Mark S Searle

List of Publications by Year
in descending order

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135 papers	6,722 citations	57758 44 h-index	69250 77 g-index
143 all docs	143 docs citations	143 times ranked	8216 citing authors

#	Article	IF	Citations
1	An ALS-associated variant of the autophagy receptor SQSTM1/p62 reprograms binding selectivity toward the autophagy-related hATG8 proteins. Journal of Biological Chemistry, 2022, 298, 101514.	3.4	3
2	Factor XII and kininogen asymmetric assembly with gC1qR/C1QBP/P32 is governed by allostery. Blood, 2020, 136, 1685-1697.	1.4	16
3	G-quadruplex ligands mediate downregulation of DUX4 expression. Nucleic Acids Research, 2020, 48, 4179-4194.	14.5	18
4	DNA replication initiation in Bacillus subtilis: structural and functional characterization of the essential DnaAâ€“DnaD interaction. Nucleic Acids Research, 2019, 47, 2101-2112.	14.5	17
5	Probing Protein-RNA Interactions Through Spin-Labelling and Paramagnetic Relaxation Enhancements. , 2018, , 2149-2161.		0
6	Probing Protein-RNA Interactions Through Spin-Labelling and Paramagnetic Relaxation Enhancements. , 2017, , 1-13.		0
7	Mass spectrometry insights into a tandem ubiquitin-binding domain hybrid engineered for the selective recognition of unanchored polyubiquitin. Proteomics, 2016, 16, 1961-1969.	2.2	11
8	SilE is an intrinsically disordered periplasmic â€œmolecular spongeâ€•involved in bacterial silver resistance. Molecular Microbiology, 2016, 101, 731-742.	2.5	38
9	Defective recognition of LC3B by mutant SQSTM1/p62 implicates impairment of autophagy as a pathogenic mechanism in ALS-FTLD. Autophagy, 2016, 12, 1094-1104.	9.1	123
10	Method for the Purification of Endogenous Unanchored Polyubiquitin Chains. Methods in Molecular Biology, 2016, 1449, 203-213.	0.9	3
11	Enantiopure titanocene complexes â€“ direct evidence for paraptosis in cancer cells. Metallomics, 2016, 8, 286-297.	2.4	19
12	ALS-FTLD associated mutations of SQSTM1 impact on Keap1-Nrf2 signalling. Molecular and Cellular Neurosciences, 2016, 76, 52-58.	2.2	52
13	Synthesis of 6-arylisocytosines and their potential for hydrogen bonding interactions. Tetrahedron, 2015, 71, 7339-7343.	1.9	9
14	The role of short RNA loops in recognition of a single-hairpin exon derived from a mammalian-wide interspersed repeat. RNA Biology, 2015, 12, 54-69.	3.1	21
15	Ubiquitinâ€binding domains: Mechanisms of ubiquitin recognition and use as tools to investigate ubiquitinâ€modified proteomes. Proteomics, 2015, 15, 844-861.	2.2	41
16	A Targeted Oligonucleotide Enhancer of SMN2 Exon 7 Splicing Forms Competing Quadruplex and Protein Complexes in Functional Conditions. Cell Reports, 2014, 9, 193-205.	6.4	12
17	A sequence-based approach for prediction of CsrA/RsmA targets in bacteria with experimental validation in Pseudomonas aeruginosa. Nucleic Acids Research, 2014, 42, 6811-6825.	14.5	54
18	Ligand selectivity in stabilising tandem parallel folded G-quadruplex motifs in human telomeric DNA sequences. Chemical Communications, 2014, 50, 15202-15205.	4.1	30

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19	Enthalpy/Entropy Compensation Effects from Cavity Desolvation Underpin Broad Ligand Binding Selectivity for Rat Odorant Binding Protein 3. Biochemistry, 2014, 53, 2371-2379.	2.5	20
20	SQSTM1 mutations â€“ Bridging Paget disease of bone and ALS/FTLD. Experimental Cell Research, 2014, 325, 27-37.	2.6	123
