

# Zsuzsanna Dosztanyi

## List of Publications by Year in descending order

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Version: 2024-02-01

64  
papers

11,448  
citations

100601

38  
h-index

134545

62  
g-index

71  
all docs

71  
docs citations

71  
times ranked

16975  
citing authors

#	ARTICLE	IF	CITATIONS
1	DisProt in 2022: improved quality and accessibility of protein intrinsic disorder annotation. <i>Nucleic Acids Research</i> , 2022, 50, D480-D487.	6.5	117
2	MobiDB: intrinsically disordered proteins in 2021. <i>Nucleic Acids Research</i> , 2021, 49, D361-D367.	6.5	183
3	MobiDB-lite 3.0: fast consensus annotation of intrinsic disorder flavors in proteins. <i>Bioinformatics</i> , 2021, 36, 5533-5534.	1.8	47
4	The MemMoRF database for recognizing disordered protein regions interacting with cellular membranes. <i>Nucleic Acids Research</i> , 2021, 49, D355-D360.	6.5	8
5	Mutations of Intrinsically Disordered Protein Regions Can Drive Cancer but Lack Therapeutic Strategies. <i>Biomolecules</i> , 2021, 11, 381.	1.8	26
6	IUPred3: prediction of protein disorder enhanced with unambiguous experimental annotation and visualization of evolutionary conservation. <i>Nucleic Acids Research</i> , 2021, 49, W297-W303.	6.5	258
7	Functions of intrinsically disordered proteins through evolutionary lenses. <i>Progress in Molecular Biology and Translational Science</i> , 2021, 183, 45-74.	0.9	10
8	PhaSePro: the database of proteins driving liquid-liquid phase separation. <i>Nucleic Acids Research</i> , 2020, 48, D360-D367.	6.5	100
9	DisProt: intrinsic protein disorder annotation in 2020. <i>Nucleic Acids Research</i> , 2020, 48, D269-D276.	6.5	141
10	Disentangling the complexity of low complexity proteins. <i>Briefings in Bioinformatics</i> , 2020, 21, 458-472.	3.2	70
11	Evolutionary Study of Disorder in Protein Sequences. <i>Biomolecules</i> , 2020, 10, 1413.	1.8	16
12	Ancient Evolutionary Origin of Intrinsically Disordered Cancer Risk Regions. <i>Biomolecules</i> , 2020, 10, 1115.	1.8	11
13	PlaToLoCo: the first web meta-server for visualization and annotation of low complexity regions in proteins. <i>Nucleic Acids Research</i> , 2020, 48, W77-W84.	6.5	71
14	Analyzing Protein Disorder with IUPred2A. <i>Current Protocols in Bioinformatics</i> , 2020, 70, e99.	25.8	233
15	Sequential, Structural and Functional Properties of Protein Complexes Are Defined by How Folding and Binding Intertwine. <i>Journal of Molecular Biology</i> , 2019, 431, 4408-4428.	2.0	12
16	Large-scale Analysis of Redox-sensitive Conditionally Disordered Protein Regions Reveals Their Widespread Nature and Key Roles in High-level Eukaryotic Processes. <i>Proteomics</i> , 2019, 19, e1800070.	1.3	17
17	Bioinformatical Approaches to Unstructured/Disordered Proteins and Their Complexes. <i>Springer Series on Bio- and Neurosystems</i> , 2019, , 561-596.	0.2	0
18	An intrinsically disordered proteins community for ELIXIR. <i>F1000Research</i> , 2019, 8, 1753.	0.8	12

#	ARTICLE	IF	CITATIONS
19	DIBS: a repository of disordered binding sites mediating interactions with ordered proteins. <i>Bioinformatics</i> , 2018, 34, 535-537.	1.8	72
20	A comprehensive assessment of long intrinsic protein disorder from the DisProt database. <i>Bioinformatics</i> , 2018, 34, 445-452.	1.8	53
21	Prediction of protein disorder based on IUPred. <i>Protein Science</i> , 2018, 27, 331-340.	3.1	164
22	IUPred2A: context-dependent prediction of protein disorder as a function of redox state and protein binding. <i>Nucleic Acids Research</i> , 2018, 46, W329-W337.	6.5	1,080
23	MobiDB 3.0: more annotations for intrinsic disorder, conformational diversity and interactions in proteins. <i>Nucleic Acids Research</i> , 2018, 46, D471-D476.	6.5	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. <i>Nucleic Acids Research</i> , 2017, 45, D219-D227.	6.5	242
26	InterPro in 2017 – beyond protein family and domain annotations. <i>Nucleic Acids Research</i> , 2017, 45, D190-D199.	6.5	1,358
27	Degrons in cancer. <i>Science Signaling</i> , 2017, 10, .	1.6	100
28	Simultaneous quantification of protein order and disorder. <i>Nature Chemical Biology</i> , 2017, 13, 339-342.	3.9	113
29	MobiDB-lite: fast and highly specific consensus prediction of intrinsic disorder in proteins. <i>Bioinformatics</i> , 2017, 33, 1402-1404.	1.8	161
30	Novel linear motif filtering protocol reveals the role of the LC8 dynein light chain in the Hippo pathway. <i>PLoS Computational Biology</i> , 2017, 13, e1005885.	1.5	20
31	Systematic analysis of somatic mutations driving cancer: uncovering functional protein regions in disease development. <i>Biology Direct</i> , 2016, 11, 23.	1.9	15
32	Systematic discovery of linear binding motifs targeting an ancient protein interaction surface on <sc>MAP</sc> kinases. <i>Molecular Systems Biology</i> , 2015, 11, 837.	3.2	60
33	Prediction and Analysis of Intrinsically Disordered Proteins. <i>Methods in Molecular Biology</i> , 2015, 1261, 35-59.	0.4	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. <i>PLoS ONE</i> , 2013, 8, e56465.	1.1	8
36	D2P2: database of disordered protein predictions. <i>Nucleic Acids Research</i> , 2012, 41, D508-D516.	6.5	570

