

Takuhiro Ito

List of Publications by Year in descending order

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Version: 2024-02-01

48
papers

1,796
citations

257357

24
h-index

302012

39
g-index

57
all docs

57
docs citations

57
times ranked

2481
citing authors

#	ARTICLE	IF	CITATIONS
1	The landscape of translational stall sites in bacteria revealed by monosome and disome profiling. <i>Rna</i> , 2022, 28, 290-302.	1.6	8
2	Conformational alterations in unidirectional ion transport of a light-driven chloride pump revealed using X-ray free electron lasers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	11
3	ISRIB Blunts the Integrated Stress Response by Allosterically Antagonising the Inhibitory Effect of Phosphorylated eIF2 on eIF2B. <i>Molecular Cell</i> , 2021, 81, 88-103.e6.	4.5	93
4	Dual targeting of DDX3 and eIF4A by the translation inhibitor rocaglamide A. <i>Cell Chemical Biology</i> , 2021, 28, 475-486.e8.	2.5	37
5	Incorporation of Halogenated Amino Acids into Antibody Fragments at Multiple Specific Sites Enhances Antigen Binding. <i>ChemBioChem</i> , 2021, 22, 120-123.	1.3	10
6	eIF2B-capturing viral protein NSs suppresses the integrated stress response. <i>Nature Communications</i> , 2021, 12, 7102.	5.8	21
7	Glial pathology in a novel spontaneous mutant mouse of the <i>Eif2b5</i> gene: a vanishing white matter disease model. <i>Journal of Neurochemistry</i> , 2020, 154, 25-40.	2.1	15
8	eIF2B and the Integrated Stress Response: A Structural and Mechanistic View. <i>Biochemistry</i> , 2020, 59, 1299-1308.	1.2	21
9	HCV IRES Captures an Actively Translating 80S Ribosome. <i>Molecular Cell</i> , 2019, 74, 1205-1214.e8.	4.5	42
10	Structural basis for eIF2B inhibition in integrated stress response. <i>Science</i> , 2019, 364, 495-499.	6.0	91
11	The Translation Inhibitor Rocaglamide Targets a Bimolecular Cavity between eIF4A and Polypurine RNA. <i>Molecular Cell</i> , 2019, 73, 738-748.e9.	4.5	128
12	Genetic Code Expansion of the Silkworm <i>Bombyx mori</i> to Functionalize Silk Fiber. <i>ACS Synthetic Biology</i> , 2018, 7, 801-806.	1.9	26
13	Dynamic interaction of poly(A)-binding protein with the ribosome. <i>Scientific Reports</i> , 2018, 8, 17435.	1.6	23
14	JQ1 affects BRD2-dependent and independent transcription regulation without disrupting H4-hyperacetylated chromatin states. <i>Epigenetics</i> , 2018, 13, 410-431.	1.3	32
15	Cell-free synthesis of functional antibody fragments to provide a structural basis for antibody-antigen interaction. <i>PLoS ONE</i> , 2018, 13, e0193158.	1.1	20
16	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
17	Crystal structure of eIF2B and insights into eIF2B interactions. <i>FEBS Journal</i> , 2017, 284, 868-874.	2.2	21
18	Trm5 and TrmD: Two Enzymes from Distinct Origins Catalyze the Identical tRNA Modification, m1G37. <i>Biomolecules</i> , 2017, 7, 32.	1.8	34

