

Frederick P Roth

List of Publications by Year in descending order

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Version: 2024-02-01

150
papers

32,457
citations

15880

67
h-index

9865

146
g-index

173
all docs

173
docs citations

173
times ranked

41675
citing authors

#	ARTICLE	IF	CITATIONS
1	MaveRegistry: a collaboration platform for multiplexed assays of variant effect. <i>Bioinformatics</i> , 2021, 37, 3382-3383.	1.8	9
2	Seeds of their own destruction: Dominant-negative peptide screening yields functional insight and therapeutic leads. <i>Cell Systems</i> , 2021, 12, 691-693.	2.9	4
3	Shifting landscapes of human MTHFR missense-variant effects. <i>American Journal of Human Genetics</i> , 2021, 108, 1283-1300.	2.6	33
4	Improved pathogenicity prediction for rare human missense variants. <i>American Journal of Human Genetics</i> , 2021, 108, 1891-1906.	2.6	51
5	Prioritizing genes for systematic variant effect mapping. <i>Bioinformatics</i> , 2021, 36, 5448-5455.	1.8	9
6	Highly Combinatorial Genetic Interaction Analysis Reveals a Multi-Drug Transporter Influence Network. <i>Cell Systems</i> , 2020, 10, 25-38.e10.	2.9	18
7	MaveQuest: a web resource for planning experimental tests of human variant effects. <i>Bioinformatics</i> , 2020, 36, 3938-3940.	1.8	7
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.	1.6	4
9	A Comprehensive, Flexible Collection of SARS-CoV-2 Coding Regions. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3399-3402.	0.8	48
10	Yeast-Based Genetic Interaction Analysis of Human Kinome. <i>Cells</i> , 2020, 9, 1156.	1.8	5
11	Systems analysis of RhoGEF and RhoGAP regulatory proteins reveals spatially organized RAC1 signalling from integrin adhesions. <i>Nature Cell Biology</i> , 2020, 22, 498-511.	4.6	154
12	A proactive genotype-to-patient-phenotype map for cystathionine beta-synthase. <i>Genome Medicine</i> , 2020, 12, 13.	3.6	45
13	A reference map of the human binary protein interactome. <i>Nature</i> , 2020, 580, 402-408.	13.7	724
14	Systematic analysis of bypass suppression of essential genes. <i>Molecular Systems Biology</i> , 2020, 16, e9828.	3.2	45
15	Multiplexed measurement of variant abundance and activity reveals VKOR topology, active site and human variant impact. <i>ELife</i> , 2020, 9, .	2.8	58
16	Assessing predictions on fitness effects of missense variants in calmodulin. <i>Human Mutation</i> , 2019, 40, 1463-1473.	1.1	8
17	Quantifying immune-based counterselection of somatic mutations. <i>PLoS Genetics</i> , 2019, 15, e1008227.	1.5	14
18	MaveDB: an open-source platform to distribute and interpret data from multiplexed assays of variant effect. <i>Genome Biology</i> , 2019, 20, 223.	3.8	130

