

Monika Fuxreiter

List of Publications by Year in descending order

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87
papers

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66343

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docs citations

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times ranked

12811
citing authors

#	ARTICLE	IF	CITATIONS
1	Sequence Determinants of the Aggregation of Proteins Within Condensates Generated by Liquid-liquid Phase Separation. <i>Journal of Molecular Biology</i> , 2022, 434, 167201.	4.2	62
2	FuzDB: a new phase in understanding fuzzy interactions. <i>Nucleic Acids Research</i> , 2022, 50, D509-D517.	14.5	25
3	Adventures on the Routes of Protein Evolutionâ€”In Memoriam Dan Salah Tawfik (1955â€”2021). <i>Journal of Molecular Biology</i> , 2022, 434, 167462.	4.2	6
4	Molecular Determinants of Selectivity in Disordered Complexes May Shed Light on Specificity in Protein Condensates. <i>Biomolecules</i> , 2022, 12, 92.	4.0	3
5	FuzDrop on AlphaFold: visualizing the sequence-dependent propensity of liquidâ€”liquid phase separation and aggregation of proteins. <i>Nucleic Acids Research</i> , 2022, 50, W337-W344.	14.5	44
6	Electrostatics tunes protein interactions to context. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	7
7	Are casein micelles extracellular condensates formed by liquidâ€”liquid phase separation?. <i>FEBS Letters</i> , 2022, 596, 2072-2085.	2.8	5
8	MobiDB: intrinsically disordered proteins in 2021. <i>Nucleic Acids Research</i> , 2021, 49, D361-D367.	14.5	183
9	Spot in a drop: mutations in aberrant condensates. <i>Nature Reviews Molecular Cell Biology</i> , 2021, 22, 162-163.	37.0	3
10	Fuzziness and Frustration in the Energy Landscape of Protein Folding, Function, and Assembly. <i>Accounts of Chemical Research</i> , 2021, 54, 1251-1259.	15.6	88
11	Frustration in Fuzzy Protein Complexes Leads to Interaction Versatility. <i>Journal of Physical Chemistry B</i> , 2021, 125, 2513-2520.	2.6	52
12	Generic nature of the condensed states of proteins. <i>Nature Cell Biology</i> , 2021, 23, 587-594.	10.3	94
13	Observation of an α -synuclein liquid droplet state and its maturation into Lewy body-like assemblies. <i>Journal of Molecular Cell Biology</i> , 2021, 13, 282-294.	3.3	65
14	Protein interactions in liquid-liquid phase separation. <i>Journal of Molecular Biology</i> , 2021, 434, 167388.	4.2	1
15	Rapid Biophysical Characterization and NMR Spectroscopy Structural Analysis of Small Proteins from Bacteria and Archaea. <i>ChemBioChem</i> , 2020, 21, 1178-1187.	2.6	24
16	Patterns of Dynamics Comprise a Conserved Evolutionary Trait. <i>Journal of Molecular Biology</i> , 2020, 432, 497-507.	4.2	8
17	Classifying the Binding Modes of Disordered Proteins. <i>International Journal of Molecular Sciences</i> , 2020, 21, 8615.	4.1	49
18	Asymmetric dynamic coupling promotes alternative evolutionary pathways in an enzyme dimer. <i>Scientific Reports</i> , 2020, 10, 18866.	3.3	2

