

Marc Vidal

List of Publications by Year in Descending Order

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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	OpenPIP: An Open-source Platform for Hosting, Visualizing and Analyzing Protein Interaction Data. <i>Journal of Molecular Biology</i> , 2022 , 167603	6.5	0
160	New views of old proteins: clarifying the enigmatic proteome. <i>Molecular and Cellular Proteomics</i> , 2022 , 100254	7.6	0
159	Alternative glycosylation controls endoplasmic reticulum dynamics and tubular extension in mammalian cells. <i>Science Advances</i> , 2021 , 7,	14.3	3
158	A comprehensive library of human transcription factors for cell fate engineering. <i>Nature Biotechnology</i> , 2021 , 39, 510-519	44.5	40
157	Comprehensive characterization of protein-protein interactions perturbed by disease mutations. <i>Nature Genetics</i> , 2021 , 53, 342-353	36.3	27
156	The HTLV-1 viral oncoproteins Tax and HBZ reprogram the cellular mRNA splicing landscape. <i>PLoS Pathogens</i> , 2021 , 17, e1009919	7.6	3
155	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
154	Yeast-Based Genetic Interaction Analysis of Human Kinome. <i>Cells</i> , 2020 , 9,	7.9	3
153	ORF Capture-Seq as a versatile method for targeted identification of full-length isoforms. <i>Nature Communications</i> , 2020 , 11, 2326	17.4	8
152	Precision medicine - networks to the rescue. <i>Current Opinion in Biotechnology</i> , 2020 , 63, 177-189	11.4	17
151	A proactive genotype-to-patient-phenotype map for cystathionine beta-synthase. <i>Genome Medicine</i> , 2020 , 12, 13	14.4	17
150	A reference map of the human binary protein interactome. <i>Nature</i> , 2020 , 580, 402-408	50.4	269
149	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
148	Maximizing binary interactome mapping with a minimal number of assays. <i>Nature Communications</i> , 2019 , 10, 3907	17.4	21
147	Network-based prediction of protein interactions. <i>Nature Communications</i> , 2019 , 10, 1240	17.4	156
146	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
145	A genome-wide positioning systems network algorithm for in silico drug repurposing. <i>Nature Communications</i> , 2019 , 10, 3476	17.4	82

144	Global Analysis of Intercellular Homeodomain Protein Transfer. <i>Cell Reports</i> , 2019 , 28, 712-722.e3	10.6	11
143	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
142	How many human proteoforms are there?. <i>Nature Chemical Biology</i> , 2018 , 14, 206-214	11.7	324
141	Protein Interactomics by Two-Hybrid Methods. <i>Methods in Molecular Biology</i> , 2018 , 1794, 1-14	1.4	5
140	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
139	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
138	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
137	HSP90 Shapes the Consequences of Human Genetic Variation. <i>Cell</i> , 2017 , 168, 856-866.e12	56.2	75
136	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
135	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
134	Proteome-Scale Human Interactomics. <i>Trends in Biochemical Sciences</i> , 2017 , 42, 342-354	10.3	95
133	Identifying pathogenicity of human variants via paralog-based yeast complementation. <i>PLoS Genetics</i> , 2017 , 13, e1006779	6	19
132	Challenges and recommendations for epigenomics in precision health. <i>Nature Biotechnology</i> , 2017 , 35, 1128-1132	44.5	16
131	A framework for exhaustively mapping functional missense variants. <i>Molecular Systems Biology</i> , 2017 , 13, 957	12.2	69
130	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
129	Network-based in silico drug efficacy screening. <i>Nature Communications</i> , 2016 , 7, 10331	17.4	240
128	Proteome-scale Binary Interactomics in Human Cells. <i>Molecular and Cellular Proteomics</i> , 2016 , 15, 3624-3639	18	
127	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