21	Paget disease of bone-associated UBA domain mutations of SQSTM1 exert distinct effects on protein structure and function. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2014, 1842, 992-1000.	3.8	28
22	Optimal antisense target reducingINSintron 1 retention is adjacent to a parallel G quadruplex. Nucleic Acids Research, 2014, 42, 8161-8173.	14.5	24
23	Structural Rearrangement in an RsmA/CsrA Ortholog of Pseudomonas aeruginosa Creates a Dimeric RNA-Binding Protein, RsmN. Structure, 2013, 21, 1659-1671.	3.3	88
24	On and off-target effects of telomere uncapping G-quadruplex selective ligands based on pentacyclic acridinium salts. Journal of Experimental and Clinical Cancer Research, 2013, 32, 68.	8.6	22
25	The S349T mutation of SQSTM1 links Keap1/Nrf2 signalling to Paget's disease of bone. Bone, 2013, 52, 699-706.	2.9	21
26	Structural insights into the targeting of mRNA GU-rich elements by the three RRMs of CELF1. Nucleic Acids Research, 2013, 41, 7153-7166.	14.5	26
27	Structural insights into specificity and diversity in mechanisms of ubiquitin recognition by ubiquitin-binding domains. Biochemical Society Transactions, 2012, 40, 404-408.	3.4	17
28	Insights into the Molecular Composition of Endogenous Unanchored Polyubiquitin Chains. Journal of Proteome Research, 2012, 11, 1969-1980.	3.7	28
29	Probing Affinity and Ubiquitin Linkage Selectivity of Ubiquitin-Binding Domains Using Mass Spectrometry. Journal of the American Chemical Society, 2012, 134, 6416-6424.	13.7	34
30	Overview of Protein Folding Mechanisms: Experimental and Theoretical Approaches to Probing Energy Landscapes. Current Protocols in Protein Science, 2012, 68, Unit 28.2.1-22.	2.8	10
31	A nonsynonymous TNFRSF11A variation increases NFÎºB activity and the severity of Paget's disease. Journal of Bone and Mineral Research, 2012, 27, 443-452.	2.8	34
32	Impact of p62/SQSTM1 UBA Domain Mutations Linked to Pagetâ€™s Disease of Bone on Ubiquitin Recognition. Biochemistry, 2011, 50, 4665-4674.	2.5	26
33	Independent Interactions of Ubiquitin-Binding Domains in a Ubiquitin-Mediated Ternary Complex. Biochemistry, 2011, 50, 9076-9087.	2.5	32
34	Structural Insights into the Two Sequential Folding Transition States of the PB1 Domain of NBR1 from Î¦ Value Analysis and Biased Molecular Dynamics Simulations. Biochemistry, 2011, 50, 125-135.	2.5	3
35	Telomestatin: Formal Total Synthesis and Cation-Mediated Interaction of Its seco-Derivatives with G-Quadruplexes. Journal of the American Chemical Society, 2011, 133, 1044-1051.	13.7	74
36	7-Deazapurine biosynthesis: NMR study of toyocamycin biosynthesis in Streptomyces rimosus using 2-13C-7-15N-adenine. Organic and Biomolecular Chemistry, 2011, 9, 2227.	2.8	19

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37	Inhibition of Cullin RING Ligases by Cycle Inhibiting Factor: Evidence for Interference with Nedd8-Induced Conformational Control. Journal of Molecular Biology, 2011, 413, 430-437.	4.2	17
38	Sequence determinants for the tandem recognition of UGU and CUG rich RNA elements by the two Nâ€"terminal RRMs of CELF1. Nucleic Acids Research, 2011, 39, 8638-8650.	14.5	21
39	Mutant p62/SQSTM1 UBA domains linked to Paget's disease of bone differ in their abilities to function as stabilization signals. FEBS Letters, 2010, 584, 1585-1590.	2.8	15
40	Occurrence of a Quadruplex Motif in a Unique Insert within Exon C of the Bovine Estrogen Receptor Î± Gene (ESR1). Biochemistry, 2010, 49, 7625-7633.	2.5	19
41	Dimerisation of the UBA Domain of p62 Inhibits Ubiquitin Binding and Regulates NF-ÎºB Signalling. Journal of Molecular Biology, 2010, 396, 178-194.	4.2	93
