

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	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
2	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
3	Immunostimulatory Cancer-Associated Fibroblast Subpopulations Can Predict Immunotherapy Response in Head and Neck Cancer. <i>Clinical Cancer Research</i> , 2022, 28, 2094-2109.	3.2	60
4	Adult enteric Dclk1-positive glial and neuronal cells reveal distinct responses to acute intestinal injury. <i>American Journal of Physiology - Renal Physiology</i> , 2022, 322, G583-G597.	1.6	2
5	Notch-mediated Ephrin signaling disrupts islet architecture and β cell function. <i>JCI Insight</i> , 2022, 7, .	2.3	5
6	A multi-organ chip with matured tissue niches linked by vascular flow. <i>Nature Biomedical Engineering</i> , 2022, 6, 351-371.	11.6	162
7	DIPG-57. A systems biology approach to defining and targeting master regulator dependencies from bulk and single-Cell RNA-seq in diffuse midline glioma (DMG). <i>Neuro-Oncology</i> , 2022, 24, i31-i32.	0.6	0
8	Abstract 2127: Master regulator analysis of the tumor microenvironment and the distinctive tumor sub-populations in pancreatic ductal adenocarcinoma. <i>Cancer Research</i> , 2022, 82, 2127-2127.	0.4	0
9	Oncoprotein-specific molecular interaction maps (SigMaps) for cancer network analyses. <i>Nature Biotechnology</i> , 2021, 39, 215-224.	9.4	21
10	Prioritizing transcriptional factors in gene regulatory networks with PageRank. <i>IScience</i> , 2021, 24, 102017.	1.9	9
11	Longitudinal Immune Profiling Reveals Unique Myeloid and T-cell Phenotypes Associated with Spontaneous Immunoediting in a Prostate Tumor Model. <i>Cancer Immunology Research</i> , 2021, 9, 529-541.	1.6	11
12	An expanded universe of cancer targets. <i>Cell</i> , 2021, 184, 1142-1155.	13.5	135
13	Single-cell protein activity analysis identifies recurrence-associated renal tumor macrophages. <i>Cell</i> , 2021, 184, 2988-3005.e16.	13.5	166
14	Targeting the T-Cell Lymphoma Epigenome Induces Cell Death, Cancer Testes Antigens, Immune-Modulatory Signaling Pathways. <i>Molecular Cancer Therapeutics</i> , 2021, 20, 1422-1430.	1.9	6
15	Promotion of cholangiocarcinoma growth by diverse cancer-associated fibroblast subpopulations. <i>Cancer Cell</i> , 2021, 39, 866-882.e11.	7.7	159
16	Discovery of widespread transcription initiation at microsatellites predictable by sequence-based deep neural network. <i>Nature Communications</i> , 2021, 12, 3297.	5.8	11
17	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
18	Abstract 645: Network-based assessment of HDAC6 activity is highly predictive of pre-clinical and clinical responses to the HDAC6 inhibitor ricolinostat. , 2021, , .		0

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19	Abstract LB247: A forward genetic screen to identify drivers of neuroendocrine prostate cancer. , 2021, , .		0
20	A 2:1 randomized, open-label, phase II study of selinexor vs. physician's choice in older patients with relapsed or refractory acute myeloid leukemia. <i>Leukemia and Lymphoma</i> , 2021, 62, 1-12.	0.6	9
21	Fimepinostat (CUDC-907) in patients with relapsed/refractory diffuse large B cell and high-grade B-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
22	A modular master regulator landscape controls cancer transcriptional identity. <i>Cell</i> , 2021, 184, 334-351.e20.	13.5	78
23	A CRISPR/Cas9-Engineered <i>ARID1A</i> -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
24	HER3 Is an Actionable Target in Advanced Prostate Cancer. <i>Cancer Research</i> , 2021, 81, 6207-6218.	0.4	25
25	BACH2 inhibition reverses β cell failure in type 2 diabetes models. <i>Journal of Clinical Investigation</i> , 2021, 131, .	3.9	43
26	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
27	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
28	Identifying the Potential Mechanism of Action of SNPs Associated With Breast Cancer Susceptibility With GVI-TamIN. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 798.	2.0	0
29	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
30	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
31	Generation of pralatrexate resistant T-cell lymphoma lines reveals two patterns of acquired drug resistance that is overcome with epigenetic modifiers. <i>Genes Chromosomes and Cancer</i> , 2020, 59, 639-651.	1.5	3
32	Mesenchymal subtype neuroblastomas are addicted to TGF- β 2R2/HMGR-driven protein geranylgeranylation. <i>Scientific Reports</i> , 2020, 10, 10748.	1.6	3
33	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
34	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
35	Preclinical evaluation of XPO1 inhibition in Wilms tumors.. <i>Journal of Clinical Oncology</i> , 2020, 38, 3580-3580.	0.8	1
36	N-quinoline-benzenesulfonamide derivatives exert potent anti-lymphoma effect by targeting NF- κ B. <i>IScience</i> , 2020, 23, 101884.	1.9	1

