

Thomas A Steitz

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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	The complete atomic structure of the large ribosomal subunit at 2.4 Å resolution. <i>Science</i> , 2000 , 289, 905-20	33.3	2807
125	The structural basis of ribosome activity in peptide bond synthesis. <i>Science</i> , 2000 , 289, 920-30	33.3	1781
124	DNA polymerases: structural diversity and common mechanisms. <i>Journal of Biological Chemistry</i> , 1999 , 274, 17395-8	5.4	629
123	Structure of catabolite gene activator protein at 2.9 Å resolution suggests binding to left-handed B-DNA. <i>Nature</i> , 1981 , 290, 744-9	50.4	624
122	Structure of the replicating complex of a pol alpha family DNA polymerase. <i>Cell</i> , 2001 , 105, 657-67	56.2	507
121	The structures of four macrolide antibiotics bound to the large ribosomal subunit. <i>Molecular Cell</i> , 2002 , 10, 117-28	17.6	448
120	Insights into Editing from an Ile-tRNA Synthetase Structure with tRNA ^{Ile} and Mupirocin. <i>Science</i> , 1999 , 285, 1074-1077	33.3	364
119	Structures of MLSBK antibiotics bound to mutated large ribosomal subunits provide a structural explanation for resistance. <i>Cell</i> , 2005 , 121, 257-70	56.2	352
118	Structures of five antibiotics bound at the peptidyl transferase center of the large ribosomal subunit. <i>Journal of Molecular Biology</i> , 2003 , 330, 1061-75	6.5	319
117	A structural understanding of the dynamic ribosome machine. <i>Nature Reviews Molecular Cell Biology</i> , 2008 , 9, 242-53	48.7	315
116	Structure of Taq polymerase with DNA at the polymerase active site. <i>Nature</i> , 1996 , 382, 278-81	50.4	291
115	An induced-fit mechanism to promote peptide bond formation and exclude hydrolysis of peptidyl-tRNA. <i>Nature</i> , 2005 , 438, 520-4	50.4	285
114	Structural basis for the transition from initiation to elongation transcription in T7 RNA polymerase. <i>Science</i> , 2002 , 298, 1387-95	33.3	283
113	The structural mechanism of translocation and helicase activity in T7 RNA polymerase. <i>Cell</i> , 2004 , 116, 393-404	56.2	277
112	Structural basis for initiation of transcription from an RNA polymerase-promoter complex. <i>Nature</i> , 1999 , 399, 80-3	50.4	267
111	Crystal structure of the site-specific recombinase gamma delta resolvase complexed with a 34 bp cleavage site. <i>Cell</i> , 1995 , 82, 193-207	56.2	240
110	Structural insights into peptide bond formation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 11670-5	11.5	233

109	Structural insights into the roles of water and the 2'hydroxyl of the P site tRNA in the peptidyl transferase reaction. <i>Molecular Cell</i> , 2005 , 20, 437-48	17.6	226
108	Crystal structure of the oxazolidinone antibiotic linezolid bound to the 50S ribosomal subunit. <i>Journal of Medicinal Chemistry</i> , 2008 , 51, 3353-6	8.3	217
107	RNA, the first macromolecular catalyst: the ribosome is a ribozyme. <i>Trends in Biochemical Sciences</i> , 2003 , 28, 411-8	10.3	214
106	Revisiting the structures of several antibiotics bound to the bacterial ribosome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 17158-63	11.5	199
105	Crystal structure of a DinB lesion bypass DNA polymerase catalytic fragment reveals a classic polymerase catalytic domain. <i>Molecular Cell</i> , 2001 , 8, 427-37	17.6	173
104	Formation of the first peptide bond: the structure of EF-P bound to the 70S ribosome. <i>Science</i> , 2009 , 325, 966-70	33.3	172
103	The structures of the anti-tuberculosis antibiotics viomycin and capreomycin bound to the 70S ribosome. <i>Nature Structural and Molecular Biology</i> , 2010 , 17, 289-93	17.6	167
102	Structural insights into the stabilization of MALAT1 noncoding RNA by a bipartite triple helix. <i>Nature Structural and Molecular Biology</i> , 2014 , 21, 633-40	17.6	156
101	Crystal structures of the E. coli transcription initiation complexes with a complete bubble. <i>Molecular Cell</i> , 2015 , 58, 534-40	17.6	153
100	Structural insights into the role of rRNA modifications in protein synthesis and ribosome assembly. <i>Nature Structural and Molecular Biology</i> , 2015 , 22, 342-344	17.6	148
99	How hibernation factors RMF, HPF, and YfiA turn off protein synthesis. <i>Science</i> , 2012 , 336, 915-8	33.3	145
98	The mechanism of E. coli RNA polymerase regulation by ppGpp is suggested by the structure of their complex. <i>Molecular Cell</i> , 2013 , 50, 430-6	17.6	133
97	U2504 determines the species specificity of the A-site cleft antibiotics: the structures of tiamulin, homoharringtonine, and bruceantin bound to the ribosome. <i>Journal of Molecular Biology</i> , 2009 , 389, 146-56	6.5	129
96	The initiation of mammalian protein synthesis and mRNA scanning mechanism. <i>Nature</i> , 2013 , 500, 307-11	30.4	128
95	A proton wire to couple aminoacyl-tRNA accommodation and peptide-bond formation on the ribosome. <i>Nature Structural and Molecular Biology</i> , 2014 , 21, 787-93	17.6	127
94	Poly(A) tail recognition by a viral RNA element through assembly of a triple helix. <i>Science</i> , 2010 , 330, 1244-7	33.3	122
93	Structures of phi29 DNA polymerase complexed with substrate: the mechanism of translocation in B-family polymerases. <i>EMBO Journal</i> , 2007 , 26, 3494-505	13	121
92	The mechanism of inhibition of protein synthesis by the proline-rich peptide oncocin. <i>Nature Structural and Molecular Biology</i> , 2015 , 22, 466-9	17.6	114

