

Monika Fuxreiter

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

83
papers

7,670
citations

38
h-index

87
g-index

95
ext. papers

9,330
ext. citations

10.1
avg, IF

6.54
L-index

#	Paper	IF	Citations
83	Adventures on the routes of protein evolution - in memoriam Dan Salah Tawfik (1955 - 2021).. <i>Journal of Molecular Biology</i> , 2022 , 434, 167462	6.5	2
82	FuzDB: a new phase in understanding fuzzy interactions. <i>Nucleic Acids Research</i> , 2021 ,	20.1	5
81	Frustration in Fuzzy Protein Complexes Leads to Interaction Versatility. <i>Journal of Physical Chemistry B</i> , 2021 , 125, 2513-2520	3.4	17
80	Generic nature of the condensed states of proteins. <i>Nature Cell Biology</i> , 2021 , 23, 587-594	23.4	25
79	MobiDB: intrinsically disordered proteins in 2021. <i>Nucleic Acids Research</i> , 2021 , 49, D361-D367	20.1	51
78	Spot in a drop: mutations in aberrant condensates. <i>Nature Reviews Molecular Cell Biology</i> , 2021 , 22, 162-167	16.7	2
77	Fuzziness and Frustration in the Energy Landscape of Protein Folding, Function, and Assembly. <i>Accounts of Chemical Research</i> , 2021 , 54, 1251-1259	24.3	28
76	Sequence Determinants of the Aggregation of Proteins Within Condensates Generated by Liquid-liquid Phase Separation. <i>Journal of Molecular Biology</i> , 2021 , 167201	6.5	4
75	Observation of an E5ynuclein liquid droplet state and its maturation into Lewy body-like assemblies. <i>Journal of Molecular Cell Biology</i> , 2021 , 13, 282-294	6.3	25
74	Sequence-based prediction of protein binding mode landscapes. <i>PLoS Computational Biology</i> , 2020 , 16, e1007864	5	21
73	Sequence-Based Prediction of Fuzzy Protein Interactions. <i>Journal of Molecular Biology</i> , 2020 , 432, 2289-2303	23.9	46
72	Fuzzy protein theory for disordered proteins. <i>Biochemical Society Transactions</i> , 2020 , 48, 2557-2564	5.1	5
71	Widespread occurrence of the droplet state of proteins in the human proteome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 33254-33262	11.5	55
70	Rapid Biophysical Characterization and NMR Spectroscopy Structural Analysis of Small Proteins from Bacteria and Archaea. <i>ChemBioChem</i> , 2020 , 21, 1178-1187	3.8	14
69	Patterns of Dynamics Comprise a Conserved Evolutionary Trait. <i>Journal of Molecular Biology</i> , 2020 , 432, 497-507	6.5	7
68	Classifying the Binding Modes of Disordered Proteins. <i>International Journal of Molecular Sciences</i> , 2020 , 21,	6.3	22
67	Asymmetric dynamic coupling promotes alternative evolutionary pathways in an enzyme dimer. <i>Scientific Reports</i> , 2020 , 10, 18866	4.9	0

66	Specific and Fuzzy Interactions Cooperate in Modulating Protein Half-Life. <i>Journal of Molecular Biology</i> , 2019 , 431, 1700-1707	6.5	1
65	Fold or not to fold upon binding - does it really matter?. <i>Current Opinion in Structural Biology</i> , 2019 , 54, 19-25	8.1	57
64	Fuzziness in Protein Interactions-A Historical Perspective. <i>Journal of Molecular Biology</i> , 2018 , 430, 2278-2287	12.8	85
63	Protein Phase Separation: A New Phase in Cell Biology. <i>Trends in Cell Biology</i> , 2018 , 28, 420-435	18.3	869
62	Simulations of Higher-Order Protein Organizations Using a Fuzzy Framework. <i>Complexity</i> , 2018 , 2018, 1-10	1.6	3
61	Experimental Characterization of Fuzzy Protein Assemblies: Interactions of Paramyxoviral N Domains With Their Functional Partners. <i>Methods in Enzymology</i> , 2018 , 611, 137-192	1.7	7
60	Towards a Stochastic Paradigm: From Fuzzy Ensembles to Cellular Functions. <i>Molecules</i> , 2018 , 23,	4.8	15
59	The Empirical Valence Bond Approach as a Tool for Designing Artificial Catalysts 2017 , 173-198		
58	Simultaneous quantification of protein order and disorder. <i>Nature Chemical Biology</i> , 2017 , 13, 339-342	11.7	83
57	Fuzziness enables context dependence of protein interactions. <i>FEBS Letters</i> , 2017 , 591, 2682-2695	3.8	46
56	FuzDB: database of fuzzy complexes, a tool to develop stochastic structure-function relationships for protein complexes and higher-order assemblies. <i>Nucleic Acids Research</i> , 2017 , 45, D228-D235	20.1	79
55	Computational analyses of the effect of novel amino acid clusters of human transglutaminase 2 on its structure and function. <i>Amino Acids</i> , 2017 , 49, 605-614	3.5	3
54	Genomic variants reveal differential evolutionary constraints on human transglutaminases and point towards unrecognized significance of transglutaminase 2. <i>PLoS ONE</i> , 2017 , 12, e0172189	3.7	4
53	The Structure and Dynamics of Higher-Order Assemblies: Amyloids, Signalosomes, and Granules. <i>Cell</i> , 2016 , 165, 1055-1066	56.2	226
52	A Derived Allosteric Switch Underlies the Evolution of Conditional Cooperativity between HOXA11 and FOXO1. <i>Cell Reports</i> , 2016 , 15, 2097-2108	10.6	17
51	Fuzziness endows viral motif-mimicry. <i>Molecular BioSystems</i> , 2015 , 11, 2821-9		9
50	Fuzzy complexes: Specific binding without complete folding. <i>FEBS Letters</i> , 2015 , 589, 2533-42	3.8	135
49	Physiological, pathological, and structural implications of non-enzymatic protein-protein interactions of the multifunctional human transglutaminase 2. <i>Cellular and Molecular Life Sciences</i> , 2015 , 72, 3009-35	10.3	46

