

# Marc Vidal

## List of Publications by Year in descending order

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160  
papers

41,535  
citations

4641

85  
h-index

5965

160  
g-index

175  
all docs

175  
docs citations

175  
times ranked

39618  
citing authors

#	ARTICLE	IF	CITATIONS
1	The human disease network. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 8685-8690.	3.3	2,924
2	Towards a proteome-scale map of the human protein-protein interaction network. Nature, 2005, 437, 1173-1178.	13.7	2,676
3	Evidence for dynamically organized modularity in the yeast protein-protein interaction network. Nature, 2004, 430, 88-93.	13.7	1,683
4	A Map of the Interactome Network of the Metazoan <i>C. elegans</i> . Science, 2004, 303, 540-543.	6.0	1,587
5	Drug-target network. Nature Biotechnology, 2007, 25, 1119-1126.	9.4	1,584
6	Interactome Networks and Human Disease. Cell, 2011, 144, 986-998.	13.5	1,543
7	High-Quality Binary Protein Interaction Map of the Yeast Interactome Network. Science, 2008, 322, 104-110.	6.0	1,297
8	Uncovering disease-disease relationships through the incomplete interactome. Science, 2015, 347, 1257601.	6.0	1,219
9	A Proteome-Scale Map of the Human Interactome Network. Cell, 2014, 159, 1212-1226.	13.5	1,199
10	Evidence for Network Evolution in an <i>Arabidopsis</i> Interactome Map. Science, 2011, 333, 601-607.	6.0	838
11	An empirical framework for binary interactome mapping. Nature Methods, 2009, 6, 83-90.	9.0	800
12	Independently Evolved Virulence Effectors Converge onto Hubs in a Plant Immune System Network. Science, 2011, 333, 596-601.	6.0	776
13	Protein Interaction Mapping in <i>C. elegans</i> Using Proteins Involved in Vulval Development. Science, 2000, 287, 116-122.	6.0	766
14	A reference map of the human binary protein interactome. Nature, 2020, 580, 402-408.	13.7	724
15	A Protein-Protein Interaction Network for Human Inherited Ataxias and Disorders of Purkinje Cell Degeneration. Cell, 2006, 125, 801-814.	13.5	714
16	Network modeling links breast cancer susceptibility and centrosome dysfunction. Nature Genetics, 2007, 39, 1338-1349.	9.4	602
17	How many human proteoforms are there?. Nature Chemical Biology, 2018, 14, 206-214.	3.9	580
18	[34] GATEWAY recombinational cloning: Application to the cloning of large numbers of open reading frames or ORFeomes. Methods in Enzymology, 2000, 328, 575-587.	0.4	570

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19	Correlation between transcriptome and interactome mapping data from <i>Saccharomyces cerevisiae</i> . <i>Nature Genetics</i> , 2001, 29, 482-486.	9.4	570
20	Proto-genes and de novo gene birth. <i>Nature</i> , 2012, 487, 370-374.	13.7	555
21	Annotation Transfer Between Genomes: Protein-Protein Interologs and Protein-DNA Regulogs. <i>Genome Research</i> , 2004, 14, 1107-1118.	2.4	516
22	Intrinsic Disorder Is a Common Feature of Hub Proteins from Four Eukaryotic Interactomes. <i>PLoS Computational Biology</i> , 2006, 2, e100.	1.5	512
23	Widespread Macromolecular Interaction Perturbations in Human Genetic Disorders. <i>Cell</i> , 2015, 161, 647-660.	13.5	482
24	Widespread Expansion of Protein Interaction Capabilities by Alternative Splicing. <i>Cell</i> , 2016, 164, 805-817.	13.5	479
25	A public genome-scale lentiviral expression library of human ORFs. <i>Nature Methods</i> , 2011, 8, 659-661.	9.0	477
26	A Chaperome Subnetwork Safeguards Proteostasis in Aging and Neurodegenerative Disease. <i>Cell Reports</i> , 2014, 9, 1135-1150.	2.9	476
27	Identification of Potential Interaction Networks Using Sequence-Based Searches for Conserved Protein-Protein Interactions or "Interologs". <i>Genome Research</i> , 2001, 11, 2120-2126.	2.4	431
28	Reverse two-hybrid and one-hybrid systems to detect dissociation of protein-protein and DNA-protein interactions.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1996, 93, 10315-10320.	3.3	416
29	Integrating omic™ information: a bridge between genomics and systems biology. <i>Trends in Genetics</i> , 2003, 19, 551-560.	2.9	407
30	An experimentally derived confidence score for binary protein-protein interactions. <i>Nature Methods</i> , 2009, 6, 91-97.	9.0	397
31	Network-based in silico drug efficacy screening. <i>Nature Communications</i> , 2016, 7, 10331.	5.8	394
32	Convergent Targeting of a Common Host Protein-Network by Pathogen Effectors from Three Kingdoms of Life. <i>Cell Host and Microbe</i> , 2014, 16, 364-375.	5.1	367
33	Interpreting cancer genomes using systematic host network perturbations by tumour virus proteins. <i>Nature</i> , 2012, 487, 491-495.	13.7	349
34	Epstein-Barr virus and virus human protein interaction maps. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 7606-7611.	3.3	348
35	<i>C. elegans</i> ORFeome version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein expression. <i>Nature Genetics</i> , 2003, 34, 35-41.	9.4	347
36	E2F-4 and E2F-5, two members of the E2F family, are expressed in the early phases of the cell cycle.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1995, 92, 2403-2407.	3.3	342

