

# Mohan Madan Babu

## List of Publications by Year in descending order

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149  
papers

23,052  
citations

17405

63  
h-index

9073

144  
g-index

163  
all docs

163  
docs citations

163  
times ranked

31895  
citing authors

#	ARTICLE	IF	CITATIONS
1	The Transcriptional Landscape of the Mammalian Genome. <i>Science</i> , 2005, 309, 1559-1563.	6.0	3,227
2	Classification of Intrinsically Disordered Regions and Proteins. <i>Chemical Reviews</i> , 2014, 114, 6589-6631.	23.0	1,618
3	Molecular signatures of G-protein-coupled receptors. <i>Nature</i> , 2013, 494, 185-194.	13.7	1,298
4	The genome of the social amoeba <i>Dictyostelium discoideum</i> . <i>Nature</i> , 2005, 435, 43-57.	13.7	1,179
5	Genomic analysis of regulatory network dynamics reveals large topological changes. <i>Nature</i> , 2004, 431, 308-312.	13.7	921
6	Structure and evolution of transcriptional regulatory networks. <i>Current Opinion in Structural Biology</i> , 2004, 14, 283-291.	2.6	683
7	Intrinsically disordered proteins: regulation and disease. <i>Current Opinion in Structural Biology</i> , 2011, 21, 432-440.	2.6	518
8	Gene regulatory network growth by duplication. <i>Nature Genetics</i> , 2004, 36, 492-496.	9.4	475
9	Pharmacogenomics of GPCR Drug Targets. <i>Cell</i> , 2018, 172, 41-54.e19.	13.5	464
10	Mechanisms of signalling and biased agonism in G protein-coupled receptors. <i>Nature Reviews Molecular Cell Biology</i> , 2018, 19, 638-653.	16.1	457
11	A Million Peptide Motifs for the Molecular Biologist. <i>Molecular Cell</i> , 2014, 55, 161-169.	4.5	429
12	Discovery of the principal specific transcription factors of Apicomplexa and their implication for the evolution of the AP2-integrase DNA binding domains. <i>Nucleic Acids Research</i> , 2005, 33, 3994-4006.	6.5	426
13	Tight Regulation of Unstructured Proteins: From Transcript Synthesis to Protein Degradation. <i>Science</i> , 2008, 322, 1365-1368.	6.0	419
14	Tissue-Specific Splicing of Disordered Segments that Embed Binding Motifs Rewires Protein Interaction Networks. <i>Molecular Cell</i> , 2012, 46, 871-883.	4.5	344
15	Common activation mechanism of class A GPCRs. <i>ELife</i> , 2019, 8, .	2.8	339
16	An Expanded Oct4 Interaction Network: Implications for Stem Cell Biology, Development, and Disease. <i>Cell Stem Cell</i> , 2010, 6, 382-395.	5.2	338
17	The contribution of intrinsically disordered regions to protein function, cellular complexity, and human disease. <i>Biochemical Society Transactions</i> , 2016, 44, 1185-1200.	1.6	323
18	Selectivity determinants of GPCR's G-protein binding. <i>Nature</i> , 2017, 545, 317-322.	13.7	297

