Rachel E Klevit

List of Publications by Year
in descending order

170 papers	13,942 citations	19657 61 h-index	23533 111 g-index
183 all docs	183 docs citations	183 times ranked	14792 citing authors

#	Article	IF	Citations
1	BRCA1/BARD1 is a nucleosome reader and writer. Trends in Biochemical Sciences, 2022, 47, 582-595.	7.5	14
2	Cullin-independent recognition of HHARI substrates by a dynamic RBR catalytic domain. Structure, 2022, , .	3.3	6
3	Neutralizing Antibodies Against Allosteric Proteins: Insights From a Bacterial Adhesin. Journal of Molecular Biology, 2022, 434, 167717.	4.2	3
4	BRCA1/BARD1 site-specific ubiquitylation of nucleosomal H2A is directed by BARD1. Nature Structural and Molecular Biology, 2021, 28, 268-277.	8.2	58
5	Mediator subunit Med15 dictates the conserved â€œfuzzyâ€•binding mechanism of yeast transcription activators Gal4 and Gcn4. Nature Communications, 2021, 12, 2220.	12.8	28
6	Toggle switch residues control allosteric transitions in bacterial adhesins by participating in a concerted repacking of the protein core. PLoS Pathogens, 2021, 17, e1009440.	4.7	6
7	The BRCA1/BARD1 ubiquitin ligase and its substrates. Biochemical Journal, 2021, 478, 3467-3483.	3.7	28
8	Edmond Fischer (1920â€"2021). Science, 2021, 374, 157-157.	12.6	0
9	RMSD analysis of structures of the bacterial protein FimH identifies five conformations of its lectin domain. Proteins: Structure, Function and Bioinformatics, 2020, 88, 593-603.	2.6	12
10	UbcH5 Interacts with Substrates to Participate in Lysine Selection with the E3 Ubiquitin Ligase CHIP. Biochemistry, 2020, 59, 2078-2088.	2.5	7
11	Legionella effector MavC targets the Ube2N~Ub conjugate for noncanonical ubiquitination. Nature Communications, 2020, 11, 2365.	12.8	21
12	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
13	Peeking from behind the veil of enigma: emerging insights on small heat shock protein structure and function. Cell Stress and Chaperones, 2020, 25, 573-580.	2.9	19
14	Who with whom: functional coordination of E2 enzymes by RING E3 ligases during polyâ€ubiquitylation. EMBO Journal, 2020, 39, e104863.	7.8	23
15	Cbl interacts with multiple E2s in vitro and in cells. PLoS ONE, 2019, 14, e0216967.	2.5	15
16	Mechanisms of Small Heat Shock Proteins. Cold Spring Harbor Perspectives in Biology, 2019, 11, a034025.	5.5	76
17	HSPB5 engages multiple states of a destabilized client to enhance chaperone activity in a stress-dependent manner. Journal of Biological Chemistry, 2019, 294, 3261-3270.	3.4	15
18	The ubiquitin ligase SspH1 from Salmonella uses a modular and dynamic E3 domain to catalyze substrate ubiquitylation. Journal of Biological Chemistry, 2019, 294, 783-793.	3.4	7

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19	Mechanistic insights revealed by a UBE2A mutation linked to intellectual disability. Nature Chemical Biology, 2019, 15, 62-70.	8.0	19
20	Interplay of disordered and ordered regions of a human small heat shock protein yields an ensemble of â€˜quasi-orderedâ€™ states. ELife, 2019, 8, .	6.0	41
21	Indirect sexual selection drives rapid sperm protein evolution in abalone. ELife, 2019, 8, .	6.0	7
22	<scp>S</scp>tructural basis for tankyraseâ€RNF146 interaction reveals noncanonical tankyraseâ€binding motifs. Protein Science, 2018, 27, 1057-1067.	7.6	24
23	De novo mutation in <i>RING1</i> with epigenetic effects on neurodevelopment. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 1558-1563.	7.1	24
