

Bong-Jin Lee

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1387408/publications.pdf>

Version: 2024-02-01

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	Antimicrobial Peptides for Therapeutic Applications: A Review. <i>Molecules</i> , 2012, 17, 12276-12286.	3.8	391
2	Paraplegia as a Complication of Percutaneous Vertebroplasty With Polymethylmethacrylate. <i>Spine</i> , 2002, 27, E419-E422.	2.0	226
3	Antimicrobial peptides: therapeutic potentials. <i>Expert Review of Anti-Infective Therapy</i> , 2014, 12, 1477-1486.	4.4	167
4	A maresin 1/ROR α /12-lipoxygenase autoregulatory circuit prevents inflammation and progression of nonalcoholic steatohepatitis. <i>Journal of Clinical Investigation</i> , 2019, 129, 1684-1698.	8.2	109
5	Bax Inhibitor-1 Is a pH-dependent Regulator of Ca ²⁺ Channel Activity in the Endoplasmic Reticulum. <i>Journal of Biological Chemistry</i> , 2008, 283, 15946-15955.	3.4	101
6	Structure, Biology, and Therapeutic Application of Toxin α Antitoxin Systems in Pathogenic Bacteria. <i>Toxins</i> , 2016, 8, 305.	3.4	101
7	Structural study of novel antimicrobial peptides, nigrocins, isolated from <i>Rana nigromaculata</i> . <i>FEBS Letters</i> , 2001, 507, 95-100.	2.8	86
8	Structural and functional studies of the <i>Mycobacterium tuberculosis</i> VapBC30 toxin-antitoxin system: implications for the design of novel antimicrobial peptides. <i>Nucleic Acids Research</i> , 2015, 43, 7624-7637.	14.5	68
9	Antimicrobial peptides: Their physicochemical properties and therapeutic application. <i>Archives of Pharmacal Research</i> , 2012, 35, 409-413.	6.3	66
10	Structural overview of toxin α 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
11	Systematic Peptide Engineering and Structural Characterization to Search for the Shortest Antimicrobial Peptide Analogue of Gaegurin 5. <i>Journal of Biological Chemistry</i> , 2004, 279, 14784-14791.	3.4	62
12	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
13	Structural Understanding of the Allosteric Conformational Change of Cyclic AMP Receptor Protein by Cyclic AMP Binding. <i>Biochemistry</i> , 2000, 39, 13953-13962.	2.5	59
14	Role of proline, cysteine and a disulphide bridge in the structure and activity of the anti-microbial peptide gaegurin 5. <i>Biochemical Journal</i> , 2002, 368, 171-182.	3.7	48
15	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
16	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
17	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
18	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

#	ARTICLE	IF	CITATIONS
19	Functional details of the Mycobacterium tuberculosis 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
20	Solution structure of the antimicrobial peptide gaegurin 4 by 1H and 15N nuclear magnetic resonance spectroscopy. <i>FEBS Journal</i> , 2000, 267, 2695-2704.	0.2	43
21	Action mechanism and structural requirements of the antimicrobial peptides, gaegurins. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2009, 1788, 1620-1629.	2.6	43
22	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
23	Structural Determinants for the Membrane Interaction of Novel Bioactive Undecapeptides Derived from Gaegurin 5. <i>Journal of Medicinal Chemistry</i> , 2006, 49, 4886-4895.	6.4	41
24	Antimicrobial activity and stability of stapled helices of polybia-MP1. <i>Archives of Pharmacal Research</i> , 2017, 40, 1414-1419.	6.3	40
25	De novo 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
26	Antimicrobial activity of doubly-stapled alanine/lysine-based peptides. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2015, 25, 4016-4019.	2.2	39
27	Effects of a tryptophanyl substitution on the structure and antimicrobial activity of C-terminally truncated gaegurin 4. <i>FEBS Journal</i> , 2002, 269, 4367-4374.	0.2	38
28	Arm flexibility of HU from <i>Staphylococcus aureus</i> dictates the DNA-binding and recognition mechanism. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 3273-3289.	2.5	36
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	Identification of H-Ras-Specific Motif for the Activation of Invasive Signaling Program in Human Breast Epithelial Cells. <i>Neoplasia</i> , 2011, 13, 98-111.	5.3	30
31	Truncated and constrained helical analogs of antimicrobial esculentin-2EM. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2013, 23, 6717-6720.	2.2	30
32	Solution structure and p43 binding of the p38 leucine zipper motif: coiled-coil interactions mediate the association between p38 and p43. <i>FEBS Letters</i> , 2003, 542, 119-124.	2.8	29
33	Structural and Biochemical Properties of Novel Self-Cleaving Ribozymes. <i>Molecules</i> , 2017, 22, 678.	3.8	29
34	Stoichiometry and Structural Effect of the Cyclic Nucleotide Binding to Cyclic AMP Receptor Protein. <i>Journal of Biological Chemistry</i> , 2002, 277, 11450-11455.	3.4	28
35	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
36	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

