

Rachel E Klevit

List of Publications by Year in descending order

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170
papers

13,942
citations

19657

61
h-index

23533

111
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183
all docs

183
docs citations

183
times ranked

14792
citing authors

#	ARTICLE	IF	CITATIONS
1	Mutant Adenosine Deaminase 2 in a Polyarteritis Nodosa Vasculopathy. <i>New England Journal of Medicine</i> , 2014, 370, 921-931.	27.0	566
2	Recognition of Antimicrobial Peptides by a Bacterial Sensor Kinase. <i>Cell</i> , 2005, 122, 461-472.	28.9	495
3	RING-type E3 ligases: Master manipulators of E2 ubiquitin-conjugating enzymes and ubiquitination. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2014, 1843, 47-60.	4.1	458
4	UBCH7 reactivity profile reveals parkin and HHARI to be RING/HECT hybrids. <i>Nature</i> , 2011, 474, 105-108.	27.8	455
5	Proof of principle for epitope-focused vaccine design. <i>Nature</i> , 2014, 507, 201-206.	27.8	451
6	Structure of a BRCA1-BARD1 heterodimeric RING-RING complex. <i>Nature Structural Biology</i> , 2001, 8, 833-837.	9.7	446
7	E2 enzymes: more than just middle men. <i>Cell Research</i> , 2016, 26, 423-440.	12.0	399
8	Binding and recognition in the assembly of an active BRCA1/BARD1 ubiquitin-ligase complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 5646-5651.	7.1	314
9	E2-BRCA1 RING interactions dictate synthesis of mono- or specific polyubiquitin chain linkages. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 941-948.	8.2	314
10	Structure of an E3:E2 ^{1/4} Ub Complex Reveals an Allosteric Mechanism Shared among RING/U-box Ligases. <i>Molecular Cell</i> , 2012, 47, 933-942.	9.7	272
11	A UbcH5/Ubiquitin Noncovalent Complex Is Required for Processive BRCA1-Directed Ubiquitination. <i>Molecular Cell</i> , 2006, 21, 873-880.	9.7	265
12	Solid-state NMR and SAXS studies provide a structural basis for the activation of β -crystallin oligomers. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 1037-1042.	8.2	263
13	Activation of the Bacterial Sensor Kinase PhoQ by Acidic pH. <i>Molecular Cell</i> , 2007, 26, 165-174.	9.7	251
14	Structural Basis for Mechanical Force Regulation of the Adhesin FimH via Finger Trap-like β Sheet Twisting. <i>Cell</i> , 2010, 141, 645-655.	28.9	239
15	Mutations in the DBP-Deficiency Protein HSD17B4 Cause Ovarian Dysgenesis, Hearing Loss, and Ataxia of Perrault Syndrome. <i>American Journal of Human Genetics</i> , 2010, 87, 282-288.	6.2	231
16	Mutations in mitochondrial histidyl tRNA synthetase <i>HARS2</i> cause ovarian dysgenesis and sensorineural hearing loss of Perrault syndrome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 6543-6548.	7.1	225
17	Mass Spectrometric and Mutational Analyses Reveal Lys-6-linked Polyubiquitin Chains Catalyzed by BRCA1-BARD1 Ubiquitin Ligase. <i>Journal of Biological Chemistry</i> , 2004, 279, 3916-3924.	3.4	202
18	Pharmacological chaperone for β -crystallin partially restores transparency in cataract models. <i>Science</i> , 2015, 350, 674-677.	12.6	195

