Thomas A Steitz

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

126 papers	16,117 citations	57 h-index	126 g-index
132 ext. papers	17,740 ext. citations	15.9 avg, IF	6.81 L-index

#	Paper	IF	Citations
126	RNA stabilization by a poly(A) tail 3U-end binding pocket and other modes of poly(A)-RNA interaction. *Science*, **2021**, 371,	33.3	12
125	Structural Insights into Transcription Initiation from De Novo RNA Synthesis to Transitioning into Elongation. *IScience*, **2020**, 23, 101445	6.1	1
124	Crystal structure of the C-terminal domain of DENR. *Computational and Structural Biotechnology Journal*, **2020**, 18, 696-704	6.8	3
123	Molecular dynamics analysis of Mg -dependent cleavage of a pistol ribozyme reveals a fail-safe secondary ion for catalysis. *Journal of Computational Chemistry*, **2020**, 41, 1345-1352	3.5	0
122	Crystal Structure of a CAP-DNA Complex: The DNA Is Bent by 90□ *journal of hand surgery Asian-Pacific volume, The*, **2020**, 210-216	0.5	
121	Building a Replisome from Interacting Pieces: Sliding Clamp Complexed to a Peptide from DNA Polymerase and a Polymerase Editing Complex. *journal of hand surgery Asian-Pacific volume, The*, **2020**, 306-317	0.5	1
120	Structural Insights into the Roles of Water and the 2? Hydroxyl of the P Site tRNA in the Peptidyl Transferase Reaction. *journal of hand surgery Asian-Pacific volume, The*, **2020**, 557-568	0.5	
119	DNA Polymerases: Structural Diversity and Common Mechanisms. *journal of hand surgery Asian-Pacific volume, The*, **2020**, 318-321	0.5	
118	The Structural Mechanism of Translocation and Helicase Activity in T7 RNA Polymerase. *journal of hand surgery Asian-Pacific volume, The*, **2020**, 342-353	0.5	
117	Structural basis for initiation of transcription from an RNA polymerase-promoter complex. *journal of hand surgery Asian-Pacific volume, The*, **2020**, 297-300	0.5	
116	Revisiting the structures of several antibiotics bound to the bacterial ribosome. *journal of hand surgery Asian-Pacific volume, The*, **2020**, 589-594	0.5	
115	Structures of Five Antibiotics Bound at the Peptidyl Transferase Center of the Large Ribosomal Subunit. *journal of hand surgery Asian-Pacific volume, The*, **2020**, 537-551	0.5	
114	Structure of Catabolite Gene Activator Protein at 2.9-□Resolution. *journal of hand surgery Asian-Pacific volume, The*, **2020**, 187-193	0.5	
113	Crystal structure of Thermus aquaticus DNA polymerase. *journal of hand surgery Asian-Pacific volume, The*, **2020**, 288-292	0.5	
112	Structure of Taq polymerase with DNA at the polymerase active site. *journal of hand surgery Asian-Pacific volume, The*, **2020**, 293-296	0.5	
111	Structural basis for the 3? □5? exonuclease activity of Escherichia coli DNA polymerase I: a two metal ion mechanism. *journal of hand surgery Asian-Pacific volume, The*, **2020**, 245-253	0.5	
110	Structure of a Complex Between Yeast Hexokinase A and Glucose. *journal of hand surgery Asian-Pacific volume, The*, **2020**, 108-127	0.5	

