

# Gary S Shaw

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4638971/publications.pdf>

Version: 2024-02-01

135  
papers

5,036  
citations

94433

37  
h-index

110387

64  
g-index

140  
all docs

140  
docs citations

140  
times ranked

4841  
citing authors

#	ARTICLE	IF	CITATIONS
1	Distinct phosphorylation signals drive acceptor versus free ubiquitin chain targeting by parkin. <i>Biochemical Journal</i> , 2022, 479, 751-766.	3.7	3
2	Acetylation, Phosphorylation, Ubiquitination (Oh My!): Following Post-Translational Modifications on the Ubiquitin Road. <i>Biomolecules</i> , 2022, 12, 467.	4.0	14
3	Structural and Functional Insights into GID/CTLH E3 Ligase Complexes. <i>International Journal of Molecular Sciences</i> , 2022, 23, 5863.	4.1	12
4	Calcium binds and rigidifies the dysferlin C2A domain in a tightly coupled manner. <i>Biochemical Journal</i> , 2021, 478, 197-215.	3.7	13
5	Age-associated insolubility of parkin in human midbrain is linked to redox balance and sequestration of reactive dopamine metabolites. <i>Acta Neuropathologica</i> , 2021, 141, 725-754.	7.7	32
6	Acetylated Ubiquitin Modulates the Catalytic Activity of the E1 Enzyme Uba1. <i>Biochemistry</i> , 2021, 60, 1276-1285.	2.5	9
7	Ubiquitin Interacting Motifs: Duality Between Structured and Disordered Motifs. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 676235.	3.5	6
8	A mechanistic review of Parkin activation. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2021, 1865, 129894.	2.4	13
9	Interactions between the Cell Membrane Repair Protein S100A10 and Phospholipid Monolayers and Bilayers. <i>Langmuir</i> , 2021, 37, 9652-9663.	3.5	5
10	Mechanism of Zn <sup>2+</sup> and Ca <sup>2+</sup> Binding to Human S100A1. <i>Biomolecules</i> , 2021, 11, 1823.	4.0	2
11	Programmed ubiquitin acetylation using genetic code expansion reveals altered ubiquitination patterns. <i>FEBS Letters</i> , 2020, 594, 1226-1234.	2.8	10
12	The Zn <sup>2+</sup> and Ca <sup>2+</sup> binding S100B and S100A1 proteins: beyond the myths. <i>Biological Reviews</i> , 2020, 95, 738-758.	10.4	19
13	Recruitment of Ubiquitin within an E2 Chain Elongation Complex. <i>Biophysical Journal</i> , 2020, 118, 1679-1689.	0.5	8
14	The mammalian CTLH complex is an E3 ubiquitin ligase that targets its subunit muskelin for degradation. <i>Scientific Reports</i> , 2019, 9, 9864.	3.3	41
15	A subset of calcium-binding S100 proteins show preferential heterodimerization. <i>FEBS Journal</i> , 2019, 286, 1859-1876.	4.7	17
16	Optimized transformation, overexpression and purification of S100A10. <i>BioTechniques</i> , 2019, 67, 246-248.	1.8	1
17	Monitoring Interactions Between S100B and the Dopamine D2 Receptor Using NMR Spectroscopy. <i>Methods in Molecular Biology</i> , 2019, 1929, 311-324.	0.9	4
18	Impact of altered phosphorylation on loss of function of juvenile Parkinsonism-associated genetic variants of the E3 ligase parkin. <i>Journal of Biological Chemistry</i> , 2018, 293, 6337-6348.	3.4	22