42	Tuneable DNA-based asymmetric catalysis using a G-quadruplex supramolecular assembly. Chemical Communications, 2010, 46, 4309.	4.1	99
43	Characterization of a Non-UBA Domain Missense Mutation of Sequestosome 1 (SQSTM1) in Paget's Disease of Bone. Journal of Bone and Mineral Research, 2009, 24, 632-642.	2.8	48
44	Mechanism of Ligand-Induced Folding of a Natively Unfolded Helixless Variant of Rabbit I-BABP. Biochemistry, 2009, 48, 7556-7564.	2.5	18
45	Repression of Translation of Human Estrogen Receptor Î± by G-Quadruplex Formation. Biochemistry, 2009, 48, 11487-11495.	2.5	70
46	Folding Topology of a Bimolecular DNA Quadruplex Containing a Stable Mini-hairpin Motif within the Diagonal Loop. Journal of Molecular Biology, 2009, 385, 1600-1615.	4.2	18
47	Folding of single-stranded DNA quadruplexes containing an autonomously stable mini-hairpin loop. Molecular BioSystems, 2009, 5, 542.	2.9	7
48	Selectivity of small molecule ligands for parallel and anti-parallel DNA G-quadruplex structures. Organic and Biomolecular Chemistry, 2009, 7, 4194.	2.8	61
49	Conformation and dynamics of the threeâ€helix bundle UBA domain of p62 from experiment and simulation. Proteins: Structure, Function and Bioinformatics, 2008, 71, 227-240.	2.6	7
50	Sequential Barriers and an Obligatory Metastable Intermediate Define the Apparent Two-state Folding Pathway of the Ubiquitin-like PB1 Domain of NBR1. Journal of Molecular Biology, 2008, 376, 1463-1477.	4.2	6
51	The Highly Repetitive Region of the Helicobacter pylori CagY Protein Comprises Tandem Arrays of an Î±-Helical Repeat Module. Journal of Molecular Biology, 2008, 377, 956-971.	4.2	29
52	Aromatic Residues Engineered into the Î²-Turn Nucleation Site of Ubiquitin Lead to a Complex Folding Landscape, Non-Native Side-Chain Interactions, and Kinetic Traps. Biochemistry, 2008, 47, 12910-12922.	2.5	18
53	Helix Mutations Stabilize a Late Productive Intermediate on the Folding Pathway of Ubiquitin. Biochemistry, 2008, 47, 8225-8236.	2.5	8
54	Ubiquitin Recognition by the Ubiquitin-associated Domain of p62 Involves a Novel Conformational Switch. Journal of Biological Chemistry, 2008, 283, 5427-5440.	3.4	129

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55	Disruption of ubiquitin-mediated processes in diseases of the brain and bone. Biochemical Society Transactions, 2008, 36, 469-471.	3.4	13
56	Bile Acid Interactions with Rabbit Ileal Lipid Binding Protein and an Engineered Helixless Variant Reveal Novel Ligand Binding Properties of a Versatile Î²-Clam Shell Protein Scaffold. Journal of Molecular Biology, 2007, 371, 1365-1377.	4.2	20
57	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. Organic and Biomolecular Chemistry, 2007, 5, 832.	2.8	12
58	Coupling ligand recognition to protein folding in an engineered variant of rabbit ileal lipid binding protein. Chemical Communications, 2006, , 4623.	4.1	15
59	Engineering Diverse Changes in Î²-Turn Propensities in the N-Terminal Î²-Hairpin of Ubiquitin Reveals Significant Effects on Stability and Kinetics but a Robust Folding Transition Stateâ€. Biochemistry, 2006, 45, 4220-4230.	2.5	16
60	Population of On-pathway Intermediates in the Folding of Ubiquitin. Journal of Molecular Biology, 2006, 360, 1053-1066.	4.2	23
61	Engineering Enhanced Protein Stability through Î²-Turn Optimization: Insights for the Design of Stable Peptide Î²-Hairpin Systems. Angewandte Chemie - International Edition, 2005, 44, 4939-4944.	13.8	35
