Rachel E Klevit

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

164	11,081	57	102
papers	citations	h-index	g-index
183	12,724 ext. citations	9.2	6.22
ext. papers		avg, IF	L-index

#	Paper	IF	Citations
164	BRCA1/BARD1 is a nucleosome reader and writer <i>Trends in Biochemical Sciences</i> , 2022 ,	10.3	1
163	The BRCA1/BARD1 ubiquitin ligase and its substrates. <i>Biochemical Journal</i> , 2021 , 478, 3467-3483	3.8	3
162	Edmond Fischer (1920-2021). <i>Science</i> , 2021 , 374, 157	33.3	
161	Mediator subunit Med15 dictates the conserved "fuzzy" binding mechanism of yeast transcription activators Gal4 and Gcn4. <i>Nature Communications</i> , 2021 , 12, 2220	17.4	3
160	Toggle switch residues control allosteric transitions in bacterial adhesins by participating in a concerted repacking of the protein core. <i>PLoS Pathogens</i> , 2021 , 17, e1009440	7.6	O
159	BRCA1/BARD1 site-specific ubiquitylation of nucleosomal H2A is directed by BARD1. <i>Nature Structural and Molecular Biology</i> , 2021 , 28, 268-277	17.6	21
158	UbcH5 Interacts with Substrates to Participate in Lysine Selection with the E3 Ubiquitin Ligase CHIP. <i>Biochemistry</i> , 2020 , 59, 2078-2088	3.2	2
157	Legionella effector MavC targets the Ube2N~Ub conjugate for noncanonical ubiquitination. <i>Nature Communications</i> , 2020 , 11, 2365	17.4	11
156	Release of a disordered domain enhances HspB1 chaperone activity toward tau. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 2923-2929	11.5	17
155	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	4	9
154	Who with whom: functional coordination of E2 enzymes by RING E3 ligases during poly-ubiquitylation. <i>EMBO Journal</i> , 2020 , 39, e104863	13	10
153	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	4.2	4
152	Cbl interacts with multiple E2s in vitro and in cells. <i>PLoS ONE</i> , 2019 , 14, e0216967	3.7	5
151	Mechanisms of Small Heat Shock Proteins. Cold Spring Harbor Perspectives in Biology, 2019, 11,	10.2	37
150	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,	8.9	23
149	Indirect sexual selection drives rapid sperm protein evolution in abalone. ELife, 2019, 8,	8.9	6
148	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	5.4	9

(2016-2019)

147	The ubiquitin ligase SspH1 from uses a modular and dynamic E3 domain to catalyze substrate ubiquitylation. <i>Journal of Biological Chemistry</i> , 2019 , 294, 783-793	5.4	2
146	Mechanistic insights revealed by a UBE2A mutation linked to intellectual disability. <i>Nature Chemical Biology</i> , 2019 , 15, 62-70	11.7	6
145	Structural basis for tankyrase-RNF146 interaction reveals noncanonical tankyrase-binding motifs. <i>Protein Science</i> , 2018 , 27, 1057-1067	6.3	15
144	De novo mutation in with epigenetic effects on neurodevelopment. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, 1558-1563	11.5	15
143	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	11.5	11
142	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	11.5	27
141	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	5.4	52
140	Gcn4-Mediator Specificity Is Mediated by a Large and Dynamic Fuzzy Protein-Protein Complex. <i>Cell Reports</i> , 2018 , 22, 3251-3264	10.6	64
139	Characterization of RING-Between-RING E3 Ubiquitin Transfer Mechanisms. <i>Methods in Molecular Biology</i> , 2018 , 1844, 3-17	1.4	10
138	A Bifunctional Role for the UHRF1 DBL Domain in the Control of Hemi-methylated DNA-Dependent Histone Ubiquitylation. <i>Molecular Cell</i> , 2018 , 72, 753-765.e6	17.6	39
137	Mechanism of phosphoribosyl-ubiquitination mediated by a single Legionella effector. <i>Nature</i> , 2018 , 557, 729-733	50.4	38
136	Structural Studies of HHARI/UbcH7~Ub Reveal Unique E2~Ub Conformational Restriction by RBR RING1. <i>Structure</i> , 2017 , 25, 890-900.e5	5.2	32
135	pH-dependent structural modulation is conserved in the human small heat shock protein HSBP1. <i>Cell Stress and Chaperones</i> , 2017 , 22, 569-575	4	21
134	The growing world of small heat shock proteins: from structure to functions. <i>Cell Stress and Chaperones</i> , 2017 , 22, 601-611	4	101
133	Tuning BRCA1 and BARD1 activity to investigate RING ubiquitin ligase mechanisms. <i>Protein Science</i> , 2017 , 26, 475-483	6.3	20
132	RING-Between-RING E3 Ligases: Emerging Themes amid the Variations. <i>Journal of Molecular Biology</i> , 2017 , 429, 3363-3375	6.5	68
131	Two functionally distinct E2/E3 pairs coordinate sequential ubiquitination of a common substrate in development. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, E6576-E6584	11.5	23
130	Molecular insights into RBR E3 ligase ubiquitin transfer mechanisms. <i>EMBO Reports</i> , 2016 , 17, 1221-35	6.5	53

