

# Kazuhiko Yamasaki

## List of Publications by Year in descending order

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72  
papers

3,212  
citations

218381

26  
h-index

155451

55  
g-index

74  
all docs

74  
docs citations

74  
times ranked

4100  
citing authors

#	ARTICLE	IF	CITATIONS
1	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, 5484-5496.	3.5	426
2	10 Residue Folded Peptide Designed by Segment Statistics. <i>Structure</i> , 2004, 12, 1507-1518.	1.6	278
3	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.	2.0	267
4	DNA-binding domains of plant-specific transcription factors: structure, function, and evolution. <i>Trends in Plant Science</i> , 2013, 18, 267-276.	4.3	229
5	Solution Structure of an Arabidopsis WRKY DNA Binding Domain. <i>Plant Cell</i> , 2005, 17, 944-956.	3.1	185
6	Regional Polyesterism in the GTP-Bound Form of the Human c-Ha-Ras Protein. <i>Biochemistry</i> , 1997, 36, 9109-9119.	1.2	168
7	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.	3.1	107
8	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, 4202-4208.	1.2	98
9	Structural Basis for Sequence-specific DNA Recognition by an Arabidopsis WRKY Transcription Factor. <i>Journal of Biological Chemistry</i> , 2012, 287, 7683-7691.	1.6	95
10	Solution Structure of the Major DNA-binding Domain of Arabidopsis thaliana Ethylene-insensitive3-like3. <i>Journal of Molecular Biology</i> , 2005, 348, 253-264.	2.0	82
11	Structures and evolutionary origins of plant-specific transcription factor DNA-binding domains. <i>Plant Physiology and Biochemistry</i> , 2008, 46, 394-401.	2.8	80
12	Mortalin sensitizes human cancer cells to MKT-077-induced senescence. <i>Cancer Letters</i> , 2007, 252, 259-269.	3.2	79
13	Folding Pathway of Escherichia coli Ribonuclease HI: A Circular Dichroism, Fluorescence, and NMR Study. <i>Biochemistry</i> , 1995, 34, 16552-16562.	1.2	69
14	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, 6587-6601.	1.2	61
15	Mutations that abolish the ability of Ha-Ras to associate with Raf-1. <i>Oncogene</i> , 1994, 9, 2153-7.	2.6	56
16	Identification of the Metal Ion Binding Site on an RNA Motif from Hammerhead Ribozymes Using 15N NMR Spectroscopy. <i>Journal of the American Chemical Society</i> , 2002, 124, 4595-4601.	6.6	52
17	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.	3.3	52
18	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.	1.3	45

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19	Structural basis for recognition of the matrix attachment region of DNA by transcription factor SATB1. <i>Nucleic Acids Research</i> , 2007, 35, 5073-5084.	6.5	44
20	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.	1.2	36
21	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, 1054-1062.	1.0	35
22	Cell-free synthesis of zinc-binding proteins. <i>Journal of Structural and Functional Genomics</i> , 2007, 7, 93-100.	1.2	34
23	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.	9.7	33
24	Development of new fusion proteins for visualizing amyloid- $\beta$ oligomers in vivo. <i>Scientific Reports</i> , 2016, 6, 22712.	1.6	32
25	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.	1.5	30
26	DNA recognition by $\beta$ -sheets. , 1997, 44, 335-359.		29
27	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, 37840-37847.	1.6	29
28	Stress Chaperones, Mortalin, and Pex19p Mediate 5-Aza-2' Deoxycytidine-Induced Senescence of Cancer Cells by DNA Methylation-Independent Pathway. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2007, 62, 246-255.	1.7	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, 744-752.	6.6	28
30	Effect of Glycosylation on <i>Cis</i> / <i>Trans</i> Isomerization of Prolines in IgA1-Hinge Peptide. <i>Journal of the American Chemical Society</i> , 2010, 132, 5548-5549.	6.6	25
31	Sequence-specific $^1\text{H}$ and $^{15}\text{N}$ 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.	1.6	24
32	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, 5319-5327.	1.6	24
33	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, 27845-27851.	1.6	21
34	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, 151-156.	1.3	19
35	$^1\text{H}$ - $^{15}\text{N}$ NMR study of human c-Ha-ras protein: Biosynthetic incorporation of $^{15}\text{N}$ -labeled amino acids. <i>Journal of Biomolecular NMR</i> , 1992, 2, 71-82.	1.6	18
36	Spectral densities of nitrogen nuclei in <i>Escherichia coli</i> ribonuclease HI obtained by $^{15}\text{N}$ NMR relaxation and molecular dynamics. <i>Journal of Biomolecular NMR</i> , 1995, 6, 217-220.	1.6	18

