Sophie Zinn-Justin

List of Publications by Year in descending order

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50 papers

1,877 citations

³⁶¹⁴¹³
20
h-index

42 g-index

52 all docs 52 docs citations

52 times ranked 2270 citing authors

#	Article	IF	CITATIONS
1	The Ig-like Structure of the C-Terminal Domain of Lamin A/C, Mutated in Muscular Dystrophies, Cardiomyopathy, and Partial Lipodystrophy. Structure, 2002, 10, 811-823.	3.3	252
2	Automated classification of tailed bacteriophages according to their neck organization. BMC Genomics, 2014, 15, 1027.	2.8	203
3	The Carboxyl-Terminal Region Common to Lamins A and C Contains a DNA Binding Domainâ€. Biochemistry, 2003, 42, 4819-4828.	2.5	157
4	Structural Characterization of the LEM Motif Common to Three Human Inner Nuclear Membrane Proteins. Structure, 2001, 9, 503-511.	3.3	107
5	Structure of bacteriophage SPP1 head-to-tail connection reveals mechanism for viral DNA gating. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 8507-8512.	7.1	107
6	The Tudor Tandem of 53BP1. Structure, 2004, 12, 1551-1562.	3.3	96
7	Compound heterozygosity for mutations in LMNA causes a progeria syndrome without prelamin A accumulation. Human Molecular Genetics, 2006, 15, 2509-2522.	2.9	83
8	Structural analysis of emerin, an inner nuclear membrane protein mutated in X-linked Emery-Dreifuss muscular dystrophy. FEBS Letters, 2001, 501, 171-176.	2.8	62
9	The Carboxyl-terminal Nucleoplasmic Region of MAN1 Exhibits a DNA Binding Winged Helix Domain. Journal of Biological Chemistry, 2006, 281, 18208-18215.	3.4	60
10	Structural analysis of the ternary complex between lamin A/C, BAF and emerin identifies an interface disrupted in autosomal recessive progeroid diseases. Nucleic Acids Research, 2018, 46, 10460-10473.	14.5	54
11	Structural rearrangements in the phage head-to-tail interface during assembly and infection. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 7009-7014.	7.1	53
12	Inhibition of TGF-Î ² Signaling at the Nuclear Envelope: Characterization of Interactions Between MAN1, Smad2 and Smad3, and PPM1A. Science Signaling, 2013, 6, ra49.	3.6	44
13	Proper chromosome alignment depends on BRCA2 phosphorylation by PLK1. Nature Communications, 2020, 11, 1819.	12.8	38
14	Architecture of the flexible tail tube of bacteriophage SPP1. Nature Communications, 2020, 11, 5759.	12.8	37
15	Structures of biomolecular complexes by combination of NMR and cryoEM methods. Current Opinion in Structural Biology, 2017, 43, 104-113.	5.7	32
16	Structural Analysis of the Smad $2\hat{a}$ MAN1 Interaction That Regulates Transforming Growth Factor- \hat{l}^2 Signaling at the Inner Nuclear Membrane. Biochemistry, 2010, 49, 8020-8032.	2.5	29
17	Bacteriophage Tailâ€Tube Assembly Studied by Protonâ€Detected 4D Solidâ€State NMR. Angewandte Chemie - International Edition, 2017, 56, 9497-9501.	13.8	27
18	The checkpoint Saccharomyces cerevisiae Rad9 protein contains a tandem tudor domain that recognizes DNA. Nucleic Acids Research, 2007, 35, 5898-5912.	14.5	26