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19	Universal allosteric mechanism for G $\beta$ activation by GPCRs. <i>Nature</i> , 2015, 524, 173-179.	13.7	291
20	Evolution of transcription factors and the gene regulatory network in <i>Escherichia coli</i> . <i>Nucleic Acids Research</i> , 2003, 31, 1234-1244.	6.5	283
21	Independence of Repressive Histone Marks and Chromatin Compaction during Senescent Heterochromatic Layer Formation. <i>Molecular Cell</i> , 2012, 47, 203-214.	4.5	258
22	A Database of Bacterial Lipoproteins (DOLOP) with Functional Assignments to Predicted Lipoproteins. <i>Journal of Bacteriology</i> , 2006, 188, 2761-2773.	1.0	255
23	Evolutionary Dynamics of Prokaryotic Transcriptional Regulatory Networks. <i>Journal of Molecular Biology</i> , 2006, 358, 614-633.	2.0	254
24	Diverse activation pathways in class A GPCRs converge near the G-protein-coupling region. <i>Nature</i> , 2016, 536, 484-487.	13.7	245
25	Interplay between gene expression noise and regulatory network architecture. <i>Trends in Genetics</i> , 2012, 28, 221-232.	2.9	235
26	High-affinity DNA binding sites for H-NS provide a molecular basis for selective silencing within proteobacterial genomes. <i>Nucleic Acids Research</i> , 2007, 35, 6330-6337.	6.5	231
27	What are TMs in a name? Why these proteins are intrinsically disordered. <i>Intrinsically Disordered Proteins</i> , 2013, 1, e24157.	1.9	226
28	Comprehensive Analysis of Combinatorial Regulation using the Transcriptional Regulatory Network of Yeast. <i>Journal of Molecular Biology</i> , 2006, 360, 213-227.	2.0	207
29	Versatility from Protein Disorder. <i>Science</i> , 2012, 337, 1460-1461.	6.0	206
30	Cells alter their tRNA abundance to selectively regulate protein synthesis during stress conditions. <i>Science Signaling</i> , 2018, 11, .	1.6	201
31	Intrinsically Disordered Segments Affect Protein Half-Life in the Cell and during Evolution. <i>Cell Reports</i> , 2014, 8, 1832-1844.	2.9	192
32	Evolving nature of the AP2 $\beta$ -appendage hub during clathrin-coated vesicle endocytosis. <i>EMBO Journal</i> , 2004, 23, 4371-4383.	3.5	177
33	Mechanistic Insight into Site-Restricted Monoubiquitination of FANCD2 by Ube2t, FANCL, and FANCI. <i>Molecular Cell</i> , 2008, 32, 767-777.	4.5	170
34	Alternative splicing of intrinsically disordered regions and rewiring of protein interactions. <i>Current Opinion in Structural Biology</i> , 2013, 23, 443-450.	2.6	166
35	The rules of disorder or why disorder rules. <i>Progress in Biophysics and Molecular Biology</i> , 2009, 99, 94-103.	1.4	160
36	The natural history of the WRKY GCM1 zinc fingers and the relationship between transcription factors and transposons. <i>Nucleic Acids Research</i> , 2006, 34, 6505-6520.	6.5	157

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37	Promiscuity as a functional trait: intrinsically disordered regions as central players of interactomes. <i>Biochemical Journal</i> , 2013, 454, 361-369.	1.7	156
38	Structural polymorphism in the N-terminal oligomerization domain of NPM1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 4466-4471.	3.3	150
39	Genomic analysis reveals a tight link between transcription factor dynamics and regulatory network architecture. <i>Molecular Systems Biology</i> , 2009, 5, 294.	3.2	146
40	Cross-species chemogenomic profiling reveals evolutionarily conserved drug mode of action. <i>Molecular Systems Biology</i> , 2010, 6, 451.	3.2	143
41	High-throughput discovery of functional disordered regions: investigation of transactivation domains. <i>Molecular Systems Biology</i> , 2018, 14, e8190.	3.2	138
42	Discovering and understanding oncogenic gene fusions through data intensive computational approaches. <i>Nucleic Acids Research</i> , 2016, 44, 4487-4503.	6.5	133
43	Controlling entropy to tune the functions of intrinsically disordered regions. <i>Current Opinion in Structural Biology</i> , 2014, 26, 62-72.	2.6	127
44	Simultaneous quantification of protein order and disorder. <i>Nature Chemical Biology</i> , 2017, 13, 339-342.	3.9	113
45	Conservation of gene co-regulation in prokaryotes and eukaryotes. <i>Trends in Biotechnology</i> , 2002, 20, 407-410.	4.9	111
46	Sequence composition of disordered regions fine-tunes protein half-life. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 214-221.	3.6	109
47	Variable Glutamine-Rich Repeats Modulate Transcription Factor Activity. <i>Molecular Cell</i> , 2015, 59, 615-627.	4.5	103
48	Visualization and analysis of non-covalent contacts using the Protein Contacts Atlas. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 185-194.	3.6	103
49	Subunit-selective N-terminal domain associations organize the formation of AMPA receptor heteromers. <i>EMBO Journal</i> , 2011, 30, 959-971.	3.5	99
50	GPCR activation mechanisms across classes and macro/microscales. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 879-888.	3.6	98
51	Structural and functional characterization of G protein-coupled receptors with deep mutational scanning. <i>ELife</i> , 2020, 9, .	2.8	91
52	Cellular Strategies for Regulating Functional and Nonfunctional Protein Aggregation. <i>Cell Reports</i> , 2012, 2, 1425-1437.	2.9	88
53	The HIRAN Domain and Recruitment of Chromatin Remodeling and Repair activities to Damaged DNA. <i>Cell Cycle</i> , 2006, 5, 775-782.	1.3	87
54	Molecular mechanism of modulating arrestin conformation by GPCR phosphorylation. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 538-545.	3.6	87

