

Mark S Searle

List of Publications by Year in descending order

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135
papers

6,722
citations

57758

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69250

77
g-index

143
all docs

143
docs citations

143
times ranked

8216
citing authors

#	ARTICLE	IF	CITATIONS
1	The cost of conformational order: entropy changes in molecular associations. <i>Journal of the American Chemical Society</i> , 1992, 114, 10690-10697.	13.7	379
2	Origin of β^2 -Hairpin Stability in Solution: A Structural and Thermodynamic Analysis of the Folding of a Model Peptide Supports Hydrophobic Stabilization in Water. <i>Journal of the American Chemical Society</i> , 1998, 120, 1996-2007.	13.7	236
3	Empirical Correlations between Thermodynamic Properties and Intermolecular Forces. <i>Journal of the American Chemical Society</i> , 1995, 117, 5013-5015.	13.7	217
4	Partitioning of free energy contributions in the estimation of binding constants: residual motions and consequences for amide-amide hydrogen bond strengths. <i>Journal of the American Chemical Society</i> , 1992, 114, 10697-10704.	13.7	214
5	Glycopeptide Antibiotic Activity and the Possible Role of Dimerization: A Model for Biological Signaling. <i>Journal of the American Chemical Society</i> , 1994, 116, 4581-4590.	13.7	210
6	Drug Recognition and Stabilisation of the Parallel-stranded DNA Quadruplex d(TTAGGGT) ₄ Containing the Human Telomeric Repeat. <i>Journal of Molecular Biology</i> , 2003, 334, 25-36.	4.2	179
7	A short linear peptide derived from the N-terminal sequence of ubiquitin folds into a water-stable non-native β^2 -hairpin. <i>Nature Structural and Molecular Biology</i> , 1995, 2, 999-1006.	8.2	172
8	Dissecting the stability of a β^2 -hairpin peptide that folds in water: NMR and molecular dynamics analysis of the β^2 -turn and β^2 -strand contributions to folding 1 Edited by P. E. Wright. <i>Journal of Molecular Biology</i> , 1999, 292, 1051-1069.	4.2	167
9	Cooperativity in Drug-DNA Recognition: A Molecular Dynamics Study. <i>Journal of the American Chemical Society</i> , 2001, 123, 12658-12663.	13.7	150
10	Novel UBA Domain Mutations of SQSTM1 in Paget's Disease of Bone: Genotype Phenotype Correlation, Functional Analysis, and Structural Consequences. <i>Journal of Bone and Mineral Research</i> , 2004, 19, 1122-1127.	2.8	142
11	Application of a generalised enthalpy-entropy relationship to binding co-operativity and weak associations in solution. <i>Journal of the Chemical Society Perkin Transactions II</i> , 1995, , 141-151.	0.9	134
12	Ubiquitin Recognition by the Ubiquitin-associated Domain of p62 Involves a Novel Conformational Switch. <i>Journal of Biological Chemistry</i> , 2008, 283, 5427-5440.	3.4	129
13	On the stability of nucleic acid structures in solution: enthalpy - entropy compensations, internal rotations and reversibility. <i>Nucleic Acids Research</i> , 1993, 21, 2051-2056.	14.5	126
14	SQSTM1 mutations " Bridging Paget disease of bone and ALS/FTLD. <i>Experimental Cell Research</i> , 2014, 325, 27-37.	2.6	123
15	Defective recognition of LC3B by mutant SQSTM1/p62 implicates impairment of autophagy as a pathogenic mechanism in ALS-FTLD. <i>Autophagy</i> , 2016, 12, 1094-1104.	9.1	123
16	Cooperative Interaction between the Three Strands of a Designed Antiparallel β^2 -Sheet. <i>Journal of the American Chemical Society</i> , 1998, 120, 5291-5300.	13.7	121
17	Structure, Folding, and Energetics of Cooperative Interactions between the β^2 -Strands of a de Novo Designed Three-Stranded Antiparallel β^2 -Sheet Peptide. <i>Journal of the American Chemical Society</i> , 2000, 122, 8350-8356.	13.7	115
18	Design of β^2 -sheet systems for understanding the thermodynamics and kinetics of protein folding. <i>Current Opinion in Structural Biology</i> , 2004, 14, 458-464.	5.7	114

