

Mohan Madan Babu

List of Publications by Year in descending order

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149
papers

23,052
citations

17440

63
h-index

9103

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.	12.6	3,227
2	Classification of Intrinsically Disordered Regions and Proteins. <i>Chemical Reviews</i> , 2014, 114, 6589-6631.	47.7	1,618
3	Molecular signatures of G-protein-coupled receptors. <i>Nature</i> , 2013, 494, 185-194.	27.8	1,298
4	The genome of the social amoeba <i>Dictyostelium discoideum</i> . <i>Nature</i> , 2005, 435, 43-57.	27.8	1,179
5	Genomic analysis of regulatory network dynamics reveals large topological changes. <i>Nature</i> , 2004, 431, 308-312.	27.8	921
6	Structure and evolution of transcriptional regulatory networks. <i>Current Opinion in Structural Biology</i> , 2004, 14, 283-291.	5.7	683
7	Intrinsically disordered proteins: regulation and disease. <i>Current Opinion in Structural Biology</i> , 2011, 21, 432-440.	5.7	518
8	Gene regulatory network growth by duplication. <i>Nature Genetics</i> , 2004, 36, 492-496.	21.4	475
9	Pharmacogenomics of GPCR Drug Targets. <i>Cell</i> , 2018, 172, 41-54.e19.	28.9	464
10	Mechanisms of signalling and biased agonism in G protein-coupled receptors. <i>Nature Reviews Molecular Cell Biology</i> , 2018, 19, 638-653.	37.0	457
11	A Million Peptide Motifs for the Molecular Biologist. <i>Molecular Cell</i> , 2014, 55, 161-169.	9.7	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.	14.5	426
13	Tight Regulation of Unstructured Proteins: From Transcript Synthesis to Protein Degradation. <i>Science</i> , 2008, 322, 1365-1368.	12.6	419
14	Tissue-Specific Splicing of Disordered Segments that Embed Binding Motifs Rewires Protein Interaction Networks. <i>Molecular Cell</i> , 2012, 46, 871-883.	9.7	344
15	Common activation mechanism of class A GPCRs. <i>ELife</i> , 2019, 8, .	6.0	339
16	An Expanded Oct4 Interaction Network: Implications for Stem Cell Biology, Development, and Disease. <i>Cell Stem Cell</i> , 2010, 6, 382-395.	11.1	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.	3.4	323
18	Selectivity determinants of GPCR's G-protein binding. <i>Nature</i> , 2017, 545, 317-322.	27.8	297

