

Trey Ideker

List of Publications by Year in descending order

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231
papers

87,229
citations

4120

87
h-index

1280

225
g-index

261
all docs

261
docs citations

261
times ranked

112567
citing authors

#	ARTICLE	IF	CITATIONS
1	Cytoscape: A Software Environment for Integrated Models of Biomolecular Interaction Networks. <i>Genome Research</i> , 2003, 13, 2498-2504.	2.4	37,062
2	Cytoscape 2.8: new features for data integration and network visualization. <i>Bioinformatics</i> , 2011, 27, 431-432.	1.8	4,228
3	A SARS-CoV-2 protein interaction map reveals targets for drug repurposing. <i>Nature</i> , 2020, 583, 459-468.	13.7	3,542
4	Genome-wide Methylation Profiles Reveal Quantitative Views of Human Aging Rates. <i>Molecular Cell</i> , 2013, 49, 359-367.	4.5	2,734
5	Integrated Genomic Characterization of Papillary Thyroid Carcinoma. <i>Cell</i> , 2014, 159, 676-690.	13.5	2,318
6	Integration of biological networks and gene expression data using Cytoscape. <i>Nature Protocols</i> , 2007, 2, 2366-2382.	5.5	2,275
7	Integrated Genomic and Proteomic Analyses of a Systematically Perturbed Metabolic Network. <i>Science</i> , 2001, 292, 929-934.	6.0	1,921
8	A NEW APPROACH TO DECODING LIFE: Systems Biology. <i>Annual Review of Genomics and Human Genetics</i> , 2001, 2, 343-372.	2.5	1,455
9	Network-based classification of breast cancer metastasis. <i>Molecular Systems Biology</i> , 2007, 3, 140.	3.2	1,320
10	A travel guide to Cytoscape plugins. <i>Nature Methods</i> , 2012, 9, 1069-1076.	9.0	1,289
11	Discovering regulatory and signalling circuits in molecular interaction networks. <i>Bioinformatics</i> , 2002, 18, S233-S240.	1.8	1,098
12	Global Analysis of Host-Pathogen Interactions that Regulate Early-Stage HIV-1 Replication. <i>Cell</i> , 2008, 135, 49-60.	13.5	881
13	Human host factors required for influenza virus replication. <i>Nature</i> , 2010, 463, 813-817.	13.7	755
14	Conserved patterns of protein interaction in multiple species. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 1974-1979.	3.3	714
15	Protein networks in disease. <i>Genome Research</i> , 2008, 18, 644-652.	2.4	712
16	Network-based stratification of tumor mutations. <i>Nature Methods</i> , 2013, 10, 1108-1115.	9.0	698
17	Differential network biology. <i>Molecular Systems Biology</i> , 2012, 8, 565.	3.2	689
18	An Atlas of Combinatorial Transcriptional Regulation in Mouse and Man. <i>Cell</i> , 2010, 140, 744-752.	13.5	667

