Shun-ichi Sekine

List of Publications by Year
in descending order

75 papers	4,166 citations	136885 32 h-index	118793 62 g-index
77 all docs	77 docs citations	77 times ranked	4350 citing authors

#	Article	IF	Citations
1	Crystal structure of a bacterial RNA polymerase holoenzyme at 2.6â€‰Ã... resolution. Nature, 2002, 417, 712-719.	13.7	698
2	Decameric SelAâ€¢tRNA ^{Sec} Ring Structure Reveals Mechanism of Bacterial Selenocysteine Formation. Science, 2013, 340, 75-78.	6.0	302
3	Structural Basis for Double-Sieve Discrimination of L-Valine from L-Isoleucine and L-Threonine by the Complex of tRNAVal and Valyl-tRNA Synthetase. Cell, 2000, 103, 793-803.	13.5	268
4	Structural Basis for Transcription Regulation by Alarmone ppGpp. Cell, 2004, 117, 299-310.	13.5	261
5	Structure of the complete elongation complex of RNA polymerase II with basal factors. Science, 2017, 357, 921-924.	6.0	162
6	Structural basis of the nucleosome transition during RNA polymerase II passage. Science, 2018, 362, 595-598.	6.0	157
7	Crystal structure of bacterial RNA polymerase bound with a transcription inhibitor protein. Nature, 2010, 468, 978-982.	13.7	140
8	ATP binding by glutamyl-tRNA synthetase is switched to the productive mode by tRNA binding. EMBO Journal, 2003, 22, 676-688.	3.5	138
9	Structural insight into nucleosome transcription by RNA polymerase II with elongation factors. Science, 2019, 363, 744-747.	6.0	126
10	Crystal structure of elongation factor P from Thermus thermophilus HB8. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 9595-9600.	3.3	102
11	Structural basis for anticodon recognition by discriminating glutamyl-tRNA synthetase. Nature Structural Biology, 2001, 8, 203-206.	9.7	101
12	Structural basis for functional mimicry of long-variable-arm tRNA by transfer-messenger RNA. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 8293-8298.	3.3	96
13	Structural basis for mutual relief of the Rac guanine nucleotide exchange factor DOCK2 and its partner ELMO1 from their autoinhibited forms. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 3305-3310.	3.3	95
14	Effect of modified nucleotides onEscherichia colitRNAGlustructure and on its aminoacylation by glutamyl-tRNA synthetase. FEBS Journal, 1999, 266, 1128-1135.	0.2	91
15	The Ratcheted and Ratchetable Structural States of RNA Polymerase Underlie Multiple Transcriptional Functions. Molecular Cell, 2015, 57, 408-421.	4.5	85
16	The selective tRNA aminoacylation mechanism based on a single Gâ€¢U pair. Nature, 2014, 510, 507-511.	13.7	80
17	Major Identity Determinants in the "Augmented D Helix" of tRNAGlufromEscherichia coli. Journal of Molecular Biology, 1996, 256, 685-700.	2.0	65
18	Crystal structure of human selenocysteine tRNA. Nucleic Acids Research, 2009, 37, 6259-6268.	6.5	64