126	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
125	Survey of variation in human transcription factors reveals prevalent DNA binding changes. <i>Science</i> , 2016 , 351, 1450-1454	33.3	78
124	A Zebrafish Genetic Screen Identifies Neuromedin U as a Regulator of Sleep/Wake States. <i>Neuron</i> , 2016 , 89, 842-56	13.9	59
123	Widespread Expansion of Protein Interaction Capabilities by Alternative Splicing. <i>Cell</i> , 2016 , 164, 805-17	56.2	308
122	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
121	An inter-species protein-protein interaction network across vast evolutionary distance. <i>Molecular Systems Biology</i> , 2016 , 12, 865	12.2	31
120	Pooled-matrix protein interaction screens using Barcode Fusion Genetics. <i>Molecular Systems Biology</i> , 2016 , 12, 863	12.2	59
119	An extended set of yeast-based functional assays accurately identifies human disease mutations. <i>Genome Research</i> , 2016 , 26, 670-80	9.7	65
118	Protein domain-level landscape of cancer-type-specific somatic mutations. <i>PLoS Computational Biology</i> , 2015 , 11, e1004147	5	46
117	Human gene-centered transcription factor networks for enhancers and disease variants. <i>Cell</i> , 2015 , 161, 661-673	56.2	80
116	Widespread macromolecular interaction perturbations in human genetic disorders. <i>Cell</i> , 2015 , 161, 647-660	56.2	343
115	Global Edgetic Rewiring in Cancer Networks. <i>Cell Systems</i> , 2015 , 1, 251-3	10.6	11
114	Selecting causal genes from genome-wide association studies via functionally coherent subnetworks. <i>Nature Methods</i> , 2015 , 12, 154-9	21.6	68
113	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
112	Disease networks. Uncovering disease-disease relationships through the incomplete interactome. <i>Science</i> , 2015 , 347, 1257601	33.3	767
111	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
110	A chaperome subnetwork safeguards proteostasis in aging and neurodegenerative disease. <i>Cell Reports</i> , 2014 , 9, 1135-50	10.6	317
109	A proteome-scale map of the human interactome network. <i>Cell</i> , 2014 , 159, 1212-1226	56.2	898

108	Multiplex single-molecule interaction profiling of DNA-barcoded proteins. <i>Nature</i> , 2014 , 515, 554-7	50.4	56
107	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
106	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
105	The yeast two-hybrid assay: still finding connections after 25 years. <i>Nature Methods</i> , 2014 , 11, 1203-6	21.6	52
104	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
103	Edgotype: a fundamental link between genotype and phenotype. <i>Current Opinion in Genetics and Development</i> , 2013 , 23, 649-57	4.9	103
102	Interactome Networks 2013 , 45-63		4
101	SH3 interactome conserves general function over specific form. <i>Molecular Systems Biology</i> , 2013 , 9, 652	12.2	47
100	Mycobacterium tuberculosis type VII secreted effector EsxH targets host ESCRT to impair trafficking. <i>PLoS Pathogens</i> , 2013 , 9, e1003734	7.6	108
99	Proto-genes and de novo gene birth. <i>Nature</i> , 2012 , 487, 370-4	50.4	379
98	A Protein Domain-Based Interactome Network for <i>C. elegans</i> Early Embryogenesis. <i>Cell</i> , 2012 , 151, 1633	56.2	3
97	Protein interactions of the transcription factor Hoxa1. <i>BMC Developmental Biology</i> , 2012 , 12, 29	3.1	33
96	Host-pathogen interactome mapping for HTLV-1 and -2 retroviruses. <i>Retrovirology</i> , 2012 , 9, 26	3.6	62
95	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
94	Interpreting cancer genomes using systematic host network perturbations by tumour virus proteins. <i>Nature</i> , 2012 , 487, 491-5	50.4	294
93	Viral perturbations of host networks reflect disease etiology. <i>PLoS Computational Biology</i> , 2012 , 8, e1002531	5.31	90
92	Identification of FAM111A as an SV40 host range restriction and adenovirus helper factor. <i>PLoS Pathogens</i> , 2012 , 8, e1002949	7.6	40
91	A public genome-scale lentiviral expression library of human ORFs. <i>Nature Methods</i> , 2011 , 8, 659-61	21.6	373