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19	Complementary Profiling of Gene Expression at the Transcriptome and Proteome Levels in <i>Saccharomyces cerevisiae</i> . <i>Molecular and Cellular Proteomics</i> , 2002, 1, 323-333.	2.5	591
20	DNA methylation aging clocks: challenges and recommendations. <i>Genome Biology</i> , 2019, 20, 249.	3.8	552
21	Network propagation: a universal amplifier of genetic associations. <i>Nature Reviews Genetics</i> , 2017, 18, 551-562.	7.7	514
22	Integrative approaches for finding modular structure in biological networks. <i>Nature Reviews Genetics</i> , 2013, 14, 719-732.	7.7	512
23	Comparative host-coronavirus protein interaction networks reveal pan-viral disease mechanisms. <i>Science</i> , 2020, 370, .	6.0	508
24	Modeling cellular machinery through biological network comparison. <i>Nature Biotechnology</i> , 2006, 24, 427-433.	9.4	492
25	Inferring Pathway Activity toward Precise Disease Classification. <i>PLoS Computational Biology</i> , 2008, 4, e1000217.	1.5	475
26	A global network of transcription factors, involving E2A, EBF1 and Foxo1, that orchestrates B cell fate. <i>Nature Immunology</i> , 2010, 11, 635-643.	7.0	475
27	Functional genomic screen for modulators of ciliogenesis and cilium length. <i>Nature</i> , 2010, 464, 1048-1051.	13.7	473
28	Conserved pathways within bacteria and yeast as revealed by global protein network alignment. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 11394-11399.	3.3	466
29	Exome Sequencing Links Corticospinal Motor Neuron Disease to Common Neurodegenerative Disorders. <i>Science</i> , 2014, 343, 506-511.	6.0	466
30	Metabolomics Reveals Signature of Mitochondrial Dysfunction in Diabetic Kidney Disease. <i>Journal of the American Society of Nephrology: JASN</i> , 2013, 24, 1901-1912.	3.0	454
31	Rewiring of Genetic Networks in Response to DNA Damage. <i>Science</i> , 2010, 330, 1385-1389.	6.0	408
32	DNA Methylation Clocks in Aging: Categories, Causes, and Consequences. <i>Molecular Cell</i> , 2018, 71, 882-895.	4.5	403
33	Host Cell Factors in HIV Replication: Meta-Analysis of Genome-Wide Studies. <i>PLoS Pathogens</i> , 2009, 5, e1000437.	2.1	396
34	Systematic interpretation of genetic interactions using protein networks. <i>Nature Biotechnology</i> , 2005, 23, 561-566.	9.4	391
35	Temporal transcriptional response to ethylene gas drives growth hormone cross-regulation in <i>Arabidopsis</i> . <i>ELife</i> , 2013, 2, e00675.	2.8	379
36	Conservation and Rewiring of Functional Modules Revealed by an Epistasis Map in Fission Yeast. <i>Science</i> , 2008, 322, 405-410.	6.0	328

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37	MHC-I Genotype Restricts the Oncogenic Mutational Landscape. <i>Cell</i> , 2017, 171, 1272-1283.e15.	13.5	307
38	Using deep learning to model the hierarchical structure and function of a cell. <i>Nature Methods</i> , 2018, 15, 290-298.	9.0	292
39	Combinatorial CRISPR-Cas9 screens for de novo mapping of genetic interactions. <i>Nature Methods</i> , 2017, 14, 573-576.	9.0	287
40	Testing for Differentially-Expressed Genes by Maximum-Likelihood Analysis of Microarray Data. <i>Journal of Computational Biology</i> , 2000, 7, 805-817.	0.8	286
41	A Decade of Systems Biology. <i>Annual Review of Cell and Developmental Biology</i> , 2010, 26, 721-744.	4.0	277
42	Comprehensive curation and analysis of global interaction networks in <i>Saccharomyces cerevisiae</i> . <i>Journal of Biology</i> , 2006, 5, 11.	2.7	276
43	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
44	Epigenetic aging signatures in mice livers are slowed by dwarfism, calorie restriction and rapamycin treatment. <i>Genome Biology</i> , 2017, 18, 57.	3.8	249
45	A Systems Approach to Mapping DNA Damage Response Pathways. <i>Science</i> , 2006, 312, 1054-1059.	6.0	248
46	Multiple Pathways Are Co-regulated by the Protein Kinase Snf1 and the Transcription Factors Adr1 and Cat8. <i>Journal of Biological Chemistry</i> , 2003, 278, 26146-26158.	1.6	247
47	NDEx, the Network Data Exchange. <i>Cell Systems</i> , 2015, 1, 302-305.	2.9	247
48	Methylome-wide Analysis of Chronic HIV Infection Reveals Five-Year Increase in Biological Age and Epigenetic Targeting of HLA. <i>Molecular Cell</i> , 2016, 62, 157-168.	4.5	233
49	Efficient Algorithms for Detecting Signaling Pathways in Protein Interaction Networks. <i>Journal of Computational Biology</i> , 2006, 13, 133-144.	0.8	225
50	A Genetic Interaction Map of RNA-Processing Factors Reveals Links between Sem1/Dss1-Containing Complexes and mRNA Export and Splicing. <i>Molecular Cell</i> , 2008, 32, 735-746.	4.5	221
51	Mitochondria, Energetics, Epigenetics, and Cellular Responses to Stress. <i>Environmental Health Perspectives</i> , 2014, 122, 1271-1278.	2.8	221
52	Predicting Drug Response and Synergy Using a Deep Learning Model of Human Cancer Cells. <i>Cancer Cell</i> , 2020, 38, 672-684.e6.	7.7	216
53	Systematic Evaluation of Molecular Networks for Discovery of Disease Genes. <i>Cell Systems</i> , 2018, 6, 484-495.e5.	2.9	215
54	A proteome-wide protein interaction map for <i>Campylobacter jejuni</i> . <i>Genome Biology</i> , 2007, 8, R130.	3.8	214

