

Yutaka Ito

List of Publications by Year in descending order

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95
papers

4,135
citations

147801

31
h-index

114465

63
g-index

98
all docs

98
docs citations

98
times ranked

3588
citing authors

#	ARTICLE	IF	CITATIONS
1	Cell-free production and stable-isotope labeling of milligram quantities of proteins. FEBS Letters, 1999, 442, 15-19.	2.8	463
2	High-resolution multi-dimensional NMR spectroscopy of proteins in human cells. Nature, 2009, 458, 106-109.	27.8	410
3	Protein structure determination in living cells by in-cell NMR spectroscopy. Nature, 2009, 458, 102-105.	27.8	317
4	Structural genomics projects in Japan. Nature Structural Biology, 2000, 7, 943-945.	9.7	316
5	Regional Polyesterism in the GTP-Bound Form of the Human c-Ha-Ras Protein., Biochemistry, 1997, 36, 9109-9119.	2.5	168
6	The N-terminal domain of the human Rad51 protein binds DNA: structure and a DNA binding surface as revealed by NMR. Journal of Molecular Biology, 1999, 290, 495-504.	4.2	134
7	Dual amino acid-selective and site-directed stable-isotope labeling of the human c-Ha-Ras protein by cell-free synthesis. Journal of Biomolecular NMR, 1998, 11, 295-306.	2.8	126
8	In-cell NMR spectroscopy of proteins inside Xenopus laevis oocytes. Journal of Biomolecular NMR, 2006, 36, 179-188.	2.8	120
9	An Approach to the Structure Determination of Larger Proteins Using Triple Resonance NMR Experiments in Conjunction with Random Fractional Deuteration. Journal of the American Chemical Society, 1996, 118, 407-415.	13.7	114
10	An extended DNA structure through deoxyribose-base stacking induced by RecA protein. Proceedings of the National Academy of Sciences of the United States of America, 1997, 94, 6623-6628.	7.1	103
11	Base pair switching by interconversion of sugar puckers in DNA extended by proteins of RecA-family: A model for homology search in homologous genetic recombination. Proceedings of the National Academy of Sciences of the United States of America, 1998, 95, 11071-11076.	7.1	82
12	High-Resolution Heteronuclear Multidimensional NMR of Proteins in Living Insect Cells Using a Baculovirus Protein Expression System. Journal of the American Chemical Society, 2013, 135, 1688-1691.	13.7	81
13	An interaction between a specified surface of the C-terminal domain of RecA protein and double-stranded DNA for homologous pairing. Journal of Molecular Biology, 1997, 274, 213-221.	4.2	80
14	Cellular structural biology. Current Opinion in Structural Biology, 2010, 20, 640-648.	5.7	75
15	Intermolecular ^{31}P - ^{15}N and ^{31}P - ^1H Scalar Couplings Across Hydrogen Bonds Formed between a Protein and a Nucleotide. Journal of the American Chemical Society, 2000, 122, 5883-5884.	13.7	64
16	Homologous genetic recombination as an intrinsic dynamic property of a DNA structure induced by RecA/Rad51-family proteins: A possible advantage of DNA over RNA as genomic material. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 8425-8432.	7.1	64
17	An approach to global fold determination using limited NMR data from larger proteins selectively protonated at specific residue types. Journal of Biomolecular NMR, 1996, 8, 360-368.	2.8	56
18	High-Resolution Protein 3D Structure Determination in Living Eukaryotic Cells. Angewandte Chemie - International Edition, 2019, 58, 7284-7288.	13.8	52