129	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	2.8	9
128	Hemi-methylated DNA regulates DNA methylation inheritance through allosteric activation of H3 ubiquitylation by UHRF1. <i>ELife</i> , 2016 , 5,	8.9	80
127	Abstract 4542: Ube2d family members, Ube2e family members and Ube2w modulate the ubiquitination and degradation of EGFR by Cbl 2016 ,		2
126	Structural insights into SAM domain-mediated tankyrase oligomerization. <i>Protein Science</i> , 2016 , 25, 174	4652	15
125	E2 enzymes: more than just middle men. <i>Cell Research</i> , 2016 , 26, 423-40	24.7	247
124	Interaction of BARD1 and HP1 Is Required for BRCA1 Retention at Sites of DNA Damage. <i>Cancer Research</i> , 2015 , 75, 1311-21	10.1	68
123	Structure of the Erystallin domain from the redox-sensitive chaperone, HSPB1. <i>Journal of Biomolecular NMR</i> , 2015 , 63, 223-8	3	30
122	A Mechanism of Subunit Recruitment in Human Small Heat Shock Protein Oligomers. <i>Biochemistry</i> , 2015 , 54, 4276-84	3.2	38
121	Pharmacological chaperone for Erystallin partially restores transparency in cataract models. <i>Science</i> , 2015 , 350, 674-7	33.3	145
120	Regulating the Regulators: Recent Revelations in the Control of E3 Ubiquitin Ligases. <i>Journal of Biological Chemistry</i> , 2015 , 290, 21244-51	5.4	51
119	Intrinsic disorder drives N-terminal ubiquitination by Ube2w. <i>Nature Chemical Biology</i> , 2015 , 11, 83-9	11.7	44
118	Allosteric activation of the RNF146 ubiquitin ligase by a poly(ADP-ribosyl)ation signal. <i>Nature</i> , 2015 , 517, 223-6	50.4	115
117	pUBLically unzipping Parkin: how phosphorylation exposes a ligase bit by bit. <i>EMBO Journal</i> , 2015 , 34, 2486-8	13	5
116	Acidic pH and divalent cation sensing by PhoQ are dispensable for systemic salmonellae virulence. <i>ELife</i> , 2015 , 4, e06792	8.9	18
115	A conserved histidine modulates HSPB5 structure to trigger chaperone activity in response to stress-related acidosis. <i>ELife</i> , 2015 , 4,	8.9	40
114	Structural, Functional, and Mechanistic Diversity in Protein Ubiquitination. FASEB Journal, 2015, 29, 355	. ħ.9	
113	Proof of principle for epitope-focused vaccine design. <i>Nature</i> , 2014 , 507, 201-6	50.4	365
112	Mutations in Twinkle primase-helicase cause Perrault syndrome with neurologic features. <i>Neurology</i> , 2014 , 83, 2054-61	6.5	73

(2012-2014)

