

Marc Vidal

List of Publications by Year in descending order

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160
papers

41,535
citations

4658

85
h-index

5988

160
g-index

175
all docs

175
docs citations

175
times ranked

39618
citing authors

#	ARTICLE	IF	CITATIONS
1	OpenPIP: An Open-source Platform for Hosting, Visualizing and Analyzing Protein Interaction Data. <i>Journal of Molecular Biology</i> , 2022, 434, 167603.	4.2	3
2	New Views of Old Proteins: Clarifying the Enigmatic Proteome. <i>Molecular and Cellular Proteomics</i> , 2022, 21, 100254.	3.8	16
3	A comprehensive library of human transcription factors for cell fate engineering. <i>Nature Biotechnology</i> , 2021, 39, 510-519.	17.5	110
4	Comprehensive characterization of protein-protein interactions perturbed by disease mutations. <i>Nature Genetics</i> , 2021, 53, 342-353.	21.4	109
5	Alternative glycosylation controls endoplasmic reticulum dynamics and tubular extension in mammalian cells. <i>Science Advances</i> , 2021, 7, .	10.3	8
6	The HTLV-1 viral oncoproteins Tax and HBZ reprogram the cellular mRNA splicing landscape. <i>PLoS Pathogens</i> , 2021, 17, e1009919.	4.7	19
7	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.	3.4	4
8	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.	7.1	16
9	Yeast-Based Genetic Interaction Analysis of Human Kinome. <i>Cells</i> , 2020, 9, 1156.	4.1	5
10	ORF Capture-Seq as a versatile method for targeted identification of full-length isoforms. <i>Nature Communications</i> , 2020, 11, 2326.	12.8	19
11	Precision medicine networks to the rescue. <i>Current Opinion in Biotechnology</i> , 2020, 63, 177-189.	6.6	30
12	A proactive genotype-to-patient-phenotype map for cystathionine beta-synthase. <i>Genome Medicine</i> , 2020, 12, 13.	8.2	45
13	A reference map of the human binary protein interactome. <i>Nature</i> , 2020, 580, 402-408.	27.8	724
14	A genome-wide positioning systems network algorithm for in silico drug repurposing. <i>Nature Communications</i> , 2019, 10, 3476.	12.8	134
15	Global Analysis of Intercellular Homeodomain Protein Transfer. <i>Cell Reports</i> , 2019, 28, 712-722.e3.	6.4	28
16	Maximizing binary interactome mapping with a minimal number of assays. <i>Nature Communications</i> , 2019, 10, 3907.	12.8	57
17	Network-based prediction of protein interactions. <i>Nature Communications</i> , 2019, 10, 1240.	12.8	293
18	APID database: redefining protein-protein interaction experimental evidences and binary interactomes. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	3.0	113

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19	Network Analysis of UBE3A/E6AP-Associated Proteins Provides Connections to Several Distinct Cellular Processes. <i>Journal of Molecular Biology</i> , 2018, 430, 1024-1050.	4.2	32
20	How many human proteoforms are there?. <i>Nature Chemical Biology</i> , 2018, 14, 206-214.	8.0	580
21	Protein Interactomics by Two-Hybrid Methods. <i>Methods in Molecular Biology</i> , 2018, 1794, 1-14.	0.9	6
22	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.	3.0	25
23	Genome-Scale Networks Link Neurodegenerative Disease Genes to α -Synuclein through Specific Molecular Pathways. <i>Cell Systems</i> , 2017, 4, 157-170.e14.	6.2	102
24	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.	6.2	91
25	HSP90 Shapes the Consequences of Human Genetic Variation. <i>Cell</i> , 2017, 168, 856-866.e12.	28.9	117
26	Dynamic Role of trans Regulation of Gene Expression in Relation to Complex Traits. <i>American Journal of Human Genetics</i> , 2017, 100, 571-580.	6.2	101
27	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.	5.5	12
28	Proteome-Scale Human Interactomics. <i>Trends in Biochemical Sciences</i> , 2017, 42, 342-354.	7.5	129
29	Challenges and recommendations for epigenomics in precision health. <i>Nature Biotechnology</i> , 2017, 35, 1128-1132.	17.5	19
30	A framework for exhaustively mapping functional missense variants. <i>Molecular Systems Biology</i> , 2017, 13, 957.	7.2	146
31	Identifying pathogenicity of human variants via paralog-based yeast complementation. <i>PLoS Genetics</i> , 2017, 13, e1006779.	3.5	30
32	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.	3.2	30
33	An inter-species protein-protein interaction network across vast evolutionary distance. <i>Molecular Systems Biology</i> , 2016, 12, 865.	7.2	42
34	Pooled-matrix protein interaction screens using Barcode Fusion Genetics. <i>Molecular Systems Biology</i> , 2016, 12, 863.	7.2	102
35	An extended set of yeast-based functional assays accurately identifies human disease mutations. <i>Genome Research</i> , 2016, 26, 670-680.	5.5	116
36	How much of the human protein interactome remains to be mapped?. <i>Science Signaling</i> , 2016, 9, eg7.	3.6	31