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37	DIPG-40. TARGETING MASTER REGULATOR DEPENDENCIES IN DIFFUSE INTRINSIC PONTINE GLIOMA (DIPG). <i>Neuro-Oncology</i> , 2020, 22, iii294-iii295.	0.6	0
38	Reply to "H-STS, L-STS and KRJ-I are not authentic GEPNET cell lines"™. <i>Nature Genetics</i> , 2019, 51, 1427-1428.	9.4	15
39	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
40	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
41	Patient-Driven Discovery, Therapeutic Targeting, and Post-Clinical Validation of a Novel <i>AKT1</i> Fusion-Driven Cancer. <i>Cancer Discovery</i> , 2019, 9, 605-616.	7.7	11
42	Experimental microdissection enables functional harmonisation of pancreatic cancer subtypes. <i>Gut</i> , 2019, 68, 1034-1043.	6.1	147
43	Elucidating synergistic dependencies in lung adenocarcinoma by proteome-wide signaling-network analysis. <i>PLoS ONE</i> , 2019, 14, e0208646.	1.1	6
44	SJARACNe: a scalable software tool for gene network reverse engineering from big data. <i>Bioinformatics</i> , 2019, 35, 2165-2166.	1.8	36
45	Cross-Cohort Analysis Identifies a <i>TEAD4</i> MYCN Positive Feedback Loop as the Core Regulatory Element of High-Risk Neuroblastoma. <i>Cancer Discovery</i> , 2018, 8, 582-599.	7.7	119
46	The Immune Landscape of Cancer. <i>Immunity</i> , 2018, 48, 812-830.e14.	6.6	3,706
47	A <i>CLK3</i> - <i>HMGA2</i> 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
48	<i>ZCCHC17</i> is a master regulator of synaptic gene expression in Alzheimer's disease. <i>Bioinformatics</i> , 2018, 34, 367-371.	1.8	14
49	The number of titrated microRNA species dictates ceRNA regulation. <i>Nucleic Acids Research</i> , 2018, 46, 4354-4369.	6.5	32
50	iterClust: a statistical framework for iterative clustering analysis. <i>Bioinformatics</i> , 2018, 34, 2865-2866.	1.8	9
51	TMOD-18. THE PATIENT DERIVED XENOGRAFT NATIONAL RESOURCE: A COMPREHENSIVE COLLECTION OF HIGH-GRADE GLIOMA MODELS FOR PRE-CLINICAL AND TRANSLATIONAL STUDIES. <i>Neuro-Oncology</i> , 2018, 20, vi272-vi272.	0.6	0
52	<i>NSD2</i> is a conserved driver of metastatic prostate cancer progression. <i>Nature Communications</i> , 2018, 9, 5201.	5.8	66
53	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
54	Differentiation-state plasticity is a targetable resistance mechanism in basal-like breast cancer. <i>Nature Communications</i> , 2018, 9, 3815.	5.8	137

