Janusz Bujnicki

List of Articles by Year in descending order

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296 peer-reviewed articles	15,462 peer-reviewed citations	20786 60 peer-reviewed h-index	184863 5.42 score
332 documents	17858 doc citations	20543 65 h-index	26420 citing authors

#	Article	IF	Citations
1	NAIRDB: a database of Fourier transform infrared (FTIR) data for nucleic acids. Nucleic Acids Research, 2025, 53, D157-D162.	10.7	16
2	Sci-ModoM: a quantitative database of transcriptome-wide high-throughput RNA modification sites. Nucleic Acids Research, 2025, 53, D310-D317.	10.7	14
3	DesiRNA: structure-based design of RNA sequences with a replica exchange Monte Carlo approach. Nucleic Acids Research, 2025, 53, .	10.7	8
4	Determining the effects of pseudouridine incorporation on human tRNAs. EMBO Journal, 2025, 44, .	5.1	15
5	ARTEM: a method for RNA and DNA tertiary motif identification with backbone permutations. Genome Biology, 2025, 26, .	4.8	7
6	Modeling flexible RNA 3D structures and RNA-protein complexes. Current Opinion in Structural Biology, 2025, 94, 103137.	4.6	8
7	MODOMICS: a database of RNA modifications and related information. 2023 update. Nucleic Acids Research, 2024, 52, D239-D244.	10.7	426
8	Discovery of a trefoil knot in the RydC RNA: Challenging previous notions of RNA topology. Journal of Molecular Biology, 2024, 436, 168455.	2.9	11
9	Conserved structures and dynamics in 5'-proximal regions of Betacoronavirus RNA genomes. Nucleic Acids Research, 2024, 52, 3419-3432.	10.7	17
10	DEGRONOPEDIA: a web server for proteome-wide inspection of degrons. Nucleic Acids Research, 2024, 52, W221-W232.	10.7	35
11	SimRNAweb v2.0: a web server for RNA folding simulations and 3D structure modeling, with optional restraints and enhanced analysis of folding trajectories. Nucleic Acids Research, 2024, 52, W368-W373.	10.7	32
12	Are there double knots in proteins? Prediction and in vitro verification based on TrmD-Tm1570 fusion from C. nitroreducens. Frontiers in Molecular Biosciences, 2024, 10, .	2.4	12
13	ARTEMIS: a method for topology-independent superposition of RNA 3D structures and structure-based sequence alignment. Nucleic Acids Research, 2024, 52, 10850-10861.	10.7	5
14	Advances in the field of RNA 3D structure prediction and modeling, with purely theoretical approaches, and with the use of experimental data. Structure, 2024, 32, 1860-1876.	2.4	32
15	The three YTHDF paralogs and VIRMA are strong cross-histotype tumor driver candidates among m6A core genes. NAR Cancer, 2024, 6, .	2.5	7
16	Cryo-EM Structure of raiA ncRNA From Clostridium Reveals a New RNA 3D Fold. Journal of Molecular Biology, 2024, 436, 168833.	2.9	6
17	NACDDB: Nucleic Acid Circular Dichroism Database. Nucleic Acids Research, 2023, 51, D226-D231.	10.7	27
18	1D2DSimScore: A novel method for comparing contacts in biomacromolecules and their complexes. Protein Science, 2023, 32, .	3.5	6

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19	Structural interaction fingerprints and machine learning for predicting and explaining binding of small molecule ligands to RNA. Briefings in Bioinformatics, 2023, 24, .	4.0	32
20	RNA target highlights in CASP15: Evaluation of predicted models by structure providers. Proteins: Structure, Function and Bioinformatics, 2023, 91, 1600-1615.	1.9	49
21	RNA tertiary structure prediction in CASP15 by the GeneSilico group: Folding simulations based on statistical potentials and spatial restraints. Proteins: Structure, Function and Bioinformatics, 2023, 91, 1800-1810.	1.9	11
22	RNA 3D structure modeling by fragment assembly with small-angle X-ray scattering restraints. Bioinformatics, 2023, 39, .	3.2	14
