

# Bong-Jin Lee

## List of Publications by Year in descending order

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187  
papers

3,440  
citations

159585

30  
h-index

175258

52  
g-index

189  
all docs

189  
docs citations

189  
times ranked

4779  
citing authors

#	ARTICLE	IF	CITATIONS
1	Role of PemI in the <i>Staphylococcus aureus</i> PemK toxin-antitoxin complex: PemI controls PemK by acting as a PemK loop mimic. <i>Nucleic Acids Research</i> , 2022, 50, 2319-2333.	14.5	1
2	The structural and functional investigation of the VapBC43 complex from <i>Mycobacterium tuberculosis</i> . <i>Biochemical and Biophysical Research Communications</i> , 2022, 616, 19-25.	2.1	2
3	Abstract 1800: Novel NSDHL inhibitor (Compound 9) exerts anti-proliferative and cytotoxic activity in breast cancer cells. <i>Cancer Research</i> , 2022, 82, 1800-1800.	0.9	0
4	Crystal structures of human NSDHL and development of its novel inhibitor with the potential to suppress EGFR activity. <i>Cellular and Molecular Life Sciences</i> , 2021, 78, 207-225.	5.4	9
5	Structure-based design of peptides that trigger <i>Streptococcus pneumoniae</i> cell death. <i>FEBS Journal</i> , 2021, 288, 1546-1564.	4.7	13
6	Toxin-Activating Stapled Peptides Discovered by Structural Analysis Were Identified as New Therapeutic Candidates That Trigger Antibacterial Activity against <i>Mycobacterium tuberculosis</i> in the <i>Mycobacterium smegmatis</i> Model. <i>Microorganisms</i> , 2021, 9, 568.	3.6	7
7	How Bacterial Redox Sensors Transmit Redox Signals via Structural Changes. <i>Antioxidants</i> , 2021, 10, 502.	5.1	5
8	Structural and functional analysis of the <i>Klebsiella pneumoniae</i> MazEF toxin-antitoxin system. <i>IUCr</i> , 2021, 8, 362-371.	2.2	4
9	Structural and functional studies of SAV1707 from <i>Staphylococcus aureus</i> elucidate its distinct metal-dependent activity and a crucial residue for catalysis. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 587-598.	2.3	0
10	Molecular Interactions between Two LMP2A PY Motifs of EBV and WW Domains of E3 Ubiquitin Ligase AIP4. <i>Life</i> , 2021, 11, 379.	2.4	2
11	Structural Investigation of Self-Assembly and Target Binding of Anti-CRISPR AcrIIc2. <i>CRISPR Journal</i> , 2021, 4, 448-458.	2.9	1
12	Structural and functional study of SaAcP, an acylphosphatase from <i>Staphylococcus aureus</i> . <i>Biochemical and Biophysical Research Communications</i> , 2020, 532, 173-178.	2.1	2
13	Structure-Based <i>De Novo</i> Design of <i>Mycobacterium Tuberculosis</i> VapC-Activating Stapled Peptides. <i>ACS Chemical Biology</i> , 2020, 15, 2493-2498.	3.4	11
14	Structural and Functional Study of the <i>Klebsiella pneumoniae</i> VapBC Toxin-Antitoxin System, Including the Development of an Inhibitor That Activates VapC. <i>Journal of Medicinal Chemistry</i> , 2020, 63, 13669-13679.	6.4	9
15	mRNA Interferase <i>Bacillus cereus</i> BC0266 Shows MazF-Like Characteristics Through Structural and Functional Study. <i>Toxins</i> , 2020, 12, 380.	3.4	4
16	Crystal structure of the YoeBSa1-YefMSa1 complex from <i>Staphylococcus aureus</i> . <i>Biochemical and Biophysical Research Communications</i> , 2020, 527, 264-269.	2.1	1
17	The grease trap: uncovering the mechanism of the hydrophobic lid in <i>Cutibacterium acnes</i> lipase. <i>Journal of Lipid Research</i> , 2020, 61, 722-733.	4.2	11
18	Crystal structure of proteolyzed VapBC and DNA-bound VapBC from <i>Salmonella enterica</i> Typhimurium LT2 and VapC as a putative Ca <sup>2+</sup> -dependent ribonuclease. <i>FASEB Journal</i> , 2020, 34, 3051-3068.	0.5	3