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55	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
56	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
57	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
58	Synergistic antileukemic therapies in <i>NOTCH1</i> -induced T-ALL. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 2006-2011.	3.3	50
59	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
60	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
61	Epigenetic Regulation of ZBTB18 Promotes Glioblastoma Progression. <i>Molecular Cancer Research</i> , 2017, 15, 998-1011.	1.5	30
62	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
63	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
64	The recurrent architecture of tumour initiation, progression and drug sensitivity. <i>Nature Reviews Cancer</i> , 2017, 17, 116-130.	12.8	170
65	PI3K β and NOTCH1 Cross-Regulate Pathways That Define the T-cell Acute Lymphoblastic Leukemia Disease Signature. <i>Molecular Cancer Therapeutics</i> , 2017, 16, 2069-2082.	1.9	8
66	PLATE-Seq for genome-wide regulatory network analysis of high-throughput screens. <i>Nature Communications</i> , 2017, 8, 105.	5.8	109
67	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
68	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
69	High-throughput validation of ceRNA regulatory networks. <i>BMC Genomics</i> , 2017, 18, 418.	1.2	46
70	Accelerated parallel algorithm for gene network reverse engineering. <i>BMC Systems Biology</i> , 2017, 11, 83.	3.0	13
71	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
72	Systematic, network-based characterization of therapeutic target inhibitors. <i>PLoS Computational Biology</i> , 2017, 13, e1005599.	1.5	23

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73	ScreenBEAM: a novel meta-analysis algorithm for functional genomics screens via Bayesian hierarchical modeling. <i>Bioinformatics</i> , 2016, 32, 260-267.	1.8	40
74	Dclk1 Defines Quiescent Pancreatic Progenitors that Promote Injury-Induced Regeneration and Tumorigenesis. <i>Cell Stem Cell</i> , 2016, 18, 441-455.	5.2	196
75	ARACNe-AP: gene network reverse engineering through adaptive partitioning inference of mutual information. <i>Bioinformatics</i> , 2016, 32, 2233-2235.	1.8	305
76	HAUSP deubiquitinates and stabilizes N-Myc in neuroblastoma. <i>Nature Medicine</i> , 2016, 22, 1180-1186.	15.2	158
77	Identification of immunotherapeutic targets by genomic profiling of rectal NET metastases. <i>Oncotarget</i> , 2016, 5, e1213931.	2.1	14
78	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
79	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
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	Mechanism and Role of SOX2 Repression in Seminoma: Relevance to Human Germline Specification. <i>Stem Cell Reports</i> , 2016, 6, 772-783.	2.3	8
82	High-definition CpG methylation of novel genes in gastric carcinogenesis identified by next-generation sequencing. <i>Modern Pathology</i> , 2016, 29, 182-193.	2.9	50
83	Detection and removal of spatial bias in multiwell assays. <i>Bioinformatics</i> , 2016, 32, 1959-1965.	1.8	13
84	An ID2-dependent mechanism for VHL inactivation in cancer. <i>Nature</i> , 2016, 529, 172-177.	13.7	108
85	Elucidation and Pharmacological Targeting of Novel Molecular Drivers of Follicular Lymphoma Progression. <i>Cancer Research</i> , 2016, 76, 664-674.	0.4	47
86	Predicting Drug Response in Human Prostate Cancer from Preclinical Analysis of In Vivo Mouse Models. <i>Cell Reports</i> , 2015, 12, 2060-2071.	2.9	34
87	Direct ChIP-Seq significance analysis improves target prediction. <i>BMC Genomics</i> , 2015, 16, S4.	1.2	8
88	Identifying candidate drivers of alcohol dependence-induced excessive drinking by assembly and interrogation of brain-specific regulatory networks. <i>Genome Biology</i> , 2015, 16, 68.	3.8	47
89	ABC Transporters and the Proteasome Complex Are Implicated in Susceptibility to Stevens-Johnson Syndrome and Toxic Epidermal Necrolysis across Multiple Drugs. <i>PLoS ONE</i> , 2015, 10, e0131038.	1.1	9
90	HDAC6 activity is a non-oncogene addiction hub for inflammatory breast cancers. <i>Breast Cancer Research</i> , 2015, 17, 149.	2.2	42