90	Protein-protein interactions and networks: forward and reverse edgetics. <i>Methods in Molecular Biology</i> , 2011 , 759, 197-213	1.4	20
89	Interactome networks and human disease. <i>Cell</i> , 2011 , 144, 986-98	56.2	1187
88	Independently evolved virulence effectors converge onto hubs in a plant immune system network. <i>Science</i> , 2011 , 333, 596-601	33.3	601
87	Knocking out multigene redundancies via cycles of sexual assortment and fluorescence selection. <i>Nature Methods</i> , 2011 , 8, 159-64	21.6	54
86	Next-generation sequencing to generate interactome datasets. <i>Nature Methods</i> , 2011 , 8, 478-80	21.6	191
85	Evidence for network evolution in an Arabidopsis interactome map. <i>Science</i> , 2011 , 333, 601-7	33.3	689
84	Reply to "Exhaustive benchmarking of the yeast two-hybrid system". <i>Nature Methods</i> , 2010 , 7, 668-668	21.6	3
83	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
82	High-quality binary interactome mapping. <i>Methods in Enzymology</i> , 2010 , 470, 281-315	1.7	104
81	A genome-wide gene function prediction resource for <i>Drosophila melanogaster</i> . <i>PLoS ONE</i> , 2010 , 5, e12139	3.7	16
80	Analysis of the human E2 ubiquitin conjugating enzyme protein interaction network. <i>Genome Research</i> , 2009 , 19, 1905-11	9.7	124
79	Shifted Transversal Design smart-pooling for high coverage interactome mapping. <i>Genome Research</i> , 2009 , 19, 1262-9	9.7	31
78	Edgetic perturbation models of human inherited disorders. <i>Molecular Systems Biology</i> , 2009 , 5, 321	12.2	278
77	A unifying view of 21st century systems biology. <i>FEBS Letters</i> , 2009 , 583, 3891-4	3.8	87
76	Empirically controlled mapping of the <i>Caenorhabditis elegans</i> protein-protein interactome network. <i>Nature Methods</i> , 2009 , 6, 47-54	21.6	224
75	An empirical framework for binary interactome mapping. <i>Nature Methods</i> , 2009 , 6, 83-90	21.6	674
74	An experimentally derived confidence score for binary protein-protein interactions. <i>Nature Methods</i> , 2009 , 6, 91-7	21.6	342
73	Literature-curated protein interaction datasets. <i>Nature Methods</i> , 2009 , 6, 39-46	21.6	237

72	'Edgetic' perturbation of a <i>C. elegans</i> BCL2 ortholog. <i>Nature Methods</i> , 2009 , 6, 843-9	21.6	63
71	Array MAPPIT: high-throughput interactome analysis in mammalian cells. <i>Journal of Proteome Research</i> , 2009 , 8, 877-86	5.6	48
70	Isoform discovery by targeted cloning, 'deep-well' pooling and parallel sequencing. <i>Nature Methods</i> , 2008 , 5, 597-600	21.6	26
69	High-quality binary protein interaction map of the yeast interactome network. <i>Science</i> , 2008 , 322, 104-109	33.3	1100
68	A protein domain-based interactome network for <i>C. elegans</i> early embryogenesis. <i>Cell</i> , 2008 , 134, 534-45	56.2	161
67	Interactome Networks. <i>FASEB Journal</i> , 2008 , 22, 262.1	0.9	
66	Drug-target network. <i>Nature Biotechnology</i> , 2007 , 25, 1119-26	44.5	1328
65	Network modeling links breast cancer susceptibility and centrosome dysfunction. <i>Nature Genetics</i> , 2007 , 39, 1338-49	36.3	516
64	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
63	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
62	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
61	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
60	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
59	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
58	Intrinsic disorder is a common feature of hub proteins from four eukaryotic interactomes. <i>PLoS Computational Biology</i> , 2006 , 2, e100	5	435
57	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
56	Reply to Toward the complete interactome. <i>Nature Biotechnology</i> , 2006 , 24, 615-615	44.5	1
55	Interactome: gateway into systems biology. <i>Human Molecular Genetics</i> , 2005 , 14 Spec No. 2, R171-81	5.6	285

