

Kazuhiko Yamasaki

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

70
papers

2,600
citations

25
h-index

50
g-index

74
ext. papers

2,966
ext. citations

5.9
avg, IF

4.25
L-index

#	Paper	IF	Citations
70	A mixing microfluidic chip for real-time NMR monitoring of macromolecular reactions. <i>Journal of Biochemistry</i> , 2021 , 170, 363-368	3.1	1
69	Development of an orally-administrable tumor vasculature-targeting therapeutic using annexin A1-binding D-peptides. <i>PLoS ONE</i> , 2021 , 16, e0241157	3.7	0
68	Enhanced affinity of racemic phosphorothioate DNA with transcription factor SATB1 arising from diastereomer-specific hydrogen bonds and hydrophobic contacts. <i>Nucleic Acids Research</i> , 2020 , 48, 4551-4561	20.1	5
67	Comprehensive analysis of PPAR α agonist activities of stereo-, regio-, and enantio-isomers of hydroxyoctadecadienoic acids. <i>Bioscience Reports</i> , 2020 , 40,	4.1	6
66	Overcoming the blood-brain barrier by Annexin A1-binding peptide to target brain tumours. <i>British Journal of Cancer</i> , 2020 , 123, 1633-1643	8.7	7
65	Specific Coordination Mode and Electrostatic Ion Atmosphere Effects of Divalent Cations Regulating Spatially Crossing Configurations of DNA Duplexes. <i>Journal of the Physical Society of Japan</i> , 2019 , 88, 044801	1.5	
64	Is it possible for short peptide composed of positively- and negatively-charged "hydrophilic" amino acid residue-clusters to form metastable "hydrophobic" packing?. <i>Physical Chemistry Chemical Physics</i> , 2019 , 21, 9683-9693	3.6	3
63	Structural basis for specific recognition of core fucosylation in N-glycans by Pholiota squarrosa lectin (PhoSL). <i>Glycobiology</i> , 2019 , 29, 576-587	5.8	4
62	Target identification reveals lanosterol synthase as a vulnerability in glioma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 7957-7962	11.5	30
61	Crystal structures of FMN-bound and FMN-free forms of dihydroorotate dehydrogenase from. <i>FEBS Open Bio</i> , 2018 , 8, 680-691	2.7	4
60	NMR Biochemical Assay for Oxidosqualene Cyclase: Evaluation of Inhibitor Activities on <i>Trypanosoma cruzi</i> and Human Enzymes. <i>Journal of Medicinal Chemistry</i> , 2018 , 61, 5047-5053	8.3	4
59	The trimeric solution structure and fucose-binding mechanism of the core fucosylation-specific lectin PhoSL. <i>Scientific Reports</i> , 2018 , 8, 7740	4.9	6
58	Biochemical and structural features of extracellular vesicle-binding RNA aptamers. <i>Biomedical Reports</i> , 2017 , 6, 615-626	1.8	7
57	Simulated Annealing-Extended Sampling for Multicomponent Decomposition of Spectral Data of DNA Complexed with Peptide. <i>Journal of the Physical Society of Japan</i> , 2017 , 86, 014802	1.5	
56	Structures, Functions, and Evolutionary Histories of DNA-Binding Domains of Plant-Specific Transcription Factors 2016 , 57-72		1
55	An NMR Biochemical Assay for Fragment-Based Drug Discovery: Evaluation of an Inhibitor Activity on Spermidine Synthase of <i>Trypanosoma cruzi</i> . <i>Journal of Medicinal Chemistry</i> , 2016 , 59, 2261-6	8.3	7
54	Development of new fusion proteins for visualizing amyloid- β oligomers in vivo. <i>Scientific Reports</i> , 2016 , 6, 22712	4.9	22