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91	A Systems Approach to Drug Discovery in Alzheimer's Disease. <i>Neurotherapeutics</i> , 2015, 12, 126-131.	2.1	8
92	<i>Cancer Systems Biology.</i> , 2015, , 297-314.e3.		0
93	Toward understanding and exploiting tumor heterogeneity. <i>Nature Medicine</i> , 2015, 21, 846-853.	15.2	604
94	Identification of neurodegenerative factors using translato ^{me} â€“regulatory network analysis. <i>Nature Neuroscience</i> , 2015, 18, 1325-1333.	7.1	113
95	Inhibition of the autocrine IL-6â€“JAK2â€“STAT3â€“calprotectin axis as targeted therapy for HR ⁺ /HER2 ⁺ breast cancers. <i>Genes and Development</i> , 2015, 29, 1631-1648.	2.7	94
96	The Regulatory Machinery of Neurodegeneration in InÂVitro Models of Amyotrophic Lateral Sclerosis. <i>Cell Reports</i> , 2015, 12, 335-345.	2.9	42
97	Elucidating Compound Mechanism of Action by Network Perturbation Analysis. <i>Cell</i> , 2015, 162, 441-451.	13.5	278
98	DIGGIT: a Bioconductor package to infer genetic variants driving cellular phenotypes. <i>Bioinformatics</i> , 2015, 31, btv499.	1.8	12
99	The Cyni framework for network inference in Cytoscape. <i>Bioinformatics</i> , 2015, 31, 1499-1501.	1.8	9
100	Interrogation of a Context-Specific Transcription Factor Network Identifies Novel Regulators of Pluripotency. <i>Stem Cells</i> , 2015, 33, 367-377.	1.4	32
101	Cupid: simultaneous reconstruction of microRNA-target and ceRNA networks. <i>Genome Research</i> , 2015, 25, 257-267.	2.4	94
102	Assembly and Interrogation of Alzheimerâ€™s Disease Genetic Networks Reveal Novel Regulators of Progression. <i>PLoS ONE</i> , 2015, 10, e0120352.	1.1	87
103	Convection-enhanced delivery of etoposide is effective against murine proneural glioblastoma. <i>Neuro-Oncology</i> , 2014, 16, 1210-1219.	0.6	34
104	Predicting protein networks in cancer. <i>Nature Genetics</i> , 2014, 46, 1252-1253.	9.4	5
105	A promoter-level mammalian expression atlas. <i>Nature</i> , 2014, 507, 462-470.	13.7	1,838
106	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
107	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
108	A community computational challenge to predict the activity of pairs of compounds. <i>Nature Biotechnology</i> , 2014, 32, 1213-1222.	9.4	264

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109	RECOMB/ISCB Systems Biology, Regulatory Genomics, and DREAM 2013 Special Issue. <i>Journal of Computational Biology</i> , 2014, 21, 371-372.	0.8	1
110	Toward better benchmarking: challenge-based methods assessment in cancer genomics. <i>Genome Biology</i> , 2014, 15, 462.	3.8	38
111	Gene expression changes consistent with neuroAIDS and impaired working memory in HIV-1 transgenic rats. <i>Molecular Neurodegeneration</i> , 2014, 9, 26.	4.4	58
112	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
113	The Transcriptional Regulatory Network of Proneural Glioma Determines the Genetic Alterations Selected during Tumor Progression. <i>Cancer Research</i> , 2014, 74, 1440-1451.	0.4	48
114	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
115	Inferring Protein Modulation from Gene Expression Data Using Conditional Mutual Information. <i>PLoS ONE</i> , 2014, 9, e109569.	1.1	21
116	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
117	Direct Reversal of Glucocorticoid Resistance by AKT Inhibition in Acute Lymphoblastic Leukemia. <i>Cancer Cell</i> , 2013, 24, 766-776.	7.7	220
118	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
119	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
120	STK38 is a critical upstream regulator of MYC's oncogenic activity in human B-cell lymphoma. <i>Oncogene</i> , 2013, 32, 5283-5291.	2.6	58
121	Pooled ShRNA Screenings: Computational Analysis. <i>Methods in Molecular Biology</i> , 2013, 980, 371-384.	0.4	7
122	Hypothalamic proteoglycan syndecan-3 is a novel cocaine addiction resilience factor. <i>Nature Communications</i> , 2013, 4, 1955.	5.8	26
123	Improving Breast Cancer Survival Analysis through Competition-Based Multidimensional Modeling. <i>PLoS Computational Biology</i> , 2013, 9, e1003047.	1.5	76
124	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
125	A Molecular Signature Predictive of Indolent Prostate Cancer. <i>Science Translational Medicine</i> , 2013, 5, 202ra122.	5.8	114
126	Survival factor NFIL3 restricts FOXO-induced gene expression in cancer. <i>Genes and Development</i> , 2013, 27, 916-927.	2.7	42

