

Takanori Kigawa

List of Publications by Year in descending order

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179
papers

8,480
citations

47006

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85
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184
all docs

184
docs citations

184
times ranked

9526
citing authors

#	ARTICLE	IF	CITATIONS
1	Cell-free production and stable-isotope labeling of milligram quantities of proteins. <i>FEBS Letters</i> , 1999, 442, 15-19.	2.8	463
2	Role of the ENTH Domain in Phosphatidylinositol-4,5-Bisphosphate Binding and Endocytosis. <i>Science</i> , 2001, 291, 1047-1051.	12.6	437
3	Structural genomics projects in Japan. <i>Nature Structural Biology</i> , 2000, 7, 943-945.	9.7	316
4	Preparation of <i>Escherichia coli</i> cell extract for highly productive cell-free protein expression. <i>Journal of Structural and Functional Genomics</i> , 2004, 5, 63-68.	1.2	301
5	An unnatural base pair for incorporating amino acid analogs into proteins. <i>Nature Biotechnology</i> , 2002, 20, 177-182.	17.5	270
6	A Novel Zinc-binding Motif Revealed by Solution Structures of DNA-binding Domains of Arabidopsis SBP-family Transcription Factors. <i>Journal of Molecular Biology</i> , 2004, 337, 49-63.	4.2	267
7	DNA-binding domains of plant-specific transcription factors: structure, function, and evolution. <i>Trends in Plant Science</i> , 2013, 18, 267-276.	8.8	229
8	A Highly Efficient Cell-Free Protein Synthesis System from <i>Escherichia coli</i> . <i>FEBS Journal</i> , 1996, 239, 881-886.	0.2	195
9	Solution Structure of an Arabidopsis WRKY DNA Binding Domain. <i>Plant Cell</i> , 2005, 17, 944-956.	6.6	185
10	Cell-free synthesis and amino acid-selective stable isotope labeling of proteins for NMR analysis. <i>Journal of Biomolecular NMR</i> , 1995, 6, 129-134.	2.8	172
11	Expression of G protein coupled receptors in a cell-free translational system using detergents and thioredoxin-fusion vectors. <i>Protein Expression and Purification</i> , 2005, 41, 27-37.	1.3	170
12	An engineered <i>Escherichia coli</i> tyrosyl-tRNA synthetase for site-specific incorporation of an unnatural amino acid into proteins in eukaryotic translation and its application in a wheat germ cell-free system. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 9715-9720.	7.1	163
13	KUJIRA, a package of integrated modules for systematic and interactive analysis of NMR data directed to high-throughput NMR structure studies. <i>Journal of Biomolecular NMR</i> , 2007, 39, 31-52.	2.8	153
14	A B-Box 2 Surface Patch Important for TRIM5 β Self-Association, Capsid Binding Avidity, and Retrovirus Restriction. <i>Journal of Virology</i> , 2009, 83, 10737-10751.	3.4	145
15	Reduced Native State Stability in Crowded Cellular Environment Due to Protein-Protein Interactions. <i>Journal of the American Chemical Society</i> , 2013, 135, 3696-3701.	13.7	145
16	Phosphatidylinositol monophosphate-binding interface in the oomycete RXLR effector AVR3a is required for its stability in host cells to modulate plant immunity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 14682-14687.	7.1	141
17	Dual amino acid-selective and site-directed stable-isotope labeling of the human c-Ha-Ras protein by cell-free synthesis. <i>Journal of Biomolecular NMR</i> , 1998, 11, 295-306.	2.8	126
18	Selenomethionine incorporation into a protein by cell-free synthesis. <i>Journal of Structural and Functional Genomics</i> , 2002, 2, 29-35.	1.2	108

