

# Weontae Lee

## List of Publications by Year in descending order

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130  
papers

2,875  
citations

159585

30  
h-index

206112

48  
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133  
all docs

133  
docs citations

133  
times ranked

3978  
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural and functional identification of the uncharacterized metallo- $\beta$ -lactamase superfamily protein TW9814 as a phosphodiesterase with unique metal coordination. <i>Acta Crystallographica Section D: Structural Biology</i> , 2022, 78, 532-541.	2.3	0
2	Crystal Structures of the Plant Phospholipase A1 Proteins Reveal a Unique Dimerization Domain. <i>Molecules</i> , 2022, 27, 2317.	3.8	0
3	Cryo-EM structure of the human somatostatin receptor 2 complex with its agonist somatostatin delineates the ligand-binding specificity. <i>ELife</i> , 2022, 11, .	6.0	10
4	Structural insights into the HBV receptor and bile acid transporter NTCP. <i>Nature</i> , 2022, 606, 1027-1031.	27.8	44
5	Substituted Syndecan-2-Derived Mimetic Peptides Show Improved Antitumor Activity over the Parent Syndecan-2-Derived Peptide. <i>International Journal of Molecular Sciences</i> , 2022, 23, 5888.	4.1	1
6	NMR spectroscopy uncovers direct interaction between BAF60A and p53. <i>Biochemical and Biophysical Research Communications</i> , 2021, 534, 815-821.	2.1	1
7	A High-Affinity Peptide Ligand Targeting Syntenin Inhibits Glioblastoma. <i>Journal of Medicinal Chemistry</i> , 2021, 64, 1423-1434.	6.4	10
8	Early-stage dynamics of chloride ion "pumping rhodopsin revealed by a femtosecond X-ray laser. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	41
9	Solution structure of the Myb domain of Terfa derived from Zebrafish interacting with both human and plant telomeric DNA. <i>Biochemical and Biophysical Research Communications</i> , 2021, 559, 252-258.	2.1	0
10	Structural and Functional Characterizations of Cancer Targeting Nanoparticles Based on Hepatitis B Virus Capsid. <i>International Journal of Molecular Sciences</i> , 2021, 22, 9140.	4.1	0
11	Advances in dermatology using DNA aptamer "Aptamin C" innovation: Oxidative stress prevention and effect maximization of vitamin C through antioxidation. <i>Journal of Cosmetic Dermatology</i> , 2020, 19, 970-976.	1.6	15
12	Bacterial overexpression and purification of soluble recombinant human serum albumin using maltose-binding protein and protein disulphide isomerase. <i>Protein Expression and Purification</i> , 2020, 167, 105530.	1.3	12
13	Crystal structure of the HMG domain of human BAF57 and its interaction with four-way junction DNA. <i>Biochemical and Biophysical Research Communications</i> , 2020, 533, 919-924.	2.1	5
14	Structure-Based Functional Modification Study of a Cyanobacterial Chloride Pump for Transporting Multiple Anions. <i>Journal of Molecular Biology</i> , 2020, 432, 5273-5286.	4.2	9
15	Characteristic Analysis of Homo- and Heterodimeric Complexes of Human Mitochondrial Pyruvate Carrier Related to Metabolic Diseases. <i>International Journal of Molecular Sciences</i> , 2020, 21, 3403.	4.1	15
16	Pumping mechanism of NM-R3, a light-driven bacterial chloride importer in the rhodopsin family. <i>Science Advances</i> , 2020, 6, eaay2042.	10.3	7
17	A Coil-to-Helix Transition Serves as a Binding Motif for hSNF5 and BAF155 Interaction. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2452.	4.1	3
18	Influence of alkyl chain substitution of ammonium ionic liquids on the activity and stability of tobacco etch virus protease. <i>International Journal of Biological Macromolecules</i> , 2020, 155, 439-446.	7.5	8