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19	Characterizing ABC-Transporter Substrate-Likeness Using a Clean-Slate Genetic Background. <i>Frontiers in Pharmacology</i> , 2019, 10, 448.	1.6	1
20	A web application and service for imputing and visualizing missense variant effect maps. <i>Bioinformatics</i> , 2019, 35, 3191-3193.	1.8	13
21	CNTN5-/+or EHMT2-/+human iPSC-derived neurons from individuals with autism develop hyperactive neuronal networks. <i>ELife</i> , 2019, 8, .	2.8	72
22	Modeling the impact of drug interactions on therapeutic selectivity. <i>Nature Communications</i> , 2018, 9, 3452.	5.8	18
23	Mapping <scp>DNA</scp> damageâ€dependent genetic interactions in yeast via party mating and barcode fusion genetics. <i>Molecular Systems Biology</i> , 2018, 14, e7985.	3.2	25
24	The Impact of Oncogenic EGFRvIII on the Proteome of Extracellular Vesicles Released from Glioblastoma Cells. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1948-1964.	2.5	116
25	Multiplexed assays of variant effects contribute to a growing genotypeâ€phenotype atlas. <i>Human Genetics</i> , 2018, 137, 665-678.	1.8	91
26	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
27	A common class of transcripts with 5â€ ² -intron depletion, distinct early coding sequence features, and <i>N</i>¹-methyladenosine modification. <i>Rna</i> , 2017, 23, 270-283.	1.6	16
28	Assessing predictions of fitness effects of missense mutations in SUMOâ€conjugating enzyme UBE2I. <i>Human Mutation</i> , 2017, 38, 1051-1063.	1.1	12
29	Variant Interpretation: Functional Assays to the Rescue. <i>American Journal of Human Genetics</i> , 2017, 101, 315-325.	2.6	275
30	Quantitative analysis of protein interaction network dynamics in yeast. <i>Molecular Systems Biology</i> , 2017, 13, 934.	3.2	41
31	A framework for exhaustively mapping functional missense variants. <i>Molecular Systems Biology</i> , 2017, 13, 957.	3.2	146
32	CRISPR/Cas9 System as a Valuable Genome Editing Tool for Wine Yeasts with Application to Decrease Urea Production. <i>Frontiers in Microbiology</i> , 2017, 8, 2194.	1.5	46
33	Identifying pathogenicity of human variants via paralog-based yeast complementation. <i>PLoS Genetics</i> , 2017, 13, e1006779.	1.5	30
34	Systematic identification of phosphorylation-mediated protein interaction switches. <i>PLoS Computational Biology</i> , 2017, 13, e1005462.	1.5	44
35	An interâ€species proteinâ€protein interaction network across vast evolutionary distance. <i>Molecular Systems Biology</i> , 2016, 12, 865.	3.2	42
36	Pooledâ€matrix protein interaction screens using Barcode Fusion Genetics. <i>Molecular Systems Biology</i> , 2016, 12, 863.	3.2	102

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37	Taking Exception to Human Eugenics. <i>Genetics</i> , 2016, 204, 821-823.	1.2	6
38	An extended set of yeast-based functional assays accurately identifies human disease mutations. <i>Genome Research</i> , 2016, 26, 670-680.	2.4	116
39	Dual action antifungal small molecule modulates multidrug efflux and TOR signaling. <i>Nature Chemical Biology</i> , 2016, 12, 867-875.	3.9	79
40	Exploring genetic suppression interactions on a global scale. <i>Science</i> , 2016, 354, .	6.0	157
41	A Proteome-wide Fission Yeast Interactome Reveals Network Evolution Principles from Yeasts to Human. <i>Cell</i> , 2016, 164, 310-323.	13.5	106
42	Widespread Expansion of Protein Interaction Capabilities by Alternative Splicing. <i>Cell</i> , 2016, 164, 805-817.	13.5	479
43	SELPHI: correlation-based identification of kinase-associated networks from global phospho-proteomics data sets. <i>Nucleic Acids Research</i> , 2015, 43, W276-W282.	6.5	24
44	Protein Domain-Level Landscape of Cancer-Type-Specific Somatic Mutations. <i>PLoS Computational Biology</i> , 2015, 11, e1004147.	1.5	59
45	Widespread Macromolecular Interaction Perturbations in Human Genetic Disorders. <i>Cell</i> , 2015, 161, 647-660.	13.5	482
46	High-Resolution CRISPR Screens Reveal Fitness Genes and Genotype-Specific Cancer Liabilities. <i>Cell</i> , 2015, 163, 1515-1526.	13.5	1,339
47	Selecting causal genes from genome-wide association studies via functionally coherent subnetworks. <i>Nature Methods</i> , 2015, 12, 154-159.	9.0	96
48	Biomolecular Network Structure and Function. , 2015, , 1-25.		0
49	Synergy and Selectivity of Antifungal Small Molecule Combinations. <i>FASEB Journal</i> , 2015, 29, 773.13.	0.2	0
50	Prioritizing causal disease genes using unbiased genomic features. <i>Genome Biology</i> , 2014, 15, 534.	3.8	40
51	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
52	The Insertion Green Monster (iGM) Method for Expression of Multiple Exogenous Genes in Yeast. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 1183-1191.	0.8	14
53	A Highly Conserved Program of Neuronal Microexons Is Misregulated in Autistic Brains. <i>Cell</i> , 2014, 159, 1511-1523.	13.5	546
54	Novel cardiovascular gene functions revealed via systematic phenotype prediction in zebrafish. <i>Development (Cambridge)</i> , 2014, 141, 224-235.	1.2	22