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55	Integrating physical and genetic maps: from genomes to interaction networks. <i>Nature Reviews Genetics</i> , 2007, 8, 699-710.	7.7	192
56	A human MAP kinase interactome. <i>Nature Methods</i> , 2010, 7, 801-805.	9.0	187
57	Hierarchical Modularity and the Evolution of Genetic Interactomes across Species. <i>Molecular Cell</i> , 2012, 46, 691-704.	4.5	185
58	A gene ontology inferred from molecular networks. <i>Nature Biotechnology</i> , 2013, 31, 38-45.	9.4	184
59	Transcriptome profiling to identify genes involved in peroxisome assembly and function. <i>Journal of Cell Biology</i> , 2002, 158, 259-271.	2.3	175
60	Building with a scaffold: emerging strategies for high- to low-level cellular modeling. <i>Trends in Biotechnology</i> , 2003, 21, 255-262.	4.9	171
61	Systematic identification of functional orthologs based on protein network comparison. <i>Genome Research</i> , 2006, 16, 428-435.	2.4	168
62	Systems biology guided by XCMS Online metabolomics. <i>Nature Methods</i> , 2017, 14, 461-462.	9.0	168
63	Boosting Signal-to-Noise in Complex Biology: Prior Knowledge Is Power. <i>Cell</i> , 2011, 144, 860-863.	13.5	167
64	Evolutionarily Conserved Herpesviral Protein Interaction Networks. <i>PLoS Pathogens</i> , 2009, 5, e1000570.	2.1	162
65	Identification of Protein Complexes by Comparative Analysis of Yeast and Bacterial Protein Interaction Data. <i>Journal of Computational Biology</i> , 2005, 12, 835-846.	0.8	161
66	Phosphorylation of LC3 by the Hippo Kinases STK3/STK4 Is Essential for Autophagy. <i>Molecular Cell</i> , 2015, 57, 55-68.	4.5	158
67	Cytoscape: the network visualization tool for GenomeSpace workflows. <i>F1000Research</i> , 2014, 3, 151.	0.8	157
68	Linking high-resolution metabolic flux phenotypes and transcriptional regulation in yeast modulated by the global regulator Gcn4p. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 6477-6482.	3.3	154
69	Physical Network Models. <i>Journal of Computational Biology</i> , 2004, 11, 243-262.	0.8	149
70	Diverse interventions that extend mouse lifespan suppress shared age-associated epigenetic changes at critical gene regulatory regions. <i>Genome Biology</i> , 2017, 18, 58.	3.8	147
71	Genetic interaction mapping in mammalian cells using CRISPR interference. <i>Nature Methods</i> , 2017, 14, 577-580.	9.0	142
72	A Network of Conserved Synthetic Lethal Interactions for Exploration of Precision Cancer Therapy. <i>Molecular Cell</i> , 2016, 63, 514-525.	4.5	140

