Martin J Scanlon

List of Publications by Year
in descending order

127 papers	4,537 citations	117453 34 h-index	123241 61 g-index
137 all docs	137 docs citations	137 times ranked	6193 citing authors

#	Article	IF	Citations
1	Selective Binding of Small Molecules to Vibrio cholerae DsbA Offers a Starting Point for the Design of Novel Antibacterials. ChemMedChem, 2022, 17, .	1.6	3
2	Identification and characterization of two drug-like fragments that bind to the same cryptic binding pocket of Burkholderia pseudomallei DsbA. Acta Crystallographica Section D: Structural Biology, 2022, 78, 75-90.	1.1	2
3	Novel small molecules that increase the susceptibility of Neisseria gonorrhoeae to cationic antimicrobial peptides by inhibiting lipid A phosphoethanolamine transferase. Journal of Antimicrobial Chemotherapy, 2022, 77, 2441-2447.	1.3	4
4	Methyl probes in proteins for determining ligand binding mode in weak proteinâ€“ligand complexes. Scientific Reports, 2022, 12, .	1.6	3
5	Binding of a pyrimidine RNA base-mimic to SARS-CoV-2 nonstructural protein 9. Journal of Biological Chemistry, 2021, 297, 101018.	1.6	10
6	Elaboration of a benzofuran scaffold and evaluation of binding affinity and inhibition of Escherichia coli DsbA: A fragment-based drug design approach to novel antivirulence compounds. Bioorganic and Medicinal Chemistry, 2021, 45, 116315.	1.4	7
7	NMR fragment screening reveals a novel small molecule binding site near the catalytic surface of the disulfideâ€“dithiol oxidoreductase enzyme DsbA from Burkholderia pseudomallei. Journal of Biomolecular NMR, 2020, 74, 595-611.	1.6	7
8	Rapid Elaboration of Fragments into Leads by X-ray Crystallographic Screening of Parallel Chemical Libraries (REFiL_X). Journal of Medicinal Chemistry, 2020, 63, 6863-6875.	2.9	16
9	Substituted 1-methyl-4-phenylpyrrolidin-2-ones â€“ Fragment-based design of N-methylpyrrolidone-derived bromodomain inhibitors. European Journal of Medicinal Chemistry, 2020, 191, 112120.	2.6	8
10	Synthesis and elaboration of N-methylpyrrolidone as an acetamide fragment substitute in bromodomain inhibition. Bioorganic and Medicinal Chemistry, 2019, 27, 115157.	1.4	9
11	A ligand-induced structural change in fatty acidâ€“binding protein 1 is associated with potentiation of peroxisome proliferatorâ€“activated receptor Î± agonists. Journal of Biological Chemistry, 2019, 294, 3720-3734.	1.6	17
12	The Fragment-Based Development of a Benzofuran Hit as a New Class of Escherichia coli DsbA Inhibitors. Molecules, 2019, 24, 3756.	1.7	22
13	Controlled Construction of Cyclic <scp>dâ€…</scp>/<scp>â€…l</scp> Peptide Nanorods. Angewandte Chemie - International Edition, 2019, 58, 596-601.	7.2	8
14	Controlled Construction of Cyclic <scp>dâ€…</scp>/<scp>â€…l</scp> Peptide Nanorods. Angewandte Chemie, 2019, 131, 606-611.	1.6	2
15	Identification of the Binding Site of Apical Membrane Antigenâ€…1 (AMA1) Inhibitors Using a Paramagnetic Probe. ChemMedChem, 2019, 14, 603-612.	1.6	9
16	Dietary docosahexaenoic acid supplementation enhances expression of fatty acidâ€binding protein 5 at the bloodâ€“brain barrier and brain docosahexaenoic acid levels. Journal of Neurochemistry, 2018, 146, 186-197.	2.1	11
17	Production, biophysical characterization and initial crystallization studies of the N- and C-terminal domains of DsbD, an essential enzyme in Neisseria meningitidis. Acta Crystallographica Section F, Structural Biology Communications, 2018, 74, 31-38.	0.4	1
18	Fatty Acidâ€“Binding Protein 5 Mediates the Uptake of Fatty Acids, but not Drugs, Into Human Brain Endothelial Cells. Journal of Pharmaceutical Sciences, 2018, 107, 1185-1193.	1.6	18