#	ARTICLE	IF	CITATIONS
37	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
38	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
39	Purification and characterization of Moran 20K from <i>Morus alba</i> . <i>Archives of Pharmacal Research</i> , 1999, 22, 9-12.	6.3	23
40	Solution structure and membrane-binding property of the N-terminal tail domain of human annexin I. <i>FEBS Letters</i> , 2000, 484, 241-245.	2.8	22
41	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
42	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
43	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
44	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
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	Effects of salt and nickel ion on the conformational stability of <i>Bacillus pasteurii</i> UreE. <i>FEBS Letters</i> , 2002, 522, 135-140.	2.8	18
47	Crystal structure of the dimerization domain of human filamin A. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 75, 258-263.	2.6	18
48	Mono-substitution effects on antimicrobial activity of stapled heptapeptides. <i>Archives of Pharmacal Research</i> , 2017, 40, 713-719.	6.3	18
49	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
50	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
51	Molecular domain organization of BldD, an essential transcriptional regulator for developmental process of <i>Streptomyces coelicolor</i> A3(2). <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 68, 344-352.	2.6	17
52	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
53	Anticancer activity of undecapeptide analogues derived from antimicrobial peptide, Brevinin-1EMa. <i>Archives of Pharmacal Research</i> , 2012, 35, 791-799.	6.3	17
54	Structures of inactive CRP species reveal the atomic details of the allosteric transition that discriminates cyclic nucleotide second messengers. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 1726-1742.	2.5	17

