

Christina Redfield

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1099697/publications.pdf>

Version: 2024-02-01

84
papers

3,197
citations

186265
28
h-index

161849
54
g-index

90
all docs

90
docs citations

90
times ranked

3141
citing authors

#	ARTICLE	IF	CITATIONS
1	A residue-specific NMR view of the non-cooperative unfolding of a molten globule. <i>Nature Structural Biology</i> , 1997, 4, 630-634.	9.7	236
2	A conserved face of the Jagged/Serrate DSL domain is involved in Notch trans-activation and cis-inhibition. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 849-857.	8.2	222
3	Structural Determinants of Protein Dynamics: Analysis of ¹⁵ N NMR Relaxation Measurements for Main-Chain and Side-Chain Nuclei of Hen Egg White Lysozyme. <i>Biochemistry</i> , 1995, 34, 4041-4055.	2.5	211
4	Different Subdomains are Most Protected From Hydrogen Exchange in the Molten Globule and Native States of Human α -Lactalbumin. <i>Journal of Molecular Biology</i> , 1995, 253, 651-657.	4.2	200
5	A refined solution structure of hen lysozyme determined using residual dipolar coupling data. <i>Protein Science</i> , 2001, 10, 677-688.	7.6	159
6	Rapid collapse and slow structural reorganisation during the refolding of bovine α -lactalbumin. <i>Journal of Molecular Biology</i> , 1999, 288, 673-688.	4.2	151
7	Structural characterization of a highly "ordered" molten globule™ at low pH. <i>Nature Structural and Molecular Biology</i> , 1994, 1, 23-29.	8.2	144
8	Analysis of ϕ and χ_1 torsion angles for hen lysozyme in solution from proton NMR spin-spin coupling constants. <i>Biochemistry</i> , 1991, 30, 986-996.	2.5	130
9	α -lactalbumin forms a compact molten globule in the absence of disulfide bonds. <i>Nature Structural Biology</i> , 1999, 6, 948-952.	9.7	121
10	NMR analysis of main-chain conformational preferences in an unfolded fibronectin-binding protein. <i>Journal of Molecular Biology</i> , 1997, 274, 152-159.	4.2	120
11	Using nuclear magnetic resonance spectroscopy to study molten globule states of proteins. <i>Methods</i> , 2004, 34, 121-132.	3.8	105
12	Exploitation of an iron transporter for bacterial protein antibiotic import. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 12051-12056.	7.1	76
13	Chemical shifts in denatured proteins: resonance assignments for denatured ubiquitin and comparisons with other denatured proteins. <i>Journal of Biomolecular NMR</i> , 2001, 19, 153-165.	2.8	71
14	Characterization of ¹⁵ N Chemical Shift Anisotropy from Orientation-Dependent Changes to ¹⁵ N Chemical Shifts in Dilute Bicelle Solutions. <i>Journal of the American Chemical Society</i> , 1999, 121, 7441-7442.	13.7	57
15	Structural Characterisation of the Human α -Lactalbumin Molten Globule at High Temperature. <i>Journal of Molecular Biology</i> , 2003, 330, 1177-1188.	4.2	52
16	The lipoprotein Pal stabilises the bacterial outer membrane during constriction by a mobilisation-and-capture mechanism. <i>Nature Communications</i> , 2020, 11, 1305.	12.8	50
17	Comparison of the denaturant-induced unfolding of the bovine and human α -lactalbumin molten globules 1 Edited by C. R. Matthews. <i>Journal of Molecular Biology</i> , 2001, 312, 261-273.	4.2	48
18	Structure and Interdomain Interactions of a Hybrid Domain: A Disulphide-Rich Module of the Fibrillin/LTBP Superfamily of Matrix Proteins. <i>Structure</i> , 2009, 17, 759-768.	3.3	44