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19	Induced DNA bending by unique dimerization of HigA antitoxin. <i>IUCr</i> , 2020, 7, 748-760.	2.2	6
20	A structural study of TatD from <i>Staphylococcus aureus</i> elucidates a putative DNA-binding mode of a Mg <sup>2+</sup> -dependent nuclease. <i>IUCr</i> , 2020, 7, 509-521.	2.2	6
21	Anti-CRISPR AcrIIIC3 discriminates between Cas9 orthologs via targeting the variable surface of the HNH nuclease domain. <i>FEBS Journal</i> , 2019, 286, 4661-4674.	4.7	27
22	The crystal structure of AcrR from <i>Mycobacterium tuberculosis</i> reveals a one-component transcriptional regulation mechanism. <i>FEBS Open Bio</i> , 2019, 9, 1713-1725.	2.3	9
23	A maresin 1/ROR $\alpha$ /12-lipoxygenase autoregulatory circuit prevents inflammation and progression of nonalcoholic steatohepatitis. <i>Journal of Clinical Investigation</i> , 2019, 129, 1684-1698.	8.2	109
24	A novel chlorination-induced ribonuclease YabJ from <i>Staphylococcus aureus</i> . <i>Bioscience Reports</i> , 2018, 38, .	2.4	12
25	A Systematic Overview of Type II and III Toxin-Antitoxin Systems with a Focus on Druggability. <i>Toxins</i> , 2018, 10, 515.	3.4	47
26	Effects of lysine-to-arginine substitution on antimicrobial activity of cationic stapled heptapeptides. <i>Archives of Pharmacal Research</i> , 2018, 41, 1092-1097.	6.3	21
27	Unique N-terminal extension domain of human asparaginyl-tRNA synthetase elicits CCR3-mediated chemokine activity. <i>International Journal of Biological Macromolecules</i> , 2018, 120, 835-845.	7.5	12
28	Regulatory mechanisms of thiol-based redox sensors: lessons learned from structural studies on prokaryotic redox sensors. <i>Archives of Pharmacal Research</i> , 2018, 41, 583-593.	6.3	18
29	Functional insights into the <i>Streptococcus pneumoniae</i> HicBA toxin-antitoxin system based on a structural study. <i>Nucleic Acids Research</i> , 2018, 46, 6371-6386.	14.5	32
30	C-terminal dimerization of apo-cyclic $\alpha$ -AMP receptor protein validated in solution. <i>FEBS Letters</i> , 2017, 591, 1064-1070.	2.8	2
31	Functional details of the <i>Mycobacterium tuberculosis</i> VapBC26 toxin-antitoxin system based on a structural study: insights into unique binding and antibiotic peptides. <i>Nucleic Acids Research</i> , 2017, 45, 8564-8580.	14.5	44
32	Structural analyses of the MazEF4 toxin-antitoxin pair in <i>Mycobacterium tuberculosis</i> provide evidence for a unique extracellular death factor. <i>Journal of Biological Chemistry</i> , 2017, 292, 18832-18847.	3.4	25
33	Structural and functional studies of SAV0551 from <i>Staphylococcus aureus</i> as a chaperone and glyoxalase III. <i>Bioscience Reports</i> , 2017, 37, .	2.4	6
34	Antimicrobial activity and stability of stapled helices of polybia-MP1. <i>Archives of Pharmacal Research</i> , 2017, 40, 1414-1419.	6.3	40
35	Mono-substitution effects on antimicrobial activity of stapled heptapeptides. <i>Archives of Pharmacal Research</i> , 2017, 40, 713-719.	6.3	18
36	Structure and dynamics study of translation initiation factor 1 from <i>Staphylococcus aureus</i> suggests its RNA binding mode. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2017, 1865, 65-75.	2.3	3

