

Shigeyuki Yokoyama

List of Publications by Year in descending order

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770
papers

40,110
citations

2696

98
h-index

7627

156
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772
all docs

772
docs citations

772
times ranked

45097
citing authors

#	ARTICLE	IF	CITATIONS
1	¹ H, ¹³ C and ¹⁵ N resonance assignments and solution structures of the two RRM domains of Matrin-3. <i>Biomolecular NMR Assignments</i> , 2022, 16, 41-49.	0.4	3
2	The two-domain architecture of LAMP2A regulates its interaction with Hsc70. <i>Experimental Cell Research</i> , 2022, 411, 112986.	1.2	10
3	Rapid cloning of antigen-specific T-cell receptors by leveraging the cis activation of T cells. <i>Nature Biomedical Engineering</i> , 2022, 6, 806-818.	11.6	7
4	¹ H, ¹³ C and ¹⁵ N resonance assignment of the YTH domain of YTHDC2. <i>Biomolecular NMR Assignments</i> , 2021, 15, 1-7.	0.4	2
5	AdipoR agonist increases insulin sensitivity and exercise endurance in AdipoR-humanized mice. <i>Communications Biology</i> , 2021, 4, 45.	2.0	20
6	A conserved PI(4,5)P2-binding domain is critical for immune regulatory function of DOCK8. <i>Life Science Alliance</i> , 2021, 4, e202000873.	1.3	9
7	An expanded genetic code facilitates antibody chemical conjugation involving the lambda light chain. <i>Biochemical and Biophysical Research Communications</i> , 2021, 546, 35-39.	1.0	3
8	Structural and functional characterization of a putative carbonic anhydrase from <i>Geobacillus kaustophilus</i> reveals its cambialistic function. <i>Biochemical and Biophysical Research Communications</i> , 2021, 547, 96-101.	1.0	3
9	Serum anti-DIDO1, anti-CPSF2, and anti-FOXJ2 antibodies as predictive risk markers for acute ischemic stroke. <i>BMC Medicine</i> , 2021, 19, 131.	2.3	13
10	Genetic incorporation of non-canonical amino acid photocrosslinkers in <i>Neisseria meningitidis</i> : New method provides insights into the physiological function of the function-unknown NMB1345 protein. <i>PLoS ONE</i> , 2020, 15, e0237883.	1.1	6
11	Human adiponectin receptor AdipoR1 assumes closed and open structures. <i>Communications Biology</i> , 2020, 3, 446.	2.0	15
12	Fully Productive Cell-Free Genetic Code Expansion by Structure-Based Engineering of <i>Methanomylophilus alvus</i> Pyrrolysyl-tRNA Synthetase. <i>ACS Synthetic Biology</i> , 2020, 9, 718-732.	1.9	21
13	Development and Structural Evaluation of <i>N</i> -alkylated <i>trans</i> -phenylcyclopropylamine-based LSD1 Inhibitors. <i>ChemMedChem</i> , 2020, 15, 787-793.	1.6	18
14	Protein ligand interaction analysis against new CaMKK2 inhibitors by use of X-ray crystallography and the fragment molecular orbital (FMO) method. <i>Journal of Molecular Graphics and Modelling</i> , 2020, 99, 107599.	1.3	19
15	Structural Basis of Activin Receptor-Like Kinase 2 (R206H) Inhibition by Bis-heteroaryl Pyrazole-Based Inhibitors for the Treatment of Fibrodysplasia Ossificans Progressiva Identified by the Integration of Ligand-Based and Structure-Based Drug Design Approaches. <i>ACS Omega</i> , 2020, 5, 11411-11423.	1.6	11
16	Cell-Free Protein Synthesis Using S30 Extracts from <i>Escherichia coli</i> RFzero Strains for Efficient Incorporation of Non-Natural Amino Acids into Proteins. <i>International Journal of Molecular Sciences</i> , 2019, 20, 492.	1.8	25
17	Structural Basis for Genetic-Code Expansion with Bulky Lysine Derivatives by an Engineered Pyrrolysyl-tRNA Synthetase. <i>Cell Chemical Biology</i> , 2019, 26, 936-949.e13.	2.5	37
18	Bis-Heteroaryl Pyrazoles: Identification of Orally Bioavailable Inhibitors of Activin Receptor-Like Kinase-2 (R206H). <i>Chemical and Pharmaceutical Bulletin</i> , 2019, 67, 224-235.	0.6	11