#	ARTICLE	IF	CITATIONS
19	¹ H-NMR sequential assignments and cation-binding studies of spinach plastocyanin. FEBS Journal, 1987, 170, 279-292.	0.2	43
20	Pressure-induced unfolding of the molten globule of all-Ala β -lactalbumin. Protein Science, 2003, 12, 66-72.	7.6	43
21	Comparison of four independently determined structures of human recombinant interleukin-4. Nature Structural and Molecular Biology, 1994, 1, 301-310.	8.2	42
22	Structure of the Fibrillin-1 N-Terminal Domains Suggests that Heparan Sulfate Regulates the Early Stages of Microfibril Assembly. Structure, 2013, 21, 1743-1756.	3.3	42
23	Characterization of the unfolded state of bovine β -lactalbumin and comparison with unfolded states of homologous proteins. Protein Science, 2006, 15, 1397-1407.	7.6	38
24	Structural Consequences of Cysteine Substitutions C1977Y and C1977R in Calcium-binding Epidermal Growth Factor-like Domain 30 of Human Fibrillin-1. Journal of Biological Chemistry, 2004, 279, 51258-51265.	3.4	36
25	The Human β -Lactalbumin Molten Globule: Comparison of Structural Preferences at pH 2 and pH 7. Journal of Molecular Biology, 2009, 394, 351-362.	4.2	35
26	Ca ²⁺ -dependent Interface Formation in Fibrillin-1. Journal of Biological Chemistry, 2005, 280, 14076-14084.	3.4	34
27	Defining the Orientation of the ¹⁵ N Shielding Tensor Using ¹⁵ N NMR Relaxation Data for a Protein in Solution. Journal of the American Chemical Society, 1998, 120, 9692-9693.	13.7	33
28	Non-Linear and Flexible Regions of the Human Notch1 Extracellular Domain Revealed by High-Resolution Structural Studies. Structure, 2016, 24, 555-566.	3.3	32
29	Complete Assignment of the ¹ H NMR Spectrum of the Aromatic Residues of Lysozyme. FEBS Journal, 1982, 128, 527-531.	0.2	29
30	Residual dipolar couplings: are multiple independent alignments always possible?. Journal of Biomolecular NMR, 2011, 49, 53-60.	2.8	29
31	Identification of glycine spin systems in ¹ H NMR spectra of proteins using multiple quantum coherences. FEBS Letters, 1985, 186, 35-40.	2.8	28
32	Active-site Properties of the Oxidized and Reduced C-terminal Domain of DsbD Obtained by NMR Spectroscopy. Journal of Molecular Biology, 2007, 370, 643-658.	4.2	28
33	Molecular Basis for Jagged-1/Serrate Ligand Recognition by the Notch Receptor. Journal of Biological Chemistry, 2013, 288, 7305-7312.	3.4	28
34	Probing the Heme-Binding Site of the Cytochrome c Maturation Protein CcmE. Biochemistry, 2009, 48, 1820-1828.	2.5	27
35	Consequences of Inducing Intrinsic Disorder in a High-Affinity Protein-Protein Interaction. Journal of the American Chemical Society, 2015, 137, 5252-5255.	13.7	23
36	Asparagine and glutamine side-chain conformation in solution and crystal: A comparison for hen egg-white lysozyme using residual dipolar couplings. Journal of Biomolecular NMR, 2004, 30, 327-346.	2.8	21