#	ARTICLE	IF	CITATIONS
55	Structure-activity relationships of antimicrobial peptides from the skin of <i>Rana esculenta</i> inhabiting in Korea. <i>Molecules and Cells</i> , 2004, 17, 469-76.	2.6	17
56	Conformational resemblance between the structures of integrin-activating pentapeptides derived from β 2ig-h3 and RGD peptide analogues in a membrane environment. <i>Peptides</i> , 2004, 25, 199-205.	2.4	16
57	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
58	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
59	Structural Characterization of the Nickel-binding Properties of <i>Bacillus pasteurii</i> Urease Accessory Protein (Ure)E in Solution. <i>Journal of Biological Chemistry</i> , 2004, 279, 17466-17472.	3.4	15
60	Asteropsins β â€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
61	NMR analyses of the interactions of human annexin I with ATP, Ca ²⁺ , and Mg ²⁺ . <i>FEBS Letters</i> , 1998, 425, 523-527.	2.8	14
62	Structure of <i>Thermoplasma volcanium</i> Ard1 belongs to N-acetyltransferase family member suggesting multiple ligand binding modes with acetyl coenzyme A and coenzyme A. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 1790-1797.	2.3	14
63	Antimicrobial and Hemolytic Activity of Stapled Heptapeptide Dimers. <i>Bulletin of the Korean Chemical Society</i> , 2016, 37, 1199-1203.	1.9	14
64	Irreducible Fracture-Dislocation of the Ankle Caused by an Entrapped Medial Malleolus at the Syndesmosis. <i>Journal of Orthopaedic Trauma</i> , 2008, 22, 209-212.	1.4	13
65	Low Grade Fibromyxoid Sarcoma in Thigh. <i>Clinics in Orthopedic Surgery</i> , 2009, 1, 240.	2.2	13
66	Structure-based functional identification of <i>Helicobacter pylori</i> HP0268 as a nuclease with both DNA nicking and RNase activities. <i>Nucleic Acids Research</i> , 2015, 43, 5194-5207.	14.5	13
67	Structureâ€based design of peptides that trigger <i>Streptococcus pneumoniae</i> cell death. <i>FEBS Journal</i> , 2021, 288, 1546-1564.	4.7	13
68	Backbone NMR assignments of a high molecular weight protein (47 kDa), cyclic AMP receptor protein (apo-CRP). <i>Journal of Biomolecular NMR</i> , 2000, 16, 79-80.	2.8	12
69	Peptide deformylase inhibitors with retro-amide scaffold: Synthesis and structureâ€activity relationships. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2010, 20, 4317-4319.	2.2	12
70	Dipeptidyl peptidase-4 inhibitor with β -amino amide scaffold: Synthesis, SAR and biological evaluation. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2012, 22, 5545-5549.	2.2	12
71	Application of Solution NMR to Structural Studies on β -Helical Integral Membrane Proteins. <i>Molecules</i> , 2017, 22, 1347.	3.8	12
72	A novel chlorination-induced ribonuclease YabJ from <i>Staphylococcus aureus</i> . <i>Bioscience Reports</i> , 2018, 38, .	2.4	12

#	ARTICLE	IF	CITATIONS
73	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
74	Solution structure of conserved hypothetical protein HP0894 from <i>Helicobacter pylori</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 61, 1114-1116.	2.6	11
75	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
76	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
77	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
78	Structural Elucidation of the Protein- and Membrane-Binding Properties of the N-Terminal Tail Domain of Human Annexin II. <i>Journal of Biochemistry</i> , 2003, 134, 427-432.	1.7	10
79	Palmar Scaphoid Dislocation Associated With Dorsal Perilunate Dislocation: Case Report. <i>Journal of Hand Surgery</i> , 2010, 35, 726-731.	1.6	10
80	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
81	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
82	N-Capping Effects of Stapled Heptapeptides on Antimicrobial and Hemolytic Activities. <i>Bulletin of the Korean Chemical Society</i> , 2015, 36, 2511-2515.	1.9	10
83	Spinal Epidural Abscess with Pyogenic Arthritis of Facet Joint Treated with Antibiotic-Bone Cement Beads - A Case Report -. <i>Asian Spine Journal</i> , 2007, 1, 61.	2.0	10
84	Structural insight into the distinct properties of copper transport by the <i>Helicobacter pylori</i> CopP protein. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 71, 1007-1019.	2.6	9
85	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
86	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
87	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
88	NMR Spectroscopic Assessment of the Structure and Dynamic Properties of an Amphibian Antimicrobial Peptide (Gaegurin 4) Bound to SDS Micelles. <i>BMB Reports</i> , 2007, 40, 261-269.	2.4	9
89	HP0902 from <i>Helicobacter pylori</i> is a thermostable, dimeric protein belonging to an all- β^2 topology of the cupin superfamily. <i>BMB Reports</i> , 2009, 42, 387-392.	2.4	9
90	Melanocortin 4 receptors interact with antimicrobial frog peptide analogues. <i>Biochemical and Biophysical Research Communications</i> , 2006, 343, 1094-1100.	2.1	8