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19	Development of a simple new flow cytometric antibody-dependent cellular cytotoxicity (ADCC) assay with excellent sensitivity. <i>Journal of Immunological Methods</i> , 2019, 464, 74-86.	0.6	5
20	Interhelical interactions between D92 and C218 in the cytoplasmic domain regulate proton uptake upon N-decay in the proton transport of <i>Acetabularia</i> rhodopsin II. <i>Journal of Photochemistry and Photobiology B: Biology</i> , 2018, 183, 35-45.	1.7	4
21	Thioether Macrocyclic Peptides Selected against TET1 Compact Catalytic Domain Inhibit TET1 Catalytic Activity. <i>ChemBioChem</i> , 2018, 19, 979-985.	1.3	14
22	Polyamines protect nucleic acids against depurination. <i>International Journal of Biochemistry and Cell Biology</i> , 2018, 99, 147-153.	1.2	28
23	Cell-Free Protein Synthesis for Multiple Site-Specific Incorporation of Noncanonical Amino Acids Using Cell Extracts from RF-1 Deletion <i>E. coli</i> Strains. <i>Methods in Molecular Biology</i> , 2018, 1728, 49-65.	0.4	14
24	Structural basis of protein arginine rhamnosylation by glycosyltransferase EarP. <i>Nature Chemical Biology</i> , 2018, 14, 368-374.	3.9	22
25	A <i>Thermus</i> phage protein inhibits host RNA polymerase by preventing template DNA strand loading during open promoter complex formation. <i>Nucleic Acids Research</i> , 2018, 46, 431-441.	6.5	8
26	Na ⁺ -mimicking ligands stabilize the inactive state of leukotriene B4 receptor BLT1. <i>Nature Chemical Biology</i> , 2018, 14, 262-269.	3.9	80
27	The Meningococcal Cysteine Transport System Plays a Crucial Role in <i>Neisseria meningitidis</i> Survival in Human Brain Microvascular Endothelial Cells. <i>MBio</i> , 2018, 9, .	1.8	8
28	Structural Basis for the Inhibition of Cyclin Gâ€Associated Kinase by Gefitinib. <i>ChemistryOpen</i> , 2018, 7, 713-719.	0.9	15
29	Ecto-F ₀ /F ₁ ATPase as a novel candidate of prothymosin Î± receptor. <i>Expert Opinion on Biological Therapy</i> , 2018, 18, 89-94.	1.4	7
30	Phosphorylated and non-phosphorylated HCK kinase domains produced by cell-free protein expression. <i>Protein Expression and Purification</i> , 2018, 150, 92-99.	0.6	6
31	Distinct ways of G:U recognition by conserved tRNA binding motifs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 7527-7532.	3.3	26
32	JQ1 affects BRD2-dependent and independent transcription regulation without disrupting H4-hyperacetylated chromatin states. <i>Epigenetics</i> , 2018, 13, 410-431.	1.3	32
33	Cell-free synthesis of functional antibody fragments to provide a structural basis for antibodyâ€antigen interaction. <i>PLoS ONE</i> , 2018, 13, e0193158.	1.1	20
34	IRS-1 acts as an endocytic regulator of IGF-I receptor to facilitate sustained IGF signaling. <i>ELife</i> , 2018, 7, .	2.8	43
35	Crystal structure of Deep Vent DNA polymerase. <i>Biochemical and Biophysical Research Communications</i> , 2017, 483, 52-57.	1.0	12
36	Crystal structure of <i>Aquifex aeolicus</i> gene product Aq1627: a putative phosphoglucosamine mutase reveals a unique C-terminal end-to-end disulfide linkage. <i>Molecular BioSystems</i> , 2017, 13, 1370-1376.	2.9	0