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127	<i>ETV4</i> 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
128	Preface: RECOMB Systems Biology, Regulatory Genomics, and DREAM 2012 Special Issue. <i>Journal of Computational Biology</i> , 2013, 20, 373-374.	0.8	0
129	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
130	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
131	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
132	Preface: RECOMB Systems Biology, Regulatory Genomics, and DREAM 2011 Special Issue. <i>Journal of Computational Biology</i> , 2012, 19, 101-101.	0.8	2
133	Using systems and structure biology tools to dissect cellular phenotypes. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2012, 19, 171-175.	2.2	6
134	Structure-based prediction of protein-protein interactions on a genome-wide scale. <i>Nature</i> , 2012, 490, 556-560.	13.7	652
135	Reverse engineering human regulatory networks. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2012, 4, 311-325.	6.6	44
136	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
137	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
138	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
139	Genome-Wide Dissection of Posttranscriptional and Posttranslational Interactions. <i>Methods in Molecular Biology</i> , 2012, 786, 131-149.	0.4	15
140	MEF2B Mutations Lead to De-Regulated Expression of the BCL6 Oncogene in Diffuse Large B-Cell Lymphoma and Follicular Lymphoma. <i>Blood</i> , 2012, 120, 1284-1284.	0.6	1
141	Keynote: A systems biology approach to integrative cancer genomics. , 2011, , .		0
142	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
143	Integrative Network-based Association Studies: Leveraging cell regulatory models in the post-GWAS era. <i>Nature Precedings</i> , 2011, , .	0.1	6
144	Gene expression analysis uncovers similarity and differences among Burkitt lymphoma subtypes. <i>Blood</i> , 2011, 117, 3596-3608.	0.6	128

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145	Rewiring makes the difference. <i>Molecular Systems Biology</i> , 2011, 7, 463.	3.2	57
146	Drawing networks of rejection - a systems biological approach to the identification of candidate genes in heart transplantation. <i>Journal of Cellular and Molecular Medicine</i> , 2011, 15, 949-956.	1.6	10
147	Tâ€cell lymphoblastic lymphoma shows differences and similarities with Tâ€cell acute lymphoblastic leukemia by genomic and gene expression analyses. <i>Genes Chromosomes and Cancer</i> , 2011, 50, 1063-1075.	1.5	44
148	Preface. <i>Journal of Computational Biology</i> , 2011, 18, 131-131.	0.8	1
149	Regulation of extra-embryonic endoderm stem cell differentiation by Nodal and Cripto signaling. <i>Development (Cambridge)</i> , 2011, 138, 3885-3895.	1.2	53
150	Verification of systems biology research in the age of collaborative competition. <i>Nature Biotechnology</i> , 2011, 29, 811-815.	9.4	83
151	Striking a Balance Between Feasible and Realistic Biological Models. <i>Science Translational Medicine</i> , 2011, 3, 103ps39.	5.8	3
152	Regulation of extra-embryonic endoderm stem cell differentiation by Nodal and Cripto signaling. <i>Journal of Cell Science</i> , 2011, 124, e1-e1.	1.2	1
153	A human Bâ€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
154	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
155	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
156	The transcriptional network for mesenchymal transformation of brain tumours. <i>Nature</i> , 2010, 463, 318-325.	13.7	1,114
157	Towards patient-based cancer therapeutics. <i>Nature Biotechnology</i> , 2010, 28, 904-906.	9.4	65
158	The TLX1 oncogene drives aneuploidy in T cell transformation. <i>Nature Medicine</i> , 2010, 16, 1321-1327.	15.2	139
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