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73	Functional landscape of SARS-CoV-2 cellular restriction. <i>Molecular Cell</i> , 2021, 81, 2656-2668.e8.	4.5	137
74	Multivariate analysis of 1.5 million people identifies genetic associations with traits related to self-regulation and addiction. <i>Nature Neuroscience</i> , 2021, 24, 1367-1376.	7.1	137
75	Damage recovery pathways in <i>Saccharomyces cerevisiae</i> revealed by genomic phenotyping and interactome mapping. <i>Molecular Cancer Research</i> , 2002, 1, 103-12.	1.5	136
76	The Plasmodium protein network diverges from those of other eukaryotes. <i>Nature</i> , 2005, 438, 108-112.	13.7	128
77	Functional Maps of Protein Complexes from Quantitative Genetic Interaction Data. <i>PLoS Computational Biology</i> , 2008, 4, e1000065.	1.5	128
78	Genotype to phenotype via network analysis. <i>Current Opinion in Genetics and Development</i> , 2013, 23, 611-621.	1.5	126
79	Multi-tiered genomic analysis of head and neck cancer ties TP53 mutation to 3p loss. <i>Nature Genetics</i> , 2014, 46, 939-943.	9.4	126
80	Multilineage Priming of Enhancer Repertoires Precedes Commitment to the B and Myeloid Cell Lineages in Hematopoietic Progenitors. <i>Immunity</i> , 2011, 35, 413-425.	6.6	125
81	Interaction Landscape of Inherited Polymorphisms with Somatic Events in Cancer. <i>Cancer Discovery</i> , 2017, 7, 410-423.	7.7	121
82	eQED: an efficient method for interpreting eQTL associations using protein networks. <i>Molecular Systems Biology</i> , 2008, 4, 162.	3.2	117
83	The Cancer Cell Map Initiative: Defining the Hallmark Networks of Cancer. <i>Molecular Cell</i> , 2015, 58, 690-698.	4.5	117
84	A global transcriptional network connecting noncoding mutations to changes in tumor gene expression. <i>Nature Genetics</i> , 2018, 50, 613-620.	9.4	116
85	Visible Machine Learning for Biomedicine. <i>Cell</i> , 2018, 173, 1562-1565.	13.5	115
86	The Psychiatric Cell Map Initiative: A Convergent Systems Biological Approach to Illuminating Key Molecular Pathways in Neuropsychiatric Disorders. <i>Cell</i> , 2018, 174, 505-520.	13.5	108
87	A Multiscale Map of the Stem Cell State in Pancreatic Adenocarcinoma. <i>Cell</i> , 2019, 177, 572-586.e22.	13.5	107
88	Rac2 Controls Tumor Growth, Metastasis and M1-M2 Macrophage Differentiation In Vivo. <i>PLoS ONE</i> , 2014, 9, e95893.	1.1	93
89	Few-shot learning creates predictive models of drug response that translate from high-throughput screens to individual patients. <i>Nature Cancer</i> , 2021, 2, 233-244.	5.7	92
90	Hot Spots for Modulating Toxicity Identified by Genomic Phenotyping and Localization Mapping. <i>Molecular Cell</i> , 2004, 16, 117-125.	4.5	90