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19	Structural modification of NADPH oxidase activator (Noxa 1) by oxidative stress: An experimental and computational study. <i>International Journal of Biological Macromolecules</i> , 2020, 163, 2405-2414.	7.5	19
20	Tyrosine 51 residue of the syndecan-2 extracellular domain is involved in the interaction with and activation of pro-matrix metalloproteinase-7. <i>Scientific Reports</i> , 2019, 9, 10625.	3.3	6
21	The XFEL Protein Crystallography: Developments and Perspectives. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3421.	4.1	13
22	Non-Cryogenic Structure and Dynamics of HIV-1 Integrase Catalytic Core Domain by X-ray Free-Electron Lasers. <i>International Journal of Molecular Sciences</i> , 2019, 20, 1943.	4.1	8
23	Computer aided protein engineering to enhance the thermo-stability of CXCR1- T4 lysozyme complex. <i>Scientific Reports</i> , 2019, 9, 5317.	3.3	3
24	Biological conversion of methane to methanol through genetic reassembly of native catalytic domains. <i>Nature Catalysis</i> , 2019, 2, 342-353.	34.4	66
25	Liquid chromatography-tandem mass spectrometry of recombinant human extracellular superoxide dismutase (rhSOD3) in mouse plasma and its application to pharmacokinetic study. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2019, 164, 590-597.	2.8	3
26	Non-cryogenic structure of a chloride pump provides crucial clues to temperature-dependent channel transport efficiency. <i>Journal of Biological Chemistry</i> , 2019, 294, 794-804.	3.4	14
27	CXXC5 mediates growth plate senescence and is a target for enhancement of longitudinal bone growth. <i>Life Science Alliance</i> , 2019, 2, e201800254.	2.8	19
28	Discovery of a small-molecule inhibitor of Dvl-CXXC5 interaction by computational approaches. <i>Journal of Computer-Aided Molecular Design</i> , 2018, 32, 643-655.	2.9	11
29	The C-Domain of the NAC Transcription Factor ANAC019 Is Necessary for pH-Tuned DNA Binding through a Histidine Switch in the N-Domain. <i>Cell Reports</i> , 2018, 22, 1141-1150.	6.4	11
30	Wnt-Catenin-RAS interaction serves as a molecular switch for RAS degradation via GSK-3 $\beta$ . <i>EMBO Reports</i> , 2018, 19, .	4.5	34
31	TOM1 Regulates Neuronal Accumulation of Amyloid- $\beta$ Oligomers by FcRIL2 Variant in Alzheimer's Disease. <i>Journal of Neuroscience</i> , 2018, 38, 9001-9018.	3.6	21
32	CAP modifies the structure of a model protein from thermophilic bacteria: mechanisms of CAP-mediated inactivation. <i>Scientific Reports</i> , 2018, 8, 10218.	3.3	25
33	The bone anabolic effects of irisin are through preferential stimulation of aerobic glycolysis. <i>Bone</i> , 2018, 114, 150-160.	2.9	32
34	Structural and functional analysis of lysozyme after treatment with dielectric barrier discharge plasma and atmospheric pressure plasma jet. <i>Scientific Reports</i> , 2017, 7, 1027.	3.3	51
35	Crystal structure of the PDZ domain of mouse Dishevelled 1 and its interaction with CXXC5. <i>Biochemical and Biophysical Research Communications</i> , 2017, 485, 584-590.	2.1	10
36	C-terminal tail of NADPH oxidase organizer 1 (Noxo1) mediates interaction with NADPH oxidase activator (Noxa1) in the NOX1 complex. <i>Biochemical and Biophysical Research Communications</i> , 2017, 490, 594-600.	2.1	6