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37	Targeting Ras-Driven Cancer Cell Survival and Invasion through Selective Inhibition of DOCK1. <i>Cell Reports</i> , 2017, 19, 969-980.	2.9	51
38	Crystal structure of RNA polymerase II from <i>Komagataella pastoris</i> . <i>Biochemical and Biophysical Research Communications</i> , 2017, 487, 230-235.	1.0	15
39	Crystal structure analysis of a hypothetical protein (MJ0366) from <i>Methanocaldococcus jannaschii</i> revealed a novel topological arrangement of the knot fold. <i>Biochemical and Biophysical Research Communications</i> , 2017, 482, 264-269.	1.0	13
40	Crystal structural characterization reveals novel oligomeric interactions of human voltage-dependent anion channel 1. <i>Protein Science</i> , 2017, 26, 1749-1758.	3.1	20
41	Development and crystallographic evaluation of histone H3 peptide with N-terminal serine substitution as a potent inhibitor of lysine-specific demethylase 1. <i>Bioorganic and Medicinal Chemistry</i> , 2017, 25, 2617-2624.	1.4	22
42	Parallel homodimer structures of the extracellular domains of the voltage-gated sodium channel β 4 subunit explain its role in cell-cell adhesion. <i>Journal of Biological Chemistry</i> , 2017, 292, 13428-13440.	1.6	16
43	Extensive Survey of Antibody Invariant Positions for Efficient Chemical Conjugation Using Expanded Genetic Codes. <i>Bioconjugate Chemistry</i> , 2017, 28, 2099-2108.	1.8	15
44	Structure of the complete elongation complex of RNA polymerase II with basal factors. <i>Science</i> , 2017, 357, 921-924.	6.0	162
45	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.	3.1	5
46	Crystal structure of eIF2B and insights into eIF2B interactions. <i>FEBS Journal</i> , 2017, 284, 868-874.	2.2	21
47	Existence of two O-like intermediates in the photocycle of <i>Acetabularia</i> rhodopsin II, a light-driven proton pump from a marine alga. <i>Biophysics and Physicobiology</i> , 2017, 14, 49-55.	0.5	7
48	Trm5 and TrmD: Two Enzymes from Distinct Origins Catalyze the Identical tRNA Modification, m1G37. <i>Biomolecules</i> , 2017, 7, 32.	1.8	34
49	Theoretical Analysis of Activity Cliffs among Benzofuranone-Class Pim1 Inhibitors Using the Fragment Molecular Orbital Method with Molecular Mechanics Poisson-Boltzmann Surface Area (FMO+MM-PBSA) Approach. <i>Journal of Chemical Information and Modeling</i> , 2017, 57, 2996-3010.	2.5	41
50	Structural Mechanism for Light-driven Transport by a New Type of Chloride Ion Pump, Nonlabens marinus Rhodopsin-3. <i>Journal of Biological Chemistry</i> , 2016, 291, 17488-17495.	1.6	34
51	Crystal structure of human nucleosome core particle containing enzymatically introduced CpG methylation. <i>FEBS Open Bio</i> , 2016, 6, 498-514.	1.0	11
52	Structure-based site-directed photo-crosslinking analyses of multimeric cell-adhesive interactions of voltage-gated sodium channel β subunits. <i>Scientific Reports</i> , 2016, 6, 26618.	1.6	13
53	Expression, purification, and crystallization of <i>Schizosaccharomyces pombe</i> eIF2B. <i>Journal of Structural and Functional Genomics</i> , 2016, 17, 33-38.	1.2	4
54	Structure, Dynamics, and Interaction of p54 ^{nrb} /NonO RRM1 with 5' Splice Site RNA Sequence. <i>Biochemistry</i> , 2016, 55, 2553-2566.	1.2	13

