

Monika Fuxreiter

List of Publications by Year in descending order

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87
papers

10,495
citations

66343

42
h-index

56724

83
g-index

95
all docs

95
docs citations

95
times ranked

12811
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | Classification of Intrinsically Disordered Regions and Proteins. <i>Chemical Reviews</i> , 2014, 114, 6589-6631. | 47.7 | 1,618 |
| 2 | Protein Phase Separation: A New Phase in Cell Biology. <i>Trends in Cell Biology</i> , 2018, 28, 420-435. | 7.9 | 1,439 |
| 3 | Fuzzy complexes: polymorphism and structural disorder in protein-protein interactions. <i>Trends in Biochemical Sciences</i> , 2008, 33, 2-8. | 7.5 | 942 |
| 4 | Preformed Structural Elements Feature in Partner Recognition by Intrinsically Unstructured Proteins. <i>Journal of Molecular Biology</i> , 2004, 338, 1015-1026. | 4.2 | 494 |
| 5 | Type II restriction endonucleases: structure and mechanism. <i>Cellular and Molecular Life Sciences</i> , 2005, 62, 685-707. | 5.4 | 452 |
| 6 | Local structural disorder imparts plasticity on linear motifs. <i>Bioinformatics</i> , 2007, 23, 950-956. | 4.1 | 376 |
| 7 | 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 |
| 8 | The Structure and Dynamics of Higher-Order Assemblies: Amyloids, Signalosomes, and Granules. <i>Cell</i> , 2016, 165, 1055-1066. | 28.9 | 311 |
| 9 | Close encounters of the third kind: disordered domains and the interactions of proteins. <i>BioEssays</i> , 2009, 31, 328-335. | 2.5 | 229 |
| 10 | What's in a name? Why these proteins are intrinsically disordered. <i>Intrinsically Disordered Proteins</i> , 2013, 1, e24157. | 1.9 | 226 |
| 11 | Malleable machines take shape in eukaryotic transcriptional regulation. <i>Nature Chemical Biology</i> , 2008, 4, 728-737. | 8.0 | 192 |
| 12 | Intrinsically Disordered Segments Affect Protein Half-Life in the Cell and during Evolution. <i>Cell Reports</i> , 2014, 8, 1832-1844. | 6.4 | 192 |
| 13 | Fuzzy Complexes: A More Stochastic View of Protein Function. <i>Advances in Experimental Medicine and Biology</i> , 2012, 725, 1-14. | 1.6 | 183 |
| 14 | MobiDB: intrinsically disordered proteins in 2021. <i>Nucleic Acids Research</i> , 2021, 49, D361-D367. | 14.5 | 183 |
| 15 | 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 |
| 16 | Fuzzy complexes: Specific binding without complete folding. <i>FEBS Letters</i> , 2015, 589, 2533-2542. | 2.8 | 177 |
| 17 | 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 |
| 18 | Fuzziness: linking regulation to protein dynamics. <i>Molecular BioSystems</i> , 2012, 8, 168-177. | 2.9 | 155 |