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19	Sequence-based prediction of protein binding mode landscapes. <i>PLoS Computational Biology</i> , 2020, 16, e1007864.	3.2	41
20	Sequence-Based Prediction of Fuzzy Protein Interactions. <i>Journal of Molecular Biology</i> , 2020, 432, 2289-2303.	4.2	77
21	Fuzzy protein theory for disordered proteins. <i>Biochemical Society Transactions</i> , 2020, 48, 2557-2564.	3.4	16
22	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.	7.1	178
23	Editorial overview: Dynamic protein interactions “ from complexes to molecular machines. <i>Current Opinion in Structural Biology</i> , 2019, 56, vi-viii.	5.7	1
24	Specific and Fuzzy Interactions Cooperate in Modulating Protein Half-Life. <i>Journal of Molecular Biology</i> , 2019, 431, 1700-1707.	4.2	2
25	Fold or not to fold upon binding “ does it really matter?. <i>Current Opinion in Structural Biology</i> , 2019, 54, 19-25.	5.7	73
26	Fuzziness in Protein Interactions“ A Historical Perspective. <i>Journal of Molecular Biology</i> , 2018, 430, 2278-2287.	4.2	118
27	Protein Phase Separation: A New Phase in Cell Biology. <i>Trends in Cell Biology</i> , 2018, 28, 420-435.	7.9	1,439
28	Simulations of Higher-Order Protein Organizations Using a Fuzzy Framework. <i>Complexity</i> , 2018, 2018, 1-10.	1.6	4
29	Experimental Characterization of Fuzzy Protein Assemblies: Interactions of Paramyxoviral NTAIL Domains With Their Functional Partners. <i>Methods in Enzymology</i> , 2018, 611, 137-192.	1.0	8
30	Towards a Stochastic Paradigm: From Fuzzy Ensembles to Cellular Functions. <i>Molecules</i> , 2018, 23, 3008.	3.8	18
31	Simultaneous quantification of protein order and disorder. <i>Nature Chemical Biology</i> , 2017, 13, 339-342.	8.0	113
32	Fuzziness enables context dependence of protein interactions. <i>FEBS Letters</i> , 2017, 591, 2682-2695.	2.8	60
33	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.	14.5	96
34	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.	2.7	4
35	Genomic variants reveal differential evolutionary constraints on human transglutaminases and point towards unrecognized significance of transglutaminase 2. <i>PLoS ONE</i> , 2017, 12, e0172189.	2.5	8
36	The Structure and Dynamics of Higher-Order Assemblies: Amyloids, Signalosomes, and Granules. <i>Cell</i> , 2016, 165, 1055-1066.	28.9	311

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37	A Derived Allosteric Switch Underlies the Evolution of Conditional Cooperativity between HOXA11 and FOXO1. <i>Cell Reports</i> , 2016, 15, 2097-2108.	6.4	25
38	Fuzzy regions in an intrinsically disordered protein impair protein-protein interactions. <i>FEBS Journal</i> , 2016, 283, 576-594.	4.7	43
39	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, 3009-3035.	5.4	52
40	Fuzziness endows viral motif-mimicry. <i>Molecular BioSystems</i> , 2015, 11, 2821-2829.	2.9	11
41	Fuzzy complexes: Specific binding without complete folding. <i>FEBS Letters</i> , 2015, 589, 2533-2542.	2.8	177
42	Fuzziness - Disorder in Protein Complexes - Imparts Versatility on Signalling. <i>FASEB Journal</i> , 2015, 29, 372.1.	0.5	0
43	Intrinsically Disordered Segments Affect Protein Half-Life in the Cell and during Evolution. <i>Cell Reports</i> , 2014, 8, 1832-1844.	6.4	192
44	The role of reorganization energy in rational enzyme design. <i>Current Opinion in Chemical Biology</i> , 2014, 21, 34-41.	6.1	27
45	Disordered Proteinaceous Machines. <i>Chemical Reviews</i> , 2014, 114, 6806-6843.	47.7	109
46	Classification of Intrinsically Disordered Regions and Proteins. <i>Chemical Reviews</i> , 2014, 114, 6589-6631.	47.7	1,618
47	Alternative splicing of intrinsically disordered regions and rewiring of protein interactions. <i>Current Opinion in Structural Biology</i> , 2013, 23, 443-450.	5.7	166
48	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, 261-272.	3.7	34
49	What's in a name? Why these proteins are intrinsically disordered. <i>Intrinsically Disordered Proteins</i> , 2013, 1, e24157.	1.9	226
50	Tissue-Specific Splicing of Disordered Segments that Embed Binding Motifs Rewires Protein Interaction Networks. <i>Molecular Cell</i> , 2012, 46, 871-883.	9.7	344
51	Fuzziness: linking regulation to protein dynamics. <i>Molecular BioSystems</i> , 2012, 8, 168-177.	2.9	155
52	QM/MM simulation of liquid water with an adaptive quantum region. <i>Physical Chemistry Chemical Physics</i> , 2012, 14, 646-656.	2.8	80
53	Fuzzy Complexes: A More Stochastic View of Protein Function. <i>Advances in Experimental Medicine and Biology</i> , 2012, 725, 1-14.	1.6	183
54	Interactions via intrinsically disordered regions: What kind of motifs?. <i>IUBMB Life</i> , 2012, 64, 513-520.	3.4	76