#	ARTICLE	IF	CITATIONS
37	Oxidation State-dependent Protein-Protein Interactions in Disulfide Cascades. <i>Journal of Biological Chemistry</i> , 2011, 286, 24943-24956.	3.4	21
38	Local and Global Cooperativity in the Human $\hat{\pm}$ -Lactalbumin Molten Globule. <i>Journal of Molecular Biology</i> , 2004, 338, 149-158.	4.2	19
39	Biophysical Characterisation of Fibulin-5 Proteins Associated with Disease. <i>Journal of Molecular Biology</i> , 2010, 401, 605-617.	4.2	19
40	¹ H-NMR analysis of turkey egg-white lysozyme and comparison with hen egg-white lysozyme. <i>FEBS Journal</i> , 1993, 215, 255-266.	0.2	17
41	Probing subtle differences in the hydrogen exchange behavior of variants of the human $\hat{\pm}$ -lactalbumin molten globule using mass spectrometry. <i>Journal of Molecular Biology</i> , 2001, 311, 909-919.	4.2	16
42	Probing the Effect of Temperature on the Backbone Dynamics of the Human $\hat{\pm}$ -Lactalbumin Molten Globule. <i>Journal of the American Chemical Society</i> , 2008, 130, 15318-15326.	13.7	16
43	Control of Periplasmic Interdomain Thiol:Disulfide Exchange in the Transmembrane Oxidoreductase DsbD. <i>Journal of Biological Chemistry</i> , 2009, 284, 3219-3226.	3.4	16
44	NMR Analysis Shows That a b-Type Variant of <i>Hydrogenobacter thermophilus</i> Cytochrome c552 Retains Its Native Structure. <i>Journal of Biological Chemistry</i> , 2004, 279, 15177-15182.	3.4	15
45	Characterization of the structure and dynamics of amyloidogenic variants of human lysozyme by NMR spectroscopy. <i>Protein Science</i> , 2001, 10, 2525-2530.	7.6	15
46	The N-Terminal Region of Fibrillin-1 Mediates a Bipartite Interaction with LTBP1. <i>Structure</i> , 2017, 25, 1208-1221.e5.	3.3	15
47	Rapid Collapse into a Molten Globule Is Followed by Simple Two-State Kinetics in the Folding of Lysozyme from Bacteriophage $\hat{\pm}$. <i>Biochemistry</i> , 2010, 49, 8646-8657.	2.5	14
48	Surface accessibility of aromatic residues in human lysozyme using photochemically induced dynamic nuclear polarization NMR spectroscopy. <i>FEBS Letters</i> , 1985, 185, 248-252.	2.8	13
49	Structural Insights into Notch Receptor-Ligand Interactions. <i>Advances in Experimental Medicine and Biology</i> , 2018, 1066, 33-46.	1.6	13
50	Local frustration determines loop opening during the catalytic cycle of an oxidoreductase. <i>ELife</i> , 2020, 9, .	6.0	13
51	Assignment of resonances in the ¹ H NMR spectrum of human lysozyme. <i>FEBS Journal</i> , 1985, 153, 383-396.	0.2	11
52	Toxin import through the antibiotic efflux channel TolC. <i>Nature Communications</i> , 2021, 12, 4625.	12.8	11
53	Conformational flexibility of GRASPs and their constituent PDZ subdomains reveals structural basis of their promiscuous interactome. <i>FEBS Journal</i> , 2020, 287, 3255-3272.	4.7	10
54	A method for the estimation of ϕ 1 torsion angles in proteins. <i>Journal of Biomolecular NMR</i> , 1993, 3, 415.	2.8	9

#	ARTICLE	IF	CITATIONS
55	The N1317H Substitution Associated with Leber Congenital Amaurosis Results in Impaired Interdomain Packing in Human CRB1 Epidermal Growth Factor-like (EGF) Domains. <i>Journal of Biological Chemistry</i> , 2007, 282, 28807-28814.	3.4	9
56	Probing the urea dependence of residual structure in denatured human α -lactalbumin. <i>Journal of Biomolecular NMR</i> , 2009, 45, 121-131.	2.8	9
57	NMR Spectroscopic and Bioinformatic Analyses of the LTBP1 C-Terminus Reveal a Highly Dynamic Domain Organisation. <i>PLoS ONE</i> , 2014, 9, e87125.	2.5	9
58	The Role of Active Site Flexible Loops in Catalysis and of Zinc in Conformational Stability of <i>Bacillus cereus</i> 569/H/9 β -Lactamase. <i>Journal of Biological Chemistry</i> , 2016, 291, 16124-16137.	3.4	9
59	Structural characterization of KKT4, an unconventional microtubule-binding kinetochore protein. <i>Structure</i> , 2021, 29, 1014-1028.e8.	3.3	9
60	The Dynamics of Lysozyme from Bacteriophage Lambda in Solution Probed by NMR and MD Simulations. <i>ChemBioChem</i> , 2013, 14, 1780-1788.	2.6	8
61	Nuclear Overhauser effects and the assignment of the proton NMR spectra of proteins. <i>FEBS Letters</i> , 1984, 176, 307-312.	2.8	7
62	An Extended Active-site Motif Controls the Reactivity of the Thioredoxin Fold. <i>Journal of Biological Chemistry</i> , 2014, 289, 8681-8696.	3.4	7
63	The CcmC-CcmE interaction during cytochrome c maturation by System I is driven by protein-protein and not protein-heme contacts. <i>Journal of Biological Chemistry</i> , 2018, 293, 16778-16790.	3.4	7
64	¹⁵ N NMR Relaxation Data Reveal Significant Chemical Exchange Broadening in the α -Domain of Human α -Lactalbumin. <i>Biochemistry</i> , 2009, 48, 4031-4039.	2.5	5
65	Backbone ¹ H, ¹³ C, and ¹⁵ N resonance assignments for lysozyme from bacteriophage lambda. <i>Biomolecular NMR Assignments</i> , 2010, 4, 111-114.	0.8	5
66	¹ H, ¹³ C and ¹⁵ N assignments of the four N-terminal domains of human fibrillin-1. <i>Biomolecular NMR Assignments</i> , 2014, 8, 75-80.	0.8	5
67	¹ H, ¹³ C and ¹⁵ N assignments of EGF domains 4 to 7 of human Notch-1. <i>Biomolecular NMR Assignments</i> , 2015, 9, 275-279.	0.8	5
68	Bacterial Expression and In Vitro Refolding of Limited Fragments of the Notch Receptor and Its Ligands. <i>Methods in Molecular Biology</i> , 2014, 1187, 193-208.	0.9	5
69	The structural basis for high affinity binding of α 1-acid glycoprotein to the potent antitumor compound UCN-01. <i>Journal of Biological Chemistry</i> , 2021, 297, 101392.	3.4	5
70	¹ H, ¹⁵ N and ¹³ C assignments of the carboxy-terminal domain of the transmembrane electron transfer protein DsbD. <i>Journal of Biomolecular NMR</i> , 2002, 24, 359-360.	2.8	4
71	¹ H, ¹³ C and ¹⁵ N resonance assignments for the oxidized and reduced states of the N-terminal domain of DsbD from <i>Escherichia coli</i> . <i>Biomolecular NMR Assignments</i> , 2012, 6, 163-167.	0.8	4
72	¹ H, ¹³ C and ¹⁵ N assignments of EGF domains 8-11 of human Notch-1. <i>Biomolecular NMR Assignments</i> , 2015, 9, 375-379.	0.8	4