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55	Large-Scale Identification and Analysis of Suppressive Drug Interactions. <i>Chemistry and Biology</i> , 2014, 21, 541-551.	6.2	27
56	A Proteome-Scale Map of the Human Interactome Network. <i>Cell</i> , 2014, 159, 1212-1226.	13.5	1,199
57	Target-Independent Prediction of Drug Synergies Using Only Drug Lipophilicity. <i>Journal of Chemical Information and Modeling</i> , 2014, 54, 2286-2293.	2.5	30
58	Systems biology and the analysis of genetic variation. <i>Current Opinion in Genetics and Development</i> , 2013, 23, 599-601.	1.5	3
59	Interactome Networks. , 2013, , 45-63.		5
60	ChromoZoom: a flexible, fluid, web-based genome browser. <i>Bioinformatics</i> , 2013, 29, 384-386.	1.8	14
61	RanBP2/Nup358 Potentiates the Translation of a Subset of mRNAs Encoding Secretory Proteins. <i>PLoS Biology</i> , 2013, 11, e1001545.	2.6	61
62	Cross-Species Protein Interactome Mapping Reveals Species-Specific Wiring of Stress Response Pathways. <i>Science Signaling</i> , 2013, 6, ra38.	1.6	47
63	Viral Perturbations of Host Networks Reflect Disease Etiology. <i>PLoS Computational Biology</i> , 2012, 8, e1002531.	1.5	102
64	A Resource of Quantitative Functional Annotation for Homo sapiens Genes. <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 223-233.	0.8	6
65	The Green Monster Process for the Generation of Yeast Strains Carrying Multiple Gene Deletions. <i>Journal of Visualized Experiments</i> , 2012, , e4072.	0.2	12
66	Introns in UTRs: Why we should stop ignoring them. <i>BioEssays</i> , 2012, 34, 1025-1034.	1.2	119
67	Genome Rearrangements Caused by Depletion of Essential DNA Replication Proteins in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2012, 192, 147-160.	1.2	25
68	Interpreting cancer genomes using systematic host network perturbations by tumour virus proteins. <i>Nature</i> , 2012, 487, 491-495.	13.7	349
69	Response to "MHC-dependent mate choice in humans: Why genomic patterns from the HapMap European American data set support the hypothesis" (DOI: 10.1002/bies.201100150). <i>BioEssays</i> , 2012, 34, 576-577.	1.2	7
70	Evidence for Network Evolution in an <i>Arabidopsis</i> Interactome Map. <i>Science</i> , 2011, 333, 601-607.	6.0	838
71	Systematic exploration of synergistic drug pairs. <i>Molecular Systems Biology</i> , 2011, 7, 544.	3.2	284
72	Independently Evolved Virulence Effectors Converge onto Hubs in a Plant Immune System Network. <i>Science</i> , 2011, 333, 596-601.	6.0	776