#	ARTICLE	IF	CITATIONS
19	Synergistic recruitment of UbcH7~Ub and phosphorylated Ubl domain triggers parkin activation. EMBO Journal, 2018, 37, .	7.8	26
20	Regulation of Shigella Effector Kinase OspG through Modulation of Its Dynamic Properties. Journal of Molecular Biology, 2018, 430, 2096-2112.	4.2	8
21	S100 Proteins. , 2018, , 4793-4801.		0
22	Parkinâ€“phosphoubiquitin complex reveals cryptic ubiquitin-binding site required for RBR ligase activity. Nature Structural and Molecular Biology, 2017, 24, 475-483.	8.2	73
23	RBR Ubiquitin Transfer: Not Simply an â€œOpenâ€“and â€œClosedâ€“Case?. Structure, 2017, 25, 817-819.	3.3	2
24	Structure of phosphorylated UBL domain and insights into PINK1-orchestrated parkin activation. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 298-303.	7.1	77
25	Cytochrome <i>c</i> as a Peroxidase: Activation of the Precatalytic Native State by H <sub>2</sub> O <sub>2</sub> -Induced Covalent Modifications. Journal of the American Chemical Society, 2017, 139, 15701-15709.	13.7	67
26	Calcium-Mediated Control of S100 Proteins: Allosteric Communication via an Agitator/Signal Blocking Mechanism. Journal of the American Chemical Society, 2017, 139, 11460-11470.	13.7	16
27	Ubiquitin phosphorylated at Ser57 hyper-activates parkin. Biochimica Et Biophysica Acta - General Subjects, 2017, 1861, 3038-3046.	2.4	15
28	Generation of phospho-ubiquitin variants by orthogonal translation reveals codon skipping. FEBS Letters, 2016, 590, 1530-1542.	2.8	32
29	Suramin inhibits cullin-RING E3 ubiquitin ligases. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E2011-8.	7.1	50
30	S100 Proteins. , 2016, , 1-10.		2
31	Disruption of the autoinhibited state primes the E3 ligase parkin for activation and catalysis. EMBO Journal, 2015, 34, 2506-2521.	7.8	160
32	The HIP2~Ubiquitin Conjugate Forms a Non-Compact Monomeric Thioester during Di-Ubiquitin Synthesis. PLoS ONE, 2015, 10, e0120318.	2.5	7
33	Switching on ubiquitylation by phosphorylating a ubiquitous activator. Biochemical Journal, 2014, 460, e1-e3.	3.7	2
34	RBR E3 ubiquitin ligases: new structures, new insights, new questions. Biochemical Journal, 2014, 458, 421-437.	3.7	220
35	Pivotal role for the ubiquitin Y59-E51 loop in lysine 48 polyubiquitination. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 8434-8439.	7.1	24
36	A Snapshot of Ubiquitin Chain Elongation. Journal of Biological Chemistry, 2014, 289, 7068-7081.	3.4	11

#	ARTICLE	IF	CITATIONS
37	Structure and Mechanism of the E3 Ligase Rbx1 in Complex with the E2 Enzyme CDC34 Charged with Ubiquitin. <i>Biophysical Journal</i> , 2014, 106, 47a.	0.5	0
38	Structural Basis for the Inhibition of Host Protein Ubiquitination by Shigella Effector Kinase OspG. <i>Structure</i> , 2014, 22, 878-888.	3.3	40
39	Ataxin-3 Is a Multivalent Ligand for the Parkin Ubl Domain. <i>Biochemistry</i> , 2013, 52, 7369-7376.	2.5	12
40	A molecular explanation for the recessive nature of parkin-linked Parkinson's disease. <i>Nature Communications</i> , 2013, 4, 1983.	12.8	123
41	Comparison of Predicted Epimerases and Reductases of the Campylobacter jejuni d-altro- and l-gluco-Heptose Synthesis Pathways. <i>Journal of Biological Chemistry</i> , 2013, 288, 19569-19580.	3.4	24
42	Structure of the HHARI Catalytic Domain Shows Glimpses of a HECT E3 Ligase. <i>PLoS ONE</i> , 2013, 8, e74047.	2.5	12
43	Architecture of the catalytic HPN motif is conserved in all E2 conjugating enzymes. <i>Biochemical Journal</i> , 2012, 445, 167-174.	3.7	35
44	Structure and functional studies of N-terminal Cx43 mutants linked to oculodentodigital dysplasia. <i>Molecular Biology of the Cell</i> , 2012, 23, 3312-3321.	2.1	41
45	Selective Recruitment of an E2-Ubiquitin Complex by an E3 Ubiquitin Ligase. <i>Journal of Biological Chemistry</i> , 2012, 287, 17374-17385.	3.4	44
46	Complete 6-Deoxy-d-altro-heptose Biosynthesis Pathway from Campylobacter jejuni. <i>Journal of Biological Chemistry</i> , 2012, 287, 29776-29788.	3.4	23
47	Conserved Region 3 of Human Papillomavirus 16 E7 Contributes to Dereglulation of the Retinoblastoma Tumor Suppressor. <i>Journal of Virology</i> , 2012, 86, 13313-13323.	3.4	44
48	Structure of an Asymmetric Ternary Protein Complex Provides Insight for Membrane Interaction. <i>Structure</i> , 2012, 20, 1737-1745.	3.3	35
49	Solution structure of the E3 ligase HOIL-Ubl domain. <i>Protein Science</i> , 2012, 21, 1085-1092.	7.6	6
50	Systematic Analysis of the Amino Acid Residues of Human Papillomavirus Type 16 E7 Conserved Region 3 Involved in Dimerization and Transformation. <i>Journal of Virology</i> , 2011, 85, 10048-10057.	3.4	36
51	Autoregulation of Parkin activity through its ubiquitin-like domain. <i>EMBO Journal</i> , 2011, 30, 2853-2867.	7.8	274
52	Impact of Autosomal Recessive Juvenile Parkinson's Disease Mutations on the Structure and Interactions of the Parkin Ubiquitin-like Domain. <i>Biochemistry</i> , 2011, 50, 2603-2610.	2.5	22
53	Identification of Calcium-Independent and Calcium-Enhanced Binding between S100B and the Dopamine D2 Receptor. <i>Biochemistry</i> , 2011, 50, 9056-9065.	2.5	16
54	Association of the Disordered C-terminus of CDC34 with a Catalytically Bound Ubiquitin. <i>Journal of Molecular Biology</i> , 2011, 407, 425-438.	4.2	18