#	ARTICLE	IF	CITATIONS
91	Solution structure of conserved hypothetical protein HP0892 from <i>Helicobacter pylori</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 70, 599-602.	2.6	8
92	Membrane binding properties of EBV gp110 C-terminal domain; evidences for structural transition in the membrane environment. <i>Virology</i> , 2008, 379, 181-190.	2.4	8
93	Interdomain interaction of cyclic AMP receptor protein in the absence of cyclic AMP. <i>Journal of Biochemistry</i> , 2008, 143, 163-167.	1.7	8
94	Identification of the WW domain-interaction sites in the unstructured N-terminal domain of EBV LMP 2A. <i>FEBS Letters</i> , 2007, 581, 65-70.	2.8	7
95	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
96	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
97	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
98	Biophysical and structural property of the putative DNA-binding protein, BldB, from <i>Streptomyces lividans</i> . <i>Biopolymers</i> , 2003, 69, 343-350.	2.4	6
99	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
100	A critical element of the light-induced quaternary structural changes in <i>YtvA</i> is a LOV domain. <i>Protein Science</i> , 2015, 24, 1997-2007.	7.6	6
101	Structural and functional insight into the different oxidation states of SAV1875 from <i>Staphylococcus aureus</i> . <i>Biochemical Journal</i> , 2016, 473, 55-66.	3.7	6
102	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
103	Induced DNA bending by unique dimerization of HigA antitoxin. <i>IUCr</i> , 2020, 7, 748-760.	2.2	6
104	A structural study of TatD from <i>Staphylococcus aureus</i> elucidates a putative DNA-binding mode of a Mg ²⁺ -dependent nuclease. <i>IUCr</i> , 2020, 7, 509-521.	2.2	6
105	Nickel-Binding Properties of the C-Terminal Tail Peptide of <i>Bacillus pasteurii</i> UreE. <i>Journal of Biochemistry</i> , 2004, 136, 635-641.	1.7	5
106	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
107	Structural insight into the interaction between the Hox and HMGB1 and understanding of the HMGB1-enhancing effect of Hox-DNA binding. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2015, 1854, 449-459.	2.3	5
108	How Bacterial Redox Sensors Transmit Redox Signals via Structural Changes. <i>Antioxidants</i> , 2021, 10, 502.	5.1	5

#	ARTICLE	IF	CITATIONS
109	Solution structure of HP1242 from <i>Helicobacter pylori</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 61, 1111-1113.	2.6	4
110	Solution structure of hypothetical protein, HP0495 (Y495_HELPY) from <i>Helicobacter pylori</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 67, 1189-1192.	2.6	4
111	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
112	Solution structure of hypothetical protein HP1423 (Y1423_HELPY) reveals the presence of $\hat{I}\pm L$ motif related to RNA binding. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 75, 252-257.	2.6	4
113	Phonetically optimized speaker modeling for robust speaker recognition. <i>Journal of the Acoustical Society of America</i> , 2009, 126, EL100-EL106.	1.1	4
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	Identification of novel scaffolds for potential anti- <i>Helicobacter pylori</i> agents based on the crystal structure of <i>H. pylori</i> 3-deoxy- d -manno-octulosonate 8-phosphate synthase (Hp KDO8PS). <i>European Journal of Medicinal Chemistry</i> , 2016, 108, 188-202.	5.5	4
116	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
117	Structural and functional analysis of the <i>Klebsiella pneumoniae</i> MazEF toxin-antitoxin system. <i>IUCr</i> , 2021, 8, 362-371.	2.2	4
118	Backbone NMR assignments of the metal-free UreE from <i>Bacillus pasteurii</i> . <i>Journal of Biomolecular NMR</i> , 2002, 24, 361-362.	2.8	3
119	Structural studies on the antimicrobial peptide Brevinin 1E by spectroscopic methods. <i>Spectroscopy</i> , 2003, 17, 127-138.	0.8	3
120	Backbone ¹ H, ¹³ C, and ¹⁵ 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
121	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
122	Structural Characterization of HP1264 Reveals a Novel Fold for the Flavin Mononucleotide Binding Protein. <i>Biochemistry</i> , 2013, 52, 1583-1593.	2.5	3
123	Crystal structure of toxin HP0892 from <i>Helicobacter pylori</i> with two Zn(II) at 1.8 Å... resolution. <i>Protein Science</i> , 2014, 23, 819-832.	7.6	3
124	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
125	Alba from <i>Thermoplasma volcanium</i> belongs to $\hat{I}\pm$ -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
126	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