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|----|---|------|-----------|
| 19 | Dynamic proteinâ€“DNA recognition: beyond what can be seen. Trends in Biochemical Sciences, 2011, 36, 415-423. | 7.5 | 137 |
| 20 | Fuzziness in Protein Interactionsâ€“A Historical Perspective. Journal of Molecular Biology, 2018, 430, 2278-2287. | 4.2 | 118 |
| 21 | Origin of the Catalytic Power of Acetylcholinesterase:Â Computer Simulation Studies. Journal of the American Chemical Society, 1998, 120, 183-194. | 13.7 | 116 |
| 22 | Simultaneous quantification of protein order and disorder. Nature Chemical Biology, 2017, 13, 339-342. | 8.0 | 113 |
| 23 | Malleable Machines in Transcription Regulation: The Mediator Complex. PLoS Computational Biology, 2008, 4, e1000243. | 3.2 | 109 |
| 24 | Disordered Proteinaceous Machines. Chemical Reviews, 2014, 114, 6806-6843. | 47.7 | 109 |
| 25 | FuzDB: database of fuzzy complexes, a tool to develop stochastic structure-function relationships for protein complexes and higher-order assemblies. Nucleic Acids Research, 2017, 45, D228-D235. | 14.5 | 96 |
| 26 | Generic nature of the condensed states of proteins. Nature Cell Biology, 2021, 23, 587-594. | 10.3 | 94 |
| 27 | Fuzziness and Frustration in the Energy Landscape of Protein Folding, Function, and Assembly. Accounts of Chemical Research, 2021, 54, 1251-1259. | 15.6 | 88 |
| 28 | QM/MM simulation of liquid water with an adaptive quantum region. Physical Chemistry Chemical Physics, 2012, 14, 646-656. | 2.8 | 80 |
| 29 | Sequence-Based Prediction of Fuzzy Protein Interactions. Journal of Molecular Biology, 2020, 432, 2289-2303. | 4.2 | 77 |
| 30 | Interactions via intrinsically disordered regions: What kind of motifs?. IUBMB Life, 2012, 64, 513-520. | 3.4 | 76 |
| 31 | Fold or not to fold upon binding â€“ does it really matter?. Current Opinion in Structural Biology, 2019, 54, 19-25. | 5.7 | 73 |
| 32 | Observation of an Î±-synuclein liquid droplet state and its maturation into Lewy body-like assemblies. Journal of Molecular Cell Biology, 2021, 13, 282-294. | 3.3 | 65 |
| 33 | Role of Base Flipping in Specific Recognition of Damaged DNA by Repair Enzymes. Journal of Molecular Biology, 2002, 323, 823-834. | 4.2 | 64 |
| 34 | Sequence Determinants of the Aggregation of Proteins Within Condensates Generated by Liquid-liquid Phase Separation. Journal of Molecular Biology, 2022, 434, 167201. | 4.2 | 62 |
| 35 | Disordered Tails of Homeodomains Facilitate DNA Recognition by Providing a Trade-Off between Folding and Specific Binding. Journal of the American Chemical Society, 2009, 131, 15084-15085. | 13.7 | 61 |
| 36 | Fuzziness enables context dependence of protein interactions. FEBS Letters, 2017, 591, 2682-2695. | 2.8 | 60 |

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|----|---|------|-----------|
| 37 | 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 |
| 38 | Evaluating Boundary Dependent Errors in QM/MM Simulations. <i>Journal of Physical Chemistry B</i> , 2009, 113, 5728-5735. | 2.6 | 53 |
| 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 | Frustration in Fuzzy Protein Complexes Leads to Interaction Versatility. <i>Journal of Physical Chemistry B</i> , 2021, 125, 2513-2520. | 2.6 | 52 |
| 41 | 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 |
| 42 | Interfacial Water as a "Hydration Fingerprint" in the Noncognate Complex of BamHI. <i>Biophysical Journal</i> , 2005, 89, 903-911. | 0.5 | 49 |
| 43 | Classifying the Binding Modes of Disordered Proteins. <i>International Journal of Molecular Sciences</i> , 2020, 21, 8615. | 4.1 | 49 |
| 44 | FuzDrop on AlphaFold: visualizing the sequence-dependent propensity of liquid-liquid phase separation and aggregation of proteins. <i>Nucleic Acids Research</i> , 2022, 50, W337-W344. | 14.5 | 44 |
| 45 | Fuzzy regions in an intrinsically disordered protein impair protein-protein interactions. <i>FEBS Journal</i> , 2016, 283, 576-594. | 4.7 | 43 |
| 46 | Flexible segments modulate co-folding of dUTPase and nucleocapsid proteins. <i>Nucleic Acids Research</i> , 2006, 35, 495-505. | 14.5 | 42 |
| 47 | Sequence-based prediction of protein binding mode landscapes. <i>PLoS Computational Biology</i> , 2020, 16, e1007864. | 3.2 | 41 |
| 48 | 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 |
| 49 | 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 |
| 50 | 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 |
| 51 | Probing the Two-Metal Ion Mechanism in the Restriction Endonuclease BamHI. <i>Biochemistry</i> , 2007, 46, 14514-14523. | 2.5 | 27 |
| 52 | The role of reorganization energy in rational enzyme design. <i>Current Opinion in Chemical Biology</i> , 2014, 21, 34-41. | 6.1 | 27 |
| 53 | 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 |
| 54 | FuzDB: a new phase in understanding fuzzy interactions. <i>Nucleic Acids Research</i> , 2022, 50, D509-D517. | 14.5 | 25 |

