

Yutaka Ito

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2888460/publications.pdf>

Version: 2024-02-01

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	Structural basis of the protochromic green/red photocycle of the chromatic acclimation sensor RcaE. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	11
2	In situ structural biology using in-cell NMR. Biochimica Et Biophysica Acta - General Subjects, 2020, 1864, 129364.	2.4	27
3	Domain selective labeling for NMR studies of multidomain proteins by domain ligation using highly active sortase A. Biochimica Et Biophysica Acta - General Subjects, 2020, 1864, 129419.	2.4	4
4	In-cell NMR as a sensitive tool to monitor physiological condition of Escherichia coli. Scientific Reports, 2020, 10, 2466.	3.3	9
5	Protein Structure Determination in Living Cells. International Journal of Molecular Sciences, 2019, 20, 2442.	4.1	25
6	High-Resolution Protein 3D Structure Determination in Living Eukaryotic Cells. Angewandte Chemie - International Edition, 2019, 58, 7284-7288.	13.8	52
7	High-Resolution Protein 3D Structure Determination in Living Eukaryotic Cells. Angewandte Chemie, 2019, 131, 7362-7366.	2.0	9
8	Solution NMR views of dynamical ordering of biomacromolecules. Biochimica Et Biophysica Acta - General Subjects, 2018, 1862, 287-306.	2.4	26
9	Advances in NMR Data Acquisition and Processing for Protein Structure Determination. , 2018, , 63-90.		0
10	Structural insights into ubiquitin phosphorylation by PINK1. Scientific Reports, 2018, 8, 10382.	3.3	35
11	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
12	Chemical shift assignments of the first and second RRM of Nrd1, a fission yeast MAPK-target RNA binding protein. Biomolecular NMR Assignments, 2017, 11, 123-126.	0.8	3
13	Parkinson's disease-related DJ-1 functions in thiol quality control against aldehyde attack in vitro. Scientific Reports, 2017, 7, 12816.	3.3	41
14	Impact of cellular health conditions on the protein folding state in mammalian cells. Chemical Communications, 2017, 53, 11245-11248.	4.1	40
15	Interactions of in vitro selected fluorogenic peptide aptamers with calmodulin. Biotechnology Letters, 2017, 39, 375-382.	2.2	3
16	Protein NMR Structure Refinement based on Bayesian Inference. Journal of Physics: Conference Series, 2016, 699, 012005.	0.4	10
17	Improved in-cell structure determination of proteins at near-physiological concentration. Scientific Reports, 2016, 6, 38312.	3.3	43
18	A specific single-stranded DNA induces a distinct conformational change in the nucleoid-associated protein HU. Biochemistry and Biophysics Reports, 2016, 8, 318-324.	1.3	1

#	ARTICLE	IF	CITATIONS
19	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
20	Efficient and cost effective production of active-form human PKB using silkworm larvae. <i>Scientific Reports</i> , 2015, 4, 6016.	3.3	9
21	The crystal and solution structure of YdiE from <i>Escherichia coli</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 919-924.	0.8	1
22	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
23	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
24	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
25	Structural Insights into the Recruitment of SMRT by the Corepressor SHARP under Phosphorylative Regulation. <i>Structure</i> , 2014, 22, 35-46.	3.3	25
26	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
27	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
28	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
29	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
30	High-Resolution Heteronuclear Multidimensional NMR of Proteins in Living Insect Cells Using a Baculovirus Protein Expression System. <i>Journal of the American Chemical Society</i> , 2013, 135, 1688-1691.	13.7	81
31	Structure, Dynamics and Folding Stability of Proteins Inside Living Cells: Recent Findings from In-cell NMR Studies. <i>Seibutsu Butsurei</i> , 2013, 53, 076-081.	0.1	1
32	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
33	Insights into substrate recognition by the <i>Escherichia coli</i> Orf135 protein through its solution structure. <i>Biochemical and Biophysical Research Communications</i> , 2012, 420, 263-268.	2.1	3
34	In-Cell NMR of Intrinsically Disordered Proteins in Prokaryotic Cells. <i>Methods in Molecular Biology</i> , 2012, 895, 19-31.	0.9	10
35	¹ H, ¹³ C and ¹⁵ N NMR assignments of the <i>Escherichia coli</i> Orf135 protein. <i>Biomolecular NMR Assignments</i> , 2012, 6, 1-4.	0.8	1
36	Exclusively NOESY-based automated NMR assignment and structure determination of proteins. <i>Journal of Biomolecular NMR</i> , 2011, 50, 137-146.	2.8	26

