

Marc Vidal

List of Publications by Citations

Source: <https://exaly.com/author-pdf/8804402/marc-vidal-publications-by-citations.pdf>

Version: 2024-04-28

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

161
papers

32,823
citations

79
h-index

175
g-index

175
ext. papers

38,365
ext. citations

18.4
avg, IF

6.68
L-index

#	Paper	IF	Citations
161	The human disease network. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 8685-90	11.5	2380
160	Towards a proteome-scale map of the human protein-protein interaction network. <i>Nature</i> , 2005 , 437, 1173-8	50.4	2287
159	A map of the interactome network of the metazoan <i>C. elegans</i> . <i>Science</i> , 2004 , 303, 540-3	33.3	1398
158	Evidence for dynamically organized modularity in the yeast protein-protein interaction network. <i>Nature</i> , 2004 , 430, 88-93	50.4	1381
157	Drug-target network. <i>Nature Biotechnology</i> , 2007 , 25, 1119-26	44.5	1328
156	Interactome networks and human disease. <i>Cell</i> , 2011 , 144, 986-98	56.2	1187
155	High-quality binary protein interaction map of the yeast interactome network. <i>Science</i> , 2008 , 322, 104-10	33.3	1100
154	A proteome-scale map of the human interactome network. <i>Cell</i> , 2014 , 159, 1212-1226	56.2	898
153	Disease networks. Uncovering disease-disease relationships through the incomplete interactome. <i>Science</i> , 2015 , 347, 1257-60	33.3	767
152	Evidence for network evolution in an Arabidopsis interactome map. <i>Science</i> , 2011 , 333, 601-7	33.3	689
151	An empirical framework for binary interactome mapping. <i>Nature Methods</i> , 2009 , 6, 83-90	21.6	674
150	Protein interaction mapping in <i>C. elegans</i> using proteins involved in vulval development. <i>Science</i> , 2000 , 287, 116-22	33.3	659
149	A protein-protein interaction network for human inherited ataxias and disorders of Purkinje cell degeneration. <i>Cell</i> , 2006 , 125, 801-14	56.2	637
148	Independently evolved virulence effectors converge onto hubs in a plant immune system network. <i>Science</i> , 2011 , 333, 596-601	33.3	601
147	Correlation between transcriptome and interactome mapping data from <i>Saccharomyces cerevisiae</i> . <i>Nature Genetics</i> , 2001 , 29, 482-6	36.3	517
146	Network modeling links breast cancer susceptibility and centrosome dysfunction. <i>Nature Genetics</i> , 2007 , 39, 1338-49	36.3	516
145	GATEWAY recombinational cloning: application to the cloning of large numbers of open reading frames or ORFeomes. <i>Methods in Enzymology</i> , 2000 , 328, 575-92	1.7	496

144	Intrinsic disorder is a common feature of hub proteins from four eukaryotic interactomes. <i>PLoS Computational Biology</i> , 2006 , 2, e100	5	435
143	Annotation transfer between genomes: protein-protein interologs and protein-DNA regulogs. <i>Genome Research</i> , 2004 , 14, 1107-18	9.7	400
142	Proto-genes and de novo gene birth. <i>Nature</i> , 2012 , 487, 370-4	50.4	379
141	A public genome-scale lentiviral expression library of human ORFs. <i>Nature Methods</i> , 2011 , 8, 659-61	21.6	373
140	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, 10315-20	11.5	372
139	Integrating 'omic' information: a bridge between genomics and systems biology. <i>Trends in Genetics</i> , 2003 , 19, 551-60	8.5	363
138	Identification of potential interaction networks using sequence-based searches for conserved protein-protein interactions or "interologs". <i>Genome Research</i> , 2001 , 11, 2120-6	9.7	344
137	Widespread macromolecular interaction perturbations in human genetic disorders. <i>Cell</i> , 2015 , 161, 647-660	56.2	343
136	An experimentally derived confidence score for binary protein-protein interactions. <i>Nature Methods</i> , 2009 , 6, 91-7	21.6	342
135	How many human proteoforms are there?. <i>Nature Chemical Biology</i> , 2018 , 14, 206-214	11.7	324
134	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, 2403-7	11.5	319
133	A chaperome subnetwork safeguards proteostasis in aging and neurodegenerative disease. <i>Cell Reports</i> , 2014 , 9, 1135-50	10.6	317
132	C. elegans 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	36.3	310
131	Widespread Expansion of Protein Interaction Capabilities by Alternative Splicing. <i>Cell</i> , 2016 , 164, 805-17	56.2	308
130	Interpreting cancer genomes using systematic host network perturbations by tumour virus proteins. <i>Nature</i> , 2012 , 487, 491-5	50.4	294
129	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, 7606-11	11.5	293
128	Interactome: gateway into systems biology. <i>Human Molecular Genetics</i> , 2005 , 14 Spec No. 2, R171-81	5.6	285
127	Edgetic perturbation models of human inherited disorders. <i>Molecular Systems Biology</i> , 2009 , 5, 321	12.2	278