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19	Solution Structure of the B3 DNA Binding Domain of the Arabidopsis Cold-Responsive Transcription Factor RAV1 [W]. <i>Plant Cell</i> , 2004, 16, 3448-3459.	6.6	107
20	Structural Insight into the Zinc Finger CW Domain as a Histone Modification Reader. <i>Structure</i> , 2010, 18, 1127-1139.	3.3	103
21	Regioselective Carbon-Carbon Bond Formation in Proteins with Palladium Catalysis; New Protein Chemistry by Organometallic Chemistry. <i>ChemBioChem</i> , 2006, 7, 134-139.	2.6	96
22	Site-Specific Functionalization of Proteins by Organopalladium Reactions. <i>ChemBioChem</i> , 2007, 8, 232-238.	2.6	96
23	Structural Basis for Sequence-specific DNA Recognition by an Arabidopsis WRKY Transcription Factor. <i>Journal of Biological Chemistry</i> , 2012, 287, 7683-7691.	3.4	95
24	Structural basis for mutual relief of the Rac guanine nucleotide exchange factor DOCK2 and its partner ELMO1 from their autoinhibited forms. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 3305-3310.	7.1	95
25	The CAP-Gly Domain of CYLD Associates with the Proline-Rich Sequence in NEMO/IKK β . <i>Structure</i> , 2004, 12, 1719-1728.	3.3	93
26	A Continuous Cell-Free Protein Synthesis System for Coupled Transcription-Translation ¹ . <i>Journal of Biochemistry</i> , 1991, 110, 166-168.	1.7	92
27	Combinatorial mutagenesis to restrict amino acid usage in an enzyme to a reduced set. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 13549-13553.	7.1	85
28	Solution Structure of the Major DNA-binding Domain of Arabidopsis thaliana Ethylene-insensitive3-like3. <i>Journal of Molecular Biology</i> , 2005, 348, 253-264.	4.2	82
29	A robust two-step PCR method of template DNA production for high-throughput cell-free protein synthesis. <i>Journal of Structural and Functional Genomics</i> , 2007, 8, 173-191.	1.2	81
30	Structures and evolutionary origins of plant-specific transcription factor DNA-binding domains. <i>Plant Physiology and Biochemistry</i> , 2008, 46, 394-401.	5.8	80
31	RING Domain Mutations Uncouple TRIM5 β Restriction of HIV-1 from Inhibition of Reverse Transcription and Acceleration of Uncoating. <i>Journal of Virology</i> , 2012, 86, 1717-1727.	3.4	78
32	Solution Structure of the SEA Domain from the Murine Homologue of Ovarian Cancer Antigen CA125 (MUC16). <i>Journal of Biological Chemistry</i> , 2004, 279, 13174-13182.	3.4	74
33	Contribution of E3-Ubiquitin Ligase Activity to HIV-1 Restriction by TRIM5 β : Structure of the RING Domain of TRIM5 β . <i>Journal of Virology</i> , 2011, 85, 8725-8737.	3.4	73
34	The C-Terminal BAG Domain of BAG5 Induces Conformational Changes of the Hsp70 Nucleotide- Binding Domain for ADP-ATP Exchange. <i>Structure</i> , 2010, 18, 309-319.	3.3	68
35	Improving cell-free protein synthesis for stable-isotope labeling. <i>Journal of Biomolecular NMR</i> , 2007, 37, 225-229.	2.8	67
36	Structural basis for the sequence-specific RNA-recognition mechanism of human CUG-BP1 RRM3. <i>Nucleic Acids Research</i> , 2009, 37, 5151-5166.	14.5	67