#	ARTICLE	IF	CITATIONS
37	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
38	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
39	3P008 Structural studies of tubulin tyrosine ligase using solution NMR spectroscopy(Protein:) Tj ETQq1 1 0.784314 rgBT /Overlock 10 S146.	0.1	0
40	Cellular structural biology. <i>Current Opinion in Structural Biology</i> , 2010, 20, 640-648.	5.7	75
41	Solution structure of a zincâ€fingering domain that binds to polyâ€ADPâ€ribose. <i>Genes To Cells</i> , 2010, 15, 101-110.	1.2	17
42	NMR protein structure determination in living E. coli cells using nonlinear sampling. <i>Nature Protocols</i> , 2010, 5, 1051-1060.	12.0	42
43	Solution structure of the HRDC domain of human Bloom syndrome protein BLM. <i>Journal of Biochemistry</i> , 2010, 148, 517-525.	1.7	27
44	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
45	Protein structure determination in living cells by in-cell NMR spectroscopy. <i>Nature</i> , 2009, 458, 102-105.	27.8	317
46	High-resolution multi-dimensional NMR spectroscopy of proteins in human cells. <i>Nature</i> , 2009, 458, 106-109.	27.8	410
47	Solution structure of the E. coli 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
48	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
49	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
50	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
51	2P014 Structural and functional analysis of split PH domain of Rho-kinase(Proteins-structure and) Tj ETQq1 1 0.784314 rgBT /Overlock 10	0.1	0
52	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
53	Backbone 1H, 13C and 15N assignments of a 59ÅkDa Salmonella typhimurium periplasmic oligopeptide binding protein, OppA. <i>Biomolecular NMR Assignments</i> , 2007, 1, 37-39.	0.8	0
54	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

#	ARTICLE	IF	CITATIONS
55	S1f2-1 NMR studies of periplasmic binding proteins(S1-f2: "Functions and dynamics of protein systems in) Tj ETQq1 1 0.784314 rgBT S119.	0.1	0
56	Heteronuclear multidimensional NMR and homology modelling studies of the C-terminal nucleotide-binding domain of the human mitochondrial ABC transporter ABCB6. Journal of Biomolecular NMR, 2006, 35, 53-71.	2.8	9
57	In-cell NMR spectroscopy of proteins inside <i>Xenopus laevis</i> oocytes. Journal of Biomolecular NMR, 2006, 36, 179-188.	2.8	120
58	Backbone ¹ H, ¹³ C, and ¹⁵ N E. coli nickel binding protein NikA. Journal of Biomolecular NMR, 2005, 32, 177-177.	2.8	3
59	Solution Structure of the C-Terminal Transcriptional Activator Domain of FixJ from <i>Sinorhizobium meliloti</i> and Its Recognition of the fixK Promoter,. Biochemistry, 2005, 44, 14835-14844.	2.5	20
60	Design of $\hat{\iota}$ Cro Fold: Solution Structure of a Monomeric Variant of the De Novo Protein. Journal of Molecular Biology, 2005, 354, 801-814.	4.2	14
61	Present Status of 920 MHz High-Resolution NMR Spectrometers. IEEE Transactions on Applied Superconductivity, 2004, 14, 1608-1612.	1.7	18
62	Letter to the Editor: Backbone ¹ H, ¹³ C, and ¹⁵ N Assignments of a 42ÅkDa RecR Homodimer. Journal of Biomolecular NMR, 2004, 28, 199-200.	2.8	4
63	Myristoylation-regulated Direct Interaction Between Calcium-bound Calmodulin and N-terminal Region of pp60v-src. Journal of Molecular Biology, 2004, 338, 169-180.	4.2	22
64	A novel method for the biosynthesis of deuterated proteins with selective protonation at the aromatic rings of Phe, Tyr and Trp. Journal of Biomolecular NMR, 2003, 27, 81-86.	2.8	32
65	An NMR study on the interaction of <i>Escherichia coli</i> DinI with RecA-ssDNA complexes. Nucleic Acids Research, 2003, 31, 1735-1743.	14.5	27
66	A Novel Approach for the Sequential Backbone Assignment of Larger Proteins: $\hat{\Lambda}$ Selective Intra-HNCA and DQ-HNCA. Journal of the American Chemical Society, 2002, 124, 11199-11207.	13.7	45
67	Solution structure of the human parvulin-like peptidyl prolyl cis/trans isomerase, hPar14. Journal of Molecular Biology, 2001, 305, 917-926.	4.2	30
68	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
69	Structural genomics projects in Japan. Nature Structural Biology, 2000, 7, 943-945.	9.7	316
70	Structural genomics projects in Japan. Progress in Biophysics and Molecular Biology, 2000, 73, 363-376.	2.9	49
71	Assignments of the ¹ H, ¹³ C, and ¹⁵ N resonances of the 21 kDa Vesl/Homer family protein, Vesl-1S. Journal of Biomolecular NMR, 2000, 18, 181-182.	2.8	2
72	Intermolecular ³¹ P $\hat{\omega}$ ¹⁵ N and ³¹ P $\hat{\omega}$ ¹ H 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

