma: Relevance to Human Germline Specification. Stem Cell Reports, 2016, 6, 772-783.	4.8	8
174	PI3KÎ³/Î´ and NOTCH1 Cross-Regulate Pathways That Define the T-cell Acute Lymphoblastic Leukemia Disease Signature. Molecular Cancer Therapeutics, 2017, 16, 2069-2082.	4.1	8
175	Oncogenic AKT Signaling Negatively Regulates Glucocorticoid Receptor Function to Promote Glucocorticoid Resistance In T Cell Acute Lymphoblastic Leukemia. Blood, 2010, 116, 11-11.	1.4	8
176	DISSECTING THE INTERFACE BETWEEN SIGNALING AND TRANSCRIPTIONAL REGULATION IN HUMAN B CELLS. , 2008, , .		7
177	MASTER REGULATORS USED AS BREAST CANCER METASTASIS CLASSIFIER. , 2008, , .		7
178	Pooled ShRNA Screenings: Computational Analysis. Methods in Molecular Biology, 2013, 980, 371-384.	0.9	7
179	A Context-Specific Network of Protein-DNA and Protein-Protein Interactions Reveals New Regulatory Motifs in Human B Cells. Lecture Notes in Computer Science, 2006, , 42-56.	1.3	7
180	Integrative Network-based Association Studies: Leveraging cell regulatory models in the post-GWAS era. Nature Precedings, 2011, , .	0.1	6

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181	Using systems and structure biology tools to dissect cellular phenotypes. Journal of the American Medical Informatics Association: JAMIA, 2012, 19, 171-175.	4.4	6
182	Elucidating synergistic dependencies in lung adenocarcinoma by proteome-wide signaling-network analysis. PLoS ONE, 2019, 14, e0208646.	2.5	6
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