

# Takanori Kigawa

## List of Publications by Year in descending order

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Version: 2024-02-01

179  
papers

8,480  
citations

47006

47  
h-index

53230

85  
g-index

184  
all docs

184  
docs citations

184  
times ranked

9526  
citing authors

| #  | ARTICLE  | IF  | CITATIONS |
|----|--|-----|-----------|
| 1  | <sup>1</sup> H, <sup>13</sup> C and <sup>15</sup> N resonance assignments and solution structures of the two RRM domains of Matrin-3. <i>Biomolecular NMR Assignments</i> , 2022, 16, 41-49.   | 0.8 | 3         |
| 2  | 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        |
| 3  | <sup>1</sup> H, <sup>13</sup> C and <sup>15</sup> N resonance assignment of the YTH domain of YTHDC2. <i>Biomolecular NMR Assignments</i> , 2021, 15, 1-7.   | 0.8 | 2         |
| 4  | DiRect: Site-directed mutagenesis method for protein engineering by rational design. <i>Biochemical and Biophysical Research Communications</i> , 2021, 551, 107-113.  | 2.1 | 5         |
| 5  | 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        |
| 6  | Changes in dynamic and static structures of the HIV $\alpha$ 1 p24 capsid protein N $\alpha$ -domain caused by amino $\alpha$ -acid substitution are associated with its viral viability. <i>Protein Science</i> , 2021, 30, 2233-2245.                      | 7.6 | 1         |
| 7  | Identification of a Proline-Kinked Amphipathic $\alpha$ -Helix Downstream from the Methyltransferase Domain of a Potexvirus Replicase and Its Role in Virus Replication and Perinuclear Complex Formation. <i>Journal of Virology</i> , 2021, 95, e0190620.  | 3.4 | 6         |
| 8  | High $\alpha$ -Efficient and Dosage $\alpha$ -Controllable Intracellular Cargo Delivery through Electrochemical Metal $\alpha$ -Organic Hybrid Nanogates. <i>Small Science</i> , 2021, 1, 2100069.   | 9.9 | 5         |
| 9  | 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        |
| 10 | Molecular mechanism of glycolytic flux control intrinsic to human phosphoglycerate kinase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .   | 7.1 | 5         |
| 11 | Simultaneous introduction of multiple biomacromolecules into plant cells using a cell-penetrating peptide nanocarrier. <i>Nanoscale</i> , 2020, 12, 18844-18856.   | 5.6 | 25        |
| 12 | Computational study on the polymerization reaction of $\alpha$ -aminopeptidase for the synthesis of $\alpha$ -peptides. <i>RSC Advances</i> , 2020, 10, 17582-17592.   | 3.6 | 5         |
| 13 | Cold shock proteins improve E. coli cell $\alpha$ -free synthesis in terms of soluble yields of aggregation $\alpha$ -prone proteins. <i>Biotechnology and Bioengineering</i> , 2020, 117, 1628-1639.  | 3.3 | 10        |
| 14 | Amino-acid selective isotope labeling enables simultaneous overlapping signal decomposition and information extraction from NMR spectra. <i>Journal of Biomolecular NMR</i> , 2020, 74, 125-137.   | 2.8 | 2         |
| 15 | 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        |
| 16 | Selective isotope labeling strategy and computational interpretation of spectra for protein NMR analyses. <i>Journal of Physics: Conference Series</i> , 2018, 1036, 012007.   | 0.4 | 0         |
| 17 | Corrigendum to $\alpha$ Multiple inhibitory factor removal from an Escherichia coli cell extract improves cell-free protein synthesis $\alpha$ [Biosci Bioeng 108 (2009) 30 $\alpha$ -35]. <i>Journal of Bioscience and Bioengineering</i> , 2017, 123, 139. | 2.2 | 1         |
| 18 | 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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|----|---|-----|-----------|
| 19 | Impact of cellular health conditions on the protein folding state in mammalian cells. <i>Chemical Communications</i> , 2017, 53, 11245-11248.   | 4.1 | 40        |
| 20 | 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        |
| 21 | Advances in stable isotope assisted labeling strategies with information science. <i>Archives of Biochemistry and Biophysics</i> , 2017, 628, 17-23.  | 3.0 | 3         |
| 22 | Solution structure of the first RNA recognition motif domain of human spliceosomal protein SF3b49 and its mode of interaction with a SF3b145 fragment. <i>Protein Science</i> , 2017, 26, 280-291.  | 7.6 | 5         |
| 23 | 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        |
| 24 | NMR Analyses of Proteins with Stable Isotope Labeling Based on Information Sciences. <i>Seibutsu Butsuri</i> , 2017, 57, 153-156.   | 0.1 | 0         |
| 25 | Molecular actions of two synthetic brassinosteroids, iso-carbaBL and 6-deoxoBL, which cause altered physiological activities between <i>Arabidopsis</i> and rice. <i>PLoS ONE</i> , 2017, 12, e0174015.   | 2.5 | 9         |
| 26 | 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        |
| 27 | Protein NMR Structure Refinement based on Bayesian Inference. <i>Journal of Physics: Conference Series</i> , 2016, 699, 012005.   | 0.4 | 10        |
| 28 | Accurate and molecular-size-tolerant NMR quantitation of diverse components in solution. <i>Scientific Reports</i> , 2016, 6, 21742.  | 3.3 | 3         |
| 29 | A pre-metazoan origin of the CRK gene family and co-opted signaling network. <i>Scientific Reports</i> , 2016, 6, 34349.  | 3.3 | 7         |
| 30 | NMR spectral analysis using prior knowledge. <i>Journal of Physics: Conference Series</i> , 2016, 699, 012003.  | 0.4 | 10        |
| 31 | Intracellular Delivery of Proteins via Fusion Peptides in Intact Plants. <i>PLoS ONE</i> , 2016, 11, e0154081.  | 2.5 | 62        |
| 32 | Effect of Glu12-His89 Interaction on Dynamic Structures in HIV-1 p17 Matrix Protein Elucidated by NMR. <i>PLoS ONE</i> , 2016, 11, e0167176.  | 2.5 | 2         |
| 33 | Comparison of residual alpha- and beta-structures between two intrinsically disordered proteins by using NMR. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2015, 1854, 229-238.   | 2.3 | 4         |
| 34 | 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        |
| 35 | Molecular level evaluation on HEMA interaction with a collagen model. <i>Dental Materials</i> , 2015, 31, 88-92.  | 3.5 | 11        |
| 36 | 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        |