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37	Structural and Biochemical Properties of Novel Self-Cleaving Ribozymes. <i>Molecules</i> , 2017, 22, 678.	3.8	29
38	Application of Solution NMR to Structural Studies on $\alpha$ -Helical Integral Membrane Proteins. <i>Molecules</i> , 2017, 22, 1347.	3.8	12
39	Solution NMR Studies of Mycobacterium tuberculosis Proteins for Antibiotic Target Discovery. <i>Molecules</i> , 2017, 22, 1447.	3.8	2
40	Cellular Membrane Composition Requirement by Antimicrobial and Anticancer Peptide GA-K4. <i>Protein and Peptide Letters</i> , 2017, 24, 197-205.	0.9	1
41	Elucidating the Dynamic Properties of Globular Protein using Predicted Order Parameters and 15N NMR Relaxation. <i>Journal of the Korean Magnetic Resonance Society</i> , 2017, 21, 26-30.	0.1	0
42	Identification of Enzymatic Catalysis of PncA using 1H-NMR. <i>Journal of the Korean Magnetic Resonance Society</i> , 2017, 21, 85-89.	0.1	0
43	Structure, Biology, and Therapeutic Application of Toxin-Antitoxin Systems in Pathogenic Bacteria. <i>Toxins</i> , 2016, 8, 305.	3.4	101
44	Quercetin Directly Interacts with Vitamin D Receptor (VDR): Structural Implication of VDR Activation by Quercetin. <i>Biomolecules and Therapeutics</i> , 2016, 24, 191-198.	2.4	21
45	Two distinct mechanisms of transcriptional regulation by the redox sensor YodB. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E5202-11.	7.1	19
46	Antimicrobial and Hemolytic Activity of Stapled Heptapeptide Dimers. <i>Bulletin of the Korean Chemical Society</i> , 2016, 37, 1199-1203.	1.9	14
47	Solution NMR studies on Helicobacter pylori proteins for antibiotic target discovery. <i>Expert Opinion on Drug Discovery</i> , 2016, 11, 681-693.	5.0	0
48	Structural and functional insight into the different oxidation states of SAV1875 from Staphylococcus aureus. <i>Biochemical Journal</i> , 2016, 473, 55-66.	3.7	6
49	Identification of novel scaffolds for potential anti-Helicobacter pylori agents based on the crystal structure of H. pylori 3-deoxy- d -manno-octulosonate 8-phosphate synthase ( Hp KDO8PS). <i>European Journal of Medicinal Chemistry</i> , 2016, 108, 188-202.	5.5	4
50	Alba from Thermoplasma volcanium belongs to $\alpha$ -NAT's: An insight into the structural aspects of Tv Alba and its acetylation by Tv Ard1. <i>Archives of Biochemistry and Biophysics</i> , 2016, 590, 90-100.	3.0	3
51	Structural and functional studies of the Mycobacterium tuberculosis VapBC30 toxin-antitoxin system. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2016, 72, s209-s209.	0.1	1
52	Secondary structure analysis of MRA1997 from Mycobacterium tuberculosis and characterization of DNA binding property. <i>Journal of the Korean Magnetic Resonance Society</i> , 2016, 20, 36-40.	0.1	0
53	Crystal structure of YwpF from Staphylococcus aureus reveals its architecture comprised of a $\beta$ -barrel core domain resembling type VI secretion system proteins and a two-helix pair. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2015, 71, s273-s273.	0.1	0
54	Crystal structure of PhoU from Pseudomonas aeruginosa, a negative regulator of the Pho regulon. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2015, 71, s231-s231.	0.1	0