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37	Interaction studies of carbon nanomaterials and plasma activated carbon nanomaterials solution with telomere binding protein. <i>Scientific Reports</i> , 2017, 7, 2636.	3.3	17
38	NMR uncovers direct interaction between human NEDD4-1 and p34SEI <sup>1</sup> . <i>Biochemical and Biophysical Research Communications</i> , 2017, 490, 984-990.	2.1	5
39	Cyclized Oligopeptide Targeting LRP5/6-DKK1 Interaction Reduces the Growth of Tumor Burden in a Multiple Myeloma Mouse Model. <i>Yonsei Medical Journal</i> , 2017, 58, 505.	2.2	14
40	Extracellular superoxide dismutase ameliorates house dust mite-induced atopic dermatitis-like skin inflammation and inhibits mast cell activation in mice. <i>Experimental Dermatology</i> , 2016, 25, 630-635.	2.9	9
41	<sup>1</sup> H-NMR Characterization of the DNA-binding Domain of <i>Arabidopsis thaliana</i> Telomere Repeat Factor. <i>Bulletin of the Korean Chemical Society</i> , 2016, 37, 485-489.	1.9	0
42	Crystal structures of human peroxiredoxin 6 in different oxidation states. <i>Biochemical and Biophysical Research Communications</i> , 2016, 477, 717-722.	2.1	30
43	Small molecule inhibitors of the Dishevelled-CXXC5 interaction are new drug candidates for bone anabolic osteoporosis therapy. <i>EMBO Molecular Medicine</i> , 2016, 8, 375-387.	6.9	32
44	Identification of small-molecule compounds targeting the dishevelled PDZ domain by virtual screening and binding studies. <i>Bioorganic and Medicinal Chemistry</i> , 2016, 24, 3259-3266.	3.0	17
45	The MPN domain of <i>Caenorhabditis elegans</i> UfSP modulates both substrate recognition and deufmylation activity. <i>Biochemical and Biophysical Research Communications</i> , 2016, 476, 450-456.	2.1	3
46	Crystal structure and functional characterization of a light-driven chloride pump having an NTQ motif. <i>Nature Communications</i> , 2016, 7, 12677.	12.8	54
47	New structural insight of C-terminal region of Syntenin-1, enhancing the molecular dimerization and inhibitory function related on Syndecan-4 signaling. <i>Scientific Reports</i> , 2016, 6, 36818.	3.3	18
48	Small-molecule binding of the axin RGS domain promotes $\beta$ -catenin and Ras degradation. <i>Nature Chemical Biology</i> , 2016, 12, 593-600.	8.0	80
49	Expression, subcellular localization, and enzyme activity of a recombinant human extra-cellular superoxide dismutase in tobacco ( <i>Nicotiana benthamiana</i> L.). <i>Protein Expression and Purification</i> , 2016, 119, 69-74.	1.3	7
50	Probing the Folding-Unfolding Transition of a Thermophilic Protein, MTH1880. <i>PLoS ONE</i> , 2016, 11, e0145853.	2.5	6
51	Cloning, Purification, and Characterization of Recombinant Human Extracellular Superoxidedismutase in SF9 Insect Cells. <i>Molecules and Cells</i> , 2016, 39, 242-249.	2.6	4
52	Protein structure determination by conformational space annealing using <sup>1</sup> H-NMR geometric restraints. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 2251-2262.	2.6	16
53	Effect of nanosecond-pulsed plasma on the structural modification of biomolecules. <i>RSC Advances</i> , 2015, 5, 47300-47308.	3.6	13
54	A Unique Phenylalanine in the Transmembrane Domain Strengthens Homodimerization of the Syndecan-2 Transmembrane Domain and Functionally Regulates Syndecan-2. <i>Journal of Biological Chemistry</i> , 2015, 290, 5772-5782.	3.4	13

