Jean Baum

List of Publications by Year
in descending order

58 papers	2,020 citations	257450 24 h-index	254184 43 g-index
61 all docs	61 docs citations	61 times ranked	2515 citing authors

#	Article	IF	Citations
1	Molecular dynamics analysis of a flexible loop at the binding interface of the <scp>SARSâ€CoV</scp>â€2 spike protein <scp>receptorâ€binding</scp> domain. Proteins: Structure, Function and Bioinformatics, 2022, 90, 1044-1053.	2.6	30
2	Evolution of the <scp>SARSâ€CoV</scp>â€2 proteome in three dimensions (3D) during the first 6 months of the <scp>COVID</scp>â€19 pandemic. Proteins: Structure, Function and Bioinformatics, 2022, 90, 1054-1080.	2.6	31
3	NMR unveils an N-terminal interaction interface on acetylated-Î±-synuclein monomers for recruitment to fibrils. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	29
4	The 2021 FASEB Virtual Science Research Conference on Protein Aggregation: Function, Dysfunction, and Disease, June 23â€“25, 2021. FASEB Journal, 2021, 35, e21884.	0.5	0
5	DJ-1 Acts as a Scavenger of Î±-Synuclein Oligomers and Restores Monomeric Glycated Î±-Synuclein. Biomolecules, 2021, 11, 1466.	4.0	8
6	Apoptosis signal regulating kinase 1 deletion mitigates Î±-synuclein pre-formed fibril propagation in mice. Neurobiology of Aging, 2020, 85, 49-57.	3.1	9
7	Collagen I Weakly Interacts with the Î²-Sheets of Î²₂-Microglobulin and Enhances Conformational Exchange To Induce Amyloid Formation. Journal of the American Chemical Society, 2020, 142, 1321-1331.	13.7	15
8	Antioxidant Nanoparticles for Concerted Inhibition of Î±-Synuclein Fibrillization, and Attenuation of Microglial Intracellular Aggregation and Activation. Frontiers in Bioengineering and Biotechnology, 2020, 8, 112.	4.1	26
9	Mimicking cotranslational folding of prosubtilisin E in vitro. Journal of Biochemistry, 2020, 167, 473-482.	1.7	3
10	PET-RAFT and SAXS: High Throughput Tools To Study Compactness and Flexibility of Single-Chain Polymer Nanoparticles. Macromolecules, 2019, 52, 8295-8304.	4.8	43
11	Molecular underpinnings of integrin binding to collagen-mimetic peptides containing vascular Ehlersâ€“Danlos syndromeâ€“associated substitutions. Journal of Biological Chemistry, 2019, 294, 14442-14453.	3.4	1
12	Extracellular matrix components modulate different stages in Î²2-microglobulin amyloid formation. Journal of Biological Chemistry, 2019, 294, 9392-9401.	3.4	19
13	Increased Dynamics of Î±-Synuclein Fibrils by Î²-Synuclein Leads to Reduced Seeding and Cytotoxicity. Scientific Reports, 2019, 9, 17579.	3.3	17
14	Cryptic binding sites become accessible through surface reconstruction of the type I collagen fibril. Scientific Reports, 2018, 8, 16646.	3.3	23
15	Multi-Pronged Interactions Underlie Inhibition of Î±-Synuclein Aggregation by Î²-Synuclein. Journal of Molecular Biology, 2018, 430, 2360-2371.	4.2	22
16	Magnesium Activates Microsecond Dynamics to Regulate Integrin-Collagen Recognition. Structure, 2018, 26, 1080-1090.e5.	3.3	15
17	Protein Aggregation. Protein Science, 2018, 27, 1149-1150.	7.6	2
18	Interactions between the Intrinsically Disordered Proteins Î²â€Synuclein and Î±â€Synuclein. Proteomics, 2018, 18, e1800109.	2.2	16