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19	Inhibition of Diverse DsbA Enzymes in Multi-DsbA Encoding Pathogens. Antioxidants and Redox Signaling, 2018, 29, 653-666.	2.5	35
20	Reduced bloodâ€brain barrier expression of fatty acidâ€binding protein 5 is associated with increased vulnerability of APP/PS1 mice to cognitive deficits from low omegaâ€3 fatty acid diets. Journal of Neurochemistry, 2018, 144, 81-92.	2.1	18
21	Design of a Fragment-Screening Library. Methods in Enzymology, 2018, 610, 97-115.	0.4	7
22	Structural and biochemical insights into the disulfide reductase mechanism of DsbD, an essential enzyme for neisserial pathogens. Journal of Biological Chemistry, 2018, 293, 16559-16571.	1.6	10
23	Applications of NMR Spectroscopy in FBDD. , 2018, , 2211-2231.		2
24	Structural basis for the inhibition of poxvirus assembly by the antibiotic rifampicin. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 8424-8429.	3.3	30
25	Fragment-Based Discovery of Inhibitors of the Bacterial DnaG-SSB Interaction. Antibiotics, 2018, 7, 14.	1.5	14
26	Cyclic Hexapeptide Mimics of the LEDGF Integrase Recognition Loop in Complex with HIVâ€1 Integrase. ChemMedChem, 2018, 13, 1555-1565.	1.6	5
27	Molecular Insights into the Interaction Between the SPRY Domain-Containing SOCS Box Protein SPSB2 and Peptides Based on the Binding Motif from iNOS. Australian Journal of Chemistry, 2017, 70, 191.	0.5	8
28	Î”â€Myrtoxinâ€Mp1a is a Helical Heterodimer from the Venom of the Jack Jumper Ant that has Antimicrobial, Membraneâ€Disrupting, and Nociceptive Activities. Angewandte Chemie - International Edition, 2017, 56, 8495-8499.	7.2	28
29	Neurokinin 1 receptor signaling in endosomes mediates sustained nociception and is a viable therapeutic target for prolonged pain relief. Science Translational Medicine, 2017, 9, .	5.8	158
30	HN, N, CÎ± and CÎ² assignments of the two periplasmic domains of Neisseria meningitidis DsbD. Biomolecular NMR Assignments, 2017, 11, 181-186.	0.4	1
31	The first total synthesis and solution structure of a polypeptin, PE2, a cyclic lipopeptide with broad spectrum antibiotic activity. Organic and Biomolecular Chemistry, 2017, 15, 7173-7180.	1.5	5
32	Fragment library screening identifies hits that bind to the non-catalytic surface of Pseudomonas aeruginosa DsbA1. PLoS ONE, 2017, 12, e0173436.	1.1	17
33	Applications of NMR Spectroscopy in FBDD. , 2017, , 1-22.		0
34	Targeting Bacterial Dsb Proteins for the Development of Anti-Virulence Agents. Molecules, 2016, 21, 811.	1.7	52
35	Solution NMR characterization of apical membrane antigen 1 and small molecule interactions as a basis for designing new antimalarials. Journal of Molecular Recognition, 2016, 29, 281-291.	1.1	8
36	Redoxâ€stable cyclic peptide inhibitors of the SPSB2â€“iNOS interaction. FEBS Letters, 2016, 590, 696-704.	1.3	17

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37	Protein unfolding is essential for cleavage within the Î±-helix of a model protein substrate by the serine protease, thrombin. Biochimie, 2016, 122, 227-234.	1.3	6
38	Structureâ€“Activity Studies of Î²-Hairpin Peptide Inhibitors of the Plasmodium falciparum AMA1â€“RON2 Interaction. Journal of Molecular Biology, 2016, 428, 3986-3998.	2.0	22
39	The ways and means of fragment-based drug design. , 2016, 167, 28-37.		67
40	Fatty Acid-Binding Protein 5 at the Bloodâ€“Brain Barrier Regulates Endogenous Brain Docosahexaenoic Acid Levels and Cognitive Function. Journal of Neuroscience, 2016, 36, 11755-11767.	1.7	61
41	Determination of ligand binding modes in weak proteinâ€“ligand complexes using sparse NMR data. Journal of Biomolecular NMR, 2016, 66, 195-208.	1.6	19