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55	Combinatorial expression of GPCR isoforms affects signalling and drug responses. <i>Nature</i> , 2020, 587, 650-656.	13.7	87
56	Dissecting the expression dynamics of RNA-binding proteins in posttranscriptional regulatory networks. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 20300-20305.	3.3	85
57	A Global Map of G Protein Signaling Regulation by RGS Proteins. <i>Cell</i> , 2020, 183, 503-521.e19.	13.5	82
58	Conservation and Evolutionary Dynamics of the <i>agr</i> Cell-to-Cell Communication System across Firmicutes. <i>Journal of Bacteriology</i> , 2008, 190, 743-746.	1.0	80
59	A C <sup>α</sup> -H <sup>α</sup> -O Hydrogen Bond Stabilized Polypeptide Chain Reversal Motif at the C Terminus of Helices in Proteins. <i>Journal of Molecular Biology</i> , 2002, 322, 871-880.	2.0	75
60	Functional determinants of transcription factors in <i>Escherichia coli</i> : protein families and binding sites. <i>Trends in Genetics</i> , 2003, 19, 75-79.	2.9	75
61	Context-Specific Striatal Astrocyte Molecular Responses Are Phenotypically Exploitable. <i>Neuron</i> , 2020, 108, 1146-1162.e10.	3.8	73
62	Transcriptional regulation constrains the organization of genes on eukaryotic chromosomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 15761-15766.	3.3	72
63	NCI: a server to identify non-canonical interactions in protein structures. <i>Nucleic Acids Research</i> , 2003, 31, 3345-3348.	6.5	68
64	Whole Genome Sequencing Highlights Genetic Changes Associated with Laboratory Domestication of <i>C. elegans</i> . <i>PLoS ONE</i> , 2010, 5, e13922.	1.1	68
65	Structured and disordered facets of the GPCR fold. <i>Current Opinion in Structural Biology</i> , 2014, 27, 129-137.	2.6	68
66	Lipolysis drives expression of the constitutively active receptor GPR3 to induce adipose thermogenesis. <i>Cell</i> , 2021, 184, 3502-3518.e33.	13.5	68
67	Human Inositol Polyphosphate Multikinase Regulates Transcript-Selective Nuclear mRNA Export to Preserve Genome Integrity. <i>Molecular Cell</i> , 2013, 51, 737-750.	4.5	65
68	Uncovering a Hidden Distributed Architecture Behind Scale-free Transcriptional Regulatory Networks. <i>Journal of Molecular Biology</i> , 2006, 360, 204-212.	2.0	64
69	Molecular Principles of Gene Fusion Mediated Rewiring of Protein Interaction Networks in Cancer. <i>Molecular Cell</i> , 2016, 63, 579-592.	4.5	63
70	Evolution of fold switching in a metamorphic protein. <i>Science</i> , 2021, 371, 86-90.	6.0	59
71	Probing G <sub>i</sub> 1 protein activation at single amino acid resolution. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 686-694.	3.6	58
72	Asymmetric mRNA localization contributes to fidelity and sensitivity of spatially localized systems. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 833-839.	3.6	57

