

ZoltÄ;n GÄ;spÄ;ri

List of Publications by Year in descending order

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Version: 2024-02-01

64
papers

2,390
citations

361413

20
h-index

214800

47
g-index

71
all docs

71
docs citations

71
times ranked

3306
citing authors

#	ARTICLE	IF	CITATIONS
1	Microsatellites in Different Eukaryotic Genomes: Survey and Analysis. <i>Genome Research</i> , 2000, 10, 967-981.	5.5	1,180
2	Vicinal disulfide turns. <i>Protein Engineering, Design and Selection</i> , 2003, 16, 637-639.	2.1	107
3	Functional aspects of the solution structure and dynamics of PAF – a highly stable antifungal protein from <i>Penicillium chrysogenum</i> . <i>FEBS Journal</i> , 2009, 276, 2875-2890.	4.7	83
4	Charged single α -helix: A versatile protein structural motif. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 74, 905-916.	2.6	72
5	Disentangling the complexity of low complexity proteins. <i>Briefings in Bioinformatics</i> , 2020, 21, 458-472.	6.5	70
6	Structure and stability of β^2 -pleated sheets. <i>Journal of Computational Chemistry</i> , 2005, 26, 1155-1168.	3.3	68
7	New Antimicrobial Potential and Structural Properties of PAFB: A Cationic, Cysteine-Rich Protein from <i>Penicillium chrysogenum</i> Q176. <i>Scientific Reports</i> , 2018, 8, 1751.	3.3	65
8	“Invisible” Conformers of an Antifungal Disulfide Protein Revealed by Constrained Cold and Heat Unfolding, CEST-NMR Experiments, and Molecular Dynamics Calculations. <i>Chemistry - A European Journal</i> , 2015, 21, 5136-5144.	3.3	47
9	A Protein Classification Benchmark collection for machine learning. <i>Nucleic Acids Research</i> , 2007, 35, D232-D236.	14.5	39
10	Estimating intrinsic structural preferences of de novo emerging random sequence proteins: Is aggregation the main bottleneck?. <i>FEBS Letters</i> , 2012, 586, 2468-2472.	2.8	36
11	The Putative HORMA Domain Protein Atg101 Dimerizes and Is Required for Starvation-Induced and Selective Autophagy in <i>Drosophila</i> . <i>BioMed Research International</i> , 2014, 2014, 1-13.	1.9	36
12	Comparative structure analysis of proteinase inhibitors from the desert locust, <i>Schistocerca gregaria</i> . <i>FEBS Journal</i> , 2002, 269, 527-537.	0.2	35
13	D19S Mutation of the Cationic, Cysteine-Rich Protein PAF: Novel Insights into Its Structural Dynamics, Thermal Unfolding and Antifungal Function. <i>PLoS ONE</i> , 2017, 12, e0169920.	2.5	35
14	Efficient recognition of folds in protein 3D structures by the improved PRIDE algorithm. <i>Bioinformatics</i> , 2005, 21, 3322-3323.	4.1	30
15	Vicinal disulfide bridge conformers by experimental methods and by ab initio and DFT molecular computations. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 55, 152-168.	2.6	28
16	Charged single alpha-helices in proteomes revealed by a consensus prediction approach. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2012, 1824, 637-646.	2.3	28
17	Distribution and evolution of short tandem repeats in closely related bacterial genomes. <i>Gene</i> , 2008, 410, 18-25.	2.2	27
18	Ensemble-Based Interpretations of NMR Structural Data to Describe Protein Internal Dynamics. <i>Molecules</i> , 2013, 18, 10548-10567.	3.8	27