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73	Identification of Neuronal RNA Targets of TDP-43-containing Ribonucleoprotein Complexes. <i>Journal of Biological Chemistry</i> , 2011, 286, 1204-1215.	1.6	366
74	PERSONALIZED MEDICINE: FROM GENOTYPES AND MOLECULAR PHENOTYPES TOWARDS COMPUTED THERAPY. , 2011, , .		0
75	Knocking out multigene redundancies via cycles of sexual assortment and fluorescence selection. <i>Nature Methods</i> , 2011, 8, 159-164.	9.0	74
76	Next-generation sequencing to generate interactome datasets. <i>Nature Methods</i> , 2011, 8, 478-480.	9.0	258
77	Reconstitution of human RNA interference in budding yeast. <i>Nucleic Acids Research</i> , 2011, 39, e43-e43.	6.5	26
78	Discovering the Targets of Drugs Via Computational Systems Biology. <i>Journal of Biological Chemistry</i> , 2011, 286, 23653-23658.	1.6	29
79	Genome Analysis Reveals Interplay between 5'UTR Introns and Nuclear mRNA Export for Secretory and Mitochondrial Genes. <i>PLoS Genetics</i> , 2011, 7, e1001366.	1.5	73
80	The Genetic Landscape of a Cell. <i>Science</i> , 2010, 327, 425-431.	6.0	1,937
81	Metabolic Signatures of Exercise in Human Plasma. <i>Science Translational Medicine</i> , 2010, 2, 33ra37.	5.8	337
82	The Tandem Inversion Duplication in <i>Salmonella enterica</i> : Selection Drives Unstable Precursors to Final Mutation Types. <i>Genetics</i> , 2010, 185, 65-80.	1.2	43
83	FuncBase : a resource for quantitative gene function annotation. <i>Bioinformatics</i> , 2010, 26, 1806-1807.	1.8	14
84	Interpreting Metabolomic Profiles using Unbiased Pathway Models. <i>PLoS Computational Biology</i> , 2010, 6, e1000692.	1.5	52
85	Absence of Evidence for MHC-Dependent Mate Selection within HapMap Populations. <i>PLoS Genetics</i> , 2010, 6, e1000925.	1.5	35
86	Numerous Conserved and Divergent MicroRNAs Expressed by Herpes Simplex Viruses 1 and 2. <i>Journal of Virology</i> , 2010, 84, 4659-4672.	1.5	145
87	Genome-wide functional analysis of human 5' untranslated region introns. <i>Genome Biology</i> , 2010, 11, R29.	13.9	68
88	A Genome-Wide Gene Function Prediction Resource for <i>Drosophila melanogaster</i> . <i>PLoS ONE</i> , 2010, 5, e12139.	1.1	17
89	Large-scale RACE approach for proactive experimental definition of <i>C. elegans</i> ORFeome. <i>Genome Research</i> , 2009, 19, 2334-2342.	2.4	12
90	Quantitative phenotyping via deep barcode sequencing. <i>Genome Research</i> , 2009, 19, 1836-1842.	2.4	275

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91	Next generation software for functional trend analysis. <i>Bioinformatics</i> , 2009, 25, 3043-3044.	1.8	248
92	Pathways of the Heart. <i>Circulation: Cardiovascular Genetics</i> , 2009, 2, 303-305.	5.1	2
93	Q&A: Epistasis. <i>Journal of Biology</i> , 2009, 8, 35.	2.7	32
94	Empirically controlled mapping of the <i>Caenorhabditis elegans</i> protein-protein interactome network. <i>Nature Methods</i> , 2009, 6, 47-54.	9.0	260
95	An empirical framework for binary interactome mapping. <i>Nature Methods</i> , 2009, 6, 83-90.	9.0	800
96	An experimentally derived confidence score for binary protein-protein interactions. <i>Nature Methods</i> , 2009, 6, 91-97.	9.0	397
97	Literature-curated protein interaction datasets. <i>Nature Methods</i> , 2009, 6, 39-46.	9.0	288
98	Biomolecular Network Structure and Function. , 2009, , 570-589.		0
99	Isoform discovery by targeted cloning, 'deep-well' pooling and parallel sequencing. <i>Nature Methods</i> , 2008, 5, 597-600.	9.0	30
100	High-Quality Binary Protein Interaction Map of the Yeast Interactome Network. <i>Science</i> , 2008, 322, 104-110.	6.0	1,297
101	A race through the maze of genomic evidence. <i>Genome Biology</i> , 2008, 9, S1.	3.8	11
102	Combining guilt-by-association and guilt-by-profiling to predict <i>Saccharomyces cerevisiae</i> gene function. <i>Genome Biology</i> , 2008, 9, S7.	13.9	78
103	A critical assessment of <i>Mus musculus</i> gene function prediction using integrated genomic evidence. <i>Genome Biology</i> , 2008, 9, S2.	13.9	214
104	An en masse phenotype and function prediction system for <i>Mus musculus</i> . <i>Genome Biology</i> , 2008, 9, S8.	13.9	20
105	Chemical substructures that enrich for biological activity. <i>Bioinformatics</i> , 2008, 24, 2518-2525.	1.8	279
106	A Protein Domain-Based Interactome Network for <i>C. elegans</i> Early Embryogenesis. <i>Cell</i> , 2008, 134, 534-545.	13.5	196
107	A <i>C. elegans</i> genome-scale microRNA network contains composite feedback motifs with high flux capacity. <i>Genes and Development</i> , 2008, 22, 2535-2549.	2.7	207
108	Challenges in translating plasma proteomics from bench to bedside: update from the NHLBI Clinical Proteomics Programs. <i>American Journal of Physiology - Lung Cellular and Molecular Physiology</i> , 2008, 295, L16-L22.	1.3	73