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73	Conserved Sequence Preferences Contribute to Substrate Recognition by the Proteasome. <i>Journal of Biological Chemistry</i> , 2016, 291, 14526-14539.	1.6	56
74	A conserved molecular switch in Class F receptors regulates receptor activation and pathway selection. <i>Nature Communications</i> , 2019, 10, 667.	5.8	56
75	Principles of transcriptional regulation and evolution of the metabolic system in <i>E. coli</i> . <i>Genome Research</i> , 2009, 19, 79-91.	2.4	55
76	Genomic neighbourhood and the regulation of gene expression. <i>Current Opinion in Cell Biology</i> , 2010, 22, 326-333.	2.6	55
77	Affinity and competition for TBP are molecular determinants of gene expression noise. <i>Nature Communications</i> , 2016, 7, 10417.	5.8	55
78	Interplay Between Network Structures, Regulatory Modes and Sensing Mechanisms of Transcription Factors in the Transcriptional Regulatory Network of <i>E. coli</i> . <i>Journal of Molecular Biology</i> , 2007, 372, 1108-1122.	2.0	53
79	Constraints and consequences of the emergence of amino acid repeats in eukaryotic proteins. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 765-777.	3.6	53
80	Dissecting ensemble networks in ES cell populations reveals micro-heterogeneity underlying pluripotency. <i>Molecular BioSystems</i> , 2012, 8, 744.	2.9	52
81	Xpf and Not the Fanconi Anaemia Proteins or Rev3 Accounts for the Extreme Resistance to Cisplatin in <i>Dictyostelium discoideum</i> . <i>PLoS Genetics</i> , 2009, 5, e1000645.	1.5	52
82	Recognition Pliability Is Coupled to Structural Heterogeneity: A Calmodulin Intrinsically Disordered Binding Region Complex. <i>Structure</i> , 2012, 20, 522-533.	1.6	51
83	Revealing the Determinants of Widespread Alternative Splicing Perturbation in Cancer. <i>Cell Reports</i> , 2017, 21, 798-812.	2.9	51
84	Fc $\gamma$ 3 Receptor I Alpha Chain (CD64) Expression in Macrophages Is Critical for the Onset of Meningitis by <i>Escherichia coli</i> K1. <i>PLoS Pathogens</i> , 2010, 6, e1001203.	2.1	45
85	The impact of genomic neighborhood on the evolution of human and chimpanzee transcriptome. <i>Genome Research</i> , 2009, 19, 785-794.	2.4	44
86	A time-invariant principle of genome evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 13004-13009.	3.3	44
87	Adaptive evolution by optimizing expression levels in different environments. <i>Trends in Microbiology</i> , 2006, 14, 11-14.	3.5	43
88	Eukaryotic gene regulation in three dimensions and its impact on genome evolution. <i>Current Opinion in Genetics and Development</i> , 2008, 18, 571-582.	1.5	43
89	Cotranslational protein assembly imposes evolutionary constraints on homomeric proteins. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 279-288.	3.6	43
90	Capturing dynamic protein interactions. <i>Science</i> , 2018, 359, 1105-1106.	6.0	42

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91	How do disordered regions achieve comparable functions to structured domains?. <i>Protein Science</i> , 2015, 24, 909-922.	3.1	41
92	Function and Regulation of Phase-Separated Biological Condensates. <i>Biochemistry</i> , 2018, 57, 2452-2461.	1.2	41
93	Integrated Genomic Analysis Identifies <i>UBTF</i> Tandem Duplications as a Recurrent Lesion in Pediatric Acute Myeloid Leukemia. <i>Blood Cancer Discovery</i> , 2022, 3, 194-207.	2.6	38
94	The Hidden Codes That Shape Protein Evolution. <i>Science</i> , 2013, 342, 1325-1326.	6.0	37
95	Human MC4R variants affect endocytosis, trafficking and dimerization revealing multiple cellular mechanisms involved in weight regulation. <i>Cell Reports</i> , 2021, 34, 108862.	2.9	37
96	Methods to Reconstruct and Compare Transcriptional Regulatory Networks. <i>Methods in Molecular Biology</i> , 2009, 541, 163-180.	0.4	36
97	The chemotherapeutic CX-5461 primarily targets TOP2B and exhibits selective activity in high-risk neuroblastoma. <i>Nature Communications</i> , 2021, 12, 6468.	5.8	35
98	Did the loss of sigma factors initiate pseudogene accumulation in <i>M. leprae</i> ?. <i>Trends in Microbiology</i> , 2003, 11, 59-61.	3.5	34
99	Disorder-to-order transition in PE/PPE proteins of <i>Mycobacterium tuberculosis</i> augments the pro-pathogen immune response. <i>FEBS Open Bio</i> , 2020, 10, 70-85.	1.0	33
100	Chemogenomics and biotechnology. <i>Trends in Biotechnology</i> , 2008, 26, 252-258.	4.9	32
101	Evolutionary selection for protein aggregation. <i>Biochemical Society Transactions</i> , 2012, 40, 1032-1037.	1.6	32
102	A complex network framework for unbiased statistical analyses of DNA-DNA contact maps. <i>Nucleic Acids Research</i> , 2013, 41, 701-710.	6.5	32
103	Amino acid homorepeats in proteins. <i>Nature Reviews Chemistry</i> , 2020, 4, 420-434.	13.8	31
104	TAT-Pathway-Dependent Lipoproteins as a Niche-Based Adaptation in Prokaryotes. <i>Journal of Molecular Evolution</i> , 2010, 70, 359-370.	0.8	29
105	Solitary and Repetitive Binding Motifs for the AP2 Complex $\pm$ -Appendage in Amphiphysin and Other Accessory Proteins. <i>Journal of Biological Chemistry</i> , 2008, 283, 5099-5109.	1.6	26
106	DNA Sequence Preferences of Transcriptional Activators Correlate More Strongly than Repressors with Nucleosomes. <i>Molecular Cell</i> , 2012, 47, 183-192.	4.5	26
107	Registering $\alpha$ -helices and $\beta$ -strands using backbone C-H $\cdots$ O interactions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 51, 167-171.	1.5	25
108	Computational approaches to study transcriptional regulation. <i>Biochemical Society Transactions</i> , 2008, 36, 758-765.	1.6	25