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37	Interactome: gateway into systems biology. <i>Human Molecular Genetics</i> , 2005, 14, R171-R181.	1.4	329
38	Edgetic perturbation models of human inherited disorders. <i>Molecular Systems Biology</i> , 2009, 5, 321.	3.2	326
39	Effect of sampling on topology predictions of protein-protein interaction networks. <i>Nature Biotechnology</i> , 2005, 23, 839-844.	9.4	302
40	Network-based prediction of protein interactions. <i>Nature Communications</i> , 2019, 10, 1240.	5.8	293
41	Literature-curated protein interaction datasets. <i>Nature Methods</i> , 2009, 6, 39-46.	9.0	288
42	Combined Functional Genomic Maps of the <i>C. elegans</i> DNA Damage Response. <i>Science</i> , 2002, 295, 127-131.	6.0	270
43	A novel member of the RING finger family, KRIP-1, associates with the KRAB-A transcriptional repressor domain of zinc finger proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1996, 93, 15299-15304.	3.3	260
44	Predictive models of molecular machines involved in <i>Caenorhabditis elegans</i> early embryogenesis. <i>Nature</i> , 2005, 436, 861-865.	13.7	260
45	Empirically controlled mapping of the <i>Caenorhabditis elegans</i> protein-protein interactome network. <i>Nature Methods</i> , 2009, 6, 47-54.	9.0	260
46	High-Throughput Yeast Two-Hybrid Assays for Large-Scale Protein Interaction Mapping. <i>Methods</i> , 2001, 24, 297-306.	1.9	258
47	Next-generation sequencing to generate interactome datasets. <i>Nature Methods</i> , 2011, 8, 478-480.	9.0	258
48	hORFeome v3.1: A resource of human open reading frames representing over 10,000 human genes. <i>Genomics</i> , 2007, 89, 307-315.	1.3	248
49	Screening patients for heterozygous p53 mutations using a functional assay in yeast. <i>Nature Genetics</i> , 1993, 5, 124-129.	9.4	243
50	Combining biological networks to predict genetic interactions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 15682-15687.	3.3	225
51	Human ORFeome Version 1.1: A Platform for Reverse Proteomics. <i>Genome Research</i> , 2004, 14, 2128-2135.	2.4	208
52	A Protein Domain-Based Interactome Network for <i>C. elegans</i> Early Embryogenesis. <i>Cell</i> , 2008, 134, 534-545.	13.5	196
53	A Gateway-Compatible Yeast One-Hybrid System. <i>Genome Research</i> , 2004, 14, 2093-2101.	2.4	189
54	A Biological Atlas of Functional Maps. <i>Cell</i> , 2001, 104, 333-339.	13.5	188