126	A reference map of the human binary protein interactome. <i>Nature</i> , 2020 , 580, 402-408	50.4	269
125	Effect of sampling on topology predictions of protein-protein interaction networks. <i>Nature Biotechnology</i> , 2005 , 23, 839-44	44.5	253
124	Combined functional genomic maps of the <i>C. elegans</i> DNA damage response. <i>Science</i> , 2002 , 295, 127-31	33.3	253
123	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, 15299-304	11.5	243
122	Convergent targeting of a common host protein-network by pathogen effectors from three kingdoms of life. <i>Cell Host and Microbe</i> , 2014 , 16, 364-75	23.4	242
121	Network-based in silico drug efficacy screening. <i>Nature Communications</i> , 2016 , 7, 10331	17.4	240
120	Literature-curated protein interaction datasets. <i>Nature Methods</i> , 2009 , 6, 39-46	21.6	237
119	hORFeome v3.1: a resource of human open reading frames representing over 10,000 human genes. <i>Genomics</i> , 2007 , 89, 307-15	4.3	229
118	Predictive models of molecular machines involved in <i>Caenorhabditis elegans</i> early embryogenesis. <i>Nature</i> , 2005 , 436, 861-5	50.4	225
117	Empirically controlled mapping of the <i>Caenorhabditis elegans</i> protein-protein interactome network. <i>Nature Methods</i> , 2009 , 6, 47-54	21.6	224
116	Screening patients for heterozygous p53 mutations using a functional assay in yeast. <i>Nature Genetics</i> , 1993 , 5, 124-9	36.3	224
115	High-throughput yeast two-hybrid assays for large-scale protein interaction mapping. <i>Methods</i> , 2001 , 24, 297-306	4.6	208
114	Next-generation sequencing to generate interactome datasets. <i>Nature Methods</i> , 2011 , 8, 478-80	21.6	191
113	Combining biological networks to predict genetic interactions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 15682-7	11.5	190
112	Human ORFeome version 1.1: a platform for reverse proteomics. <i>Genome Research</i> , 2004 , 14, 2128-35	9.7	182
111	A biological atlas of functional maps. <i>Cell</i> , 2001 , 104, 333-9	56.2	165
110	A gateway-compatible yeast one-hybrid system. <i>Genome Research</i> , 2004 , 14, 2093-101	9.7	162
109	A protein domain-based interactome network for <i>C. elegans</i> early embryogenesis. <i>Cell</i> , 2008 , 134, 534-45	56.2	161