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91	Cost-effective strategies for completing the interactome. <i>Nature Methods</i> , 2009, 6, 55-61.	9.0	88
92	Protein Networks as Logic Functions in Development and Cancer. <i>PLoS Computational Biology</i> , 2011, 7, e1002180.	1.5	86
93	Dissection of DNA Damage Responses Using Multiconditional Genetic Interaction Maps. <i>Molecular Cell</i> , 2013, 49, 346-358.	4.5	86
94	De novo emergence of adaptive membrane proteins from thymine-rich genomic sequences. <i>Nature Communications</i> , 2020, 11, 781.	5.8	84
95	Understudied proteins: opportunities and challenges for functional proteomics. <i>Nature Methods</i> , 2022, 19, 774-779.	9.0	83
96	Integrated Assessment and Prediction of Transcription Factor Binding. <i>PLoS Computational Biology</i> , 2006, 2, e70.	1.5	82
97	High Temperature Requirement Factor A1 (HTRA1) Gene Regulates Angiogenesis through Transforming Growth Factor- β Family Member Growth Differentiation Factor 6. <i>Journal of Biological Chemistry</i> , 2012, 287, 1520-1526.	1.6	82
98	Combinatorial CRISPR-Cas9 Metabolic Screens Reveal Critical Redox Control Points Dependent on the KEAP1-NRF2 Regulatory Axis. <i>Molecular Cell</i> , 2018, 69, 699-708.e7.	4.5	81
99	Identifying Epistasis in Cancer Genomes: A Delicate Affair. <i>Cell</i> , 2019, 177, 1375-1383.	13.5	81
100	Inferring gene ontologies from pairwise similarity data. <i>Bioinformatics</i> , 2014, 30, i34-i42.	1.8	78
101	Improving Breast Cancer Survival Analysis through Competition-Based Multidimensional Modeling. <i>PLoS Computational Biology</i> , 2013, 9, e1003047.	1.5	76
102	The Dfm1 Derlin Is Required for ERAD Retrotranslocation of Integral Membrane Proteins. <i>Molecular Cell</i> , 2018, 69, 306-320.e4.	4.5	76
103	Network propagation in the cytoscape cyberinfrastructure. <i>PLoS Computational Biology</i> , 2017, 13, e1005598.	1.5	73
104	Translation of Genotype to Phenotype by a Hierarchy of Cell Subsystems. <i>Cell Systems</i> , 2016, 2, 77-88.	2.9	72
105	Systems biology 101—what you need to know. <i>Nature Biotechnology</i> , 2004, 22, 473-475.	9.4	71
106	Protein networks markedly improve prediction of subcellular localization in multiple eukaryotic species. <i>Nucleic Acids Research</i> , 2008, 36, e136-e136.	6.5	69
107	PKC μ Promotes Oncogenic Functions of ATF2 in the Nucleus while Blocking Its Apoptotic Function at Mitochondria. <i>Cell</i> , 2012, 148, 543-555.	13.5	69
108	Multiple Routes to Oncogenesis Are Promoted by the Human Papillomavirus—Host Protein Network. <i>Cancer Discovery</i> , 2018, 8, 1474-1489.	7.7	67

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109	Quantitative Translation of Dog-to-Human Aging by Conserved Remodeling of the DNA Methylome. <i>Cell Systems</i> , 2020, 11, 176-185.e6.	2.9	67
110	Using Functional Signature Ontology (FUSION) to Identify Mechanisms of Action for Natural Products. <i>Science Signaling</i> , 2013, 6, ra90.	1.6	66
111	A protein interaction landscape of breast cancer. <i>Science</i> , 2021, 374, eabf3066.	6.0	66
112	DNA replication stress differentially regulates G1/S genes via Rad53-dependent inactivation of Nrm1. <i>EMBO Journal</i> , 2012, 31, 1811-1822.	3.5	65
113	Functional genome-wide siRNA screen identifies KIAA0586 as mutated in Joubert syndrome. <i>ELife</i> , 2015, 4, e06602.	2.8	64
114	Yeast PP4 Interacts with ATR Homolog Ddc2-Mec1 and Regulates Checkpoint Signaling. <i>Molecular Cell</i> , 2015, 57, 273-289.	4.5	63
115	NDEx 2.0: A Clearinghouse for Research on Cancer Pathways. <i>Cancer Research</i> , 2017, 77, e58-e61.	0.4	63
116	Coevolution within a transcriptional network by compensatory <i>trans</i> and <i>cis</i> mutations. <i>Genome Research</i> , 2010, 20, 1672-1678.	2.4	62
117	Subnetwork-based analysis of chronic lymphocytic leukemia identifies pathways that associate with disease progression. <i>Blood</i> , 2012, 120, 2639-2649.	0.6	61
118	Chromatin dysregulation and DNA methylation at transcription start sites associated with transcriptional repression in cancers. <i>Nature Communications</i> , 2019, 10, 2188.	5.8	61
119	A census of pathway maps in cancer systems biology. <i>Nature Reviews Cancer</i> , 2020, 20, 233-246.	12.8	60
120	Leveraging premalignant biology for immune-based cancer prevention. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 10750-10758.	3.3	57
121	Decoupling Epigenetic and Genetic Effects through Systematic Analysis of Gene Position. <i>Cell Reports</i> , 2013, 3, 128-137.	2.9	56
122	A systems approach to delineate functions of paralogous transcription factors: Role of the Yap family in the DNA damage response. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 2934-2939.	3.3	55
123	Transcriptional regulation of protein complexes within and across species. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 1283-1288.	3.3	52
124	Genome-Wide Association Data Reveal a Global Map of Genetic Interactions among Protein Complexes. <i>PLoS Genetics</i> , 2009, 5, e1000782.	1.5	52
125	Genome-Wide Fitness and Expression Profiling Implicate Mga2 in Adaptation to Hydrogen Peroxide. <i>PLoS Genetics</i> , 2009, 5, e1000488.	1.5	51
126	Unveiling Complexity and Multipotentiality of Early Heart Fields. <i>Circulation Research</i> , 2021, 129, 474-487.	2.0	50