	111	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	11.5	55
	110	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, 4004-14	1 ^{3.2}	18
	109	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	4.9	345
	108	E2~Ub conjugates regulate the kinase activity of Shigella effector OspG during pathogenesis. <i>EMBO Journal</i> , 2014 , 33, 437-49	13	46
	107	Mutant adenosine deaminase 2 in a polyarteritis nodosa vasculopathy. <i>New England Journal of Medicine</i> , 2014 , 370, 921-31	59.2	409
;	106	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, 103-10	3.2	10
:	105	One size does not fit all: the oligomeric states of B crystallin. <i>FEBS Letters</i> , 2013 , 587, 1073-80	3.8	108
:	104	Mutations in LARS2, encoding mitochondrial leucyl-tRNA synthetase, lead to premature ovarian failure and hearing loss in Perrault syndrome. <i>American Journal of Human Genetics</i> , 2013 , 92, 614-20	11	153
:	103	Structural Biology: Parkin's Serpentine Shape Revealed in the Year of the Snake. <i>Current Biology</i> , 2013 , 23, R691-3	6.3	9
:	102	Activation of UbcH5c~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, 2991-9	3.2	35
	101	Flavonoid regulation of HCN2 channels. Journal of Biological Chemistry, 2013, 288, 33136-45	5.4	10
:	100	Activity-enhancing mutations in an E3 ubiquitin ligase identified by high-throughput mutagenesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, E1263-72	11.5	108
	99	Following Ariadne's thread: a new perspective on RBR ubiquitin ligases. <i>BMC Biology</i> , 2012 , 10, 24	7.3	69
	98	Binding determinants of the small heat shock protein, B -crystallin: recognition of the 'IxI' motif. <i>EMBO Journal</i> , 2012 , 31, 4587-94	13	88
	97	Structural insights into the conformation and oligomerization of E2~ubiquitin conjugates. <i>Biochemistry</i> , 2012 , 51, 4175-87	3.2	58
	96	OTUB1 co-opts Lys48-linked ubiquitin recognition to suppress E2 enzyme function. <i>Molecular Cell</i> , 2012 , 45, 384-97	17.6	135
	95	Structure of an E3:E2~Ub complex reveals an allosteric mechanism shared among RING/U-box ligases. <i>Molecular Cell</i> , 2012 , 47, 933-42	17.6	217
	94	RING-between-RINGskeeping the safety on loaded guns. <i>EMBO Journal</i> , 2012 , 31, 3792-4	13	10

93	The acidic transcription activator Gcn4 binds the mediator subunit Gal11/Med15 using a simple protein interface forming a fuzzy complex. <i>Molecular Cell</i> , 2011 , 44, 942-53	17.6	120
92	E2s: structurally economical and functionally replete. <i>Biochemical Journal</i> , 2011 , 433, 31-42	3.8	137
91	UBCH7 reactivity profile reveals parkin and HHARI to be RING/HECT hybrids. <i>Nature</i> , 2011 , 474, 105-8	50.4	369
90	Ubiquitin in motion: structural studies of the ubiquitin-conjugating enzyme~ubiquitin conjugate. <i>Biochemistry</i> , 2011 , 50, 1624-33	3.2	99
89	Mutations in mitochondrial histidyl tRNA synthetase HARS2 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, 6543-8	11.5	200
88	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, 1516.	5 ⁵ 7⁄0	20
87	N-terminal domain of alphaB-crystallin provides a conformational switch for multimerization and structural heterogeneity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 6409-14	11.5	159
86	A pH-dependent Switch Regulates Chaperone Activity. FASEB Journal, 2011, 25, 907.4	0.9	
85	Solid-state NMR and SAXS studies provide a structural basis for the activation of alphaB-crystallin oligomers. <i>Nature Structural and Molecular Biology</i> , 2010 , 17, 1037-42	17.6	228
84	Identification of an unconventional E3 binding surface on the UbcH5 ~ 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, 2848-53	11.5	45
83	Structural and functional characterization of the monomeric U-box domain from E4B. <i>Biochemistry</i> , 2010 , 49, 347-55	3.2	27
82	Structural basis for mechanical force regulation of the adhesin FimH via finger trap-like beta sheet twisting. <i>Cell</i> , 2010 , 141, 645-55	56.2	204
81	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, 282-8	11	209
80	Engineering a ubiquitin ligase reveals conformational flexibility required for ubiquitin transfer. Journal of Biological Chemistry, 2009 , 284, 26797-802	5.4	34
79	Cyclic nucleotide binding GAF domains from phosphodiesterases: structural and mechanistic insights. <i>Structure</i> , 2009 , 17, 1551-1557	5.2	76
78	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, 5381-5	95.7	38
77	alphaB-crystallin: a hybrid solid-state/solution-state NMR investigation reveals structural aspects of the heterogeneous oligomer. <i>Journal of Molecular Biology</i> , 2009 , 385, 1481-97	6.5	97
76	The PhoQ histidine kinases of Salmonella and Pseudomonas spp. are structurally and functionally different: evidence that pH and antimicrobial peptide sensing contribute to mammalian pathogenesis. Molecular Microbiology 2008, 69, 503-19	4.1	37