24	Solution structure of sperm lysin yields novel insights into molecular dynamics of rapid protein evolution. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 1310-1315.	7.1	14
25	BARD1 is necessary for ubiquitylation of nucleosomal histone H2A and for transcriptional regulation of estrogen metabolism genes. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 1316-1321.	7.1	43
26	HspB1 and Hsc70 chaperones engage distinct tau species and have different inhibitory effects on amyloid formation. Journal of Biological Chemistry, 2018, 293, 2687-2700.	3.4	81
27	Gcn4-Mediator Specificity Is Mediated by a Large and Dynamic Fuzzy Protein-Protein Complex. Cell Reports, 2018, 22, 3251-3264.	6.4	110
28	Characterization of RING-Between-RING E3 Ubiquitin Transfer Mechanisms. Methods in Molecular Biology, 2018, 1844, 3-17.	0.9	17
29	A Bifunctional Role for the UHRF1ÂUBL Domain in the Control of Hemi-methylated DNA-Dependent Histone Ubiquitylation. Molecular Cell, 2018, 72, 753-765.e6.	9.7	58
30	Mechanism of phosphoribosyl-ubiquitination mediated by a single Legionella effector. Nature, 2018, 557, 729-733.	27.8	75
31	Structural Studies of HHARI/UbcH7âˆ¼Ub Reveal Unique E2âˆ¼Ub Conformational Restriction by RBR RING1. Structure, 2017, 25, 890-900.e5.	3.3	45
32	pH-dependent structural modulation is conserved in the human small heat shock protein HSBP1. Cell Stress and Chaperones, 2017, 22, 569-575.	2.9	24
33	The growing world of small heat shock proteins: from structure to functions. Cell Stress and Chaperones, 2017, 22, 601-611.	2.9	158
34	Tuning BRCA1 and BARD1 activity to investigate RING ubiquitin ligase mechanisms. Protein Science, 2017, 26, 475-483.	7.6	30
35	RING-Between-RING E3 Ligases: Emerging Themes amid the Variations. Journal of Molecular Biology, 2017, 429, 3363-3375.	4.2	110
36	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

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37	Structural insights into SAM domainâ€mediated tankyrase oligomerization. Protein Science, 2016, 25, 1744-1752.	7.6	25
38	E2 enzymes: more than just middle men. Cell Research, 2016, 26, 423-440.	12.0	399
39	Intrinsically-Disordered Region of Human Small Heat Shock Protein HSPB1 Affects Structure and Function. Biophysical Journal, 2016, 110, 43a.	0.5	0
40	The Disparate Effects of two Molecular Chaperones on Tau Amyloid Formation. Biophysical Journal, 2016, 110, 554a.	0.5	0
41	Molecular insights into <scp>RBR</scp> E3 ligase ubiquitin transfer mechanisms. EMBO Reports, 2016, 17, 1221-1235.	4.5	73
42	Infantile onset spinocerebellar ataxia caused by compound heterozygosity for Twinkle mutations and modeling of Twinkle mutations causing recessive disease. Journal of Physical Education and Sports Management, 2016, 2, a001107.	1.2	13
43	Hemi-methylated DNA regulates DNA methylation inheritance through allosteric activation of H3 ubiquitylation by UHRF1. ELife, 2016, 5, .	6.0	111
44	Abstract 4542: Ube2d family members, Ube2e family members and Ube2w modulate the ubiquitination and degradation of EGFR by Cbl. , 2016, , .		3
45	pUBLically unzipping Parkin: how phosphorylation exposes a ligase bit by bit. EMBO Journal, 2015, 34, 2486-2488.	7.8	5
46	Acidic pH and divalent cation sensing by PhoQ are dispensable for systemic salmonellae virulence. ELife, 2015, 4, e06792.	6.0	34
47	Interaction of BARD1 and HP1 Is Required for BRCA1 Retention at Sites of DNA Damage. Cancer Research, 2015, 75, 1311-1321.	0.9	83
