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List of Publications by Year
in descending order

101 papers	7,129 citations	87888 38 h-index	71685 76 g-index
106 all docs	106 docs citations	106 times ranked	6056 citing authors

#	Article	IF	Citations
1	NR5A1 c.991â€1 GÂ>ÂC spliceâ€site variant causes familial 46,XY partial gonadal dysgenesis with incomplete penetrance. Clinical Endocrinology, 2021, 94, 656-666.	2.4	9
2	Genome Replication of Bacterial and Archaeal Viruses. , 2021, , 429-438.		2
3	VoroCNN: deep convolutional neural network built on 3D Voronoi tessellation of protein structures. Bioinformatics, 2021, 37, 2332-2339.	4.1	27
4	VoroContacts: a tool for the analysis of interatomic contacts in macromolecular structures. Bioinformatics, 2021, 37, 4873-4875.	4.1	10
5	Modeling of protein complexes in <scp>CASP14</scp> with emphasis on the interaction interface prediction. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1834-1843.	2.6	14
6	Modeling SARSâ€CoVâ€2 proteins in the CASPâ€commons experiment. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1987-1996.	2.6	24
7	Prediction of protein assemblies, the next frontier: The <scp>CASP14â€CAPRI</scp> experiment. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1800-1823.	2.6	73
8	Transposon-associated TnpB is a programmable RNA-guided DNA endonuclease. Nature, 2021, 599, 692-696.	27.8	125
9	Templateâ€based modeling of diverse protein interactions in CAPRI rounds 38â€45. Proteins: Structure, Function and Bioinformatics, 2020, 88, 939-947.	2.6	3
10	Evolutionary classification of CRISPRâ€"Cas systems: a burst of class 2 and derived variants. Nature Reviews Microbiology, 2020, 18, 67-83.	28.6	1,427
11	Diversity and evolution of B-family DNA polymerases. Nucleic Acids Research, 2020, 48, 10142-10156.	14.5	52
12	Evolutionary and functional classification of the CARF domain superfamily, key sensors in prokaryotic antivirus defense. Nucleic Acids Research, 2020, 48, 8828-8847.	14.5	66
13	HEPN-MNT Toxin-Antitoxin System: The HEPN Ribonuclease Is Neutralized by OligoAMPylation. Molecular Cell, 2020, 80, 955-970.e7.	9.7	19
14	A catalogue of biochemically diverse CRISPR-Cas9 orthologs. Nature Communications, 2020, 11, 5512.	12.8	116
15	PAM recognition by miniature CRISPRâ€"Cas12f nucleases triggers programmable double-stranded DNA target cleavage. Nucleic Acids Research, 2020, 48, 5016-5023.	14.5	175
16	Contact Area-Based Structural Analysis of Proteins and Their Complexes Using CAD-Score. Methods in Molecular Biology, 2020, 2112, 75-90.	0.9	6
17	Template-Based Modeling of Protein Complexes Using the PPI3D Web Server. Methods in Molecular Biology, 2020, 2165, 139-155.	0.9	6
18	Structural modeling of protein complexes: Current capabilities and challenges. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1222-1232.	2.6	12