#	ARTICLE	IF	CITATIONS
127	Crystal structure of proteolyzed VapBC and DNA-bound VapBC from Salmonella enterica Typhimurium LT2 and VapC as a putative Ca ²⁺ -dependent ribonuclease. <i>FASEB Journal</i> , 2020, 34, 3051-3068.	0.5	3
128	Lumbar Pyogenic Spondylodiscitis and Bilateral Psoas Abscesses Extending to the Gluteal Muscles and Intrapelvic Area Treated with CT-guided Percutaneous Drainage - A Case Report -. <i>Asian Spine Journal</i> , 2008, 2, 51.	2.0	3
129	Backbone ¹ H, ¹⁵ N, and ¹³ C Resonance Assignment and Secondary Structure Prediction of HP0495 from Helicobacter pylori. <i>BMB Reports</i> , 2007, 40, 839-843.	2.4	3
130	Conformational change of cyclic AMP Receptor Protein by the binding of cyclic nucleotide. <i>IUBMB Life</i> , 1996, 40, 93-100.	3.4	2
131	Interaction of T4 Endonuclease V with DNA. <i>Journal of Biological Chemistry</i> , 2003, 278, 30985-30992.	3.4	2
132	NMR Study on Small Proteins from Helicobacter pylori for Antibiotic Target Discovery: A Review. <i>Molecules</i> , 2013, 18, 13410-13424.	3.8	2
133	C-terminal dimerization of apo-cyclic <i>scp</i> -AMP receptor protein validated in solution. <i>FEBS Letters</i> , 2017, 591, 1064-1070.	2.8	2
134	Solution NMR Studies of Mycobacterium tuberculosis Proteins for Antibiotic Target Discovery. <i>Molecules</i> , 2017, 22, 1447.	3.8	2
135	Structural and functional study of SaAcp, an acylphosphatase from Staphylococcus aureus. <i>Biochemical and Biophysical Research Communications</i> , 2020, 532, 173-178.	2.1	2
136	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
137	Backbone ¹ H, ¹⁵ N, and ¹³ C Resonance Assignment of HP1242 from Helicobacter pylori. <i>BMB Reports</i> , 2005, 38, 591-594.	2.4	2
138	Backbone ¹ H, ¹⁵ N, and ¹³ C resonance assignments and secondary-structure of the conserved hypothetical protein HP0892 of Helicobacter pylori. <i>Molecules and Cells</i> , 2008, 25, 138-41.	2.6	2
139	Thermal denaturation of the apo-cyclic AMP receptor protein and noncovalent interactions between its domains. <i>Molecules and Cells</i> , 2008, 26, 61-6.	2.6	2
140	The structural and functional investigation of the VapBC43 complex from Mycobacterium tuberculosis. <i>Biochemical and Biophysical Research Communications</i> , 2022, 616, 19-25.	2.1	2
141	Backbone assignments for endonuclease V from bacteriophage T4 with deuterium labeling. <i>Journal of Biomolecular NMR</i> , 2002, 22, 383-384.	2.8	1
142	¹ H, ¹³ C and ¹⁵ N chemical shift assignments of Ninjurin1 Extracellular N-terminal Domain. <i>Biomolecular NMR Assignments</i> , 2013, 7, 159-162.	0.8	1
143	Bacterial peptide deformylase inhibitor PMT analogs inhibit cancer cell growth by interacting with human peptide deformylase. <i>Science Bulletin</i> , 2014, 59, 4274-4282.	1.7	1
144	Solution structure of Rv0569, potent hypoxic signal transduction protein, from Mycobacterium tuberculosis. <i>Tuberculosis</i> , 2014, 94, 43-50.	1.9	1