[1999-2008]

75	Crystal structure of the BARD1 ankyrin repeat domain and its functional consequences. <i>Journal of Biological Chemistry</i> , 2008 , 283, 21179-86	5.4	29
74	Solution structure of the cGMP binding GAF domain from phosphodiesterase 5: insights into nucleotide specificity, dimerization, and cGMP-dependent conformational change. <i>Journal of Biological Chemistry</i> , 2008 , 283, 22749-59	5.4	31
73	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, 25913-9	5.4	40
72	E2-BRCA1 RING interactions dictate synthesis of mono- or specific polyubiquitin chain linkages. <i>Nature Structural and Molecular Biology</i> , 2007 , 14, 941-8	17.6	265
71	Estrogen receptor alpha is a putative substrate for the BRCA1 ubiquitin ligase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 5794-9	11.5	140
70	Activation of the bacterial sensor kinase PhoQ by acidic pH. <i>Molecular Cell</i> , 2007 , 26, 165-74	17.6	200
69	Ubiquitin transfer from the E2 perspective: why is UbcH5 so promiscuous?. <i>Cell Cycle</i> , 2006 , 5, 2867-73	4.7	66
68	Metal bridges between the PhoQ sensor domain and the membrane regulate transmembrane signaling. <i>Journal of Molecular Biology</i> , 2006 , 356, 1193-206	6.5	101
67	A UbcH5/ubiquitin noncovalent complex is required for processive BRCA1-directed ubiquitination. <i>Molecular Cell</i> , 2006 , 21, 873-80	17.6	229
66	Recognition of antimicrobial peptides by a bacterial sensor kinase. <i>Cell</i> , 2005 , 122, 461-72	56.2	439
65	Backbone 1H, 13C, and 15N resonance assignment of the 46 kDa dimeric GAF A domain of phosphodiesterase 5. <i>Journal of Biomolecular NMR</i> , 2005 , 33, 75	3	2
64	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, 3916-24	5.4	174
63	Mechanism of DNA binding by the ADR1 zinc finger transcription factor as determined by SPR. Journal of Molecular Biology, 2003 , 329, 931-9	6.5	19
62	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, 5646-51	11.5	280
61	Structure of a BRCA1-BARD1 heterodimeric RING-RING complex. <i>Nature Structural Biology</i> , 2001 , 8, 833	3-7	381
60	BRCA1 RING domain cancer-predisposing mutations. Structural consequences and effects on protein-protein interactions. <i>Journal of Biological Chemistry</i> , 2001 , 276, 41399-406	5.4	103
59	The whole is not the simple sum of its parts in calmodulin from S. cerevisiae. <i>Biochemistry</i> , 2000 , 39, 422	2 5. 30	25
58	Mapping the functional domains of BRCA1. Interaction of the ring finger domains of BRCA1 and BARD1. <i>Journal of Biological Chemistry</i> , 1999 , 274, 5659-65	5.4	109