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19	Estimation of model accuracy in CASP13. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1361-1377.	2.6	78
20	Blind prediction of homo‐and hetero‐protein complexes: The CASP13‐CAPRI experiment. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1200-1221.	2.6	99
21	VoroMQA web server for assessing three-dimensional structures of proteins and protein complexes. Nucleic Acids Research, 2019, 47, W437-W442.	14.5	32
22	New insights into the structures and interactions of bacterial Y-family DNA polymerases. Nucleic Acids Research, 2019, 47, 4393-4405.	14.5	27
23	Comparative analysis of methods for evaluation of protein models against native structures. Bioinformatics, 2019, 35, 937-944.	4.1	34
24	The H-subunit of the restriction endonuclease CglI contains a prototype DEAD-Z1 helicase-like motor. Nucleic Acids Research, 2018, 46, 2560-2572.	14.5	1
25	Novel Families of Archaeo-Eukaryotic Primases Associated with Mobile Genetic Elements of Bacteria and Archaea. Journal of Molecular Biology, 2018, 430, 737-750.	4.2	31
26	Modeling of protein complexes in CAPRI Round 37 using template‐based approach combined with model selection. Proteins: Structure, Function and Bioinformatics, 2018, 86, 292-301.	2.6	9
27	DnaQ exonuclease‐like domain of Cas2 promotes spacer integration in a type I‐E CRISPR‐Cas system. EMBO Reports, 2018, 19, .	4.5	31
28	The PPI3D web server for searching, analyzing and modeling protein–protein interactions in the context of 3D structures. Bioinformatics, 2017, 33, 935-937.	4.1	39
29	VoroMQA: Assessment of protein structure quality using interatomic contact areas. Proteins: Structure, Function and Bioinformatics, 2017, 85, 1131-1145.	2.6	149
30	A structure–function analysis of the yeast Elg1 protein reveals the importance of PCNA unloading in genome stability maintenance. Nucleic Acids Research, 2017, 45, gkw1348.	14.5	34
31	Cover Image, Volume 85, Issue 6. Proteins: Structure, Function and Bioinformatics, 2017, 85, C1.	2.6	0
32	A cyclic oligonucleotide signaling pathway in type III CRISPR-Cas systems. Science, 2017, 357, 605-609.	12.6	382
33	Type III CRISPR-Cas Immunity: Major Differences Brushed Aside. Trends in Microbiology, 2017, 25, 49-61.	7.7	133
34	Structure of Csm2 elucidates the relationship between small subunits of CRISPR‐Cas effector complexes. FEBS Letters, 2016, 590, 1521-1529.	2.8	21
35	The logic of DNA replication in double-stranded DNA viruses: insights from global analysis of viral genomes. Nucleic Acids Research, 2016, 44, 4551-4564.	14.5	80
36	Spatiotemporal Control of Type III-A CRISPR-Cas Immunity: Coupling DNA Degradation with the Target RNA Recognition. Molecular Cell, 2016, 62, 295-306.	9.7	224

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37	Viral DNA replication: new insights and discoveries from large scale computational analysis. BMC Bioinformatics, 2015, 16, .	2.6	3
38	Human HLTF mediates postreplication repair by its HIRAN domain-dependent replication fork remodelling. Nucleic Acids Research, 2015, 43, gkv896.	14.5	51
39	Functional mapping of the plant small RNA methyltransferase: HEN1 physically interacts with HYL1 and DICER-LIKE 1 proteins. Nucleic Acids Research, 2015, 43, 2802-2812.	14.5	67
40	The Cytolytic Activity of Vaginolysin Strictly Depends on Cholesterol and Is Potentiated by Human CD59. Toxins, 2015, 7, 110-128.	3.4	34
41	The use of interatomic contact areas to quantify discrepancies between RNA 3D models and reference structures. Nucleic Acids Research, 2014, 42, 5407-5415.	14.5	8
42	Voronota: A fast and reliable tool for computing the vertices of the Voronoi diagram of atomic balls. Journal of Computational Chemistry, 2014, 35, 672-681.	3.3	62
43	The CAD-score web server: contact area-based comparison of structures and interfaces of proteins, nucleic acids and their complexes. Nucleic Acids Research, 2014, 42, W259-W263.	14.5	15
44	Conformational Analysis of Processivity Clamps in Solution Demonstrates that Tertiary Structure Does Not Correlate with Protein Dynamics. Structure, 2014, 22, 572-581.	3.3	30
45	Herpesviral helicase-primase subunit UL8 is inactivated B-family polymerase. Bioinformatics, 2014, 30, 2093-2097.	4.1	11
46	Programmable RNA Shredding by the Type III-A CRISPR-Cas System of Streptococcus thermophilus. Molecular Cell, 2014, 56, 506-517.	9.7	278
47	Comprehensive analysis of DNA polymerase III α subunits and their homologs in bacterial genomes. Nucleic Acids Research, 2014, 42, 1393-1413.	14.5	59
48	CAD‑score: A new contact area difference‑based function for evaluation of protein structural models. Proteins: Structure, Function and Bioinformatics, 2013, 81, 149-162.	2.6	123
49	A vitamin B$_{12}$ transporter in *Mycobacterium tuberculosis*. Open Biology, 2013, 3, 120175.	3.6	83
50	Structural and functional analysis of rare missense mutations in human chorionic gonadotrophin β-subunit. Molecular Human Reproduction, 2012, 18, 379-390.	2.8	21
51	Two distinct SSB protein families in nucleo-cytoplasmic large DNA viruses. Bioinformatics, 2012, 28, 3186-3190.	4.1	15
52	A novel inducible mutagenesis system in Mycobacterium tuberculosis. FASEB Journal, 2012, 26, 222.1.	0.5	2
53	The N‑terminal region of the bacterial DNA polymerase PolC features a pair of domains, both distantly related to domain ƒV of the DNA polymerase III τ subunit. FEBS Journal, 2011, 278, 3109-3118.	4.7	4
54	Methods for Sequence‑Structure Alignment. Methods in Molecular Biology, 2011, 857, 55-82.	0.9	10