48	Structure of the Î±-crystallin domain from the redox-sensitive chaperone, HSPB1. Journal of Biomolecular NMR, 2015, 63, 223-228.	2.8	38
49	A Mechanism of Subunit Recruitment in Human Small Heat Shock Protein Oligomers. Biochemistry, 2015, 54, 4276-4284.	2.5	53
50	Pharmacological chaperone for Î±-crystallin partially restores transparency in cataract models. Science, 2015, 350, 674-677.	12.6	195
51	Regulating the Regulators: Recent Revelations in the Control of E3 Ubiquitin Ligases. Journal of Biological Chemistry, 2015, 290, 21244-21251.	3.4	61
52	Intrinsic disorder drives N-terminal ubiquitination by Ube2w. Nature Chemical Biology, 2015, 11, 83-89.	8.0	68
53	Allosteric activation of the RNF146 ubiquitin ligase by a poly(ADP-ribosyl)ation signal. Nature, 2015, 517, 223-226.	27.8	177
54	A conserved histidine modulates HSPB5 structure to trigger chaperone activity in response to stress-related acidosis. ELife, 2015, 4, .	6.0	52

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55	Structural, Functional, and Mechanistic Diversity in Protein Ubiquitination. FASEB Journal, 2015, 29, 355.1.	0.5	0
56	Abstract 4965: Multiple ubiquitin-conjugating enzymes modulate the ubiquitination and downregulation of the EGFR by the Cbl RING finger ubiquitin ligase. , 2015, , .		0
57	E2~Ub conjugates regulate the kinase activity ofShigellaeffector OspG during pathogenesis. EMBO Journal, 2014, 33, n/a-n/a.	7.8	53
58	Mutant Adenosine Deaminase 2 in a Polyarteritis Nodosa Vasculopathy. New England Journal of Medicine, 2014, 370, 921-931.	27.0	566
59	Proof of principle for epitope-focused vaccine design. Nature, 2014, 507, 201-206.	27.8	451
60	Mutations in Twinkle primase-helicase cause Perrault syndrome with neurologic features. Neurology, 2014, 83, 2054-2061.	1.1	86
61	A sequence-specific transcription activator motif and powerful synthetic variants that bind Mediator using a fuzzy protein interface. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E3506-13.	7.1	84
62	The Ubiquitin-Conjugating Enzyme, UbcM2, Is Restricted to Monoubiquitylation by a Two-Fold Mechanism That Involves Backside Residues of E2 and Lys48 of Ubiquitin. Biochemistry, 2014, 53, 4004-4014.	2.5	18
63	RING-type E3 ligases: Master manipulators of E2 ubiquitin-conjugating enzymes and ubiquitination. Biochimica Et Biophysica Acta - Molecular Cell Research, 2014, 1843, 47-60.	4.1	458
64	Abstract 4441: Ube2e inhibits the ubiquitination and degradation of EGFR mediated by Cbl and Ube2d. , 2014, , .		2
65	Biochemical and Structural Characterization of the Ubiquitin-Conjugating Enzyme UBE2W Reveals the Formation of a Noncovalent Homodimer. Cell Biochemistry and Biophysics, 2013, 67, 103-110.	1.8	15
66	One size does not fit all: The oligomeric states of Î±B crystallin. FEBS Letters, 2013, 587, 1073-1080.	2.8	157
67	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
68	Structural Biology: Parkinâ€™s Serpentine Shape Revealed in the Year of the Snake. Current Biology, 2013, 23, R691-R693.	3.9	11
69	Activation of UbcH5câˆ¼Ub Is the Result of a Shift in Interdomain Motions of the Conjugate Bound to U-Box E3 Ligase E4B. Biochemistry, 2013, 52, 2991-2999.	2.5	47
70	Flavonoid Regulation of HCN2 Channels. Journal of Biological Chemistry, 2013, 288, 33136-33145.	3.4	12
71	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
72	RING-between-RINGs-keeping the safety on loaded guns. EMBO Journal, 2012, 31, 3792-3794.	7.8	10

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73	Binding determinants of the small heat shock protein, Î±B-crystallin: recognition of the â€˜IxIâ€™ motif. EMBO Journal, 2012, 31, 4587-4594.	7.8	104
