Zsuzsanna Dosztanyi

List of Publications by Year
in descending order

65 papers	11,448 citations	87888 38 h-index	118850 62 g-index
71 all docs	71 docs citations	71 times ranked	15239 citing authors

#	Article	IF	Citations
1	DisProt in 2022: improved quality and accessibility of protein intrinsic disorder annotation. Nucleic Acids Research, 2022, 50, D480-D487.	14.5	117
2	MobiDB: intrinsically disordered proteins in 2021. Nucleic Acids Research, 2021, 49, D361-D367.	14.5	183
3	MobiDB-lite 3.0: fast consensus annotation of intrinsic disorder flavors in proteins. Bioinformatics, 2021, 36, 5533-5534.	4.1	47
4	The MemMoRF database for recognizing disordered protein regions interacting with cellular membranes. Nucleic Acids Research, 2021, 49, D355-D360.	14.5	8
5	Mutations of Intrinsically Disordered Protein Regions Can Drive Cancer but Lack Therapeutic Strategies. Biomolecules, 2021, 11, 381.	4.0	26
6	IUPred3: prediction of protein disorder enhanced with unambiguous experimental annotation and visualization of evolutionary conservation. Nucleic Acids Research, 2021, 49, W297-W303.	14.5	258
7	Functions of intrinsically disordered proteins through evolutionary lenses. Progress in Molecular Biology and Translational Science, 2021, 183, 45-74.	1.7	10
8	PhaSePro: the database of proteins driving liquidâ€"liquid phase separation. Nucleic Acids Research, 2020, 48, D360-D367.	14.5	100
9	DisProt: intrinsic protein disorder annotation in 2020. Nucleic Acids Research, 2020, 48, D269-D276.	14.5	141
10	Disentangling the complexity of low complexity proteins. Briefings in Bioinformatics, 2020, 21, 458-472.	6.5	70
11	Evolutionary Study of Disorder in Protein Sequences. Biomolecules, 2020, 10, 1413.	4.0	16
12	Ancient Evolutionary Origin of Intrinsically Disordered Cancer Risk Regions. Biomolecules, 2020, 10, 1115.	4.0	11
13	PlaToLoCo: the first web meta-server for visualization and annotation of low complexity regions in proteins. Nucleic Acids Research, 2020, 48, W77-W84.	14.5	71
14	Analyzing Protein Disorder with IUPred2A. Current Protocols in Bioinformatics, 2020, 70, e99.	25.8	233
15	Sequential, Structural and FunctionalÂProperties of Protein Complexes Are Defined by How Folding and Binding Intertwine. Journal of Molecular Biology, 2019, 431, 4408-4428.	4.2	12
16	Largeâ€Scale Analysis of Redoxâ€Sensitive Conditionally Disordered Protein Regions Reveals Their Widespread Nature and Key Roles in Highâ€Level Eukaryotic Processes. Proteomics, 2019, 19, e1800070.	2.2	17
17	Bioinformatical Approaches to Unstructured/Disordered Proteins and Their Complexes. Springer Series on Bio- and Neurosystems, 2019, , 561-596.	0.2	0
18	An intrinsically disordered proteins community for ELIXIR. F1000Research, 2019, 8, 1753.	1.6	12

#	Article	IF	Citations
19	DIBS: a repository of disordered binding sites mediating interactions with ordered proteins. Bioinformatics, 2018, 34, 535-537.	4.1	72
20	A comprehensive assessment of long intrinsic protein disorder from the DisProt database. Bioinformatics, 2018, 34, 445-452.	4.1	53
21	Prediction of protein disorder based on IUPred. Protein Science, 2018, 27, 331-340.	7.6	164
22	IUPred2A: context-dependent prediction of protein disorder as a function of redox state and protein binding. Nucleic Acids Research, 2018, 46, W329-W337.	14.5	1,080
23	MobiDB 3.0: more annotations for intrinsic disorder, conformational diversity and interactions in proteins. Nucleic Acids Research, 2018, 46, D471-D476.	14.5	190
24	Bioinformatics Approaches to the Structure and Function of Intrinsically Disordered Proteins. , 2017, , 167-203.		5
25	DisProt 7.0: a major update of the database of disordered proteins. Nucleic Acids Research, 2017, 45, D219-D227.	14.5	242
26	InterPro in 2017â€"beyond protein family and domain annotations. Nucleic Acids Research, 2017, 45, D190-D199.	14.5	1,358
27	Degrons in cancer. Science Signaling, 2017, 10, .	3.6	100
28	Simultaneous quantification of protein order and disorder. Nature Chemical Biology, 2017, 13, 339-342.	8.0	113
29	MobiDB-lite: fast and highly specific consensus prediction of intrinsic disorder in proteins. Bioinformatics, 2017, 33, 1402-1404.	4.1	161
30	Novel linear motif filtering protocol reveals the role of the LC8 dynein light chain in the Hippo pathway. PLoS Computational Biology, 2017, 13, e1005885.	3.2	20
31	Systematic analysis of somatic mutations driving cancer: uncovering functional protein regions in disease development. Biology Direct, 2016, 11, 23.	4.6	15
32	Systematic discovery of linear binding motifs targeting an ancient protein interaction surface on <scp>MAP</scp> kinases. Molecular Systems Biology, 2015, 11, 837.	7.2	60
33	Prediction and Analysis of Intrinsically Disordered Proteins. Methods in Molecular Biology, 2015, 1261, 35-59.	0.9	9
34	Bioinformatical Approaches to Unstructured/Disordered Proteins and Their Interactions. Springer Series in Bio-/neuroinformatics, 2014, , 525-556.	0.1	1
35	The N-Terminal Intrinsically Disordered Domain of Mgm101p Is Localized to the Mitochondrial Nucleoid. PLoS ONE, 2013, 8, e56465.	2.5	8
36	D2P2: database of disordered protein predictions. Nucleic Acids Research, 2012, 41, D508-D516.	14.5	570