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55	Identification of Cyproheptadine as an Inhibitor of SET Domain Containing Lysine Methyltransferase 7/9 (Set7/9) That Regulates Estrogen-Dependent Transcription. <i>Journal of Medicinal Chemistry</i> , 2016, 59, 3650-3660.	2.9	47
56	Inhibition of translation initiation complex formation by GE81112 unravels a 16S rRNA structural switch involved in P-site decoding. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E2286-95.	3.3	28
57	Cell-Free Synthesis of Membrane Proteins. <i>Springer Protocols</i> , 2016, , 123-135.	0.1	1
58	Methyl transfer by substrate signaling from a knotted protein fold. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 941-948.	3.6	74
59	Cell-Free Protein Production for Structural Biology. <i>Springer Protocols</i> , 2016, , 83-102.	0.1	5
60	Crystal structures of a subunit of the formylglycinamide ribonucleotide amidotransferase, PurS, from <i>Thermus thermophilus</i> , <i>Sulfolobus tokodaii</i> and <i>Methanocaldococcus jannaschii</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2016, 72, 627-635.	0.4	1
61	SARS-CoV 3CL protease cleaves its C-terminal autoprocessing site by novel subsite cooperativity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 12997-13002.	3.3	224
62	Crystal structures of the ATP-binding and ADP-release dwells of the V1 rotary motor. <i>Nature Communications</i> , 2016, 7, 13235.	5.8	40
63	Cell-free methods to produce structurally intact mammalian membrane proteins. <i>Scientific Reports</i> , 2016, 6, 30442.	1.6	56
64	Structural basis for disruption of claudin assembly in tight junctions by an enterotoxin. <i>Scientific Reports</i> , 2016, 6, 33632.	1.6	85
65	Histone H4 lysine 20 acetylation is associated with gene repression in human cells. <i>Scientific Reports</i> , 2016, 6, 24318.	1.6	40
66	Atomic structure of Hsp90-Cdc37-Cdk4 reveals that Hsp90 traps and stabilizes an unfolded kinase. <i>Science</i> , 2016, 352, 1542-1547.	6.0	354
67	Incorporation of a Doubly Functionalized Synthetic Amino Acid into Proteins for Creating Chemical and Light-Induced Conjugates. <i>Bioconjugate Chemistry</i> , 2016, 27, 198-206.	1.8	37
68	Binding interactions of the peripheral stalk subunit isoforms from human V-ATPase. <i>Bioscience, Biotechnology and Biochemistry</i> , 2016, 80, 878-890.	0.6	2
69	Crystal structure of eukaryotic translation initiation factor 2B. <i>Nature</i> , 2016, 531, 122-125.	13.7	103
70	<i>Neisseria meningitidis</i> Translation Elongation Factor P and Its Active-Site Arginine Residue Are Essential for Cell Viability. <i>PLoS ONE</i> , 2016, 11, e0147907.	1.1	40
71	<i>Escherichia coli</i> Cell-Free Protein Synthesis and Isotope Labeling of Mammalian Proteins. <i>Methods in Enzymology</i> , 2015, 565, 311-345.	0.4	11
72	Intra- and inter-nucleosomal interactions of the histone H4 tail revealed with a human nucleosome core particle with genetically-incorporated H4 tetra-acetylation. <i>Scientific Reports</i> , 2015, 5, 17204.	1.6	67