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19	Sequence-specific interaction of Hoechst 33258 with the minor groove of an adenine-tract DNA duplex studied in solution by ¹ H NMR spectroscopy. <i>Nucleic Acids Research</i> , 1990, 18, 3753-3762.	14.5	112
20	Structure of the Ubiquitin-associated Domain of p62 (SQSTM1) and Implications for Mutations That Cause Paget's Disease of Bone. <i>Journal of Biological Chemistry</i> , 2003, 278, 37409-37412.	3.4	111
21	Stabilization of \hat{I}^2 -Hairpin Peptides by Salt Bridges: Role of Preorganization in the Energetic Contribution of Weak Interactions. <i>Journal of the American Chemical Society</i> , 2003, 125, 9038-9047.	13.7	100
22	Tunable DNA-based asymmetric catalysis using a G-quadruplex supramolecular assembly. <i>Chemical Communications</i> , 2010, 46, 4309.	4.1	99
23	NMR studies of the interaction of the antibiotic nogalamycin with the hexadeoxyribonucleotide duplex d(5'-GCATGC) ₂ . <i>Biochemistry</i> , 1988, 27, 4340-4349.	2.5	97
24	Loss of Ubiquitin-Binding Associated With Paget's Disease of Bone p62 (SQSTM1) Mutations. <i>Journal of Bone and Mineral Research</i> , 2004, 20, 619-624.	2.8	97
25	Dimerisation of the UBA Domain of p62 Inhibits Ubiquitin Binding and Regulates NF- \hat{I}^B Signalling. <i>Journal of Molecular Biology</i> , 2010, 396, 178-194.	4.2	93
26	Recognition and Stabilization of Quadruplex DNA by a Potent New Telomerase Inhibitor: NMR Studies of the 2:1 Complex of a Pentacyclic Methylacridinium Cation with d(TTAGGGT) ₄ . <i>Angewandte Chemie - International Edition</i> , 2001, 40, 4749-4751.	13.8	90
27	Structural Rearrangement in an RsmA/CsrA Ortholog of <i>Pseudomonas aeruginosa</i> Creates a Dimeric RNA-Binding Protein, RsmN. <i>Structure</i> , 2013, 21, 1659-1671.	3.3	88
28	Interaction of Hoechst 33258 with the minor groove of the A + T-rich DNA duplex d(GGTAATTACC) ₂ studied in solution by NMR spectroscopy. <i>FEBS Journal</i> , 1993, 211, 437-447.	0.2	84
29	Structure of the parallel-stranded DNA quadruplex d(TTAGGGT) ₄ containing the human telomeric repeat: evidence for A-tetrad formation from NMR and molecular dynamics simulations. <i>Organic and Biomolecular Chemistry</i> , 2003, 1, 1650-1656.	2.8	79
30	Energetics of Weak Interactions in a \hat{I}^2 -hairpin Peptide: Electrostatic and Hydrophobic Contributions to Stability from Lysine Salt Bridges. <i>Journal of the American Chemical Society</i> , 1999, 121, 11615-11620.	13.7	78
31	The structure of an asymmetric dimer relevant to the mode of action of the glycopeptide antibiotics. <i>Structure</i> , 1994, 2, 747-754.	3.3	77
32	Peptide models of protein \hat{I}^2 -sheets: design, folding and insights into stabilising weak interactions. <i>Perkin Transactions II RSC</i> , 2001, , 1011-1020.	1.1	75
33	Telomestatin: Formal Total Synthesis and Cation-Mediated Interaction of Its <i>sec</i> -Derivatives with G-Quadruplexes. <i>Journal of the American Chemical Society</i> , 2011, 133, 1044-1051.	13.7	74
34	Native-like \hat{I}^2 -hairpin structure in an isolated fragment from ferredoxin: NMR and CD studies of solvent effects on the N-terminal 20 residues. <i>Protein Engineering, Design and Selection</i> , 1996, 9, 559-565.	2.1	70
35	Repression of Translation of Human Estrogen Receptor \hat{I}^{\pm} by G-Quadruplex Formation. <i>Biochemistry</i> , 2009, 48, 11487-11495.	2.5	70
36	NMR Studies of Drug-DNA interactions. <i>Progress in Nuclear Magnetic Resonance Spectroscopy</i> , 1993, 25, 403-480.	7.5	68