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55	Crystal structure of M. tuberculosis' toxin in complex with its neutralizing antitoxin. Acta Crystallographica Section A: Foundations and Advances, 2015, 71, s229-s229.	0.1	0
56	A critical element of the light-induced quaternary structural changes in $\gamma$ -TV-A $\alpha$ -LOV. Protein Science, 2015, 24, 1997-2007.	7.6	6
57	$\alpha$ -Capping Effects of Stapled Heptapeptides on Antimicrobial and Hemolytic Activities. Bulletin of the Korean Chemical Society, 2015, 36, 2511-2515.	1.9	10
58	Structure-based functional identification of Helicobacter pylori HP0268 as a nuclease with both DNA nicking and RNase activities. Nucleic Acids Research, 2015, 43, 5194-5207.	14.5	13
59	Crystal structure of YwpF from <i>S. taphylococcus aureus</i> reveals its architecture comprised of a $\beta$ -barrel core domain resembling type VI secretion system proteins and a two-helix pair. Proteins: Structure, Function and Bioinformatics, 2015, 83, 781-788.	2.6	0
60	Structural insight into the interaction between the Hox and HMGB1 and understanding of the HMGB1-enhancing effect of Hox-DNA binding. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2015, 1854, 449-459.	2.3	5
61	Structural and functional studies of the <i>Mycobacterium tuberculosis</i> VapBC30 toxin-antitoxin system: implications for the design of novel antimicrobial peptides. Nucleic Acids Research, 2015, 43, 7624-7637.	14.5	68
62	Antimicrobial activity of doubly-stapled alanine/lysine-based peptides. Bioorganic and Medicinal Chemistry Letters, 2015, 25, 4016-4019.	2.2	39
63	Radiological Assessment of the Effect of Congenital C3-4 Synostosis on Adjacent Segments. Asian Spine Journal, 2015, 9, 895.	2.0	1
64	Backbone assignments of $^1\text{H}$ , $^{15}\text{N}$ and $^{13}\text{C}$ resonances and secondary structure prediction of MRA1997 from <i>Mycobacterium tuberculosis</i> H37Rv. Journal of the Korean Magnetic Resonance Society, 2015, 19, 49-53.	0.1	1
65	Structural stability of CD1 domain of human mitotic checkpoint serine/threonine-protein kinase, Bub1. Journal of the Korean Magnetic Resonance Society, 2015, 19, 88-94.	0.1	1
66	pH Effect on the Structure of Reduced NifU-like Protein from Helicobacter pylori. Journal of the Korean Magnetic Resonance Society, 2015, 19, 106-111.	0.1	0
67	Bacterial peptide deformylase inhibitor PMT analogs inhibit cancer cell growth by interacting with human peptide deformylase. Science Bulletin, 2014, 59, 4274-4282.	1.7	1
68	Crystal structure of toxin HP0892 from <i>Helicobacter pylori</i> with two Zn(II) at 1.8 Å... resolution. Protein Science, 2014, 23, 819-832.	7.6	3
69	Antimicrobial peptides: therapeutic potentials. Expert Review of Anti-Infective Therapy, 2014, 12, 1477-1486.	4.4	167
70	Structures of inactive CRP species reveal the atomic details of the allosteric transition that discriminates cyclic nucleotide second messengers. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 1726-1742.	2.5	17
71	$\beta$ -Arm flexibility of HU from <i>Staphylococcus aureus</i> dictates the DNA-binding and recognition mechanism. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 3273-3289.	2.5	36
72	Structure of Thermoplasma volcanium Ard1 belongs to N-acetyltransferase family member suggesting multiple ligand binding modes with acetyl coenzyme A and coenzyme A. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 1790-1797.	2.3	14