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37	Solution structure of the RWD domain of the mouse GCN2 protein. <i>Protein Science</i> , 2004, 13, 2089-2100.	7.6	66
38	Cell-free protein synthesis system from <i>Escherichia coli</i> cells cultured at decreased temperatures improves productivity by decreasing DNA template degradation. <i>Analytical Biochemistry</i> , 2008, 377, 156-161.	2.4	65
39	Aberrant Assembly of RNA Recognition Motif 1 Links to Pathogenic Conversion of TAR DNA-binding Protein of 43 kDa (TDP-43). <i>Journal of Biological Chemistry</i> , 2013, 288, 14886-14905.	3.4	65
40	Structural basis for the dual RNA-recognition modes of human Tra2- $\hat{1}$ RRM. <i>Nucleic Acids Research</i> , 2011, 39, 1538-1553.	14.5	62
41	Intracellular Delivery of Proteins via Fusion Peptides in Intact Plants. <i>PLoS ONE</i> , 2016, 11, e0154081.	2.5	62
42	Solution Structure of the SWIRM Domain of Human Histone Demethylase LSD1. <i>Structure</i> , 2006, 14, 457-468.	3.3	59
43	Functional and structural basis of the nuclear localization signal in the ZIC3 zinc finger domain. <i>Human Molecular Genetics</i> , 2008, 17, 3459-3473.	2.9	53
44	Automated system for high-throughput protein production using the dialysis cell-free method. <i>Protein Expression and Purification</i> , 2009, 68, 128-136.	1.3	53
45	A practical method for cell-free protein synthesis to avoid stable isotope scrambling and dilution. <i>Analytical Biochemistry</i> , 2011, 411, 223-229.	2.4	53
46	The solution structure of the pleckstrin homology domain of mouse son-of-sevenless 1 (msos1). <i>Journal of Molecular Biology</i> , 1997, 269, 579-591.	4.2	51
47	Structures of the first and second double-stranded RNA-binding domains of human TAR RNA-binding protein. <i>Protein Science</i> , 2011, 20, 118-130.	7.6	50
48	Structural genomics projects in Japan. <i>Progress in Biophysics and Molecular Biology</i> , 2000, 73, 363-376.	2.9	49
49	Solution structure of a BolA-like protein from <i>Mus musculus</i> . <i>Protein Science</i> , 2004, 13, 545-548.	7.6	49
50	Solution structure of the PWWP domain of the hepatoma-derived growth factor family. <i>Protein Science</i> , 2005, 14, 756-764.	7.6	48
51	Solution Structure of the Catalytic Domain of the Mitochondrial Protein ICT1 That Is Essential for Cell Vitality. <i>Journal of Molecular Biology</i> , 2010, 404, 260-273.	4.2	48
52	Characterization of acyl-CoA-binding protein (ACBP) in the pheromone gland of the silkworm, <i>Bombyx mori</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2001, 31, 603-609.	2.7	47
53	Structural insight into the interaction of ADP-ribose with the PARP WWE domains. <i>FEBS Letters</i> , 2012, 586, 3858-3864.	2.8	47
54	Novel dimerization mode of the human Bcl-2 family protein Bak, a mitochondrial apoptosis regulator. <i>Journal of Structural Biology</i> , 2009, 166, 32-37.	2.8	46

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55	Nuclear magnetic resonance and molecular dynamics studies on the interactions of the ras-binding domain of raf-1 with wild-type and mutant ras proteins. <i>Journal of Molecular Biology</i> , 1999, 286, 219-232.	4.2	45
56	An Arabidopsis SBP-domain fragment with a disrupted C-terminal zinc-binding site retains its tertiary structure. <i>FEBS Letters</i> , 2006, 580, 2109-2116.	2.8	45
57	The Crystal Structure of Mouse Nup35 Reveals Atypical RNP Motifs and Novel Homodimerization of the RRM Domain. <i>Journal of Molecular Biology</i> , 2006, 363, 114-124.	4.2	45
58	Solution structure of the extraterminal domain of the bromodomain-containing protein BRD4. <i>Protein Science</i> , 2008, 17, 2174-2179.	7.6	43
59	NMR solution structures of actin depolymerizing factor homology domains. <i>Protein Science</i> , 2009, 18, 2384-2392.	7.6	43
60	Structural and Functional Differences of SWIRM Domain Subtypes. <i>Journal of Molecular Biology</i> , 2007, 369, 222-238.	4.2	41
61	The RRM domain of poly(A)-specific ribonuclease has a noncanonical binding site for mRNA cap analog recognition. <i>Nucleic Acids Research</i> , 2008, 36, 4754-4767.	14.5	41
62	Solution Structure of the DFF-C Domain of DFF45/ICAD. A Structural Basis for the Regulation of Apoptotic DNA Fragmentation. <i>Journal of Molecular Biology</i> , 2002, 321, 317-327.	4.2	40
63	NMR Solution Structure of Human Vaccinia-related Kinase 1 (VRK1) Reveals the C-terminal Tail Essential for Its Structural Stability and Autocatalytic Activity. <i>Journal of Biological Chemistry</i> , 2011, 286, 22131-22138.	3.4	40
64	Impact of cellular health conditions on the protein folding state in mammalian cells. <i>Chemical Communications</i> , 2017, 53, 11245-11248.	4.1	40
65	Solution structure of the kinase-associated domain 1 of mouse microtubule-associated protein/microtubule affinity-regulating kinase 3. <i>Protein Science</i> , 2006, 15, 2534-2543.	7.6	38
66	Effects of Escherichia coli ribosomal protein S12 mutations on cell-free protein synthesis. <i>FEBS Journal</i> , 2004, 271, 1127-1134.	0.2	37
67	Crystal Structure of the RUN Domain of the RAP2-interacting Protein x. <i>Journal of Biological Chemistry</i> , 2006, 281, 31843-31853.	3.4	36
68	Solution Structure of Histone Chaperone ANP32B: Interaction with Core Histones H3 and H4 through Its Acidic Concave Domain. <i>Journal of Molecular Biology</i> , 2010, 401, 97-114.	4.2	35
69	Cell-free synthesis of zinc-binding proteins. <i>Journal of Structural and Functional Genomics</i> , 2007, 7, 93-100.	1.2	34
70	A novel sphingomyelin/cholesterol domain-specific probe reveals the dynamics of the membrane domains during virus release and in Niemann-Pick type C. <i>FASEB Journal</i> , 2017, 31, 1301-1322.	0.5	34
71	Solution structure of an atypical WW domain in a novel β^2 -clam-like dimeric form. <i>FEBS Letters</i> , 2007, 581, 462-468.	2.8	33
72	Angucycline antibiotic waldiomycin recognizes common structural motif conserved in bacterial histidine kinases. <i>Journal of Antibiotics</i> , 2017, 70, 251-258.	2.0	32