91	The crystal structure of the catalytic domain of the site-specific recombination enzyme gamma delta resolvase at 2.7 Å resolution. <i>Cell</i> , 1990 , 63, 1323-9	56.2	110
90	The structure of <i>T. aquaticus</i> DNA polymerase III is distinct from eukaryotic replicative DNA polymerases. <i>Cell</i> , 2006 , 126, 893-904	56.2	109
89	Structure of a synaptic gammadelta resolvase tetramer covalently linked to two cleaved DNAs. <i>Science</i> , 2005 , 309, 1210-5	33.3	105
88	Mechanism of transfer RNA maturation by CCA-adding enzyme without using an oligonucleotide template. <i>Nature</i> , 2004 , 430, 640-5	50.4	105
87	Crystal structures of the <i>Bacillus stearothermophilus</i> CCA-adding enzyme and its complexes with ATP or CTP. <i>Cell</i> , 2002 , 111, 815-24	56.2	104
86	Structures of proline-rich peptides bound to the ribosome reveal a common mechanism of protein synthesis inhibition. <i>Nucleic Acids Research</i> , 2016 , 44, 2439-50	20.1	99
85	Ribosome-Targeting Antibiotics: Modes of Action, Mechanisms of Resistance, and Implications for Drug Design. <i>Annual Review of Biochemistry</i> , 2018 , 87, 451-478	29.1	98
84	Conformational changes of elongation factor G on the ribosome during tRNA translocation. <i>Cell</i> , 2015 , 160, 219-27	56.2	89
83	Structural basis for the rescue of stalled ribosomes: structure of YaeJ bound to the ribosome. <i>Science</i> , 2012 , 335, 1370-2	33.3	87
82	The structure of a transcribing T7 RNA polymerase in transition from initiation to elongation. <i>Science</i> , 2008 , 322, 553-7	33.3	83
81	Structures of deacylated tRNA mimics bound to the E site of the large ribosomal subunit. <i>Rna</i> , 2003 , 9, 1345-52	5.8	76
80	Polyspecific pyrrolysyl-tRNA synthetases from directed evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 16724-9	11.5	75
79	Visualizing polynucleotide polymerase machines at work. <i>EMBO Journal</i> , 2006 , 25, 3458-68	13	73
78	Mutations outside the anisomycin-binding site can make ribosomes drug-resistant. <i>Journal of Molecular Biology</i> , 2008 , 379, 505-19	6.5	69
77	Structures of normal single-stranded DNA and deoxyribo-3 [′] S-phosphorothiolates bound to the 3 [′] U ₅ exonucleolytic active site of DNA polymerase I from <i>Escherichia coli</i> . <i>Biochemistry</i> , 1999 , 38, 696-704	2.2	68
76	Structural basis for the fast self-cleavage reaction catalyzed by the twister ribozyme. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 13028-33	11.5	65
75	The structural changes of T7 RNA polymerase from transcription initiation to elongation. <i>Current Opinion in Structural Biology</i> , 2009 , 19, 683-90	8.1	65
74	Insights into the replisome from the structure of a ternary complex of the DNA polymerase III alpha-subunit. <i>Journal of Molecular Biology</i> , 2008 , 382, 859-69	6.5	65