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55	A protein-protein interaction map of the <i>Caenorhabditis elegans</i> 26S proteasome. <i>EMBO Reports</i> , 2001, 2, 821-828.	2.0	173
56	Integrating Interactome, Phenome, and Transcriptome Mapping Data for the <i>C. elegans</i> Germline. <i>Current Biology</i> , 2002, 12, 1952-1958.	1.8	170
57	<i>Mycobacterium tuberculosis</i> Type VII Secreted Effector EsxH Targets Host ESCRT to Impair Trafficking. <i>PLoS Pathogens</i> , 2013, 9, e1003734.	2.1	167
58	A disease module in the interactome explains disease heterogeneity, drug response and captures novel pathways and genes in asthma. <i>Human Molecular Genetics</i> , 2015, 24, 3005-3020.	1.4	162
59	Open-reading-frame sequence tags (OSTs) support the existence of at least 17,300 genes in <i>C. elegans</i> . <i>Nature Genetics</i> , 2001, 27, 332-336.	9.4	159
60	Dominant-negative p53 mutations selected in yeast hit cancer hot spots.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1996, 93, 4091-4095.	3.3	158
61	A First Version of the <i>Caenorhabditis elegans</i> Promoterome. <i>Genome Research</i> , 2004, 14, 2169-2175.	2.4	155
62	A framework for exhaustively mapping functional missense variants. <i>Molecular Systems Biology</i> , 2017, 13, 957.	3.2	146
63	Protein interaction maps for model organisms. <i>Nature Reviews Molecular Cell Biology</i> , 2001, 2, 55-63.	16.1	139
64	Spatiotemporal 16p11.2 Protein Network Implicates Cortical Late Mid-Fetal Brain Development and KCTD13-Cul3-RhoA Pathway in Psychiatric Diseases. <i>Neuron</i> , 2015, 85, 742-754.	3.8	139
65	Systematic Interactome Mapping and Genetic Perturbation Analysis of a <i>C. elegans</i> TGF- $\beta$ Signaling Network. <i>Molecular Cell</i> , 2004, 13, 469-482.	4.5	136
66	Increasing specificity in high-throughput yeast two-hybrid experiments. <i>Methods</i> , 2004, 32, 363-370.	1.9	135
67	Analysis of the human E2 ubiquitin conjugating enzyme protein interaction network. <i>Genome Research</i> , 2009, 19, 1905-1911.	2.4	134
68	A genome-wide positioning systems network algorithm for in silico drug repurposing. <i>Nature Communications</i> , 2019, 10, 3476.	5.8	134
69	Protein interaction network of alternatively spliced isoforms from brain links genetic risk factors for autism. <i>Nature Communications</i> , 2014, 5, 3650.	5.8	131
70	Edgotype: a fundamental link between genotype and phenotype. <i>Current Opinion in Genetics and Development</i> , 2013, 23, 649-657.	1.5	129
71	Proteome-Scale Human Interactomics. <i>Trends in Biochemical Sciences</i> , 2017, 42, 342-354.	3.7	129
72	High-Quality Binary Interactome Mapping. <i>Methods in Enzymology</i> , 2010, 470, 281-315.	0.4	126

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73	Yeast Two-Hybrid Systems and Protein Interaction Mapping Projects for Yeast and Worm. <i>Yeast</i> , 2000, 1, 88-94.	0.8	121
74	Insight into transcription factor gene duplication from <i>Caenorhabditis elegans</i> Promoterome-driven expression patterns. <i>BMC Genomics</i> , 2007, 8, 27.	1.2	120
75	HSP90 Shapes the Consequences of Human Genetic Variation. <i>Cell</i> , 2017, 168, 856-866.e12.	13.5	117
76	An extended set of yeast-based functional assays accurately identifies human disease mutations. <i>Genome Research</i> , 2016, 26, 670-680.	2.4	116
77	Survey of variation in human transcription factors reveals prevalent DNA binding changes. <i>Science</i> , 2016, 351, 1450-1454.	6.0	114
78	APID database: redefining protein-protein interaction experimental evidences and binary interactomes. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	1.4	113
79	Human Gene-Centered Transcription Factor Networks for Enhancers and Disease Variants. <i>Cell</i> , 2015, 161, 661-673.	13.5	111
80	A comprehensive library of human transcription factors for cell fate engineering. <i>Nature Biotechnology</i> , 2021, 39, 510-519.	9.4	110
81	Comprehensive characterization of protein-protein interactions perturbed by disease mutations. <i>Nature Genetics</i> , 2021, 53, 342-353.	9.4	109
82	<i>C. elegans</i> ORFeome Version 3.1: Increasing the Coverage of ORFeome Resources With Improved Gene Predictions. <i>Genome Research</i> , 2004, 14, 2064-2069.	2.4	107
83	A unifying view of 21st century systems biology. <i>FEBS Letters</i> , 2009, 583, 3891-3894.	1.3	105
84	A Novel Human DnaJ Protein, hTid-1, a Homolog of the <i>Drosophila</i> Tumor Suppressor Protein Tid56, Can Interact with the Human Papillomavirus Type 16 E7 Oncoprotein. <i>Virology</i> , 1998, 247, 74-85.	1.1	102
85	Viral Perturbations of Host Networks Reflect Disease Etiology. <i>PLoS Computational Biology</i> , 2012, 8, e1002531.	1.5	102
86	Pooled-matrix protein interaction screens using Barcode Fusion Genetics. <i>Molecular Systems Biology</i> , 2016, 12, 863.	3.2	102
87	Genome-Scale Networks Link Neurodegenerative Disease Genes to $\alpha$ -Synuclein through Specific Molecular Pathways. <i>Cell Systems</i> , 2017, 4, 157-170.e14.	2.9	102
88	Dynamic Role of trans Regulation of Gene Expression in Relation to Complex Traits. <i>American Journal of Human Genetics</i> , 2017, 100, 571-580.	2.6	101
89	Interactome modeling. <i>FEBS Letters</i> , 2005, 579, 1834-1838.	1.3	99
90	Selecting causal genes from genome-wide association studies via functionally coherent subnetworks. <i>Nature Methods</i> , 2015, 12, 154-159.	9.0	96