42	Design, Synthesis, and Characterization of Cyclic Peptidomimetics of the Inducible Nitric Oxide Synthase Binding Epitope That Disrupt the Proteinâ€“Protein Interaction Involving SPRY Domain-Containing Suppressor of Cytokine Signaling Box Protein (SPSB) 2 and Inducible Nitric Oxide Synthase. Journal of Medicinal Chemistry, 2016, 59, 5799-5809.	2.9	19
43	Binding of CFA/I Pili of Enterotoxigenic Escherichia coli to Asialo-GM1 Is Mediated by the Minor Pilin CfaE. Infection and Immunity, 2016, 84, 1642-1649.	1.0	11
44	Propargyloxyproline Regio- and Stereoisomers for Click-Conjugation of Peptides: Synthesis and Application in Linear and Cyclic Peptides. Australian Journal of Chemistry, 2015, 68, 1365.	0.5	11
45	Conserved features in TamA enable interaction with TamB to drive the activity of the translocation and assembly module. Scientific Reports, 2015, 5, 12905.	1.6	35
46	Solution structure and DNA binding of the catalytic domain of the large serine resolvase TnpX. Journal of Molecular Recognition, 2015, 28, 316-324.	1.1	1
47	Fatty Acid-binding Proteins 1 and 2 Differentially Modulate the Activation of Peroxisome Proliferator-activated Receptor Î± in a Ligand-selective Manner. Journal of Biological Chemistry, 2015, 290, 13895-13906.	1.6	49
48	Application of Fragmentâ€Based Screening to the Design of Inhibitors of Escherichia coli DsbA. Angewandte Chemie - International Edition, 2015, 54, 2179-2184.	7.2	46
49	Small Molecule Inhibitors of Disulfide Bond Formation by the Bacterial DsbAâ€“DsbB Dual Enzyme System. ACS Chemical Biology, 2015, 10, 957-964.	1.6	27
50	Promiscuous 2-Aminothiazoles (PrATs): A Frequent Hitting Scaffold. Journal of Medicinal Chemistry, 2015, 58, 1205-1214.	2.9	75
51	Inhibitors of BCATm: A Tough Nut To Crack. Journal of Medicinal Chemistry, 2015, 58, 7138-7139.	2.9	4
52	Fatty Acid-Binding Protein 5 Facilitates the Bloodâ€“Brain Barrier Transport of Docosahexaenoic Acid. Molecular Pharmaceutics, 2015, 12, 4375-4385.	2.3	88
53	Determinants of Proteolysis and Cell-Binding for the Shigella flexneri Cytotoxin, SigA. Current Microbiology, 2015, 71, 613-617.	1.0	4
54	Fatty Acid Binding Proteins Expressed at the Human Bloodâ€“Brain Barrier Bind Drugs in an Isoform-Specific Manner. Pharmaceutical Research, 2015, 32, 3432-3446.	1.7	9

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55	Targeting virulence not viability in the search for future antibacterials. British Journal of Clinical Pharmacology, 2015, 79, 208-215.	1.1	144
56	Sent packing: protein engineering generates a new crystal form ofPseudomonas aeruginosaDsbA1 with increased catalytic surface accessibility. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 2386-2395.	2.5	5
57	¹⁹F NMR as a Probe of Ligand Interactions with the iNOS Binding site of SPRY Domainâ€Containing SOCS Box Protein 2. Chemical Biology and Drug Design, 2014, 84, 616-625.	1.5	26
58	Assignments of human integrin Î±1I domain in the apo and Mg2+ bound states. Biomolecular NMR Assignments, 2014, 8, 117-121.	0.4	4
59	Structure of the Chicken CD3ÏµÎ´/Î³ Heterodimer and Its Assembly with the Î±Î²T Cell Receptor. Journal of Biological Chemistry, 2014, 289, 8240-8251.	1.6	13
60	Characterization of Two Distinct Modes of Drug Binding to Human Intestinal Fatty Acid Binding Protein. ACS Chemical Biology, 2014, 9, 2526-2534.	1.6	24
61	Structure and Dynamics of Apical Membrane Antigen 1 from Plasmodium falciparum FVO. Biochemistry, 2014, 53, 7310-7320.	1.2	23
62	A critical evaluation of pyrrolo[2,3-d]pyrimidine-4-amines as Plasmodium falciparum apical membrane antigen 1 (AMA1) inhibitors. MedChemComm, 2014, 5, 1500-1506.	3.5	8
63	Ligand-Induced Conformational Change of Plasmodium falciparum AMA1 Detected Using ¹⁹F NMR. Journal of Medicinal Chemistry, 2014, 57, 6419-6427.	2.9	33