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|----|--|-----|-----------|
| 55 | 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 |
| 56 | 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 |
| 57 | 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 |
| 58 | 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 |
| 59 | Towards a Stochastic Paradigm: From Fuzzy Ensembles to Cellular Functions. <i>Molecules</i> , 2018, 23, 3008. | 3.8 | 18 |
| 60 | 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 |
| 61 | Fuzzy protein theory for disordered proteins. <i>Biochemical Society Transactions</i> , 2020, 48, 2557-2564. | 3.4 | 16 |
| 62 | Assessing Conservation of Disordered Regions in Proteins. <i>The Open Proteomics Journal</i> , 2008, 1, 46-53. | 0.4 | 15 |
| 63 | Checking nucleic acid crystal structures. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 813-828. | 2.5 | 12 |
| 64 | Fuzzy interactome: the limitations of models in molecular biology. <i>Trends in Biochemical Sciences</i> , 2009, 34, 3. | 7.5 | 11 |
| 65 | Fuzziness endows viral motif-mimicry. <i>Molecular BioSystems</i> , 2015, 11, 2821-2829. | 2.9 | 11 |
| 66 | 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 |
| 67 | Experimental Characterization of Fuzzy Protein Assemblies: Interactions of Paramyxoviral N-TAIL Domains With Their Functional Partners. <i>Methods in Enzymology</i> , 2018, 611, 137-192. | 1.0 | 8 |
| 68 | Patterns of Dynamics Comprise a Conserved Evolutionary Trait. <i>Journal of Molecular Biology</i> , 2020, 432, 497-507. | 4.2 | 8 |
| 69 | 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 |
| 70 | 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 |
| 71 | 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 |
| 72 | 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 |

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|----|--|------|-----------|
| 73 | 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 |
| 74 | Are casein micelles extracellular condensates formed by liquidâ€“liquid phase separation?. <i>FEBS Letters</i> , 2022, 596, 2072-2085. | 2.8 | 5 |
| 75 | 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 |
| 76 | 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 |
| 77 | Simulations of Higher-Order Protein Organizations Using a Fuzzy Framework. <i>Complexity</i> , 2018, 2018, 1-10. | 1.6 | 4 |
| 78 | 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 |
| 79 | Spot in a drop: mutations in aberrant condensates. <i>Nature Reviews Molecular Cell Biology</i> , 2021, 22, 162-163. | 37.0 | 3 |
| 80 | Molecular Determinants of Selectivity in Disordered Complexes May Shed Light on Specificity in Protein Condensates. <i>Biomolecules</i> , 2022, 12, 92. | 4.0 | 3 |
| 81 | Editorial: Fuzzy Interactions: Many Facets of Protein Binding. <i>Frontiers in Molecular Biosciences</i> , 0, 9, . | 3.5 | 3 |
| 82 | Specific and Fuzzy Interactions Cooperate in Modulating Protein Half-Life. <i>Journal of Molecular Biology</i> , 2019, 431, 1700-1707. | 4.2 | 2 |
| 83 | Asymmetric dynamic coupling promotes alternative evolutionary pathways in an enzyme dimer. <i>Scientific Reports</i> , 2020, 10, 18866. | 3.3 | 2 |
| 84 | Editorial overview: Dynamic protein interactions â€” from complexes to molecular machines. <i>Current Opinion in Structural Biology</i> , 2019, 56, vi-viii. | 5.7 | 1 |
| 85 | Protein interactions in liquid-liquid phase separation. <i>Journal of Molecular Biology</i> , 2021, 434, 167388. | 4.2 | 1 |
| 86 | Fuzzy Complexes: Polymorphism And Structural Disorder In Protein-protein Interactions. <i>Biophysical Journal</i> , 2009, 96, 319a. | 0.5 | 0 |
| 87 | Fuzziness â€“ Disorder in Protein Complexes â€“ Imparts Versatility on Signalling. <i>FASEB Journal</i> , 2015, 29, 372.1. | 0.5 | 0 |