62	Extending the Folding Nucleus of Ubiquitin with an Independently Folding Î²-Hairpin Finger: Hurdles to Rapid Folding Arising from the Stabilisation of Local Interactions. Journal of Molecular Biology, 2005, 349, 205-221.	4.2	26
63	Engineering Stabilising Î²-Sheet Interactions into a Conformationally Flexible Region of the Folding Transition State of Ubiquitin. Journal of Molecular Biology, 2005, 353, 373-384.	4.2	11
64	Context-dependent effects of proline residues on the stability and folding pathway of ubiquitin. FEBS Journal, 2004, 271, 4474-4484.	0.2	20
65	Design of Î²-sheet systems for understanding the thermodynamics and kinetics of protein folding. Current Opinion in Structural Biology, 2004, 14, 458-464.	5.7	114
66	Novel UBA Domain Mutations of SQSTM1 in Paget's Disease of Bone: Genotype Phenotype Correlation, Functional Analysis, and Structural Consequences. Journal of Bone and Mineral Research, 2004, 19, 1122-1127.	2.8	142
67	Loss of Ubiquitin-Binding Associated With Paget's Disease of Bone p62 (SQSTM1) Mutations. Journal of Bone and Mineral Research, 2004, 20, 619-624.	2.8	97
68	Incremental Contribution to Protein Stability from aÎ² HairpinâEœFingerâ€• Limits on the Stability of DesignedÎ² Hairpin Peptides. Angewandte Chemie - International Edition, 2004, 43, 1991-1994.	13.8	14
69	Insights into stabilizing weak interactions in designed peptide ?-hairpins. Biopolymers, 2004, 76, 185-195.	2.4	44
70	Structure and K+ ion-dependent stability of a parallel-stranded DNA quadruplex containing a core A-tetrad. Organic and Biomolecular Chemistry, 2004, 2, 810.	2.8	31
71	Drug-induced stabilisation of a mismatched C-T base pair in a DNA hairpinElectronic supplementary information (ESI) available: 1H NMR spectra of the hairpin sequence. See http://www.rsc.org/suppdata/cc/b3/b305337g/. Chemical Communications, 2003, , 1814.	4.1	6
72	Stabilization of Î²-Hairpin Peptides by Salt Bridges:â€‰ Role of Preorganization in the Energetic Contribution of Weak Interactions. Journal of the American Chemical Society, 2003, 125, 9038-9047.	13.7	100

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73	Stability and Folding Kinetics of a Ubiquitin Mutant with a Strong Propensity for Nonnative Î²-Hairpin Conformation in the Unfolded State. Biochemistry, 2003, 42, 13762-13771.	2.5	34
74	Drug Recognition and Stabilisation of the Parallel-stranded DNA Quadruplex d(TTAGGGT)4 Containing the Human Telomeric Repeat. Journal of Molecular Biology, 2003, 334, 25-36.	4.2	179
75	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. Organic and Biomolecular Chemistry, 2003, 1, 1650-1656.	2.8	79
76	DNA recognition by the anthracycline antibiotic respinomycin D: NMR structure of the intercalation complex with d(AGACGTCT)2. Organic and Biomolecular Chemistry, 2003, 1, 60-66.	2.8	43
77	Structure of the Ubiquitin-associated Domain of p62 (SQSTM1) and Implications for Mutations That Cause Paget's Disease of Bone. Journal of Biological Chemistry, 2003, 278, 37409-37412.	3.4	111
78	Structure of a Drug-Induced DNA T-Bulge: Implications for DNA Frameshift Mutations. Angewandte Chemie - International Edition, 2002, 41, 4754-4756.	13.8	16
79	Drug recognition of a DNA single strand break. FEBS Journal, 2002, 269, 1726-1733.	0.2	10
80	Insights into the Stability of Native and Partially Folded States of Ubiquitin:Â Effects of Cosolvents and Denaturants on the Thermodynamics of Protein Foldingâ€. Biochemistry, 2001, 40, 10317-10325.	2.5	39