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19	Same Fold with Different Mobility: A Backbone Dynamics of Small Protease Inhibitors from the Desert Locust, <i>Schistocerca gregaria</i> . <i>Biochemistry</i> , 2004, 43, 3376-3384.	2.5	25
20	Folded and unfolded cross predictions and protein evolution: The case study of coiled coils. <i>FEBS Letters</i> , 2010, 584, 1623-1627.	2.8	24
21	Speciation in Chlamydia : Genomewide Phylogenetic Analyses Identified a Reliable Set of Acquired Genes. <i>Journal of Molecular Evolution</i> , 2003, 57, 672-680.	1.8	20
22	When the Surface Tells What Lies Beneath: Combinatorial Phage-display Mutagenesis Reveals Complex Networks of Surface Core Interactions in the Pacifastin Protease Inhibitor Family. <i>Journal of Molecular Biology</i> , 2007, 370, 63-79.	4.2	20
23	Reconciling the lock and key and dynamic views of canonical serine protease inhibitor action. <i>FEBS Letters</i> , 2010, 584, 203-206.	2.8	20
24	A simple fold with variations: the pacifastin inhibitor family. <i>Bioinformatics</i> , 2004, 20, 448-451.	4.1	17
25	Protein Dynamics as Reported by NMR. <i>Annual Reports on NMR Spectroscopy</i> , 2010, , 35-75.	1.5	17
26	Divergent microsatellite evolution in the human and chimpanzee lineages. <i>FEBS Letters</i> , 2007, 581, 2523-2526.	2.8	14
27	Multidimensional NMR Identifies the Conformational Shift Essential for Catalytic Competence in the 60-kDa <i>Drosophila melanogaster</i> dUTPase Trimer. <i>Journal of Biological Chemistry</i> , 2004, 279, 17945-17950.	3.4	13
28	CoNSEnsX: an ensemble view of protein structures and NMR-derived experimental data. <i>BMC Structural Biology</i> , 2010, 10, 39.	2.3	13
29	A conserved charged single α -helix with a putative steric role in paraspeckle formation. <i>Rna</i> , 2015, 21, 2023-2029.	3.5	13
30	CoNSEnsX Webserver for the Analysis of Protein Structural Ensembles Reflecting Experimentally Determined Internal Dynamics. <i>Journal of Chemical Information and Modeling</i> , 2017, 57, 1728-1734.	5.4	12
31	Accurate NMR Determinations of Proton Proton Distances. <i>Annual Reports on NMR Spectroscopy</i> , 2018, 94, 1-39.	1.5	12
32	Generation and analysis of the conformational potential energy surfaces of N-acetyl-N-methyl-L-alanine-N ² -methylamide. An exploratory ab initio study. <i>Computational and Theoretical Chemistry</i> , 2003, 625, 121-136.	1.5	11
33	MAP Kinase-Mediated Activation of RSK1 and MK2 Substrate Kinases. <i>Structure</i> , 2020, 28, 1101-1113.e5.	3.3	11
34	Coiled coils as possible models of protein structure evolution. <i>Biomolecular Concepts</i> , 2011, 2, 199-210.	2.2	10
35	Fast protein fold estimation from NMR-derived distance restraints. <i>Bioinformatics</i> , 2008, 24, 272-275.	4.1	9
36	Ligand dependent intra and interdomain motions in the PDZ12 tandem regulate binding interfaces in postsynaptic density protein 95. <i>FEBS Letters</i> , 2020, 594, 887-902.	2.8	8