108	Integrating interactome, phenome, and transcriptome mapping data for the <i>C. elegans</i> germline. <i>Current Biology</i> , 2002 , 12, 1952-8	6.3	157
107	Network-based prediction of protein interactions. <i>Nature Communications</i> , 2019 , 10, 1240	17.4	156
106	A protein-protein interaction map of the <i>Caenorhabditis elegans</i> 26S proteasome. <i>EMBO Reports</i> , 2001 , 2, 821-8	6.5	156
105	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, 332-6	36.3	145
104	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, 4091-5	11.5	135
103	A first version of the <i>Caenorhabditis elegans</i> Promoterome. <i>Genome Research</i> , 2004 , 14, 2169-75	9.7	133
102	Analysis of the human E2 ubiquitin conjugating enzyme protein interaction network. <i>Genome Research</i> , 2009 , 19, 1905-11	9.7	124
101	Protein interaction maps for model organisms. <i>Nature Reviews Molecular Cell Biology</i> , 2001 , 2, 55-62	48.7	118
100	Increasing specificity in high-throughput yeast two-hybrid experiments. <i>Methods</i> , 2004 , 32, 363-70	4.6	117
99	Systematic interactome mapping and genetic perturbation analysis of a <i>C. elegans</i> TGF-beta signaling network. <i>Molecular Cell</i> , 2004 , 13, 469-82	17.6	115
98	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, 3005-20	5.6	108
97	<i>Mycobacterium tuberculosis</i> type VII secreted effector EsxH targets host ESCRT to impair trafficking. <i>PLoS Pathogens</i> , 2013 , 9, e1003734	7.6	108
96	High-quality binary interactome mapping. <i>Methods in Enzymology</i> , 2010 , 470, 281-315	1.7	104
95	Edgotype: a fundamental link between genotype and phenotype. <i>Current Opinion in Genetics and Development</i> , 2013 , 23, 649-57	4.9	103
94	Insight into transcription factor gene duplication from <i>Caenorhabditis elegans</i> Promoterome-driven expression patterns. <i>BMC Genomics</i> , 2007 , 8, 27	4.5	103
93	Protein interaction network of alternatively spliced isoforms from brain links genetic risk factors for autism. <i>Nature Communications</i> , 2014 , 5, 3650	17.4	101
92	Yeast two-hybrid systems and protein interaction mapping projects for yeast and worm. <i>Yeast</i> , 2000 , 17, 88-94	3.4	101
91	<i>C. elegans</i> ORFeome version 3.1: increasing the coverage of ORFeome resources with improved gene predictions. <i>Genome Research</i> , 2004 , 14, 2064-9	9.7	97

90	Proteome-Scale Human Interactomics. <i>Trends in Biochemical Sciences</i> , 2017 , 42, 342-354	10.3	95
89	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, 742-54	13.9	94
88	Interactome modeling. <i>FEBS Letters</i> , 2005 , 579, 1834-8	3.8	94
87	Viral perturbations of host networks reflect disease etiology. <i>PLoS Computational Biology</i> , 2012 , 8, e1002531	3.5	90
86	A novel human DnaJ protein, hTid-1, a homolog of the Drosophila tumor suppressor protein Tid56, can interact with the human papillomavirus type 16 E7 oncoprotein. <i>Virology</i> , 1998 , 247, 74-85	3.6	90
85	A unifying view of 21st century systems biology. <i>FEBS Letters</i> , 2009 , 583, 3891-4	3.8	87
84	A genome-wide positioning systems network algorithm for in silico drug repurposing. <i>Nature Communications</i> , 2019 , 10, 3476	17.4	82
83	Human gene-centered transcription factor networks for enhancers and disease variants. <i>Cell</i> , 2015 , 161, 661-673	56.2	80
82	Survey of variation in human transcription factors reveals prevalent DNA binding changes. <i>Science</i> , 2016 , 351, 1450-1454	33.3	78
81	Prospects for drug screening using the reverse two-hybrid system. <i>Trends in Biotechnology</i> , 1999 , 17, 374-81	15.1	78
80	Genome-Scale Networks Link Neurodegenerative Disease Genes to β -Synuclein through Specific Molecular Pathways. <i>Cell Systems</i> , 2017 , 4, 157-170.e14	10.6	76
79	HSP90 Shapes the Consequences of Human Genetic Variation. <i>Cell</i> , 2017 , 168, 856-866.e12	56.2	75
78	A framework for exhaustively mapping functional missense variants. <i>Molecular Systems Biology</i> , 2017 , 13, 957	12.2	69
77	Selecting causal genes from genome-wide association studies via functionally coherent subnetworks. <i>Nature Methods</i> , 2015 , 12, 154-9	21.6	68
76	Systematic screening reveals a role for BRCA1 in the response to transcription-associated DNA damage. <i>Genes and Development</i> , 2014 , 28, 1957-75	12.6	66
75	An extended set of yeast-based functional assays accurately identifies human disease mutations. <i>Genome Research</i> , 2016 , 26, 670-80	9.7	65
74	'Edgetic' perturbation of a C. elegans BCL2 ortholog. <i>Nature Methods</i> , 2009 , 6, 843-9	21.6	63
73	ORFeome cloning and systems biology: standardized mass production of the parts from the parts-list. <i>Genome Research</i> , 2004 , 14, 2001-9	9.7	63