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55	Computational analysis of DNA replicases in double-stranded DNA viruses: relationship with the genome size. Nucleic Acids Research, 2011, 39, 8291-8305.	14.5	17
56	Identification of new homologs of PD-(D/E)XK nucleases by support vector machines trained on data derived from profileâ€"profile alignments. Nucleic Acids Research, 2011, 39, 1187-1196.	14.5	34
57	Voroprot: an interactive tool for the analysis and visualization of complex geometric features of protein structure. Bioinformatics, 2011, 27, 723-724.	4.1	18
58	Detection of distant evolutionary relationships between protein families using theory of sequence profile-profile comparison. BMC Bioinformatics, 2010, 11, 89.	2.6	43
59	Thermodynamics of radicicol binding to human Hsp90 alpha and beta isoforms. Biophysical Chemistry, 2010, 152, 153-163.	2.8	23
60	Essential roles for <i>imuA</i> â€²- and <i>imuB</i> -encoded accessory factors in DnaE2-dependent mutagenesis in <i>Mycobacterium tuberculosis</i>. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 13093-13098.	7.1	113
61	COMA server for protein distant homology search. Bioinformatics, 2010, 26, 1905-1906.	4.1	30
62	How Proteins Slide on DNA. Biological and Medical Physics Series, 2010, , 39-68.	0.4	4
63	The use of automatic tools and human expertise in templateâ€"based modeling of CASP8 target proteins. Proteins: Structure, Function and Bioinformatics, 2009, 77, 81-88.	2.6	20
64	Re-searcher: a system for recurrent detection of homologous protein sequences. BMC Bioinformatics, 2008, 9, 296.	2.6	5
65	Molecular modeling-based analysis of interactions in the RFC-dependent clamp-loading process. Protein Science, 2008, 11, 2403-2416.	7.6	33
66	Distinct Double- and Single-Stranded DNA Binding of <i>E. coli</i> Replicative DNA Polymerase III Î± Subunit. ACS Chemical Biology, 2008, 3, 577-587.	3.4	32
67	Generation of DNA cleavage specificities of type II restriction endonucleases by reassortment of target recognition domains. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 10358-10363.	7.1	38
68	Restriction endonuclease BpuJI specific for the 5â€²-CCCGT sequence is related to the archaeal Holliday junction resolvase family. Nucleic Acids Research, 2007, 35, 2377-2389.	14.5	9
69	Physical and functional interactions between MutY glycosylase homologue (MYH) and checkpoint proteins Rad9â€"Rad1â€"Hus1. Biochemical Journal, 2006, 400, 53-62.	3.7	83
70	DNA Sliding Clamps: Just the Right Twist to Load onto DNA. Current Biology, 2005, 15, R989-R992.	3.9	10
71	PSI-BLAST-ISS: an intermediate sequence search tool for estimation of the position-specific alignment reliability. BMC Bioinformatics, 2005, 6, 185.	2.6	32
72	Comparative modeling in CASP6 using consensus approach to template selection, sequence-structure alignment, and structure assessment. Proteins: Structure, Function and Bioinformatics, 2005, 61, 99-105.	2.6	66