109	A general two-metal-ion mechanism for catalytic RNA. *journal of hand surgery Asian-Pacific volume, The*, **2020**, 597-601	0.5	
108	Structure of a Complex of Catabolite Gene Activator Protein and Cyclic AMP Refined at 2□5 □ Resolution. *journal of hand surgery Asian-Pacific volume, The*, **2020**, 194-209	0.5	
107	Structure of DNA Polymerase I Klenow Fragment Bound to Duplex DNA. *journal of hand surgery Asian-Pacific volume, The*, **2020**, 270-273	0.5	0
106	Structure of a Synaptic □Resolvase Tetramer Covalently Linked to Two Cleaved DNAs. *journal of hand surgery Asian-Pacific volume, The*, **2020**, 447-452	0.5	
105	Glucose-induced conformational change in yeast hexokinase. *journal of hand surgery Asian-Pacific volume, The*, **2020**, 65-69	0.5	
104	Structural Basis for the Transition from Initiation to Elongation Transcription in T7 RNA Polymerase. *journal of hand surgery Asian-Pacific volume, The*, **2020**, 333-341	0.5	
103	Structural Basis for Transfer RNA Aminoacylation by Escherichia coli Glutaminyl-tRNA Synthetase. *journal of hand surgery Asian-Pacific volume, The*, **2020**, 401-414	0.5	
102	Structure of a Complex Between Yeast Hexokinase A and Glucose. *journal of hand surgery Asian-Pacific volume, The*, **2020**, 81-107	0.5	
101	The Hexameric Helicase DnaB Adopts a Nonplanar Conformation during Translocation. *journal of hand surgery Asian-Pacific volume, The*, **2020**, 365-375	0.5	
100	The Structures of Four Macrolide Antibiotics Bound to the Large Ribosomal Subunit. *journal of hand surgery Asian-Pacific volume, The*, **2020**, 525-536	0.5	0
99	The Structural Basis of Ribosome Activity in Peptide Bond Synthesis. *journal of hand surgery Asian-Pacific volume, The*, **2020**, 501-511	0.5	1
98	Crystal structure of the DENR-MCT-1 complex revealed zinc-binding site essential for heterodimer formation. *Proceedings of the National Academy of Sciences of the United States of America*, **2019**, 116, 528-533	11.5	10
97	Identification of Dihydrofuro[3,4- d]pyrimidine Derivatives as Novel HIV-1 Non-Nucleoside Reverse Transcriptase Inhibitors with Promising Antiviral Activities and Desirable Physicochemical Properties. *Journal of Medicinal Chemistry*, **2019**, 62, 1484-1501	8.3	41
96	Ribosome-Targeting Antibiotics: Modes of Action, Mechanisms of Resistance, and Implications for Drug Design. *Annual Review of Biochemistry*, **2018**, 87, 451-478	29.1	98
95	Structural basis for potent and broad inhibition of HIV-1 RT by thiophene[3,2-]pyrimidine non-nucleoside inhibitors. *ELife*, **2018**, 7,	8.9	41
94	Crystal structure of Pistol, a class of self-cleaving ribozyme. *Proceedings of the National Academy of Sciences of the United States of America*, **2017**, 114, 1021-1026	11.5	45
93	Perspectives on the ribosome. *Philosophical Transactions of the Royal Society B: Biological Sciences*, **2017**, 372,	5.8	3
92	Structural insights into NusG regulating transcription elongation. *Nucleic Acids Research*, **2017**, 45, 968-974	16.1	22

91	Crystal Structure of the Human Ribosome in Complex with DENR-MCT-1. *Cell Reports*, **2017**, 20, 521-528	10.6	29
90	Crystal Structure of the C-terminal Domain of Human eIF2D and Its Implications on Eukaryotic Translation Initiation. *Journal of Molecular Biology*, **2017**, 429, 2765-2771	6.5	9
89	Structural basis of bacterial transcription activation. *Science*, **2017**, 358, 947-951	33.3	32
88	A structure-based kinetic model of transcription. *Transcription*, **2017**, 8, 1-8	4.8	9
87	Insights into RNA binding by the anticancer drug cisplatin from the crystal structure of cisplatin-modified ribosome. *Nucleic Acids Research*, **2016**, 44, 4978-87	20.1	50
86	Structures of E. coli σ-transcription initiation complexes provide new insights into polymerase mechanism. *Proceedings of the National Academy of Sciences of the United States of America*, **2016**, 113, 4051-6	11.5	50
85	Structures of proline-rich peptides bound to the ribosome reveal a common mechanism of protein synthesis inhibition. *Nucleic Acids Research*, **2016**, 44, 2439-50	20.1	99
84	Elongation factor 4 remodels the A-site tRNA on the ribosome. *Proceedings of the National Academy of Sciences of the United States of America*, **2016**, 113, 4994-9	11.5	17
83	Crystal Structure of Human Profilaggrin S100 Domain and Identification of Target Proteins Annexin II, Stratifin, and HSP27. *Journal of Investigative Dermatology*, **2015**, 135, 1801-1809	4.3	12
82	Crystal structures of the E. coli transcription initiation complexes with a complete bubble. *Molecular Cell*, **2015**, 58, 534-40	17.6	153
81	Structural insights into the role of rRNA modifications in protein synthesis and ribosome assembly. *Nature Structural and Molecular Biology*, **2015**, 22, 342-344	17.6	148
80	The mechanism of inhibition of protein synthesis by the proline-rich peptide oncocin. *Nature Structural and Molecular Biology*, **2015**, 22, 466-9	17.6	114
79	Distinct tRNA Accommodation Intermediates Observed on the Ribosome with the Antibiotics Hygromycin A and A201A. *Molecular Cell*, **2015**, 58, 832-44	17.6	57
78	Conformational changes of elongation factor G on the ribosome during tRNA translocation. *Cell*, **2015**, 160, 219-27	56.2	89
77	Structural basis for transcription reactivation by RapA. *Proceedings of the National Academy of Sciences of the United States of America*, **2015**, 112, 2006-10	11.5	35
76	Amicoumacin a inhibits translation by stabilizing mRNA interaction with the ribosome. *Molecular Cell*, **2014**, 56, 531-40	17.6	58
75	Polyspecific pyrrolysyl-tRNA synthetases from directed evolution. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, 16724-9	11.5	75
74	A proton wire to couple aminoacyl-tRNA accommodation and peptide-bond formation on the ribosome. *Nature Structural and Molecular Biology*, **2014**, 21, 787-93	17.6	127