#	ARTICLE	IF	CITATIONS
73	Cell-free production and stable-isotope labeling of milligram quantities of proteins. FEBS Letters, 1999, 442, 15-19.	2.8	463
74	Ubiquitin Binding Interface Mapping on Yeast Ubiquitin Hydrolase by NMR Chemical Shift Perturbation. Biochemistry, 1999, 38, 9242-9253.	2.5	26
75	An NMR Analysis of Ubiquitin Recognition by Yeast Ubiquitin Hydrolase: Evidence for Novel Substrate Recognition by a Cysteine Protease. Biochemistry, 1999, 38, 11634-11642.	2.5	25
76	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. Journal of Molecular Biology, 1999, 286, 219-232.	4.2	45
77	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
78	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
79	Solution structure of the Ras-binding domain of RGL. FEBS Letters, 1998, 441, 413-418.	2.8	24
80	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
81	Regional Polyesterism in the GTP-Bound Form of the Human c-Ha-Ras Protein. Biochemistry, 1997, 36, 9109-9119.	2.5	168
82	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
83	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
84	Characterization of the Structural Difference between Active and Inactive Forms of the Ras Protein by Chemical Modification Followed by Mass Spectrometric Peptide Mapping. Analytical Biochemistry, 1997, 248, 15-25.	2.4	21
85	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
86	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
87	New Techniques for NMR Structural Biology. Journal of Pesticide Sciences, 1996, 21, 450-459.	1.4	0
88	A Constitutive Effector Region on the C-terminal Side of Switch I of the Ras Protein. Journal of Biological Chemistry, 1995, 270, 4661-4667.	3.4	24
89	Site-directed mutagenesis, fluorescence, and two-dimensional NMR studies on microenvironments of effector region aromatic residues of human c-Ha-Ras protein. Biochemistry, 1994, 33, 65-73.	2.5	36
90	Sequence-specific ¹ H and ¹⁵ N resonance assignments and secondary structure of GDP-bound human c-Ha-Ras protein in solution. Journal of Biomolecular NMR, 1993, 3, 165-84.	2.8	24

#	ARTICLE	IF	CITATIONS
91	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
92	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
93	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
94	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
95	Conformation change of effector-region residues in antiparallel β -sheet of human c-Ha-ras protein on GDP \rightarrow GTP \rightarrow ³ S exchange: A two-dimensional NMR study. <i>Biochemical and Biophysical Research Communications</i> , 1989, 162, 1054-1062.	2.1	35