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19	N-terminal domain of $\hat{I}\pm$ B-crystallin provides a conformational switch for multimerization and structural heterogeneity. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 6409-6414.	7.1	185
20	Allosteric activation of the RNF146 ubiquitin ligase by a poly(ADP-ribosyl)ation signal. Nature, 2015, 517, 223-226.	27.8	177
21	Mutations in LARS2, Encoding Mitochondrial Leucyl-tRNA Synthetase, Lead to Premature Ovarian Failure and Hearing Loss in Perrault Syndrome. American Journal of Human Genetics, 2013, 92, 614-620.	6.2	176
22	OTUB1 Co-opts Lys48-Linked Ubiquitin Recognition to Suppress E2 Enzyme Function. Molecular Cell, 2012, 45, 384-397.	9.7	174
23	The Acidic Transcription Activator Gcn4 Binds the Mediator Subunit Gal11/Med15 Using a Simple Protein Interface Forming a Fuzzy Complex. Molecular Cell, 2011, 44, 942-953.	9.7	172
24	Estrogen receptor \hat{A} is a putative substrate for the BRCA1 ubiquitin ligase. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 5794-5799.	7.1	166
25	E2s: structurally economical and functionally replete. Biochemical Journal, 2011, 433, 31-42.	3.7	164
26	Proton NMR studies on the interaction between distamycin A and a symmetrical DNA dodecamer. Biochemistry, 1986, 25, 3296-3303.	2.5	163
27	Activity-enhancing mutations in an E3 ubiquitin ligase identified by high-throughput mutagenesis. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E1263-72.	7.1	158
28	The growing world of small heat shock proteins: from structure to functions. Cell Stress and Chaperones, 2017, 22, 601-611.	2.9	158
29	One size does not fit all: The oligomeric states of $\hat{I}\pm$ B crystallin. FEBS Letters, 2013, 587, 1073-1080.	2.8	157
30	Involvement of the carboxy-terminal residue in the active site of the histidine-containing protein, HPr, of the phosphoenolpyruvate:sugar phosphotransferase system of Escherichia coli. Biochemistry, 1991, 30, 9601-9607.	2.5	145
31	Interaction of calmodulin and a calmodulin-binding peptide from myosin light chain kinase: major spectral changes in both occur as the result of complex formation. Biochemistry, 1985, 24, 8152-8157.	2.5	142
32	Binding of the Catabolite Repressor Protein CcpA to Its DNA Target Is Regulated by Phosphorylation of its Corepressor HPr. Journal of Biological Chemistry, 1997, 272, 26530-26535.	3.4	133
33	Solution Structure of the Sodium Channel Inactivation Gate,. Biochemistry, 1999, 38, 855-861.	2.5	130
34	Mapping the Functional Domains of BRCA1. Journal of Biological Chemistry, 1999, 274, 5659-5665.	3.4	124
35	Ubiquitin in Motion: Structural Studies of the Ubiquitin-Conjugating Enzyme $\hat{1}\frac{1}{4}$ Ubiquitin Conjugate. Biochemistry, 2011, 50, 1624-1633.	2.5	124
36	BRCA1 RING Domain Cancer-predisposing Mutations. Journal of Biological Chemistry, 2001, 276, 41399-41406.	3.4	118