74	Structural Insights into the Conformation and Oligomerization of E2â̂¼Ubiquitin Conjugates. Biochemistry, 2012, 51, 4175-4187.	2.5	78
75	OTUB1 Co-opts Lys48-Linked Ubiquitin Recognition to Suppress E2 Enzyme Function. Molecular Cell, 2012, 45, 384-397.	9.7	174
76	Structure of an E3:E2â̂¼Ub Complex Reveals an Allosteric Mechanism Shared among RING/U-box Ligases. Molecular Cell, 2012, 47, 933-942.	9.7	272
77	Following Ariadne's thread: a new perspective on RBR ubiquitin ligases. BMC Biology, 2012, 10, 24.	3.8	74
78	Ubiquitin in Motion: Structural Studies of the Ubiquitin-Conjugating Enzymeâ̂¼Ubiquitin Conjugate. Biochemistry, 2011, 50, 1624-1633.	2.5	124
79	The Acidic Transcription Activator Gcn4 Binds the Mediator Subunit Gal11/Med15Â Using a Simple Protein Interface Forming a Fuzzy Complex. Molecular Cell, 2011, 44, 942-953.	9.7	172
80	E2s: structurally economical and functionally replete. Biochemical Journal, 2011, 433, 31-42.	3.7	164
81	UBCH7 reactivity profile reveals parkin and HHARI to be RING/HECT hybrids. Nature, 2011, 474, 105-108.	27.8	455
82	Mutations in mitochondrial histidyl tRNA synthetase <i>HARS2</i> cause ovarian dysgenesis and sensorineural hearing loss of Perrault syndrome. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 6543-6548.	7.1	225
83	The Essential Ubc4/Ubc5 Function in Yeast Is HECT E3-dependent, and RING E3-dependent Pathways Require Only Monoubiquitin Transfer by Ubc4. Journal of Biological Chemistry, 2011, 286, 15165-15170.	3.4	25
84	N-terminal domain of Î±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
85	A pHâ€dependent Switch Regulates Chaperone Activity. FASEB Journal, 2011, 25, 907.4.	0.5	0
86	Mutations in the DBP-Deficiency Protein HSD17B4 Cause Ovarian Dysgenesis, Hearing Loss, and Ataxia of Perrault Syndrome. American Journal of Human Genetics, 2010, 87, 282-288.	6.2	231
87	Solid-state NMR and SAXS studies provide a structural basis for the activation of Î±B-crystallin oligomers. Nature Structural and Molecular Biology, 2010, 17, 1037-1042.	8.2	263
88	Identification of an unconventional E3 binding surface on the UbcH5Ââ̂¼ÂUb conjugate recognized by a pathogenic bacterial E3 ligase.. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 2848-2853.	7.1	53
89	Structural and Functional Characterization of the Monomeric U-Box Domain from E4B. Biochemistry, 2010, 49, 347-355.	2.5	35
90	Structural Basis for Mechanical Force Regulation of the Adhesin FimH via Finger Trap-like Î² Sheet Twisting. Cell, 2010, 141, 645-655.	28.9	239

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91	Engineering a Ubiquitin Ligase Reveals Conformational Flexibility Required for Ubiquitin Transfer. Journal of Biological Chemistry, 2009, 284, 26797-26802.	3.4	46
92	Cyclic Nucleotide Binding GAF Domains from Phosphodiesterases: Structural and Mechanistic Insights. Structure, 2009, 17, 1551-1557.	3.3	109
93	Dynamic interactions of proteins in complex networks: identifying the complete set of interacting E2s for functional investigation of E3â€dependent protein ubiquitination. FEBS Journal, 2009, 276, 5381-5389.	4.7	45
94	Î±B-Crystallin: A Hybrid Solid-State/Solution-State NMR Investigation Reveals Structural Aspects of the Heterogeneous Oligomer. Journal of Molecular Biology, 2009, 385, 1481-1497.	4.2	106
95	Structural and Biophysical Characterization of the GAF Domains from Phosphodiesterases 5 and 6. Biophysical Journal, 2009, 96, 547a.	0.5	0