81	Cooperativity in Drugâ˜DNA Recognition:â€‰ A Molecular Dynamics Study. Journal of the American Chemical Society, 2001, 123, 12658-12663.	13.7	150
82	Peptide models of protein Î²-sheets: design, folding and insights into stabilising weak interactions. Perkin Transactions II RSC, 2001, , 1011-1020.	1.1	75
83	Design of histidine-Zn2+ binding sites within a Î²-hairpin peptide: enhancement of Î²-sheet stability through metal complexation. Chemical Communications, 2001, , 1162-1163.	4.1	30
84	Effects of Amino Acid Ït‚Ï^ Propensities and Secondary Structure Interactions in Modulating HÎ± Chemical Shifts in Peptide and Protein Î²-Sheet. Journal of the American Chemical Society, 2001, 123, 12318-12324.	13.7	38
85	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. Angewandte Chemie - International Edition, 2001, 40, 4749-4751.	13.8	90
86	Folding of a Î²-hairpin peptide derived from the N-terminus of ubiquitin. FEBS Journal, 2000, 267, 3539-3548.	0.2	28
87	Templating peptide folding on the surface of a micelle. Bioorganic and Medicinal Chemistry Letters, 2000, 10, 1139-1142.	2.2	9
88	Do interstrand hydrogen bonds contribute to Î²-hairpin peptide stability in solution? IR analysis of peptide folding in water. Chemical Communications, 2000, , 593-594.	4.1	20
89	Evidence for Î²-sheet conformation in vesicle-bound peptides derived from the transmembrane bacterial flagellar motor protein MotB from Rhodobacter sphaeroides. Perkin Transactions II RSC, 2000, , 479-483.	1.1	0
90	Structure, Folding, and Energetics of Cooperative Interactions between the Î²-Strands of a de Novo Designed Three-Stranded Antiparallel Î²-Sheet Peptide. Journal of the American Chemical Society, 2000, 122, 8350-8356.	13.7	115

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91	Cooperative Assembly of a Nativelike Ubiquitin Structure through Peptide Fragment Complexation:â€‰Energetics of Peptide Association and Folding. Biochemistry, 2000, 39, 12355-12364.	2.5	40
92	Energetics of Weak Interactions in a Î²-hairpin Peptide:Â Electrostatic and Hydrophobic Contributions to Stability from Lysine Salt Bridges. Journal of the American Chemical Society, 1999, 121, 11615-11620.	13.7	78
93	DNA minor groove recognition by bis-benzimidazole analogues of Hoechst 33258: insights into structure-DNA affinity relationships assessed by fluorescence titration measurements. Nucleic Acids Research, 1999, 27, 1619-1624.	14.5	64
94	Molecular Recognition between a New Pentacyclic Acridinium Salt and DNA Sequences Investigated by Optical Spectroscopic Techniques, Proton Nuclear Magnetic Resonance Spectroscopy, and Molecular Modeling. Biochemistry, 1999, 38, 6723-6731.	2.5	21
95	Structure, dynamics and hydration of the nogalamycin-d(ATGCAT) 2 complex determined by NMR and molecular dynamics simulations in solution 1 1Edited by I. Tinoco. Journal of Molecular Biology, 1999, 290, 699-716.	4.2	47
96	Dissecting the stability of a Î²-hairpin peptide that folds in water: NMR and molecular dynamics analysis of the Î²-turn and Î²-strand contributions to folding 1 1Edited by P. E. Wright. Journal of Molecular Biology, 1999, 292, 1051-1069.	4.2	167
97	Solution structure and dynamics of the A-T tract DNA decamer duplex d(GGTAATTACC)2: implications for recognition by minor groove binding drugs. Biochemical Journal, 1999, 342, 125.	3.7	7
98	Solution structure and dynamics of the A-T tract DNA decamer duplex d(GGTAATTACC)2: implications for recognition by minor groove binding drugs. Biochemical Journal, 1999, 342, 125-132.	3.7	16