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109	The Synergizer service for translating gene, protein and other biological identifiers. <i>Bioinformatics</i> , 2008, 24, 2272-2273.	1.8	48
110	Defining genetic interaction. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 3461-3466.	3.3	399
111	Metabolite profiling of blood from individuals undergoing planned myocardial infarction reveals early markers of myocardial injury. <i>Journal of Clinical Investigation</i> , 2008, 118, 3503-3512.	3.9	244
112	Systematic quantitative function annotation of mouse genes. <i>FASEB Journal</i> , 2008, 22, 100.3.	0.2	0
113	Confirmation of Organized Modularity in the Yeast Interactome. <i>PLoS Biology</i> , 2007, 5, e153.	2.6	86
114	Genetic interaction screens advance in reverse. <i>Genes and Development</i> , 2007, 21, 137-142.	2.7	8
115	Functional Specificity among Ribosomal Proteins Regulates Gene Expression. <i>Cell</i> , 2007, 131, 557-571.	13.5	323
116	Genome-scale analysis of in vivo spatiotemporal promoter activity in <i>Caenorhabditis elegans</i> . <i>Nature Biotechnology</i> , 2007, 25, 663-668.	9.4	286
117	Systematic pathway analysis using high-resolution fitness profiling of combinatorial gene deletions. <i>Nature Genetics</i> , 2007, 39, 199-206.	9.4	294
118	Probabilistic Paths for Protein Complex Inference. <i>Lecture Notes in Computer Science</i> , 2007, , 14-28.	1.0	6
119	Using High-Throughput Screening Data To Discriminate Compounds with Single-Target Effects from Those with Side Effects. <i>Journal of Chemical Information and Modeling</i> , 2006, 46, 1549-1562.	2.5	26
120	Systematic genetics swims forward elegantly. <i>Molecular Systems Biology</i> , 2006, 2, 48.	3.2	2
121	Mammalian ultraconserved elements are strongly depleted among segmental duplications and copy number variants. <i>Nature Genetics</i> , 2006, 38, 1216-1220.	9.4	105
122	Query Chem: a Google-powered web search combining text and chemical structures. <i>Bioinformatics</i> , 2006, 22, 1670-1673.	1.8	16
123	Predictive models of molecular machines involved in <i>Caenorhabditis elegans</i> early embryogenesis. <i>Nature</i> , 2005, 436, 861-865.	13.7	260
124	Towards a proteome-scale map of the human protein-protein interaction network. <i>Nature</i> , 2005, 437, 1173-1178.	13.7	2,676
125	Discovering functional relationships: biochemistry versus genetics. <i>Trends in Genetics</i> , 2005, 21, 424-427.	2.9	22
126	Motifs, themes and thematic maps of an integrated <i>Saccharomyces cerevisiae</i> interaction network. <i>Journal of Biology</i> , 2005, 4, 6.	2.7	154