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73	Crystal structure of JHP933 from <i>Helicobacter pylori</i> J99 shows two-domain architecture with a DUF1814 family nucleotidyltransferase domain and a helical bundle domain. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 2275-2281.	2.6	3
74	Crystal structure of PhoU from <i>Pseudomonas aeruginosa</i> , a negative regulator of the Pho regulon. <i>Journal of Structural Biology</i> , 2014, 188, 22-29.	2.8	11
75	Asteropsins B $\alpha$ -D, sponge-derived knottins with potential utility as a novel scaffold for oral peptide drugs. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2014, 1840, 977-984.	2.4	15
76	Solution structure of Rv0569, potent hypoxic signal transduction protein, from <i>Mycobacterium tuberculosis</i> . <i>Tuberculosis</i> , 2014, 94, 43-50.	1.9	1
77	De Novo Design and Their Antimicrobial Activity of Stapled Amphipathic Helices of Heptapeptides. <i>Bulletin of the Korean Chemical Society</i> , 2014, 35, 3632-3636.	1.9	18
78	Enhanced Chemical Shift Analysis for Secondary Structure prediction of protein. <i>Journal of the Korean Magnetic Resonance Society</i> , 2014, 18, 36-40.	0.1	1
79	<sup>1</sup> H, <sup>13</sup> C and <sup>15</sup> N chemical shift assignments of Ninjurin1 Extracellular N-terminal Domain. <i>Biomolecular NMR Assignments</i> , 2013, 7, 159-162.	0.8	1
80	Crystal structure of apo and copper bound HP0894 toxin from <i>Helicobacter pylori</i> 26695 and insight into mRNase activity. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013, 1834, 2579-2590.	2.3	7
81	Truncated and constrained helical analogs of antimicrobial esculentin-2EM. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2013, 23, 6717-6720.	2.2	30
82	Structural overview of toxin-antitoxin systems in infectious bacteria: A target for developing antimicrobial agents. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013, 1834, 1155-1167.	2.3	66
83	Structural Characterization of HP1264 Reveals a Novel Fold for the Flavin Mononucleotide Binding Protein. <i>Biochemistry</i> , 2013, 52, 1583-1593.	2.5	3
84	Identification of Chromosomal HP0892-HP0893 Toxin-Antitoxin Proteins in <i>Helicobacter pylori</i> and Structural Elucidation of Their Protein-Protein Interaction. <i>Journal of Biological Chemistry</i> , 2013, 288, 6004-6013.	3.4	16
85	Overexpression, crystallization and preliminary X-ray crystallographic analysis of hypothetical protein SAV0479 from <i>Staphylococcus aureus</i> Mu50. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 405-407.	0.7	0
86	NMR Study on Small Proteins from <i>Helicobacter pylori</i> for Antibiotic Target Discovery: A Review. <i>Molecules</i> , 2013, 18, 13410-13424.	3.8	2
87	Structural Characterization of de Novo Designed L5K5W Model Peptide Isomers with Potent Antimicrobial and Varied Hemolytic Activities. <i>Molecules</i> , 2013, 18, 859-876.	3.8	16
88	Backbone <sup>1</sup> H, <sup>15</sup> N, and <sup>13</sup> C Resonances Assignment and Secondary Structure Prediction of SAV0506 from <i>Staphylococcus aureus</i> . <i>Journal of the Korean Magnetic Resonance Society</i> , 2013, 17, 54-58.	0.1	1
89	Identification of Potent Inhibitors against Human Peptide Deformylase as Anticancer Agents. <i>Bulletin of the Korean Chemical Society</i> , 2013, 34, 3885-3887.	1.9	0
90	Backbone <sup>1</sup> H, <sup>15</sup> N, and <sup>13</sup> C resonance assignments and secondary structure prediction of NifU-like protein, HP1492 from <i>Helicobacter Pylori</i> . <i>Journal of the Korean Magnetic Resonance Society</i> , 2013, 17, 105-110.	0.1	1