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55	Solution structure of the transmembrane 2 domain of the human melanocortin-4 receptor in sodium dodecyl sulfate (SDS) micelles and the functional implication of the D90N mutant. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2015, 1848, 1294-1302.	2.6	6
56	Trans-regulation of Syndecan Functions by Hetero-oligomerization. <i>Journal of Biological Chemistry</i> , 2015, 290, 16943-16953.	3.4	24
57	Influence of reactive species on the modification of biomolecules generated from the soft plasma. <i>Scientific Reports</i> , 2015, 5, 8221.	3.3	100
58	Crystal structure of syndesmos and its interaction with Syndecan-4 proteoglycan. <i>Biochemical and Biophysical Research Communications</i> , 2015, 463, 762-767.	2.1	7
59	AMIGO2, a novel membrane anchor of PDK1, controls cell survival and angiogenesis via Akt activation. <i>Journal of Cell Biology</i> , 2015, 211, 619-637.	5.2	49
60	Co-expression of human agouti-related protein enhances expression and stability of human melanocortin-4 receptor. <i>Biochemical and Biophysical Research Communications</i> , 2015, 456, 116-121.	2.1	1
61	AMIGO2, a novel membrane anchor of PDK1, controls cell survival and angiogenesis via Akt activation. <i>Journal of Experimental Medicine</i> , 2015, 212, 212120IA105.	8.5	1
62	Heteronuclear NMR studies on 44 kDa dimer, syndesmos. <i>Journal of the Korean Magnetic Resonance Society</i> , 2015, 19, 83-87.	0.1	1
63	Solution structure of CEH-37 homeodomain of the nematode <i>Caenorhabditis elegans</i> . <i>Biochemical and Biophysical Research Communications</i> , 2014, 443, 370-375.	2.1	1
64	Plasma modification of poly(2-heptadecyl-4-vinylthieno[3,4-d]thiazole) low bandgap polymer and its application in solar cells. <i>Physical Chemistry Chemical Physics</i> , 2014, 16, 27043-27052.	2.8	12
65	Pleiotropic effects of a vibrio extracellular protease on the activation of contact system. <i>Biochemical and Biophysical Research Communications</i> , 2014, 450, 1099-1103.	2.1	6
66	Solution structure of telomere binding domain of AtTRB2 derived from <i>Arabidopsis thaliana</i> . <i>Biochemical and Biophysical Research Communications</i> , 2014, 452, 436-442.	2.1	6
67	Inhibition of human neutrophil activity by an RNA aptamer bound to interleukin-8. <i>Biomaterials</i> , 2014, 35, 578-589.	11.4	37
68	Backbone Dynamics of an Atypical Orphan Response Regulator Protein, <i>Helicobacter pylori</i> 1043. <i>Molecules and Cells</i> , 2013, 35, 158-165.	2.6	5
69	<sup>1</sup> H, <sup>15</sup> N, and <sup>13</sup> C Resonance Assignments and Secondary Structure of the SWIRM Domain of Human BAF155, a Chromatin Remodeling Complex Component. <i>Molecules and Cells</i> , 2013, 36, 333-339.	2.6	0
70	Solution Structure and Rpn1 Interaction of the UBL Domain of Human RNA Polymerase II C-Terminal Domain Phosphatase. <i>PLoS ONE</i> , 2013, 8, e62981.	2.5	8
71	A High-Content Subtractive Screen for Selecting Small Molecules Affecting Internalization of GPCRs. <i>Journal of Biomolecular Screening</i> , 2012, 17, 379-385.	2.6	3
72	DNA-Binding Domain of AtTRB2 Reveals Unique Features of a Single Myb Histone Protein Family that Binds to Both <i>Arabidopsis</i> - and Human-Type Telomeric DNA Sequences. <i>Molecular Plant</i> , 2012, 5, 1406-1408.	8.3	8

