

Shun-ichi Sekine

List of Publications by Year in descending order

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75
papers

4,166
citations

136885

32
h-index

118793

62
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77
all docs

77
docs citations

77
times ranked

4350
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	Structural and biochemical analyses of the nucleosome containing <i>Komagataella pastoris</i> histones. Journal of Biochemistry, 2022, 172, 79-88.	0.9	11
3	CHAPTER 4. RNA Polymerase-associated Transcription Elongation Factors. Chemical Biology, 2021, , 72-99.	0.1	0
4	Overview of the α 1SBA: integrative approaches towards understanding of gene expression session at the 57th BSJ meeting. Biophysical Reviews, 2020, 12, 253-254.	1.5	1
5	Structural insight into nucleosome transcription by RNA polymerase II with elongation factors. Science, 2019, 363, 744-747.	6.0	126
6	Discovery of a small molecule inhibitor targeting dengue virus NS5 RNA-dependent RNA polymerase. PLoS Neglected Tropical Diseases, 2019, 13, e0007894.	1.3	49
7	Architecture of the RNA polymerase II elongation complex: new insights into Spt4/5 and Elf1. Transcription, 2018, 9, 286-291.	1.7	13
8	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
9	Structural basis of the nucleosome transition during RNA polymerase II passage. Science, 2018, 362, 595-598.	6.0	157
10	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
11	Distinct ways of C: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
12	Crystal structure of RNA polymerase II from <i>Komagataella pastoris</i> . Biochemical and Biophysical Research Communications, 2017, 487, 230-235.	1.0	15
13	Parallel homodimer structures of the extracellular domains of the voltage-gated sodium channel β 2 subunit explain its role in cell-cell adhesion. Journal of Biological Chemistry, 2017, 292, 13428-13440.	1.6	16
14	Structure of the complete elongation complex of RNA polymerase II with basal factors. Science, 2017, 357, 921-924.	6.0	162
15	Structure-based site-directed photo-crosslinking analyses of multimeric cell-adhesive interactions of voltage-gated sodium channel β 2 subunits. Scientific Reports, 2016, 6, 26618.	1.6	13
16	Crystal structure of nanoKAZ: The mutated 19 kDa component of <i>Oplophorus</i> luciferase catalyzing the bioluminescent reaction with coelenterazine. Biochemical and Biophysical Research Communications, 2016, 470, 88-93.	1.0	44
17	Crystal Structure of Okadaic Acid Binding Protein 2.1: A Sponge Protein Implicated in Cytotoxin Accumulation. ChemBioChem, 2015, 16, 1435-1439.	1.3	7
18	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

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19	The Ratcheted and Ratchetable Structural States of RNA Polymerase Underlie Multiple Transcriptional Functions. <i>Molecular Cell</i> , 2015, 57, 408-421.	4.5	85
20	A SelB/EF-Tu/aIF2 ³ -like protein from <i>Methanosarcina mazei</i> in the GTP-bound form binds cysteinyl-tRNA ^{Cys} . <i>Journal of Structural and Functional Genomics</i> , 2015, 16, 25-41.	1.2	1
21	Crystal structure of the full-length bacterial selenocysteine-specific elongation factor SelB. <i>Nucleic Acids Research</i> , 2015, 43, 9028-9038.	6.5	19
22	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
23	Ratcheting of RNA polymerase toward structural principles of RNA polymerase operations. <i>Transcription</i> , 2015, 6, 56-60.	1.7	5
24	Structural basis for promoter specificity switching of RNA polymerase by a phage factor. <i>Genes and Development</i> , 2014, 28, 521-531.	2.7	31
25	Development of a hexahistidine-3 ^Å -FLAG-tandem affinity purification method for endogenous protein complexes in <i>Pichia pastoris</i> . <i>Journal of Structural and Functional Genomics</i> , 2014, 15, 191-199.	1.2	12
26	Dimer-Dimer Interaction of the Bacterial Selenocysteine Synthase Sela Promotes Functional Active-Site Formation and Catalytic Specificity. <i>Journal of Molecular Biology</i> , 2014, 426, 1723-1735.	2.0	17
27	Molecular basis of RNA polymerase promoter specificity switch revealed through studies of <i>Thermus</i> bacteriophage transcription regulator. <i>Bacteriophage</i> , 2014, 4, e29399.	1.9	3
28	The selective tRNA aminoacylation mechanism based on a single G-CU pair. <i>Nature</i> , 2014, 510, 507-511.	13.7	80
29	Crystallization and preliminary X-ray crystallographic analyses of <i>Thermus thermophilus</i> backtracked RNA polymerase. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 174-177.	0.7	1
30	Tertiary structure of bacterial selenocysteine tRNA. <i>Nucleic Acids Research</i> , 2013, 41, 6729-6738.	6.5	35
31	Decameric Sela-tRNA ^{Sec} Ring Structure Reveals Mechanism of Bacterial Selenocysteine Formation. <i>Science</i> , 2013, 340, 75-78.	6.0	302
32	Crystallographic and mutational studies on the tRNA thiouridine synthetase TtuA. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 1232-1244.	1.5	28
33	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
34	Crystallization and preliminary X-ray crystallographic analysis of <i>Aquifex aeolicus</i> Sela, a bacterial selenocysteine synthase. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 1128-1133.	0.7	3
35	Structural basis of transcription by bacterial and eukaryotic RNA polymerases. <i>Current Opinion in Structural Biology</i> , 2012, 22, 110-118.	2.6	34
36	Crystallization and preliminary X-ray crystallographic analysis of bacterial tRNA ^{Sec} in complex with seryl-tRNA synthetase. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 678-682.	0.7	2