23	A comprehensive survey of long-range tertiary interactions and motifs in non-coding RNA structures. Nucleic Acids Research, 2023, 51, 8367-8382.	10.7	17
24	MODOMICS: a database of RNA modification pathways. 2021 update. Nucleic Acids Research, 2022, 50, D231-D235.	10.7	809
25	DNAzymeBuilder, a web application for in situ generation of RNA/DNA-cleaving deoxyribozymes. Nucleic Acids Research, 2022, 50, W261-W265.	10.7	19
26	Molecular insights into RNA recognition and gene regulation by the TRIM-NHL protein Mei-P26. Life Science Alliance, 2022, 5, e202201418.	1.9	9
27	fingeRNAt—A novel tool for high-throughput analysis of nucleic acid-ligand interactions. PLoS Computational Biology, 2022, 18, e1009783.	1.9	29
28	Computational Pipeline for Reference-Free Comparative Analysis of RNA 3D Structures Applied to SARS-CoV-2 UTR Models. International Journal of Molecular Sciences, 2022, 23, 9630.	3.2	29
29	DNAmoreDB, a database of DNAzymes. Nucleic Acids Research, 2021, 49, D76-D81.	10.7	40
30	AnnapuRNA: A scoring function for predicting RNA-small molecule binding poses. PLoS Computational Biology, 2021, 17, e1008309.	1.9	84
31	RNA and DNA G-quadruplexes bind to human dicer and inhibit its activity. Cellular and Molecular Life Sciences, 2021, 78, 3709-3724.	3.5	21
32	Constrained peptides mimic a viral suppressor of RNA silencing. Nucleic Acids Research, 2021, 49, 12622-12633.	10.7	21
33	A combined structural and biochemical approach reveals translocation and stalling of UvrB on the DNA lesion as a mechanism of damage verification in bacterial nucleotide excision repair. DNA Repair, 2020, 85, 102746.	1.8	18
34	Genome-wide mapping of SARS-CoV-2 RNA structures identifies therapeutically-relevant elements. Nucleic Acids Research, 2020, 48, 12436-12452.	10.7	303
35	RNAProbe: a web server for normalization and analysis of RNA structure probing data. Nucleic Acids Research, 2020, 48, W292-W299.	10.7	25
36	RNA-Puzzles Round IV: 3D structure predictions of four ribozymes and two aptamers. Rna, 2020, 26, 982-995.	2.5	168

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37	RNA 3D structure prediction guided by independent folding of homologous sequences. BMC Bioinformatics, 2019, 20, .	2.5	27
38	Petri net–based model of the human DNA base excision repair pathway. PLoS ONE, 2019, 14, e0217913.	1.5	5
39	Matching tRNA modifications in humans to their known and predicted enzymes. Nucleic Acids Research, 2019, 47, 2143-2159.	10.7	172
40	Computational modeling of RNA 3D structure based on experimental data. Bioscience Reports, 2019, 39, .	2.5	57
41	Specific interaction of zinc finger protein Com with RNA and the crystal structure of a self-complementary RNA duplex recognized by Com. PLoS ONE, 2019, 14, e0214481.	1.5	8
42	Crystal Structure and Directed Evolution of Specificity of NlaIV Restriction Endonuclease. Journal of Molecular Biology, 2019, 431, 2082-2094.	2.9	3
43	Structural bases of peptidoglycan recognition by lysostaphin SH3b domain. Scientific Reports, 2019, 9, .	2.7	96
44	RRMdb—an evolutionary-oriented database of RNA recognition motif sequences. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	1.2	12
45	Evolutionary plasticity of the NHL domain underlies distinct solutions to RNA recognition. Nature Communications, 2018, 9, .	10.8	54
46	MODOMICS: a database of RNA modification pathways. 2017 update. Nucleic Acids Research, 2018, 46, D303-D307.	10.7	1,709
47	Novel inhibitors of the rRNA ErmC' methyltransferase to block resistance to macrolides, lincosamides, streptogramine B antibiotics. European Journal of Medicinal Chemistry, 2018, 146, 60-67.	4.4	21
48	Human RNA cap1 methyltransferase CMTr1 cooperates with RNA helicase DHX15 to modify RNAs with highly structured 5' termini. Philosophical Transactions of the Royal Society B: Biological Sciences, 2018, 373, 20180161.	2.6	28