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|----|--|------|-----------|
| 37 | Stable isotope labeling strategy based on coding theory. <i>Journal of Biomolecular NMR</i> , 2015, 63, 213-221.   | 2.8  | 12        |
| 38 | Novel RNA recognition motif domain in the cytoplasmic polyadenylation element binding protein 3. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 2879-2886.  | 2.6  | 4         |
| 39 | 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        |
| 40 | 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         |
| 41 | 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         |
| 42 | 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        |
| 43 | Long-range effects of tag sequence on marginally stabilized structure in HIV-1 p24 capsid protein monitored using NMR. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 1638-1647.   | 2.3  | 0         |
| 44 | Cell-free synthesis system suitable for disulfide-containing proteins. <i>Biochemical and Biophysical Research Communications</i> , 2013, 431, 296-301.  | 2.1  | 24        |
| 45 | 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        |
| 46 | 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       |
| 47 | 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       |
| 48 | 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        |
| 49 | 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        |
| 50 | RING Domain Mutations Uncouple TRIM5 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        |
| 51 | Simplification of the genetic code: restricted diversity of genetically encoded amino acids. <i>Nucleic Acids Research</i> , 2012, 40, 10576-10584.  | 14.5 | 18        |
| 52 | 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        |
| 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 | 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        |

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|----|---|------|-----------|
| 55 | Active Intermediates of Polyhydroxyalkanoate Synthase from <i>Aeromonas caviae</i> in Polymerization Reaction. <i>Biomacromolecules</i> , 2012, 13, 3450-3455.  | 5.4  | 21        |
| 56 | 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        |
| 57 | Rapid biochemical synthesis of <sup>11</sup> 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        |
| 58 | A Multiphysics Model of In Vitro Transcription Coupling Enzymatic Reaction and Precipitation Formation. <i>Biophysical Journal</i> , 2012, 102, 221-230.  | 0.5  | 13        |
| 59 | Solution structure of the splicing factor motif of the human Prp18 protein. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 968-974.  | 2.6  | 3         |
| 60 | 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         |
| 61 | Crystal structure of <i>Sulfolobus tokodaii</i> sua5 complexed with <i>ScpL</i> threonine and AMPPNP. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 2065-2075.  | 2.6  | 21        |
| 62 | 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        |
| 63 | 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        |
| 64 | Structural basis for the dual RNA-recognition modes of human Tra2- $\beta$ RRM. <i>Nucleic Acids Research</i> , 2011, 39, 1538-1553.  | 14.5 | 62        |
| 65 | Contribution of E3-Ubiquitin Ligase Activity to HIV-1 Restriction by TRIM5 $\alpha$ : Structure of the RING Domain of TRIM5 $\alpha$ . <i>Journal of Virology</i> , 2011, 85, 8725-8737.  | 3.4  | 73        |
| 66 | 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        |
| 67 | 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        |
| 68 | 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       |
| 69 | Multi-Objective Robust Optimization for In Vitro RNA Synthesis. , 2011, , .   |      | 0         |
| 70 | Cell-Free Protein Preparation Through Prokaryotic Transcription-Translation Methods. <i>Methods in Molecular Biology</i> , 2010, 607, 1-10.   | 0.9  | 10        |
| 71 | Analysis of Protein Functions Through a Bacterial Cell-Free Protein Expression System. <i>Methods in Molecular Biology</i> , 2010, 607, 53-62.  | 0.9  | 2         |
| 72 | An economical method for producing stable-isotope labeled proteins by the E. coli cell-free system. <i>Journal of Biomolecular NMR</i> , 2010, 48, 193-201.   | 2.8  | 17        |