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37	Network-based in silico drug efficacy screening. <i>Nature Communications</i> , 2016, 7, 10331.	12.8	394
38	Proteome-scale Binary Interactomics in Human Cells. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 3624-3639.	3.8	23
39	The transcription factor ERG recruits CCR4â€“NOT to control mRNA decay and mitotic progression. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 663-672.	8.2	35
40	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.	7.1	67
41	Survey of variation in human transcription factors reveals prevalent DNA binding changes. <i>Science</i> , 2016, 351, 1450-1454.	12.6	114
42	A Zebrafish Genetic Screen Identifies Neuromedin U as a Regulator of Sleep/Wake States. <i>Neuron</i> , 2016, 89, 842-856.	8.1	81
43	Widespread Expansion of Protein Interaction Capabilities by Alternative Splicing. <i>Cell</i> , 2016, 164, 805-817.	28.9	479
44	<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.	9.4	57
45	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.	8.1	139
46	Uncovering disease-disease relationships through the incomplete interactome. <i>Science</i> , 2015, 347, 1257601.	12.6	1,219
47	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.	2.9	162
48	Protein Domain-Level Landscape of Cancer-Type-Specific Somatic Mutations. <i>PLoS Computational Biology</i> , 2015, 11, e1004147.	3.2	59
49	Human Gene-Centered Transcription Factor Networks for Enhancers and Disease Variants. <i>Cell</i> , 2015, 161, 661-673.	28.9	111
50	Widespread Macromolecular Interaction Perturbations in Human Genetic Disorders. <i>Cell</i> , 2015, 161, 647-660.	28.9	482
51	Global Edgetic Rewiring in Cancer Networks. <i>Cell Systems</i> , 2015, 1, 251-253.	6.2	28
52	Selecting causal genes from genome-wide association studies via functionally coherent subnetworks. <i>Nature Methods</i> , 2015, 12, 154-159.	19.0	96
53	Protein interaction network of alternatively spliced isoforms from brain links genetic risk factors for autism. <i>Nature Communications</i> , 2014, 5, 3650.	12.8	131
54	The yeast two-hybrid assay: still finding connections after 25 years. <i>Nature Methods</i> , 2014, 11, 1203-1206.	19.0	68

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55	Systematic screening reveals a role for BRCA1 in the response to transcription-associated DNA damage. <i>Genes and Development</i> , 2014, 28, 1957-1975.	5.9	86
56	A Chaperome Subnetwork Safeguards Proteostasis in Aging and Neurodegenerative Disease. <i>Cell Reports</i> , 2014, 9, 1135-1150.	6.4	476
57	A Proteome-Scale Map of the Human Interactome Network. <i>Cell</i> , 2014, 159, 1212-1226.	28.9	1,199
58	Multiplex single-molecule interaction profiling of DNA-barcoded proteins. <i>Nature</i> , 2014, 515, 554-557.	27.8	72
59	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.	11.0	367
60	Edgotype: a fundamental link between genotype and phenotype. <i>Current Opinion in Genetics and Development</i> , 2013, 23, 649-657.	3.3	129
61	Interactome Networks. , 2013, , 45-63.		5
62	SH3 interactome conserves general function over specific form. <i>Molecular Systems Biology</i> , 2013, 9, 652.	7.2	61
63	<i>Mycobacterium tuberculosis</i> Type VII Secreted Effector EsxH Targets Host ESCRT to Impair Trafficking. <i>PLoS Pathogens</i> , 2013, 9, e1003734.	4.7	167
64	Viral Perturbations of Host Networks Reflect Disease Etiology. <i>PLoS Computational Biology</i> , 2012, 8, e1002531.	3.2	102
65	Identification of FAM111A as an SV40 Host Range Restriction and Adenovirus Helper Factor. <i>PLoS Pathogens</i> , 2012, 8, e1002949.	4.7	58
66	Proto-genes and de novo gene birth. <i>Nature</i> , 2012, 487, 370-374.	27.8	555
67	A Protein Domain-Based Interactome Network for <i>C.Âelegans</i> Early Embryogenesis. <i>Cell</i> , 2012, 151, 1633.	28.9	4
68	Protein interactions of the transcription factor Hoxa1. <i>BMC Developmental Biology</i> , 2012, 12, 29.	2.1	43
69	Host-pathogen interactome mapping for HTLV-1 and -2 retroviruses. <i>Retrovirology</i> , 2012, 9, 26.	2.0	64
70	Comparative analysis of virusâ€host interactomes with a mammalian high-throughput protein complementation assay based on <i>Gaussia princeps</i> luciferase. <i>Methods</i> , 2012, 58, 349-359.	3.8	59
71	Interpreting cancer genomes using systematic host network perturbations by tumour virus proteins. <i>Nature</i> , 2012, 487, 491-495.	27.8	349
72	Evidence for Network Evolution in an <i>Arabidopsis</i> Interactome Map. <i>Science</i> , 2011, 333, 601-607.	12.6	838