#	Article	IF	Citations
19	Di-phosphorylated BAF shows altered structural dynamics and binding to DNA, but interacts with its nuclear envelope partners. Nucleic Acids Research, 2021, 49, 3841-3855.	14.5	25
20	Variability in automated assignment of NOESY spectra and three-dimensional structure determination: a test case on three small disulfide-bonded proteins. Journal of Biomolecular NMR, 2001, 19, 49-62.	2.8	24
21	Bacteriophage SPP1 Tail Tube Protein Self-assembles into \hat{l}^2 -Structure-rich Tubes. Journal of Biological Chemistry, 2015, 290, 3836-3849.	3.4	24
22	Protein structural and mechanistic basis of progeroid laminopathies. FEBS Journal, 2021, 288, 2757-2772.	4.7	23
23	High affinity anchoring of the decoration protein pb10 onto the bacteriophage T5 capsid. Scientific Reports, 2017, 7, 41662.	3.3	21
24	Combining Homologous Recombination and Phosphopeptide-binding Data to Predict the Impact of <i>BRCA1</i> BRCT Variants on Cancer Risk. Molecular Cancer Research, 2019, 17, 54-69.	3.4	21
25	Lamin B1 sequesters 53BP1 to control its recruitment to DNA damage. Science Advances, 2021, 7, .	10.3	21
26	A Tandem of SH3-like Domains Participates in RNA Binding in KIN17, a Human Protein Activated in Response to Genotoxics. Journal of Molecular Biology, 2006, 364, 764-776.	4.2	20
27	Solution structure of the region 51–160 of human KIN17 reveals an atypical winged helix domain. Protein Science, 2007, 16, 2750-2755.	7.6	20
28	Cyclic imine toxins survey in coastal european shellfish samples: Bioaccumulation and mode of action of 28-O-palmitoyl ester of pinnatoxin-G. first report of portimine-A bioaccumulation Harmful Algae, 2020, 98, 101887.	4.8	18
29	Muscular Dystrophy Mutations Impair the Nuclear Envelope Emerin Self-assembly Properties. ACS Chemical Biology, 2015, 10, 2733-2742.	3.4	16
30	Emerin selfâ€assembly mechanism: role of the LEM domain. FEBS Journal, 2017, 284, 338-352.	4.7	16
31	Solution structure of gp17 from the <i>Siphoviridae</i> bacteriophage SPP1: Insights into its role in virion assembly. Proteins: Structure, Function and Bioinformatics, 2012, 80, 319-326.	2.6	15
32	Proteinâ^'Protein Interfaces Probed by Methyl Labeling and Protonâ€Detected Solidâ€State NMR Spectroscopy. ChemPhysChem, 2018, 19, 2457-2460.	2.1	15
33	Sensitivityâ€Enhanced ¹³ Câ€NMR Spectroscopy for Monitoring Multisite Phosphorylation at Physiological Temperature and pH. Angewandte Chemie - International Edition, 2020, 59, 10411-10415.	13.8	15
34	An Emerin LEM-Domain Mutation Impairs Cell Response to Mechanical Stress. Cells, 2019, 8, 570.	4.1	14
35	Boundaries and physical characterization of a new domain shared between mammalian 53BP1 and yeast Rad9 checkpoint proteins. Protein Science, 2005, 14, 1827-1839.	7.6	13
36	1H, 13C and 15N backbone resonance assignment of the intrinsically disordered region of the nuclear envelope protein emerin. Biomolecular NMR Assignments, 2016, 10, 179-182.	0.8	8

#	Article	IF	CITATIONS
37	BRCA2 binding through a cryptic repeated motif to HSF2BP oligomers does not impact meiotic recombination. Nature Communications, 2021, 12, 4605.	12.8	8
38	Dissecting the roles of Haspin and VRK1 in histone H3 phosphorylation during mitosis. Scientific Reports, 2022, 12 , .	3.3	8
39	Crystallization and halide phasing of the C-terminal domain of human KIN17. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 245-248.	0.7	7
40	Purification and Structural Analysis of LEM-Domain Proteins. Methods in Enzymology, 2016, 569, 43-61.	1.0	7
41	Bacteriophage Tailâ€Tube Assembly Studied by Protonâ€Detected 4D Solidâ€State NMR. Angewandte Chemie, 2017, 129, 9625-9629.	2.0	6
42	1H, 13C and 15N backbone resonance assignment of the human BRCA2 N-terminal region. Biomolecular NMR Assignments, 2020, 14, 79-85.	0.8	6
43	Sensitivityâ€Enhanced 13 Câ€NMR Spectroscopy for Monitoring Multisite Phosphorylation at Physiological Temperature and pH. Angewandte Chemie, 2020, 132, 10497-10501.	2.0	6
44	Intrinsic Disorder and Phosphorylation in BRCA2 Facilitate Tight Regulation of Multiple Conserved Binding Events. Biomolecules, 2021, 11, 1060.	4.0	6
45	The high protein expression of FOXO3, but not that of FOXO1, is associated with markers of good prognosis. Scientific Reports, 2020, 10, 6920.	3.3	5
46	1H, 13C and 15N resonance assignments of the C-terminal domain of human lamin A/C. Journal of Biomolecular NMR, 2002, 22, 371-372.	2.8	4
47	Letter to the Editor:1H,13C and15N Resonance Assignments of the Region 1463-1617 of the Mouse p53 Binding Protein 1 (53BP1). Journal of Biomolecular NMR, 2004, 28, 303-304.	2.8	4
48	NMR Assignment of Region 51–160 of Human KIN17, a DNA and RNA-binding Protein. Journal of Biomolecular NMR, 2006, 36, 29-29.	2.8	3
49	The phospho-dependent role of BRCA2 on the maintenance of chromosome integrity. Cell Cycle, 2021, 20, 731-741.	2.6	3
50	1H, 13C and 15N backbone resonance assignment of the lamin C-terminal region specific to prelamin A. Biomolecular NMR Assignments, 2018, 12, 225-229.	0.8	1