

# Bálint Mácsáros

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7621475/publications.pdf>

Version: 2024-02-01

36  
papers

4,124  
citations

331670

21  
h-index

361022

35  
g-index

43  
all docs

43  
docs citations

43  
times ranked

7069  
citing authors

#	ARTICLE	IF	CITATIONS
1	The IntAct database: efficient access to fine-grained molecular interaction data. <i>Nucleic Acids Research</i> , 2022, 50, D648-D653.	14.5	89
2	DisProt in 2022: improved quality and accessibility of protein intrinsic disorder annotation. <i>Nucleic Acids Research</i> , 2022, 50, D480-D487.	14.5	117
3	ECO: the Evidence and Conclusion Ontology, an update for 2022. <i>Nucleic Acids Research</i> , 2022, 50, D1515-D1521.	14.5	21
4	The Eukaryotic Linear Motif resource: 2022 release. <i>Nucleic Acids Research</i> , 2022, 50, D497-D508.	14.5	144
5	PSINDB: the postsynaptic proteinâ€“protein interaction database. <i>Database: the Journal of Biological Databases and Curation</i> , 2022, 2022, .	3.0	3
6	Short linear motif candidates in the cell entry system used by SARS-CoV-2 and their potential therapeutic implications. <i>Science Signaling</i> , 2021, 14, .	3.6	61
7	Computational resources for identifying and describing proteins driving liquidâ€“liquid phase separation. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	40
8	Mutations of Intrinsically Disordered Protein Regions Can Drive Cancer but Lack Therapeutic Strategies. <i>Biomolecules</i> , 2021, 11, 381.	4.0	26
9	PhaSePro: the database of proteins driving liquidâ€“liquid phase separation. <i>Nucleic Acids Research</i> , 2020, 48, D360-D367.	14.5	100
10	DisProt: intrinsic protein disorder annotation in 2020. <i>Nucleic Acids Research</i> , 2020, 48, D269-D276.	14.5	141
11	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
12	A guide to regulation of the formation of biomolecular condensates. <i>FEBS Journal</i> , 2020, 287, 1924-1935.	4.7	48
13	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.	4.2	12
14	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.	2.2	17
15	Sequence and Structure Properties Uncover the Natural Classification of Protein Complexes Formed by Intrinsically Disordered Proteins via Mutual Synergistic Folding. <i>International Journal of Molecular Sciences</i> , 2019, 20, 5460.	4.1	3
16	Bioinformatical Approaches to Unstructured/Disordered Proteins and Their Complexes. <i>Springer Series on Bio- and Neurosystems</i> , 2019, , 561-596.	0.2	0
17	An intrinsically disordered proteins community for ELIXIR. <i>F1000Research</i> , 2019, 8, 1753.	1.6	12
18	DIBS: a repository of disordered binding sites mediating interactions with ordered proteins. <i>Bioinformatics</i> , 2018, 34, 535-537.	4.1	72

#	ARTICLE	IF	CITATIONS
19	Structural Principles Governing Disease-Causing Germline Mutations. <i>Journal of Molecular Biology</i> , 2018, 430, 4955-4970.	4.2	9
20	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.	14.5	1,080
21	MobiDB 3.0: more annotations for intrinsic disorder, conformational diversity and interactions in proteins. <i>Nucleic Acids Research</i> , 2018, 46, D471-D476.	14.5	190
22	Degrans in cancer. <i>Science Signaling</i> , 2017, 10, .	3.6	100
23	MFIB: a repository of protein complexes with mutual folding induced by binding. <i>Bioinformatics</i> , 2017, 33, 3682-3684.	4.1	61
24	Systematic analysis of somatic mutations driving cancer: uncovering functional protein regions in disease development. <i>Biology Direct</i> , 2016, 11, 23.	4.6	15
25	Systematic discovery of linear binding motifs targeting an ancient protein interaction surface on <scp>MAP</scp> kinases. <i>Molecular Systems Biology</i> , 2015, 11, 837.	7.2	60
26	A word of caution about biological inference – Revisiting cysteine covalent state predictions. <i>FEBS Open Bio</i> , 2014, 4, 310-314.	2.3	2
27	Bioinformatical Approaches to Unstructured/Disordered Proteins and Their Interactions. Springer Series in Bio-/neuroinformatics, 2014, , 525-556.	0.1	1
28	Is there a biological cost of protein disorder? Analysis of cancer-associated mutations. <i>Molecular BioSystems</i> , 2012, 8, 296-307.	2.9	43
29	Disordered Binding Regions and Linear Motifs – Bridging the Gap between Two Models of Molecular Recognition. <i>PLoS ONE</i> , 2012, 7, e46829.	2.5	60
30	The expanding view of protein – protein interactions: complexes involving intrinsically disordered proteins. <i>Physical Biology</i> , 2011, 8, 035003.	1.8	55
31	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.	3.2	21
32	Bioinformatical approaches to characterize intrinsically disordered/unstructured proteins. <i>Briefings in Bioinformatics</i> , 2010, 11, 225-243.	6.5	107
33	ANCHOR: web server for predicting protein binding regions in disordered proteins. <i>Bioinformatics</i> , 2009, 25, 2745-2746.	4.1	527
34	Prediction of Protein Binding Regions in Disordered Proteins. <i>PLoS Computational Biology</i> , 2009, 5, e1000376.	3.2	523
35	Assessing Conservation of Disordered Regions in Proteins. <i>The Open Proteomics Journal</i> , 2008, 1, 46-53.	0.4	15
36	Molecular Principles of the Interactions of Disordered Proteins. <i>Journal of Molecular Biology</i> , 2007, 372, 549-561.	4.2	242