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37	DNA minor groove recognition by bis-benzimidazole analogues of Hoechst 33258: insights into structure-DNA affinity relationships assessed by fluorescence titration measurements. <i>Nucleic Acids Research</i> , 1999, 27, 1619-1624.	14.5	64
38	Selectivity of small molecule ligands for parallel and anti-parallel DNA G-quadruplex structures. <i>Organic and Biomolecular Chemistry</i> , 2009, 7, 4194.	2.8	61
39	Modulation of intrinsic β , γ propensities of amino acids by neighbouring residues in the coil regions of protein structures: NMR analysis and dissection of a β^2 -hairpin peptide 1 Edited by P. E. Wright. <i>Journal of Molecular Biology</i> , 1998, 284, 1597-1609.	4.2	56
40	A sequence-based approach for prediction of CsrA/RsmA targets in bacteria with experimental validation in <i>Pseudomonas aeruginosa</i> . <i>Nucleic Acids Research</i> , 2014, 42, 6811-6825.	14.5	54
41	ALS-FTLD associated mutations of SQSTM1 impact on Keap1-Nrf2 signalling. <i>Molecular and Cellular Neurosciences</i> , 2016, 76, 52-58.	2.2	52
42	Characterization of a Non-UBA Domain Missense Mutation of Sequestosome 1 (SQSTM1) in Paget's Disease of Bone. <i>Journal of Bone and Mineral Research</i> , 2009, 24, 632-642.	2.8	48
43	Structure, dynamics and hydration of the nogalamycin-d(ATGCAT) ₂ complex determined by NMR and molecular dynamics simulations in solution 1 Edited by I. Tinoco. <i>Journal of Molecular Biology</i> , 1999, 290, 699-716.	4.2	47
44	Insights into stabilizing weak interactions in designed peptide β -hairpins. <i>Biopolymers</i> , 2004, 76, 185-195.	2.4	44
45	DNA recognition by the anthracycline antibiotic respinomycin D: NMR structure of the intercalation complex with d(AGACGTCT) ₂ . <i>Organic and Biomolecular Chemistry</i> , 2003, 1, 60-66.	2.8	43
46	Ubiquitin-binding domains: Mechanisms of ubiquitin recognition and use as tools to investigate ubiquitin-modified proteomes. <i>Proteomics</i> , 2015, 15, 844-861.	2.2	41
47	Cooperative Assembly of a Nativelike Ubiquitin Structure through Peptide Fragment Complexation: Energetics of Peptide Association and Folding. <i>Biochemistry</i> , 2000, 39, 12355-12364.	2.5	40
48	Insights into the Stability of Native and Partially Folded States of Ubiquitin: Effects of Cosolvents and Denaturants on the Thermodynamics of Protein Folding. <i>Biochemistry</i> , 2001, 40, 10317-10325.	2.5	39
49	Effects of Amino Acid β , γ Propensities and Secondary Structure Interactions in Modulating ^1H Chemical Shifts in Peptide and Protein β -Sheet. <i>Journal of the American Chemical Society</i> , 2001, 123, 12318-12324.	13.7	38
50	SilE is an intrinsically disordered periplasmic α -molecular sponge involved in bacterial silver resistance. <i>Molecular Microbiology</i> , 2016, 101, 731-742.	2.5	38
51	NMR structural analysis of a β^2 -hairpin peptide designed for DNA binding. <i>Chemical Communications</i> , 1997, , 1297-1298.	4.1	37
52	Asymmetry in the structure of glycopeptide antibiotic dimers: NMR studies of the ristocetin A complex with a bacterial cell wall analog. <i>Journal of the American Chemical Society</i> , 1995, 117, 7958-7964.	13.7	35
53	Engineering Enhanced Protein Stability through β^2 -Turn Optimization: Insights for the Design of Stable Peptide β^2 -Hairpin Systems. <i>Angewandte Chemie - International Edition</i> , 2005, 44, 4939-4944.	13.8	35
54	Stability and Folding Kinetics of a Ubiquitin Mutant with a Strong Propensity for Nonnative β^2 -Hairpin Conformation in the Unfolded State. <i>Biochemistry</i> , 2003, 42, 13762-13771.	2.5	34