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73	Content of intrinsic disorder influences the outcome of cell-free protein synthesis. <i>Scientific Reports</i> , 2015, 5, 14079.	1.6	9
74	Crystal structures and ligand binding of PurM proteins from <i>Thermus thermophilus</i> and <i>Geobacillus kaustophilus</i> . <i>Journal of Biochemistry</i> , 2015, 159, mvv107.	0.9	4
75	Questionable expression of unstable <sc>DQ</sc> heterodimer containing HLA*01:07. <i>Tissue Antigens</i> , 2015, 86, 413-418.	1.0	5
76	Crystal Structure of Okadaic Acid Binding Protein 2.1: A Sponge Protein Implicated in Cytotoxin Accumulation. <i>ChemBioChem</i> , 2015, 16, 1435-1439.	1.3	7
77	Investigating the Roles of the C-Terminal Domain of <i>Plasmodium falciparum</i> GyrA. <i>PLoS ONE</i> , 2015, 10, e0142313.	1.1	6
78	Protein stabilization utilizing a redefined codon. <i>Scientific Reports</i> , 2015, 5, 9762.	1.6	35
79	Cavity as a Source of Conformational Fluctuation and High-Energy State: High-Pressure NMR Study of a Cavity-Enlarged Mutant of T4Lysozyme. <i>Biophysical Journal</i> , 2015, 108, 133-145.	0.2	36
80	Time-Resolved Raman and Polyacrylamide Gel Electrophoresis Observations of Nucleotide Incorporation and Misincorporation in RNA within a Bacterial RNA Polymerase Crystal. <i>Biochemistry</i> , 2015, 54, 652-665.	1.2	6
81	The Ratcheted and Ratchetable Structural States of RNA Polymerase Underlie Multiple Transcriptional Functions. <i>Molecular Cell</i> , 2015, 57, 408-421.	4.5	85
82	Lysine-Specific Demethylase 2 Suppresses Lipid Influx and Metabolism in Hepatic Cells. <i>Molecular and Cellular Biology</i> , 2015, 35, 1068-1080.	1.1	28
83	Expression, purification, crystallization, and preliminary X-ray crystallographic studies of the human adiponectin receptors, AdipoR1 and AdipoR2. <i>Journal of Structural and Functional Genomics</i> , 2015, 16, 11-23.	1.2	14
84	A SelB/EF-Tu/αIF2 ³ -like protein from <i>Methanosarcina mazei</i> in the GTP-bound form binds cysteinyl-tRNA ^{Cys} . <i>Journal of Structural and Functional Genomics</i> , 2015, 16, 25-41.	1.2	1
85	Highly reproductive <i>Escherichia coli</i> cells with no specific assignment to the UAG codon. <i>Scientific Reports</i> , 2015, 5, 9699.	1.6	126
86	Crystal structure of the MazG-related nucleoside triphosphate pyrophosphohydrolase from <i>Thermotoga maritima</i> MSB8. <i>Journal of Structural and Functional Genomics</i> , 2015, 16, 81-89.	1.2	1
87	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
88	Crystal structures of the human adiponectin receptors. <i>Nature</i> , 2015, 520, 312-316.	18.7	176
89	Crystal structure of the full-length bacterial selenocysteine-specific elongation factor SelB. <i>Nucleic Acids Research</i> , 2015, 43, 9028-9038.	6.5	19
90	Structural basis for the slow photocycle and late proton release in <i>Acetabularia</i> rhodopsin I from the marine plant <i>Acetabularia acetabulum</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 2203-2216.	2.5	21