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127	Proteome-wide discovery of mislocated proteins in cancer. <i>Genome Research</i> , 2013, 23, 1283-1294.	2.4	49
128	Bayesian network analysis of targeting interactions in chromatin. <i>Genome Research</i> , 2010, 20, 190-200.	2.4	48
129	HPV E2, E4, E5 drive alternative carcinogenic pathways in HPV positive cancers. <i>Oncogene</i> , 2020, 39, 6327-6339.	2.6	48
130	Effect of Electrode Position on Outcome of Low-Energy Intracardiac Cardioversion of Atrial Fibrillation. <i>American Journal of Cardiology</i> , 1997, 79, 621-625.	0.7	45
131	Disruption of <i>NSD1</i> in Head and Neck Cancer Promotes Favorable Chemotherapeutic Responses Linked to Hypomethylation. <i>Molecular Cancer Therapeutics</i> , 2018, 17, 1585-1594.	1.9	45
132	Characterization of functionally active gene fusions in human papillomavirus related oropharyngeal squamous cell carcinoma. <i>International Journal of Cancer</i> , 2016, 139, 373-382.	2.3	44
133	Integrative genomic analysis by interoperation of bioinformatics tools in GenomeSpace. <i>Nature Methods</i> , 2016, 13, 245-247.	9.0	44
134	Cytoscape tools for the web age: D3.js and Cytoscape.js exporters. <i>F1000Research</i> , 2014, 3, 143.	0.8	44
135	Dynamic post-translational modification profiling of <i>Mycobacterium tuberculosis</i> -infected primary macrophages. <i>ELife</i> , 2020, 9, .	2.8	44
136	A multi-scale map of cell structure fusing protein images and interactions. <i>Nature</i> , 2021, 600, 536-542.	13.7	43
137	Network approaches and applications in biology. <i>PLoS Computational Biology</i> , 2017, 13, e1005771.	1.5	40
138	Genome Wide Proteomics of ERBB2 and EGFR and Other Oncogenic Pathways in Inflammatory Breast Cancer. <i>Journal of Proteome Research</i> , 2013, 12, 2805-2817.	1.8	38
139	An Integrated Systems Analysis Implicates EGR1 Downregulation in Simian Immunodeficiency Virus Encephalitis-Induced Neural Dysfunction. <i>Journal of Neuroscience</i> , 2009, 29, 12467-12476.	1.7	37
140	Cell-autonomous circadian clock of hepatocytes drives rhythms in transcription and polyamine synthesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 18560-18565.	3.3	37
141	Landscape of protein-protein interactions in <i>Drosophila</i> immune deficiency signaling during bacterial challenge. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 10717-10722.	3.3	37
142	A protein network map of head and neck cancer reveals PIK3CA mutant drug sensitivity. <i>Science</i> , 2021, 374, eabf2911.	6.0	37
143	Analysis of Matched Tumor and Normal Profiles Reveals Common Transcriptional and Epigenetic Signals Shared across Cancer Types. <i>PLoS ONE</i> , 2015, 10, e0142618.	1.1	36
144	Pan-cancer analysis reveals technical artifacts in TCGA germline variant calls. <i>BMC Genomics</i> , 2017, 18, 458.	1.2	36