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37	Crystal structure of the C17/25 subcomplex from <i>Schizosaccharomyces pombe</i> RNA polymerase III. <i>Protein Science</i> , 2011, 20, 1558-1565.	3.1	4
38	A novel conformation of RNA polymerase sheds light on the mechanism of transcription. <i>Transcription</i> , 2011, 2, 162-167.	1.7	10
39	Structural Basis of Selenocysteine tRNA Recognition by PSTK for the Accurate Selenium Incorporation into Proteins. <i>Seibutsu Butsuri</i> , 2011, 51, 272-273.	0.0	0
40	Structure of an archaeal homologue of the bacterial Fmu/RsmB/RrmB rRNA cytosine 5-methyltransferase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 1301-1307.	2.5	6
41	Crystallization and preliminary X-ray crystallographic analysis of <i>Thermus thermophilus</i> transcription elongation complex bound to Gfh1. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 64-68.	0.7	4
42	Crystal structure of bacterial RNA polymerase bound with a transcription inhibitor protein. <i>Nature</i> , 2010, 468, 978-982.	13.7	140
43	Structural Basis for the Major Role of O-Phosphoseryl-tRNA Kinase in the UGA-Specific Encoding of Selenocysteine. <i>Molecular Cell</i> , 2010, 39, 410-420.	4.5	48
44	Crystal Structure of <i>Methanocaldococcus jannaschii</i> Trm4 Complexed with Sinefungin. <i>Journal of Molecular Biology</i> , 2010, 401, 323-333.	2.0	14
45	Unique protein architecture of alanyl-tRNA synthetase for aminoacylation, editing, and dimerization. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 8489-8494.	3.3	51
46	Crystal structure of human selenocysteine tRNA. <i>Nucleic Acids Research</i> , 2009, 37, 6259-6268.	6.5	64
47	Modeling of tRNA-assisted mechanism of Arg activation based on a structure of Arg-tRNA synthetase, tRNA, and an ATP analog (ANP). <i>FEBS Journal</i> , 2009, 276, 4763-4779.	2.2	21
48	Structure of Selenophosphate Synthetase Essential for Selenium Incorporation into Proteins and RNAs. <i>Journal of Molecular Biology</i> , 2009, 385, 1456-1469.	2.0	39
49	Structure of an N-terminally truncated selenophosphate synthetase from <i>Aquifex aeolicus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 453-458.	0.7	7
50	Crystallographic and mutational studies of seryl-tRNA synthetase from the archaeon <i>Pyrococcus horikoshii</i> . <i>RNA Biology</i> , 2008, 5, 169-177.	1.5	28
51	Structural basis for functional mimicry of long-variable-arm tRNA by transfer-messenger RNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 8293-8298.	3.3	96
52	The Putative DNA-Binding Protein Sto12a from the Thermoacidophilic Archaeon <i>Sulfolobus tokodaii</i> Contains Intrachain and Interchain Disulfide Bonds. <i>Journal of Molecular Biology</i> , 2007, 372, 1293-1304.	2.0	8
53	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
54	Structural basis of CoA recognition by the <i>Pyrococcus</i> single-domain CoA-binding proteins. <i>Journal of Structural and Functional Genomics</i> , 2007, 7, 119-129.	1.2	3