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|----|---|------|-----------|
| 73 | 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        |
| 74 | Structural basis for the recognition of nucleophosmin-anaplastic lymphoma kinase oncoprotein by the phosphotyrosine binding domain of Suc1-associated neurotrophic factor-induced tyrosine-phosphorylated target-2. <i>Journal of Structural and Functional Genomics</i> , 2010, 11, 125-141. | 1.2  | 5         |
| 75 | 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         |
| 76 | 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        |
| 77 | Structural Insight into the Zinc Finger CW Domain as a Histone Modification Reader. <i>Structure</i> , 2010, 18, 1127-1139.   | 3.3  | 103       |
| 78 | 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        |
| 79 | Site-specific incorporation of 4-Iodo-L-phenylalanine through opal suppression. <i>Journal of Biochemistry</i> , 2010, 148, 179-187.  | 1.7  | 4         |
| 80 | Solution Structure of Histone Chaperone ANP32B: Interaction with Core Histones H3&H4 through Its Acidic Concave Domain. <i>Journal of Molecular Biology</i> , 2010, 401, 97-114.  | 4.2  | 35        |
| 81 | 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        |
| 82 | An Accurate Prediction Method for Protein Structural Class from Signal Patterns of NMR Spectra in the Absence of Chemical Shift Assignments. , 2010, , .  |      | 3         |
| 83 | 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        |
| 84 | 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        |
| 85 | A B-Box 2 Surface Patch Important for TRIM5 $\alpha$ Self-Association, Capsid Binding Avidity, and Retrovirus Restriction. <i>Journal of Virology</i> , 2009, 83, 10737-10751.  | 3.4  | 145       |
| 86 | 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        |
| 87 | A new modeling method in feature construction for the HSQC spectra screening problem. <i>Bioinformatics</i> , 2009, 25, 948-953.  | 4.1  | 2         |
| 88 | 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        |
| 89 | Solution structure of the GUCT domain from human RNA helicase II/Gu $\alpha$ reveals the RRM fold, but implausible RNA interactions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 74, 133-144.   | 2.6  | 11        |
| 90 | NMR solution structures of actin depolymerizing factor homology domains. <i>Protein Science</i> , 2009, 18, 2384-2392.  | 7.6  | 43        |

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|-----|--|------|-----------|
| 91  | 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        |
| 92  | 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        |
| 93  | 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        |
| 94  | Structural and Functional Characterization of the NHR1 Domain of the Drosophila Neuralized E3 Ligase in the Notch Signaling Pathway. <i>Journal of Molecular Biology</i> , 2009, 393, 478-495.   | 4.2  | 27        |
| 95  | 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        |
| 96  | 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        |
| 97  | 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        |
| 98  | 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         |
| 99  | Solution structure of the extraterminal domain of the bromodomain-containing protein BRD4. <i>Protein Science</i> , 2008, 17, 2174-2179.   | 7.6  | 43        |
| 100 | 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        |
| 101 | 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        |
| 102 | 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        |
| 103 | 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        |
| 104 | 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        |
| 105 | 2P039 One sequence, two folds? : Solution structures of the B-box from human tripartite motif 39 protein (Proteins-structure and structure-function relationship, Poster Presentations). <i>Seibutsu Butsuri</i> , 2007, 47, S122.               | 0.1  | 0         |
| 106 | 3P067 Natural Design in Controlling Dimerization of a Protein Module : Lessons from the WW domains (Proteins-stability, folding, and other physicochemical properties, Oral Presentations). <i>Seibutsu Butsuri</i> , 2007, 47, S219.            | 0.1  | 0         |
| 107 | Structural and Functional Differences of SWIRM Domain Subtypes. <i>Journal of Molecular Biology</i> , 2007, 369, 222-238.  | 4.2  | 41        |
| 108 | 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        |

