

Fred F Damberger

List of Publications by Year in descending order

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Version: 2024-02-01

40
papers

2,903
citations

236925

25
h-index

276875

41
g-index

43
all docs

43
docs citations

43
times ranked

3467
citing authors

#	ARTICLE	IF	CITATIONS
1	NMR and EPR reveal a compaction of the RNA-binding protein FUS upon droplet formation. <i>Nature Chemical Biology</i> , 2021, 17, 608-614.	8.0	63
2	Recognition of N6-Methyladenosine by the YTHDC1 YTH Domain Studied by Molecular Dynamics and NMR Spectroscopy: The Role of Hydration. <i>Journal of Physical Chemistry B</i> , 2021, 125, 7691-7705.	2.6	15
3	A transient $\hat{\text{I}}\pm$ -helix in the N-terminal RNA recognition motif of polypyrimidine tract binding protein senses RNA secondary structure. <i>Nucleic Acids Research</i> , 2020, 48, 4521-4537.	14.5	16
4	Distinct G protein-coupled receptor phosphorylation motifs modulate arrestin affinity and activation and global conformation. <i>Nature Communications</i> , 2019, 10, 1261.	12.8	86
5	Prokaryotic ubiquitin-like protein remains intrinsically disordered when covalently attached to proteasomal target proteins. <i>BMC Structural Biology</i> , 2018, 17, 1.	2.3	17
6	Modification of Cassava Root Starch Phosphorylation Enhances Starch Functional Properties. <i>Frontiers in Plant Science</i> , 2018, 9, 1562.	3.6	27
7	Repression of Sex4 and Like Sex Four2 Orthologs in Potato Increases Tuber Starch Bound Phosphate With Concomitant Alterations in Starch Physical Properties. <i>Frontiers in Plant Science</i> , 2018, 9, 1044.	3.6	16
8	Molecular basis for disassembly of an importin:ribosomal protein complex by the escortin Tsr2. <i>Nature Communications</i> , 2018, 9, 3669.	12.8	17
9	Aromatic side-chain conformational switch on the surface of the RNA Recognition Motif enables RNA discrimination. <i>Nature Communications</i> , 2017, 8, 654.	12.8	23
10	Structural study of the Fox-1 RRM protein hydration reveals a role for key water molecules in RRM-RNA recognition. <i>Nucleic Acids Research</i> , 2017, 45, 8046-8063.	14.5	28
11	Evidence for cooperative tandem binding of hnRNP C RRMs in mRNA processing. <i>Rna</i> , 2015, 21, 1931-1942.	3.5	29
12	Structural and Mechanistic Insights into Poly(uridine) Tract Recognition by the hnRNP $\hat{\text{A}}\text{C}$ RNA Recognition Motif. <i>Journal of the American Chemical Society</i> , 2014, 136, 14536-14544.	13.7	62
13	Structural plasticity of the cellular prion protein and implications in health and disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 8549-8554.	7.1	35
14	Molecular basis of UG-rich RNA recognition by the human splicing factor TDP-43. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 1443-1449.	8.2	293
15	Pheromone discrimination by a pH-tuned polymorphism of the <i>Bombyx mori</i> pheromone-binding protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 18680-18685.	7.1	59
16	Prion Protein mPrP[F175A](121 $\hat{\text{A}}$ 231): Structure and Stability in Solution. <i>Journal of Molecular Biology</i> , 2012, 423, 496-502.	4.2	16
17	Structures of Pup ligase PafA and depupylase Dop from the prokaryotic ubiquitin-like modification pathway. <i>Nature Communications</i> , 2012, 3, 1014.	12.8	58
18	Structural basis for sigma factor mimicry in the general stress response of Alphaproteobacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E1405-14.	7.1	49