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19	Structural genomics projects in Japan. <i>Progress in Biophysics and Molecular Biology</i> , 2000, 73, 363-376.	2.9	49
20	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
21	A Novel Approach for the Sequential Backbone Assignment of Larger Proteins: A Selective Intra-HNCA and DQ-HNCA. <i>Journal of the American Chemical Society</i> , 2002, 124, 11199-11207.	13.7	45
22	Improved in-cell structure determination of proteins at near-physiological concentration. <i>Scientific Reports</i> , 2016, 6, 38312.	3.3	43
23	NMR protein structure determination in living <i>E. coli</i> cells using nonlinear sampling. <i>Nature Protocols</i> , 2010, 5, 1051-1060.	12.0	42
24	A new carbamidemethyl-linked lanthanoid chelating tag for PCS NMR spectroscopy of proteins in living HeLa cells. <i>Journal of Biomolecular NMR</i> , 2016, 66, 99-110.	2.8	42
25	Parkinson's disease-related DJ-1 functions in thiol quality control against aldehyde attack in vitro. <i>Scientific Reports</i> , 2017, 7, 12816.	3.3	41
26	Impact of cellular health conditions on the protein folding state in mammalian cells. <i>Chemical Communications</i> , 2017, 53, 11245-11248.	4.1	40
27	Identification of the RecR Toprim Domain as the Binding Site for both RecF and RecO. <i>Journal of Biological Chemistry</i> , 2006, 281, 18549-18559.	3.4	39
28	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.	2.5	36
29	Conformation change of effector-region residues in antiparallel β -sheet of human c-Ha-ras protein on GDP \rightarrow GTP γ S exchange: A two-dimensional NMR study. <i>Biochemical and Biophysical Research Communications</i> , 1989, 162, 1054-1062.	2.1	35
30	A Mechanism for Single-stranded DNA-binding Protein (SSB) Displacement from Single-stranded DNA upon SSB-RecO Interaction. <i>Journal of Biological Chemistry</i> , 2011, 286, 6720-6732.	3.4	35
31	Structural insights into ubiquitin phosphorylation by PINK1. <i>Scientific Reports</i> , 2018, 8, 10382.	3.3	35
32	A novel method for the biosynthesis of deuterated proteins with selective protonation at the aromatic rings of Phe, Tyr and Trp. <i>Journal of Biomolecular NMR</i> , 2003, 27, 81-86.	2.8	32
33	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
34	An NMR study on the interaction of <i>Escherichia coli</i> DinI with RecA-ssDNA complexes. <i>Nucleic Acids Research</i> , 2003, 31, 1735-1743.	14.5	27
35	Solution structure of the HRDC domain of human Bloom syndrome protein BLM. <i>Journal of Biochemistry</i> , 2010, 148, 517-525.	1.7	27
36	In situ structural biology using in-cell NMR. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2020, 1864, 129364.	2.4	27

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37	Ubiquitin Binding Interface Mapping on Yeast Ubiquitin Hydrolase by NMR Chemical Shift Perturbation. <i>Biochemistry</i> , 1999, 38, 9242-9253.	2.5	26
38	Exclusively NOESY-based automated NMR assignment and structure determination of proteins. <i>Journal of Biomolecular NMR</i> , 2011, 50, 137-146.	2.8	26
39	An in-cell NMR study of monitoring stress-induced increase of cytosolic Ca ²⁺ concentration in HeLa cells. <i>Biochemical and Biophysical Research Communications</i> , 2013, 438, 653-659.	2.1	26
40	Solution NMR views of dynamical ordering of biomacromolecules. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2018, 1862, 287-306.	2.4	26
41	An NMR Analysis of Ubiquitin Recognition by Yeast Ubiquitin Hydrolase: Evidence for Novel Substrate Recognition by a Cysteine Protease. <i>Biochemistry</i> , 1999, 38, 11634-11642.	2.5	25
42	Structural Insights into the Recruitment of SMRT by the Corepressor SHARP under Phosphorylative Regulation. <i>Structure</i> , 2014, 22, 35-46.	3.3	25
43	Protein Structure Determination in Living Cells. <i>International Journal of Molecular Sciences</i> , 2019, 20, 2442.	4.1	25
44	Conformation of guanosine 5'-diphosphate as bound to a human c-Ha-ras mutant protein: a nuclear Overhauser effect study. <i>Biochemistry</i> , 1989, 28, 8411-8416.	2.5	24
45	Sequence-specific ¹ H and ¹⁵ 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.	2.8	24
46	A Constitutive Effector Region on the C-terminal Side of Switch I of the Ras Protein. <i>Journal of Biological Chemistry</i> , 1995, 270, 4661-4667.	3.4	24
47	Solution structure of the Ras-binding domain of RGL. <i>FEBS Letters</i> , 1998, 441, 413-418.	2.8	24
48	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
49	Myristoylation-regulated Direct Interaction Between Calcium-bound Calmodulin and N-terminal Region of pp60v-src. <i>Journal of Molecular Biology</i> , 2004, 338, 169-180.	4.2	22
50	Understanding the roles of amino acid residues in tertiary structure formation of chignolin by using molecular dynamics simulation. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 73, 621-631.	2.6	22
51	Characterization of the Structural Difference between Active and Inactive Forms of the Ras Protein by Chemical Modification Followed by Mass Spectrometric Peptide Mapping. <i>Analytical Biochemistry</i> , 1997, 248, 15-25.	2.4	21
52	Solution Structure of the C-Terminal Transcriptional Activator Domain of FixJ from <i>Sinorhizobium meliloti</i> and Its Recognition of the fixK Promoter. <i>Biochemistry</i> , 2005, 44, 14835-14844.	2.5	20
53	Solution structure of the <i>E. coli</i> ribosome hibernation promoting factor HPF: Implications for the relationship between structure and function. <i>Biochemical and Biophysical Research Communications</i> , 2009, 389, 580-585.	2.1	20
54	A ¹ H- ¹⁵ N NMR study of human c-Ha-ras protein: Biosynthetic incorporation of ¹⁵ N-labeled amino acids. <i>Journal of Biomolecular NMR</i> , 1992, 2, 71-82.	2.8	18