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37	Is there a biological cost of protein disorder? Analysis of cancer-associated mutations. <i>Molecular BioSystems</i> , 2012, 8, 296-307.	2.9	43
38	Disordered Binding Regions and Linear Motifs—Bridging the Gap between Two Models of Molecular Recognition. <i>PLoS ONE</i> , 2012, 7, e46829.	1.1	60
39	The expanding view of protein—protein interactions: complexes involving intrinsically disordered proteins. <i>Physical Biology</i> , 2011, 8, 035003.	0.8	55
40	Proteins with Complex Architecture as Potential Targets for Drug Design: A Case Study of <i>Mycobacterium tuberculosis</i> . <i>PLoS Computational Biology</i> , 2011, 7, e1002118.	1.5	21
41	Bioinformatical approaches to characterize intrinsically disordered/unstructured proteins. <i>Briefings in Bioinformatics</i> , 2010, 11, 225-243.	3.2	107
42	ANCHOR: web server for predicting protein binding regions in disordered proteins. <i>Bioinformatics</i> , 2009, 25, 2745-2746.	1.8	527
43	Prediction of Protein Binding Regions in Disordered Proteins. <i>PLoS Computational Biology</i> , 2009, 5, e1000376.	1.5	523
44	Prediction of Protein Disorder. <i>Methods in Molecular Biology</i> , 2008, 426, 103-115.	0.4	56
45	Substrate Preference of Transglutaminase 2 Revealed by Logistic Regression Analysis and Intrinsic Disorder Examination. <i>Journal of Molecular Biology</i> , 2008, 383, 390-402.	2.0	35
46	Prediction of Protein Disorder at the Domain Level. <i>Current Protein and Peptide Science</i> , 2007, 8, 161-171.	0.7	71
47	Towards Proteomic Approaches for the Identification of Structural Disorder. <i>Current Protein and Peptide Science</i> , 2007, 8, 173-179.	0.7	20
48	Molecular Principles of the Interactions of Disordered Proteins. <i>Journal of Molecular Biology</i> , 2007, 372, 549-561.	2.0	242
49	Disorder and Sequence Repeats in Hub Proteins and Their Implications for Network Evolution. <i>Journal of Proteome Research</i> , 2006, 5, 2985-2995.	1.8	312
50	Prevalent Structural Disorder in <i>E.coli</i> and <i>S.cerevisiae</i> Proteomes. <i>Journal of Proteome Research</i> , 2006, 5, 1996-2000.	1.8	119
51	TMDET: web server for detecting transmembrane regions of proteins by using their 3D coordinates. <i>Bioinformatics</i> , 2005, 21, 1276-1277.	1.8	132
52	IUPred: web server for the prediction of intrinsically unstructured regions of proteins based on estimated energy content. <i>Bioinformatics</i> , 2005, 21, 3433-3434.	1.8	1,832
53	Integron-associated Mobile Gene Cassettes Code for Folded Proteins: The Structure of Bal32a, a New Member of the Adaptable $\beta$ -Barrel Family. <i>Journal of Molecular Biology</i> , 2005, 346, 1229-1241.	2.0	20
54	The Pairwise Energy Content Estimated from Amino Acid Composition Discriminates between Folded and Intrinsically Unstructured Proteins. <i>Journal of Molecular Biology</i> , 2005, 347, 827-839.	2.0	911

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55	PDB_TM: selection and membrane localization of transmembrane proteins in the protein data bank. <i>Nucleic Acids Research</i> , 2004, 33, D275-D278.	6.5	245
56	Transmembrane proteins in the Protein Data Bank: identification and classification. <i>Bioinformatics</i> , 2004, 20, 2964-2972.	1.8	216
57	Noncovalent Cross-Links in Context with Other Structural and Functional Elements of Proteins.. <i>ChemInform</i> , 2004, 35, no.	0.1	0
58	Noncovalent Cross-links in Context with Other Structural and Functional Elements of Proteinsâ€. <i>Journal of Chemical Information and Computer Sciences</i> , 2004, 44, 347-351.	2.8	7
59	Servers for sequence-structure relationship analysis and prediction. <i>Nucleic Acids Research</i> , 2003, 31, 3359-3363.	6.5	12
60	SCide: identification of stabilization centers in proteins. <i>Bioinformatics</i> , 2003, 19, 899-900.	1.8	99
61	Amino acid similarity matrices based on force fields. <i>Bioinformatics</i> , 2001, 17, 686-699.	1.8	22
62	Stabilization centers in various proteins. <i>Theoretical Chemistry Accounts</i> , 1999, 101, 27-32.	0.5	8
63	The role of long-range interactions in defining the secondary structure of proteins is overestimated. <i>Bioinformatics</i> , 1997, 13, 297-301.	1.8	6
64	Stabilization centers in proteins: Identification, characterization and predictions. <i>Journal of Molecular Biology</i> , 1997, 272, 597-612.	2.0	144