73	A story with a good ending: tRNA 3'end maturation by CCA-adding enzymes. <i>Current Opinion in Structural Biology</i> , 2006 , 16, 12-7	8.1	65
72	Crystal structures of an archaeal class I CCA-adding enzyme and its nucleotide complexes. <i>Molecular Cell</i> , 2003 , 12, 1165-72	17.6	59
71	Amicoumacin a inhibits translation by stabilizing mRNA interaction with the ribosome. <i>Molecular Cell</i> , 2014 , 56, 531-40	17.6	58
70	Distinct tRNA Accommodation Intermediates Observed on the Ribosome with the Antibiotics Hygromycin A and A201A. <i>Molecular Cell</i> , 2015 , 58, 832-44	17.6	57
69	The structure of LepA, the ribosomal back translocase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 4673-8	11.5	56
68	The structural basis of the transition from initiation to elongation phases of transcription, as well as translocation and strand separation, by T7 RNA polymerase. <i>Current Opinion in Structural Biology</i> , 2004 , 14, 4-9	8.1	54
67	Insights into RNA binding by the anticancer drug cisplatin from the crystal structure of cisplatin-modified ribosome. <i>Nucleic Acids Research</i> , 2016 , 44, 4978-87	20.1	50
66	Structures of E. coli β -transcription initiation complexes provide new insights into polymerase mechanism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 4051-6	11.5	50
65	Crystal structure of Pistol, a class of self-cleaving ribozyme. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, 1021-1026	11.5	45
64	Implications of structures of synaptic tetramers of gamma delta resolvase for the mechanism of recombination. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 10642-7	11.5	45
63	Structures of triacetyloleandomycin and mycalamide A bind to the large ribosomal subunit of <i>Haloarcula marismortui</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2009 , 53, 5010-4	5.9	43
62	The structures of antibiotics bound to the E site region of the 50 S ribosomal subunit of <i>Haloarcula marismortui</i> : 13-deoxytedanolide and girodazole. <i>Journal of Molecular Biology</i> , 2007 , 367, 1471-9	6.5	41
61	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. <i>Journal of Medicinal Chemistry</i> , 2019 , 62, 1484-1501	8.3	41
60	Structural basis for potent and broad inhibition of HIV-1 RT by thiophene[3,2-]pyrimidine non-nucleoside inhibitors. <i>ELife</i> , 2018 , 7,	8.9	41
59	Negamycin interferes with decoding and translocation by simultaneous interaction with rRNA and tRNA. <i>Molecular Cell</i> , 2014 , 56, 541-50	17.6	38
58	Structural basis for transcription reactivation by RapA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 2006-10	11.5	35
57	Accuracy, lesion bypass, strand displacement and translocation by DNA polymerases. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2004 , 359, 17-23	5.8	35
56	Crystal structure of elongation factor 4 bound to a clockwise ratcheted ribosome. <i>Science</i> , 2014 , 345, 684-7	33.3	32