72	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, 1771-5	6.3	63
71	Host-pathogen interactome mapping for HTLV-1 and -2 retroviruses. <i>Retrovirology</i> , 2012 , 9, 26	3.6	62
70	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	10.6	61
69	A Zebrafish Genetic Screen Identifies Neuromedin U as a Regulator of Sleep/Wake States. <i>Neuron</i> , 2016 , 89, 842-56	13.9	59
68	Pooled-matrix protein interaction screens using Barcode Fusion Genetics. <i>Molecular Systems Biology</i> , 2016 , 12, 863	12.2	59
67	Multiplex single-molecule interaction profiling of DNA-barcoded proteins. <i>Nature</i> , 2014 , 515, 554-7	50.4	56
66	Knocking out multigene redundancies via cycles of sexual assortment and fluorescence selection. <i>Nature Methods</i> , 2011 , 8, 159-64	21.6	54
65	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	11.5	52
64	The yeast two-hybrid assay: still finding connections after 25 years. <i>Nature Methods</i> , 2014 , 11, 1203-6	21.6	52
63	Dynamic Role of trans Regulation of Gene Expression in Relation to Complex Traits. <i>American Journal of Human Genetics</i> , 2017 , 100, 571-580	11	50
62	APID database: redefining protein-protein interaction experimental evidences and binary interactomes. <i>Database: the Journal of Biological Databases and Curation</i> , 2019 , 2019,	5	50
61	Array MAPPIT: high-throughput interactome analysis in mammalian cells. <i>Journal of Proteome Research</i> , 2009 , 8, 877-86	5.6	48
60	A genetic strategy to eliminate self-activator baits prior to high-throughput yeast two-hybrid screens. <i>Genome Research</i> , 1999 , 9, 1128-34	9.7	48
59	SH3 interactome conserves general function over specific form. <i>Molecular Systems Biology</i> , 2013 , 9, 652	12.2	47
58	Protein domain-level landscape of cancer-type-specific somatic mutations. <i>PLoS Computational Biology</i> , 2015 , 11, e1004147	5	46
57	InSite: a computational method for identifying protein-protein interaction binding sites on a proteome-wide scale. <i>Genome Biology</i> , 2007 , 8, R192	18.3	45
56	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, 349-59	4.6	43
55	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, 1578-93	7.6	43

54	Identification of FAM111A as an SV40 host range restriction and adenovirus helper factor. <i>PLoS Pathogens</i> , 2012 , 8, e1002949	7.6	40
53	A comprehensive library of human transcription factors for cell fate engineering. <i>Nature Biotechnology</i> , 2021 , 39, 510-519	44.5	40
52	MECP2 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	24.4	35
51	Protein interactions of the transcription factor Hoxa1. <i>BMC Developmental Biology</i> , 2012 , 12, 29	3.1	33
50	Shifted Transversal Design smart-pooling for high coverage interactome mapping. <i>Genome Research</i> , 2009 , 19, 1262-9	9.7	31
49	An inter-species protein-protein interaction network across vast evolutionary distance. <i>Molecular Systems Biology</i> , 2016 , 12, 865	12.2	31
48	WorfDB: the Caenorhabditis elegans ORFeome Database. <i>Nucleic Acids Research</i> , 2003 , 31, 237-40	20.1	29
47	Comprehensive characterization of protein-protein interactions perturbed by disease mutations. <i>Nature Genetics</i> , 2021 , 53, 342-353	36.3	27
46	Isoform discovery by targeted cloning, 'deep-well' pooling and parallel sequencing. <i>Nature Methods</i> , 2008 , 5, 597-600	21.6	26
45	The transcription factor ERG recruits CCR4-NOT to control mRNA decay and mitotic progression. <i>Nature Structural and Molecular Biology</i> , 2016 , 23, 663-72	17.6	25
44	Network Analysis of UBE3A/E6AP-Associated Proteins Provides Connections to Several Distinct Cellular Processes. <i>Journal of Molecular Biology</i> , 2018 , 430, 1024-1050	6.5	24
43	From genome to proteome: developing expression clone resources for the human genome. <i>Human Molecular Genetics</i> , 2006 , 15 Spec No 1, R31-43	5.6	24
42	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, 8720-5	11.5	24
41	Maximizing binary interactome mapping with a minimal number of assays. <i>Nature Communications</i> , 2019 , 10, 3907	17.4	21
40	Protein-protein interactions and networks: forward and reverse edgetics. <i>Methods in Molecular Biology</i> , 2011 , 759, 197-213	1.4	20
39	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	5	20
38	Identifying pathogenicity of human variants via paralog-based yeast complementation. <i>PLoS Genetics</i> , 2017 , 13, e1006779	6	19
37	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, 4639-46		19