49	Bioinformatics Tools and Benchmarks for Computational Docking and 3D Structure Prediction of RNA-Protein Complexes. Genes, 2018, 9, 432.	1.8	47
50	RNA-Puzzles Round III: 3D RNA structure prediction of five riboswitches and one ribozyme. Rna, 2017, 23, 655-672.	2.5	198
51	Defining the crucial domain and amino acid residues in bacterial Lon protease for DNA binding and processing of DNA-interacting substrates. Journal of Biological Chemistry, 2017, 292, 7507-7518.	1.3	40
52	Structural studies of RNA-protein complexes: A hybrid approach involving hydrodynamics, scattering, and computational methods. Methods, 2017, 118-119, 146-162.	2.0	46
53	Mutations in human AID differentially affect its ability to deaminate cytidine and 5-methylcytidine in ssDNA substrates in vitro. Scientific Reports, 2017, 7, .	2.7	9
54	Occurrence and stability of lone pair–π stacking interactions between ribose and nucleobases in functional RNAs. Nucleic Acids Research, 2017, 45, 11019-11032.	10.7	65

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55	SupeRNAlign: a new tool for flexible superposition of homologous RNA structures and inference of accurate structure-based sequence alignments. Nucleic Acids Research, 2017, 45, e150-e150.	10.7	13
56	Impact of the structural integrity of the three-way junction of adenovirus VAI RNA on PKR inhibition. PLoS ONE, 2017, 12, e0186849.	1.5	24
57	Identification of protein structural elements responsible for the diversity of sequence preferences among Mini-III RNases. Scientific Reports, 2016, 6, .	2.7	12
58	Coarse-grained modeling of RNA 3D structure. Methods, 2016, 103, 138-156.	2.0	64
59	SimRNA: a coarse-grained method for RNA folding simulations and 3D structure prediction. Nucleic Acids Research, 2016, 44, e63-e63.	10.7	437
60	SimRNAweb: a web server for RNA 3D structure modeling with optional restraints. Nucleic Acids Research, 2016, 44, W315-W319.	10.7	134
61	Asymmetric DNA methylation by dimeric EcoP15I DNA methyltransferase. Biochimie, 2016, 128-129, 70-82.	2.1	5
62	tRNAmodpred: A computational method for predicting posttranscriptional modifications in tRNAs. Methods, 2016, 107, 34-41.	2.0	12
63	Loss of Conserved Noncoding RNAs in Genomes of Bacterial Endosymbionts. Genome Biology and Evolution, 2016, 8, 426-438.	1.7	12
64	Computational modeling of RNA 3D structures and interactions. Current Opinion in Structural Biology, 2016, 37, 22-28.	4.6	50
65	Structural and functional insights into tRNA binding and adenosine N1-methylation by an archaeal Trm10 homologue. Nucleic Acids Research, 2016, 44, 940-953.	10.7	37
66	The architecture of the Schizosaccharomyces pombe CCR4-NOT complex. Nature Communications, 2016, 7, .	10.8	56
67	Genome-wide survey of codons under diversifying selection in a highly recombining bacterial species,Helicobacter pylori. DNA Research, 2016, 23, 135-143.	1.5	8
68	Sequence-specific cleavage of dsRNA by Mini-III RNase. Nucleic Acids Research, 2015, 43, 2864-2873.	10.7	33
69	Phylogenomics and sequence-structure-function relationships in the GmrSD family of Type IV restriction enzymes. BMC Bioinformatics, 2015, 16, .	2.5	47
70	Modeling of ribonucleic acid–ligand interactions. Wiley Interdisciplinary Reviews: Computational Molecular Science, 2015, 5, 425-439.	6.5	18
71	Biochemical Characterization and Validation of a Catalytic Site of a Highly Thermostable Ts2631 Endolysin from the Thermus scotoductus Phage vB_Tsc2631. PLoS ONE, 2015, 10, e0137374.	1.5	59
72	Magnesium-binding architectures in RNA crystal structures: validation, binding preferences, classification and motif detection. Nucleic Acids Research, 2015, 43, 3789-3801.	10.7	121