73	Crystal structure of elongation factor 4 bound to a clockwise ratcheted ribosome. *Science*, **2014**, 345, 684-7	33.3	32
72	Negamycin interferes with decoding and translocation by simultaneous interaction with rRNA and tRNA. *Molecular Cell*, **2014**, 56, 541-50	17.6	38
71	Structural basis for the fast self-cleavage reaction catalyzed by the twister ribozyme. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, 13028-33	11.5	65
70	Structural insights into the stabilization of MALAT1 noncoding RNA by a bipartite triple helix. *Nature Structural and Molecular Biology*, **2014**, 21, 633-40	17.6	156
69	The antibiotics dityromycin and GE82832 bind protein S12 and block EF-G-catalyzed translocation. *Cell Reports*, **2014**, 6, 357-65	10.6	30
68	Exploiting large non-isomorphous differences for phase determination of a G-segment invertase-DNA complex. *Acta Crystallographica Section D: Biological Crystallography*, **2014**, 70, 685-93		4
67	The initiation of mammalian protein synthesis and mRNA scanning mechanism. *Nature*, **2013**, 500, 307-11	50.4	128
66	Structure of the PolIII□c-DNA complex suggests an atomic model of the replisome. *Structure*, **2013**, 21, 658-64	5.2	7
65	The mechanism of E. coli RNA polymerase regulation by ppGpp is suggested by the structure of their complex. *Molecular Cell*, **2013**, 50, 430-6	17.6	133
64	Crystal structure of an intermediate of rotating dimers within the synaptic tetramer of the G-segment invertase. *Nucleic Acids Research*, **2013**, 41, 2673-82	20.1	21
63	The antibiotic thermorubin inhibits protein synthesis by binding to inter-subunit bridge B2a of the ribosome. *Journal of Molecular Biology*, **2012**, 416, 571-8	6.5	32
62	Elements of ribosomal drug resistance and specificity. *Current Opinion in Structural Biology*, **2012**, 22, 750-8	8.1	13
61	Structural basis for the rescue of stalled ribosomes: structure of YaeJ bound to the ribosome. *Science*, **2012**, 335, 1370-2	33.3	87
60	How hibernation factors RMF, HPF, and YfiA turn off protein synthesis. *Science*, **2012**, 336, 915-8	33.3	145
59	Crystallization of Escherichia coli 70S Ribosome in complex with tRNAs. *FASEB Journal*, **2012**, 26, 550.1	0.9	
58	Revisiting the structures of several antibiotics bound to the bacterial ribosome. *Proceedings of the National Academy of Sciences of the United States of America*, **2010**, 107, 17158-63	11.5	199
57	Poly(A) tail recognition by a viral RNA element through assembly of a triple helix. *Science*, **2010**, 330, 1244-7	33.3	122
56	The structures of the anti-tuberculosis antibiotics viomycin and capreomycin bound to the 70S ribosome. *Nature Structural and Molecular Biology*, **2010**, 17, 289-93	17.6	167