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19	Mechanism of molecular interactions for tRNAVal recognition by valyl-tRNA synthetase. Rna, 2003, 9, 100-111.	1.6	59
20	Structural basis for methyl-donorâ€“dependent and sequence-specific binding to tRNA substrates by knotted methyltransferase TrmD. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E4197-205.	3.3	54
21	Unique protein architecture of alanyl-tRNA synthetase for aminoacylation, editing, and dimerization. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 8489-8494.	3.3	51
22	Crystal Structure of tRNA Adenosine Deaminase (TadA) from Aquifex aeolicus. Journal of Biological Chemistry, 2005, 280, 16002-16008.	1.6	49
23	Discovery of a small molecule inhibitor targeting dengue virus NS5 RNA-dependent RNA polymerase. PLoS Neglected Tropical Diseases, 2019, 13, e0007894.	1.3	49
24	Structural Bases of Transfer RNA-Dependent Amino Acid Recognition and Activation by Glutamyl-tRNA Synthetase. Structure, 2006, 14, 1791-1799.	1.6	48
25	Structural Basis for the Major Role of O-Phosphoseryl-tRNA Kinase in the UGA-Specific Encoding of Selenocysteine. Molecular Cell, 2010, 39, 410-420.	4.5	48
26	Structure of an archaeal TYW1, the enzyme catalyzing the second step of wye-base biosynthesis. Acta Crystallographica Section D: Biological Crystallography, 2007, 63, 1059-1068.	2.5	44
27	Crystal structure of nanoKAZ: The mutated 19ÂkDa component of Oplophorus luciferase catalyzing the bioluminescent reaction with coelenterazine. Biochemical and Biophysical Research Communications, 2016, 470, 88-93.	1.0	44
28	Purification, crystallization and initial crystallographic analysis of RNA polymerase holoenzyme fromThermus thermophilus. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 1497-1500.	2.5	40
29	Structure of Selenophosphate Synthetase Essential for Selenium Incorporation into Proteins and RNAs. Journal of Molecular Biology, 2009, 385, 1456-1469.	2.0	39
30	Structural and mutational studies of the amino acid-editing domain from archaeal/eukaryal phenylalanyl-tRNA synthetase. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 14744-14749.	3.3	35
31	Tertiary structure of bacterial selenocysteine tRNA. Nucleic Acids Research, 2013, 41, 6729-6738.	6.5	35
32	Structural basis of transcription by bacterial and eukaryotic RNA polymerases. Current Opinion in Structural Biology, 2012, 22, 110-118.	2.6	34
33	tRNA Recognition by Glutamyl-tRNA Reductase. Journal of Biological Chemistry, 2004, 279, 34931-34937.	1.6	31
34	Structural basis for promoter specificity switching of RNA polymerase by a phage factor. Genes and Development, 2014, 28, 521-531.	2.7	31
35	Crystallographic and mutational studies of seryl-tRNA synthetase from the archaeonPyrococcus horikoshii. RNA Biology, 2008, 5, 169-177.	1.5	28
36	Crystallographic and mutational studies on the tRNA thiouridine synthetase TtuA. Proteins: Structure, Function and Bioinformatics, 2013, 81, 1232-1244.	1.5	28

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37	Crystal Structures of Tyrosyl-tRNA Synthetases from Archaea. Journal of Molecular Biology, 2006, 355, 395-408.	2.0	27
38	Distinct ways of G:U recognition by conserved tRNA binding motifs. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 7527-7532.	3.3	26
39	Structural Basis of the Water-assisted Asparagine Recognition by Asparaginyl-tRNA Synthetase. Journal of Molecular Biology, 2006, 360, 329-342.	2.0	24
40	Modeling of tRNAâ€assisted mechanism of Arg activation based on a structure of Argâ€tRNA synthetase, tRNA, and an ATP analog (ANP). FEBS Journal, 2009, 276, 4763-4779.	2.2	21
41	Crystal structure of the full-length bacterial selenocysteine-specific elongation factor SelB. Nucleic Acids Research, 2015, 43, 9028-9038.	6.5	19
42	The identity determinants required for the discrimination between tRNAGlu and tRNAAsp by glutamyl-tRNA synthetase from Escherichia coli. FEBS Journal, 1999, 261, 354-360.	0.2	18
43	Crystal Structure of a Lysine Biosynthesis Enzyme, LysX, from Thermus thermophilus HB8. Journal of Molecular Biology, 2003, 332, 729-740.	2.0	18
44	Dimerâ€“Dimer Interaction of the Bacterial Selenocysteine Synthase SelA Promotes Functional Active-Site Formation and Catalytic Specificity. Journal of Molecular Biology, 2014, 426, 1723-1735.	2.0	17
45	Parallel homodimer structures of the extracellular domains of the voltage-gated sodium channel Î²4 subunit explain its role in cellâ€“cell adhesion. Journal of Biological Chemistry, 2017, 292, 13428-13440.	1.6	16
46	Crucial Role of the HIGH-loop Lysine for the Catalytic Activity of Arginyl-tRNA Synthetase. Journal of Biological Chemistry, 2001, 276, 3723-3726.	1.6	15
47	Crystal structure of RNA polymerase II from Komagataella pastoris. Biochemical and Biophysical Research Communications, 2017, 487, 230-235.	1.0	15
48	Crystal Structure of Methanocaldococcus jannaschii Trm4 Complexed with Sinefungin. Journal of Molecular Biology, 2010, 401, 323-333.	2.0	14
49	Structure-based site-directed photo-crosslinking analyses of multimeric cell-adhesive interactions of voltage-gated sodium channel Î² subunits. Scientific Reports, 2016, 6, 26618.	1.6	13
50	Architecture of the RNA polymerase II elongation complex: new insights into Spt4/5 and Elf1. Transcription, 2018, 9, 286-291.	1.7	13
51	Development of a hexahistidine-3Ã— FLAG-tandem affinity purification method for endogenous protein complexes in Pichia pastoris. Journal of Structural and Functional Genomics, 2014, 15, 191-199.	1.2	12
52	A three-dimensional structure model of the complex of glutamyl-tRNA synthetase and its cognate tRNA. FEBS Letters, 1995, 377, 77-81.	1.3	11
53	Conformational alterations in unidirectional ion transport of a light-driven chloride pump revealed using X-ray free electron lasers. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	11
54	Structural and biochemical analyses of the nucleosome containing Komagataella pastoris histones. Journal of Biochemistry, 2022, 172, 79-88.	0.9	11