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73	An atlas of RNA base pairs involving modified nucleobases with optimal geometries and accurate energies. Nucleic Acids Research, 2015, 43, 9573-9573.	10.7	21
74	The Signature of the Five-Stranded vRRM Fold Defined by Functional, Structural and Computational Analysis of the hnRNP L Protein. Journal of Molecular Biology, 2015, 427, 3001-3022.	2.9	29
75	Brickworxbuilds recurrent RNA and DNA structural motifs into medium- and low-resolution electron-density maps. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 697-705.	3.1	16
76	Characterization of the termini of the West Nile virus genome and their interactions with the small isoform of the 2' 5'-oligoadenylate synthetase family. Journal of Structural Biology, 2015, 190, 236-249.	1.5	26
77	RNAcentral: an international database of ncRNA sequences. Nucleic Acids Research, 2015, 43, D123-D129.	10.7	122
78	An atlas of RNA base pairs involving modified nucleobases with optimal geometries and accurate energies. Nucleic Acids Research, 2015, 43, 6714-6729.	10.7	66
79	NPDock: a web server for protein–nucleic acid docking. Nucleic Acids Research, 2015, 43, W425-W430.	10.7	238
80	GDFuzz3D: a method for protein 3D structure reconstruction from contact maps, based on a non-Euclidean distance function. Bioinformatics, 2015, 31, 3499-3505.	3.2	39
81	Structure and intrinsic disorder of the proteins of theTrypanosoma brucei editosome. FEBS Letters, 2015, 589, 2603-2610.	1.8	7
82	RNA-Puzzles Round II: assessment of RNA structure prediction programs applied to three large RNA structures. Rna, 2015, 21, 1066-1084.	2.5	196
83	Distribution and frequencies of post-transcriptional modifications in tRNAs. RNA Biology, 2014, 11, 1619-1629.	2.4	203
84	RNA methyltransferases involved in 5' cap biosynthesis. RNA Biology, 2014, 11, 1597-1607.	2.4	90
85	Computational modeling of RNA 3D structures, with the aid of experimental restraints. RNA Biology, 2014, 11, 522-536.	2.4	40
86	Structural analysis of human 2'-O-ribose methyltransferases involved in mRNA cap structure formation. Nature Communications, 2014, 5, .	10.8	102
87	CompaRNA: a server for continuous benchmarking of automated methods for RNA secondary structure prediction. Nucleic Acids Research, 2014, 42, 5403-5406.	10.7	17
88	RNA Bricks—a database of RNA 3D motifs and their interactions. Nucleic Acids Research, 2014, 42, D123-D131.	10.7	99
89	Structural basis of the methylation specificity of R.DpnI. Nucleic Acids Research, 2014, 42, 8745-8754.	10.7	39
90	ClaRNA: a classifier of contacts in RNA 3D structures based on a comparative analysis of various classification schemes. Nucleic Acids Research, 2014, 42, e151-e151.	10.7	58

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91	The RNase H-like superfamily: new members, comparative structural analysis and evolutionary classification. Nucleic Acids Research, 2014, 42, 4160-4179.	10.7	171
92	Solution conformation of adenovirus virus associated RNA-I and its interaction with PKR. Journal of Structural Biology, 2014, 185, 48-57.	1.5	23
93	Computational modeling of protein–RNA complex structures. Methods, 2014, 65, 310-319.	2.0	32
94	Designability landscape reveals sequence features that define axial helix rotation in four-helical homo-oligomeric antiparallel coiled-coil structures. Journal of Structural Biology, 2014, 188, 123-133.	1.5	20
95	Female-specific gene expression in dioecious liverwort Pellia endiviifolia is developmentally regulated and connected to archegonia production. BMC Plant Biology, 2014, 14, 168.	3.0	6
96	Functional and Bioinformatics Analysis of Two Campylobacter jejuni Homologs of the Thiol-Disulfide Oxidoreductase, DsbA. PLoS ONE, 2014, 9, e106247.	1.5	21