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91	Structural Analysis of Hypothetical Proteins from <i>Helicobacter pylori</i> : An Approach to Estimate Functions of Unknown or Hypothetical Proteins. <i>International Journal of Molecular Sciences</i> , 2012, 13, 7109-7137.	4.1	17
92	Tetraspan TM4SF5-dependent direct activation of FAK and metastatic potential of hepatocarcinoma cells. <i>Journal of Cell Science</i> , 2012, 125, 5960-5973.	2.0	45
93	Structural and biochemical characterization of HP0315 from <i>Helicobacter pylori</i> as a VapD protein with an endoribonuclease activity. <i>Nucleic Acids Research</i> , 2012, 40, 4216-4228.	14.5	46
94	Antimicrobial Peptides for Therapeutic Applications: A Review. <i>Molecules</i> , 2012, 17, 12276-12286.	3.8	391
95	Dipeptidyl peptidase-4 inhibitor with $\hat{1}^2$ -amino amide scaffold: Synthesis, SAR and biological evaluation. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2012, 22, 5545-5549.	2.2	12
96	Backbone resonances assignment of 19 kDa CD1 domain of human mitotic checkpoint serine/threonine-protein kinase, Bub1. <i>Biomolecular NMR Assignments</i> , 2012, 6, 109-113.	0.8	3
97	Antimicrobial peptides: Their physicochemical properties and therapeutic application. <i>Archives of Pharmacal Research</i> , 2012, 35, 409-413.	6.3	66
98	Anticancer activity of undecapeptide analogues derived from antimicrobial peptide, Brevinin-1EMa. <i>Archives of Pharmacal Research</i> , 2012, 35, 791-799.	6.3	17
99	Solid-state NMR Study on Membrane Protein Structure in Biological Condition. <i>Journal of the Korean Magnetic Resonance Society</i> , 2012, 16, 103-110.	0.1	0
100	Backbone <sup>1</sup> H, <sup>15</sup> N, and <sup>13</sup> C resonance assignments and secondary structure prediction of SAV2228 (translation initiation factor-1) from <i>Staphylococcus aureus</i> . <i>Journal of the Korean Magnetic Resonance Society</i> , 2012, 16, 162-171.	0.1	0
101	Identification of H-Ras-Specific Motif for the Activation of Invasive Signaling Program in Human Breast Epithelial Cells. <i>Neoplasia</i> , 2011, 13, 98-IN1.	5.3	30
102	Solution structure of UIM and interaction of tandem ubiquitin binding domains in STAM1 with ubiquitin. <i>Biochemical and Biophysical Research Communications</i> , 2011, 405, 24-30.	2.1	10
103	Radiographic Outcomes After Treatment of Pediatric Supracondylar Humerus Fractures Using a Treatment-Based Classification System. <i>Journal of Orthopaedic Trauma</i> , 2011, 25, 18-25.	1.4	5
104	Activity Optimization of an Undecapeptide Analogue Derived from a Frog-Skin Antimicrobial Peptide. <i>Molecules and Cells</i> , 2011, 31, 49-54.	2.6	22
105	Backbone <sup>1</sup> H, <sup>13</sup> C, and <sup>15</sup> N assignments for the tandem ubiquitin binding domains of signal transducing adapter molecule 1. <i>Biomolecular NMR Assignments</i> , 2011, 5, 51-54.	0.8	3
106	Peptide deformylase inhibitors with non-peptide scaffold: Synthesis and structure-activity relationships. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2011, 21, 133-136.	2.2	10
107	Separation and structural elucidation of a novel analogue of vardenafil included as an adulterant in a dietary supplement by liquid chromatography-electrospray ionization mass spectrometry, infrared spectroscopy and nuclear magnetic resonance spectroscopy. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2011, 54, 491-496.	2.8	43
108	A novel approach to simultaneous screening and confirmation of regulated pharmaceutical compounds in dietary supplements by LC/MS/MS with an information-dependent acquisition method. <i>Food Additives and Contaminants - Part A Chemistry, Analysis, Control, Exposure and Risk Assessment</i> , 2011, 28, 396-407.	2.3	45