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73	Progress over the first decade of CASP experiments. Proteins: Structure, Function and Bioinformatics, 2005, 61, 225-236.	2.6	172
74	HhaI DNA Methyltransferase Uses the Protruding Gln237 for Active Flipping of Its Target Cytosine. Structure, 2004, 12, 1047-1055.	3.3	36
75	Sequence-structure mapping errors in the PDB: OB-fold domains. Protein Science, 2004, 13, 1594-1602.	7.6	15
76	Assessment of progress over the CASP experiments. Proteins: Structure, Function and Bioinformatics, 2003, 53, 585-595.	2.6	110
77	Comparative modeling in CASP5: Progress is evident, but alignment errors remain a significant hindrance. Proteins: Structure, Function and Bioinformatics, 2003, 53, 380-388.	2.6	52
78	Selection and characterization of anti-MUC-1 scFvs intended for targeted therapy. Clinical Cancer Research, 2003, 9, 3845S-53S.	7.0	8
79	Comparative modeling of CASP4 target proteins: Combining results of sequence search with three-dimensional structure assessment. Proteins: Structure, Function and Bioinformatics, 2001, 45, 47-54.	2.6	40
80	Processing and evaluation of predictions in CASP4. Proteins: Structure, Function and Bioinformatics, 2001, 45, 13-21.	2.6	131
81	Comparison of performance in successive CASP experiments. Proteins: Structure, Function and Bioinformatics, 2001, 45, 163-170.	2.6	62
82	Structure-based predictions of Rad1, Rad9, Hus1 and Rad17 participation in sliding clamp and clamp-loading complexes. Nucleic Acids Research, 2000, 28, 2481-2493.	14.5	247
83	Structure-based sequence alignment for the Î²-trefoil subdomain of the clostridial neurotoxin family provides residue level information about the putative ganglioside binding site. FEBS Letters, 2000, 482, 119-124.	2.8	39
84	Processing and analysis of CASP3 protein structure predictions. Proteins: Structure, Function and Bioinformatics, 1999, 37, 22-29.	2.6	206
85	Some measures of comparative performance in the three CASPs. Proteins: Structure, Function and Bioinformatics, 1999, 37, 231-237.	2.6	39
86	Addressing the issue of sequence-to-structure alignments in comparative modeling of CASP3 target proteins. Proteins: Structure, Function and Bioinformatics, 1999, 37, 73-80.	2.6	21
87	A modified definition of Sov, a segment-based measure for protein secondary structure prediction assessment. , 1999, 34, 220-223.		323
88	A Sliding Clamp Model for the Rad1 Family of Cell Cycle Checkpoint Proteins. Cell, 1999, 96, 769-770.	28.9	143
89	Processing and analysis of CASP3 protein structure predictions. Proteins: Structure, Function and Bioinformatics, 1999, 37, 22-29.	2.6	142
90	Some measures of comparative performance in the three CASPs. Proteins: Structure, Function and Bioinformatics, 1999, 37, 231-237.	2.6	4

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91	Addressing the issue of sequenceâ€toâ€structure alignments in comparative modeling of CASP3 target proteins. Proteins: Structure, Function and Bioinformatics, 1999, 37, 73-80.	2.6	0
92	Numerical criteria for the evaluation of ab initio predictions of protein structure. Proteins: Structure, Function and Bioinformatics, 1997, 29, 140-150.	2.6	21
93	Criteria for evaluating protein structures derived from comparative modeling. Proteins: Structure, Function and Bioinformatics, 1997, 29, 7-13.	2.6	28
94	Numerical criteria for the evaluation of ab initio predictions of protein structure. Proteins: Structure, Function and Bioinformatics, 1997, 29, 140-150.	2.6	2
95	Numerical criteria for the evaluation of ab initio predictions of protein structure. Proteins: Structure, Function and Bioinformatics, 1997, 29, 140-150.	2.6	12
96	Criteria for evaluating protein structures derived from comparative modeling. Proteins: Structure, Function and Bioinformatics, 1997, 29, 7-13.	2.6	4
97	Different enzymes with similar structures involved in Mg^{2+}-mediated polynucleotidyl transfer. Nature Structural Biology, 1995, 2, 838-841.	9.7	29
98	Five-stranded Î²-sheet sandwiched with two Î±-helices: A structural link between restriction endonucleasesEcoRI andEcoRV. Proteins: Structure, Function and Bioinformatics, 1994, 20, 279-282.	2.6	64
99	How are tRNAs and mRNA arranged in the ribosome? An attempt to correlate the stereochemistry of the tRNA-mRNA interaction with constraints imposed by the ribosomal topography. Nucleic Acids Research, 1992, 20, 2627-2637.	14.5	64
100	The path of a protein chain can be approximated by the conformation dictated by interpeptide ionic bridges. FEBS Letters, 1992, 302, 57-60.	2.8	0
101	Codon-anticodon pairing A model for interacting codon-anticodon duplexes located at the ribosomal A- and P-sites. FEBS Letters, 1992, 313, 133-137.	2.8	24