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19	Universal allosteric mechanism for G β activation by GPCRs. <i>Nature</i> , 2015, 524, 173-179.	27.8	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.	14.5	283
21	Independence of Repressive Histone Marks and Chromatin Compaction during Senescent Heterochromatic Layer Formation. <i>Molecular Cell</i> , 2012, 47, 203-214.	9.7	258
22	A Database of Bacterial Lipoproteins (DOLOP) with Functional Assignments to Predicted Lipoproteins. <i>Journal of Bacteriology</i> , 2006, 188, 2761-2773.	2.2	255
23	Evolutionary Dynamics of Prokaryotic Transcriptional Regulatory Networks. <i>Journal of Molecular Biology</i> , 2006, 358, 614-633.	4.2	254
24	Diverse activation pathways in class A GPCRs converge near the G-protein-coupling region. <i>Nature</i> , 2016, 536, 484-487.	27.8	245
25	Interplay between gene expression noise and regulatory network architecture. <i>Trends in Genetics</i> , 2012, 28, 221-232.	6.7	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.	14.5	231
27	Whatâ€™s 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.	4.2	207
29	Versatility from Protein Disorder. <i>Science</i> , 2012, 337, 1460-1461.	12.6	206
30	Cells alter their tRNA abundance to selectively regulate protein synthesis during stress conditions. <i>Science Signaling</i> , 2018, 11, .	3.6	201
31	Intrinsically Disordered Segments Affect Protein Half-Life in the Cell and during Evolution. <i>Cell Reports</i> , 2014, 8, 1832-1844.	6.4	192
32	Evolving nature of the AP2 β -appendage hub during clathrin-coated vesicle endocytosis. <i>EMBO Journal</i> , 2004, 23, 4371-4383.	7.8	177
33	Mechanistic Insight into Site-Restricted Monoubiquitination of FANCD2 by Ube2t, FANCL, and FANCI. <i>Molecular Cell</i> , 2008, 32, 767-777.	9.7	170
34	Alternative splicing of intrinsically disordered regions and rewiring of protein interactions. <i>Current Opinion in Structural Biology</i> , 2013, 23, 443-450.	5.7	166
35	The rules of disorder or why disorder rules. <i>Progress in Biophysics and Molecular Biology</i> , 2009, 99, 94-103.	2.9	160
36	The natural history of the WRKYâ€™GCM1 zinc fingers and the relationship between transcription factors and transposons. <i>Nucleic Acids Research</i> , 2006, 34, 6505-6520.	14.5	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.	3.7	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.	7.1	150
39	Genomic analysis reveals a tight link between transcription factor dynamics and regulatory network architecture. <i>Molecular Systems Biology</i> , 2009, 5, 294.	7.2	146
40	Cross-species chemogenomic profiling reveals evolutionarily conserved drug mode of action. <i>Molecular Systems Biology</i> , 2010, 6, 451.	7.2	143
41	High-throughput discovery of functional disordered regions: investigation of transactivation domains. <i>Molecular Systems Biology</i> , 2018, 14, e8190.	7.2	138
42	Discovering and understanding oncogenic gene fusions through data intensive computational approaches. <i>Nucleic Acids Research</i> , 2016, 44, 4487-4503.	14.5	133
43	Controlling entropy to tune the functions of intrinsically disordered regions. <i>Current Opinion in Structural Biology</i> , 2014, 26, 62-72.	5.7	127
44	Simultaneous quantification of protein order and disorder. <i>Nature Chemical Biology</i> , 2017, 13, 339-342.	8.0	113
45	Conservation of gene co-regulation in prokaryotes and eukaryotes. <i>Trends in Biotechnology</i> , 2002, 20, 407-410.	9.3	111
46	Sequence composition of disordered regions fine-tunes protein half-life. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 214-221.	8.2	109
47	Variable Glutamine-Rich Repeats Modulate Transcription Factor Activity. <i>Molecular Cell</i> , 2015, 59, 615-627.	9.7	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.	8.2	103
49	Subunit-selective N-terminal domain associations organize the formation of AMPA receptor heteromers. <i>EMBO Journal</i> , 2011, 30, 959-971.	7.8	99
50	GPCR activation mechanisms across classes and macro/microscales. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 879-888.	8.2	98
51	Structural and functional characterization of G protein-coupled receptors with deep mutational scanning. <i>ELife</i> , 2020, 9, .	6.0	91
52	Cellular Strategies for Regulating Functional and Nonfunctional Protein Aggregation. <i>Cell Reports</i> , 2012, 2, 1425-1437.	6.4	88
53	The HIRAN Domain and Recruitment of Chromatin Remodeling and Repair activities to Damaged DNA. <i>Cell Cycle</i> , 2006, 5, 775-782.	2.6	87
54	Molecular mechanism of modulating arrestin conformation by GPCR phosphorylation. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 538-545.	8.2	87

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55	Combinatorial expression of GPCR isoforms affects signalling and drug responses. <i>Nature</i> , 2020, 587, 650-656.	27.8	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.	7.1	85
57	A Global Map of G Protein Signaling Regulation by RGS Proteins. <i>Cell</i> , 2020, 183, 503-521.e19.	28.9	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.	2.2	80
59	A C ^α -H ^α -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.	4.2	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.	6.7	75
61	Context-Specific Striatal Astrocyte Molecular Responses Are Phenotypically Exploitable. <i>Neuron</i> , 2020, 108, 1146-1162.e10.	8.1	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.	7.1	72
63	NCI: a server to identify non-canonical interactions in protein structures. <i>Nucleic Acids Research</i> , 2003, 31, 3345-3348.	14.5	68
64	Whole Genome Sequencing Highlights Genetic Changes Associated with Laboratory Domestication of <i>C. elegans</i> . <i>PLoS ONE</i> , 2010, 5, e13922.	2.5	68
65	Structured and disordered facets of the GPCR fold. <i>Current Opinion in Structural Biology</i> , 2014, 27, 129-137.	5.7	68
66	Lipolysis drives expression of the constitutively active receptor GPR3 to induce adipose thermogenesis. <i>Cell</i> , 2021, 184, 3502-3518.e33.	28.9	68
67	Human Inositol Polyphosphate Multikinase Regulates Transcript-Selective Nuclear mRNA Export to Preserve Genome Integrity. <i>Molecular Cell</i> , 2013, 51, 737-750.	9.7	65
68	Uncovering a Hidden Distributed Architecture Behind Scale-free Transcriptional Regulatory Networks. <i>Journal of Molecular Biology</i> , 2006, 360, 204-212.	4.2	64
69	Molecular Principles of Gene Fusion Mediated Rewiring of Protein Interaction Networks in Cancer. <i>Molecular Cell</i> , 2016, 63, 579-592.	9.7	63
70	Evolution of fold switching in a metamorphic protein. <i>Science</i> , 2021, 371, 86-90.	12.6	59
71	Probing G _i 1 protein activation at single amino acid resolution. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 686-694.	8.2	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.	8.2	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.	3.4	56
74	A conserved molecular switch in Class F receptors regulates receptor activation and pathway selection. <i>Nature Communications</i> , 2019, 10, 667.	12.8	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.	5.5	55
76	Genomic neighbourhood and the regulation of gene expression. <i>Current Opinion in Cell Biology</i> , 2010, 22, 326-333.	5.4	55
77	Affinity and competition for TBP are molecular determinants of gene expression noise. <i>Nature Communications</i> , 2016, 7, 10417.	12.8	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.	4.2	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.	8.2	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.	3.5	52
82	Recognition Pliability Is Coupled to Structural Heterogeneity: A Calmodulin Intrinsically Disordered Binding Region Complex. <i>Structure</i> , 2012, 20, 522-533.	3.3	51
83	Revealing the Determinants of Widespread Alternative Splicing Perturbation in Cancer. <i>Cell Reports</i> , 2017, 21, 798-812.	6.4	51
84	Fc γ 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.	4.7	45
85	The impact of genomic neighborhood on the evolution of human and chimpanzee transcriptome. <i>Genome Research</i> , 2009, 19, 785-794.	5.5	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.	7.1	44
87	Adaptive evolution by optimizing expression levels in different environments. <i>Trends in Microbiology</i> , 2006, 14, 11-14.	7.7	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.	3.3	43
89	Cotranslational protein assembly imposes evolutionary constraints on homomeric proteins. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 279-288.	8.2	43
90	Capturing dynamic protein interactions. <i>Science</i> , 2018, 359, 1105-1106.	12.6	42