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55	Probing Affinity and Ubiquitin Linkage Selectivity of Ubiquitin-Binding Domains Using Mass Spectrometry. <i>Journal of the American Chemical Society</i> , 2012, 134, 6416-6424.	13.7	34
56	A nonsynonymous <i>TNFRSF11A</i> variation increases NF κ B activity and the severity of Paget's disease. <i>Journal of Bone and Mineral Research</i> , 2012, 27, 443-452.	2.8	34
57	Independent Interactions of Ubiquitin-Binding Domains in a Ubiquitin-Mediated Ternary Complex. <i>Biochemistry</i> , 2011, 50, 9076-9087.	2.5	32
58	Rational design and binding of modified cell-wall peptides to vancomycin-group antibiotics: Factorising free energy contributions to binding. <i>Tetrahedron</i> , 1993, 49, 9171-9182.	1.9	31
59	Structure and K ⁺ ion-dependent stability of a parallel-stranded DNA quadruplex containing a core A-tetrad. <i>Organic and Biomolecular Chemistry</i> , 2004, 2, 810.	2.8	31
60	Design of histidine-Zn ²⁺ binding sites within a β -hairpin peptide: enhancement of β -sheet stability through metal complexation. <i>Chemical Communications</i> , 2001, , 1162-1163.	4.1	30
61	Ligand selectivity in stabilising tandem parallel folded G-quadruplex motifs in human telomeric DNA sequences. <i>Chemical Communications</i> , 2014, 50, 15202-15205.	4.1	30
62	Burial of Hydrocarbon Causes Cooperative Enhancement of Electrostatic Binding. <i>Angewandte Chemie International Edition in English</i> , 1995, 34, 1483-1485.	4.4	29
63	The Highly Repetitive Region of the <i>Helicobacter pylori</i> CagY Protein Comprises Tandem Arrays of an α -Helical Repeat Module. <i>Journal of Molecular Biology</i> , 2008, 377, 956-971.	4.2	29
64	Expression of electrostatic binding cooperativity in the recognition of cell-wall peptide analogues by vancomycin group antibiotics. <i>Journal of the Chemical Society Chemical Communications</i> , 1994, , 1519.	2.0	28
65	Folding of a β -hairpin peptide derived from the N-terminus of ubiquitin. <i>FEBS Journal</i> , 2000, 267, 3539-3548.	0.2	28
66	Insights into the Molecular Composition of Endogenous Unanchored Polyubiquitin Chains. <i>Journal of Proteome Research</i> , 2012, 11, 1969-1980.	3.7	28
67	Paget disease of bone-associated UBA domain mutations of SQSTM1 exert distinct effects on protein structure and function. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2014, 1842, 992-1000.	3.8	28
68	Extending the Folding Nucleus of Ubiquitin with an Independently Folding β -Hairpin Finger: Hurdles to Rapid Folding Arising from the Stabilisation of Local Interactions. <i>Journal of Molecular Biology</i> , 2005, 349, 205-221.	4.2	26
69	Impact of p62/SQSTM1 UBA Domain Mutations Linked to Paget's Disease of Bone on Ubiquitin Recognition. <i>Biochemistry</i> , 2011, 50, 4665-4674.	2.5	26
70	Structural insights into the targeting of mRNA GU-rich elements by the three RRM of CELF1. <i>Nucleic Acids Research</i> , 2013, 41, 7153-7166.	14.5	26
71	Optimal antisense target reducing <i>INS</i> intron 1 retention is adjacent to a parallel G quadruplex. <i>Nucleic Acids Research</i> , 2014, 42, 8161-8173.	14.5	24
72	Anthracycline antibiotic arugomycin binds in both grooves of the DNA helix simultaneously: an NMR and molecular modelling study. <i>Nucleic Acids Research</i> , 1991, 19, 2897-2906.	14.5	23

