

# Mohan Madan Babu

## List of Publications by Year in descending order

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Version: 2024-02-01

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	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.	5.0	38
2	CCL22 mutations drive natural killer cell lymphoproliferative disease by deregulating microenvironmental crosstalk. <i>Nature Genetics</i> , 2022, 54, 637-648.	21.4	13
3	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, .	13.8	24
4	Conformational selection guides $\beta^2$ -arrestin recruitment at a biased G protein-coupled receptor. <i>Science</i> , 2022, 377, 222-228.	12.6	16
5	Biophysicists' outstanding response to Covid-19. <i>Biophysical Journal</i> , 2021, 120, E1-E2.	0.5	2
6	Human MC4R variants affect endocytosis, trafficking and dimerization revealing multiple cellular mechanisms involved in weight regulation. <i>Cell Reports</i> , 2021, 34, 108862.	6.4	37
7	Biological impact of mutually exclusive exon switching. <i>PLoS Computational Biology</i> , 2021, 17, e1008708.	3.2	12
8	A community effort to bring structure to disorder. <i>Nature Methods</i> , 2021, 18, 454-455.	19.0	19
9	Lipolysis drives expression of the constitutively active receptor GPR3 to induce adipose thermogenesis. <i>Cell</i> , 2021, 184, 3502-3518.e33.	28.9	68
10	Biophysicists' continued outstanding response to COVID-19. <i>Biophysical Journal</i> , 2021, 120, E1.	0.5	2
11	Evolution of fold switching in a metamorphic protein. <i>Science</i> , 2021, 371, 86-90.	12.6	59
12	The chemotherapeutic CX-5461 primarily targets TOP2B and exhibits selective activity in high-risk neuroblastoma. <i>Nature Communications</i> , 2021, 12, 6468.	12.8	35
13	GPCR activation mechanisms across classes and macro/microscales. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 879-888.	8.2	98
14	Pathway perturbations in signaling networks: Linking genotype to phenotype. <i>Seminars in Cell and Developmental Biology</i> , 2020, 99, 3-11.	5.0	13
15	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.	2.3	33
16	Context-Specific Striatal Astrocyte Molecular Responses Are Phenotypically Exploitable. <i>Neuron</i> , 2020, 108, 1146-1162.e10.	8.1	73
17	Amino acid homorepeats in proteins. <i>Nature Reviews Chemistry</i> , 2020, 4, 420-434.	30.2	31
18	Combinatorial expression of GPCR isoforms affects signalling and drug responses. <i>Nature</i> , 2020, 587, 650-656.	27.8	87

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19	Molecular determinants underlying functional innovations of TBP and their impact on transcription initiation. <i>Nature Communications</i> , 2020, 11, 2384.	12.8	17
20	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
21	A Global Map of G Protein Signaling Regulation by RGS Proteins. <i>Cell</i> , 2020, 183, 503-521.e19.	28.9	82
22	Combinatorial multivalent interactions drive cooperative assembly of the COPII coat. <i>Journal of Cell Biology</i> , 2020, 219, .	5.2	20
23	Structural and functional characterization of G protein-coupled receptors with deep mutational scanning. <i>ELife</i> , 2020, 9, .	6.0	91
24	Molecular Signatures of Fusion Proteins in Cancer. <i>ACS Pharmacology and Translational Science</i> , 2019, 2, 122-133.	4.9	20
25	The fitness cost and benefit of phase-separated protein deposits. <i>Molecular Systems Biology</i> , 2019, 15, e8075.	7.2	10
26	A conserved molecular switch in Class F receptors regulates receptor activation and pathway selection. <i>Nature Communications</i> , 2019, 10, 667.	12.8	56
27	An intrinsically disordered proteins community for ELIXIR. <i>F1000Research</i> , 2019, 8, 1753.	1.6	12
28	Common activation mechanism of class A GPCRs. <i>ELife</i> , 2019, 8, .	6.0	339
29	Enabling next generation systems biology: a conversation with M. Madan Babu. <i>Molecular Systems Biology</i> , 2019, 15, e9376.	7.2	1
30	Capturing dynamic protein interactions. <i>Science</i> , 2018, 359, 1105-1106.	12.6	42
31	Function and Regulation of Phase-Separated Biological Condensates. <i>Biochemistry</i> , 2018, 57, 2452-2461.	2.5	41
32	Cotranslational protein assembly imposes evolutionary constraints on homomeric proteins. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 279-288.	8.2	43
33	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
34	Pharmacogenomics of GPCR Drug Targets. <i>Cell</i> , 2018, 172, 41-54.e19.	28.9	464
35	From prioritisation to understanding: mechanistic predictions of variant effects. <i>Molecular Systems Biology</i> , 2018, 14, e8741.	7.2	2
36	Human Diseases from Gain-of-Function Mutations in Disordered Protein Regions. <i>Cell</i> , 2018, 175, 40-42.	28.9	21