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73	A public genome-scale lentiviral expression library of human ORFs. <i>Nature Methods</i> , 2011, 8, 659-661.	19.0	477
74	Protein-Protein Interactions and Networks: Forward and Reverse Edgetics. <i>Methods in Molecular Biology</i> , 2011, 759, 197-213.	0.9	24
75	Interactome Networks and Human Disease. <i>Cell</i> , 2011, 144, 986-998.	28.9	1,543
76	Independently Evolved Virulence Effectors Converge onto Hubs in a Plant Immune System Network. <i>Science</i> , 2011, 333, 596-601.	12.6	776
77	Knocking out multigene redundancies via cycles of sexual assortment and fluorescence selection. <i>Nature Methods</i> , 2011, 8, 159-164.	19.0	74
78	Next-generation sequencing to generate interactome datasets. <i>Nature Methods</i> , 2011, 8, 478-480.	19.0	258
79	Reply to "Exhaustive benchmarking of the yeast two-hybrid system". <i>Nature Methods</i> , 2010, 7, 668-668.	19.0	3
80	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.	3.8	51
81	High-Quality Binary Interactome Mapping. <i>Methods in Enzymology</i> , 2010, 470, 281-315.	1.0	126
82	A Genome-Wide Gene Function Prediction Resource for <i>Drosophila melanogaster</i> . <i>PLoS ONE</i> , 2010, 5, e12139.	2.5	17
83	Analysis of the human E2 ubiquitin conjugating enzyme protein interaction network. <i>Genome Research</i> , 2009, 19, 1905-1911.	5.5	134
84	Shifted Transversal Design smart-pooling for high coverage interactome mapping. <i>Genome Research</i> , 2009, 19, 1262-1269.	5.5	36
85	Edgetic perturbation models of human inherited disorders. <i>Molecular Systems Biology</i> , 2009, 5, 321.	7.2	326
86	A unifying view of 21st century systems biology. <i>FEBS Letters</i> , 2009, 583, 3891-3894.	2.8	105
87	Empirically controlled mapping of the <i>Caenorhabditis elegans</i> protein-protein interactome network. <i>Nature Methods</i> , 2009, 6, 47-54.	19.0	260
88	An empirical framework for binary interactome mapping. <i>Nature Methods</i> , 2009, 6, 83-90.	19.0	800
89	An experimentally derived confidence score for binary protein-protein interactions. <i>Nature Methods</i> , 2009, 6, 91-97.	19.0	397
90	Literature-curated protein interaction datasets. <i>Nature Methods</i> , 2009, 6, 39-46.	19.0	288