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73	Crystal structure of an enhancer of rudimentary homolog (ERH) at 2.1 Å... resolution. <i>Protein Science</i> , 2005, 14, 1888-1893.	7.6	31
74	Solution structure of the human parvulin-like peptidyl prolyl cis/trans isomerase, hPar14. <i>Journal of Molecular Biology</i> , 2001, 305, 917-926.	4.2	30
75	Solution structure of the Eps15 homology domain of a human POB1 (partner of RalBP1). <i>FEBS Letters</i> , 1999, 442, 138-142.	2.8	29
76	Translation of "rare" Codons in a Cell-free Protein Synthesis System from <i>Escherichia coli</i> . <i>Journal of Structural and Functional Genomics</i> , 2006, 7, 31-36.	1.2	28
77	Structural and Functional Characterization of the NHR1 Domain of the <i>Drosophila</i> Neuralized E3 Ligase in the Notch Signaling Pathway. <i>Journal of Molecular Biology</i> , 2009, 393, 478-495.	4.2	27
78	Solution structure and siRNA-mediated knockdown analysis of the mitochondrial disease-related protein C12orf65. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 2629-2642.	2.6	27
79	Native protein delivery into rice callus using ionic complexes of protein and cell-penetrating peptides. <i>PLoS ONE</i> , 2019, 14, e0214033.	2.5	27
80	Solution structure of the cysteine-rich domain in Fn14, a member of the tumor necrosis factor receptor superfamily. <i>Protein Science</i> , 2009, 18, 650-656.	7.6	26
81	An automated system designed for large scale NMR data deposition and annotation: application to over 600 assigned chemical shift data entries to the BioMagResBank from the Riken Structural Genomics/Proteomics Initiative internal database. <i>Journal of Biomolecular NMR</i> , 2012, 53, 311-320.	2.8	26
82	Structure of the C-terminal Phosphotyrosine Interaction Domain of Fe65L1 Complexed with the Cytoplasmic Tail of Amyloid Precursor Protein Reveals a Novel Peptide Binding Mode. <i>Journal of Biological Chemistry</i> , 2008, 283, 27165-27178.	3.4	25
83	Simultaneous introduction of multiple biomacromolecules into plant cells using a cell-penetrating peptide nanocarrier. <i>Nanoscale</i> , 2020, 12, 18844-18856.	5.6	25
84	A characteristic arrangement of aromatic amino acid residues in the solution structure of the amino-terminal RNA-binding domain of <i>Drosophila</i> sex-lethal 1 Edited by K. Nagai. <i>Journal of Molecular Biology</i> , 1997, 272, 82-94.	4.2	24
85	Solution structure of the Ras-binding domain of RGL. <i>FEBS Letters</i> , 1998, 441, 413-418.	2.8	24
86	Solution structure of the rhodanese homology domain At4g01050(175-295) from <i>Arabidopsis thaliana</i> . <i>Protein Science</i> , 2009, 14, 224-230.	7.6	24
87	Cell-free synthesis system suitable for disulfide-containing proteins. <i>Biochemical and Biophysical Research Communications</i> , 2013, 431, 296-301.	2.1	24
88	A fluorogenic peptide probe developed by in vitro selection using tRNA carrying a fluorogenic amino acid. <i>Chemical Communications</i> , 2014, 50, 2962-2964.	4.1	24
89	Crystal Structure Analysis of the PHD Domain of the Transcription Co-activator Pygopus. <i>Journal of Molecular Biology</i> , 2007, 370, 80-92.	4.2	23
90	Solution structure of the zinc finger HIT domain in protein FON. <i>Protein Science</i> , 2007, 16, 1577-1587.	7.6	23