53	The combination of sequence-specific and nonspecific DNA-binding modes of transcription factor SATB1. <i>Biochemical Journal</i> , 2016 , 473, 3321-39	3.8	6
52	Analysis of ATP and AMP binding to a DNA aptamer and its imidazole-tethered derivatives by surface plasmon resonance. <i>Analyst, The</i> , 2015 , 140, 5881-4	5	9
51	Tracing primordial protein evolution through structurally guided stepwise segment elongation. <i>Journal of Biological Chemistry</i> , 2014 , 289, 3394-404	5.4	12
50	Real-time NMR monitoring of protein-folding kinetics by a recycle flow system for temperature jump. <i>Analytical Chemistry</i> , 2013 , 85, 9439-43	7.8	7
49	DNA-binding domains of plant-specific transcription factors: structure, function, and evolution. <i>Trends in Plant Science</i> , 2013 , 18, 267-76	13.1	167
48	Domain structures and inter-domain interactions defining the holoenzyme architecture of archaeal d-family DNA polymerase. <i>Life</i> , 2013 , 3, 375-85	3	3
47	Structural basis for sequence-specific DNA recognition by an Arabidopsis WRKY transcription factor. <i>Journal of Biological Chemistry</i> , 2012 , 287, 7683-91	5.4	62
46	Effect of glycosylation on cis/trans isomerization of prolines in IgA1-hinge peptide. <i>Journal of the American Chemical Society</i> , 2010 , 132, 5548-9	16.4	24
45	Solution structure of the N-terminal domain of the archaeal D-family DNA polymerase small subunit reveals evolutionary relationship to eukaryotic B-family polymerases. <i>FEBS Letters</i> , 2010 , 584, 3370-5	3.8	11
44	Glycerol stimulates innate chaperoning, proteasomal and stress-resistance functions: implications for geronto-manipulation. <i>Biogerontology</i> , 2008 , 9, 269-82	4.5	12
43	Structures and evolutionary origins of plant-specific transcription factor DNA-binding domains. <i>Plant Physiology and Biochemistry</i> , 2008 , 46, 394-401	5.4	58
42	Structural basis for recognition of the matrix attachment region of DNA by transcription factor SATB1. <i>Nucleic Acids Research</i> , 2007 , 35, 5073-84	20.1	35
41	Stress chaperones, mortalin, and pex19p mediate 5-aza-2Tdeoxycytidine-induced senescence of cancer cells by DNA methylation-independent pathway. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2007 , 62, 246-55	6.4	19
40	Mortalin sensitizes human cancer cells to MKT-077-induced senescence. <i>Cancer Letters</i> , 2007 , 252, 259-69	6.9	72
39	Cell-free synthesis of zinc-binding proteins. <i>Journal of Structural and Functional Genomics</i> , 2006 , 7, 93-100		31
38	Solution structure and DNA-binding mode of the matrix attachment region-binding domain of the transcription factor SATB1 that regulates the T-cell maturation. <i>Journal of Biological Chemistry</i> , 2006 , 281, 5319-27	5.4	23
37	An Arabidopsis SBP-domain fragment with a disrupted C-terminal zinc-binding site retains its tertiary structure. <i>FEBS Letters</i> , 2006 , 580, 2109-16	3.8	25
36	Structural and functional differences between mouse mot-1 and mot-2 proteins that differ in two amino acids. <i>Annals of the New York Academy of Sciences</i> , 2006 , 1067, 220-3	6.5	9

35	Geroprotection by glycerol: insights to its mechanisms and clinical potentials. <i>Annals of the New York Academy of Sciences</i> , 2006 , 1067, 488-92	6.5	10
34	Solution structure of an Arabidopsis WRKY DNA binding domain. <i>Plant Cell</i> , 2005 , 17, 944-56	11.6	143
33	Solution structure of the major DNA-binding domain of Arabidopsis thaliana ethylene-insensitive3-like3. <i>Journal of Molecular Biology</i> , 2005 , 348, 253-64	6.5	68
32	Solution structure of the B3 DNA binding domain of the Arabidopsis cold-responsive transcription factor RAV1. <i>Plant Cell</i> , 2004 , 16, 3448-59	11.6	91
31	10 residue folded peptide designed by segment statistics. <i>Structure</i> , 2004 , 12, 1507-18	5.2	230
30	Structural and sequence comparisons arising from the solution structure of the transcription elongation factor NusG from <i>Thermus thermophilus</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2004 , 56, 40-51	4.2	29
29	Nature of the chemical bond formed with the structural metal ion at the A9/G10.1 motif derived from hammerhead ribozymes. <i>Journal of the American Chemical Society</i> , 2004 , 126, 744-52	16.4	27
28	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	6.5	178
27	Acid-induced denaturation of Escherichia coli ribonuclease HI analyzed by CD and NMR spectroscopies. <i>Biopolymers</i> , 2003 , 69, 176-88	2.2	5
26	A modified sensor chip for surface plasmon resonance enables a rapid determination of sequence specificity of DNA-binding proteins. <i>FEBS Letters</i> , 2003 , 536, 151-6	3.8	17
25	Molecular structure and novel DNA binding sites located in loops of flap endonuclease-1 from <i>Pyrococcus horikoshii</i> . <i>Journal of Biological Chemistry</i> , 2002 , 277, 37840-7	5.4	27
24	Identification of the metal ion binding site on an RNA motif from hammerhead ribozymes using (15)N NMR spectroscopy. <i>Journal of the American Chemical Society</i> , 2002 , 124, 4595-601	16.4	48
23	Determinants in the sequence specific binding of two plant transcription factors, CBF1 and NtERF2, to the DRE and GCC motifs. <i>Biochemistry</i> , 2002 , 41, 4202-8	3.2	82
22	NMR structure of ribonuclease HI from Escherichia coli. <i>Biological and Pharmaceutical Bulletin</i> , 2000 , 23, 1147-52	2.3	10
21	A novel mode of DNA recognition by a beta-sheet revealed by the solution structure of the GCC-box binding domain in complex with DNA. <i>EMBO Journal</i> , 1998 , 17, 5484-96	13	363
20	Structural stability and internal motions of Escherichia coli ribonuclease HI: 15N relaxation and hydrogen-deuterium exchange analyses. <i>Journal of Molecular Biology</i> , 1998 , 277, 707-22	6.5	14
19	Pressure-denatured state of Escherichia coli ribonuclease HI as monitored by Fourier transform infrared and NMR spectroscopy. <i>Biochemistry</i> , 1998 , 37, 18001-9	3.2	15
18	Zinc finger proteins of the archaebacterial origin. <i>Proceedings of the Japan Academy Series B: Physical and Biological Sciences</i> , 1998 , 74, 227-232	4	