55	Structural basis of bacterial transcription activation. <i>Science</i> , 2017 , 358, 947-951	33.3	32
54	The antibiotic thermorubin inhibits protein synthesis by binding to inter-subunit bridge B2a of the ribosome. <i>Journal of Molecular Biology</i> , 2012 , 416, 571-8	6.5	32
53	The antibiotics dityromycin and GE82832 bind protein S12 and block EF-G-catalyzed translocation. <i>Cell Reports</i> , 2014 , 6, 357-65	10.6	30
52	On the structural basis of peptide-bond formation and antibiotic resistance from atomic structures of the large ribosomal subunit. <i>FEBS Letters</i> , 2005 , 579, 955-8	3.8	30
51	Crystal Structure of the Human Ribosome in Complex with DENR-MCT-1. <i>Cell Reports</i> , 2017 , 20, 521-528	10.6	29
50	Use of chemically modified nucleotides to determine a 62-nucleotide RNA crystal structure: a survey of phosphorothioates, Br, Pt and Hg. <i>Journal of Biomolecular Structure and Dynamics</i> , 1997 , 15, 165-72	3.6	27
49	How the CCA-adding enzyme selects adenine over cytosine at position 76 of tRNA. <i>Science</i> , 2010 , 330, 937-40	33.3	26
48	Structural insights into NusG regulating transcription elongation. <i>Nucleic Acids Research</i> , 2017 , 45, 968-974	11.1	22
47	Crystal structure of an intermediate of rotating dimers within the synaptic tetramer of the G-segment invertase. <i>Nucleic Acids Research</i> , 2013 , 41, 2673-82	20.1	21
46	Elongation factor 4 remodels the A-site tRNA on the ribosome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 4994-9	11.5	17
45	Elements of ribosomal drug resistance and specificity. <i>Current Opinion in Structural Biology</i> , 2012 , 22, 750-8	8.1	13
44	Crystal Structure of Human Profilaggrin S100 Domain and Identification of Target Proteins Annexin II, Stratifin, and HSP27. <i>Journal of Investigative Dermatology</i> , 2015 , 135, 1801-1809	4.3	12
43	RNA stabilization by a poly(A) tail 3' end binding pocket and other modes of poly(A)-RNA interaction. <i>Science</i> , 2021 , 371,	33.3	12
42	Crystal structure of the DENR-MCT-1 complex revealed zinc-binding site essential for heterodimer formation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 528-533	11.5	10
41	Crystal Structure of the C-terminal Domain of Human eIF2D and Its Implications on Eukaryotic Translation Initiation. <i>Journal of Molecular Biology</i> , 2017 , 429, 2765-2771	6.5	9
40	A structure-based kinetic model of transcription. <i>Transcription</i> , 2017 , 8, 1-8	4.8	9
39	Structure of the PolIII-DNA complex suggests an atomic model of the replisome. <i>Structure</i> , 2013 , 21, 658-64	5.2	7
38	Protomer structure of oligomeric enzymes: symmetry and allosteric interactions in yeast hexokinase. <i>Biochemical Society Transactions</i> , 1977 , 5, 620-3	5.1	5

37	Exploiting large non-isomorphous differences for phase determination of a G-segment invertase-DNA complex. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014 , 70, 685-93		4
36	Structural insights into the functions of the large ribosomal subunit, a major antibiotic target. <i>Keio Journal of Medicine</i> , 2008 , 57, 1-14	1.6	4
35	Perspectives on the ribosome. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2017 , 372,	5.8	3
34	Crystal structure of the C-terminal domain of DENR. <i>Computational and Structural Biotechnology Journal</i> , 2020 , 18, 696-704	6.8	3
33	Collecting butterflies and the protein structure initiative: the right questions?. <i>Structure</i> , 2007 , 15, 1523-42	4.2	3
32	The Structure of Yeast Hexokinase and its Complexes with Substrates. <i>Biochemical Society Transactions</i> , 1974 , 2, 52-54	5.1	3
31	Retrospective. Frederic M. Richards (1925-2009). <i>Science</i> , 2009 , 323, 1181	33.3	2
30	Structural Insights into Transcription Initiation from De Novo RNA Synthesis to Transitioning into Elongation. <i>IScience</i> , 2020 , 23, 101445	6.1	1
29	Building a Replisome from Interacting Pieces: Sliding Clamp Complexed to a Peptide from DNA Polymerase and a Polymerase Editing Complex. <i>journal of hand surgery Asian-Pacific volume, The</i> , 2020 , 306-317	0.5	1
28	The Structural Basis of Ribosome Activity in Peptide Bond Synthesis. <i>journal of hand surgery Asian-Pacific volume, The</i> , 2020 , 501-511	0.5	1
27	Molecular dynamics analysis of Mg ²⁺ -dependent cleavage of a pistol ribozyme reveals a fail-safe secondary ion for catalysis. <i>Journal of Computational Chemistry</i> , 2020 , 41, 1345-1352	3.5	0
26	Structure of DNA Polymerase I Klenow Fragment Bound to Duplex DNA. <i>journal of hand surgery Asian-Pacific volume, The</i> , 2020 , 270-273	0.5	0
25	The Structures of Four Macrolide Antibiotics Bound to the Large Ribosomal Subunit. <i>journal of hand surgery Asian-Pacific volume, The</i> , 2020 , 525-536	0.5	0
24	The roles of RNA in the peptidyl transferase reaction and its inhibition by antibiotics. <i>FASEB Journal</i> , 2006 , 20, A422	0.9	
23	Structural basis for base discrimination by RB69 DNA polymerase. <i>FASEB Journal</i> , 2008 , 22, 593.2	0.9	
22	Crystal Structure of a CAP-DNA Complex: The DNA Is Bent by 90°. <i>journal of hand surgery Asian-Pacific volume, The</i> , 2020 , 210-216	0.5	
21	Structural Insights into the Roles of Water and the 2'-OH of the P Site tRNA in the Peptidyl Transferase Reaction. <i>journal of hand surgery Asian-Pacific volume, The</i> , 2020 , 557-568	0.5	
20	DNA Polymerases: Structural Diversity and Common Mechanisms. <i>journal of hand surgery Asian-Pacific volume, The</i> , 2020 , 318-321	0.5	

