ZoltÃ¡n GÃ¡spÃ¡ri

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/6555231/publications.pdf

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	Diversity of synaptic protein complexes as a function of the abundance of their constituent proteins: A modeling approach. PLoS Computational Biology, 2022, 18, e1009758.	3.2	3
2	Resonance assignment of the Shank1 PDZ domain. Biomolecular NMR Assignments, 2022, , 1.	0.8	0
3	Charged sequence motifs increase the propensity towards liquidâ€“liquid phase separation. FEBS Letters, 2022, 596, 1013-1028.	2.8	5
4	PSINDB: the postsynaptic proteinâ€“protein interaction database. Database: the Journal of Biological Databases and Curation, 2022, 2022, .	3.0	3
5	Directed Evolution-Driven Increase of Structural Plasticity Is a Prerequisite for Binding the Complement Lectin Pathway Blocking MASP-Inhibitor Peptides. ACS Chemical Biology, 2022, , .	3.4	1
6	DIPEND: An Open-Source Pipeline to Generate Ensembles of Disordered Segments Using Neighbor-Dependent Backbone Preferences. Biomolecules, 2021, 11, 1505.	4.0	2
7	Disentangling the complexity of low complexity proteins. Briefings in Bioinformatics, 2020, 21, 458-472.	6.5	70
8	Ligandâ€dependent intraâ€and interdomain motions in the PDZ12 tandem regulate binding interfaces in postsynaptic density proteinâ€95. FEBS Letters, 2020, 594, 887-902.	2.8	8
9	Ensemble-Based Analysis of the Dynamic Allostery in the PSD-95 PDZ3 Domain in Relation to the General Variability of PDZ Structures. International Journal of Molecular Sciences, 2020, 21, 8348.	4.1	4
10	MAP Kinase-Mediated Activation of RSK1 and MK2 Substrate Kinases. Structure, 2020, 28, 1101-1113.e5.	3.3	11
11	Distribution of disease-causing germline mutations in coiled-coils implies an important role of their N-terminal region. Scientific Reports, 2020, 10, 17333.	3.3	4
12	Structure and Oxidative Folding of AAI, the Major Alfa-Amylase Inhibitor From Amaranth Seeds. Frontiers in Chemistry, 2020, 8, 180.	3.6	5
13	Evaluation and Selection of Dynamic Protein Structural Ensembles with CoNSEnsX+. Methods in Molecular Biology, 2020, 2112, 241-254.	0.9	0
14	Assessing Protein Function Through Structural Similarities with CATH. Methods in Molecular Biology, 2020, 2112, 43-57.	0.9	2
15	Occurrence of Ordered and Disordered Structural Elements in Postsynaptic Proteins Supports Optimization for Interaction Diversity. Entropy, 2019, 21, 761.	2.2	6
16	Different modes of barrel opening suggest a complex pathway of ligand binding in human gastrotropin. PLoS ONE, 2019, 14, e0216142.	2.5	2
17	New Antimicrobial Potential and Structural Properties of PAFB: A Cationic, Cysteine-Rich Protein from Penicillium chrysogenum Q176. Scientific Reports, 2018, 8, 1751.	3.3	65
18	Accurate NMR Determinations of Protonâ€“Proton Distances. Annual Reports on NMR Spectroscopy, 2018, 94, 1-39.	1.5	12

#	Article	IF	Citations
19	Detection of single alpha-helices in large protein sequence sets using hardware acceleration. Journal of Structural Biology, 2018, 204, 109-116.	2.8	6
20	CoNSEnsX⁺ Webserver for the Analysis of Protein Structural Ensembles Reflecting Experimentally Determined Internal Dynamics. Journal of Chemical Information and Modeling, 2017, 57, 1728-1734.	5.4	12
21	Fine-tuning the extent and dynamics of binding cleft opening as a potential general regulatory mechanism in parvulin-type peptidyl prolyl isomerases. Scientific Reports, 2017, 7, 44504.	3.3	7
22	Consensus Prediction of Charged Single Alpha-Helices with CSAHserver. Methods in Molecular Biology, 2017, 1484, 25-34.	0.9	7
23	Acceleration of a protein structure comparison algorithm on FPGA. , 2017, , .		0
24	D19S Mutation of the Cationic, Cysteine-Rich Protein PAF: Novel Insights into Its Structural Dynamics, Thermal Unfolding and Antifungal Function. PLoS ONE, 2017, 12, e0169920.	2.5	35
25	â€œInvisibleâ€•Conformers of an Antifungal Disulfide Protein Revealed by Constrained Cold and Heat Unfolding, CESTâ€NMR Experiments, and Molecular Dynamics Calculations. Chemistry - A European Journal, 2015, 21, 5136-5144.	3.3	47
26	A conserved charged single Î±-helix with a putative steric role in paraspeckle formation. Rna, 2015, 21, 2023-2029.	3.5	13
27	The Role of Structural Flexibility and Stability in the Interaction of Serine Proteases with their Inhibitors. Current Protein and Peptide Science, 2015, 16, 521-531.	1.4	5
28	Is Five Percent Too Small? Analysis of the Overlaps between Disorder, Coiled Coil and Collagen Predictions in Complete Proteomes. Proteomes, 2014, 2, 72-83.	3.5	5
29	The Putative HORMA Domain Protein Atg101 Dimerizes and Is Required for Starvation-Induced and Selective Autophagy inDrosophila. BioMed Research International, 2014, 2014, 1-13.	1.9	36
30	Are Proposed Early Genetic Codes Capable of Encoding Viable Proteins?. Journal of Molecular Evolution, 2014, 78, 263-274.	1.8	5
31	Ensemble-Based Interpretations of NMR Structural Data to Describe Protein Internal Dynamics. Molecules, 2013, 18, 10548-10567.	3.8	27
32	Charged single alpha-helices in proteomes revealed by a consensus prediction approach. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2012, 1824, 637-646.	2.3	28
33	Estimating intrinsic structural preferences of de novo emerging randomâ€sequence proteins: Is aggregation the main bottleneck?. FEBS Letters, 2012, 586, 2468-2472.	2.8	36
34	Coiled coils as possible models of protein structure evolution. Biomolecular Concepts, 2011, 2, 199-210.	2.2	10
35	Detecting Atypical Examples of Known Domain Types by Sequence Similarity Searching: The SBASE Domain Library Approach. Current Protein and Peptide Science, 2010, 11, 538-549.	1.4	6
36	Probing Dynamic Protein Ensembles with Atomic Proximity Measures. Current Protein and Peptide Science, 2010, 11, 515-522.	1.4	6