#	ARTICLE	IF	CITATIONS
55	Temporal Development of Protein Structure during S100A11 Folding and Dimerization Probed by Oxidative Labeling and Mass Spectrometry. <i>Journal of Molecular Biology</i> , 2011, 409, 669-679.	4.2	20
56	Discovery and Characterization of a Nonphosphorylated Cyclic Peptide Inhibitor of the Peptidylprolyl Isomerase, Pin1. <i>Journal of Medicinal Chemistry</i> , 2011, 54, 3854-3865.	6.4	49
57	Identification of regions responsible for the open conformation of S100A10 using chimaeric S100A11-S100A10 proteins. <i>Biochemical Journal</i> , 2011, 434, 37-48.	3.7	11
58	Characterization of the dehydratase WcbK and the reductase WcaG involved in GDP-6-deoxy-manno-heptose biosynthesis in <i>Campylobacter jejuni</i> . <i>Biochemical Journal</i> , 2011, 439, 235-248.	3.7	18
59	The S100A10-Annexin A2 Complex Provides a Novel Asymmetric Platform for Membrane Repair. <i>Journal of Biological Chemistry</i> , 2011, 286, 40174-40183.	3.4	57
60	Identification of a molecular recognition feature in the E1A oncoprotein that binds the SUMO conjugase UBC9 and likely interferes with polySUMOylation. <i>Oncogene</i> , 2010, 29, 4693-4704.	5.9	28
61	Differential Interaction of the E3 Ligase Parkin with the Proteasomal Subunit S5a and the Endocytic Protein Eps15. <i>Journal of Biological Chemistry</i> , 2010, 285, 1424-1434.	3.4	19
62	Codon optimization for enhanced <i>Escherichia coli</i> expression of human S100A11 and S100A1 proteins. <i>Protein Expression and Purification</i> , 2010, 73, 58-64.	1.3	17
63	Identification of a Novel Zn <sup>2+</sup> -binding Domain in the Autosomal Recessive Juvenile Parkinson-related E3 Ligase Parkin. <i>Journal of Biological Chemistry</i> , 2009, 284, 14978-14986.	3.4	113
64	Design of high-affinity S100-target hybrid proteins. <i>Protein Science</i> , 2009, 18, 2528-2536.	7.6	16
65	Elucidating the Formation of 6-Deoxyheptose: Biochemical Characterization of the GDP-glycero-manno-heptose C6 Dehydratase, DmhA, and Its Associated C4 Reductase, DmhB. <i>Biochemistry</i> , 2009, 48, 7764-7775.	2.5	23
66	The Structure of the UbcH8-Ubiquitin Complex Shows a Unique Ubiquitin Interaction Site. <i>Biochemistry</i> , 2009, 48, 12169-12179.	2.5	46
67	Formation of Monomeric S100B and S100A11 Proteins at Low Ionic Strength. <i>Biochemistry</i> , 2009, 48, 1954-1963.	2.5	11
68	Unique S100 target protein interactions. <i>General Physiology and Biophysics</i> , 2009, 28 Spec No Focus, F39-46.	0.9	23
69	<sup>1</sup> H, <sup>13</sup> C and <sup>15</sup> N resonance assignments for the human E2 conjugating enzyme, UbcH7. <i>Biomolecular NMR Assignments</i> , 2008, 2, 21-23.	0.8	7
70	Analysis of the structure of human apo-S100B at low temperature indicates a unimodal conformational distribution is adopted by calcium-free S100 proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 73, 28-42.	2.6	23
71	S100-annexin complexes - structural insights. <i>FEBS Journal</i> , 2008, 275, 4956-4966.	4.7	77
72	Identification of a Dimeric Intermediate in the Unfolding Pathway for the Calcium-Binding Protein S100B. <i>Journal of Molecular Biology</i> , 2008, 382, 1075-1088.	4.2	3