#	ARTICLE	IF	CITATIONS
73	¹ H, ¹³ C and ¹⁵ N resonance assignments for the microtubule-binding domain of the kinetoplastid kinetochore protein KKT4 from <i>Trypanosoma brucei</i> . <i>Biomolecular NMR Assignments</i> , 2020, 14, 309-315.	0.8	4
74	Backbone ¹ H, ¹³ C and ¹⁵ N resonance assignment of the C-terminal EGF-cbEGF pair of LTBP1 and flanking residues. <i>Biomolecular NMR Assignments</i> , 2014, 8, 159-163.	0.8	3
75	¹ H, ¹³ C and ¹⁵ N resonance assignments for the response regulator CheY3 from <i>Rhodobacter sphaeroides</i> . <i>Biomolecular NMR Assignments</i> , 2016, 10, 373-378.	0.8	3
76	An NMR and MD study of complexes of bacteriophage lambda lysozyme with tetra- and hexa- <i>N</i> -acetylchitohexaose. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020, 88, 82-93.	2.6	3
77	Assignment of Protein NMR Spectra Using Heteronuclear NMR – A Tutorial. <i>Biological Magnetic Resonance</i> , 2015, , 1-42.	0.4	3
78	¹ H, ¹³ C and ¹⁵ N resonance assignments for the fibrillin-1 EGF2-EGF3-hybrid1-cbEGF1 four-domain fragment. <i>Biomolecular NMR Assignments</i> , 2014, 8, 189-194.	0.8	2
79	Modular, triple-resonance, transmission line DNP MAS probe for 500- ¹ MHz/ ³³⁰ -GHz. <i>Journal of Magnetic Resonance</i> , 2019, 307, 106573.	2.1	2
80	Iain D Campbell 1941-2014. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 427-428.	8.2	1
81	Comparison of the backbone dynamics of wild-type <i>Hydrogenobacter thermophilus</i> cytochrome c 552 and its b-type variant. <i>Journal of Biomolecular NMR</i> , 2015, 62, 221-231.	2.8	1
82	¹ H, ¹³ C and ¹⁵ N resonance assignments for the tandem CUE domains from chromatin remodeler SMARCAD1. <i>Biomolecular NMR Assignments</i> , 2019, 13, 261-265.	0.8	1
83	The "Shape-Shifter"™ Peptide from the Disulphide Isomerase PmScsC Shows Context-Dependent Conformational Preferences. <i>Biomolecules</i> , 2021, 11, 642.	4.0	1
84	¹ H, ¹³ C, and ¹⁵ N resonance assignments for the tandem PHD finger motifs of human CHD4. <i>Biomolecular NMR Assignments</i> , 2015, 9, 239-242.	0.8	0