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91	Multiple Functions of Glutamate Uptake via Meningococcal GltT-GltM -Glutamate ABC Transporter in <i>Neisseria meningitidis</i> Internalization into Human Brain Microvascular Endothelial Cells. <i>Infection and Immunity</i> , 2015, 83, 3555-3567.	1.0	6
92	Structural basis for methyl-donor-dependent and sequence-specific binding to tRNA substrates by knotted methyltransferase TrmD. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E4197-205.	3.3	54
93	Reassignment of a rare sense codon to a non-canonical amino acid in <i>Escherichia coli</i> . <i>Nucleic Acids Research</i> , 2015, 43, 8111-8122.	6.5	70
94	Distribution of histone H4 modifications as revealed by a panel of specific monoclonal antibodies. <i>Chromosome Research</i> , 2015, 23, 753-766.	1.0	49
95	Ratcheting of RNA polymerase toward structural principles of RNA polymerase operations. <i>Transcription</i> , 2015, 6, 56-60.	1.7	5
96	Crystal structure analysis of ornithine transcarbamylase from <i>Thermus thermophilus</i> HB8 provides insights on the plasticity of the active site. <i>Biochemical and Biophysical Research Communications</i> , 2015, 465, 174-179.	1.0	3
97	A redox switch shapes the Lon protease exit pore to facultatively regulate proteolysis. <i>Nature Chemical Biology</i> , 2015, 11, 46-51.	3.9	25
98	Structural basis for promoter specificity switching of RNA polymerase by a phage factor. <i>Genes and Development</i> , 2014, 28, 521-531.	2.7	31
99	Allosteric regulation of β -secretase activity by a phenylimidazole-type β -secretase modulator. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 10544-10549.	3.3	72
100	Kinase crystal identification and ATP-competitive inhibitor screening using the fluorescent ligand SKF86002. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 392-404.	2.5	8
101	Application of plug-plug technique to ACE experiments for discovery of peptides binding to a larger target protein: A model study of calmodulin-binding fragments selected from a digested mixture of reduced BSA. <i>Electrophoresis</i> , 2014, 35, 846-854.	1.3	6
102	Novel RNA recognition motif domain in the cytoplasmic polyadenylation element binding protein 3. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 2879-2886.	1.5	4
103	Multiple Site-Specific Installations of N^{μ} -Monomethyl-L-Lysine into Histone Proteins by Cell-Based and Cell-Free Protein Synthesis. <i>ChemBioChem</i> , 2014, 15, 1830-1838.	1.3	36
104	Molecular pathogenesis of Spondylocheirodysplastic Ehlers-Danlos syndrome caused by mutant ZIP13 proteins. <i>EMBO Molecular Medicine</i> , 2014, 6, 1028-1042.	3.3	56
105	Development of a hexahistidine-3 \times FLAG-tandem affinity purification method for endogenous protein complexes in <i>Pichia pastoris</i> . <i>Journal of Structural and Functional Genomics</i> , 2014, 15, 191-199.	1.2	12
106	Crystal structure and in silico studies of dihydrodipicolinate synthase (DHDPS) from <i>Aquifex aeolicus</i> . <i>Extremophiles</i> , 2014, 18, 973-985.	0.9	5
107	Crystal structure of the eukaryotic translation initiation factor 2A from <i>Schizosaccharomyces pombe</i> . <i>Journal of Structural and Functional Genomics</i> , 2014, 15, 125-130.	1.2	8
108	Dimer-Dimer Interaction of the Bacterial Selenocysteine Synthase SelA Promotes Functional Active-Site Formation and Catalytic Specificity. <i>Journal of Molecular Biology</i> , 2014, 426, 1723-1735.	2.0	17

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109	Cell-Free Membrane Protein Expression. <i>Methods in Molecular Biology</i> , 2014, 1118, 267-273.	0.4	11
110	Bioinformatics Analysis and Optimization of Cell-Free Protein Synthesis. <i>Methods in Molecular Biology</i> , 2014, 1118, 17-33.	0.4	6
111	Cell-Free Expression of Protein Complexes for Structural Biology. <i>Methods in Molecular Biology</i> , 2014, 1091, 151-159.	0.4	25
112	RNA Targeting by the Type III-A CRISPR-Cas Csm Complex of <i>Thermus thermophilus</i> . <i>Molecular Cell</i> , 2014, 56, 518-530.	4.5	267
113	Molecular basis of RNA polymerase promoter specificity switch revealed through studies of <i>Thermus</i> bacteriophage transcription regulator. <i>Bacteriophage</i> , 2014, 4, e29399.	1.9	3
114	Expanded Genetic Code Technologies for Incorporating Modified Lysine at Multiple Sites. <i>ChemBioChem</i> , 2014, 15, 2181-2187.	1.3	29
115	The Histidine Transporter SLC15A4 Coordinates mTOR-Dependent Inflammatory Responses and Pathogenic Antibody Production. <i>Immunity</i> , 2014, 41, 375-388.	6.6	121
116	The zinc-binding region (ZBR) fragment of Emi2 can inhibit APC/C by targeting its association with the coactivator Cdc20 and UBE2C-mediated ubiquitylation. <i>FEBS Open Bio</i> , 2014, 4, 689-703.	1.0	17
117	Structural Basis for the Specific Recognition of the Major Antigenic Peptide from the Japanese Cedar Pollen Allergen Cry j 1 by HLA-DP5. <i>Journal of Molecular Biology</i> , 2014, 426, 3016-3027.	2.0	37
118	RBFOX and SUP-12 sandwich a G base to cooperatively regulate tissue-specific splicing. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 778-786.	3.6	27
119	A new manual dispensing system for in meso membrane protein crystallization with using a stepping motor-based dispenser. <i>Journal of Structural and Functional Genomics</i> , 2014, 15, 165-171.	1.2	7
120	Crystal structures of the S6K1 kinase domain in complexes with inhibitors. <i>Journal of Structural and Functional Genomics</i> , 2014, 15, 153-164.	1.2	13
121	Crystal structure of tRNA m1A58 methyltransferase Trml from <i>Aquifex aeolicus</i> in complex with S-adenosyl-l-methionine. <i>Journal of Structural and Functional Genomics</i> , 2014, 15, 173-180.	1.2	9
122	The selective tRNA aminoacylation mechanism based on a single G-CU pair. <i>Nature</i> , 2014, 510, 507-511.	13.7	80
123	Conserved Neutralizing Epitope at Globular Head of Hemagglutinin in H3N2 Influenza Viruses. <i>Journal of Virology</i> , 2014, 88, 7130-7144.	1.5	67
124	MicroRNA-Mediated Deadenylation in a Mammalian Cell-Free System. <i>Methods in Molecular Biology</i> , 2014, 1125, 341-351.	0.4	3
125	Posttranscriptional Control of Protein Synthesis in <i>Drosophila</i> S2 Cell-Free System. <i>Methods in Molecular Biology</i> , 2014, 1118, 257-266.	0.4	0
126	Thermostable Mismatch-Recognizing Protein MutS Suppresses Nonspecific Amplification during Polymerase Chain Reaction (PCR). <i>International Journal of Molecular Sciences</i> , 2013, 14, 6436-6453.	1.8	11