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19	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
20	Methyl transfer by substrate signaling from a knotted protein fold. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 941-948.	3.6	74
21	Crystal structure of eukaryotic translation initiation factor 2B. <i>Nature</i> , 2016, 531, 122-125.	13.7	103
22	Controlling the Fluorescence of Benzofuran-Modified Uracil Residues in Oligonucleotides by Triple-Helix Formation. <i>ChemBioChem</i> , 2015, 16, 167-176.	1.3	27
23	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
24	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
25	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
26	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
27	Crystallographic and mutational studies on the tRNA thouridine synthetase TtuA. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 1232-1244.	1.5	28
28	Structural basis for mutual relief of the Rac guanine nucleotide exchange factor DOCK2 and its partner ELMO1 from their autoinhibited forms. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 3305-3310.	3.3	95
29	Plasma-Assisted Biological Macromolecular Crystallization. <i>Applied Physics Express</i> , 2011, 4, 026201.	1.1	10
30	Differentiating analogous tRNA methyltransferases by fragments of the methyl donor. <i>Rna</i> , 2011, 17, 1236-1246.	1.6	33
31	2P004 Crystallization of the complex of Gly-tRNA synthetase and tRNA(Gly) from <i>Pyrococcus horikoshii</i> (The 48th Annual Meeting of the Biophysical Society of Japan). <i>Seibutsu Butsuri</i> , 2010, 50, S82.	0.0	0
32	Structure of nondiscriminating glutamyl-tRNA synthetase from <i>Thermotoga maritima</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 813-820.	2.5	9
33	Two enzymes bound to one transfer RNA assume alternative conformations for consecutive reactions. <i>Nature</i> , 2010, 467, 612-616.	13.7	57
34	Crystal Structure of <i>Methanocaldococcus jannaschii</i> Trm4 Complexed with Sinefungin. <i>Journal of Molecular Biology</i> , 2010, 401, 323-333.	2.0	14
35	Tertiary structure checkpoint at anticodon loop modification in tRNA functional maturation. <i>Nature Structural and Molecular Biology</i> , 2009, 16, 1109-1115.	3.6	97
36	Crystal Structure of the β Subunit of Human Translation Initiation Factor 2B. <i>Journal of Molecular Biology</i> , 2009, 392, 937-951.	2.0	26

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37	Crystal structure of archaeal tRNA(m ¹ G37)methyltransferase aTrm5. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 72, 1274-1289.	1.5	53
38	Structure of an archaeal TYW1, the enzyme catalyzing the second step of wye-base biosynthesis. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2007, 63, 1059-1068.	2.5	44
39	Resonance assignments of the Î± subunit of human eukaryotic initiation factor 2 (eIF2Î±). <i>Journal of Biomolecular NMR</i> , 2007, 38, 173-173.	1.6	0
40	Mapping of the Auto-inhibitory Interactions of Protein Kinase R by Nuclear Magnetic Resonance. <i>Journal of Molecular Biology</i> , 2006, 364, 352-363.	2.0	35
41	Sensitivity enhancement in NMR of macromolecules by application of optimal control theory. <i>Journal of Biomolecular NMR</i> , 2005, 32, 23-30.	1.6	35
42	A Molecular Handoff between Bacteriophage T7 DNA Primase and T7 DNA Polymerase Initiates DNA Synthesis. <i>Journal of Biological Chemistry</i> , 2004, 279, 30554-30562.	1.6	36
43	Solution Structure of Human Initiation Factor eIF2Î± Reveals Homology to the Elongation Factor eEF1B. <i>Structure</i> , 2004, 12, 1693-1704.	1.6	82
44	Using codon optimization, chaperone co-expression, and rational mutagenesis for production and NMR assignments of human eIF2Î±. <i>Journal of Biomolecular NMR</i> , 2004, 28, 357-367.	1.6	24
45	Modular Architecture of the Bacteriophage T7 Primase Couples RNA Primer Synthesis to DNA Synthesis. <i>Molecular Cell</i> , 2003, 11, 1349-1360.	4.5	103
46	Solution structure of an RNA fragment with the P7/P9.0 region and the 3' terminal guanosine of the Tetrahymena group I intron. <i>Rna</i> , 2002, 8, 440-451.	1.6	17
47	Solution structures of the first and second RNA-binding domains of human U2 small nuclear ribonucleoprotein particle auxiliary factor (U2AF65). <i>EMBO Journal</i> , 1999, 18, 4523-4534.	3.5	39
48	METTL18-mediated histidine methylation of RPL3 modulates translation elongation for proteostasis maintenance. <i>ELife</i> , 0, 11, .	2.8	11