96	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. Molecular Microbiology, 2008, 69, 503-519.	2.5	44
97	Crystal Structure of the BARD1 Ankyrin Repeat Domain and Its Functional Consequences. Journal of Biological Chemistry, 2008, 283, 21179-21186.	3.4	35
98	Solution Structure of the cGMP Binding GAF Domain from Phosphodiesterase 5. Journal of Biological Chemistry, 2008, 283, 22749-22759.	3.4	32
99	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. Journal of Biological Chemistry, 2008, 283, 25913-25919.	3.4	42
100	Estrogen receptor Â 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
101	Activation of the Bacterial Sensor Kinase PhoQ by Acidic pH. Molecular Cell, 2007, 26, 165-174.	9.7	251
102	E2â€"BRCA1 RING interactions dictate synthesis of mono- or specific polyubiquitin chain linkages. Nature Structural and Molecular Biology, 2007, 14, 941-948.	8.2	314
103	Metal Bridges between the PhoQ Sensor Domain and the Membrane Regulate Transmembrane Signaling. Journal of Molecular Biology, 2006, 356, 1193-1206.	4.2	116
104	A UbcH5/Ubiquitin Noncovalent Complex Is Required for Processive BRCA1-Directed Ubiquitination. Molecular Cell, 2006, 21, 873-880.	9.7	265
105	Ubiquitin Transfer from the E2 Perspective: Why is UbcH5 So Promiscuous?. Cell Cycle, 2006, 5, 2867-2873.	2.6	77
106	Backbone 1H, 13C, and 15N Resonance Assignment of the 46ÂkDa Dimeric GAF A Domain of Phosphodiesterase 5. Journal of Biomolecular NMR, 2005, 33, 75-75.	2.8	2
107	Recognition of Antimicrobial Peptides by a Bacterial Sensor Kinase. Cell, 2005, 122, 461-472.	28.9	495
108	Mass Spectrometric and Mutational Analyses Reveal Lys-6-linked Polyubiquitin Chains Catalyzed by BRCA1-BARD1 Ubiquitin Ligase. Journal of Biological Chemistry, 2004, 279, 3916-3924.	3.4	202

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109	Mechanism of DNA Binding by the ADR1 Zinc Finger Transcription Factor as Determined by SPR. Journal of Molecular Biology, 2003, 329, 931-939.	4.2	22
110	Binding and recognition in the assembly of an active BRCA1/BARD1 ubiquitin-ligase complex. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 5646-5651.	7.1	314
111	Structure of a BRCA1-BARD1 heterodimeric RING-RING complex. Nature Structural Biology, 2001, 8, 833-837.	9.7	446
112	BRCA1 RING Domain Cancer-predisposing Mutations. Journal of Biological Chemistry, 2001, 276, 41399-41406.	3.4	118
113	The Whole Is Not the Simple Sum of Its Parts in Calmodulin fromS.cerevisiaeâ€. Biochemistry, 2000, 39, 4225-4230.	2.5	29
114	Mapping the Functional Domains of BRCA1. Journal of Biological Chemistry, 1999, 274, 5659-5665.	3.4	124
115	A folding transition and novel zinc finger accessory domain in the transcription factor ADR1. Nature Structural Biology, 1999, 6, 478-485.	9.7	33
116	Solution Structure of the Sodium Channel Inactivation Gate,. Biochemistry, 1999, 38, 855-861.	2.5	130
117	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
118	Solvent exchange rates of side-chain amide protons in proteins. Journal of Biomolecular NMR, 1998, 11, 205-212.	2.8	6
119	Ca²⁺â€dependent conformational changes in bovine GCAPâ€2. Protein Science, 1998, 7, 2675-2680.	7.6	45
120	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
121	Prediction and structural characterization of an independently folding substructure in the src SH3 domain. Journal of Molecular Biology, 1998, 283, 293-300.	4.2	42