97	Structural analysis of monomeric retroviral reverse transcriptase in complex with an RNA/DNA hybrid. Nucleic Acids Research, 2013, 41, 3874-3887.	10.7	52
98	S6:S18 ribosomal protein complex interacts with a structural motif present in its own mRNA. Rna, 2013, 19, 1341-1348.	2.5	23
99	LigandRNA: computational predictor of RNA–ligand interactions. Rna, 2013, 19, 1605-1616.	2.5	100
100	CompaRNA: a server for continuous benchmarking of automated methods for RNA secondary structure prediction. Nucleic Acids Research, 2013, 41, 4307-4323.	10.7	113
101	QA-RecombineIt: a server for quality assessment and recombination of protein models. Nucleic Acids Research, 2013, 41, W389-W397.	10.7	10
102	RNAlyzer—novel approach for quality analysis of RNA structural models. Nucleic Acids Research, 2013, 41, 5978-5990.	10.7	26
103	Crystal structures of the tRNA:m 2 G6 methyltransferase Trm14/TrmN from two domains of life. Nucleic Acids Research, 2012, 40, 5149-5161.	10.7	50
104	Crohn's Disease Risk Alleles on the NOD2 Locus Have Been Maintained by Natural Selection on Standing Variation. Molecular Biology and Evolution, 2012, 29, 1569-1585.	3.1	24
105	MetalionRNA: computational predictor of metal-binding sites in RNA structures. Bioinformatics, 2012, 28, 198-205.	3.2	51
106	RNApathwaysDB—a database of RNA maturation and decay pathways. Nucleic Acids Research, 2012, 41, D268-D272.	10.7	10
107	Rational engineering of sequence specificity in R.MwoI restriction endonuclease. Nucleic Acids Research, 2012, 40, 8579-8592.	10.7	3
108	Structural bioinformatics of the human spliceosomal proteome. Nucleic Acids Research, 2012, 40, 7046-7065.	10.7	44

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109	Sequence-specific cleavage of the RNA strand in DNA–RNA hybrids by the fusion of ribonuclease H with a zinc finger. Nucleic Acids Research, 2012, 40, 11563-11570.	10.7	20
110	MODOMICS: a database of RNA modification pathways—2013 update. Nucleic Acids Research, 2012, 41, D262-D267.	10.7	1,001
111	RNA-Puzzles : A CASP-like evaluation of RNA three-dimensional structure prediction. Rna, 2012, 18, 610-625.	2.5	304
112	The open reading frame TTC1157 of Thermus thermophilus HB27 encodes the methyltransferase forming N2-methylguanosine at position 6 in tRNA. Rna, 2012, 18, 815-824.	2.5	23
113	RIBER/DIBER: a software suite for crystal content analysis in the studies of protein–nucleic acid complexes. Bioinformatics, 2012, 28, 880-881.	3.2	5
114	Delineation of structural domains and identification of functionally important residues in DNA repair enzyme exonuclease VII. Nucleic Acids Research, 2012, 40, 8163-8174.	10.7	18
115	Structure of eukaryotic 2'-O-ribose methyltransferase in complex with mRNA cap analogue. Acta Crystallographica Section A: Foundations and Advances, 2012, 68, s144-s144.	0.2	0
116	Computational methods for prediction of protein–RNA interactions. Journal of Structural Biology, 2012, 179, 261-268.	1.5	125
117	Statins Impair Glucose Uptake in Tumor Cells. Neoplasia, 2012, 14, 311-323.	2.7	39
118	Novel non-specific DNA adenine methyltransferases. Nucleic Acids Research, 2012, 40, 2119-2130.	10.7	64
119	Crystal structure and mechanism of action of the N6-methyladenine-dependent type IIM restriction endonuclease R.DpnI. Nucleic Acids Research, 2012, 40, 7563-7572.	10.7	62
120	MetaDisorder: a meta-server for the prediction of intrinsic disorder in proteins. BMC Bioinformatics, 2012, 13, .	2.5	315
121	Molecular evolution of dihydrouridine synthases. BMC Bioinformatics, 2012, 13, .	2.5	40
122	The utility of comparative models and the local model quality for protein crystal structure determination by Molecular Replacement. BMC Bioinformatics, 2012, 13, .	2.5	10