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37	Cells alter their tRNA abundance to selectively regulate protein synthesis during stress conditions. <i>Science Signaling</i> , 2018, 11, .	3.6	201
38	High-throughput discovery of functional disordered regions: investigation of transactivation domains. <i>Molecular Systems Biology</i> , 2018, 14, e8190.	7.2	138
39	Molecular Deconvolution Platform to Establish Disease Mechanisms by Surveying GPCR Signaling. <i>Cell Reports</i> , 2018, 24, 557-568.e5.	6.4	12
40	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
41	Molecular mechanism of modulating arrestin conformation by GPCR phosphorylation. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 538-545.	8.2	87
42	Intrinsically Disordered Proteins Adaptively Reorganize Cellular Matter During Stress. <i>Trends in Biochemical Sciences</i> , 2017, 42, 410-412.	7.5	24
43	Selectivity determinants of GPCR-G-protein binding. <i>Nature</i> , 2017, 545, 317-322.	27.8	297
44	Simultaneous quantification of protein order and disorder. <i>Nature Chemical Biology</i> , 2017, 13, 339-342.	8.0	113
45	Revealing the Determinants of Widespread Alternative Splicing Perturbation in Cancer. <i>Cell Reports</i> , 2017, 21, 798-812.	6.4	51
46	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
47	Conserved Sequence Preferences Contribute to Substrate Recognition by the Proteasome. <i>Journal of Biological Chemistry</i> , 2016, 291, 14526-14539.	3.4	56
48	Molecular Principles of Gene Fusion Mediated Rewiring of Protein Interaction Networks in Cancer. <i>Molecular Cell</i> , 2016, 63, 579-592.	9.7	63
49	Diverse activation pathways in class A GPCRs converge near the G-protein-coupling region. <i>Nature</i> , 2016, 536, 484-487.	27.8	245
50	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
51	Affinity and competition for TBP are molecular determinants of gene expression noise. <i>Nature Communications</i> , 2016, 7, 10417.	12.8	55
52	Discovering and understanding oncogenic gene fusions through data intensive computational approaches. <i>Nucleic Acids Research</i> , 2016, 44, 4487-4503.	14.5	133
53	Sequence composition of disordered regions fine-tunes protein half-life. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 214-221.	8.2	109
54	Universal allosteric mechanism for G $\pm$ activation by GPCRs. <i>Nature</i> , 2015, 524, 173-179.	27.8	291

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55	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
56	Classifying pairs with trees for supervised biological network inference. <i>Molecular BioSystems</i> , 2015, 11, 2116-2125.	2.9	13
57	Proteome response at the edge of protein aggregation. <i>Open Biology</i> , 2015, 5, 140221.	3.6	9
58	How do disordered regions achieve comparable functions to structured domains?. <i>Protein Science</i> , 2015, 24, 909-922.	7.6	41
59	Probing G $\beta$ 1 protein activation at single amino acid resolution. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 686-694.	8.2	58
60	Variable Glutamine-Rich Repeats Modulate Transcription Factor Activity. <i>Molecular Cell</i> , 2015, 59, 615-627.	9.7	103
61	Structure and Evolution of Transcriptional Regulatory Networks. , 2014, , 1-16.		1
62	Intrinsically Disordered Segments Affect Protein Half-Life in the Cell and during Evolution. <i>Cell Reports</i> , 2014, 8, 1832-1844.	6.4	192
63	Optimizing membrane-protein biogenesis through nonoptimal-codon usage. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 1023-1025.	8.2	11
64	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
65	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
66	Controlling entropy to tune the functions of intrinsically disordered regions. <i>Current Opinion in Structural Biology</i> , 2014, 26, 62-72.	5.7	127
67	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
68	Structured and disordered facets of the GPCR fold. <i>Current Opinion in Structural Biology</i> , 2014, 27, 129-137.	5.7	68
69	A Million Peptide Motifs for the Molecular Biologist. <i>Molecular Cell</i> , 2014, 55, 161-169.	9.7	429
70	Classification of Intrinsically Disordered Regions and Proteins. <i>Chemical Reviews</i> , 2014, 114, 6589-6631.	47.7	1,618
71	Promiscuity as a functional trait: intrinsically disordered regions as central players of interactomes. <i>Biochemical Journal</i> , 2013, 454, 361-369.	3.7	156
72	The Hidden Codes That Shape Protein Evolution. <i>Science</i> , 2013, 342, 1325-1326.	12.6	37