57	A folding transition and novel zinc finger accessory domain in the transcription factor ADR1. <i>Nature Structural Biology</i> , 1999 , 6, 478-85		27
56	Solution structure of the sodium channel inactivation gate. <i>Biochemistry</i> , 1999 , 38, 855-61	3.2	116
55	Increased helix and protein stability through the introduction of a new tertiary hydrogen bond. <i>Journal of Molecular Biology</i> , 1999 , 286, 1609-19	6.5	28
54	Solvent exchange rates of side-chain amide protons in proteins. <i>Journal of Biomolecular NMR</i> , 1998 , 11, 205-12	3	6
53	Ca2+-dependent conformational changes in bovine GCAP-2. <i>Protein Science</i> , 1998 , 7, 2675-80	6.3	42
52	A disorder-to-order transition coupled to DNA binding in the essential zinc-finger DNA-binding domain of yeast ADR1. <i>Journal of Molecular Biology</i> , 1998 , 279, 929-43	6.5	32
51	Prediction and structural characterization of an independently folding substructure in the src SH3 domain. <i>Journal of Molecular Biology</i> , 1998 , 283, 293-300	6.5	38
50	The cancer-predisposing mutation C61G disrupts homodimer formation in the NH2-terminal BRCA1 RING finger domain. <i>Journal of Biological Chemistry</i> , 1998 , 273, 7795-9	5.4	67
49	Binding of the catabolite repressor protein CcpA to its DNA target is regulated by phosphorylation of its corepressor HPr. <i>Journal of Biological Chemistry</i> , 1997 , 272, 26530-5	5.4	110
48	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, 14003-11	3.2	14
47	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, 1835-48	6.3	20
46	Phosphorylation on histidine is accompanied by localized structural changes in the phosphocarrier protein, HPr from Bacillus subtilis. <i>Protein Science</i> , 1997 , 6, 2107-19	6.3	29
45	Demonstration of protein-protein interaction specificity by NMR chemical shift mapping. <i>Protein Science</i> , 1997 , 6, 2624-7	6.3	30
44	Influence of N-cap mutations on the structure and stability of Escherichia coli HPr. <i>Biochemistry</i> , 1996 , 35, 11268-77	3.2	27
43	Hydrogen bonding and equilibrium isotope enrichment in histidine-containing proteins. <i>Nature Structural and Molecular Biology</i> , 1996 , 3, 522-31	17.6	28
42	Investigation of a side-chain-side-chain hydrogen bond by mutagenesis, thermodynamics, and NMR spectroscopy. <i>Protein Science</i> , 1995 , 4, 936-44	6.3	15
41	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, 2478-86	6.3	41
40	Ca2+ binding to calmodulin and its role in Schizosaccharomyces pombe as revealed by mutagenesis and NMR spectroscopy. <i>Journal of Biological Chemistry</i> , 1995 , 270, 20643-52	5.4	34

39	Sequence-specific DNA recognition by Cys2, His2 zinc fingers. <i>Annals of the New York Academy of Sciences</i> , 1994 , 726, 92-102; discussion 102-4	6.5	10
38	Unraveling a bacterial hexose transport pathway. Current Opinion in Structural Biology, 1994 , 4, 814-22	8.1	46
37	Zinc finger diversity. Current Opinion in Structural Biology, 1994 , 4, 28-35	8.1	33
36	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, 15271-82	3.2	52
35	Structure of a histidine-X4-histidine zinc finger domain: insights into ADR1-UAS1 protein-DNA recognition. <i>Biochemistry</i> , 1994 , 33, 4460-70	3.2	23
34	Mapping of Specific Protein-Protein Interactions by NMR. <i>Techniques in Protein Chemistry</i> , 1994 , 5, 439-	445	2
33	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, 3261-70	3.2	50
32	Structures of DNA-binding mutant zinc finger domains: implications for DNA binding. <i>Protein Science</i> , 1993 , 2, 951-65	6.3	27
31	A series of point mutations reveal interactions between the calcium-binding sites of calmodulin. <i>Protein Science</i> , 1992 , 1, 245-53	6.3	42
30	Solution structure of the phosphocarrier protein HPr from Bacillus subtilis by two-dimensional NMR spectroscopy. <i>Protein Science</i> , 1992 , 1, 1363-76	6.3	59
29	Multidimensional nuclear magnetic resonance spectroscopy of DNA-binding proteins. <i>Methods in Enzymology</i> , 1991 , 208, 63-82	1.7	6
28	Reexamination of the secondary and tertiary structure of histidine-containing protein from Escherichia coli by homonuclear and heteronuclear NMR spectroscopy. <i>Biochemistry</i> , 1991 , 30, 11842-5	0 ^{3.2}	41
27	ADR1a, a zinc finger peptide, exists in two folded conformations. <i>Biochemistry</i> , 1991 , 30, 3365-71	3.2	20
26	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. <i>Biochemistry</i> , 1991 , 30, 9601-7	3.2	129
25	NMR studies of two related phosphotransfer proteins 1991 , 40-44		1
24	Solution structure of a zinc finger domain of yeast ADR1. <i>Proteins: Structure, Function and Bioinformatics</i> , 1990 , 7, 215-26	4.2	105
23	Sequence-specific 1H NMR resonance assignments of Bacillus subtilis HPr: use of spectra obtained from mutants to resolve spectral overlap. <i>Biochemistry</i> , 1990 , 29, 7191-200	3.2	49
22	The structure of HPr and site-directed mutagenesis. <i>FEMS Microbiology Letters</i> , 1989 , 5, 43-52	2.9	3