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|-----|--|-----|-----------|
| 109 | Solution structure of an atypical WW domain in a novel Î²-clam-like dimeric form. FEBS Letters, 2007, 581, 462-468.  | 2.8 | 33        |
| 110 | Site-Specific Functionalization of Proteins by Organopalladium Reactions. ChemBioChem, 2007, 8, 232-238.   | 2.6 | 96        |
| 111 | Regioselective Carbon-Carbon Bond Formation in Proteins with Palladium Catalysis; New Protein Chemistry by Organometallic Chemistry. ChemBioChem, 2007, 8, 159-159.  | 2.6 | 0         |
| 112 | Solution structure of the zinc finger HIT domain in protein FON. Protein Science, 2007, 16, 1577-1587.   | 7.6 | 23        |
| 113 | Solution structure of the general transcription factor 2I domain in mouse TFII-I protein. Protein Science, 2007, 16, 1788-1792.  | 7.6 | 10        |
| 114 | Cell-free synthesis of zinc-binding proteins. Journal of Structural and Functional Genomics, 2007, 7, 93-100.  | 1.2 | 34        |
| 115 | A robust two-step PCR method of template DNA production for high-throughput cell-free protein synthesis. Journal of Structural and Functional Genomics, 2007, 8, 173-191.  | 1.2 | 81        |
| 116 | Improving cell-free protein synthesis for stable-isotope labeling. Journal of Biomolecular NMR, 2007, 37, 225-229.   | 2.8 | 67        |
| 117 | KUJIRA, a package of integrated modules for systematic and interactive analysis of NMR data directed to high-throughput NMR structure studies. Journal of Biomolecular NMR, 2007, 39, 31-52.                         | 2.8 | 153       |
| 118 | An Arabidopsis SBP-domain fragment with a disrupted C-terminal zinc-binding site retains its tertiary structure. FEBS Letters, 2006, 580, 2109-2116.   | 2.8 | 45        |
| 119 | The Crystal Structure of Mouse Nup35 Reveals Atypical RNP Motifs and Novel Homodimerization of the RRM Domain. Journal of Molecular Biology, 2006, 363, 114-124.   | 4.2 | 45        |
| 120 | Structure of the UNC5H2 death domain. Acta Crystallographica Section D: Biological Crystallography, 2006, 62, 1502-1509.   | 2.5 | 4         |
| 121 | Solution structure of the antifreeze-like domain of human sialic acid synthase. Protein Science, 2006, 15, 1010-1016.  | 7.6 | 20        |
| 122 | Solution structure of the kinase-associated domain 1 of mouse microtubule-associated protein/microtubule affinity-regulating kinase 3. Protein Science, 2006, 15, 2534-2543.   | 7.6 | 38        |
| 123 | Translation of "rare" Codons in a Cell-free Protein Synthesis System from Escherichia coli. Journal of Structural and Functional Genomics, 2006, 7, 31-36.   | 1.2 | 28        |
| 124 | Solution Structure of the SWIRM Domain of Human Histone Demethylase LSD1. Structure, 2006, 14, 457-468.  | 3.3 | 59        |
| 125 | Regioselective Carbon-Carbon Bond Formation in Proteins with Palladium Catalysis; New Protein Chemistry by Organometallic Chemistry. ChemBioChem, 2006, 7, 134-139.  | 2.6 | 96        |
| 126 | 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. ChemBioChem, 2006, 7, 1577-1581. | 2.6 | 10        |

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|-----|--|-----|-----------|
| 127 | Crystal Structure of the RUN Domain of the RAP2-interacting Protein x. Journal of Biological Chemistry, 2006, 281, 31843-31853.  | 3.4 | 36        |
| 128 | Crystal Structure of the RUN Domain of the RAP2-interacting Protein x. Journal of Biological Chemistry, 2006, 281, 31843-31853.  | 3.4 | 9         |
| 129 | Solution structure of the PWWP domain of the hepatoma-derived growth factor family. Protein Science, 2005, 14, 756-764.  | 7.6 | 48        |
| 130 | Crystal structure of an enhancer of rudimentary homolog (ERH) at 2.1 Å... resolution. Protein Science, 2005, 14, 1888-1893.  | 7.6 | 31        |
| 131 | Solution structure of the Src homology 2 domain from the human feline sarcoma oncogene Fes. Journal of Biomolecular NMR, 2005, 31, 357-361.  | 2.8 | 16        |
| 132 | Solution Structure of the Mouse Enhancer of Rudimentary Protein Reveals a Novel Fold. Journal of Biomolecular NMR, 2005, 32, 329-334.  | 2.8 | 17        |
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