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91	How do disordered regions achieve comparable functions to structured domains?. Protein Science, 2015, 24, 909-922.	7.6	41
92	Function and Regulation of Phase-Separated Biological Condensates. Biochemistry, 2018, 57, 2452-2461.	2.5	41
93	Integrated Genomic Analysis Identifies <i>UBTF</i> Tandem Duplications as a Recurrent Lesion in Pediatric Acute Myeloid Leukemia. Blood Cancer Discovery, 2022, 3, 194-207.	5.0	38
94	The Hidden Codes That Shape Protein Evolution. Science, 2013, 342, 1325-1326.	12.6	37
95	Human MC4R variants affect endocytosis, trafficking and dimerization revealing multiple cellular mechanisms involved in weight regulation. Cell Reports, 2021, 34, 108862.	6.4	37
96	Methods to Reconstruct and Compare Transcriptional Regulatory Networks. Methods in Molecular Biology, 2009, 541, 163-180.	0.9	36
97	The chemotherapeutic CX-5461 primarily targets TOP2B and exhibits selective activity in high-risk neuroblastoma. Nature Communications, 2021, 12, 6468.	12.8	35
98	Did the loss of sigma factors initiate pseudogene accumulation in <i>M. leprae</i> ?. Trends in Microbiology, 2003, 11, 59-61.	7.7	34
99	Disorder-to-order transition in PE/PPE proteins of <i>Mycobacterium tuberculosis</i> augments the pro-pathogen immune response. FEBS Open Bio, 2020, 10, 70-85.	2.3	33
100	Chemogenomics and biotechnology. Trends in Biotechnology, 2008, 26, 252-258.	9.3	32
101	Evolutionary selection for protein aggregation. Biochemical Society Transactions, 2012, 40, 1032-1037.	3.4	32
102	A complex network framework for unbiased statistical analyses of DNA-DNA contact maps. Nucleic Acids Research, 2013, 41, 701-710.	14.5	32
103	Amino acid homorepeats in proteins. Nature Reviews Chemistry, 2020, 4, 420-434.	30.2	31
104	TAT-Pathway-Dependent Lipoproteins as a Niche-Based Adaptation in Prokaryotes. Journal of Molecular Evolution, 2010, 70, 359-370.	1.8	29
105	Solitary and Repetitive Binding Motifs for the AP2 Complex \pm -Appendage in Amphiphysin and Other Accessory Proteins. Journal of Biological Chemistry, 2008, 283, 5099-5109.	3.4	26
106	DNA Sequence Preferences of Transcriptional Activators Correlate More Strongly than Repressors with Nucleosomes. Molecular Cell, 2012, 47, 183-192.	9.7	26
107	Registering α -helices and β -strands using backbone C-H \cdots O interactions. Proteins: Structure, Function and Bioinformatics, 2003, 51, 167-171.	2.6	25
108	Computational approaches to study transcriptional regulation. Biochemical Society Transactions, 2008, 36, 758-765.	3.4	25