48	Fuzziness - Disorder in Protein Complexes - Imparts Versatility on Signalling. <i>FASEB Journal</i> , 2015 , 29, 372.1	0.9	
47	Disordered proteinaceous machines. <i>Chemical Reviews</i> , 2014 , 114, 6806-43	68.1	92
46	Classification of intrinsically disordered regions and proteins. <i>Chemical Reviews</i> , 2014 , 114, 6589-631	68.1	1141
45	Intrinsically disordered segments affect protein half-life in the cell and during evolution. <i>Cell Reports</i> , 2014 , 8, 1832-1844	10.6	136
44	The role of reorganization energy in rational enzyme design. <i>Current Opinion in Chemical Biology</i> , 2014 , 21, 34-41	9.7	23
43	Alternative splicing of intrinsically disordered regions and rewiring of protein interactions. <i>Current Opinion in Structural Biology</i> , 2013 , 23, 443-50	8.1	134
42	Identification of a specific one amino acid change in recombinant human transglutaminase 2 that regulates its activity and calcium sensitivity. <i>Biochemical Journal</i> , 2013 , 455, 261-72	3.8	25
41	What's in a name? Why these proteins are intrinsically disordered: Why these proteins are intrinsically disordered. <i>Intrinsically Disordered Proteins</i> , 2013 , 1, e24157		171
40	Tissue-specific splicing of disordered segments that embed binding motifs rewires protein interaction networks. <i>Molecular Cell</i> , 2012 , 46, 871-83	17.6	272
39	Fuzziness: linking regulation to protein dynamics. <i>Molecular BioSystems</i> , 2012 , 8, 168-77		128
38	QM/MM simulation of liquid water with an adaptive quantum region. <i>Physical Chemistry Chemical Physics</i> , 2012 , 14, 646-56	3.6	74
37	Fuzzy complexes: a more stochastic view of protein function. <i>Advances in Experimental Medicine and Biology</i> , 2012 , 725, 1-14	3.6	162
36	Interactions via intrinsically disordered regions: what kind of motifs?. <i>IUBMB Life</i> , 2012 , 64, 513-20	4.7	62
35	Active site residue involvement in monoamine or diamine oxidation catalysed by pea seedling amine oxidase. <i>FEBS Journal</i> , 2011 , 278, 1232-43	5.7	5
34	Dynamic protein-DNA recognition: beyond what can be seen. <i>Trends in Biochemical Sciences</i> , 2011 , 36, 415-23	10.3	116
33	Fuzzy interactome: the limitations of models in molecular biology. <i>Trends in Biochemical Sciences</i> , 2009 , 34, 3	10.3	10
32	Close encounters of the third kind: disordered domains and the interactions of proteins. <i>BioEssays</i> , 2009 , 31, 328-35	4.1	197
31	Evaluating boundary dependent errors in QM/MM simulations. <i>Journal of Physical Chemistry B</i> , 2009 , 113, 5728-35	3.4	49