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19	Structural Insights into the Glycine Pair Motifs in Type III Collagen. ACS Biomaterials Science and Engineering, 2017, 3, 269-278.	5.2	3
20	A pH-dependent switch promotes Î²-synuclein fibril formation via glutamate residues. Journal of Biological Chemistry, 2017, 292, 16368-16379.	3.4	41
21	Revealing Accessibility of Cryptic Protein Binding Sites within the Functional Collagen Fibril. Biomolecules, 2017, 7, 76.	4.0	21
22	The loss of inhibitory Câ€terminal conformations in disease associated P123H Î²â€synuclein. Protein Science, 2016, 25, 286-294.	7.6	13
23	Polymer brain-nanotherapeutics for multipronged inhibition of microglial Î±-synuclein aggregation, activation, and neurotoxicity. Biomaterials, 2016, 111, 179-189.	11.4	19
24	Intrinsic local destabilization of the Câ€terminus predisposes integrin Î±1 I domain to a conformational switch induced by collagen binding. Protein Science, 2016, 25, 1672-1681.	7.6	4
25	Intermolecular Paramagnetic Relaxation Enhancement (PRE) Studies of Transient Complexes in Intrinsically Disordered Proteins. Methods in Molecular Biology, 2016, 1345, 45-53.	0.9	7
26	Unveiling transient protein-protein interactions that modulate inhibition of alpha-synuclein aggregation by beta-synuclein, a pre-synaptic protein that co-localizes with alpha-synuclein. Scientific Reports, 2015, 5, 15164.	3.3	53
27	Local amino acid sequence patterns dominate the heterogeneous phenotype for the collagen connective tissue disease Osteogenesis Imperfecta resulting from Gly mutations. Journal of Structural Biology, 2015, 192, 127-137.	2.8	14
28	Dynamic Water-Mediated Hydrogen Bonding in a Collagen Model Peptide. Biochemistry, 2015, 54, 6029-6037.	2.5	26
29	NMR Studies Demonstrate a Unique AAB Composition and Chain Register for a Heterotrimeric Type IV Collagen Model Peptide Containing a Natural Interruption Site. Journal of Biological Chemistry, 2015, 290, 24201-24209.	3.4	19
30	A Revised Picture of the Cu(II)âˆ’Î±-Synuclein Complex: The Role of N-Terminal Acetylation. Biochemistry, 2014, 53, 2815-2817.	2.5	71
31	Fast hydrogen exchange affects 15N relaxation measurements in intrinsically disordered proteins. Journal of Biomolecular NMR, 2013, 55, 249-256.	2.8	18
32	Exploring the accessible conformations of Nâ€terminal acetylated Î±â€synuclein. FEBS Letters, 2013, 587, 1128-1138.	2.8	29
33	Mechanistic Insight into the Relationship between N-Terminal Acetylation of Î±-Synuclein and Fibril Formation Rates by NMR and Fluorescence. PLoS ONE, 2013, 8, e75018.	2.5	43
34	Investigation of the Polymeric Properties of Î±-Synuclein and Comparison with NMR Experiments: A Replica Exchange Molecular Dynamics Study. Journal of Chemical Theory and Computation, 2012, 8, 3929-3942.	5.3	31
35	Nâ€terminal acetylation of Î±â€synuclein induces increased transient helical propensity and decreased aggregation rates in the intrinsically disordered monomer. Protein Science, 2012, 21, 911-917.	7.6	161
36	The A53T Mutation is Key in Defining the Differences in the Aggregation Kinetics of Human and Mouse Î±-Synuclein. Journal of the American Chemical Society, 2011, 133, 13465-13470.	13.7	45