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127	Transcriptional Compensation for Gene Loss Plays a Minor Role in Maintaining Genetic Robustness in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2005, 171, 829-833.	1.2	22
128	Genomewide Identification of Sko1 Target Promoters Reveals a Regulatory Network That Operates in Response to Osmotic Stress in <i>Saccharomyces cerevisiae</i> . <i>Eukaryotic Cell</i> , 2005, 4, 1343-1352.	3.4	68
129	Metabolomic Identification of Novel Biomarkers of Myocardial Ischemia. <i>Circulation</i> , 2005, 112, 3868-3875.	1.6	443
130	Chipper: discovering transcription-factor targets from chromatin immunoprecipitation microarrays using variance stabilization. <i>Genome Biology</i> , 2005, 6, R96.	13.9	37
131	Prediction of similarly acting cis-regulatory modules by subsequence profiling and comparative genomics in <i>Drosophila melanogaster</i> and <i>D.pseudoobscura</i> . <i>Bioinformatics</i> , 2004, 20, 2738-2750.	1.8	59
132	Predicting Protein Complex Membership Using Probabilistic Network Reliability. <i>Genome Research</i> , 2004, 14, 1170-1175.	2.4	166
133	Intensity-based protein identification by machine learning from a library of tandem mass spectra. <i>Nature Biotechnology</i> , 2004, 22, 214-219.	9.4	294
134	Evidence for dynamically organized modularity in the yeast protein-protein interaction network. <i>Nature</i> , 2004, 430, 88-93.	13.7	1,683
135	Predicting co-complexed protein pairs using genomic and proteomic data integration. <i>BMC Bioinformatics</i> , 2004, 5, 38.	1.2	139
136	Global Mapping of the Yeast Genetic Interaction Network. <i>Science</i> , 2004, 303, 808-813.	6.0	1,908
137	SILVER helps assign peptides to tandem mass spectra using intensity-based scoring. <i>Journal of the American Society for Mass Spectrometry</i> , 2004, 15, 910-912.	1.2	24
138	A Map of the Interactome Network of the Metazoan <i>C. elegans</i> . <i>Science</i> , 2004, 303, 540-543.	6.0	1,587
139	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
140	Predicting Gene Function From Patterns of Annotation. <i>Genome Research</i> , 2003, 13, 896-904.	2.4	121
141	Characterizing gene sets with FuncAssociate. <i>Bioinformatics</i> , 2003, 19, 2502-2504.	1.8	431
142	GoFish finds genes with combinations of Gene Ontology attributes. <i>Bioinformatics</i> , 2003, 19, 788-789.	1.8	14
143	Latent Herpes Simplex Virus Infection of Sensory Neurons Alters Neuronal Gene Expression. <i>Journal of Virology</i> , 2003, 77, 9533-9541.	1.5	58
144	Assessing experimentally derived interactions in a small world. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 4372-4376.	3.3	387

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145	Predicting phenotype from patterns of annotation. <i>Bioinformatics</i> , 2003, 19, i183-i189.	1.8	27
146	Regulating General Mutation Rates: Examination of the Hypermutable State Model for Cairnsian Adaptive Mutation. <i>Genetics</i> , 2003, 163, 1483-1496.	1.2	55
147	Judging the Quality of Gene Expression-Based Clustering Methods Using Gene Annotation. <i>Genome Research</i> , 2002, 12, 1574-1581.	2.4	259
148	The Genome-Wide Localization of Rsc9, a Component of the RSC Chromatin-Remodeling Complex, Changes in Response to Stress. <i>Molecular Cell</i> , 2002, 9, 563-573.	4.5	135
149	Bringing Out the Best Features of Expression Data. <i>Genome Research</i> , 2001, 11, 1801-1802.	2.4	10
150	Finding DNA regulatory motifs within unaligned noncoding sequences clustered by whole-genome mRNA quantitation. <i>Nature Biotechnology</i> , 1998, 16, 939-945.	9.4	835