21	Common structural changes accompany the functional inactivation of HPr by seryl phosphorylation or by serine to aspartate substitution. <i>Biochemistry</i> , 1989 , 28, 9908-12	3.2	99
20	The uses and limitations of calmodulin antagonists 1989 , 44, 181-239		37
19	Proton nuclear magnetic resonance studies on the variant-3 neurotoxin from Centruroides sculpturatus Ewing: sequential assignment of resonances. <i>Biochemistry</i> , 1989 , 28, 1548-55	3.2	11
18	Proton nuclear magnetic resonance characterization of the aromatic residues in the variant-3 neurotoxin from Centruroides sculpturatus Ewing. <i>Biochemistry</i> , 1989 , 28, 1555-62	3.2	9
17	STUDY OF A PHOSPHORYLATED PROTEIN BY TWO-DIMENSIONAL NMR SPECTROSCOPY 1989 , 233-238	3	
16	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, 5845-62	20.1	76
15	Study of calmodulin-peptide interactions by NMR spectroscopy. <i>Methods in Enzymology</i> , 1987 , 139, 197	-20/6	1
14	Ovothiols, a family of redox-active mercaptohistidine compounds from marine invertebrate eggs. <i>Biochemistry</i> , 1987 , 26, 4028-36	3.2	70
13	1H NMR Studies of Calmodulin-Peptide Interactions 1987 , 333-347		1
12	ORGANIZATION OF MYOSIN LIGHT CHAIN KINASE FROM RABBIT SKELETAL MUSCLE 1987 , 494-504		1
11	Determination of Secondary and Tertiary Structures of Proteins in Solution by Two-Dimensional NMR 1987 , 587-599		
10	Two-dimensional 1H NMR studies of histidine-containing protein from Escherichia coli. 2. Leucine resonance assignments by long-range coherence transfer. <i>Biochemistry</i> , 1986 , 25, 7770-3	3.2	24
9	Two-dimensional 1H NMR studies of histidine-containing protein from Escherichia coli. 1. Sequential resonance assignments. <i>Biochemistry</i> , 1986 , 25, 7760-9	3.2	45
8	Two-dimensional 1H NMR studies of histidine-containing protein from Escherichia coli. 3. Secondary and tertiary structure as determined by NMR. <i>Biochemistry</i> , 1986 , 25, 7774-81	3.2	91
7	1H NMR studies on the interaction between distamycin A and a symmetrical DNA dodecamer. <i>Biochemistry</i> , 1986 , 25, 3296-303	3.2	150
6	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. <i>Biochemistry</i> , 1985 , 24, 8152-7	3.2	130
5	1H NMR studies of calmodulin. Resonance assignments by use of tryptic fragments. <i>FEBS Journal</i> , 1984 , 138, 281-9		70
4	1H-NMR studies of calmodulin. The nature of the Ca2+-dependent conformational change. <i>FEBS Journal</i> , 1984 , 139, 109-14		84

LIST OF PUBLICATIONS

3 Spectroscopic analyses of calmodulin and its interactions. *Methods in Enzymology*, **1983**, 102, 82-104 1.7 22

2	Mediator subunit Med15 dictates the conserved f uzzy [b inding mechanism of yeast transcription activators Gal4 and Gcn4	2
1	Interplay of disordered and ordered regions of a human small heat shock protein yields an ensemble of quasi-orderedIstates	1