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109	Investigations on C $\pi$ -H $\pi$ interactions in RNA binding proteins. <i>International Journal of Biological Macromolecules</i> , 2007, 41, 251-259.	3.6	24
110	Intrinsically Disordered Proteins Adaptively Reorganize Cellular Matter During Stress. <i>Trends in Biochemical Sciences</i> , 2017, 42, 410-412.	3.7	24
111	Discovery and Genetic Code Expansion of a Polyethylene Terephthalate (PET) Hydrolase from the Human Saliva Metagenome for the Degradation and Biofunctionalization of PET. <i>Angewandte Chemie - International Edition</i> , 2022, 61, .	7.2	24
112	Exploring the environmental preference of weak interactions in ( $\beta$ / $\alpha$ ) <sub>8</sub> barrel proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 65, 75-86.	1.5	21
113	Structure, evolution and dynamics of transcriptional regulatory networks. <i>Biochemical Society Transactions</i> , 2010, 38, 1155-1178.	1.6	21
114	Human Diseases from Gain-of-Function Mutations in Disordered Protein Regions. <i>Cell</i> , 2018, 175, 40-42.	13.5	21
115	Molecular Signatures of Fusion Proteins in Cancer. <i>ACS Pharmacology and Translational Science</i> , 2019, 2, 122-133.	2.5	20
116	Combinatorial multivalent interactions drive cooperative assembly of the COPII coat. <i>Journal of Cell Biology</i> , 2020, 219, .	2.3	20
117	A community effort to bring structure to disorder. <i>Nature Methods</i> , 2021, 18, 454-455.	9.0	19
118	Comparison of transcription regulatory interactions inferred from high-throughput methods: what do they reveal?. <i>Trends in Genetics</i> , 2008, 24, 319-323.	2.9	18
119	p53 shapes genome-wide and cell type-specific changes in microRNA expression during the human DNA damage response. <i>Cell Cycle</i> , 2014, 13, 2572-2586.	1.3	18
120	Molecular determinants underlying functional innovations of TBP and their impact on transcription initiation. <i>Nature Communications</i> , 2020, 11, 2384.	5.8	17
121	Conformational selection guides $\beta$ -arrestin recruitment at a biased G protein-coupled receptor. <i>Science</i> , 2022, 377, 222-228.	6.0	16
122	Shigellaapyrase - a novel variant of bacterial acid phosphatases?. <i>FEBS Letters</i> , 2002, 512, 8-12.	1.3	14
123	Transcript stability in the protein interaction network of <i>Escherichia coli</i> . <i>Molecular BioSystems</i> , 2009, 5, 154-162.	2.9	14
124	Duel of the fates: the role of transcriptional circuits and noise in CD4+ cells. <i>Current Opinion in Cell Biology</i> , 2012, 24, 350-358.	2.6	14
125	Classifying pairs with trees for supervised biological network inference. <i>Molecular BioSystems</i> , 2015, 11, 2116-2125.	2.9	13
126	Pathway perturbations in signaling networks: Linking genotype to phenotype. <i>Seminars in Cell and Developmental Biology</i> , 2020, 99, 3-11.	2.3	13