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37	Solution structure of a zinc finger domain of yeast ADR1. <i>Proteins: Structure, Function and Bioinformatics</i> , 1990, 7, 215-226.	2.6	116
38	Metal Bridges between the PhoQ Sensor Domain and the Membrane Regulate Transmembrane Signaling. <i>Journal of Molecular Biology</i> , 2006, 356, 1193-1206.	4.2	116
39	Hemi-methylated DNA regulates DNA methylation inheritance through allosteric activation of H3 ubiquitylation by UHRF1. <i>ELife</i> , 2016, 5, .	6.0	111
40	RING-Between-RING E3 Ligases: Emerging Themes amid the Variations. <i>Journal of Molecular Biology</i> , 2017, 429, 3363-3375.	4.2	110
41	Gcn4-Mediator Specificity Is Mediated by a Large and Dynamic Fuzzy Protein-Protein Complex. <i>Cell Reports</i> , 2018, 22, 3251-3264.	6.4	110
42	Cyclic Nucleotide Binding GAF Domains from Phosphodiesterases: Structural and Mechanistic Insights. <i>Structure</i> , 2009, 17, 1551-1557.	3.3	109
43	Common structural changes accompany the functional inactivation of HPr by seryl phosphorylation or by serine to aspartate substitution. <i>Biochemistry</i> , 1989, 28, 9908-9912.	2.5	107
44	$\hat{\pm}$ B-Crystallin: A Hybrid Solid-State/Solution-State NMR Investigation Reveals Structural Aspects of the Heterogeneous Oligomer. <i>Journal of Molecular Biology</i> , 2009, 385, 1481-1497.	4.2	106
45	Binding determinants of the small heat shock protein, $\hat{\pm}$ B-crystallin: recognition of the $\hat{\epsilon}$ -I $\hat{\epsilon}$ ™ motif. <i>EMBO Journal</i> , 2012, 31, 4587-4594.	7.8	104
46	Two-dimensional proton NMR studies of histidine-containing protein from <i>Escherichia coli</i> . 3. Secondary and tertiary structure as determined by NMR. <i>Biochemistry</i> , 1986, 25, 7774-7781.	2.5	102
47	¹ H-NMR studies of calmodulin. The nature of the Ca ²⁺ -dependent conformational change. <i>FEBS Journal</i> , 1984, 139, 109-114.	0.2	97
48	Mutations in Twinkle primase-helicase cause Perrault syndrome with neurologic features. <i>Neurology</i> , 2014, 83, 2054-2061.	1.1	86
49	¹ H NMR studies of calmodulin. Resonance assignments by use of tryptic fragments. <i>FEBS Journal</i> , 1984, 138, 281-289.	0.2	85
50	A sequence-specific transcription activator motif and powerful synthetic variants that bind Mediator using a fuzzy protein interface. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E3506-13.	7.1	84
51	Interaction of BARD1 and HP1 Is Required for BRCA1 Retention at Sites of DNA Damage. <i>Cancer Research</i> , 2015, 75, 1311-1321.	0.9	83
52	Two-dimensional NMR investigation of a bent DNA fragment: assignment of the proton resonances and preliminary structure analysis. <i>Nucleic Acids Research</i> , 1987, 15, 5845-5862.	14.5	82
53	HspB1 and Hsc70 chaperones engage distinct tau species and have different inhibitory effects on amyloid formation. <i>Journal of Biological Chemistry</i> , 2018, 293, 2687-2700.	3.4	81
54	Ovothiols, a family of redox-active mercaptohistidine compounds from marine invertebrate eggs. <i>Biochemistry</i> , 1987, 26, 4028-4036.	2.5	79

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55	The Cancer-predisposing Mutation C61G Disrupts Homodimer Formation in the NH ₂ -terminal BRCA1 RING Finger Domain. <i>Journal of Biological Chemistry</i> , 1998, 273, 7795-7799.	3.4	79
56	Structural Insights into the Conformation and Oligomerization of E2 ^{1/4} Ubiquitin Conjugates. <i>Biochemistry</i> , 2012, 51, 4175-4187.	2.5	78
57	Ubiquitin Transfer from the E2 Perspective: Why is UbcH5 So Promiscuous?. <i>Cell Cycle</i> , 2006, 5, 2867-2873.	2.6	77
58	Mechanisms of Small Heat Shock Proteins. <i>Cold Spring Harbor Perspectives in Biology</i> , 2019, 11, a034025.	5.5	76
59	Mechanism of phosphoribosyl-ubiquitination mediated by a single Legionella effector. <i>Nature</i> , 2018, 557, 729-733.	27.8	75
60	Following Ariadne's thread: a new perspective on RBR ubiquitin ligases. <i>BMC Biology</i> , 2012, 10, 24.	3.8	74
61	Molecular insights into <sc>RBR</sc> E3 ligase ubiquitin transfer mechanisms. <i>EMBO Reports</i> , 2016, 17, 1221-1235.	4.5	73
62	Intrinsic disorder drives N-terminal ubiquitination by Ube2w. <i>Nature Chemical Biology</i> , 2015, 11, 83-89.	8.0	68
63	Solution structure of the phosphocarrier protein HPr from <i>Bacillus subtilis</i> by two-dimensional NMR spectroscopy. <i>Protein Science</i> , 1992, 1, 1363-1376.	7.6	65
64	Regulating the Regulators: Recent Revelations in the Control of E3 Ubiquitin Ligases. <i>Journal of Biological Chemistry</i> , 2015, 290, 21244-21251.	3.4	61
65	A Bifunctional Role for the UHRF1 ^U UBL Domain in the Control of Hemi-methylated DNA-Dependent Histone Ubiquitylation. <i>Molecular Cell</i> , 2018, 72, 753-765.e6.	9.7	58
66	BRCA1/BARD1 site-specific ubiquitylation of nucleosomal H2A is directed by BARD1. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 268-277.	8.2	58
67	Sequence-specific proton NMR resonance assignments of Bacillus subtilis HPr: use of spectra obtained from mutants to resolve spectral overlap. <i>Biochemistry</i> , 1990, 29, 7191-7200.	2.5	56
68	Structural Consequences of Histidine Phosphorylation: NMR Characterization of the Phosphohistidine Form of Histidine-Containing Protein from Bacillus subtilis and Escherichia coli. <i>Biochemistry</i> , 1994, 33, 15271-15282.	2.5	54
69	Similarities and differences between yeast and vertebrate calmodulin: An examination of the calcium-binding and structural properties of calmodulin from the yeast Saccharomyces cerevisiae. <i>Biochemistry</i> , 1993, 32, 3261-3270.	2.5	53
70	Identification of an unconventional E3 binding surface on the UbcH5 ^{1/4} Ub conjugate recognized by a pathogenic bacterial E3 ligase.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 2848-2853.	7.1	53
71	E2~Ub conjugates regulate the kinase activity of Shigella effector OspG during pathogenesis. <i>EMBO Journal</i> , 2014, 33, n/a-n/a.	7.8	53
72	A Mechanism of Subunit Recruitment in Human Small Heat Shock Protein Oligomers. <i>Biochemistry</i> , 2015, 54, 4276-4284.	2.5	53