36	Proteome-scale Binary Interactomics in Human Cells. <i>Molecular and Cellular Proteomics</i> , 2016 , 15, 3624-3639	11.4	18
35	Precision medicine - networks to the rescue. <i>Current Opinion in Biotechnology</i> , 2020 , 63, 177-189	11.4	17
34	A proactive genotype-to-patient-phenotype map for cystathionine beta-synthase. <i>Genome Medicine</i> , 2020 , 12, 13	14.4	17
33	A model of elegance. <i>American Journal of Human Genetics</i> , 1998 , 63, 955-61	11	17
32	Challenges and recommendations for epigenomics in precision health. <i>Nature Biotechnology</i> , 2017 , 35, 1128-1132	44.5	16
31	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, 74-88	1.7	16
30	A genome-wide gene function prediction resource for <i>Drosophila melanogaster</i> . <i>PLoS ONE</i> , 2010 , 5, e12139	13.9	16
29	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	5	14
28	Yeast Two-Hybrid Systems and Protein Interaction Mapping Projects for Yeast and Worm. <i>Yeast</i> , 2000 , 1, 88-94	3.4	13
27	A reference map of the human protein interactome		13
26	Global Edgetic Rewiring in Cancer Networks. <i>Cell Systems</i> , 2015 , 1, 251-3	10.6	11
25	Global Analysis of Intercellular Homeodomain Protein Transfer. <i>Cell Reports</i> , 2019 , 28, 712-722.e3	10.6	11
24	Use of protein-interaction maps to formulate biological questions. <i>Current Opinion in Chemical Biology</i> , 2001 , 5, 57-62	9.7	9
23	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	9.7	8
22	ORF Capture-Seq as a versatile method for targeted identification of full-length isoforms. <i>Nature Communications</i> , 2020 , 11, 2326	17.4	8
21	Integrated version of reverse two-hybrid system for the postproteomic era. <i>Methods in Enzymology</i> , 2002 , 350, 525-45	1.7	8
20	Network-based prediction of protein interactions		7
19	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	11.5	6

18	Reply to "Does mapping reveal correlation between gene expression and protein-protein interaction?". <i>Nature Genetics</i> , 2003 , 33, 16-17	36.3	6
17	Protein Interactomics by Two-Hybrid Methods. <i>Methods in Molecular Biology</i> , 2018 , 1794, 1-14	1.4	5
16	Interactome Networks 2013 , 45-63		4
15	Yeast-Based Genetic Interaction Analysis of Human Kinome. <i>Cells</i> , 2020 , 9,	7.9	3
14	A Protein Domain-Based Interactome Network for <i>C. elegans</i> Early Embryogenesis. <i>Cell</i> , 2012 , 151, 1633-1642	56.2	3
13	Reply to "Exhaustive benchmarking of the yeast two-hybrid system". <i>Nature Methods</i> , 2010 , 7, 668-668	21.6	3
12	Alternative glycosylation controls endoplasmic reticulum dynamics and tubular extension in mammalian cells. <i>Science Advances</i> , 2021 , 7,	14.3	3
11	The HTLV-1 viral oncoproteins Tax and HBZ reprogram the cellular mRNA splicing landscape. <i>PLoS Pathogens</i> , 2021 , 17, e1009919	7.6	3
10	Expanding the Atlas of Functional Missense Variation for Human Genes		2
9	Towards an Essayome for binary interactome mapping		2
8	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	5.4	2
7	A map of binary SARS-CoV-2 protein interactions implicates host immune regulation and ubiquitination		2
6	Reply to Toward the complete interactome. <i>Nature Biotechnology</i> , 2006 , 24, 615-615	44.5	1
5	Controllability in an islet specific regulatory network identifies the transcriptional factor NFATC4, which regulates Type 2 Diabetes associated genes		1
4	OpenPIP: An Open-source Platform for Hosting, Visualizing and Analyzing Protein Interaction Data. <i>Journal of Molecular Biology</i> , 2022 , 167603	6.5	0
3	New views of old proteins: clarifying the enigmatic proteome. <i>Molecular and Cellular Proteomics</i> , 2022 , 100254	7.6	0
2	Forward and Reverse Proteomics 2003 , 255-276		
1	Interactome Networks. <i>FASEB Journal</i> , 2008 , 22, 262.1	0.9	