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37	Pressure-Denatured State of Escherichia coli Ribonuclease HI As Monitored by Fourier Transform Infrared and NMR Spectroscopy. <i>Biochemistry</i> , 1998, 37, 18001-18009.	1.2	16
38	Comprehensive analysis of PPAR $\beta$ agonist activities of stereo-, regio-, and enantio-isomers of hydroxyoctadecadienoic acids. <i>Bioscience Reports</i> , 2020, 40, .	1.1	16
39	Structural stability and internal motions of Escherichia coli ribonuclease HI: 15 N relaxation and hydrogen-deuterium exchange analyses 1 Edited by P. E. Wright. <i>Journal of Molecular Biology</i> , 1998, 277, 707-722.	2.0	14
40	Glycerol stimulates innate chaperoning, proteasomal and stress-resistance functions: implications for geronto-manipulation. <i>Biogerontology</i> , 2008, 9, 269-282.	2.0	14
41	Solution structure of the N-terminal domain of the archaeal DNA polymerase small subunit reveals evolutionary relationship to eukaryotic DNA polymerases. <i>FEBS Letters</i> , 2010, 584, 3370-3375.	1.3	14
42	Tracing Primordial Protein Evolution through Structurally Guided Stepwise Segment Elongation. <i>Journal of Biological Chemistry</i> , 2014, 289, 3394-3404.	1.6	14
43	The trimeric solution structure and fucose-binding mechanism of the core fucosylation-specific lectin PhoSL. <i>Scientific Reports</i> , 2018, 8, 7740.	1.6	14
44	Geroprotection by Glycerol: Insights to Its Mechanisms and Clinical Potentials. <i>Annals of the New York Academy of Sciences</i> , 2006, 1067, 488-492.	1.8	13
45	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, 9550-9556.	1.2	12
46	NMR Structure of Ribonuclease HI from Escherichia coli.. <i>Biological and Pharmaceutical Bulletin</i> , 2000, 23, 1147-1152.	0.6	11
47	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, 220-223.	1.8	11
48	Overcoming the blood-brain barrier by Annexin A1-binding peptide to target brain tumours. <i>British Journal of Cancer</i> , 2020, 123, 1633-1643.	2.9	11
49	Real-Time NMR Monitoring of Protein-Folding Kinetics by a Recycle Flow System for Temperature Jump. <i>Analytical Chemistry</i> , 2013, 85, 9439-9443.	3.2	9
50	Analysis of ATP and AMP binding to a DNA aptamer and its imidazole-tethered derivatives by surface plasmon resonance. <i>Analyt. The</i> , 2015, 140, 5881-5884.	1.7	9
51	The combination of sequence-specific and nonspecific DNA-binding modes of transcription factor SATB1. <i>Biochemical Journal</i> , 2016, 473, 3321-3339.	1.7	9
52	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.	6.5	9
53	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, 731-739.	1.1	8
54	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, 2261-2266.	2.9	8

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55	Biochemical and structural features of extracellular vesicle-binding RNA aptamers. <i>Biomedical Reports</i> , 2017, 6, 615-626.	0.9	8
56	Structural basis for specific recognition of core fucosylation in N-glycans by <i>Pholiota squarrosa</i> lectin (PhoSL). <i>Glycobiology</i> , 2019, 29, 576-587.	1.3	8
57	Application of the quasi-spectral density function of <sup>15</sup> N nuclei to the selection of a motional model for model-free analysis. <i>Journal of Biomolecular NMR</i> , 1995, 6, 423-6.	1.6	7
58	Crystal structures of FMN bound and FMN free forms of dihydroorotate dehydrogenase from <i>Trypanosoma brucei</i> . <i>FEBS Open Bio</i> , 2018, 8, 680-691.	1.0	7
59	Acid-induced denaturation of <i>Escherichia coli</i> ribonuclease HI analyzed by CD and NMR spectroscopies. <i>Biopolymers</i> , 2003, 69, 176-188.	1.2	6
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.	2.9	5
61	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.	1.3	5
62	Development of an orally-administrable tumor vasculature-targeting therapeutic using annexin A1-binding D-peptides. <i>PLoS ONE</i> , 2021, 16, e0241157.	1.1	5
63	Domain Structures and Inter-Domain Interactions Defining the Holoenzyme Architecture of Archaeal D-Family DNA Polymerase. <i>Life</i> , 2013, 3, 375-385.	1.1	4
64	Methylation of adenine bases at the N <sup>6</sup> H <sub>2</sub> 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.	1.6	3
65	Structures, Functions, and Evolutionary Histories of DNA-Binding Domains of Plant-Specific Transcription Factors. , 2016, , 57-72.		1
66	A mixing microfluidic chip for real-time NMR monitoring of macromolecular reactions. <i>Journal of Biochemistry</i> , 2021, 170, 363-368.	0.9	1
67	DNA recognition by $\beta$ -sheets. , 1997, 44, 335.		1
68	Fragment-Based Drug Discovery for <i>Trypanosoma brucei</i> Glycosylphosphatidylinositol-Specific Phospholipase C through Biochemical and WaterLOGSY-NMR Methods. <i>Journal of Biochemistry</i> , 2022, , .	0.9	1
69	Old yellow enzyme of a novel fungi-specific class. <i>FEBS Journal</i> , 2022, , .	2.2	1
70	Zinc finger proteins of the archaeobacterial origin. <i>Proceedings of the Japan Academy Series B: Physical and Biological Sciences</i> , 1998, 74, 227-232.	1.6	0
71	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.	0.7	0
72	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.	0.7	0