17	Methylation of adenine bases at the N6H2 groups decreases the melting temperature of the DNA duplex independently of the nucleotide sequence. <i>Proceedings of the Japan Academy Series B: Physical and Biological Sciences</i> , 1998 , 74, 210-215	4	3
16	Regional polyesterism in the GTP-bound form of the human c-Ha-Ras protein. <i>Biochemistry</i> , 1997 , 36, 9109-19	150	
15	Solution structure of an extracellular domain containing the WSxWS motif of the granulocyte colony-stimulating factor receptor and its interaction with ligand. <i>Nature Structural Biology</i> , 1997 , 4, 498-504		30
14	DNA recognition by beta-sheets. <i>Biopolymers</i> , 1997 , 44, 335-59	2.2	25
13	DNA recognition by β sheets 1997 , 44, 335		1
12	Application of the quasi-spectral density function of $(15)\text{N}$ nuclei to the selection of a motional model for model-free analysis. <i>Journal of Biomolecular NMR</i> , 1995 , 6, 423-6	3	6
11	Spectral densities of nitrogen nuclei in Escherichia coli ribonuclease HI obtained by 15N NMR relaxation and molecular dynamics. <i>Journal of Biomolecular NMR</i> , 1995 , 6, 217-20	3	17
10	Ligand binding characteristics of the carboxyl-terminal domain of the cytokine receptor homologous region of the granulocyte colony-stimulating factor receptor. <i>Journal of Biological Chemistry</i> , 1995 , 270, 27845-51	5.4	16
9	Characterization of the internal motions of Escherichia coli ribonuclease HI by a combination of 15N -NMR relaxation analysis and molecular dynamics simulation: examination of dynamic models. <i>Biochemistry</i> , 1995 , 34, 6587-601	3.2	59
8	Folding pathway of Escherichia coli ribonuclease HI: a circular dichroism, fluorescence, and NMR study. <i>Biochemistry</i> , 1995 , 34, 16552-62	3.2	65
7	Site-directed mutagenesis, fluorescence, and two-dimensional NMR studies on microenvironments of effector region aromatic residues of human c-Ha-Ras protein. <i>Biochemistry</i> , 1994 , 33, 65-73	3.2	30
6	Mutations that abolish the ability of Ha-Ras to associate with Raf-1. <i>Oncogene</i> , 1994 , 9, 2153-7	9.2	53
5	Sequence-specific 1H and 15N resonance assignments and secondary structure of GDP-bound human c-Ha-Ras protein in solution. <i>Journal of Biomolecular NMR</i> , 1993 , 3, 165-84	3	24
4	Guanine-nucleotide binding activity, interaction with GTPase-activating protein and solution conformation of the human c-Ha-Ras protein catalytic domain are retained upon deletion of C-terminal 18 amino acid residues. <i>The Protein Journal</i> , 1992 , 11, 731-9		8
3	A 1H - 15N NMR study of human c-Ha-ras protein: biosynthetic incorporation of 15N -labeled amino acids. <i>Journal of Biomolecular NMR</i> , 1992 , 2, 71-82	3	18
2	Spin-labeling proton NMR study on aromatic amino acid residues in the guanine nucleotide binding site of human c-Ha-ras(1-171) protein. <i>Biochemistry</i> , 1989 , 28, 9550-6	3.2	12
1	Conformation change of effector-region residues in antiparallel beta-sheet of human c-Ha-ras protein on GDP \rightarrow GTP gamma S exchange: a two-dimensional NMR study. <i>Biochemical and Biophysical Research Communications</i> , 1989 , 162, 1054-62	3.4	34