#	ARTICLE	IF	CITATIONS
73	Structure of the Parkin in-between-ring domain provides insights for E3-ligase dysfunction in autosomal recessive Parkinson's disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 3095-3100.	7.1	81
74	Amide Exchange Shows Calcium-Induced Conformational Changes Are Transmitted to the Dimer Interface of S100B. <i>Biochemistry</i> , 2007, 46, 7478-7487.	2.5	9
75	A Disease State Mutation Unfolds the Parkin Ubiquitin-like Domain. <i>Biochemistry</i> , 2007, 46, 14162-14169.	2.5	41
76	Insights into S100 Target Specificity Examined by a New Interaction between S100A11 and Annexin A2. <i>Biochemistry</i> , 2006, 45, 14695-14705.	2.5	49
77	Folding Kinetics of the S100A11 Protein Dimer Studied by Time-Resolved Electrospray Mass Spectrometry and Pulsed Hydrogen-Deuterium Exchange. <i>Biochemistry</i> , 2006, 45, 3005-3013.	2.5	49
78	Calcium-dependent and -independent interactions of the S100 protein family. <i>Biochemical Journal</i> , 2006, 396, 201-214.	3.7	516
79	The solution structure of the protein ydhA from <i>Escherichia coli</i> . <i>Journal of Biomolecular NMR</i> , 2006, 35, 295-300.	2.8	11
80	Solution structure of the <i>Escherichia coli</i> protein ydhR: A putative mono-oxygenase. <i>Protein Science</i> , 2005, 14, 3115-3120.	7.6	6
81	Ubiquitin Manipulation by an E2 Conjugating Enzyme Using a Novel Covalent Intermediate. <i>Journal of Biological Chemistry</i> , 2005, 280, 31732-31738.	3.4	38
82	Solution Structure of the Flexible Class II Ubiquitin-conjugating Enzyme Ubc1 Provides Insights for Polyubiquitin Chain Assembly. <i>Journal of Biological Chemistry</i> , 2004, 279, 47139-47147.	3.4	50
83	Human S100B Protein Interacts with the <i>Escherichia coli</i> Division Protein FtsZ in a Calcium-sensitive Manner. <i>Journal of Biological Chemistry</i> , 2004, 279, 18806-18813.	3.4	14
84	Letter to the editor: Assignment of the <sup>1</sup> H, <sup>13</sup> C and <sup>15</sup> N resonances of the class II E2 conjugating enzyme, Ubc1. <i>Journal of Biomolecular NMR</i> , 2004, 30, 369-370.	2.8	0
85	Solution NMR Structure and X-ray Absorption Analysis of the C-Terminal Zinc-Binding Domain of the SecA ATPase. <i>Biochemistry</i> , 2004, 43, 9361-9371.	2.5	30
86	Interaction of the tail with the catalytic region of a class II E2 conjugating enzyme. <i>Journal of Biomolecular NMR</i> , 2003, 26, 147-155.	2.8	9
87	Unmasking the Annexin I Interaction from the Structure of Apo-S100A11. <i>Structure</i> , 2003, 11, 887-897.	3.3	59
88	A Novel S100 Target Conformation Is Revealed by the Solution Structure of the Ca <sup>2+</sup> -S100B-TRTK-12 Complex. <i>Journal of Biological Chemistry</i> , 2003, 278, 6251-6257.	3.4	49
89	Synthetic Calcium-Binding Peptides. , 2002, 173, 175-182.		2
90	Role of the N-Terminal Helix I for Dimerization and Stability of the Calcium-Binding Protein S100B. <i>Biochemistry</i> , 2002, 41, 3637-3646.	2.5	20