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91	Co-expression of Two Polyhydroxyalkanoate Synthase Subunits from <i>Synechocystis</i> sp. PCC 6803 by Cell-Free Synthesis and Their Specific Activity for Polymerization of 3-Hydroxybutyryl-Coenzyme A. <i>Biochemistry</i> , 2015, 54, 1401-1407.	2.5	22
92	Crystal structure of <i>Sulfolobus tokodaii</i> sua5 complexed with methionine and AMPPNP. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 2065-2075.	2.6	21
93	Active Intermediates of Polyhydroxyalkanoate Synthase from <i>Aeromonas caviae</i> in Polymerization Reaction. <i>Biomacromolecules</i> , 2012, 13, 3450-3455.	5.4	21
94	Solution structure of the antifreeze-like domain of human sialic acid synthase. <i>Protein Science</i> , 2006, 15, 1010-1016.	7.6	20
95	Solution structure of the RNA binding domain in the human muscleblind-like protein 2. <i>Protein Science</i> , 2009, 18, 80-91.	7.6	20
96	A Fluorescent-Based High-Throughput Screening Assay for Small Molecules That Inhibit the Interaction of MdmX with p53. <i>Journal of Biomolecular Screening</i> , 2013, 18, 191-198.	2.6	20
97	Role of 2-hydroxyethyl methacrylate in the interaction of dental monomers with collagen studied by saturation transfer difference NMR. <i>Journal of Dentistry</i> , 2014, 42, 484-489.	4.1	20
98	Letter to the Editor: NMR assignment of the hypothetical ENTH-VHS domain At3g16270 from <i>Arabidopsis thaliana</i> . <i>Journal of Biomolecular NMR</i> , 2004, 29, 205-206.	2.8	18
99	Simplification of the genetic code: restricted diversity of genetically encoded amino acids. <i>Nucleic Acids Research</i> , 2012, 40, 10576-10584.	14.5	18
100	Receptor-Binding Affinities of Human Epidermal Growth Factor Variants Having Unnatural Amino Acid Residues in Position 23. <i>Biochemistry</i> , 1994, 33, 7470-7476.	2.5	17
101	Solution structure determination of the two DNA-binding domains in the <i>Schizosaccharomyces pombe</i> Abp1 protein by a combination of dipolar coupling and diffusion anisotropy restraints. <i>Journal of Biomolecular NMR</i> , 2002, 22, 333-347.	2.8	17
102	Structure of a conserved CoA-binding protein synthesized by a cell-free system. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 1213-1218.	2.5	17
103	Solution Structure of the Mouse Enhancer of Rudimentary Protein Reveals a Novel Fold. <i>Journal of Biomolecular NMR</i> , 2005, 32, 329-334.	2.8	17
104	An economical method for producing stable-isotope labeled proteins by the <i>E. coli</i> cell-free system. <i>Journal of Biomolecular NMR</i> , 2010, 48, 193-201.	2.8	17
105	Rapid biochemical synthesis of ¹³ C-labeled single chain variable fragment antibody for immuno-PET by cell-free protein synthesis. <i>Bioorganic and Medicinal Chemistry</i> , 2012, 20, 6579-6582.	3.0	17
106	Solution structures of the DNA-binding domains of immune-related zinc-finger protein ZFAT. <i>Journal of Structural and Functional Genomics</i> , 2015, 16, 55-65.	1.2	17
107	Cell-Free Protein Production System with the <i>E. coli</i> Crude Extract for Determination of Protein Folds. <i>Methods in Molecular Biology</i> , 2010, 607, 101-111.	0.9	17
108	Solution structure of the Src homology 2 domain from the human feline sarcoma oncogene Fes. <i>Journal of Biomolecular NMR</i> , 2005, 31, 357-361.	2.8	16