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73	A conserved histidine modulates HSPB5 structure to trigger chaperone activity in response to stress-related acidosis. <i>ELife</i> , 2015, 4, .	6.0	52
74	Two-dimensional proton NMR studies of histidine-containing protein from <i>Escherichia coli</i> . 1. Sequential resonance assignments. <i>Biochemistry</i> , 1986, 25, 7760-7769.	2.5	51
75	A series of point mutations reveal interactions between the calcium-binding sites of calmodulin. <i>Protein Science</i> , 1992, 1, 245-253.	7.6	50
76	Reexamination of the secondary and tertiary structure of histidine-containing protein from <i>Escherichia coli</i> by homonuclear and heteronuclear NMR spectroscopy. <i>Biochemistry</i> , 1991, 30, 11842-11850.	2.5	47
77	Unraveling a bacterial hexose transport pathway. <i>Current Opinion in Structural Biology</i> , 1994, 4, 814-822.	5.7	47
78	Activation of UbcH5c ^{1/4} Ub Is the Result of a Shift in Interdomain Motions of the Conjugate Bound to U-Box E3 Ligase E4B. <i>Biochemistry</i> , 2013, 52, 2991-2999.	2.5	47
79	Engineering a Ubiquitin Ligase Reveals Conformational Flexibility Required for Ubiquitin Transfer. <i>Journal of Biological Chemistry</i> , 2009, 284, 26797-26802.	3.4	46
80	Ca ²⁺ -dependent conformational changes in bovine GCAP ² . <i>Protein Science</i> , 1998, 7, 2675-2680.	7.6	45
81	Dynamic interactions of proteins in complex networks: identifying the complete set of interacting E2s for functional investigation of E3-dependent protein ubiquitination. <i>FEBS Journal</i> , 2009, 276, 5381-5389.	4.7	45
82	Structural Studies of HHARI/UbcH7 ^{1/4} Ub Reveal Unique E2 ^{1/4} Ub Conformational Restriction by RBR RING1. <i>Structure</i> , 2017, 25, 890-900.e5.	3.3	45
83	The PhoQ histidine kinases of <i>Salmonella</i> and <i>Pseudomonas</i> spp. are structurally and functionally different: evidence that pH and antimicrobial peptide sensing contribute to mammalian pathogenesis. <i>Molecular Microbiology</i> , 2008, 69, 503-519.	2.5	44
84	Phosphorylation of serine ⁴⁶ in HPr, a key regulatory protein in bacteria, results in stabilization of its solution structure. <i>Protein Science</i> , 1995, 4, 2478-2486.	7.6	43
85	BARD1 is necessary for ubiquitylation of nucleosomal histone H2A and for transcriptional regulation of estrogen metabolism genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 1316-1321.	7.1	43
86	The uses and limitations of calmodulin antagonists. , 1989, 44, 181-239.		42
87	Prediction and structural characterization of an independently folding substructure in the src SH3 domain. <i>Journal of Molecular Biology</i> , 1998, 283, 293-300.	4.2	42
88	The Structure of the GAF A Domain from Phosphodiesterase 6C Reveals Determinants of cGMP Binding, a Conserved Binding Surface, and a Large cGMP-dependent Conformational Change. <i>Journal of Biological Chemistry</i> , 2008, 283, 25913-25919.	3.4	42
89	Interplay of disordered and ordered regions of a human small heat shock protein yields an ensemble of "quasi-ordered" states. <i>ELife</i> , 2019, 8, .	6.0	41
90	Ca ²⁺ Binding to Calmodulin and Its Role in <i>Schizosaccharomyces pombe</i> as Revealed by Mutagenesis and NMR Spectroscopy. <i>Journal of Biological Chemistry</i> , 1995, 270, 20643-20652.	3.4	40