#	Article	IF	Citations
37	Is there a biological cost of protein disorder? Analysis of cancer-associated mutations. Molecular BioSystems, 2012, 8, 296-307.	2.9	43
38	Disordered Binding Regions and Linear Motifsâ€"Bridging the Gap between Two Models of Molecular Recognition. PLoS ONE, 2012, 7, e46829.	2.5	60
39	The expanding view of proteinâ€"protein interactions: complexes involving intrinsically disordered proteins. Physical Biology, 2011, 8, 035003.	1.8	55
40	Proteins with Complex Architecture as Potential Targets for Drug Design: A Case Study of Mycobacterium tuberculosis. PLoS Computational Biology, 2011, 7, e1002118.	3.2	21
41	Bioinformatical approaches to characterize intrinsically disordered/unstructured proteins. Briefings in Bioinformatics, 2010, 11, 225-243.	6.5	107
42	ANCHOR: web server for predicting protein binding regions in disordered proteins. Bioinformatics, 2009, 25, 2745-2746.	4.1	527
43	Prediction of Protein Binding Regions in Disordered Proteins. PLoS Computational Biology, 2009, 5, e1000376.	3.2	523
44	Prediction of Protein Disorder. Methods in Molecular Biology, 2008, 426, 103-115.	0.9	56
45	Substrate Preference of Transglutaminase 2 Revealed by Logistic Regression Analysis and Intrinsic Disorder Examination. Journal of Molecular Biology, 2008, 383, 390-402.	4.2	35
46	Prediction of Protein Disorder at the Domain Level. Current Protein and Peptide Science, 2007, 8, 161-171.	1.4	71
47	Towards Proteomic Approaches for the Identification of Structural Disorder. Current Protein and Peptide Science, 2007, 8, 173-179.	1.4	20
48	Molecular Principles of the Interactions of Disordered Proteins. Journal of Molecular Biology, 2007, 372, 549-561.	4.2	242
49	Disorder and Sequence Repeats in Hub Proteins and Their Implications for Network Evolution. Journal of Proteome Research, 2006, 5, 2985-2995.	3.7	312
50	Prevalent Structural Disorder inE.coliandS.cerevisiaeProteomes. Journal of Proteome Research, 2006, 5, 1996-2000.	3.7	119
51	TMDET: web server for detecting transmembrane regions of proteins by using their 3D coordinates. Bioinformatics, 2005, 21, 1276-1277.	4.1	132
52	IUPred: web server for the prediction of intrinsically unstructured regions of proteins based on estimated energy content. Bioinformatics, 2005, 21, 3433-3434.	4.1	1,832
53	Integron-associated Mobile Gene Cassettes Code for Folded Proteins: The Structure of Bal32a, a New Member of the Adaptable Î±+Î² Barrel Family. Journal of Molecular Biology, 2005, 346, 1229-1241.	4.2	20
54	The Pairwise Energy Content Estimated from Amino Acid Composition Discriminates between Folded and Intrinsically Unstructured Proteins. Journal of Molecular Biology, 2005, 347, 827-839.	4.2	911

#	Article	IF	Citations
55	PDB_TM: selection and membrane localization of transmembrane proteins in the protein data bank. Nucleic Acids Research, 2004, 33, D275-D278.	14.5	245
56	Transmembrane proteins in the Protein Data Bank: identification and classification. Bioinformatics, 2004, 20, 2964-2972.	4.1	216
57	Noncovalent Cross-Links in Context with Other Structural and Functional Elements of Proteins.. ChemInform, 2004, 35, no.	0.0	0
58	Noncovalent Cross-links in Context with Other Structural and Functional Elements of Proteinsâ€. Journal of Chemical Information and Computer Sciences, 2004, 44, 347-351.	2.8	7
59	Servers for sequence-structure relationship analysis and prediction. Nucleic Acids Research, 2003, 31, 3359-3363.	14.5	12
60	SCide: identification of stabilization centers in proteins. Bioinformatics, 2003, 19, 899-900.	4.1	99
61	Amino acid similarity matrices based on force fields. Bioinformatics, 2001, 17, 686-699.	4.1	22
62	Stabilization centers in various proteins. Theoretical Chemistry Accounts, 1999, 101, 27-32.	1.4	8
63	The role of long-range interactions in defining the secondary structure of proteins is overestimated. Bioinformatics, 1997, 13, 297-301.	4.1	6
64	Stabilization centers in proteins:Identification, characterization and predictions. Journal of Molecular Biology, 1997, 272, 597-612.	4.2	144
65	Interresidue interactions in protein classes. Proteins: Structure, Function and Bioinformatics, 1997, 27, 360-366.	2.6	0