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37	Structure-oriented rational design of chymotrypsin inhibitor models. <i>Protein Engineering, Design and Selection</i> , 2003, 16, 673-681.	2.1	7
38	Fine-tuning the extent and dynamics of binding cleft opening as a potential general regulatory mechanism in parvulin-type peptidyl prolyl isomerases. <i>Scientific Reports</i> , 2017, 7, 44504.	3.3	7
39	Consensus Prediction of Charged Single Alpha-Helices with CSAHserver. <i>Methods in Molecular Biology</i> , 2017, 1484, 25-34.	0.9	7
40	Detecting Atypical Examples of Known Domain Types by Sequence Similarity Searching: The SBASE Domain Library Approach. <i>Current Protein and Peptide Science</i> , 2010, 11, 538-549.	1.4	6
41	Probing Dynamic Protein Ensembles with Atomic Proximity Measures. <i>Current Protein and Peptide Science</i> , 2010, 11, 515-522.	1.4	6
42	Detection of single alpha-helices in large protein sequence sets using hardware acceleration. <i>Journal of Structural Biology</i> , 2018, 204, 109-116.	2.8	6
43	Occurrence of Ordered and Disordered Structural Elements in Postsynaptic Proteins Supports Optimization for Interaction Diversity. <i>Entropy</i> , 2019, 21, 761.	2.2	6
44	Local binding with globally distributed changes in a small protease inhibitor upon enzyme binding. <i>FEBS Journal</i> , 2006, 273, 1831-1842.	4.7	5
45	Is Five Percent Too Small? Analysis of the Overlaps between Disorder, Coiled Coil and Collagen Predictions in Complete Proteomes. <i>Proteomes</i> , 2014, 2, 72-83.	3.5	5
46	Are Proposed Early Genetic Codes Capable of Encoding Viable Proteins?. <i>Journal of Molecular Evolution</i> , 2014, 78, 263-274.	1.8	5
47	Structure and Oxidative Folding of AAI, the Major Alfa-Amylase Inhibitor From Amaranth Seeds. <i>Frontiers in Chemistry</i> , 2020, 8, 180.	3.6	5
48	The Role of Structural Flexibility and Stability in the Interaction of Serine Proteases with their Inhibitors. <i>Current Protein and Peptide Science</i> , 2015, 16, 521-531.	1.4	5
49	Charged sequence motifs increase the propensity towards liquidâ€“liquid phase separation. <i>FEBS Letters</i> , 2022, 596, 1013-1028.	2.8	5
50	Interaction between separated consecutive complement control modules of human C1r: Implications for dimerization of the fullâ€“length protease. <i>FEBS Letters</i> , 2010, 584, 4565-4569.	2.8	4
51	Ensemble-Based Analysis of the Dynamic Allostery in the PSD-95 PDZ3 Domain in Relation to the General Variability of PDZ Structures. <i>International Journal of Molecular Sciences</i> , 2020, 21, 8348.	4.1	4
52	Distribution of disease-causing germline mutations in coiled-coils implies an important role of their N-terminal region. <i>Scientific Reports</i> , 2020, 10, 17333.	3.3	4
53	Is there an excuse for the non-conformist? Notes on the calculated energies, atomâ€“atom contacts and natural abundance of the different conformers of alanine in proteins. <i>Computational and Theoretical Chemistry</i> , 2004, 675, 141-148.	1.5	3
54	A redesigned genetic code for selective labeling in protein NMR. <i>BioEssays</i> , 2008, 30, 772-780.	2.5	3

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55	Diversity of synaptic protein complexes as a function of the abundance of their constituent proteins: A modeling approach. <i>PLoS Computational Biology</i> , 2022, 18, e1009758.	3.2	3
56	PSINDB: the postsynaptic protein-protein interaction database. <i>Database: the Journal of Biological Databases and Curation</i> , 2022, 2022, .	3.0	3
57	Role of Cationic Residues in Fine Tuning the Flexibility of Charged Single α -helices. <i>Biophysical Journal</i> , 2009, 96, 322a.	0.5	2
58	Different modes of barrel opening suggest a complex pathway of ligand binding in human gastrotropin. <i>PLoS ONE</i> , 2019, 14, e0216142.	2.5	2
59	DIPEND: An Open-Source Pipeline to Generate Ensembles of Disordered Segments Using Neighbor-Dependent Backbone Preferences. <i>Biomolecules</i> , 2021, 11, 1505.	4.0	2
60	Assessing Protein Function Through Structural Similarities with CATH. <i>Methods in Molecular Biology</i> , 2020, 2112, 43-57.	0.9	2
61	Directed Evolution-Driven Increase of Structural Plasticity Is a Prerequisite for Binding the Complement Lectin Pathway Blocking MASP-Inhibitor Peptides. <i>ACS Chemical Biology</i> , 2022, , .	3.4	1
62	Acceleration of a protein structure comparison algorithm on FPGA. , 2017, , .		0
63	Evaluation and Selection of Dynamic Protein Structural Ensembles with CoNSEnsX+. <i>Methods in Molecular Biology</i> , 2020, 2112, 241-254.	0.9	0
64	Resonance assignment of the Shank1 PDZ domain. <i>Biomolecular NMR Assignments</i> , 2022, , 1.	0.8	0