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73	A methodology to infer gene networks from spatial patterns of expression – an application to fluorescence in situ hybridization images. <i>Molecular BioSystems</i> , 2013, 9, 1926.	2.9	0
74	Molecular signatures of G-protein-coupled receptors. <i>Nature</i> , 2013, 494, 185-194.	27.8	1,298
75	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
76	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
77	What’s in a name? Why these proteins are intrinsically disordered. <i>Intrinsically Disordered Proteins</i> , 2013, 1, e24157.	1.9	226
78	A complex network framework for unbiased statistical analyses of DNA–DNA contact maps. <i>Nucleic Acids Research</i> , 2013, 41, 701-710.	14.5	32
79	Reconfiguring Regulation. <i>Science</i> , 2012, 335, 1050-1051.	12.6	3
80	Versatility from Protein Disorder. <i>Science</i> , 2012, 337, 1460-1461.	12.6	206
81	Cellular Strategies for Regulating Functional and Nonfunctional Protein Aggregation. <i>Cell Reports</i> , 2012, 2, 1425-1437.	6.4	88
82	Dissecting ensemble networks in ES cell populations reveals micro-heterogeneity underlying pluripotency. <i>Molecular BioSystems</i> , 2012, 8, 744.	2.9	52
83	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
84	Independence of Repressive Histone Marks and Chromatin Compaction during Senescent Heterochromatic Layer Formation. <i>Molecular Cell</i> , 2012, 47, 203-214.	9.7	258
85	DNA Sequence Preferences of Transcriptional Activators Correlate More Strongly than Repressors with Nucleosomes. <i>Molecular Cell</i> , 2012, 47, 183-192.	9.7	26
86	Evolutionary selection for protein aggregation. <i>Biochemical Society Transactions</i> , 2012, 40, 1032-1037.	3.4	32
87	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
88	Recognition Pliability Is Coupled to Structural Heterogeneity: A Calmodulin Intrinsically Disordered Binding Region Complex. <i>Structure</i> , 2012, 20, 522-533.	3.3	51
89	Interplay between gene expression noise and regulatory network architecture. <i>Trends in Genetics</i> , 2012, 28, 221-232.	6.7	235
90	Subunit-selective N-terminal domain associations organize the formation of AMPA receptor heteromers. <i>EMBO Journal</i> , 2011, 30, 959-971.	7.8	99

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91	Intrinsically disordered proteins: regulation and disease. <i>Current Opinion in Structural Biology</i> , 2011, 21, 432-440.	5.7	518
92	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
93	Structure, evolution and dynamics of transcriptional regulatory networks. <i>Biochemical Society Transactions</i> , 2010, 38, 1155-1178.	3.4	21
94	TAT-Pathway-Dependent Lipoproteins as a Niche-Based Adaptation in Prokaryotes. <i>Journal of Molecular Evolution</i> , 2010, 70, 359-370.	1.8	29
95	Genomic neighbourhood and the regulation of gene expression. <i>Current Opinion in Cell Biology</i> , 2010, 22, 326-333.	5.4	55
96	Scaling up synthetic gene circuits. <i>Nature Nanotechnology</i> , 2010, 5, 631-633.	31.5	3
97	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
98	Cross-species chemogenomic profiling reveals evolutionarily conserved drug mode of action. <i>Molecular Systems Biology</i> , 2010, 6, 451.	7.2	143
99	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
100	Fcγ3 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
101	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
102	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
103	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
104	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
105	The impact of genomic neighborhood on the evolution of human and chimpanzee transcriptome. <i>Genome Research</i> , 2009, 19, 785-794.	5.5	44
106	The rules of disorder or why disorder rules. <i>Progress in Biophysics and Molecular Biology</i> , 2009, 99, 94-103.	2.9	160
107	The efficiency of mitochondrial electron transport chain is increased in the long-lived <i>mrg19</i> <i>Saccharomyces cerevisiae</i> . <i>Aging Cell</i> , 2009, 8, 643-653.	6.7	12
108	Methods to Reconstruct and Compare Transcriptional Regulatory Networks. <i>Methods in Molecular Biology</i> , 2009, 541, 163-180.	0.9	36