64	Activation of the pseudokinase MLKL unleashes the four-helix bundle domain to induce membrane localization and necroptotic cell death. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 15072-15077.	3.3	484
65	The Role of Oxidoreductases in Determining the Function of the Neisserial Lipid A Phosphoethanolamine Transferase Required for Resistance to Polymyxin. PLoS ONE, 2014, 9, e106513.	1.1	24
66	Molecular Insights into the Interaction between Plasmodium falciparum Apical Membrane Antigen 1 and an Invasion-Inhibitory Peptide. PLoS ONE, 2014, 9, e109674.	1.1	10
67	Design and Evaluation of the Performance of an NMR Screening Fragment Library. Australian Journal of Chemistry, 2013, 66, 1465.	0.5	33
68	Parallel Screening of Low Molecular Weight Fragment Libraries: Do Differences in Methodology Affect Hit Identification?. Journal of Biomolecular Screening, 2013, 18, 147-159.	2.6	61
69	The Structure of Integrin Î±1I Domain in Complex with a Collagen-mimetic Peptide. Journal of Biological Chemistry, 2013, 288, 36796-36809.	1.6	22
70	Distinct binding properties of TIAR RRMs and linker region. RNA Biology, 2013, 10, 579-589.	1.5	25
71	Development of Inhibitors of Plasmodium falciparum Apical Membrane Antigen 1 Based on Fragment Screening. Australian Journal of Chemistry, 2013, 66, 1530.	0.5	20
72	Interrogating Fragments Using a Protein Thermal Shift Assay. Australian Journal of Chemistry, 2013, 66, 1502.	0.5	10

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73	Detection and Prevention of Aggregation-based False Positives in STD-NMR-based Fragment Screening. Australian Journal of Chemistry, 2013, 66, 1518.	0.5	9
74	Blind Manâ€™s Bluff â€“ Elaboration of Fragment Hits in the Absence of Structure for the Development of Antitrypsin Deficiency Inhibitors. Australian Journal of Chemistry, 2013, 66, 1525.	0.5	3
75	Comparative Sequence, Structure and Redox Analyses of Klebsiella pneumoniae DsbA Show That Anti-Virulence Target DsbA Enzymes Fall into Distinct Classes. PLoS ONE, 2013, 8, e80210.	1.1	24
76	Colloidal characteristics and formulation of pure protein particulate vaccines. Journal of Pharmacy and Pharmacology, 2012, 64, 1386-1393.	1.2	2
77	The 1.2â€…Ã… resolution crystal structure of TcpG, theVibrio choleraeDsbA disulfide-forming protein required for pilus and cholera-toxin production. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 1290-1302.	2.5	20
78	Synthesis of Unsymmetrical 1,1â€²-Disubstituted Bis(1,2,3-triazole)s Using Monosilylbutadiynes. Organic Letters, 2011, 13, 537-539.	2.4	43
79	Fatty Acid Binding Proteins: Potential Chaperones of Cytosolic Drug Transport in the Enterocyte?. Pharmaceutical Research, 2011, 28, 2176-2190.	1.7	17
80	Preparation, crystallization and preliminary X-ray diffraction analysis of two intestinal fatty-acid binding proteins in the presence of 11-(dansylamino)undecanoic acid. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 291-295.	0.7	4
81	Fragmentâ€Based Design of Ligands Targeting a Novel Site on the Integrase Enzyme of Human Immunodeficiency Virusâ€…1. ChemMedChem, 2011, 6, 258-261.	1.6	24
82	Characterization of the N-Methyltransferase Activities of the Multifunctional Polypeptide Cyclosporin Synthetase. Chemistry and Biology, 2011, 18, 464-475.	6.2	21
83	Backbone and side chain 1H, 15N and 13C assignments for the oxidised and reduced forms of the oxidoreductase protein DsbA from Staphylococcus aureus. Biomolecular NMR Assignments, 2010, 4, 25-28.	0.4	3
84	Crystal structure of the HIVâ€1 integrase core domain in complex with sucrose reveals details of an allosteric inhibitory binding site. FEBS Letters, 2010, 584, 1455-1462.	1.3	38