30	The energy gap as a universal reaction coordinate for the simulation of chemical reactions. <i>Journal of Physical Chemistry B</i> , 2009 , 113, 7867-73	3.4	34
29	On the divalent metal ion dependence of DNA cleavage by restriction endonucleases of the EcoRI family. <i>Journal of Molecular Biology</i> , 2009 , 393, 140-60	6.5	49
28	Disordered tails of homeodomains facilitate DNA recognition by providing a trade-off between folding and specific binding. <i>Journal of the American Chemical Society</i> , 2009 , 131, 15084-5	16.4	53
27	Malleable machines take shape in eukaryotic transcriptional regulation. <i>Nature Chemical Biology</i> , 2008 , 4, 728-37	11.7	161
26	Fuzzy complexes: polymorphism and structural disorder in protein-protein interactions. <i>Trends in Biochemical Sciences</i> , 2008 , 33, 2-8	10.3	788
25	Malleable machines in transcription regulation: the mediator complex. <i>PLoS Computational Biology</i> , 2008 , 4, e1000243	5	91
24	Assessing Conservation of Disordered Regions in Proteins. <i>The Open Proteomics Journal</i> , 2008 , 1, 46-53		13
23	Probing the two-metal ion mechanism in the restriction endonuclease BamHI. <i>Biochemistry</i> , 2007 , 46, 14514-23	3.2	24
22	Metal-binding sites at the active site of restriction endonuclease BamHI can conform to a one-ion mechanism. <i>Biological Chemistry</i> , 2007 , 388, 73-8	4.5	9
21	An EcoRI-RsrI chimeric restriction endonuclease retains parental sequence specificity. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2007 , 1774, 583-94	4	3
20	Flexible segments modulate co-folding of dUTPase and nucleocapsid proteins. <i>Nucleic Acids Research</i> , 2007 , 35, 495-505	20.1	40
19	Local structural disorder imparts plasticity on linear motifs. <i>Bioinformatics</i> , 2007 , 23, 950-6	7.2	335
18	Electrostatic versus nonelectrostatic effects in DNA sequence discrimination by divalent ions Mg ²⁺ and Mn ²⁺ . <i>Journal of Physical Chemistry B</i> , 2007 , 111, 6272-9	3.4	23
17	Phosphorylation-induced transient intrinsic structure in the kinase-inducible domain of CREB facilitates its recognition by the KIX domain of CBP. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006 , 64, 749-57	4.2	27
16	Interfacial water as a "hydration fingerprint" in the noncognate complex of BamHI. <i>Biophysical Journal</i> , 2005 , 89, 903-11	2.9	49
15	Type II restriction endonucleases: structure and mechanism. <i>Cellular and Molecular Life Sciences</i> , 2005 , 62, 685-707	10.3	385
14	Flexibility of prolyl oligopeptidase: molecular dynamics and molecular framework analysis of the potential substrate pathways. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005 , 60, 504-12	4.2	49
13	Noncovalent cross-links in context with other structural and functional elements of proteins. <i>Journal of Chemical Information and Computer Sciences</i> , 2004 , 44, 347-51		4

12	Preformed structural elements feature in partner recognition by intrinsically unstructured proteins. <i>Journal of Molecular Biology</i> , 2004 , 338, 1015-26	6.5	448
11	Protein stability indicates divergent evolution of PD-(D/E)XK type II restriction endonucleases. <i>Protein Science</i> , 2002 , 11, 1978-83	6.3	14
10	Role of base flipping in specific recognition of damaged DNA by repair enzymes. <i>Journal of Molecular Biology</i> , 2002 , 323, 823-34	6.5	59
9	Checking nucleic acid crystal structures. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001 , 57, 813-28		8
8	Crystallization and preliminary X-ray analysis of porcine muscle prolyl oligopeptidase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1998 , 54, 1414-5		2
7	Origin of the Catalytic Power of Acetylcholinesterase: Computer Simulation Studies. <i>Journal of the American Chemical Society</i> , 1998 , 120, 183-194	16.4	106
6	Role of electrostatics at the catalytic metal binding site in xylose isomerase action: Ca(2+)-inhibition and metal competence in the double mutant D254E/D256E. <i>Proteins: Structure, Function and Bioinformatics</i> , 1997 , 28, 183-93	4.2	18
5	Molecular modelling of xylose isomerase catalysis: the role of electrostatics and charge transfer to metals. <i>Protein Engineering, Design and Selection</i> , 1995 , 8, 925-33	1.9	18
4	Observation of an β -synuclein liquid droplet state and its maturation into Lewy body-like assemblies		5
3	Widespread occurrence of the droplet state of proteins in the human proteome		3
2	Frustration in protein complexes leads to interaction versatility		3
1	Sequence determinants of the aggregation of proteins within condensates generated by liquid-liquid phase separation		2