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73	PACSY, a relational database management system for protein structure and chemical shift analysis. <i>Journal of Biomolecular NMR</i> , 2012, 54, 169-179.	2.8	33
74	Uncovering symmetry-breaking vector and reliability order for assigning secondary structures of proteins from atomic NMR chemical shifts in amino acids. <i>Journal of Biomolecular NMR</i> , 2011, 51, 411-424.	2.8	5
75	Solution structure of MTH1821, a putative structure homologue to RNA polymerase $\hat{\pm}$ subunit from <i>Methanobacterium thermoautotrophicum</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 1347-1351.	2.6	2
76	Crystal Structure of Fushi Tarazu Factor 1 Ligand Binding Domain/Fushi Tarazu Peptide Complex Identifies New Class of Nuclear Receptors. <i>Journal of Biological Chemistry</i> , 2011, 286, 31225-31231.	3.4	16
77	Solution Structures and Molecular Interactions of Selective Melanocortin Receptor Antagonists. <i>Molecules and Cells</i> , 2010, 30, 551-556.	2.6	3
78	Structural Basis of E2 $\hat{\epsilon}$ 25K/UBB+1 Interaction Leading to Proteasome Inhibition and Neurotoxicity. <i>Journal of Biological Chemistry</i> , 2010, 285, 36070-36080.	3.4	47
79	Prediction of Parathyroid Hormone Signalling Potency Using SVMs. <i>Molecules and Cells</i> , 2009, 27, 547-556.	2.6	1
80	Solution Structure of the DNA Binding Domain of Rice Telomere Binding Protein RTBP1 <sup>&lt;sup&gt;&lt;/sup&gt;</sup> . <i>Biochemistry</i> , 2009, 48, 827-838.	2.5	17
81	Structural basis of the auto-inhibition mechanism of nonreceptor tyrosine kinase PTK6. <i>Biochemical and Biophysical Research Communications</i> , 2009, 384, 236-242.	2.1	6
82	Crystal Structures and Enzyme Mechanisms of a Dual Fucose Mutarotase/Ribose Pyranase. <i>Journal of Molecular Biology</i> , 2009, 391, 178-191.	4.2	8
83	The solution structure of ribosomal protein S17E from <i>Methanobacterium thermoautotrophicum</i> : A structural homolog of the FF domain. <i>Protein Science</i> , 2008, 17, 583-588.	7.6	3
84	The oligomeric status of syndecan-4 regulates syndecan-4 interaction with $\hat{\pm}$ -actinin. <i>European Journal of Cell Biology</i> , 2008, 87, 807-815.	3.6	47
85	Structural proteomics by NMR spectroscopy. <i>Expert Review of Proteomics</i> , 2008, 5, 589-601.	3.0	42
86	Structural and Cell Adhesion Properties of Zebrafish Syndecan-4 Are Shared with Higher Vertebrates. <i>Journal of Biological Chemistry</i> , 2008, 283, 29322-29330.	3.4	33
87	Structure of the DNA-binding domain of NgTRF1 reveals unique features of plant telomere-binding proteins. <i>Nucleic Acids Research</i> , 2008, 36, 2739-2755.	14.5	28
88	Structure of an Atypical Orphan Response Regulator Protein Supports a New Phosphorylation-independent Regulatory Mechanism. <i>Journal of Biological Chemistry</i> , 2007, 282, 20667-20675.	3.4	49
89	Molecular dissection of the interaction between the SH3 domain and the SH2-Kinase Linker region in PTK6. <i>Biochemical and Biophysical Research Communications</i> , 2007, 362, 829-834.	2.1	17
90	Solution structure of the hypothetical novel $\hat{\epsilon}$ fold protein TA0956 from <i>Thermoplasma acidophilum</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 69, 444-447.	2.6	3