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127	1H, 13C, and 15N resonance assignments of the dsRBDs of mouse RNA helicase A. <i>Biomolecular NMR Assignments</i> , 2013, 7, 69-72.	0.4	1
128	Structural basis for the altered drug sensitivities of non-small cell lung cancer-associated mutants of human epidermal growth factor receptor. <i>Oncogene</i> , 2013, 32, 27-38.	2.6	114
129	A small-molecule AdipoR agonist for type 2 diabetes and short life in obesity. <i>Nature</i> , 2013, 503, 493-499.	13.7	565
130	Immune regulatory functions of DOCK family proteins in health and disease. <i>Experimental Cell Research</i> , 2013, 319, 2343-2349.	1.2	70
131	Mutant LV476-7AA of A-subunit of <i>Enterococcus hirae</i> V1-ATPase: High affinity of A3B3 complex to DF axis and low ATPase activity. <i>SpringerPlus</i> , 2013, 2, 689.	1.2	0
132	Rotation mechanism of <i>Enterococcus hirae</i> V1-ATPase based on asymmetric crystal structures. <i>Nature</i> , 2013, 493, 703-707.	13.7	114
133	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
134	Prediction of Ligand-Induced Structural Polymorphism of Receptor Interaction Sites Using Machine Learning. <i>Journal of Chemical Information and Modeling</i> , 2013, 53, 704-716.	2.5	4
135	Reconstitution of eukaryotic translation initiation factor 3 by co-expression of the subunits in a human cell-derived in vitro protein synthesis system. <i>Protein Expression and Purification</i> , 2013, 87, 5-10.	0.6	12
136	Comparative functional analysis of CYP71AV1 natural variants reveals an important residue for the successive oxidation of amorpha-4,11-diene. <i>FEBS Letters</i> , 2013, 587, 278-284.	1.3	21
137	Crystal structure of type I 3-dehydroquinase of <i>Aquifex aeolicus</i> suggests closing of active site flap is not essential for enzyme action. <i>Biochemical and Biophysical Research Communications</i> , 2013, 432, 350-354.	1.0	2
138	A novel crystal form of pyrrolysyl-tRNA synthetase reveals the pre- and post-aminoacyl-tRNA synthesis conformational states of the adenylate and aminoacyl moieties and an asparagine residue in the catalytic site. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 5-15.	2.5	15
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