99	Prion protein fragments spanning helix 1 and both strands of Î² sheet (residues 125â€“170) show evidence for predominantly helical propensity by CD and NMR. Folding & Design, 1998, 3, 313-320.	4.5	17
100	Structure of the nogalamycinâ€“d(ATGCAT)2 complex in solution: DNA recognition at an isolated TpG site. Journal of the Chemical Society Perkin Transactions 1, 1998, , 3-6.	0.9	3
101	Cooperative Interaction between the Three Strands of a Designed Antiparallel Î²-Sheet. Journal of the American Chemical Society, 1998, 120, 5291-5300.	13.7	121
102	Origin of Î²-Hairpin Stability in Solution:Â Structural and Thermodynamic Analysis of the Folding of a Model Peptide Supports Hydrophobic Stabilization in Water. Journal of the American Chemical Society, 1998, 120, 1996-2007.	13.7	236
103	Modulation of intrinsic Ï†,Ï^ propensities of amino acids by neighbouring residues in the coil regions of protein structures: NMR analysis and dissection of a Î²-hairpin peptide 1 1Edited by P. E. Wright. Journal of Molecular Biology, 1998, 284, 1597-1609.	4.2	56
104	NMR structural analysis of a Î²-hairpin peptide designed for DNA binding. Chemical Communications, 1997, , 1297-1298.	4.1	37
105	The â€˜nâ€™ effect in molecular recognition. , 1996, 9, 88-94.		13
106	Native-like Î²-hairpin structure in an isolated fragment from ferredoxin: NMR and CD studies of solvent effects on the N-terminal 20 residues. Protein Engineering, Design and Selection, 1996, 9, 559-565.	2.1	70
107	Kooperative VerstÃrkung elektrostatischer Bindungen durch das Verbergen von Kohlenwasserstoffen. Angewandte Chemie, 1995, 107, 1644-1646.	2.0	3
108	Burial of Hydrocarbon Causes Cooperative Enhancement of Electrostatic Binding. Angewandte Chemie International Edition in English, 1995, 34, 1483-1485.	4.4	29

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109	A short linear peptide derived from the N-terminal sequence of ubiquitin folds into a water-stable non-native Î²-hairpin. Nature Structural and Molecular Biology, 1995, 2, 999-1006.	8.2	172
110	Empirical Correlations between Thermodynamic Properties and Intermolecular Forces. Journal of the American Chemical Society, 1995, 117, 5013-5015.	13.7	217
111	Asymmetry in the structure of glycopeptide antibiotic dimers: NMR studies of the ristocetin A complex with a bacterial cell wall analog. Journal of the American Chemical Society, 1995, 117, 7958-7964.	13.7	35
112	Application of a generalised enthalpyâ€“entropy relationship to binding co-operativity and weak associations in solution. Journal of the Chemical Society Perkin Transactions II, 1995, , 141-151.	0.9	134
113	Enhancement of Electrostatic Binding Through Cooperative Interactions: Enthalpy/Entropy Compensation and Peptideâ€”Peptide Recognition. , 1995, , 151-159.		0
114	Glycopeptide Antibiotic Activity and the Possible Role of Dimerization: A Model for Biological Signaling. Journal of the American Chemical Society, 1994, 116, 4581-4590.	13.7	210
115	The structure of an asymmetric dimer relevant to the mode of action of the glycopeptide antibiotics. Structure, 1994, 2, 747-754.	3.3	77
116	Expression of electrostatic binding cooperativity in the recognition of cell-wall peptide analogues by vancomycin group antibiotics. Journal of the Chemical Society Chemical Communications, 1994, , 1519.	2.0	28