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55	Crystal Structures of Tyrosyl-tRNA Synthetases from Archaea. <i>Journal of Molecular Biology</i> , 2006, 355, 395-408.	2.0	27
56	Structural Basis of the Water-assisted Asparagine Recognition by Asparaginyl-tRNA Synthetase. <i>Journal of Molecular Biology</i> , 2006, 360, 329-342.	2.0	24
57	Structural Bases of Transfer RNA-Dependent Amino Acid Recognition and Activation by Glutamyl-tRNA Synthetase. <i>Structure</i> , 2006, 14, 1791-1799.	1.6	48
58	Structural and mutational studies of the amino acid-editing domain from archaeal/eukaryal phenylalanyl-tRNA synthetase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 14744-14749.	3.3	35
59	Crystal Structure of tRNA Adenosine Deaminase (TadA) from <i>Aquifex aeolicus</i> . <i>Journal of Biological Chemistry</i> , 2005, 280, 16002-16008.	1.6	49
60	Crystal structure of elongation factor P from <i>Thermus thermophilus</i> HB8. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 9595-9600.	3.3	102
61	tRNA Recognition by Glutamyl-tRNA Reductase. <i>Journal of Biological Chemistry</i> , 2004, 279, 34931-34937.	1.6	31
62	Structural Basis for Transcription Regulation by Alarmone ppGpp. <i>Cell</i> , 2004, 117, 299-310.	13.5	261
63	ATP binding by glutamyl-tRNA synthetase is switched to the productive mode by tRNA binding. <i>EMBO Journal</i> , 2003, 22, 676-688.	3.5	138
64	Cloning, expression, purification, crystallization and initial crystallographic analysis of the lysine-biosynthesis LysX protein from <i>Thermus thermophilus</i> HB8. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 1651-1652.	2.5	2
65	Crystal Structure of a Lysine Biosynthesis Enzyme, LysX, from <i>Thermus thermophilus</i> HB8. <i>Journal of Molecular Biology</i> , 2003, 332, 729-740.	2.0	18
66	Mechanism of molecular interactions for tRNA ^{Val} recognition by valyl-tRNA synthetase. <i>Rna</i> , 2003, 9, 100-111.	1.6	59
67	Purification, crystallization and initial crystallographic analysis of RNA polymerase holoenzyme from <i>Thermus thermophilus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 1497-1500.	2.5	40
68	Crystal structure of a bacterial RNA polymerase holoenzyme at 2.6 Å resolution. <i>Nature</i> , 2002, 417, 712-719.	13.7	698
69	Structural basis for anticodon recognition by discriminating glutamyl-tRNA synthetase. <i>Nature Structural Biology</i> , 2001, 8, 203-206.	9.7	101
70	Crucial Role of the HIGH-loop Lysine for the Catalytic Activity of Arginyl-tRNA Synthetase. <i>Journal of Biological Chemistry</i> , 2001, 276, 3723-3726.	1.6	15
71	Structural Basis for Double-Sieve Discrimination of L-Valine from L-Isoleucine and L-Threonine by the Complex of tRNA ^{Val} and Valyl-tRNA Synthetase. <i>Cell</i> , 2000, 103, 793-803.	13.5	268
72	Effect of modified nucleotides on <i>Escherichia coli</i> tRNA ^{Glu} structure and on its aminoacylation by glutamyl-tRNA synthetase. <i>FEBS Journal</i> , 1999, 266, 1128-1135.	0.2	91

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73	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
74	Major Identity Determinants in the "Augmented D Helix" of tRNAGlu from Escherichia coli. Journal of Molecular Biology, 1996, 256, 685-700.	2.0	65
75	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