122	The Cancer-predisposing Mutation C61G Disrupts Homodimer Formation in the NH2-terminal BRCA1 RING Finger Domain. Journal of Biological Chemistry, 1998, 273, 7795-7799.	3.4	79
123	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
124	Paramagnetic Cobalt as a Probe of the Orientation of an Accessory DNA-Binding Region of the Yeast ADR1 Zinc-Finger Proteinâ€. Biochemistry, 1997, 36, 14003-14011.	2.5	17
125	NMR chemical shift perturbation mapping of dna binding by a zincâ€finger domain from the yeast transcription factor ADR1. Protein Science, 1997, 6, 1835-1848.	7.6	20
126	Phosphorylation on histidine is accompanied by localized structural changes in the phosphocarrier protein, HPr from <i>Bacillus subtilis</i>. Protein Science, 1997, 6, 2107-2119.	7.6	29

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127	Demonstration of proteinâ€"protein interaction specificity by NMR chemical shift mapping. Protein Science, 1997, 6, 2624-2627.	7.6	32
128	Influence of N-Cap Mutations on the Structure and Stability of Escherichia coli HPr. Biochemistry, 1996, 35, 11268-11277.	2.5	30
129	Hydrogen bonding and equilibrium isotope enrichment in histidine-containing proteins. Nature Structural and Molecular Biology, 1996, 3, 522-531.	8.2	32
130	Phosphorylation of serineâ€46 in HPr, a key regulatory protein in bacteria, results in stabilization of its solution structure. Protein Science, 1995, 4, 2478-2486.	7.6	43
131	Ca2+ Binding to Calmodulin and Its Role in Schizosaccharomyces pombe as Revealed by Mutagenesis and NMR Spectroscopy. Journal of Biological Chemistry, 1995, 270, 20643-20652.	3.4	40
132	Investigation of a sideâ€chainâ€sideâ€chain hydrogen bond by mutagenesis, thermodynamics, and NMR spectroscopy. Protein Science, 1995, 4, 936-944.	7.6	17
133	Sequence-Specific DNA Recognition by Cys2, His2Zinc Fingers. Annals of the New York Academy of Sciences, 1994, 726, 92-104.	3.8	13
134	Unraveling a bacterial hexose transport pathway. Current Opinion in Structural Biology, 1994, 4, 814-822.	5.7	47
135	Zinc finger diversity. Current Opinion in Structural Biology, 1994, 4, 28-35.	5.7	37
136	Structural Consequences of Histidine Phosphorylation: NMR Characterization of the Phosphohistidine Form of Histidine-Containing Protein from Bacillus subtilis and Escherichia coli. Biochemistry, 1994, 33, 15271-15282.	2.5	54
137	Structure of a Histidine-X4-Histidine Zinc Finger Domain: Insights into ADR1-UAS1 Protein-DNA Recognition. Biochemistry, 1994, 33, 4460-4470.	2.5	26
138	Mapping of Specific Protein-Protein Interactions by NMR. Techniques in Protein Chemistry, 1994, 5, 439-445.	0.3	2
139	Structures of DNAâ€binding mutant zinc finger domains: Implications for DNA binding. Protein Science, 1993, 2, 951-965.	7.6	31
140	Similarities and differences between yeast and vertebrate calmodulin: An examination of the calcium-binding and structural properties of calmodulin from the yeast Saccharomyces cerevisiae. Biochemistry, 1993, 32, 3261-3270.	2.5	53
141	A series of point mutations reveal interactions between the calciumâ€binding sites of calmodulin. Protein Science, 1992, 1, 245-253.	7.6	50
142	Solution structure of the phosphocarrier protein HPr from <i>Bacillus subtilis</i> by twoâ€dimensional NMR spectroscopy. Protein Science, 1992, 1, 1363-1376.	7.6	65
143	Reexamination of the secondary and tertiary structure of histidine-containing protein from Escherichia coli by homonuclear and heteronuclear NMR spectroscopy. Biochemistry, 1991, 30, 11842-11850.	2.5	47