#	ARTICLE	IF	CITATIONS
91	The C-Terminus and Linker Region of S100B Exert Dual Control on Protein-Protein Interactions with TRTK-12. <i>Biochemistry</i> , 2002, 41, 5421-5428.	2.5	27
92	<sup>1</sup> H, <sup>15</sup> N and <sup>13</sup> C resonance assignments of rabbit apo-S100A11. <i>Journal of Biomolecular NMR</i> , 2002, 22, 191-192.	2.8	8
93	Assignment of <sup>1</sup> H, <sup>13</sup> C and <sup>15</sup> N resonances of human Ca <sup>2+</sup> -S100B in complex with the TRTK-12 peptide. <i>Journal of Biomolecular NMR</i> , 2002, 23, 255-256.	2.8	3
94	Folding and stability of the subunit of the F1FOATP synthase. <i>Protein Science</i> , 2002, 11, 1227-1238.	7.6	27
95	Structure of a Conjugating Enzyme-Ubiquitin Thiolester Intermediate Reveals a Novel Role for the Ubiquitin Tail. <i>Structure</i> , 2001, 9, 897-904.	3.3	157
96	Sequence specific analysis of the heterogeneous glycan chain from peanut peroxidase by <sup>1</sup> H-NMR spectroscopy. <i>Phytochemistry</i> , 2000, 53, 135-144.	2.9	10
97	Letter to the editor: <sup>1</sup> H, <sup>15</sup> N and <sup>13</sup> C resonance assignments for the catalytic domain of the yeast E2, UBC1. <i>Journal of Biomolecular NMR</i> , 2000, 16, 351-352.	2.8	7
98	For the record: A logical sequence search for S100B target proteins. <i>Protein Science</i> , 2000, 9, 2043-2046.	7.6	29
99	The solution structure of the C-terminal domain of the Mu B transposition protein. <i>EMBO Journal</i> , 2000, 19, 5625-5634.	7.8	10
100	Identification of the ubiquitin interfacial residues in a ubiquitin-E2 covalent complex. <i>Journal of Biomolecular NMR</i> , 2000, 18, 319-327.	2.8	30
101	Specificity and Zn <sup>2+</sup> Enhancement of the S100B Binding Epitope TRTK-12. <i>Journal of Biological Chemistry</i> , 1999, 274, 1502-1508.	3.4	48
102	The Dimerization Domain of the $\beta$ Subunit of the Escherichia coli F1FO-ATPase. <i>Journal of Biological Chemistry</i> , 1999, 274, 31094-31101.	3.4	51
103	A novel calcium-sensitive switch revealed by the structure of human S100B in the calcium-bound form. <i>Structure</i> , 1998, 6, 211-222.	3.3	128
104	Solution and solid state conformation of the human EGF receptor transmembrane region. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 1998, 1371, 241-253.	2.6	13
105	A change-in-hand mechanism for S100 signalling. <i>Biochemistry and Cell Biology</i> , 1998, 76, 324-333.	2.0	62
106	A change-in-hand mechanism for S100 signalling. <i>Biochemistry and Cell Biology</i> , 1998, 76, 324-333.	2.0	32
107	Assignment and secondary structure of calcium-bound human S100B. <i>Journal of Biomolecular NMR</i> , 1997, 10, 77-88.	2.8	24
108	Identification and structural influence of a differentially modified N-terminal methionine in human S100b. <i>Protein Science</i> , 1997, 6, 1110-1113.	7.6	23