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91	In Situ Peroxidase Labeling and Mass-Spectrometry Connects Alpha-Synuclein Directly to Endocytic Trafficking and mRNA Metabolism in Neurons. <i>Cell Systems</i> , 2017, 4, 242-250.e4.	2.9	91
92	Prospects for drug screening using the reverse two-hybrid system. <i>Trends in Biotechnology</i> , 1999, 17, 374-381.	4.9	88
93	Systematic screening reveals a role for BRCA1 in the response to transcription-associated DNA damage. <i>Genes and Development</i> , 2014, 28, 1957-1975.	2.7	86
94	A Zebrafish Genetic Screen Identifies Neuromedin U as a Regulator of Sleep/Wake States. <i>Neuron</i> , 2016, 89, 842-856.	3.8	81
95	Knocking out multigene redundancies via cycles of sexual assortment and fluorescence selection. <i>Nature Methods</i> , 2011, 8, 159-164.	9.0	74
96	Human T cell leukemia virus type 1 Tax associates with a molecular chaperone complex containing hTid-1 and Hsp70. <i>Current Biology</i> , 2001, 11, 1771-1775.	1.8	73
97	Multiplex single-molecule interaction profiling of DNA-barcoded proteins. <i>Nature</i> , 2014, 515, 554-557.	13.7	72
98	'Edgetic' perturbation of a <i>C. elegans</i> BCL2 ortholog. <i>Nature Methods</i> , 2009, 6, 843-849.	9.0	71
99	ORFeome Cloning and Systems Biology: Standardized Mass Production of the Parts From the Parts-List. <i>Genome Research</i> , 2004, 14, 2001-2009.	2.4	69
100	The yeast two-hybrid assay: still finding connections after 25 years. <i>Nature Methods</i> , 2014, 11, 1203-1206.	9.0	68
101	Mapping transcription factor interactome networks using HaloTag protein arrays. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E4238-47.	3.3	67
102	Host-pathogen interactome mapping for HTLV-1 and -2 retroviruses. <i>Retrovirology</i> , 2012, 9, 26.	0.9	64
103	SH3 interactome conserves general function over specific form. <i>Molecular Systems Biology</i> , 2013, 9, 652.	3.2	61
104	Comparative analysis of virus-host interactomes with a mammalian high-throughput protein complementation assay based on <i>Gaussia princeps</i> luciferase. <i>Methods</i> , 2012, 58, 349-359.	1.9	59
105	Protein Domain-Level Landscape of Cancer-Type-Specific Somatic Mutations. <i>PLoS Computational Biology</i> , 2015, 11, e1004147.	1.5	59
106	Identification of FAM111A as an SV40 Host Range Restriction and Adenovirus Helper Factor. <i>PLoS Pathogens</i> , 2012, 8, e1002949.	2.1	58
107	<i>MECP2</i> Is a Frequently Amplified Oncogene with a Novel Epigenetic Mechanism That Mimics the Role of Activated RAS in Malignancy. <i>Cancer Discovery</i> , 2016, 6, 45-58.	7.7	57
108	Maximizing binary interactome mapping with a minimal number of assays. <i>Nature Communications</i> , 2019, 10, 3907.	5.8	57