#	ARTICLE	IF	CITATIONS
37	Reconciling the lockâ€andâ€key and dynamic views of canonical serine protease inhibitor action. FEBS Letters, 2010, 584, 203-206.	2.8	20
38	Foldedâ€unfolded crossâ€predictions and protein evolution: The case study of coiledâ€coils. FEBS Letters, 2010, 584, 1623-1627.	2.8	24
39	Interaction between separated consecutive complement control modules of human C1r: Implications for dimerization of the fullâ€length protease. FEBS Letters, 2010, 584, 4565-4569.	2.8	4
40	CoNSEnsX: an ensemble view of protein structures and NMR-derived experimental data. BMC Structural Biology, 2010, 10, 39.	2.3	13
41	Protein Dynamics as Reported by NMR. Annual Reports on NMR Spectroscopy, 2010, , 35-75.	1.5	17
42	Charged single Î±â€helix: A versatile protein structural motif. Proteins: Structure, Function and Bioinformatics, 2009, 74, 905-916.	2.6	72
43	Functional aspects of the solution structure and dynamics of PAF â€“ a highlyâ€stable antifungal protein from PenicilliumÂchrysogenum. FEBS Journal, 2009, 276, 2875-2890.	4.7	83
44	Role of Cationic Residues in Fine Tuning the Flexibility of Charged Single Î±-helices. Biophysical Journal, 2009, 96, 322a.	0.5	2
45	A redesigned genetic code for selective labeling in protein NMR. BioEssays, 2008, 30, 772-780.	2.5	3
46	Distribution and evolution of short tandem repeats in closely related bacterial genomes. Gene, 2008, 410, 18-25.	2.2	27
47	Fast protein fold estimation from NMR-derived distance restraints. Bioinformatics, 2008, 24, 272-275.	4.1	9
48	A Protein Classification Benchmark collection for machine learning. Nucleic Acids Research, 2007, 35, D232-D236.	14.5	39
49	When the Surface Tells What Lies Beneath: Combinatorial Phage-display Mutagenesis Reveals Complex Networks of Surfaceâ€“Core Interactions in the Pacifastin Protease Inhibitor Family. Journal of Molecular Biology, 2007, 370, 63-79.	4.2	20
50	Divergent microsatellite evolution in the human and chimpanzee lineages. FEBS Letters, 2007, 581, 2523-2526.	2.8	14
51	Local binding with globally distributed changes in a small protease inhibitor upon enzyme binding. FEBS Journal, 2006, 273, 1831-1842.	4.7	5
52	Structure and stability of Î²-pleated sheets. Journal of Computational Chemistry, 2005, 26, 1155-1168.	3.3	68
53	Efficient recognition of folds in protein 3D structures by the improved PRIDE algorithm. Bioinformatics, 2005, 21, 3322-3323.	4.1	30
54	A simple fold with variations: the pacifastin inhibitor family. Bioinformatics, 2004, 20, 448-451.	4.1	17

#	Article	IF	Citations
55	Multidimensional NMR Identifies the Conformational Shift Essential for Catalytic Competence in the 60-kDa Drosophila melanogaster dUTPase Trimer. Journal of Biological Chemistry, 2004, 279, 17945-17950.	3.4	13
56	Vicinal disulfide bridge conformers by experimental methods and by ab initio and DFT molecular computations. Proteins: Structure, Function and Bioinformatics, 2004, 55, 152-168.	2.6	28
57	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. Computational and Theoretical Chemistry, 2004, 675, 141-148.	1.5	3
58	Same Fold with Different Mobility:Â Backbone Dynamics of Small Protease Inhibitors from the Desert Locust,Schistocerca gregariaâ€. Biochemistry, 2004, 43, 3376-3384.	2.5	25
59	Speciation in Chlamydia : Genomewide Phylogenetic Analyses Identified a Reliable Set of Acquired Genes. Journal of Molecular Evolution, 2003, 57, 672-680.	1.8	20
60	Generation and analysis of the conformational potential energy surfaces of N-acetyl-N-methyl-l-alanine-Nâ€²-methylamide. An exploratory ab initio study. Computational and Theoretical Chemistry, 2003, 625, 121-136.	1.5	11
61	Structure-oriented rational design of chymotrypsin inhibitor models. Protein Engineering, Design and Selection, 2003, 16, 673-681.	2.1	7
62	Vicinal disulfide turns. Protein Engineering, Design and Selection, 2003, 16, 637-639.	2.1	107
63	Comparative structure analysis of proteinase inhibitors from the desert locust, Schistocerca gregaria. FEBS Journal, 2002, 269, 527-537.	0.2	35
64	Microsatellites in Different Eukaryotic Genomes: Survey and Analysis. Genome Research, 2000, 10, 967-981.	5.5	1,180