55	How the CCA-adding enzyme selects adenine over cytosine at position 76 of tRNA. *Science*, **2010**, 330, 937-40	33.3	26
54	Retrospective. Frederic M. Richards (1925-2009). *Science*, **2009**, 323, 1181	33.3	2
53	Structures of triacetyloleandomycin and mycalamide A bind to the large ribosomal subunit of Haloarcula marismortui. *Antimicrobial Agents and Chemotherapy*, **2009**, 53, 5010-4	5.9	43
52	The structural changes of T7 RNA polymerase from transcription initiation to elongation. *Current Opinion in Structural Biology*, **2009**, 19, 683-90	8.1	65
51	U2504 determines the species specificity of the A-site cleft antibiotics: the structures of tiamulin, homoharringtonine, and bruceantin bound to the ribosome. *Journal of Molecular Biology*, **2009**, 389, 146-56	6.5	129
50	Formation of the first peptide bond: the structure of EF-P bound to the 70S ribosome. *Science*, **2009**, 325, 966-70	33.3	172
49	A structural understanding of the dynamic ribosome machine. *Nature Reviews Molecular Cell Biology*, **2008**, 9, 242-53	48.7	315
48	Crystal structure of the oxazolidinone antibiotic linezolid bound to the 50S ribosomal subunit. *Journal of Medicinal Chemistry*, **2008**, 51, 3353-6	8.3	217
47	Mutations outside the anisomycin-binding site can make ribosomes drug-resistant. *Journal of Molecular Biology*, **2008**, 379, 505-19	6.5	69
46	Insights into the replisome from the structure of a ternary complex of the DNA polymerase III alpha-subunit. *Journal of Molecular Biology*, **2008**, 382, 859-69	6.5	65
45	The structure of a transcribing T7 RNA polymerase in transition from initiation to elongation. *Science*, **2008**, 322, 553-7	33.3	83
44	The structure of LepA, the ribosomal back translocase. *Proceedings of the National Academy of Sciences of the United States of America*, **2008**, 105, 4673-8	11.5	56
43	Structural insights into the functions of the large ribosomal subunit, a major antibiotic target. *Keio Journal of Medicine*, **2008**, 57, 1-14	1.6	4
42	Structural basis for base discrimination by RB69 DNA polymerase. *FASEB Journal*, **2008**, 22, 593.2	0.9	
41	Structures of phi29 DNA polymerase complexed with substrate: the mechanism of translocation in B-family polymerases. *EMBO Journal*, **2007**, 26, 3494-505	13	121
40	Collecting butterflies and the protein structure initiative: the right questions?. *Structure*, **2007**, 15, 1523-4	5.2	3
39	The structures of antibiotics bound to the E site region of the 50 S ribosomal subunit of Haloarcula marismortui: 13-deoxytedanolide and girodazole. *Journal of Molecular Biology*, **2007**, 367, 1471-9	6.5	41
38	A story with a good ending: tRNA 3U-end maturation by CCA-adding enzymes. *Current Opinion in Structural Biology*, **2006**, 16, 12-7	8.1	65

(2002-2006)

37	Implications of structures of synaptic tetramers of gamma delta resolvase for the mechanism of recombination. *Proceedings of the National Academy of Sciences of the United States of America*, **2006**, 103, 10642-7	11.5	45
36	The structure of T. aquaticus DNA polymerase III is distinct from eukaryotic replicative DNA polymerases. *Cell*, **2006**, 126, 893-904	56.2	109
35	Visualizing polynucleotide polymerase machines at work. *EMBO Journal*, **2006**, 25, 3458-68	13	73
34	The roles of RNA in the peptidyl transferase reaction and its inhibition by antibiotics. *FASEB Journal* , **2006**, 20, A422	0.9	
33	Structural insights into the roles of water and the 2Uhydroxyl of the P site tRNA in the peptidyl transferase reaction. *Molecular Cell*, **2005**, 20, 437-48	17.6	226
32	Structures of MLSBK antibiotics bound to mutated large ribosomal subunits provide a structural explanation for resistance. *Cell*, **2005**, 121, 257-70	56.2	352
31	On the structural basis of peptide-bond formation and antibiotic resistance from atomic structures of the large ribosomal subunit. *FEBS Letters*, **2005**, 579, 955-8	3.8	30
30	Structure of a synaptic gammadelta resolvase tetramer covalently linked to two cleaved DNAs. *Science*, **2005**, 309, 1210-5	33.3	105
29	An induced-fit mechanism to promote peptide bond formation and exclude hydrolysis of peptidyl-tRNA. *Nature*, **2005**, 438, 520-4	50.4	285
28	Accuracy, lesion bypass, strand displacement and translocation by DNA polymerases. *Philosophical Transactions of the Royal Society B: Biological Sciences*, **2004**, 359, 17-23	5.8	35
27	Mechanism of transfer RNA maturation by CCA-adding enzyme without using an oligonucleotide template. *Nature*, **2004**, 430, 640-5	50.4	105
26	The structural basis of the transition from initiation to elongation phases of transcription, as well as translocation and strand separation, by T7 RNA polymerase. *Current Opinion in Structural Biology*, **2004**, 14, 4-9	8.1	54
25	The structural mechanism of translocation and helicase activity in T7 RNA polymerase. *Cell*, **2004**, 116, 393-404	56.2	277
24	Structures of deacylated tRNA mimics bound to the E site of the large ribosomal subunit. *Rna*, **2003** , 9, 1345-52	5.8	76
23	RNA, the first macromolecular catalyst: the ribosome is a ribozyme. *Trends in Biochemical Sciences*, **2003**, 28, 411-8	10.3	214
22	Structures of five antibiotics bound at the peptidyl transferase center of the large ribosomal subunit. *Journal of Molecular Biology*, **2003**, 330, 1061-75	6.5	319
21	Crystal structures of an archaeal class I CCA-adding enzyme and its nucleotide complexes. *Molecular Cell*, **2003**, 12, 1165-72	17.6	59
20	Structural basis for the transition from initiation to elongation transcription in T7 RNA polymerase. *Science*, **2002**, 298, 1387-95	33.3	283