85	Characterization of the DsbA Oxidative Folding Catalyst fromPseudomonas aeruginosaReveals a Highly Oxidizing Protein that Binds Small Molecules. Antioxidants and Redox Signaling, 2010, 12, 921-931.	2.5	28
86	Small heat-shock proteins interact with a flanking domain to suppress polyglutamine aggregation. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 10424-10429.	3.3	77
87	The Structure of the Bacterial Oxidoreductase Enzyme DsbA in Complex with a Peptide Reveals a Basis for Substrate Specificity in the Catalytic Cycle of DsbA Enzymes. Journal of Biological Chemistry, 2009, 284, 17835-17845.	1.6	62
88	Characterization of lipophilic drug binding to rat intestinal fatty acid binding protein. Molecular and Cellular Biochemistry, 2009, 326, 87-95.	1.4	18
89	DSB proteins and bacterial pathogenicity. Nature Reviews Microbiology, 2009, 7, 215-225.	13.6	260
90	Probing the Fibrate Binding Specificity of Rat Liver Fatty Acid Binding Protein. Journal of Medicinal Chemistry, 2009, 52, 5344-5355.	2.9	17

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91	Structure and Function of the Oxidoreductase DsbA1 from Neisseria meningitidis. Journal of Molecular Biology, 2009, 394, 931-943.	2.0	36
92	Molecular Dynamics of Poly(<scp>l</scp>-lysine) Dendrimers with Naphthalene Disulfonate Caps. Macromolecules, 2009, 42, 2775-2783.	2.2	37
93	Molecular Dynamics of Variegated Polyamide Dendrimers. Macromolecules, 2009, 42, 2784-2794.	2.2	22
94	Backbone assignments of the 34ÂkDa ketopantoate reductase from E. coli. Biomolecular NMR Assignments, 2008, 2, 93-96.	0.4	2
95	The Structural Impact of a Polyglutamine Tract Is Location-Dependent. Biophysical Journal, 2008, 95, 5922-5930.	0.2	29
96	Characterization of the Drug Binding Specificity of Rat Liver Fatty Acid Binding Protein. Journal of Medicinal Chemistry, 2008, 51, 3755-3764.	2.9	63
97	The Dotted Cap Notation: A concise notation for describing variegated dendrimers. New Journal of Chemistry, 2008, 32, 1543.	1.4	4
98	Structural and Biochemical Characterization of the Oxidoreductase NmDsbA3 from Neisseria meningitidis. Journal of Biological Chemistry, 2008, 283, 32452-32461.	1.6	23
99	Probing the Flexibility of the DsbA Oxidoreductase from Vibrio choleraeâ€"a 15N - 1H Heteronuclear NMR Relaxation Analysis of Oxidized and Reduced Forms of DsbA. Journal of Molecular Biology, 2007, 371, 703-716.	2.0	21
100	Examination of the Role of Intestinal Fatty Acid-Binding Protein in Drug Absorption Using a Parallel Artificial Membrane Permeability Assay. Chemistry and Biology, 2007, 14, 453-465.	6.2	36
101	Backbone and side chain 1H, 15N and 13C assignments for the reduced form of the oxidoreductase protein DsbA from Vibrio cholerae. Biomolecular NMR Assignments, 2007, 1, 75-76.	0.4	2
102	The binding interaction of synthetic ozonide antimalarials with natural and modified Î²-cyclodextrins. Journal of Pharmaceutical Sciences, 2006, 95, 146-158.	1.6	32
103	The Cysteine-rich Secretory Protein Domain of Tpx-1 Is Related to Ion Channel Toxins and Regulates Ryanodine Receptor Ca2+ Signaling. Journal of Biological Chemistry, 2006, 281, 4156-4163.	1.6	118
104	The Interaction of Lipophilic Drugs with Intestinal Fatty Acid-binding Protein. Journal of Biological Chemistry, 2005, 280, 17769-17776.	1.6	52
105	Isolation, Solution Structure, and Insecticidal Activity of Kalata B2, a Circular Protein with a Twist:Â Do MÃ¶bius Strips Exist in Nature?â€,â€¡. Biochemistry, 2005, 44, 851-860.	1.2	225
106	An improved method for the purification of rat liver-type fatty acid binding protein from Escherichia coli. Protein Expression and Purification, 2005, 44, 23-31.	0.6	13
107	Structural and functional analysis of the Josephin domain of the polyglutamine protein ataxin-3. Biochemical and Biophysical Research Communications, 2004, 322, 387-394.	1.0	58