117	Recognition of the cell-wall binding site of the vancomycin-group antibiotics by unnatural structural motifs: 1H NMR studies of the effects of ligand binding on antibiotic dimerisation. Journal of the Chemical Society Perkin Transactions 1, 1994, , 659.	0.9	9
118	Rationally designed ligands as models for bacterial cell-wall recognition by vancomycin-group antibiotics. Journal of Chemical Sciences, 1994, 106, 937-954.	1.5	1
119	NMR Studies of Drugâ€”DNA interactions. Progress in Nuclear Magnetic Resonance Spectroscopy, 1993, 25, 403-480.	7.5	68
120	Rational design and binding of modified cell-wall peptides to vancomycin-group antibiotics: Factorising free energy contributions to binding. Tetrahedron, 1993, 49, 9171-9182.	1.9	31
121	The free energy change of restricting a bond rotation in the binding of peptide analogues to vancomycin group antibiotics. Bioorganic and Medicinal Chemistry Letters, 1993, 3, 803-808.	2.2	20
122	Interaction of Hoechst 33258 with the minor groove of the A + T-rich DNA duplex d(GGTAATTACC)2 studied in solution by NMR spectroscopy. FEBS Journal, 1993, 211, 437-447.	0.2	84
123	On the stability of nucleic acid structures in solution: enthalpy - entropy compensations, internal rotations and reversibility. Nucleic Acids Research, 1993, 21, 2051-2056.	14.5	126
124	Relationships between structure and activity based on a partitioning of free energy contributions in the estimation of binding constants. , 1993, , 86-92.		0
125	Consequences for molecular recognition and ligand-receptor complementary of entropy changes in phase transitions. Bioorganic and Medicinal Chemistry Letters, 1992, 2, 993-996.	2.2	3
126	Partitioning of free energy contributions in the estimation of binding constants: residual motions and consequences for amide-amide hydrogen bond strengths. Journal of the American Chemical Society, 1992, 114, 10697-10704.	13.7	214

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127	The cost of conformational order: entropy changes in molecular associations. Journal of the American Chemical Society, 1992, 114, 10690-10697.	13.7	379
128	31P NMR investigation of the backbone conformation and dynamics of the hexamer duplex d(5â€²-GCATGC)2in its complex with the antibiotic nogalamycin. FEBS Letters, 1992, 297, 292-296.	2.8	22
129	Interaction of the anthracycline antibiotic nogalamycin with the hexamer duplex d(5'-GACGTC)2.. An NMR and molecular modelling study. FEBS Journal, 1992, 205, 45-58.	0.2	22
130	Probing the interaction of Hoechst 33258 with an Aâ€“T rich oligonucleotide duplex using1H NMR spectroscopy. Journal of the Chemical Society Chemical Communications, 1991, , 1770-1771.	2.0	6
131	Anthracycline antibiotic arugomycin binds in both grooves of the DNA helix simultaneously: an NMR and molecular modelling study. Nucleic Acids Research, 1991, 19, 2897-2906.	14.5	23
132	Sequence-specific interaction of Hoescht 33258 with the minor grooVe of an adenine-tract DNA duplex studied in solution by1H NMR spectroscopy. Nucleic Acids Research, 1990, 18, 3753-3762.	14.5	112
133	Sequence specific conformation of a DNA decamer containing an adenine tract studied in solution by 1H-NMR spectroscopy. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 1990, 1049, 69-77.	2.4	5
134	Hoogsteen versus Watson-Crick A-T basepairing in DNA complexes of a new group of â€˜quinomycin-likeâ€™ antibiotics. FEBS Letters, 1990, 272, 171-174.	2.8	10
135	NMR studies of the interaction of the antibiotic nogalamycin with the hexadeoxyribonucleotide duplex d(5'-GCATGC)2. Biochemistry, 1988, 27, 4340-4349.	2.5	97