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109	Crystal structure of the N-terminal RecA-like domain of a DEAD-box RNA helicase, the <i>Dugesia japonica</i> vasa-like gene B protein. <i>Journal of Structural Biology</i> , 2005, 150, 58-68.	2.8	16
110	Solution Structure of the Second RNA Recognition Motif (RRM) Domain of Murine T Cell Intracellular Antigen-1 (TIA-1) and Its RNA Recognition Mode. <i>Biochemistry</i> , 2008, 47, 6437-6450.	2.5	16
111	Basic Folded and Low-Populated Locally Disordered Conformers of SUMO-2 Characterized by NMR Spectroscopy at Varying Pressures. <i>Biochemistry</i> , 2008, 47, 30-39.	2.5	14
112	The NMR solution structures of the five constituent cold-shock domains (CSD) of the human UNR (upstream of N-ras) protein. <i>Journal of Structural and Functional Genomics</i> , 2010, 11, 181-188.	1.2	14
113	ZF21 Protein, a Regulator of the Disassembly of Focal Adhesions and Cancer Metastasis, Contains a Novel Noncanonical Pleckstrin Homology Domain. <i>Journal of Biological Chemistry</i> , 2011, 286, 31598-31609.	3.4	14
114	Direct introduction of neomycin phosphotransferase II protein into apple leaves to confer kanamycin resistance. <i>Plant Biotechnology</i> , 2016, 33, 403-407.	1.0	14
115	Letter to the Editor: NMR assignment of the SH2 domain from the human feline sarcoma oncogene FES. <i>Journal of Biomolecular NMR</i> , 2004, 30, 463-464.	2.8	13
116	Bacterial Cell-Free System for Highly Efficient Protein Synthesis. , 0, , 83-97.		13
117	A Multiphysics Model of In Vitro Transcription Coupling Enzymatic Reaction and Precipitation Formation. <i>Biophysical Journal</i> , 2012, 102, 221-230.	0.5	13
118	Letter to the Editor: NMR assignment of the hypothetical rhodanese domain At4g01050 from <i>Arabidopsis thaliana</i> . <i>Journal of Biomolecular NMR</i> , 2004, 29, 207-208.	2.8	12
119	Multiple inhibitory factor removal from an <i>Escherichia coli</i> cell extract improves cell-free protein synthesis. <i>Journal of Bioscience and Bioengineering</i> , 2009, 108, 30-35.	2.2	12
120	Stable isotope labeling strategy based on coding theory. <i>Journal of Biomolecular NMR</i> , 2015, 63, 213-221.	2.8	12
121	Class I Polyhydroxyalkanoate Synthase from the Purple Photosynthetic Bacterium <i>Rhodovulum sulfidophilum</i> Predominantly Exists as a Functional Dimer in the Absence of a Substrate. <i>ACS Omega</i> , 2017, 2, 5071-5078.	3.5	12
122	Peptide-Based Polyion Complex Vesicles That Deliver Enzymes into Intact Plants To Provide Antibiotic Resistance without Genetic Modification. <i>Biomacromolecules</i> , 2021, 22, 1080-1090.	5.4	12
123	Dosage effect of minor arginyl- and isoleucyl-tRNAs on protein synthesis in an <i>Escherichia coli</i> in vitro coupled transcription/translation system. <i>Journal of Bioscience and Bioengineering</i> , 2001, 91, 53-57.	2.2	11
124	Solution structure of the GUCT domain from human RNA helicase II/Gu ^{h2} reveals the RRM fold, but implausible RNA interactions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 74, 133-144.	2.6	11
125	Solution structure of the C-terminal DUF1000 domain of the human thioredoxin-like 1 protein. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 2176-2180.	2.6	11
126	Molecular level evaluation on HEMA interaction with a collagen model. <i>Dental Materials</i> , 2015, 31, 88-92.	3.5	11