108	Self-micellization of gemfibrozil 1-O-beta acyl glucuronide in aqueous solution. Pharmaceutical Research, 2003, 20, 465-470.	1.7	6

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109	The Three-dimensional Solution Structure of NaD1, a New Floral Defensin from Nicotiana alata and its Application to a Homology Model of the Crop Defense Protein alfAFP. Journal of Molecular Biology, 2003, 325, 175-188.	2.0	124
110	Difficult Macrocyclizations:â€‰ New Strategies for Synthesizing Highly Strained Cyclic Tetrapeptides. Organic Letters, 2003, 5, 2711-2714.	2.4	76
111	Conformationally Constrained Macrocycles That Mimic Tripeptide Î²-Strands in Water and Aprotic Solvents. Journal of the American Chemical Society, 2002, 124, 5673-5683.	6.6	56
112	Enhancing the immunogenicity and modulating the fine epitope recognition of antisera to a helical group A streptococcal peptide vaccine candidate from the M protein using lipidâ€core peptide technology. Immunology and Cell Biology, 2002, 80, 178-187.	1.0	38
113	The solution structure of C1-T1, a two-domain proteinase inhibitor derived from a circular precursor protein from Nicotiana alata11Edited by P. E. Wright. Journal of Molecular Biology, 2001, 306, 69-79.	2.0	20
114	Solution Structure of BSTI:Â A New Trypsin Inhibitor from Skin Secretions ofBombina bombinaâ€,â€¡. Biochemistry, 2001, 40, 4601-4609.	1.2	25
115	Conformational Selection of Inhibitors and Substrates by Proteolytic Enzymes:Â Implications for Drug Design and Polypeptide Processing. Journal of Medicinal Chemistry, 2000, 43, 1271-1281.	2.9	146
116	A Marine Snail Neurotoxin Shares with Scorpion Toxins a Convergent Mechanism of Blockade on the Pore of Voltage-Gated K Channels. Journal of General Physiology, 1999, 114, 141-158.	0.9	26
117	A novel two-chain proteinase inhibitor generated by circularization of a multidomain precursor protein. Nature Structural Biology, 1999, 6, 526-530.	9.7	51
118	Structure of a putative ancestral protein encoded by a single sequence repeat from a multidomain proteinase inhibitor gene fromNicotiana alata. Structure, 1999, 7, 793-802.	1.6	21
119	Cyclooligomerization of Thiazole-Containing Tetrapeptides. Symmetrical Macrocycles with up to 76 Amino Acids. Journal of the American Chemical Society, 1999, 121, 2603-2604.	6.6	42
120	A Backbone Linker for BOC-Based Peptide Synthesis and On-Resin Cyclization:Â Synthesis of Stylostatin 1â€,Â§. Journal of Organic Chemistry, 1999, 64, 3095-3101.	1.7	73
121	Solution structure and proposed binding mechanism of a novel potassium channel toxin Îº-conotoxin PVIIA. Structure, 1997, 5, 1585-1597.	1.6	88
122	Solution structure of the cardiostimulant polypeptide anthopleurin-B and comparison with anthopleurin-A. Structure, 1995, 3, 791-803.	1.6	59
123	A simplified liquid chromatography assay for the quantitation of halofantrine and desbutylhalofantrine in plasma and identification of a degradation product of desbutylhalofantrine formed under alkaline conditions. Journal of Pharmaceutical and Biomedical Analysis, 1995, 13, 265-272.	1.4	46
124	Three-Dimensional Structure in Solution of the Polypeptide Cardiac Stimulant Anthopleurin-A. Biochemistry, 1995, 34, 3782-3794.	1.2	47
125	NMR solution structure of the RNA-binding peptide from HIV-1 Rev protein. Biochemistry, 1995, 34, 8242-8249.	1.2	31
126	Multiple conformations of the sea anemone polypeptide anthopleurinâ€A in solution. Protein Science, 1994, 3, 1121-1124.	3.1	19

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127	Peptide epitope binding and fluorescence quenching with the anti-mucin antibody C595. Cancer Letters, 1992, 63, 199-202.	3.2	1