123	Related bifunctional restriction endonuclease-methyltransferase triplets: TspDTI, Tth111II/TthHB27I and TsoI with distinct specificities. BMC Molecular Biology, 2012, 13, .	4.0	21
124	MetaLocGramN: A meta-predictor of protein subcellular localization for Gram-negative bacteria. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2012, 1824, 1425-1433.	1.3	29
125	A novel homozygous p.Arg527Leu LMNA mutation in two unrelated Egyptian families causes overlapping mandibuloacral dysplasia and progeria syndrome. European Journal of Human Genetics, 2012, 20, 1134-1140.	2.1	34
126	Intrinsic Disorder in the Human Spliceosomal Proteome. PLoS Computational Biology, 2012, 8, e1002641.	1.9	87

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127	A toolbox for developing bioinformatics software. Briefings in Bioinformatics, 2012, 13, 244-257.	4.0	20
128	REPAIRtoire--a database of DNA repair pathways. Nucleic Acids Research, 2011, 39, D788-D792.	10.7	64
129	STAT1 as a novel therapeutical target in pro-atherogenic signal integration of IFNγ, TLR4 and IL-6 in vascular disease. Cytokine and Growth Factor Reviews, 2011, 22, 211-219.	7.3	103
130	Common Design Principles in the Spliceosomal RNA Helicase Brr2 and in the Hel308 DNA Helicase. Molecular Cell, 2011, 41, 366.	8.6	0
131	REVIEW PAPER Virtual screening strategies in drug design – methods and applications. Biotechnologia, 2011, 92, 249-264.	1.3	46
132	Effect of substrate features and mutagenesis of active site tyrosine residues on the reaction course catalysed byTrypanosoma bruceisterol C-24-methyltransferase. Biochemical Journal, 2011, 439, 413-428.	2.3	12
133	RNA tertiary structure prediction with ModeRNA. Briefings in Bioinformatics, 2011, 12, 601-613.	4.0	18
134	RNA and protein 3D structure modeling: similarities and differences. Journal of Molecular Modeling, 2011, 17, 2325-2336.	1.9	86
135	ModeRNA: a tool for comparative modeling of RNA 3D structure. Nucleic Acids Research, 2011, 39, 4007-4022.	10.7	289
136	Evidence for an evolutionary antagonism between Mrr and Type III modification systems. Nucleic Acids Research, 2011, 39, 5991-6001.	10.7	27
137	Structural basis for the methylation of A1408 in 16S rRNA by a panaminoglycoside resistance methyltransferase NpmA from a clinical isolate and analysis of the NpmA interactions with the 30S ribosomal subunit. Nucleic Acids Research, 2011, 39, 1903-1918.	10.7	32
138	A Single Zinc Ion Is Sufficient for an Active Trypanosoma brucei tRNA Editing Deaminase. Journal of Biological Chemistry, 2011, 286, 20366-20374.	1.3	19
139	2'-O-ribose methylation of cap2 in human: function and evolution in a horizontally mobile family. Nucleic Acids Research, 2011, 39, 4756-4768.	10.7	155
140	ModeRNA server: an online tool for modeling RNA 3D structures. Bioinformatics, 2011, 27, 2441-2442.	3.2	65
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142	Physiological truncation and domain organization of a novel uracil-DNA-degrading factor. FEBS Journal, 2010, 277, 1245-1259.	3.3	5
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144	New archaeal methyltransferases forming 1-methyladenosine or 1-methyladenosine and 1-methylguanosine at position 9 of tRNA. Nucleic Acids Research, 2010, 38, 6533-6543.	10.7	51

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145	FILTREST3D: discrimination of structural models using restraints from experimental data. Bioinformatics, 2010, 26, 2986-2987.	3.2	21
146	Insights into the structure, function and evolution of the radical-SAM 23S rRNA methyltransferase Cfr that confers antibiotic resistance in bacteria. Nucleic Acids Research, 2010, 38, 1652-1663.	10.7	82
147	A putative mobile genetic element carrying a novel type IIF restriction-modification system (PluTI). Nucleic Acids Research, 2010, 38, 3019-3030.	10.7	14