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55	Active site residue involvement in monoamine or diamine oxidation catalysed by pea seedling amine oxidase. <i>FEBS Journal</i> , 2011, 278, 1232-1243.	4.7	6
56	Dynamic proteinâ€“DNA recognition: beyond what can be seen. <i>Trends in Biochemical Sciences</i> , 2011, 36, 415-423.	7.5	137
57	Fuzzy interactome: the limitations of models in molecular biology. <i>Trends in Biochemical Sciences</i> , 2009, 34, 3.	7.5	11
58	Close encounters of the third kind: disordered domains and the interactions of proteins. <i>BioEssays</i> , 2009, 31, 328-335.	2.5	229
59	Evaluating Boundary Dependent Errors in QM/MM Simulations. <i>Journal of Physical Chemistry B</i> , 2009, 113, 5728-5735.	2.6	53
60	The Energy Gap as a Universal Reaction Coordinate for the Simulation of Chemical Reactions. <i>Journal of Physical Chemistry B</i> , 2009, 113, 7867-7873.	2.6	36
61	On the Divalent Metal Ion Dependence of DNA Cleavage by Restriction Endonucleases of the EcoRI Family. <i>Journal of Molecular Biology</i> , 2009, 393, 140-160.	4.2	59
62	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, 15084-15085.	13.7	61
63	Fuzzy Complexes: Polymorphism And Structural Disorder In Protein-protein Interactions. <i>Biophysical Journal</i> , 2009, 96, 319a.	0.5	0
64	Malleable machines take shape in eukaryotic transcriptional regulation. <i>Nature Chemical Biology</i> , 2008, 4, 728-737.	8.0	192
65	Fuzzy complexes: polymorphism and structural disorder in proteinâ€“protein interactions. <i>Trends in Biochemical Sciences</i> , 2008, 33, 2-8.	7.5	942
66	Malleable Machines in Transcription Regulation: The Mediator Complex. <i>PLoS Computational Biology</i> , 2008, 4, e1000243.	3.2	109
67	Assessing Conservation of Disordered Regions in Proteins. <i>The Open Proteomics Journal</i> , 2008, 1, 46-53.	0.4	15
68	Local structural disorder imparts plasticity on linear motifs. <i>Bioinformatics</i> , 2007, 23, 950-956.	4.1	376
69	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, 6272-6279.	2.6	23
70	Probing the Two-Metal Ion Mechanism in the Restriction Endonuclease BamHI. <i>Biochemistry</i> , 2007, 46, 14514-14523.	2.5	27
71	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.	2.5	10
72	An EcoRIâ€“RsrI chimeric restriction endonuclease retains parental sequence specificity. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2007, 1774, 583-594.	2.3	3

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73	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, 749-757.	2.6	31
74	Flexible segments modulate co-folding of dUTPase and nucleocapsid proteins. <i>Nucleic Acids Research</i> , 2006, 35, 495-505.	14.5	42
75	Type II restriction endonucleases: structure and mechanism. <i>Cellular and Molecular Life Sciences</i> , 2005, 62, 685-707.	5.4	452
76	Flexibility of prolyl oligopeptidase: Molecular dynamics and molecular framework analysis of the potential substrate pathways. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 60, 504-512.	2.6	51
77	Interfacial Water as a "Hydration Fingerprint" in the Noncognate Complex of BamHI. <i>Biophysical Journal</i> , 2005, 89, 903-911.	0.5	49
78	Noncovalent Cross-links in Context with Other Structural and Functional Elements of Proteins. <i>Journal of Chemical Information and Computer Sciences</i> , 2004, 44, 347-351.	2.8	7
79	Preformed Structural Elements Feature in Partner Recognition by Intrinsically Unstructured Proteins. <i>Journal of Molecular Biology</i> , 2004, 338, 1015-1026.	4.2	494
80	Role of Base Flipping in Specific Recognition of Damaged DNA by Repair Enzymes. <i>Journal of Molecular Biology</i> , 2002, 323, 823-834.	4.2	64
81	Protein stability indicates divergent evolution of PD-(D/E)XK type II restriction endonucleases. <i>Protein Science</i> , 2002, 11, 1978-1983.	7.6	17
82	Checking nucleic acid crystal structures. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 813-828.	2.5	12
83	Crystallization and preliminary X-ray analysis of porcine muscle prolyl oligopeptidase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1998, 54, 1414-1415.	2.5	4
84	Origin of the Catalytic Power of Acetylcholinesterase: A Computer Simulation Studies. <i>Journal of the American Chemical Society</i> , 1998, 120, 183-194.	13.7	116
85	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. , 1997, 28, 183-193.		19
86	Molecular modelling of xylose isomerase catalysis: the role of electrostatics and charge transfer to metals. <i>Protein Engineering, Design and Selection</i> , 1995, 8, 925-933.	2.1	21
87	Editorial: Fuzzy Interactions: Many Facets of Protein Binding. <i>Frontiers in Molecular Biosciences</i> , 0, 9, .	3.5	3