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109	Investigations on C ⁺ H ⁻ interactions in RNA binding proteins. <i>International Journal of Biological Macromolecules</i> , 2007, 41, 251-259.	7.5	24
110	Intrinsically Disordered Proteins Adaptively Reorganize Cellular Matter During Stress. <i>Trends in Biochemical Sciences</i> , 2017, 42, 410-412.	7.5	24
111	Discovery and Genetic Code Expansion of a Polyethylene Terephthalate (PET) Hydrolase from the Human Saliva Metagenome for the Degradation and Bio ⁺ Functionalization of PET. <i>Angewandte Chemie - International Edition</i> , 2022, 61, .	13.8	24
112	Exploring the environmental preference of weak interactions in (1 ⁺ /1 ⁻) ₈ barrel proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 65, 75-86.	2.6	21
113	Structure, evolution and dynamics of transcriptional regulatory networks. <i>Biochemical Society Transactions</i> , 2010, 38, 1155-1178.	3.4	21
114	Human Diseases from Gain-of-Function Mutations in Disordered Protein Regions. <i>Cell</i> , 2018, 175, 40-42.	28.9	21
115	Molecular Signatures of Fusion Proteins in Cancer. <i>ACS Pharmacology and Translational Science</i> , 2019, 2, 122-133.	4.9	20
116	Combinatorial multivalent interactions drive cooperative assembly of the COPII coat. <i>Journal of Cell Biology</i> , 2020, 219, .	5.2	20
117	A community effort to bring structure to disorder. <i>Nature Methods</i> , 2021, 18, 454-455.	19.0	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.	6.7	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.	2.6	18
120	Molecular determinants underlying functional innovations of TBP and their impact on transcription initiation. <i>Nature Communications</i> , 2020, 11, 2384.	12.8	17
121	Conformational selection guides 1 ⁺ -arrestin recruitment at a biased G protein ⁺ -coupled receptor. <i>Science</i> , 2022, 377, 222-228.	12.6	16
122	Shigellaapyrase - a novel variant of bacterial acid phosphatases?. <i>FEBS Letters</i> , 2002, 512, 8-12.	2.8	14
123	Transcript stability in the protein interaction network of Escherichia coli. <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.	5.4	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.	5.0	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.	5.3	13
128	CCL22 mutations drive natural killer cell lymphoproliferative disease by deregulating microenvironmental crosstalk. <i>Nature Genetics</i> , 2022, 54, 637-648.	21.4	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.	6.7	12
130	Molecular Deconvolution Platform to Establish Disease Mechanisms by Surveying GPCR Signaling. <i>Cell Reports</i> , 2018, 24, 557-568.e5.	6.4	12
131	Biological impact of mutually exclusive exon switching. <i>PLoS Computational Biology</i> , 2021, 17, e1008708.	3.2	12
132	An intrinsically disordered proteins community for ELIXIR. <i>F1000Research</i> , 2019, 8, 1753.	1.6	12
133	Optimizing membrane-protein biogenesis through nonoptimal-codon usage. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 1023-1025.	8.2	11
134	The fitness cost and benefit of phase-separated protein deposits. <i>Molecular Systems Biology</i> , 2019, 15, e8075.	7.2	10
135	Proteome response at the edge of protein aggregation. <i>Open Biology</i> , 2015, 5, 140221.	3.6	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.	2.5	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.	2.6	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.	5.7	5
139	GenCompass: a universal system for analysing gene expression for any genome. <i>Trends in Biotechnology</i> , 2004, 22, 552-555.	9.3	3
140	Functional and Transcriptional Coherency of Modules in the Human Protein Interaction Network. <i>Journal of Integrative Bioinformatics</i> , 2007, 4, 198-207.	1.5	3
141	Scaling up synthetic gene circuits. <i>Nature Nanotechnology</i> , 2010, 5, 631-633.	31.5	3
142	Reconfiguring Regulation. <i>Science</i> , 2012, 335, 1050-1051.	12.6	3
143	From prioritisation to understanding: mechanistic predictions of variant effects. <i>Molecular Systems Biology</i> , 2018, 14, e8741.	7.2	2
144	Biophysicists' outstanding response to Covid-19. <i>Biophysical Journal</i> , 2021, 120, E1-E2.	0.5	2

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145	Biophysicistsâ€™ continued outstanding response to COVID-19. Biophysical Journal, 2021, 120, E1.	0.5	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, , .	2.0	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.	7.2	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