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145	Systems biology analysis reveals role of MDM2 in diabetic nephropathy. JCI Insight, 2016, 1, e87877.	2.3	34
146	Network-driven plasma proteomics expose molecular changes in the Alzheimer's brain. Molecular Neurodegeneration, 2016, 11, 31.	4.4	34
147	Challenges in identifying cancer genes by analysis of exome sequencing data. Nature Communications, 2016, 7, 12096.	5.8	34
148	Classifying tumors by supervised network propagation. Bioinformatics, 2018, 34, i484-i493.	1.8	34
149	The great hairball gambit. PLoS Genetics, 2019, 15, e1008519.	1.5	34
150	Multiscale community detection in Cytoscape. PLoS Computational Biology, 2020, 16, e1008239.	1.5	34
151	Bioengineering and Systems Biology. Annals of Biomedical Engineering, 2006, 34, 257-264.	1.3	33
152	Mapping Plant Interactomes Using Literature Curated and Predicted Protein-Protein Interaction Data Sets. Plant Cell, 2010, 22, 997-1005.	3.1	33
153	Parenchymal Volumetric Assessment as a Predictive Tool to Determine Renal Function Benefit of Nephron-Sparing Surgery Compared with Radical Nephrectomy. Journal of Endourology, 2016, 30, 114-121.	1.1	32
154	Siri of the Cell: What Biology Could Learn from the iPhone. Cell, 2014, 157, 534-538.	18.5	31
155	Active Interaction Mapping Reveals the Hierarchical Organization of Autophagy. Molecular Cell, 2017, 65, 761-774.e5.	4.5	31
156	A Fast and Flexible Framework for Network-Assisted Genomic Association. IScience, 2019, 16, 155-161.	1.9	31
157	Matrix-Metalloproteinases in Head and Neck Carcinoma-Cancer Genome Atlas Analysis and Fluorescence Imaging in Mice. Otolaryngology - Head and Neck Surgery, 2014, 151, 612-618.	1.1	30
158	Development of Ultra-High-Density Screening Tools for Microbial 'Omics. PLoS ONE, 2014, 9, e85177.	1.1	30
159	Global architecture of genetic interactions on the protein network. Nature Biotechnology, 2003, 21, 490-491.	9.4	29
160	Interpretation of cancer mutations using a multiscale map of protein systems. Science, 2021, 374, eabf3067.	6.0	29
161	HiDeF: identifying persistent structures in multiscale 'omics data. Genome Biology, 2021, 22, 21.	3.8	29
162	A Systems Approach to Discovering Signaling and Regulatory Pathways-or, how to digest large interaction networks into relevant pieces. Advances in Experimental Medicine and Biology, 2004, 547, 21-30.	0.8	28

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163	Bioengineering and Systems Biology. <i>Annals of Biomedical Engineering</i> , 2006, 34, 1226-1233.	1.3	27
164	Evidence for a common evolutionary rate in metazoan transcriptional networks. <i>ELife</i> , 2015, 4, .	2.8	26
165	Parallel genome-wide screens identify synthetic viable interactions between the BLM helicase complex and Fanconi anemia. <i>Nature Communications</i> , 2017, 8, 1238.	5.8	25
166	An open invitation to the Understudied Proteins Initiative. <i>Nature Biotechnology</i> , 2022, 40, 815-817.	9.4	25
167	Quantitative Proteomics Reveal ATM Kinase-dependent Exchange in DNA Damage Response Complexes. <i>Journal of Proteome Research</i> , 2012, 11, 4983-4991.	1.8	24
168	ERCC1 and TS Expression as Prognostic and Predictive Biomarkers in Metastatic Colon Cancer. <i>PLoS ONE</i> , 2015, 10, e0126898.	1.1	24
169	Dot1 promotes H2B ubiquitination by a methyltransferase-independent mechanism. <i>Nucleic Acids Research</i> , 2018, 46, 11251-11261.	6.5	24
170	Epigenetic aging: Biological age prediction and informing a mechanistic theory of aging. <i>Journal of Internal Medicine</i> , 2022, 292, 733-744.	2.7	24
171	Assembling global maps of cellular function through integrative analysis of physical and genetic networks. <i>Nature Protocols</i> , 2011, 6, 1308-1323.	5.5	23
172	Transcriptional repression of IFN β by ATF2 confers melanoma resistance to therapy. <i>Oncogene</i> , 2015, 34, 5739-5748.	2.6	23
173	Genomic Landscape of Appendiceal Neoplasms. <i>JCO Precision Oncology</i> , 2018, 2, 1-18.	1.5	23
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