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55	A novel conformation of RNA polymerase sheds light on the mechanism of transcription. Transcription, 2011, 2, 162-167.	1.7	10
56	The Putative DNA-Binding Protein Sto12a from the Thermoacidophilic Archaeon Sulfolobus tokodaii Contains Intrachain and Interchain Disulfide Bonds. Journal of Molecular Biology, 2007, 372, 1293-1304.	2.0	8
57	A Thermus phage protein inhibits host RNA polymerase by preventing template DNA strand loading during open promoter complex formation. Nucleic Acids Research, 2018, 46, 431-441.	6.5	8
58	Structure of an N-terminally truncated selenophosphate synthetase fromAquifex aeolicus. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 453-458.	0.7	7
59	Crystal Structure of Okadaic Acid Binding Protein 2.1: A Sponge Protein Implicated in Cytotoxin Accumulation. ChemBioChem, 2015, 16, 1435-1439.	1.3	7
60	Structure of an archaeal homologue of the bacterial Fmu/RsmB/RrmB rRNA cytosine 5-methyltransferase. Acta Crystallographica Section D: Biological Crystallography, 2010, 66, 1301-1307.	2.5	6
61	Time-Resolved Raman and Polyacrylamide Gel Electrophoresis Observations of Nucleotide Incorporation and Misincorporation in RNA within a Bacterial RNA Polymerase Crystal. Biochemistry, 2015, 54, 652-665.	1.2	6
62	Slow luminescence kinetics of semi-synthetic aequorin: expression, purification and structure determination of cf3-aequorin. Journal of Biochemistry, 2018, 164, 247-255.	0.9	6
63	Ratcheting of RNA polymerase toward structural principles of RNA polymerase operations. Transcription, 2015, 6, 56-60.	1.7	5
64	Crystallization and preliminary X-ray crystallographic analysis ofThermus thermophilustranscription elongation complex bound to Gfh1. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 64-68.	0.7	4
65	Crystal structure of the C17/25 subcomplex from Schizosaccharomyces pombe RNA polymerase III. Protein Science, 2011, 20, 1558-1565.	3.1	4
66	Structural basis of CoA recognition by the Pyrococcus single-domain CoA-binding proteins. Journal of Structural and Functional Genomics, 2007, 7, 119-129.	1.2	3
67	Crystallization and preliminary X-ray crystallographic analysis ofAquifex aeolicusSelA, a bacterial selenocysteine synthase. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 1128-1133.	0.7	3
68	Molecular basis of RNA polymerase promoter specificity switch revealed through studies ofThermusbacteriophage transcription regulator. Bacteriophage, 2014, 4, e29399.	1.9	3
69	Cloning, expression, purification, crystallization and initial crystallographic analysis of the lysine-biosynthesis LysX protein fromThermus thermophilusHB8. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 1651-1652.	2.5	2
70	Crystallization and preliminary X-ray crystallographic analysis of bacterial tRNA^{Sec}in complex with seryl-tRNA synthetase. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 678-682.	0.7	2
71	Crystallization and preliminary X-ray crystallographic analyses ofThermus thermophilusbacktracked RNA polymerase. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 174-177.	0.7	1
72	A SelB/EF-Tu/aIF2Î³-like protein from Methanosarcina mazei in the GTP-bound form binds cysteinyl-tRNACys. Journal of Structural and Functional Genomics, 2015, 16, 25-41.	1.2	1

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73	Overview of the â€œ1SBA: integrative approaches towards understanding of gene expressionâ€•session at the 57th BSJ meeting. Biophysical Reviews, 2020, 12, 253-254.	1.5	1
74	Structural Basis of Selenocysteine tRNA Recognition by PSTK for the Accurate Selenium Incorporation into Proteins. Seibutsu Butsuri, 2011, 51, 272-273.	0.0	0
75	CHAPTER 4. RNA Polymerase-associated Transcription Elongation Factors. Chemical Biology, 2021, , 72-99.	0.1	0