#	ARTICLE	IF	CITATIONS
145	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
146	Structural Investigation of Self-Assembly and Target Binding of Anti-CRISPR AcrIIc2. <i>CRISPR Journal</i> , 2021, 4, 448-458.	2.9	1
147	Structural and functional studies of the <i>Mycobacterium tuberculosis</i> VapBC30 toxin-antitoxin system. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2016, 72, s209-s209.	0.1	1
148	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
149	Backbone ¹ H, ¹⁵ N, and ¹³ 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
150	Backbone ¹ H, ¹⁵ N, and ¹³ 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
151	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
152	Radiological Assessment of the Effect of Congenital C3-4 Synostosis on Adjacent Segments. <i>Asian Spine Journal</i> , 2015, 9, 895.	2.0	1
153	Backbone assignments of ¹ H, ¹⁵ N and ¹³ C resonances and secondary structure prediction of MRA1997 from <i>Mycobacterium tuberculosis</i> H37Rv. <i>Journal of the Korean Magnetic Resonance Society</i> , 2015, 19, 49-53.	0.1	1
154	Structural stability of CD1 domain of human mitotic checkpoint serine/threonine-protein kinase, Bub1. <i>Journal of the Korean Magnetic Resonance Society</i> , 2015, 19, 88-94.	0.1	1
155	Cellular Membrane Composition Requirement by Antimicrobial and Anticancer Peptide GA-K4. <i>Protein and Peptide Letters</i> , 2017, 24, 197-205.	0.9	1
156	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
157	Backbone ¹ H, ¹⁵ N, and ¹³ C resonance assignments and secondary-structure of conserved hypothetical protein HP0894 from <i>Helicobacter pylori</i> . <i>Molecules and Cells</i> , 2005, 20, 442-5.	2.6	1
158	Backbone ¹ H, ¹⁵ N, and ¹³ C resonance assignments of the repeated domain of human beta ig-h3 protein. <i>Journal of Biomolecular NMR</i> , 2002, 24, 367-368.	2.8	0
159	S2c2-1 Structure and Protein-Protein Interaction of <i>Helicobacter Pylori</i> Proteins(S2-c2: "Structural) Tj ETQq1 1 0.784314 rgBT /Overlock 0.1 S127. <i>Seibutsu Butsuri</i> , 2006, 46, S127.	0.1	0
160	S2g2-5 Mongolian Biophysical Education System and Research Exchange with Seoul National University(S2-g2: "Education and Capacity Building in Biophysics in Asian) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 142 Id (Countries",Sym S133.	0.1	0
161	2P048 Structural Studies on Conserved Hypothetical Protein HP0894 and its Complex from <i>Helicobacter pylori</i> (29. Protein structure and dynamics (II),Poster Session,Abstract,Meeting Program) Tj ETQq1 1 0.784314 rgBT /Overlock 0.1	0.1	0
162	¹ H, ¹³ C and ¹⁵ N resonance assignments of the pyrazinamidase from <i>Mycobacterium tuberculosis</i> . <i>Journal of Biomolecular NMR</i> , 2006, 36, 60-60.	2.8	0