54	Interactome modeling. <i>FEBS Letters</i> , 2005 , 579, 1834-8	3.8	94
53	Effect of sampling on topology predictions of protein-protein interaction networks. <i>Nature Biotechnology</i> , 2005 , 23, 839-44	44.5	253
52	Predictive models of molecular machines involved in <i>Caenorhabditis elegans</i> early embryogenesis. <i>Nature</i> , 2005 , 436, 861-5	50.4	225
51	Towards a proteome-scale map of the human protein-protein interaction network. <i>Nature</i> , 2005 , 437, 1173-8	50.4	2287
50	A first version of the <i>Caenorhabditis elegans</i> Promoterome. <i>Genome Research</i> , 2004 , 14, 2169-75	9.7	133
49	A gateway-compatible yeast one-hybrid system. <i>Genome Research</i> , 2004 , 14, 2093-101	9.7	162
48	Annotation transfer between genomes: protein-protein interologs and protein-DNA regulogs. <i>Genome Research</i> , 2004 , 14, 1107-18	9.7	400
47	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
46	<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
45	Human ORFeome version 1.1: a platform for reverse proteomics. <i>Genome Research</i> , 2004 , 14, 2128-35	9.7	182
44	Evidence for dynamically organized modularity in the yeast protein-protein interaction network. <i>Nature</i> , 2004 , 430, 88-93	50.4	1381
43	A map of the interactome network of the metazoan <i>C. elegans</i> . <i>Science</i> , 2004 , 303, 540-3	33.3	1398
42	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
41	Increasing specificity in high-throughput yeast two-hybrid experiments. <i>Methods</i> , 2004 , 32, 363-70	4.6	117
40	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
39	Integrating 'omic' information: a bridge between genomics and systems biology. <i>Trends in Genetics</i> , 2003 , 19, 551-60	8.5	363
38	Reply to "Does mapping reveal correlation between gene expression and protein-protein interaction?". <i>Nature Genetics</i> , 2003 , 33, 16-17	36.3	6
37	<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	36.3	310

36	WorfDB: the Caenorhabditis elegans ORFeome Database. <i>Nucleic Acids Research</i> , 2003 , 31, 237-40	20.1	29
35	Forward and Reverse Proteomics 2003 , 255-276		
34	Integrating interactome, phenome, and transcriptome mapping data for the C. elegans germline. <i>Current Biology</i> , 2002 , 12, 1952-8	6.3	157
33	Combined functional genomic maps of the C. elegans DNA damage response. <i>Science</i> , 2002 , 295, 127-31	33.3	253
32	Integrated version of reverse two-hybrid system for the postproteomic era. <i>Methods in Enzymology</i> , 2002 , 350, 525-45	1.7	8
31	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
30	Use of protein-interaction maps to formulate biological questions. <i>Current Opinion in Chemical Biology</i> , 2001 , 5, 57-62	9.7	9
29	A protein-protein interaction map of the Caenorhabditis elegans 26S proteasome. <i>EMBO Reports</i> , 2001 , 2, 821-8	6.5	156
28	Open-reading-frame sequence tags (OSTs) support the existence of at least 17,300 genes in C. elegans. <i>Nature Genetics</i> , 2001 , 27, 332-6	36.3	145
27	Correlation between transcriptome and interactome mapping data from Saccharomyces cerevisiae. <i>Nature Genetics</i> , 2001 , 29, 482-6	36.3	517
26	Protein interaction maps for model organisms. <i>Nature Reviews Molecular Cell Biology</i> , 2001 , 2, 55-62	48.7	118
25	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
24	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
23	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
22	High-throughput yeast two-hybrid assays for large-scale protein interaction mapping. <i>Methods</i> , 2001 , 24, 297-306	4.6	208
21	A biological atlas of functional maps. <i>Cell</i> , 2001 , 104, 333-9	56.2	165
20	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
19	Yeast two-hybrid systems and protein interaction mapping projects for yeast and worm. <i>Yeast</i> , 2000 , 17, 88-94	3.4	101

18	Protein interaction mapping in <i>C. elegans</i> using proteins involved in vulval development. <i>Science</i> , 2000 , 287, 116-22	33.3	659
17	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
16	Yeast Two-Hybrid Systems and Protein Interaction Mapping Projects for Yeast and Worm. <i>Yeast</i> , 2000 , 1, 88-94	3.4	13
15	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
14	Prospects for drug screening using the reverse two-hybrid system. <i>Trends in Biotechnology</i> , 1999 , 17, 374-81	15.1	78
13	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	3.6	90
12	A model of elegance. <i>American Journal of Human Genetics</i> , 1998 , 63, 955-61	11	17
11	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
10	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
9	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
8	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
7	Screening patients for heterozygous p53 mutations using a functional assay in yeast. <i>Nature Genetics</i> , 1993 , 5, 124-9	36.3	224
6	Expanding the Atlas of Functional Missense Variation for Human Genes		2
5	Controllability in an islet specific regulatory network identifies the transcriptional factor NFATC4, which regulates Type 2 Diabetes associated genes		1
4	Network-based prediction of protein interactions		7
3	Towards an Essayome[For binary interactome mapping		2
2	A reference map of the human protein interactome		13
1	A map of binary SARS-CoV-2 protein interactions implicates host immune regulation and ubiquitination		2