144	ADR1a, a zinc finger peptide, exists in two folded conformations. Biochemistry, 1991, 30, 3365-3371.	2.5	23

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145	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
146	[6] Multidimensional nuclear magnetic resonance spectroscopy of DNA-binding proteins. Methods in Enzymology, 1991, 208, 63-82.	1.0	8
147	NMR studies of two related phosphotransfer proteins. , 1991, , 40-44.		1
148	Solution structure of a zinc finger domain of yeast ADR1. Proteins: Structure, Function and Bioinformatics, 1990, 7, 215-226.	2.6	116
149	Sequence-specific proton NMR resonance assignments of Bacillus subtilus HPr: use of spectra obtained from mutants to resolve spectral overlap. Biochemistry, 1990, 29, 7191-7200.	2.5	56
150	The structure of HPr and site-directed mutagenesis. FEMS Microbiology Letters, 1989, 63, 43-52.	1.8	8
151	Common structural changes accompany the functional inactivation of HPr by seryl phosphorylation or by serine to aspartate substitution. Biochemistry, 1989, 28, 9908-9912.	2.5	107
152	The uses and limitations of calmodulin antagonists. , 1989, 44, 181-239.		42
153	Proton nuclear magnetic resonance studies on the variant-3 neurotoxin from Centruroides sculpturatus Ewing: sequential assignment of resonances. Biochemistry, 1989, 28, 1548-1555.	2.5	11
154	Proton nuclear magnetic resonance characterization of the aromatic residues in the variant-3 neurotoxin from Centruroides sculpturatus Ewing. Biochemistry, 1989, 28, 1556-1562.	2.5	9
155	STUDY OF A PHOSPHORYLATED PROTEIN BY TWO-DIMENSIONAL NMR SPECTROSCOPY. , 1989, , 233-238.		0
156	Two-dimensional NMR investigation of a bent DNA fragment: assignment of the proton resonances and preliminary structure analysis. Nucleic Acids Research, 1987, 15, 5845-5862.	14.5	82
157	[17] Study of calmodulin-peptide interactions by NMR spectroscopy. Methods in Enzymology, 1987, 139, 197-206.	1.0	1
158	Ovothiols, a family of redox-active mercaptohistidine compounds from marine invertebrate eggs. Biochemistry, 1987, 26, 4028-4036.	2.5	79
159	1H NMR Studies of Calmodulin-Peptide Interactions. , 1987, , 333-347.		4
160	Determination of Secondary and Tertiary Structures of Proteins in Solution by Two-Dimensional NMR. , 1987, , 587-599.		0
161	ORGANIZATION OF MYOSIN LIGHT CHAIN KINASE FROM RABBIT SKELETAL MUSCLE. , 1987, , 494-504.		1
162	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

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163	Two-dimensional proton NMR studies of histidine-containing protein from Escherichia coli. 1. Sequential resonance assignments. Biochemistry, 1986, 25, 7760-7769.	2.5	51
164	Two-dimensional proton NMR studies of histidine-containing protein from Escherichia coli. 3. Secondary and tertiary structure as determined by NMR. Biochemistry, 1986, 25, 7774-7781.	2.5	102
165	Proton NMR studies on the interaction between distamycin A and a symmetrical DNA dodecamer. Biochemistry, 1986, 25, 3296-3303.	2.5	163
166	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
167	1H NMR studies of calmodulin. Resonance assignments by use of tryptic fragments. FEBS Journal, 1984, 138, 281-289.	0.2	85
168	1H-NMR studies of calmodulin. The nature of the Ca2+ -dependent conformational change. FEBS Journal, 1984, 139, 109-114.	0.2	97
169	[8] Spectroscopic analyses of calmodulin and its interactions. Methods in Enzymology, 1983, 102, 82-104.	1.0	22
170	A native chemical chaperone in the human eye lens. ELife, 0, 11, .	6.0	8