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73	Population of On-pathway Intermediates in the Folding of Ubiquitin. <i>Journal of Molecular Biology</i> , 2006, 360, 1053-1066.	4.2	23
74	³¹ P NMR investigation of the backbone conformation and dynamics of the hexamer duplex d(5'-GACATGC) ₂ in its complex with the antibiotic nogalamycin. <i>FEBS Letters</i> , 1992, 297, 292-296.	2.8	22
75	Interaction of the anthracycline antibiotic nogalamycin with the hexamer duplex d(5'-GACGTC) ₂ . An NMR and molecular modelling study. <i>FEBS Journal</i> , 1992, 205, 45-58.	0.2	22
76	On and off-target effects of telomere uncapping G-quadruplex selective ligands based on pentacyclic acridinium salts. <i>Journal of Experimental and Clinical Cancer Research</i> , 2013, 32, 68.	8.6	22
77	Molecular Recognition between a New Pentacyclic Acridinium Salt and DNA Sequences Investigated by Optical Spectroscopic Techniques, Proton Nuclear Magnetic Resonance Spectroscopy, and Molecular Modeling. <i>Biochemistry</i> , 1999, 38, 6723-6731.	2.5	21
78	Sequence determinants for the tandem recognition of UGU and CUG rich RNA elements by the two N-terminal RRM of CELF1. <i>Nucleic Acids Research</i> , 2011, 39, 8638-8650.	14.5	21
79	The S349T mutation of SQSTM1 links Keap1/Nrf2 signalling to Paget's disease of bone. <i>Bone</i> , 2013, 52, 699-706.	2.9	21
80	The role of short RNA loops in recognition of a single-hairpin exon derived from a mammalian-wide interspersed repeat. <i>RNA Biology</i> , 2015, 12, 54-69.	3.1	21
81	The free energy change of restricting a bond rotation in the binding of peptide analogues to vancomycin group antibiotics. <i>Bioorganic and Medicinal Chemistry Letters</i> , 1993, 3, 803-808.	2.2	20
82	Do interstrand hydrogen bonds contribute to β^2 -hairpin peptide stability in solution? IR analysis of peptide folding in water. <i>Chemical Communications</i> , 2000, , 593-594.	4.1	20
83	Context-dependent effects of proline residues on the stability and folding pathway of ubiquitin. <i>FEBS Journal</i> , 2004, 271, 4474-4484.	0.2	20
84	Bile Acid Interactions with Rabbit Ileal Lipid Binding Protein and an Engineered Helixless Variant Reveal Novel Ligand Binding Properties of a Versatile β^2 -Clam Shell Protein Scaffold. <i>Journal of Molecular Biology</i> , 2007, 371, 1365-1377.	4.2	20
85	Enthalpy/Entropy Compensation Effects from Cavity Desolvation Underpin Broad Ligand Binding Selectivity for Rat Odorant Binding Protein 3. <i>Biochemistry</i> , 2014, 53, 2371-2379.	2.5	20
86	Occurrence of a Quadruplex Motif in a Unique Insert within Exon C of the Bovine Estrogen Receptor β Gene (ESR1). <i>Biochemistry</i> , 2010, 49, 7625-7633.	2.5	19
87	7-Deazapurine biosynthesis: NMR study of toyocamycin biosynthesis in <i>Streptomyces rimosus</i> using 2- ¹³ C-7- ¹⁵ N-adenine. <i>Organic and Biomolecular Chemistry</i> , 2011, 9, 2227.	2.8	19
88	Enantiopure titanocene complexes – direct evidence for paraptosis in cancer cells. <i>Metallomics</i> , 2016, 8, 286-297.	2.4	19
89	Aromatic Residues Engineered into the β^2 -Turn Nucleation Site of Ubiquitin Lead to a Complex Folding Landscape, Non-Native Side-Chain Interactions, and Kinetic Traps. <i>Biochemistry</i> , 2008, 47, 12910-12922.	2.5	18
90	Mechanism of Ligand-Induced Folding of a Natively Unfolded Helixless Variant of Rabbit I-BABP. <i>Biochemistry</i> , 2009, 48, 7556-7564.	2.5	18