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109	Functional Identification of Toxin-Antitoxin Molecules from <i>Helicobacter pylori</i> 26695 and Structural Elucidation of the Molecular Interactions. <i>Journal of Biological Chemistry</i> , 2011, 286, 4842-4853.	3.4	26
110	Solution Structure of Water-soluble Mutant of Crambin and Implication for Protein Solubility. <i>Bulletin of the Korean Chemical Society</i> , 2011, 32, 1640-1644.	1.9	1
111	<sup>1</sup> H, <sup>15</sup> N and <sup>13</sup> C resonance assignment and secondary structure prediction of ss-DNA binding protein 12RNP2 precursor, HP0827 from <i>Helicobacter pylori</i> . <i>Journal of the Korean Magnetic Resonance Society</i> , 2011, 15, 69-79.	0.1	0
112	On the Importance of Transition Regions for Automatic Speaker Recognition. <i>IEICE Transactions on Information and Systems</i> , 2010, E93-D, 197-200.	0.7	0
113	Solution Structure of Antimicrobial Peptide Esculentin-1c from Skin Secretion of <i>Rana esculenta</i> . <i>Molecules and Cells</i> , 2010, 30, 435-441.	2.6	7
114	Expression, crystallization, and preliminary X-ray crystallographic analysis of putative SpoVG from <i>Staphylococcus aureus</i> . <i>Archives of Pharmacal Research</i> , 2010, 33, 1285-1288.	6.3	4
115	Palmar Scaphoid Dislocation Associated With Dorsal Perilunate Dislocation: Case Report. <i>Journal of Hand Surgery</i> , 2010, 35, 726-731.	1.6	10
116	Codon optimization enhances protein expression of human peptide deformylase in <i>E. coli</i> . <i>Protein Expression and Purification</i> , 2010, 70, 224-230.	1.3	24
117	Peptide deformylase inhibitors with retro-amide scaffold: Synthesis and structure-activity relationships. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2010, 20, 4317-4319.	2.2	12
118	Low Grade Fibromyxoid Sarcoma in Thigh. <i>Clinics in Orthopedic Surgery</i> , 2009, 1, 240.	2.2	13
119	NMR Solution Structure of HP0827 (O25501_HELPY) from <i>Helicobacter pylori</i> : Model of the Possible RNA-binding Site. <i>Journal of Biochemistry</i> , 2009, 146, 667-674.	1.7	4
120	Crystal Structure of Hypothetical Protein HP0062 (O24902_HELPY) from <i>Helicobacter pylori</i> at 1.65 Å Resolution. <i>Journal of Biochemistry</i> , 2009, 146, 535-540.	1.7	6
121	Identification of a novel ubiquitin binding site of STAM1 VHS domain by NMR spectroscopy. <i>FEBS Letters</i> , 2009, 583, 287-292.	2.8	22
122	Solution structure of hypothetical protein HP1423 (Y1423_HELPY) reveals the presence of $\hat{1}\pm$ L motif related to RNA binding. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 75, 252-257.	2.6	4
123	Crystal structure of the dimerization domain of human filamin A. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 75, 258-263.	2.6	18
124	<i>De novo</i> generation of antimicrobial LK peptides with a single tryptophan at the critical amphipathic interface. <i>Journal of Peptide Science</i> , 2009, 15, 583-588.	1.4	39
125	Structural overview on the allosteric activation of cyclic AMP receptor protein. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2009, 1794, 1299-1308.	2.3	61
126	Action mechanism and structural requirements of the antimicrobial peptides, gaegurins. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2009, 1788, 1620-1629.	2.6	43



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127	Phonetically optimized speaker modeling for robust speaker recognition. Journal of the Acoustical Society of America, 2009, 126, EL100-EL106.	1.1	4
128	HP0902 from <i>Helicobacter pylori</i> is a thermostable, dimeric protein belonging to an all- $\beta^2$ topology of the cupin superfamily. BMB Reports, 2009, 42, 387-392.	2.4	9
129	Solution structure of conserved hypothetical protein HP0892 from <i>Helicobacter pylori</i> . Proteins: Structure, Function and Bioinformatics, 2008, 70, 599-602.	2.6	8
130	Structural insight into the distinct properties of copper transport by the <i>Helicobacter pylori</i> CopP protein. Proteins: Structure, Function and Bioinformatics, 2008, 71, 1007-1019.	2.6	9
131	Bax Inhibitor-1 Is a pH-dependent Regulator of Ca <sup>2+</sup> Channel Activity in the Endoplasmic Reticulum. Journal of Biological Chemistry, 2008, 283, 15946-15955.	3.4	101
132	Membrane binding properties of EBV gp110 C-terminal domain; evidences for structural transition in the membrane environment. Virology, 2008, 379, 181-190.	2.4	8
133	Interdomain interaction of cyclic AMP receptor protein in the absence of cyclic AMP. Journal of Biochemistry, 2008, 143, 163-167.	1.7	8
134	2P-006 Structural studies of the VHS domain of human STAM1 protein Structural studies of the VHS domain of human STAM1 protein(The 46th Annual Meeting of the Biophysical Society of Japan). Seibutsu Butsuri, 2008, 48, S75-S76.	0.1	0
135	2P-053 Structural and Functional Studies on the conserved hypothetical protein HP0894 from <i>Helicobacter pylori</i> (The 46th Annual Meeting of the Biophysical Society of Japan). Seibutsu Butsuri, 2008, 48, S83.	0.1	0
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