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91	Structure of the Î±-crystallin domain from the redox-sensitive chaperone, HSPB1. Journal of Biomolecular NMR, 2015, 63, 223-228.	2.8	38
92	Zinc finger diversity. Current Opinion in Structural Biology, 1994, 4, 28-35.	5.7	37
93	Release of a disordered domain enhances HspB1 chaperone activity toward tau. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 2923-2929.	7.1	37
94	A disorder-to-order transition coupled to DNA binding in the essential zinc-finger DNA-binding domain of yeast ADR1. Journal of Molecular Biology, 1998, 279, 929-943.	4.2	36
95	Crystal Structure of the BARD1 Ankyrin Repeat Domain and Its Functional Consequences. Journal of Biological Chemistry, 2008, 283, 21179-21186.	3.4	35
96	Structural and Functional Characterization of the Monomeric U-Box Domain from E4B. Biochemistry, 2010, 49, 347-355.	2.5	35
97	Two-dimensional proton NMR studies of histidine-containing protein from Escherichia coli. 2. Leucine resonance assignments by long-range coherence transfer. Biochemistry, 1986, 25, 7770-7773.	2.5	34
98	Acidic pH and divalent cation sensing by PhoQ are dispensable for systemic salmonellae virulence. ELife, 2015, 4, e06792.	6.0	34
99	A folding transition and novel zinc finger accessory domain in the transcription factor ADR1. Nature Structural Biology, 1999, 6, 478-485.	9.7	33
100	Hydrogen bonding and equilibrium isotope enrichment in histidine-containing proteins. Nature Structural and Molecular Biology, 1996, 3, 522-531.	8.2	32
101	Demonstration of protein-protein interaction specificity by NMR chemical shift mapping. Protein Science, 1997, 6, 2624-2627.	7.6	32
102	Solution Structure of the cGMP Binding GAF Domain from Phosphodiesterase 5. Journal of Biological Chemistry, 2008, 283, 22749-22759.	3.4	32
103	Structures of DNA-binding mutant zinc finger domains: Implications for DNA binding. Protein Science, 1993, 2, 951-965.	7.6	31
104	Two functionally distinct E2/E3 pairs coordinate sequential ubiquitination of a common substrate in <i>Caenorhabditis elegans</i> development. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E6576-E6584.	7.1	31
105	Influence of N-Cap Mutations on the Structure and Stability of Escherichia coli HPr. Biochemistry, 1996, 35, 11268-11277.	2.5	30
106	Increased helix and protein stability through the introduction of a new tertiary hydrogen bond 1 1P.E. Wright. Journal of Molecular Biology, 1999, 286, 1609-1619.	4.2	30
107	Tuning BRCA1 and BARD1 activity to investigate RING ubiquitin ligase mechanisms. Protein Science, 2017, 26, 475-483.	7.6	30
108	The Whole Is Not the Simple Sum of Its Parts in Calmodulin from <i>S.cerevisiae</i> . Biochemistry, 2000, 39, 4225-4230.	2.5	29