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109	InSite: a computational method for identifying protein-protein interaction binding sites on a proteome-wide scale. <i>Genome Biology</i> , 2007, 8, R192.	13.9	53
110	Array MAPPIT: High-Throughput Interactome Analysis in Mammalian Cells. <i>Journal of Proteome Research</i> , 2009, 8, 877-886.	1.8	53
111	A Genetic Strategy to Eliminate Self-Activator Baits Prior to High-Throughput Yeast Two-Hybrid Screens. <i>Genome Research</i> , 1999, 9, 1128-1134.	2.4	51
112	Interactome Mapping of the Phosphatidylinositol 3-Kinase-Mammalian Target of Rapamycin Pathway Identifies Deformed Epidermal Autoregulatory Factor-1 as a New Glycogen Synthase Kinase-3 Interactor. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 1578-1593.	2.5	51
113	A proactive genotype-to-patient-phenotype map for cystathionine beta-synthase. <i>Genome Medicine</i> , 2020, 12, 13.	3.6	45
114	Protein interactions of the transcription factor Hoxa1. <i>BMC Developmental Biology</i> , 2012, 12, 29.	2.1	43
115	An inter-species protein-protein interaction network across vast evolutionary distance. <i>Molecular Systems Biology</i> , 2016, 12, 865.	3.2	42
116	Shifted Transversal Design smart-pooling for high coverage interactome mapping. <i>Genome Research</i> , 2009, 19, 1262-1269.	2.4	36
117	WorfDB: the <i>Caenorhabditis elegans</i> ORFeome Database. <i>Nucleic Acids Research</i> , 2003, 31, 237-240.	6.5	35
118	The transcription factor ERG recruits CCR4-NOT to control mRNA decay and mitotic progression. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 663-672.	3.6	35
119	Network Analysis of UBE3A/E6AP-Associated Proteins Provides Connections to Several Distinct Cellular Processes. <i>Journal of Molecular Biology</i> , 2018, 430, 1024-1050.	2.0	32
120	How much of the human protein interactome remains to be mapped?. <i>Science Signaling</i> , 2016, 9, eg7.	1.6	31
121	Isoform discovery by targeted cloning, 'deep-well' pooling and parallel sequencing. <i>Nature Methods</i> , 2008, 5, 597-600.	9.0	30
122	Identifying pathogenicity of human variants via paralog-based yeast complementation. <i>PLoS Genetics</i> , 2017, 13, e1006779.	1.5	30
123	Precision medicine - networks to the rescue. <i>Current Opinion in Biotechnology</i> , 2020, 63, 177-189.	3.3	30
124	Domain-based prediction of the human isoform interactome provides insights into the functional impact of alternative splicing. <i>PLoS Computational Biology</i> , 2017, 13, e1005717.	1.5	30
125	Global Edgetic Rewiring in Cancer Networks. <i>Cell Systems</i> , 2015, 1, 251-253.	2.9	28
126	Global Analysis of Intercellular Homeodomain Protein Transfer. <i>Cell Reports</i> , 2019, 28, 712-722.e3.	2.9	28