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91	'Edgetic' perturbation of a <i>C. elegans</i> BCL2 ortholog. <i>Nature Methods</i> , 2009, 6, 843-849.	19.0	71
92	Array MAPPIT: High-Throughput Interactome Analysis in Mammalian Cells. <i>Journal of Proteome Research</i> , 2009, 8, 877-886.	3.7	53
93	Isoform discovery by targeted cloning, 'deep-well' pooling and parallel sequencing. <i>Nature Methods</i> , 2008, 5, 597-600.	19.0	30
94	High-Quality Binary Protein Interaction Map of the Yeast Interactome Network. <i>Science</i> , 2008, 322, 104-110.	12.6	1,297
95	A Protein Domain-Based Interactome Network for <i>C. elegans</i> Early Embryogenesis. <i>Cell</i> , 2008, 134, 534-545.	28.9	196
96	Interactome Networks. <i>FASEB Journal</i> , 2008, 22, 262.1.	0.5	0
97	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.	7.1	348
98	The human disease network. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 8685-8690.	7.1	2,924
99	hORFeome v3.1: A resource of human open reading frames representing over 10,000 human genes. <i>Genomics</i> , 2007, 89, 307-315.	2.9	248
100	InSite: a computational method for identifying protein-protein interaction binding sites on a proteome-wide scale. <i>Genome Biology</i> , 2007, 8, R192.	9.6	53
101	Drug-target network. <i>Nature Biotechnology</i> , 2007, 25, 1119-1126.	17.5	1,584
102	Network modeling links breast cancer susceptibility and centrosome dysfunction. <i>Nature Genetics</i> , 2007, 39, 1338-1349.	21.4	602
103	Insight into transcription factor gene duplication from <i>Caenorhabditis elegans</i> Promoterome-driven expression patterns. <i>BMC Genomics</i> , 2007, 8, 27.	2.8	120
104	A Protein-Protein Interaction Network for Human Inherited Ataxias and Disorders of Purkinje Cell Degeneration. <i>Cell</i> , 2006, 125, 801-814.	28.9	714
105	Reply to Toward the complete interactome. <i>Nature Biotechnology</i> , 2006, 24, 615-615.	17.5	1
106	QUICKstep and GS-TAP: new moves for protein-interaction analysis. <i>Nature Methods</i> , 2006, 3, 975-976.	19.0	5
107	From genome to proteome: developing expression clone resources for the human genome. <i>Human Molecular Genetics</i> , 2006, 15, R31-R43.	2.9	26
108	Intrinsic Disorder Is a Common Feature of Hub Proteins from Four Eukaryotic Interactomes. <i>PLoS Computational Biology</i> , 2006, 2, e100.	3.2	512

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109	From genome to proteome: developing expression clone resources for the human genome. Human Molecular Genetics, 2006, 15, 2184-2184.	2.9	1
110	The C.elegans interactome project. , 2005, , .		0
111	Effect of sampling on topology predictions of protein-protein interaction networks. Nature Biotechnology, 2005, 23, 839-844.	17.5	302
112	Perturbing interactions. Nature Methods, 2005, 2, 412-414.	19.0	6
113	Predictive models of molecular machines involved in Caenorhabditis elegans early embryogenesis. Nature, 2005, 436, 861-865.	27.8	260
114	Towards a proteome-scale map of the human protein-protein interaction network. Nature, 2005, 437, 1173-1178.	27.8	2,676
115	Interactome: gateway into systems biology. Human Molecular Genetics, 2005, 14, R171-R181.	2.9	329
116	Interactome modeling. FEBS Letters, 2005, 579, 1834-1838.	2.8	99
117	A First Version of the Caenorhabditis elegans Promoterome. Genome Research, 2004, 14, 2169-2175.	5.5	155
118	A Gateway-Compatible Yeast One-Hybrid System. Genome Research, 2004, 14, 2093-2101.	5.5	189
119	Annotation Transfer Between Genomes: Protein-Protein Interologs and Protein-DNA Regulogs. Genome Research, 2004, 14, 1107-1118.	5.5	516
120	ORFeome Cloning and Systems Biology: Standardized Mass Production of the Parts From the Parts-List. Genome Research, 2004, 14, 2001-2009.	5.5	69
121	C. elegans ORFeome Version 3.1: Increasing the Coverage of ORFeome Resources With Improved Gene Predictions. Genome Research, 2004, 14, 2064-2069.	5.5	107
122	Human ORFeome Version 1.1: A Platform for Reverse Proteomics. Genome Research, 2004, 14, 2128-2135.	5.5	208
123	Evidence for dynamically organized modularity in the yeast protein-protein interaction network. Nature, 2004, 430, 88-93.	27.8	1,683
124	A Map of the Interactome Network of the Metazoan <i>C. elegans</i> . Science, 2004, 303, 540-543.	12.6	1,587
125	Combining biological networks to predict genetic interactions. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 15682-15687.	7.1	225
126	Increasing specificity in high-throughput yeast two-hybrid experiments. Methods, 2004, 32, 363-370.	3.8	135