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37	Backbone assignment and dynamics of human Î±-synuclein in viscous 2ÂM glucose solution. Biomolecular NMR Assignments, 2011, 5, 43-46.	0.8	13
38	Detection of Transient Interchain Interactions in the Intrinsically Disordered Protein Î±-Synuclein by NMR Paramagnetic Relaxation Enhancement. Journal of the American Chemical Society, 2010, 132, 5546-5547.	13.7	93
39	Structural Reorganization of Î±-Synuclein at Low pH Observed by NMR and REMD Simulations. Journal of Molecular Biology, 2009, 391, 784-796.	4.2	170
40	Structure and dynamics of de novo proteins from a designed superfamily of 4â€helix bundles. Protein Science, 2008, 17, 821-832.	7.6	48
41	Characterization of Conformational and Dynamic Properties of Natively Unfolded Human and Mouse Î±-Synuclein Ensembles by NMR: Implication for Aggregation. Journal of Molecular Biology, 2008, 378, 1104-1115.	4.2	112
42	NMR assignment of S836: a de novo protein from a designed superfamily. Biomolecular NMR Assignments, 2007, 1, 213-215.	0.8	2
43	Conformational Features of a Natural Break in the Type IV Collagen Gly-X-Y Repeat. Journal of Biological Chemistry, 2006, 281, 17197-17202.	3.4	37
44	Identification of Partially Disordered Peptide Intermediates through Residue-Specific NMR Diffusion Measurements. Journal of the American Chemical Society, 2005, 127, 10490-10491.	13.7	12
45	1H, 13C and 15N resonance assignments of S-824, a de novo four-helix bundle from a designed combinatorial library. Journal of Biomolecular NMR, 2003, 27, 395-396.	2.8	5
46	Solution structure of a de novo protein from a designed combinatorial library. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 13270-13273.	7.1	107
47	NMR structure determination and DNA binding properties of GCN4 peptidomimetics designed for Î±-helix initiation and stabilization. , 2002, , 463-464.		0
48	Backbone dynamics of the natively unfolded pro-peptide of subtilisin by heteronuclear NMR relaxation studies. Journal of Biomolecular NMR, 2001, 20, 233-249.	2.8	68
49	Nuclear magnetic resonance characterization of peptide models of collagenâ€“folding diseases. Philosophical Transactions of the Royal Society B: Biological Sciences, 2001, 356, 159-168.	4.0	21
50	Site-Specific NMR Monitoring of cisâ^'trans Isomerization in the Folding of the Proline-Rich Collagen Triple Helixâ€. Biochemistry, 2000, 39, 4299-4308.	2.5	57
51	Dynamics of Unfolded Proteins:Â Incorporation of Distributions of Correlation Times in the Model Free Analysis of NMR Relaxation Data. Journal of the American Chemical Society, 1999, 121, 8671-8672.	13.7	55
52	Electrostatic interactions in the acid denaturation of Î±â€lactalbumin determined by nmr. Protein Science, 1998, 7, 1930-1938.	7.6	22
53	Tertiary Contacts in Î±a-Lactalbumin at pH 7 and pH 2: A Molecular Dynamics Study. Journal of Biomolecular Structure and Dynamics, 1998, 16, 355-365.	3.5	3
54	Nuclear Magnetic Resonance Shows Asymmetric Loss of Triple Helix in Peptides Modeling a Collagen Mutation in Brittle Bone Disease. Biochemistry, 1998, 37, 15528-15533.	2.5	56

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55	Crystal structure and nmr conformation of a cyclic pseudotetrapeptide containing urethane backbone linkages. Biopolymers, 1994, 34, 403-414.	2.4	3
56	Synthesis and Nuclear Magnetic Resonance Structure Determination of an .alpha.-Helical, Bicyclic, Lactam-Bridged Hexapeptide. Journal of the American Chemical Society, 1994, 116, 6431-6432.	13.7	96
57	1H-NMR assignments and local environments of aromatic residues in bovine, human and guinea pig variants of alpha-lactalbumin. FEBS Journal, 1992, 210, 699-709.	0.2	51
58	NMR and CD studies of triple-helical peptides. Biopolymers, 1992, 32, 447-451.	2.4	61