19	The Structural Mechanism of Translocation and Helicase Activity in T7 RNA Polymerase. <i>journal of hand surgery Asian-Pacific volume, The, 2020</i> , 342-353	0.5
18	Structural basis for initiation of transcription from an RNA polymerase-promoter complex. <i>journal of hand surgery Asian-Pacific volume, The, 2020</i> , 297-300	0.5
17	Revisiting the structures of several antibiotics bound to the bacterial ribosome. <i>journal of hand surgery Asian-Pacific volume, The, 2020</i> , 589-594	0.5
16	Structures of Five Antibiotics Bound at the Peptidyl Transferase Center of the Large Ribosomal Subunit. <i>journal of hand surgery Asian-Pacific volume, The, 2020</i> , 537-551	0.5
15	Structure of Catabolite Gene Activator Protein at 2.9-Å Resolution. <i>journal of hand surgery Asian-Pacific volume, The, 2020</i> , 187-193	0.5
14	Crystal structure of <i>Thermus aquaticus</i> DNA polymerase. <i>journal of hand surgery Asian-Pacific volume, The, 2020</i> , 288-292	0.5
13	Structure of Taq polymerase with DNA at the polymerase active site. <i>journal of hand surgery Asian-Pacific volume, The, 2020</i> , 293-296	0.5
12	Structural basis for the 3' to 5' exonuclease activity of <i>Escherichia coli</i> DNA polymerase I: a two metal ion mechanism. <i>journal of hand surgery Asian-Pacific volume, The, 2020</i> , 245-253	0.5
11	Structure of a Complex Between Yeast Hexokinase A and Glucose. <i>journal of hand surgery Asian-Pacific volume, The, 2020</i> , 108-127	0.5
10	A general two-metal-ion mechanism for catalytic RNA. <i>journal of hand surgery Asian-Pacific volume, The, 2020</i> , 597-601	0.5
9	Structure of a Complex of Catabolite Gene Activator Protein and Cyclic AMP Refined at 2.5 Å Resolution. <i>journal of hand surgery Asian-Pacific volume, The, 2020</i> , 194-209	0.5
8	Structure of a Synaptic Endonuclease Tetramer Covalently Linked to Two Cleaved DNAs. <i>journal of hand surgery Asian-Pacific volume, The, 2020</i> , 447-452	0.5
7	Glucose-induced conformational change in yeast hexokinase. <i>journal of hand surgery Asian-Pacific volume, The, 2020</i> , 65-69	0.5
6	Structural Basis for the Transition from Initiation to Elongation Transcription in T7 RNA Polymerase. <i>journal of hand surgery Asian-Pacific volume, The, 2020</i> , 333-341	0.5
5	Structural Basis for Transfer RNA Aminoacylation by <i>Escherichia coli</i> Glutamyl-tRNA Synthetase. <i>journal of hand surgery Asian-Pacific volume, The, 2020</i> , 401-414	0.5
4	Structure of a Complex Between Yeast Hexokinase A and Glucose. <i>journal of hand surgery Asian-Pacific volume, The, 2020</i> , 81-107	0.5
3	The Hexameric Helicase DnaB Adopts a Nonplanar Conformation during Translocation. <i>journal of hand surgery Asian-Pacific volume, The, 2020</i> , 365-375	0.5
2	Crystal Structure of the Large Ribosomal Subunit at 5-Angstrom Resolution	11-20

- 1 Crystallization of Escherichia coli 70S Ribosome in complex with tRNAs. *FASEB Journal*, **2012**, 26, 550.1 o.9