

David Neuhaus

List of Publications by Year in descending order

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33
papers

2,803
citations

279798

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docs citations

39
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2622
citing authors

#	ARTICLE	IF	CITATIONS
1	Molecular mechanisms underlying the role of the centriolar CEP164-TTBK2 complex in ciliopathies. <i>Structure</i> , 2022, 30, 114-128.e9.	3.3	11
2	Zinc finger structure determination by NMR: Why zinc fingers can be a handful. <i>Progress in Nuclear Magnetic Resonance Spectroscopy</i> , 2022, 130-131, 62-105.	7.5	11
3	Dynamics of the HD regulatory subdomain of PARP-1; substrate access and allostery in PARP activation and inhibition. <i>Nucleic Acids Research</i> , 2021, 49, 2266-2288.	14.5	30
4	RING domains act as both substrate and enzyme in a catalytic arrangement to drive self-anchored ubiquitination. <i>Nature Communications</i> , 2021, 12, 1220.	12.8	26
5	Mechanism and evolution of the Zn-fingernail required for interaction of VARP with VPS29. <i>Nature Communications</i> , 2020, 11, 5031.	12.8	21
6	HPF1 completes the PARP active site for DNA damage-induced ADP-ribosylation. <i>Nature</i> , 2020, 579, 598-602.	27.8	172
7	Temporal Ordering in Endocytic Clathrin-Coated Vesicle Formation via AP2 Phosphorylation. <i>Developmental Cell</i> , 2019, 50, 494-508.e11.	7.0	40
8	A tri-ionic anchor mechanism drives Ube2N-specific recruitment and K63-chain ubiquitination in TRIM ligases. <i>Nature Communications</i> , 2019, 10, 4502.	12.8	32
9	Intracellular antibody signalling is regulated by phosphorylation of the Fc receptor TRIM21. <i>ELife</i> , 2018, 7, .	6.0	57
10	Homeodomain-like DNA binding proteins control the haploid-to-diploid transition in <i>Dictyostelium</i> . <i>Science Advances</i> , 2017, 3, e1602937.	10.3	21
11	¹¹³ Cd NMR Experiments Reveal an Unusual Metal Cluster in the Solution Structure of the Yeast Splicing Protein Bud31p. <i>Angewandte Chemie - International Edition</i> , 2015, 54, 4861-4864.	13.8	9
12	¹¹³ Cd NMR Experiments Reveal an Unusual Metal Cluster in the Solution Structure of the Yeast Splicing Protein Bud31p. <i>Angewandte Chemie</i> , 2015, 127, 4943-4946.	2.0	2
13	Structural Basis of Detection and Signaling of DNA Single-Strand Breaks by Human PARP-1. <i>Molecular Cell</i> , 2015, 60, 742-754.	9.7	245
14	DNA-dependent SUMO modification of PARP-1. <i>DNA Repair</i> , 2013, 12, 761-773.	2.8	24
15	The DNA-Binding Domain of Human PARP-1 Interacts with DNA Single-Strand Breaks as a Monomer through Its Second Zinc Finger. <i>Journal of Molecular Biology</i> , 2011, 407, 149-170.	4.2	138
16	Solution structures of the two PBZ domains from human APLF and their interaction with poly(ADP-ribose). <i>Nature Structural and Molecular Biology</i> , 2010, 17, 241-243.	8.2	89
17	Structural consequences of disease-causing mutations in the ATRX-DNMT3-DNMT3L (ADD) domain of the chromatin-associated protein ATRX. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 11939-11944.	7.1	138
18	How the N-terminal Domain of the OSCP Subunit of Bovine F1Fo-ATP Synthase Interacts with the N-terminal Region of an Alpha Subunit. <i>Journal of Molecular Biology</i> , 2007, 368, 310-318.	4.2	30

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19	Structure of the F1-binding Domain of the Stator of Bovine F1Fo-ATPase and How it Binds an \hat{I} -Subunit. <i>Journal of Molecular Biology</i> , 2005, 351, 824-838.	4.2	59
20	Solution Structure and DNA Binding of the Zinc-finger Domain from DNA Ligase III \hat{I} . <i>Journal of Molecular Biology</i> , 2004, 341, 723-738.	4.2	29
21	Solution Structure of Subunit F6 from the Peripheral Stalk Region of ATP Synthase from Bovine Heart Mitochondria. <i>Journal of Molecular Biology</i> , 2004, 342, 593-603.	4.2	23
22	Early heteronuclear NMR studies with rabbit liver metallothionein MT2. <i>Magnetic Resonance in Chemistry</i> , 2003, 41, S70-S79.	1.9	1
23	HMG-D complexed to a bulge DNA: An NMR model. <i>Protein Science</i> , 2001, 10, 504-518.	7.6	19
24	Determination of the NMR structure of the complex between U1A protein and its RNA polyadenylation inhibition element. <i>Journal of Biomolecular NMR</i> , 1998, 11, 59-84.	2.8	25
25	The solution structure of the first zinc finger domain of SWI5: a novel structural extension to a common fold. <i>Structure</i> , 1996, 4, 599-611.	3.3	41
26	Treatment of NOE constraints involving equivalent or nonstereoassigned protons in calculations of biomacromolecular structures. <i>Journal of Biomolecular NMR</i> , 1996, 8, 292-310.	2.8	129
27	The solution structure and dynamics of the DNA-binding domain of HMG-D from <i>Drosophila melanogaster</i> . <i>Structure</i> , 1994, 2, 609-627.	3.3	120
28	Solution structure of the DNA-binding domain of the oestrogen receptor. <i>Nature</i> , 1990, 348, 458-461.	27.8	478
29	Nuclear magnetic resonance identification of \hat{I} -turn and 310-helix secondary structure in rabbit liver metallothionein-2. <i>Journal of Molecular Biology</i> , 1986, 187, 131-135.	4.2	198
30	Sequence-specific ^1H -NMR assignments in rabbit-liver metallothionein-2. <i>FEBS Journal</i> , 1986, 157, 275-289.	0.2	59
31	Systematic application of high-resolution, phase-sensitive two-dimensional ^1H -NMR techniques for the identification of the amino-acid-proton spin systems in proteins. Rabbit metallothionein-2. <i>FEBS Journal</i> , 1985, 151, 257-273.	0.2	286
32	Polypeptide-metal cluster connectivities in metallothionein 2 by novel proton-cadmium-113 heteronuclear two-dimensional NMR experiments. <i>Journal of the American Chemical Society</i> , 1985, 107, 6847-6851.	13.7	165
33	^{113}Cd - ^1H spin-spin couplings in homonuclear ^1H correlated spectroscopy of metallothionein. Identification of the cysteine ^1H spin systems. <i>FEBS Journal</i> , 1984, 143, 659-667.	0.2	55