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91	Folding Topology of a Bimolecular DNA Quadruplex Containing a Stable Mini-hairpin Motif within the Diagonal Loop. <i>Journal of Molecular Biology</i> , 2009, 385, 1600-1615.	4.2	18
92	G-quadruplex ligands mediate downregulation of DUX4 expression. <i>Nucleic Acids Research</i> , 2020, 48, 4179-4194.	14.5	18
93	Prion protein fragments spanning helix 1 and both strands of β^2 sheet (residues 125-170) show evidence for predominantly helical propensity by CD and NMR. <i>Folding & Design</i> , 1998, 3, 313-320.	4.5	17
94	Inhibition of Cullin RING Ligases by Cycle Inhibiting Factor: Evidence for Interference with Nedd8-Induced Conformational Control. <i>Journal of Molecular Biology</i> , 2011, 413, 430-437.	4.2	17
95	Structural insights into specificity and diversity in mechanisms of ubiquitin recognition by ubiquitin-binding domains. <i>Biochemical Society Transactions</i> , 2012, 40, 404-408.	3.4	17
96	DNA replication initiation in <i>Bacillus subtilis</i> : structural and functional characterization of the essential DnaA-DnaD interaction. <i>Nucleic Acids Research</i> , 2019, 47, 2101-2112.	14.5	17
97	Solution structure and dynamics of the A-T tract DNA decamer duplex d(GGTAATTACC) ₂ : implications for recognition by minor groove binding drugs. <i>Biochemical Journal</i> , 1999, 342, 125-132.	3.7	16
98	Structure of a Drug-Induced DNA T-Bulge: Implications for DNA Frameshift Mutations. <i>Angewandte Chemie - International Edition</i> , 2002, 41, 4754-4756.	13.8	16
99	Engineering Diverse Changes in β^2 -Turn Propensities in the N-Terminal β^2 -Hairpin of Ubiquitin Reveals Significant Effects on Stability and Kinetics but a Robust Folding Transition State. <i>Biochemistry</i> , 2006, 45, 4220-4230.	2.5	16
100	Factor XII and kininogen asymmetric assembly with gC1qR/C1QBP/P32 is governed by allostery. <i>Blood</i> , 2020, 136, 1685-1697.	1.4	16
101	Coupling ligand recognition to protein folding in an engineered variant of rabbit ileal lipid binding protein. <i>Chemical Communications</i> , 2006, , 4623.	4.1	15
102	Mutant p62/SQSTM1 UBA domains linked to Paget's disease of bone differ in their abilities to function as stabilization signals. <i>FEBS Letters</i> , 2010, 584, 1585-1590.	2.8	15
103	Incremental Contribution to Protein Stability from α^2 Hairpin-Finger: Limits on the Stability of Designed β^2 Hairpin Peptides. <i>Angewandte Chemie - International Edition</i> , 2004, 43, 1991-1994.	13.8	14
104	The π - π effect in molecular recognition. , 1996, 9, 88-94.		13
105	Disruption of ubiquitin-mediated processes in diseases of the brain and bone. <i>Biochemical Society Transactions</i> , 2008, 36, 469-471.	3.4	13
106	Structure and folding dynamics of a DNA hairpin with a stabilising d(GNA) trinucleotide loop: influence of base pair mis-matches and point mutations on conformational equilibria. <i>Organic and Biomolecular Chemistry</i> , 2007, 5, 832.	2.8	12
107	A Targeted Oligonucleotide Enhancer of SMN2 Exon 7 Splicing Forms Competing Quadruplex and Protein Complexes in Functional Conditions. <i>Cell Reports</i> , 2014, 9, 193-205.	6.4	12
108	Engineering Stabilising β^2 -Sheet Interactions into a Conformationally Flexible Region of the Folding Transition State of Ubiquitin. <i>Journal of Molecular Biology</i> , 2005, 353, 373-384.	4.2	11