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127	Characterizing Interhelical Interactions of G-Protein Coupled Receptors with the Fragment Molecular Orbital Method. <i>Journal of Chemical Theory and Computation</i> , 2020, 16, 2814-2824.	2.3	13
128	CCL22 mutations drive natural killer cell lymphoproliferative disease by deregulating microenvironmental crosstalk. <i>Nature Genetics</i> , 2022, 54, 637-648.	9.4	13
129	The efficiency of mitochondrial electron transport chain is increased in the long-lived <i>Saccharomyces cerevisiae</i> . <i>Aging Cell</i> , 2009, 8, 643-653.	3.0	12
130	Molecular Deconvolution Platform to Establish Disease Mechanisms by Surveying GPCR Signaling. <i>Cell Reports</i> , 2018, 24, 557-568.e5.	2.9	12
131	Biological impact of mutually exclusive exon switching. <i>PLoS Computational Biology</i> , 2021, 17, e1008708.	1.5	12
132	An intrinsically disordered proteins community for ELIXIR. <i>F1000Research</i> , 2019, 8, 1753.	0.8	12
133	Optimizing membrane-protein biogenesis through nonoptimal-codon usage. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 1023-1025.	3.6	11
134	The fitness cost and benefit of phase-separated protein deposits. <i>Molecular Systems Biology</i> , 2019, 15, e8075.	3.2	10
135	Proteome response at the edge of protein aggregation. <i>Open Biology</i> , 2015, 5, 140221.	1.5	9
136	Evolution of eukaryotic genome architecture: Insights from the study of a rapidly evolving metazoan, <i>Oikopleura dioica</i> . <i>BioEssays</i> , 2011, 33, 592-601.	1.2	8
137	Estimating the Prevalence and Regulatory Potential of the Telomere Looping Effect in Yeast Transcription Regulation. <i>Cell Cycle</i> , 2006, 5, 2354-2363.	1.3	7
138	Editorial overview: Linking protein sequence and structural changes to function in the era of next-generation sequencing. <i>Current Opinion in Structural Biology</i> , 2015, 32, viii-x.	2.6	5
139	GenCompass: a universal system for analysing gene expression for any genome. <i>Trends in Biotechnology</i> , 2004, 22, 552-555.	4.9	3
140	Functional and Transcriptional Coherency of Modules in the Human Protein Interaction Network. <i>Journal of Integrative Bioinformatics</i> , 2007, 4, 198-207.	1.0	3
141	Scaling up synthetic gene circuits. <i>Nature Nanotechnology</i> , 2010, 5, 631-633.	15.6	3
142	Reconfiguring Regulation. <i>Science</i> , 2012, 335, 1050-1051.	6.0	3
143	From prioritisation to understanding: mechanistic predictions of variant effects. <i>Molecular Systems Biology</i> , 2018, 14, e8741.	3.2	2
144	Biophysicists' outstanding response to Covid-19. <i>Biophysical Journal</i> , 2021, 120, E1-E2.	0.2	2

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145	Biophysicistsâ€™ continued outstanding response to COVID-19. Biophysical Journal, 2021, 120, E1.	0.2	2
146	Discovery and Genetic Code Expansion of a Polyethylene Terephthalate (PET) Hydrolase from the Human Saliva Metagenome for the Degradation and Bioâ€Functionalization of PET. Angewandte Chemie, 0, , .	1.6	2
147	Structure and Evolution of Transcriptional Regulatory Networks. , 2014, , 1-16.		1
148	Enabling next generation systems biology: a conversation with M. Madan Babu. Molecular Systems Biology, 2019, 15, e9376.	3.2	1
149	A methodology to infer gene networks from spatial patterns of expression â€“ an application to fluorescence in situ hybridization images. Molecular BioSystems, 2013, 9, 1926.	2.9	0