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109	Phosphorylation on histidine is accompanied by localized structural changes in the phosphocarrier protein, HPr from <i>Bacillus subtilis</i> . <i>Protein Science</i> , 1997, 6, 2107-2119.	7.6	29
110	Mediator subunit Med15 dictates the conserved "fuzzy" binding mechanism of yeast transcription activators Gal4 and Gcn4. <i>Nature Communications</i> , 2021, 12, 2220.	12.8	28
111	The BRCA1/BARD1 ubiquitin ligase and its substrates. <i>Biochemical Journal</i> , 2021, 478, 3467-3483.	3.7	28
112	Structure of a Histidine-X4-Histidine Zinc Finger Domain: Insights into ADR1-UAS1 Protein-DNA Recognition. <i>Biochemistry</i> , 1994, 33, 4460-4470.	2.5	26
113	The Essential Ubc4/Ubc5 Function in Yeast Is HECT E3-dependent, and RING E3-dependent Pathways Require Only Monoubiquitin Transfer by Ubc4. <i>Journal of Biological Chemistry</i> , 2011, 286, 15165-15170.	3.4	25
114	Structural insights into SAM domain-mediated tankyrase oligomerization. <i>Protein Science</i> , 2016, 25, 1744-1752.	7.6	25
115	pH-dependent structural modulation is conserved in the human small heat shock protein HSBP1. <i>Cell Stress and Chaperones</i> , 2017, 22, 569-575.	2.9	24
116	Structural basis for tankyrase-RNF146 interaction reveals noncanonical tankyrase binding motifs. <i>Protein Science</i> , 2018, 27, 1057-1067.	7.6	24
117	De novo mutation in <i>RING1</i> with epigenetic effects on neurodevelopment. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 1558-1563.	7.1	24
118	ADR1a, a zinc finger peptide, exists in two folded conformations. <i>Biochemistry</i> , 1991, 30, 3365-3371.	2.5	23
119	Who with whom: functional coordination of E2 enzymes by RING E3 ligases during polyubiquitylation. <i>EMBO Journal</i> , 2020, 39, e104863.	7.8	23
120	[8] Spectroscopic analyses of calmodulin and its interactions. <i>Methods in Enzymology</i> , 1983, 102, 82-104.	1.0	22
121	Mechanism of DNA Binding by the ADR1 Zinc Finger Transcription Factor as Determined by SPR. <i>Journal of Molecular Biology</i> , 2003, 329, 931-939.	4.2	22
122	Legionella effector MavC targets the Ube2N-Ub conjugate for noncanonical ubiquitination. <i>Nature Communications</i> , 2020, 11, 2365.	12.8	21
123	NMR chemical shift perturbation mapping of dna binding by a zinc finger domain from the yeast transcription factor ADR1. <i>Protein Science</i> , 1997, 6, 1835-1848.	7.6	20
124	Mechanistic insights revealed by a UBE2A mutation linked to intellectual disability. <i>Nature Chemical Biology</i> , 2019, 15, 62-70.	8.0	19
125	Peeking from behind the veil of enigma: emerging insights on small heat shock protein structure and function. <i>Cell Stress and Chaperones</i> , 2020, 25, 573-580.	2.9	19
126	The Ubiquitin-Conjugating Enzyme, UbcM2, Is Restricted to Monoubiquitylation by a Two-Fold Mechanism That Involves Backside Residues of E2 and Lys48 of Ubiquitin. <i>Biochemistry</i> , 2014, 53, 4004-4014.	2.5	18