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91	Structural Basis of Syndecan-4 Phosphorylation as a Molecular Switch to Regulate Signaling. <i>Journal of Molecular Biology</i> , 2006, 355, 651-663.	4.2	82
92	Lys296 and Arg299 residues in the C-terminus of MD-ACO1 are essential for a 1-aminocyclopropane-1-carboxylate oxidase enzyme activity. <i>Journal of Structural Biology</i> , 2006, 156, 407-420.	2.8	29
93	Solution structure of TA1092, a ribosomal protein S24e from <i>Thermoplasma acidophilum</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 64, 1095-1097.	2.6	7
94	Solution structure of TA0895, a MoaD homologue from <i>Thermoplasma acidophilum</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 65, 1055-1057.	2.6	1
95	Crystallization and preliminary X-ray crystallographic study of HP1043, a <i>Helicobacter pylori</i> orphan response regulator. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2006, 1764, 989-991.	2.3	4
96	Protein folding using fragment assembly and physical energy function. <i>Journal of Chemical Physics</i> , 2006, 125, 194908.	3.0	9
97	In Vitro & In Vivo Effect of Parathyroid Hormone Analogue (1-14) Containing $\hat{\pm}$ -amino-iso-butyric Acid Residue (Aib)1,3. <i>Yonsei Medical Journal</i> , 2006, 47, 214.	2.2	3
98	Letter to the Editor: Resonance assignments and secondary structure of hPrxVI, a 25 kDa 1-cys human peroxiredoxin enzyme. <i>Journal of Biomolecular NMR</i> , 2005, 31, 267-268.	2.8	0
99	Functional and structural characteristics of anticancer peptide Pep27 analogues. <i>Cancer Cell International</i> , 2005, 5, 21.	4.1	48
100	NMR structure of the conserved novel-fold protein TA0743 from <i>Thermoplasma acidophilum</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 62, 819-821.	2.6	2
101	Structure and function of the potent cyclic and linear melanocortin analogues. <i>Journal of Structural Biology</i> , 2005, 150, 300-308.	2.8	10
102	Dynamic regulation of hypothalamic neuropeptide gene expression and food intake by melanocortin analogues and reversal with melanocortin-4 receptor antagonist. <i>Biochemical and Biophysical Research Communications</i> , 2005, 329, 1178-1185.	2.1	11
103	Structure and Function of a Minimal Receptor Activation Domain of Parathyroid Hormone. <i>Yonsei Medical Journal</i> , 2004, 45, 419.	2.2	4
104	Solution Structure and Backbone Dynamics of the Non-receptor Protein-tyrosine Kinase-6 Src Homology 2 Domain. <i>Journal of Biological Chemistry</i> , 2004, 279, 29700-29708.	3.4	23
105	Solution structure of a novel calcium binding protein, MTH1880, from <i>Methanobacterium thermoautotrophicum</i> . <i>Protein Science</i> , 2004, 13, 1148-1154.	7.6	10
106	Letter to the Editor: Backbone $^1H$ , $^{13}C$ and $^{15}N$ resonance assignments of the response regulator HP1043 from <i>Helicobacter pylori</i> . <i>Journal of Biomolecular NMR</i> , 2004, 28, 85-86.	2.8	5
107	The active site and substrate-binding mode of 1-aminocyclopropane-1-carboxylate oxidase determined by site-directed mutagenesis and comparative modelling studies. <i>Biochemical Journal</i> , 2004, 380, 339-346.	3.7	27
108	Structure-based Functional Discovery of Proteins: Structural Proteomics. <i>BMB Reports</i> , 2004, 37, 28-34.	2.4	12