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109	Mass spectrometry insights into a tandem ubiquitin-binding domain hybrid engineered for the selective recognition of unanchored polyubiquitin. <i>Proteomics</i> , 2016, 16, 1961-1969.	2.2	11
110	Hoogsteen versus Watson-Crick A-T basepairing in DNA complexes of a new group of α -quinomycin-like TM antibiotics. <i>FEBS Letters</i> , 1990, 272, 171-174.	2.8	10
111	Drug recognition of a DNA single strand break. <i>FEBS Journal</i> , 2002, 269, 1726-1733.	0.2	10
112	Overview of Protein Folding Mechanisms: Experimental and Theoretical Approaches to Probing Energy Landscapes. <i>Current Protocols in Protein Science</i> , 2012, 68, Unit 28.2.1-22.	2.8	10
113	Recognition of the cell-wall binding site of the vancomycin-group antibiotics by unnatural structural motifs: ¹ H NMR studies of the effects of ligand binding on antibiotic dimerisation. <i>Journal of the Chemical Society Perkin Transactions 1</i> , 1994, , 659.	0.9	9
114	Templating peptide folding on the surface of a micelle. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2000, 10, 1139-1142.	2.2	9
115	Synthesis of 6-arylisocytosines and their potential for hydrogen bonding interactions. <i>Tetrahedron</i> , 2015, 71, 7339-7343.	1.9	9
116	Helix Mutations Stabilize a Late Productive Intermediate on the Folding Pathway of Ubiquitin. <i>Biochemistry</i> , 2008, 47, 8225-8236.	2.5	8
117	Solution structure and dynamics of the A-T tract DNA decamer duplex d(GGTAATTACC) ₂ : implications for recognition by minor groove binding drugs. <i>Biochemical Journal</i> , 1999, 342, 125.	3.7	7
118	Conformation and dynamics of the three α -helix bundle UBA domain of p62 from experiment and simulation. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 71, 227-240.	2.6	7
119	Folding of single-stranded DNA quadruplexes containing an autonomously stable mini-hairpin loop. <i>Molecular BioSystems</i> , 2009, 5, 542.	2.9	7
120	Probing the interaction of Hoechst 33258 with an A ⁺ T rich oligonucleotide duplex using ¹ H NMR spectroscopy. <i>Journal of the Chemical Society Chemical Communications</i> , 1991, , 1770-1771.	2.0	6
121	Drug-induced stabilisation of a mismatched C-T base pair in a DNA hairpin Electronic supplementary information (ESI) available: ¹ H NMR spectra of the hairpin sequence. See http://www.rsc.org/suppdata/cc/b3/b305337g/ . <i>Chemical Communications</i> , 2003, , 1814.	4.1	6
122	Sequential Barriers and an Obligatory Metastable Intermediate Define the Apparent Two-state Folding Pathway of the Ubiquitin-like PB1 Domain of NBR1. <i>Journal of Molecular Biology</i> , 2008, 376, 1463-1477.	4.2	6
123	Sequence specific conformation of a DNA decamer containing an adenine tract studied in solution by ¹ H-NMR spectroscopy. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 1990, 1049, 69-77.	2.4	5
124	Consequences for molecular recognition and ligand-receptor complementarity of entropy changes in phase transitions. <i>Bioorganic and Medicinal Chemistry Letters</i> , 1992, 2, 993-996.	2.2	3
125	Kooperative Verstärkung elektrostatischer Bindungen durch das Verbergen von Kohlenwasserstoffen. <i>Angewandte Chemie</i> , 1995, 107, 1644-1646.	2.0	3
126	Structure of the nogalamycin ^d (ATGCAAT) ₂ complex in solution: DNA recognition at an isolated TpG site. <i>Journal of the Chemical Society Perkin Transactions 1</i> , 1998, , 3-6.	0.9	3

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127	Structural Insights into the Two Sequential Folding Transition States of the PB1 Domain of NBR1 from \hat{I} Value Analysis and Biased Molecular Dynamics Simulations. <i>Biochemistry</i> , 2011, 50, 125-135.	2.5	3
128	Method for the Purification of Endogenous Unanchored Polyubiquitin Chains. <i>Methods in Molecular Biology</i> , 2016, 1449, 203-213.	0.9	3
129	An ALS-associated variant of the autophagy receptor SQSTM1/p62 reprograms binding selectivity toward the autophagy-related hATG8 proteins. <i>Journal of Biological Chemistry</i> , 2022, 298, 101514.	3.4	3
130	Rationally designed ligands as models for bacterial cell-wall recognition by vancomycin-group antibiotics. <i>Journal of Chemical Sciences</i> , 1994, 106, 937-954.	1.5	1
131	Evidence for \hat{I}^2 -sheet conformation in vesicle-bound peptides derived from the transmembrane bacterial flagellar motor protein MotB from <i>Rhodobacter sphaeroides</i> . <i>Perkin Transactions II RSC</i> , 2000, , 479-483.	1.1	0
132	Probing Protein-RNA Interactions Through Spin-Labeling and Paramagnetic Relaxation Enhancements. , 2018, , 2149-2161.		0
133	Relationships between structure and activity based on a partitioning of free energy contributions in the estimation of binding constants. , 1993, , 86-92.		0
134	Enhancement of Electrostatic Binding Through Cooperative Interactions: Enthalpy/Entropy Compensation and Peptideâ€™Peptide Recognition. , 1995, , 151-159.		0
135	Probing Protein-RNA Interactions Through Spin-Labeling and Paramagnetic Relaxation Enhancements. , 2017, , 1-13.		0