#	ARTICLE	IF	CITATIONS
163	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 Butsurei, 2008, 48, S75-S76.	0.1	0
164	2P-053 Structural and Functional Studies on the conserved hypothetical protein HP0894 from Helicobacter pylori(The 46th Annual Meeting of the Biophysical Society of Japan). Seibutsu Butsurei, 2008, 48, S83.	0.1	0
165	On the Importance of Transition Regions for Automatic Speaker Recognition. IEICE Transactions on Information and Systems, 2010, E93-D, 197-200.	0.7	0
166	Overexpression, crystallization and preliminary X-ray crystallographic analysis of hypothetical protein SAV0479 from Staphylococcus aureus Mu50. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 405-407.	0.7	0
167	Crystal structure of YwpF from Staphylococcus aureus reveals its architecture comprised of a β -barrel core domain resembling type VI secretion system proteins and a two-helix pair. Acta Crystallographica Section A: Foundations and Advances, 2015, 71, s273-s273.	0.1	0
168	Crystal structure of PhoU from Pseudomonas aeruginosa, a negative regulator of the Pho regulon. Acta Crystallographica Section A: Foundations and Advances, 2015, 71, s231-s231.	0.1	0
169	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
170	Crystal structure of YwpF from Staphylococcus aureus reveals its architecture comprised of a β -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
171	Solution NMR studies on Helicobacter pylori proteins for antibiotic target discovery. Expert Opinion on Drug Discovery, 2016, 11, 681-693.	5.0	0
172	Structural and functional studies of SAV1707 from Staphylococcus aureus elucidate its distinct metal-dependent activity and a crucial residue for catalysis. Acta Crystallographica Section D: Structural Biology, 2021, 77, 587-598.	2.3	0
173	Structure-Activity Relationship of Antimicrobial Peptide, Gaegurin 4, Isolated from Korean Frog. , 2001, , 291-292.		0
174	Backbone 1H, 15N, and 13C Resonance Assignments of the Helicobacter pylori Acyl Carrier Protein. BMB Reports, 2003, 36, 505-507.	2.4	0
175	Lumbar Wedge Resection Osteotomy for Congenital Scoliosis due to a Sacral Malformation - A Case Report -. The Journal of the Korean Orthopaedic Association, 2007, 42, 828.	0.1	0
176	Cemented Bipolar Hemiarthroplasty for the Femoral Neck or Intertrochanteric Fracture in Elderly Patients - Multicenter Study -. The Journal of the Korean Orthopaedic Association, 2007, 42, 53.	0.1	0
177	Multiple Pyogenic Spondylodiscitis with Bilateral Psoas Abscesses Accompanying Osteomyelitis of Lateral Malleolus - A Case Report -. Asian Spine Journal, 2008, 2, 102.	2.0	0
178	Backbone 1H, 15N, and 13C Resonance Assignment and Secondary Structure Prediction of HP1298 from Helicobacter pylori. Journal of the Korean Magnetic Resonance Society, 2008, 12, 65-73.	0.1	0
179	1H, 15N and 13C resonance assignment and secondary structure prediction of ss-DNA binding protein 12RNP2 precursor, HP0827 from Helicobacter pylori. Journal of the Korean Magnetic Resonance Society, 2011, 15, 69-79.	0.1	0
180	Solid-state NMR Study on Membrane Protein Structure in Biological Condition. Journal of the Korean Magnetic Resonance Society, 2012, 16, 103-110.	0.1	0

#	ARTICLE	IF	CITATIONS
181	Backbone ¹ H, ¹⁵ N, and ¹³ C resonance assignments and secondary structure prediction of SAV2228 (translation initiation factor-1) from Staphylococcus aureus. Journal of the Korean Magnetic Resonance Society, 2012, 16, 162-171.	0.1	0
182	Identification of Potent Inhibitors against Human Peptide Deformylase as Anticancer Agents. Bulletin of the Korean Chemical Society, 2013, 34, 3885-3887.	1.9	0
183	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
184	Secondary structure analysis of MRA1997 from Mycobacterium tuberculosis and characterization of DNA binding property. Journal of the Korean Magnetic Resonance Society, 2016, 20, 36-40.	0.1	0
185	Elucidating the Dynamic Properties of Globular Protein using Predicted Order Parameters and ¹⁵ N NMR Relaxation. Journal of the Korean Magnetic Resonance Society, 2017, 21, 26-30.	0.1	0
186	Identification of Enzymatic Catalysis of PncA using ¹ H-NMR. Journal of the Korean Magnetic Resonance Society, 2017, 21, 85-89.	0.1	0
187	Abstract 1800: Novel NSDHL inhibitor (Compound 9) exerts anti-proliferative and cytotoxic activity in breast cancer cells. Cancer Research, 2022, 82, 1800-1800.	0.9	0