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109	<sup>1</sup> H, <sup>13</sup> C and <sup>15</sup> N resonance assignments of rice telomere binding domain from <i>Oryza sativa</i> . <i>Journal of Biomolecular NMR</i> , 2003, 27, 89-90.	2.8	1
110	Crystal Structures of RbsD Leading to the Identification of Cytoplasmic Sugar-binding Proteins with a Novel Folding Architecture. <i>Journal of Biological Chemistry</i> , 2003, 278, 28173-28180.	3.4	20
111	NMR Studies on Turn Mimetic Analogs Derived from Melanocyte-stimulating Hormones. <i>BMB Reports</i> , 2003, 36, 552-557.	2.4	3
112	An NMR approach to structural proteomics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 1825-1830.	7.1	195
113	Regulation of Inositol Phospholipid Binding and Signaling through Syndecan-4. <i>Journal of Biological Chemistry</i> , 2002, 277, 49296-49303.	3.4	49
114	Identification of Domains Directing Specificity of Coupling to G-proteins for the Melanocortin MC3 and MC4 Receptors. <i>Journal of Biological Chemistry</i> , 2002, 277, 31310-31317.	3.4	37
115	Purification and Spectroscopic Characterization of the Human Protein Tyrosine Kinase-6 SH3 Domain. <i>BMB Reports</i> , 2002, 35, 343-347.	2.4	4
116	Chiral recognition of (18-crown-6)-tetracarboxylic acid as a chiral selector determined by NMR spectroscopy. <i>Perkin Transactions II RSC</i> , 2001, , 1685-1692.	1.1	67
117	Solution Structure of the Dimeric Cytoplasmic Domain of Syndecan-4,. <i>Biochemistry</i> , 2001, 40, 8471-8478.	2.5	48
118	Differential regulation of cAMP-mediated gene transcription and ligand selectivity by MC3R and MC4R melanocortin receptors. <i>FEBS Journal</i> , 2001, 268, 582-591.	0.2	38
119	Minimization of MC1R selectivity by modification of the core structure of $\hat{I}\pm$ -MSH-ND. <i>Chemistry and Biology</i> , 2001, 8, 857-870.	6.0	8
120	Complete sequence-specific <sup>1</sup> H, <sup>13</sup> C and <sup>15</sup> N resonance assignments of the human PTK6 SH2 domain. <i>Journal of Biomolecular NMR</i> , 2001, 19, 291-292.	2.8	8
121	Folding and Stability of Sweet Protein Single-chain Monellin. <i>Journal of Biological Chemistry</i> , 2001, 276, 44229-44238.	3.4	15
122	Solution structure of p21 <sup>Waf1/Cip1/Sdi1</sup> C-terminal domain bound to Cdk4. <i>Journal of Biomolecular Structure and Dynamics</i> , 2001, 19, 419-427.	3.5	4
123	The active site and substrates binding mode of malonyl-CoA synthetase determined by transferred nuclear Overhauser effect spectroscopy, site-directed mutagenesis, and comparative modeling studies. <i>Protein Science</i> , 2000, 9, 1294-1303.	7.6	16
124	Synthesis of Optically Active Phthaloyld-Aminoxy Acids from $\alpha$ -Amino Acids or $\beta$ -Hydroxy Acids as Building Blocks for the Preparation of Aminoxy Peptides. <i>Journal of Organic Chemistry</i> , 2000, 65, 7667-7675.	3.2	68
125	Type I beta-turn conformation is important for biological activity of the melanocyte-stimulating hormone analogues. <i>FEBS Journal</i> , 1999, 265, 430-440.	0.2	30
126	Solution structure of a new hypothalamic neuropeptide, human hypocretin-2/orexin-B. <i>FEBS Journal</i> , 1999, 266, 831-839.	0.2	68

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127	Identification of residues essential for a two-step reaction by malonyl-CoA synthetase from <i>Rhizobium trifolii</i> . <i>Biochemical Journal</i> , 1999, 344, 159-166.	3.7	27
128	Solution structures of the melanocyte-stimulating hormones by two-dimensional NMR spectroscopy and dynamical simulated-annealing calculations. <i>FEBS Journal</i> , 1998, 257, 31-40.	0.2	22
129	Solution Structure of a Syndecan-4 Cytoplasmic Domain and Its Interaction with Phosphatidylinositol 4,5-Bisphosphate. <i>Journal of Biological Chemistry</i> , 1998, 273, 13022-13029.	3.4	86
130	Solution structure of the tetrameric minimum transforming domain of p53. <i>Nature Structural and Molecular Biology</i> , 1994, 1, 877-890.	8.2	267