148	Predicting Atomic Details of the Unfolding Pathway for YibK, a Knotted Protein from the SPOUT Superfamily. Journal of Biomolecular Structure and Dynamics, 2010, 27, 511-520.	1.8	36
149	The crystal structure of Escherichia coli spermidine synthase SpeE reveals a unique substrate-binding pocket. Journal of Structural Biology, 2010, 169, 277-285.	1.5	21
150	Crystal structure of a fructokinase homolog from Halothermothrix orenii. Journal of Structural Biology, 2010, 171, 397-401.	1.5	21
151	Fast Structural Alignment of Biomolecules Using a Hash Table, N-Grams and String Descriptors. Algorithms, 2009, 2, 692-709.	1.5	25
152	The structure of M.EcoKI Type I DNA methyltransferase with a DNA mimic antirestriction protein. Nucleic Acids Research, 2009, 37, 762-770.	10.7	85
153	SMN-assisted assembly of snRNP-specific Sm cores in trypanosomes. Genes and Development, 2009, 23, 1650-1664.	2.8	42
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155	MODOMICS: a database of RNA modification pathways. 2008 update. Nucleic Acids Research, 2009, 37, D118-D121.	10.7	191
156	Functional Analysis of MmeI from Methanol UtilizerMethylophilus methylotrophus, a Subtype IIC Restriction-Modification Enzyme Related to Type I Enzymes. Applied and Environmental Microbiology, 2009, 75, 212-223.	2.4	20
157	Cloning and analysis of a bifunctional methyltransferase/restriction endonuclease TspGWI, the prototype of a Thermus sp. enzyme family. BMC Molecular Biology, 2009, 10, .	4.0	24
158	YgdE is the 2'-O-ribose methyltransferase RlmM specific for nucleotide C2498 in bacterial 23S rRNA. Molecular Microbiology, 2009, 72, 1147-1158.	1.8	70
159	Integrating ELF4 into the circadian system through combined structural and functional studies. HFSP Journal, 2009, 3, 350-366.	2.2	109
160	Common Design Principles in the Spliceosomal RNA Helicase Brr2 and in the Hel308 DNA Helicase. Molecular Cell, 2009, 35, 454-466.	8.6	85
161	Probabilistic cross-link analysis and experiment planning for high-throughput elucidation of protein structure. Protein Science, 2009, 13, 3298-3313.	3.5	14
162	Type II restriction endonuclease R.Hpy188I belongs to the GIY-YIG nuclease superfamily, but exhibits an unusual active site. BMC Structural Biology, 2008, 8, .	1.8	15

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164	Virtual Screening and Experimental Verification to Identify Potential Inhibitors of the ErmC Methyltransferase Responsible for Bacterial Resistance against Macrolide Antibiotics. ChemMedChem, 2008, 3, 316-322.	2.2	36
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167	Pcons: A neural-network-based consensus predictor that improves fold recognition. Protein Science, 2008, 10, 2354-2362.	3.5	207
168	Predicting the Complex Structure and Functional Motions of the Outer Membrane Transporter and Signal Transducer FecA. Biophysical Journal, 2008, 94, 2482-2491.	1.5	11
169	Cell death upon epigenetic genome methylation: a novel function of methyl-specific deoxyribonucleases. Genome Biology, 2008, 9, .	12.2	50
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171	The PMS2 Subunit of Human MutLα Contains a Metal Ion Binding Domain of the Iron-Dependent Repressor Protein Family. Journal of Molecular Biology, 2008, 382, 610-627.	2.9	57
172	YccW is the m5C Methyltransferase Specific for 23S rRNA Nucleotide 1962. Journal of Molecular Biology, 2008, 383, 641-651.	2.9	62
173	Crystal Structure of the Escherichia coli 23S rRNA:m5C Methyltransferase RlmI (YccW) Reveals Evolutionary Links between RNA Modification Enzymes. Journal of Molecular Biology, 2008, 383, 652-666.	2.9	39
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