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55	Present Status of 920 MHz High-Resolution NMR Spectrometers. <i>IEEE Transactions on Applied Superconductivity</i> , 2004, 14, 1608-1612.	1.7	18
56	A Non-canonical DNA Structure Enables Homologous Recombination in Various Genetic Systems. <i>Journal of Biological Chemistry</i> , 2009, 284, 30230-30239.	3.4	18
57	Solution structure of a zinc-finger domain that binds to poly(ADP-ribose). <i>Genes To Cells</i> , 2010, 15, 101-110.	1.2	17
58	Design of λ Cro Fold: Solution Structure of a Monomeric Variant of the De Novo Protein. <i>Journal of Molecular Biology</i> , 2005, 354, 801-814.	4.2	14
59	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.	2.5	12
60	Microtubule-binding sites of the CH domain of EB1 and its autoinhibition revealed by NMR. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013, 1834, 499-507.	2.3	11
61	Structural basis of the photochromic green/red photocycle of the chromatic acclimation sensor RcaE. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	11
62	In-Cell NMR of Intrinsically Disordered Proteins in Prokaryotic Cells. <i>Methods in Molecular Biology</i> , 2012, 895, 19-31.	0.9	10
63	Protein NMR Structure Refinement based on Bayesian Inference. <i>Journal of Physics: Conference Series</i> , 2016, 699, 012005.	0.4	10
64	Heteronuclear multidimensional NMR and homology modelling studies of the C-terminal nucleotide-binding domain of the human mitochondrial ABC transporter ABCB6. <i>Journal of Biomolecular NMR</i> , 2006, 35, 53-71.	2.8	9
65	NMR assignments of SPOC domain of the human transcriptional corepressor SHARP in complex with a C-terminal SMRT peptide. <i>Biomolecular NMR Assignments</i> , 2013, 7, 267-270.	0.8	9
66	Efficient and cost effective production of active-form human PKB using silkworm larvae. <i>Scientific Reports</i> , 2015, 4, 6016.	3.3	9
67	High-Resolution Protein 3D Structure Determination in Living Eukaryotic Cells. <i>Angewandte Chemie</i> , 2019, 131, 7362-7366.	2.0	9
68	In-cell NMR as a sensitive tool to monitor physiological condition of Escherichia coli. <i>Scientific Reports</i> , 2020, 10, 2466.	3.3	9
69	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
70	Automated resonance assignment of the 21 kDa stereo-array isotope labeled thioldisulfide oxidoreductase DsbA. <i>Journal of Magnetic Resonance</i> , 2014, 249, 88-93.	2.1	7
71	Evaluation of the reliability of the maximum entropy method for reconstructing 3D and 4D NOESY-type NMR spectra of proteins. <i>Biochemical and Biophysical Research Communications</i> , 2015, 457, 200-205.	2.1	5
72	Letter to the Editor: Backbone ^1H , ^{13}C , and ^{15}N Assignments of a 42 kDa RecR Homodimer. <i>Journal of Biomolecular NMR</i> , 2004, 28, 199-200.	2.8	4