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127	Paramagnetic Cobalt as a Probe of the Orientation of an Accessory DNA-Binding Region of the Yeast ADR1 Zinc-Finger Protein. <i>Biochemistry</i> , 1997, 36, 14003-14011.	2.5	17
128	Investigation of a side-chain-side-chain hydrogen bond by mutagenesis, thermodynamics, and NMR spectroscopy. <i>Protein Science</i> , 1995, 4, 936-944.	7.6	17
129	Characterization of RING-Between-RING E3 Ubiquitin Transfer Mechanisms. <i>Methods in Molecular Biology</i> , 2018, 1844, 3-17.	0.9	17
130	Biochemical and Structural Characterization of the Ubiquitin-Conjugating Enzyme UBE2W Reveals the Formation of a Noncovalent Homodimer. <i>Cell Biochemistry and Biophysics</i> , 2013, 67, 103-110.	1.8	15
131	Cbl interacts with multiple E2s in vitro and in cells. <i>PLoS ONE</i> , 2019, 14, e0216967.	2.5	15
132	HSPB5 engages multiple states of a destabilized client to enhance chaperone activity in a stress-dependent manner. <i>Journal of Biological Chemistry</i> , 2019, 294, 3261-3270.	3.4	15
133	Solution structure of sperm lysin yields novel insights into molecular dynamics of rapid protein evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 1310-1315.	7.1	14
134	BRCA1/BARD1 is a nucleosome reader and writer. <i>Trends in Biochemical Sciences</i> , 2022, 47, 582-595.	7.5	14
135	Sequence-Specific DNA Recognition by Cys2, His2Zinc Fingers. <i>Annals of the New York Academy of Sciences</i> , 1994, 726, 92-104.	3.8	13
136	Infantile onset spinocerebellar ataxia caused by compound heterozygosity for Twinkle mutations and modeling of Twinkle mutations causing recessive disease. <i>Journal of Physical Education and Sports Management</i> , 2016, 2, a001107.	1.2	13
137	Flavonoid Regulation of HCN2 Channels. <i>Journal of Biological Chemistry</i> , 2013, 288, 33136-33145.	3.4	12
138	RMSD analysis of structures of the bacterial protein FimH identifies five conformations of its lectin domain. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020, 88, 593-603.	2.6	12
139	Proton nuclear magnetic resonance studies on the variant-3 neurotoxin from <i>Centruroides sculpturatus</i> Ewing: sequential assignment of resonances. <i>Biochemistry</i> , 1989, 28, 1548-1555.	2.5	11
140	Structural Biology: Parkin's Serpentine Shape Revealed in the Year of the Snake. <i>Current Biology</i> , 2013, 23, R691-R693.	3.9	11
141	RING-between-RINGs-keeping the safety on loaded guns. <i>EMBO Journal</i> , 2012, 31, 3792-3794.	7.8	10
142	Proton nuclear magnetic resonance characterization of the aromatic residues in the variant-3 neurotoxin from <i>Centruroides sculpturatus</i> Ewing. <i>Biochemistry</i> , 1989, 28, 1556-1562.	2.5	9
143	The structure of HPr and site-directed mutagenesis. <i>FEMS Microbiology Letters</i> , 1989, 63, 43-52.	1.8	8
144	[6] Multidimensional nuclear magnetic resonance spectroscopy of DNA-binding proteins. <i>Methods in Enzymology</i> , 1991, 208, 63-82.	1.0	8

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145	A native chemical chaperone in the human eye lens. <i>ELife</i> , 0, 11, .	6.0	8
146	The ubiquitin ligase SspH1 from <i>Salmonella</i> uses a modular and dynamic E3 domain to catalyze substrate ubiquitylation. <i>Journal of Biological Chemistry</i> , 2019, 294, 783-793.	3.4	7
147	UbcH5 Interacts with Substrates to Participate in Lysine Selection with the E3 Ubiquitin Ligase CHIP. <i>Biochemistry</i> , 2020, 59, 2078-2088.	2.5	7
148	Indirect sexual selection drives rapid sperm protein evolution in abalone. <i>ELife</i> , 2019, 8, .	6.0	7
149	Solvent exchange rates of side-chain amide protons in proteins. <i>Journal of Biomolecular NMR</i> , 1998, 11, 205-212.	2.8	6
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151	Cullin-independent recognition of HHARI substrates by a dynamic RBR catalytic domain. <i>Structure</i> , 2022, , .	3.3	6
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