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127	Histone deacetylase-dependent transcriptional repression by pRB in yeast occurs independently of interaction through the LXCXE binding cleft. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 8720-8725.	3.3	26
128	From genome to proteome: developing expression clone resources for the human genome. <i>Human Molecular Genetics</i> , 2006, 15, R31-R43.	1.4	26
129	Controllability in an islet specific regulatory network identifies the transcriptional factor NFATC4, which regulates Type 2 Diabetes associated genes. <i>Npj Systems Biology and Applications</i> , 2018, 4, 25.	1.4	25
130	Protein-Protein Interactions and Networks: Forward and Reverse Edgetics. <i>Methods in Molecular Biology</i> , 2011, 759, 197-213.	0.4	24
131	Proteome-scale Binary Interactomics in Human Cells. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 3624-3639.	2.5	23
132	A Model of Elegance. <i>American Journal of Human Genetics</i> , 1998, 63, 955-961.	2.6	22
133	Mutational analysis of the J recombination signal sequence binding protein (RBP-J)/Epstein-Barr virus nuclear antigen 2 (EBNA2) and RBP-J/Notch interaction. <i>FEBS Journal</i> , 2001, 268, 4639-4646.	0.2	21
134	[6] A green fluorescent protein-based reverse two-hybrid system: Application to the characterization of large numbers of potential protein-protein interactions. <i>Methods in Enzymology</i> , 2000, 328, 74-IN1.	0.4	19
135	Challenges and recommendations for epigenomics in precision health. <i>Nature Biotechnology</i> , 2017, 35, 1128-1132.	9.4	19
136	ORF Capture-Seq as a versatile method for targeted identification of full-length isoforms. <i>Nature Communications</i> , 2020, 11, 2326.	5.8	19
137	The HTLV-1 viral oncoproteins Tax and HBZ reprogram the cellular mRNA splicing landscape. <i>PLoS Pathogens</i> , 2021, 17, e1009919.	2.1	19
138	A Genome-Wide Gene Function Prediction Resource for <i>Drosophila melanogaster</i> . <i>PLoS ONE</i> , 2010, 5, e12139.	1.1	17
139	A massively parallel barcoded sequencing pipeline enables generation of the first ORFeome and interactome map for rice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 11836-11842.	3.3	16
140	Yeast Two-Hybrid Systems and Protein Interaction Mapping Projects for Yeast and Worm. <i>Yeast</i> , 2000, 1, 88-94.	0.8	16
141	New Views of Old Proteins: Clarifying the Enigmatic Proteome. <i>Molecular and Cellular Proteomics</i> , 2022, 21, 100254.	2.5	16
142	Yeast genetic interaction screen of human genes associated with amyotrophic lateral sclerosis: identification of MAP2K5 kinase as a potential drug target. <i>Genome Research</i> , 2017, 27, 1487-1500.	2.4	12
143	Use of protein-interaction maps to formulate biological questions. <i>Current Opinion in Chemical Biology</i> , 2001, 5, 57-62.	2.8	11
144	Integrated version of reverse two-hybrid system for the postproteomic era. <i>Methods in Enzymology</i> , 2002, 350, 525-545.	0.4	10

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145	Alternative glycosylation controls endoplasmic reticulum dynamics and tubular extension in mammalian cells. <i>Science Advances</i> , 2021, 7, .	4.7	8
146	Reply to "Does mapping reveal correlation between gene expression and proteinâ€“protein interaction?". <i>Nature Genetics</i> , 2003, 33, 16-17.	9.4	7
147	Perturbing interactions. <i>Nature Methods</i> , 2005, 2, 412-414.	9.0	6
148	Protein Interactomics by Two-Hybrid Methods. <i>Methods in Molecular Biology</i> , 2018, 1794, 1-14.	0.4	6
149	QUICKstep and GS-TAP: new moves for protein-interaction analysis. <i>Nature Methods</i> , 2006, 3, 975-976.	9.0	5
150	Interactome Networks. , 2013, , 45-63.		5
151	Yeast-Based Genetic Interaction Analysis of Human Kinome. <i>Cells</i> , 2020, 9, 1156.	1.8	5
152	A Protein Domain-Based Interactome Network for <i>C.Âlegans</i> Early Embryogenesis. <i>Cell</i> , 2012, 151, 1633.	13.5	4
153	Interrogation of kinase genetic interactions provides a global view of PAK1-mediated signal transduction pathways. <i>Journal of Biological Chemistry</i> , 2020, 295, 16906-16919.	1.6	4
154	Reply to "Exhaustive benchmarking of the yeast two-hybrid system". <i>Nature Methods</i> , 2010, 7, 668-668.	9.0	3
155	OpenPIP: An Open-source Platform for Hosting, Visualizing and Analyzing Protein Interaction Data. <i>Journal of Molecular Biology</i> , 2022, 434, 167603.	2.0	3
156	Reply to Toward the complete interactome. <i>Nature Biotechnology</i> , 2006, 24, 615-615.	9.4	1
157	From genome to proteome: developing expression clone resources for the human genome. <i>Human Molecular Genetics</i> , 2006, 15, 2184-2184.	1.4	1
158	TheC.elegansinteractome project. , 2005, , .		0
159	Forward and Reverse Proteomics. , 2003, , 255-276.		0
160	Interactome Networks. <i>FASEB Journal</i> , 2008, 22, 262.1.	0.2	0