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127	Nanoscale Polyion Complex Vesicles for Delivery of Cargo Proteins and Cas9 Ribonucleoprotein Complexes to Plant Cells. <i>ACS Applied Nano Materials</i> , 2021, 4, 5630-5635.	5.0	11
128	Solution structure of the epsin N-terminal homology (ENTH) domain of human epsin. <i>Journal of Structural and Functional Genomics</i> , 2002, 2, 1-8.	1.2	10
129	A New Protein Engineering Approach Combining Chemistry and Biology, Part I; Site-Specific Incorporation of 4-Iodo-L-phenylalanine in vitro by Using Misacylated Suppressor tRNAPhe. <i>ChemBioChem</i> , 2006, 7, 1577-1581.	2.6	10
130	Solution structure of the general transcription factor 2I domain in mouse TFII protein. <i>Protein Science</i> , 2007, 16, 1788-1792.	7.6	10
131	Cell-Free Protein Preparation Through Prokaryotic Transcription-Translation Methods. <i>Methods in Molecular Biology</i> , 2010, 607, 1-10.	0.9	10
132	Protein NMR Structure Refinement based on Bayesian Inference. <i>Journal of Physics: Conference Series</i> , 2016, 699, 012005.	0.4	10
133	Cold shock proteins improve E. coli cell-free synthesis in terms of soluble yields of aggregation-prone proteins. <i>Biotechnology and Bioengineering</i> , 2020, 117, 1628-1639.	3.3	10
134	NMR spectral analysis using prior knowledge. <i>Journal of Physics: Conference Series</i> , 2016, 699, 012003.	0.4	10
135	A Synthetic Multidomain Peptide That Drives a Macropinocytosis-Like Mechanism for Cytosolic Transport of Exogenous Proteins into Plants. <i>Jacs Au</i> , 2022, 2, 223-233.	7.9	10
136	Discovery of small molecule inhibitors targeting the SUMO-SIM interaction using a protein interface consensus approach. <i>MedChemComm</i> , 2014, 5, 783-786.	3.4	9
137	Crystal Structure of the RUN Domain of the RAP2-interacting Protein x. <i>Journal of Biological Chemistry</i> , 2006, 281, 31843-31853.	3.4	9
138	Molecular actions of two synthetic brassinosteroids, iso-carbaBL and 6-deoxoBL, which cause altered physiological activities between Arabidopsis and rice. <i>PLoS ONE</i> , 2017, 12, e0174015.	2.5	9
139	Structural basis for controlling the dimerization and stability of the WW domains of an atypical subfamily. <i>Protein Science</i> , 2008, 17, 1531-1541.	7.6	8
140	NMR and X-ray structures of the putative sterol carrier protein 2 from <i>Thermus thermophilus</i> HB8 show conformational changes. <i>Journal of Structural and Functional Genomics</i> , 2010, 11, 247-256.	1.2	8
141	Solution structures of the double-stranded RNA-binding domains from rna helicase A. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 1699-1706.	2.6	7
142	A pre-metazoan origin of the CRK gene family and co-opted signaling network. <i>Scientific Reports</i> , 2016, 6, 34349.	3.3	7
143	Synthesis of N-acetylglucosaminyl asparagine-substituted puromycin analogues. <i>Bioorganic and Medicinal Chemistry</i> , 1995, 3, 1631-1636.	3.0	6
144	The Use of the <i>Escherichia coli</i> Cell-Free Protein Synthesis for Structural Biology and Structural Proteomics. , 0, , 99-109.		6

#	ARTICLE	IF	CITATIONS
145	Flexible and rigid structures in HIV-1 p17 matrix protein monitored by relaxation and amide proton exchange with NMR. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 520-526.	2.3	6
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