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127	Systematic Interactome Mapping and Genetic Perturbation Analysis of a <i>C. elegans</i> TGF- β Signaling Network. <i>Molecular Cell</i> , 2004, 13, 469-482.	9.7	136
128	Integrating \sim omic TM information: a bridge between genomics and systems biology. <i>Trends in Genetics</i> , 2003, 19, 551-560.	6.7	407
129	Reply to "Does mapping reveal correlation between gene expression and protein TM protein interaction?". <i>Nature Genetics</i> , 2003, 33, 16-17.	21.4	7
130	<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.	21.4	347
131	WorfDB: the <i>Caenorhabditis elegans</i> ORFeome Database. <i>Nucleic Acids Research</i> , 2003, 31, 237-240.	14.5	35
132	Forward and Reverse Proteomics. , 2003, , 255-276.		0
133	Combined Functional Genomic Maps of the <i>C. elegans</i> DNA Damage Response. <i>Science</i> , 2002, 295, 127-131.	12.6	270
134	Integrated version of reverse two-hybrid system for the postproteomic era. <i>Methods in Enzymology</i> , 2002, 350, 525-545.	1.0	10
135	Integrating Interactome, Phenome, and Transcriptome Mapping Data for the <i>C. elegans</i> Germline. <i>Current Biology</i> , 2002, 12, 1952-1958.	3.9	170
136	High-Throughput Yeast Two-Hybrid Assays for Large-Scale Protein Interaction Mapping. <i>Methods</i> , 2001, 24, 297-306.	3.8	258
137	A Biological Atlas of Functional Maps. <i>Cell</i> , 2001, 104, 333-339.	28.9	188
138	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
139	Use of protein-interaction maps to formulate biological questions. <i>Current Opinion in Chemical Biology</i> , 2001, 5, 57-62.	6.1	11
140	A protein TM protein interaction map of the <i>Caenorhabditis elegans</i> 26S proteasome. <i>EMBO Reports</i> , 2001, 2, 821-828.	4.5	173
141	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.	21.4	159
142	Correlation between transcriptome and interactome mapping data from <i>Saccharomyces cerevisiae</i> . <i>Nature Genetics</i> , 2001, 29, 482-486.	21.4	570
143	Protein interaction maps for model organisms. <i>Nature Reviews Molecular Cell Biology</i> , 2001, 2, 55-63.	37.0	139
144	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.	3.9	73

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145	Identification of Potential Interaction Networks Using Sequence-Based Searches for Conserved Protein-Protein Interactions or "Interologs". <i>Genome Research</i> , 2001, 11, 2120-2126.	5.5	431
146	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.	7.1	26
147	[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.	1.0	19
148	Yeast Two-Hybrid Systems and Protein Interaction Mapping Projects for Yeast and Worm. <i>Yeast</i> , 2000, 1, 88-94.	1.7	121
149	Protein Interaction Mapping in <i>C. elegans</i> Using Proteins Involved in Vulval Development. <i>Science</i> , 2000, 287, 116-122.	12.6	766
150	[34] GATEWAY recombinational cloning: Application to the cloning of large numbers of open reading frames or ORFeomes. <i>Methods in Enzymology</i> , 2000, 328, 575-IN7.	1.0	570
151	Yeast Two-Hybrid Systems and Protein Interaction Mapping Projects for Yeast and Worm. <i>Yeast</i> , 2000, 1, 88-94.	1.7	16
152	A Genetic Strategy to Eliminate Self-Activator Baits Prior to High-Throughput Yeast Two-Hybrid Screens. <i>Genome Research</i> , 1999, 9, 1128-1134.	5.5	51
153	Prospects for drug screening using the reverse two-hybrid system. <i>Trends in Biotechnology</i> , 1999, 17, 374-381.	9.3	88
154	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.	2.4	102
155	A Model of Elegance. <i>American Journal of Human Genetics</i> , 1998, 63, 955-961.	6.2	22
156	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.	7.1	158
157	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.	7.1	416
158	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.	7.1	260
159	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.	7.1	342
160	Screening patients for heterozygous p53 mutations using a functional assay in yeast. <i>Nature Genetics</i> , 1993, 5, 124-129.	21.4	243