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19	Solution Structure and Activation Mechanism of Ubiquitin-Like Small Archaeal Modifier Proteins. <i>Journal of Molecular Biology</i> , 2011, 405, 1040-1055.	4.2	29
20	Dynamic Conformational Equilibria in the Physiological Function of the <i>Bombyx mori</i> Pheromone-Binding Protein. <i>Journal of Molecular Biology</i> , 2011, 408, 922-931.	4.2	29
21	Cellular prion protein conformation and function. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 17308-17313.	7.1	60
22	Molecular Insights into Mammalian End-binding Protein Heterodimerization. <i>Journal of Biological Chemistry</i> , 2010, 285, 5802-5814.	3.4	48
23	Prokaryotic Ubiquitin-like Protein (Pup) Is Coupled to Substrates via the Side Chain of Its C-Terminal Glutamate. <i>Journal of the American Chemical Society</i> , 2010, 132, 5610-5612.	13.7	62
24	Horse Prion Protein NMR Structure and Comparisons with Related Variants of the Mouse Prion Protein. <i>Journal of Molecular Biology</i> , 2010, 400, 121-128.	4.2	120
25	Prion Protein-Detergent Micelle Interactions Studied by NMR in Solution. <i>Journal of Biological Chemistry</i> , 2009, 284, 22713-22721.	3.4	29
26	A distinct structural region of the prokaryotic ubiquitin-like protein (Pup) is recognized by the N-terminal domain of the proteasomal ATPase Mpa. <i>FEBS Letters</i> , 2009, 583, 3151-3157.	2.8	80
27	An EB1-Binding Motif Acts as a Microtubule Tip Localization Signal. <i>Cell</i> , 2009, 138, 366-376.	28.9	594
28	Prion Protein NMR Structure from Tammar Wallaby (<i>Macropus eugenii</i>) Shows that the $\beta_2\alpha_1$ Loop Is Modulated by Long-Range Sequence Effects. <i>Journal of Molecular Biology</i> , 2009, 389, 833-845.	4.2	84
29	Automated amino acid side-chain NMR assignment of proteins using ^{13}C - and ^{15}N -resolved 3D $[\text{1H},\text{1H}]$ -NOESY. <i>Journal of Biomolecular NMR</i> , 2008, 42, 23-33.	2.8	66
30	Structural Basis of Ligand Binding and Release in Insect Pheromone-binding Proteins: NMR Structure of <i>Antheraea polyphemus</i> PB1 at pH 4.5. <i>Journal of Molecular Biology</i> , 2007, 373, 811-819.	4.2	84
31	Letters to the Editor. <i>Journal of Biomolecular NMR</i> , 2005, 31, 65-65.	2.8	6
32	NMR structure of the unliganded <i>Bombyx mori</i> pheromone-binding protein at physiological pH. <i>FEBS Letters</i> , 2002, 531, 314-318.	2.8	91
33	A Structurally Deviant Member of the <i>Euplotes raikovi</i> Pheromone Family: Er-23. <i>Journal of Eukaryotic Microbiology</i> , 2002, 49, 86-92.	1.7	23
34	NMR structure of the <i>Euplotes raikovi</i> pheromone Er-23 and identification of its five disulfide bonds 1 Edited by M. F. Summers. <i>Journal of Molecular Biology</i> , 2001, 313, 923-931.	4.2	33
35	NMR assignment of the A form of the pheromone-binding protein of <i>Bombyx mori</i> . <i>Journal of Biomolecular NMR</i> , 2001, 19, 79-80.	2.8	16
36	NMR structure reveals intramolecular regulation mechanism for pheromone binding and release. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 14374-14379.	7.1	261

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37	NMR characterization of a pH-dependent equilibrium between two folded solution conformations of the pheromone-binding protein from <i>Bombyx mori</i> . Protein Science, 2000, 9, 1038-1041.	7.6	129
38	Yeast heat shock transcription factor N-terminal activation domains are unstructured as probed by heteronuclear NMR spectroscopy. Protein Science, 1996, 5, 262-269.	7.6	52
39	Refined Solution Structure and Dynamics of the DNA-binding Domain of the Heat Shock Factor from <i>Kluyveromyces lactis</i> . Journal of Molecular Biology, 1995, 254, 704-719.	4.2	19
40	Solution structure of the DNA-binding domain of the heat shock transcription factor determined by multidimensional heteronuclear magnetic resonance spectroscopy. Protein Science, 1994, 3, 1806-1821.	7.6	77