#	ARTICLE	IF	CITATIONS
109	NMR Solution Structure of a Synthetic Troponin C Heterodimeric Domain. <i>Biochemistry</i> , 1996, 35, 7429-7438.	2.5	20
110	Transmembrane Region of the Epidermal Growth Factor Receptor: Behavior and Interactions via 2H NMR. <i>Biochemistry</i> , 1996, 35, 12591-12601.	2.5	33
111	Anatomy of a Flexer DNA Complex inside a Higher-Order Transposition Intermediate. <i>Cell</i> , 1996, 85, 761-771.	28.9	115
112	Structural Influence of Cation Binding to Recombinant Human Brain S100b: Evidence for Calcium-Induced Exposure of a Hydrophobic Surface. <i>Biochemistry</i> , 1996, 35, 8805-8814.	2.5	72
113	Structural Influence of Calcium on the Heme Cavity of Cationic Peanut Peroxidase as Determined by 1H-NMR Spectroscopy. <i>FEBS Journal</i> , 1995, 232, 825-833.	0.2	0
114	Human S100b protein: Formation of a tetramer from synthetic calcium-binding site peptides. <i>Protein Science</i> , 1995, 4, 765-772.	7.6	13
115	Structural Influence of Calcium on the Heme Cavity of Cationic Peanut Peroxidase as Determined by <sup>1</sup> H-NMR Spectroscopy. <i>FEBS Journal</i> , 1995, 232, 825-833.	0.2	8
116	Structural Influence of Calcium on the Heme Cavity of Cationic Peanut Peroxidase as Determined by 1H-NMR Spectroscopy. <i>FEBS Journal</i> , 1995, 232, 825-833.	0.2	28
117	Relative stabilities of synthetic peptide homo- and heterodimeric troponin C domains. <i>Protein Science</i> , 1994, 3, 1010-1019.	7.6	19
118	Metal ion binding by proteins. <i>Current Opinion in Structural Biology</i> , 1992, 2, 57-60.	5.7	5
119	Thermal cyclizations of protonated poly-unsaturated aldehydes. <i>Canadian Journal of Chemistry</i> , 1992, 70, 2065-2069.	1.1	8
120	Determination of the solution structure of a synthetic two-site calcium-binding homodimeric protein domain by NMR spectroscopy. <i>Biochemistry</i> , 1992, 31, 9572-9580.	2.5	42
121	Specific formation of a heterodimeric two-site calcium-binding domain from synthetic peptides. <i>Journal of the American Chemical Society</i> , 1992, 114, 6258-6259.	13.7	25
122	Role of interchain helical hydrophobic interactions in Ca <sup>2+</sup> affinity, formation, and stability of a two-site domain in troponin C. <i>Protein Science</i> , 1992, 1, 945-955.	7.6	34
123	A <sup>1</sup> H NMR study of a ternary peptide complex that mimics the interaction between troponin C and troponin I. <i>Protein Science</i> , 1992, 1, 1595-1603.	7.6	18
124	Stoichiometry of calcium binding to a synthetic heterodimeric troponin-C domain. <i>Biopolymers</i> , 1992, 32, 391-397.	2.4	13
125	Calcium-Induced Folding of Troponin-C: Formation of Homodimeric and Heterodimeric Two-Site Domains From Synthetic Peptides. , 1992, , 347-353.		1
126	Interactions between paired calcium-binding sites in proteins: NMR determination of the stoichiometry of calcium binding to a synthetic troponin-C peptide. <i>Journal of the American Chemical Society</i> , 1991, 113, 5557-5563.	13.7	39



#	ARTICLE	IF	CITATIONS
127	Probing the relationship between .alpha.-helix formation and calcium affinity in troponin C: proton NMR studies of calcium binding to synthetic and variant site III helix-loop-helix peptides. <i>Biochemistry</i> , 1991, 30, 8339-8347.	2.5	54
128	[11] Characterization of retinylidene iminium salts by high-field 1H and 13C nuclear magnetic resonance spectroscopy. <i>Methods in Enzymology</i> , 1990, 189, 112-122.	1.0	4
129	Calcium-induced peptide association to form an intact protein domain: 1H NMR structural evidence. <i>Science</i> , 1990, 249, 280-283.	12.6	125
130	Calcium binding proteins. Elucidating the contributions to calcium affinity from an analysis of species variants and peptide fragments. <i>Biochemistry and Cell Biology</i> , 1990, 68, 587-601.	2.0	180
131	Comparison of the structure and charge delocalization in an unsaturated imine and its corresponding iminium salt. <i>Journal of the American Chemical Society</i> , 1989, 111, 5424-5429.	13.7	23
132	Quantitative examination of the photoisomerization of retinal iminium salts by high-field proton NMR spectroscopy. <i>Journal of the American Chemical Society</i> , 1988, 110, 3013-3017.	13.7	13
133	Solid-state studies of some retinal iminium salts and related compounds: evidence for a 6-s-trans conformation. <i>Journal of the American Chemical Society</i> , 1987, 109, 5362-5366.	13.7	19
134	Photoisomerization of protonated 5-deuterio-5-methylhex-3-en-2-one. Evidence for a photochemical 1,2 hydride shift. <i>Journal of the Chemical Society Chemical Communications</i> , 1983, , 261.	2.0	1
135	One-Step Syntheses of Bicyclo[3.1.0]hex-3-en-2-one and Methyl-Substituted Derivatives. <i>Synthesis</i> , 1982, 1982, 198-199.	2.3	4