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109	Transcript stability in the protein interaction network of Escherichia coli. <i>Molecular BioSystems</i> , 2009, 5, 154-162.	2.9	14
110	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
111	Chemogenomics and biotechnology. <i>Trends in Biotechnology</i> , 2008, 26, 252-258.	9.3	32
112	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
113	Mechanistic Insight into Site-Restricted Monoubiquitination of FANCD2 by Ube2t, FANCL, and FANCI. <i>Molecular Cell</i> , 2008, 32, 767-777.	9.7	170
114	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
115	Tight Regulation of Unstructured Proteins: From Transcript Synthesis to Protein Degradation. <i>Science</i> , 2008, 322, 1365-1368.	12.6	419
116	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
117	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.	3.4	26
118	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
119	Computational approaches to study transcriptional regulation. <i>Biochemical Society Transactions</i> , 2008, 36, 758-765.	3.4	25
120	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
121	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
122	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
123	Investigations on $\pi$ - $\pi$ interactions in RNA binding proteins. <i>International Journal of Biological Macromolecules</i> , 2007, 41, 251-259.	7.5	24
124	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.	14.5	157
125	Evolutionary Dynamics of Prokaryotic Transcriptional Regulatory Networks. <i>Journal of Molecular Biology</i> , 2006, 358, 614-633.	4.2	254
126	Uncovering a Hidden Distributed Architecture Behind Scale-free Transcriptional Regulatory Networks. <i>Journal of Molecular Biology</i> , 2006, 360, 204-212.	4.2	64



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127	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
128	Adaptive evolution by optimizing expression levels in different environments. <i>Trends in Microbiology</i> , 2006, 14, 11-14.	7.7	43
129	Exploring the environmental preference of weak interactions in ( $\pm$ )-8 barrel proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 65, 75-86.	2.6	21
130	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
131	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
132	A Database of Bacterial Lipoproteins (DOLOP) with Functional Assignments to Predicted Lipoproteins. <i>Journal of Bacteriology</i> , 2006, 188, 2761-2773.	2.2	255
133	The genome of the social amoeba <i>Dictyostelium discoideum</i> . <i>Nature</i> , 2005, 435, 43-57.	27.8	1,179
134	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
135	The Transcriptional Landscape of the Mammalian Genome. <i>Science</i> , 2005, 309, 1559-1563.	12.6	3,227
136	Gene regulatory network growth by duplication. <i>Nature Genetics</i> , 2004, 36, 492-496.	21.4	475
137	Evolving nature of the AP2 $\pm$ -appendage hub during clathrin-coated vesicle endocytosis. <i>EMBO Journal</i> , 2004, 23, 4371-4383.	7.8	177
138	Genomic analysis of regulatory network dynamics reveals large topological changes. <i>Nature</i> , 2004, 431, 308-312.	27.8	921
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	Structure and evolution of transcriptional regulatory networks. <i>Current Opinion in Structural Biology</i> , 2004, 14, 283-291.	5.7	683
141	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
142	Registering $\alpha$ -helices and $\beta$ -strands using backbone C $\cdots$ H $\cdots$ O interactions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 51, 167-171.	2.6	25
143	Did the loss of sigma factors initiate pseudogene accumulation in <i>M. leprae</i> ?. <i>Trends in Microbiology</i> , 2003, 11, 59-61.	7.7	34
144	NCI: a server to identify non-canonical interactions in protein structures. <i>Nucleic Acids Research</i> , 2003, 31, 3345-3348.	14.5	68

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145	Evolution of transcription factors and the gene regulatory network in Escherichia coli. Nucleic Acids Research, 2003, 31, 1234-1244.	14.5	283
146	Shigellaapyrase - a novel variant of bacterial acid phosphatases?. FEBS Letters, 2002, 512, 8-12.	2.8	14
147	A Câ€“Hâ€“O Hydrogen Bond Stabilized Polypeptide Chain Reversal Motif at the C Terminus of Helices in Proteins. Journal of Molecular Biology, 2002, 322, 871-880.	4.2	75
148	Conservation of gene co-regulation in prokaryotes and eukaryotes. Trends in Biotechnology, 2002, 20, 407-410.	9.3	111
149	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