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73	Structure of the second RRM domain of Nrd1, a fission yeast MAPK target RNA binding protein, and implication for its RNA recognition and regulation. <i>Biochemical and Biophysical Research Communications</i> , 2013, 437, 12-17.	2.1	4
74	Domain selective labeling for NMR studies of multidomain proteins by domain ligation using highly active sortase A. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2020, 1864, 129419.	2.4	4
75	Backbone ¹ H, ¹³ C, and ¹⁵ N E. coli nickel binding protein NikA. <i>Journal of Biomolecular NMR</i> , 2005, 32, 177-177.	2.8	3
76	Insights into substrate recognition by the Escherichia coli Orf135 protein through its solution structure. <i>Biochemical and Biophysical Research Communications</i> , 2012, 420, 263-268.	2.1	3
77	Chemical shift assignments of the first and second RRM of Nrd1, a fission yeast MAPK-target RNA binding protein. <i>Biomolecular NMR Assignments</i> , 2017, 11, 123-126.	0.8	3
78	Interactions of in vitro selected fluorogenic peptide aptamers with calmodulin. <i>Biotechnology Letters</i> , 2017, 39, 375-382.	2.2	3
79	Assignments of the ¹ H, ¹³ C, and ¹⁵ N resonances of the 21 kDa Vesl/Homer family protein, Vesl-1S. <i>Journal of Biomolecular NMR</i> , 2000, 18, 181-182.	2.8	2
80	¹ H, ¹³ C and ¹⁵ N NMR assignments of the Escherichia coli Orf135 protein. <i>Biomolecular NMR Assignments</i> , 2012, 6, 1-4.	0.8	1
81	The crystal and solution structure of YdiE from Escherichia coli. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 919-924.	0.8	1
82	A specific single-stranded DNA induces a distinct conformational change in the nucleoid-associated protein HU. <i>Biochemistry and Biophysics Reports</i> , 2016, 8, 318-324.	1.3	1
83	Structure, Dynamics and Folding Stability of Proteins Inside Living Cells: Recent Findings from In-cell NMR Studies. <i>Seibutsu Butsuri</i> , 2013, 53, 076-081.	0.1	1
84	S1f2-1 NMR studies of periplasmic binding proteins(S1-f2: "Functions and dynamics of protein systems in) Tj ETQq0 0 0 rgBT /Overlock S119.	0.1	0
85	2P014 Structural and functional analysis of split PH domain of Rho-kinase(Proteins-structure and) Tj ETQq1 1 0.784314 rgBT /Overlock 0,1	0.1	0
86	1P060 Applications of nonlinear sampling scheme for four dimensional triple resonance NMR spectroscopy(Proteins-methodology,Poster Presentations). <i>Seibutsu Butsuri</i> , 2007, 47, S38.	0.1	0
87	Backbone ¹ H, ¹³ C and ¹⁵ N assignments of a 59 kDa Salmonella typhimurium periplasmic oligopeptide binding protein, OppA. <i>Biomolecular NMR Assignments</i> , 2007, 1, 37-39.	0.8	0
88	3P-051 Applications of nonlinear sampling scheme to four dimensional triple resonance NMR spectroscopy(The 46th Annual Meeting of the Biophysical Society of Japan). <i>Seibutsu Butsuri</i> , 2008, 48, S135.	0.1	0
89	2P-022 Investigating protein three-dimensional structures inside living cells by in-cell NMR spectroscopy(The 46th Annual Meeting of the Biophysical Society of Japan). <i>Seibutsu Butsuri</i> , 2008, 48, S78.	0.1	0
90	3P004 Structural studies of microtubule pulse-end tracking protein EB1 by solution NMR spectroscopy(Protein: Structure,The 48th Annual Meeting of the Biophysical Society of Japan). <i>Seibutsu Butsuri</i> , 2010, 50, S145.	0.1	0

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91	3P008 Structural studies of tubulin tyrosine ligase using solution NMR spectroscopy(Protein:) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T S146.	0.1	0
92	2SB-02 Protein NMR spectroscopy in the cellular environment(2SB Symposium organized by younger) Tj ETQq0 0 0 rgBT /Overlock 10 T	0.1	0
93	Advances in NMR Data Acquisition and Processing for Protein Structure Determination. , 2018, , 63-90.		0
94	New Techniques for NMR Structural Biology. Journal of Pesticide Sciences, 1996, 21, 450-459.	1.4	0
95	Protein NMR Structure Refinement Based on Bayesian Inference for Dynamical Ordering of Biomacromolecules. Journal of Computer Chemistry Japan, 2018, 17, 65-75.	0.1	0