19	Structural insights into peptide bond formation. *Proceedings of the National Academy of Sciences of the United States of America*, **2002**, 99, 11670-5	11.5	233
18	Crystal structures of the Bacillus stearothermophilus CCA-adding enzyme and its complexes with ATP or CTP. *Cell*, **2002**, 111, 815-24	56.2	104
17	The structures of four macrolide antibiotics bound to the large ribosomal subunit. *Molecular Cell*, **2002**, 10, 117-28	17.6	448
16	Crystal structure of a DinB lesion bypass DNA polymerase catalytic fragment reveals a classic polymerase catalytic domain. *Molecular Cell*, **2001**, 8, 427-37	17.6	173
15	Structure of the replicating complex of a pol alpha family DNA polymerase. *Cell*, **2001**, 105, 657-67	56.2	507
14	The complete atomic structure of the large ribosomal subunit at 2.4 A resolution. *Science*, **2000**, 289, 905-20	33.3	2807
13	The structural basis of ribosome activity in peptide bond synthesis. *Science*, **2000**, 289, 920-30	33.3	1781
12	Structural basis for initiation of transcription from an RNA polymerase-promoter complex. *Nature*, **1999**, 399, 80-3	50.4	267
11	DNA polymerases: structural diversity and common mechanisms. *Journal of Biological Chemistry*, **1999**, 274, 17395-8	5.4	629
10	Insights into Editing from an Ile-tRNA Synthetase Structure with tRNAIle and Mupirocin. *Science*, **1999**, 285, 1074-1077	33.3	364
9	Structures of normal single-stranded DNA and deoxyribo-3ɄS-phosphorothiolates bound to the 3Ʉ5Ʉexonucleolytic active site of DNA polymerase I from Escherichia coli. *Biochemistry*, **1999**, 38, 696-704	3.2	68
8	Use of chemically modified nucleotides to determine a 62-nucleotide RNA crystal structure: a survey of phosphorothioates, Br, Pt and Hg. *Journal of Biomolecular Structure and Dynamics*, **1997**, 15, 165-72	3.6	27
7	Structure of Taq polymerase with DNA at the polymerase active site. *Nature*, **1996**, 382, 278-81	50.4	291
6	Crystal structure of the site-specific recombinase gamma delta resolvase complexed with a 34 bp cleavage site. *Cell*, **1995**, 82, 193-207	56.2	240
5	The crystal structure of the catalytic domain of the site-specific recombination enzyme gamma delta resolvase at 2.7 A resolution. *Cell*, **1990**, 63, 1323-9	56.2	110
4	Structure of catabolite gene activator protein at 2.9 A resolution suggests binding to left-handed B-DNA. *Nature*, **1981**, 290, 744-9	50.4	624
3	Protomer structure of oligomeric enzymes: symmetry and allosteric interactions in yeast hexokinase. *Biochemical Society Transactions*, **1977**, 5, 620-3	5.1	5
2	The Structure of Yeast Hexokinase and its Complexes with Substrates. *Biochemical Society Transactions*, **1974**, 2, 52-54	5.1	3

LIST OF PUBLICATIONS

1 Crystal Structure of the Large Ribosomal Subunit at 5-Angstrom Resolution11-20