

Thomas A Steitz

List of Publications by Year in descending order

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128
papers

18,920
citations

20797

60
h-index

30058

103
g-index

132
all docs

132
docs citations

132
times ranked

12620
citing authors

#	ARTICLE	IF	CITATIONS
1	The Complete Atomic Structure of the Large Ribosomal Subunit at 2.4 Å Resolution. <i>Science</i> , 2000, 289, 905-920.	6.0	3,132
2	The Structural Basis of Ribosome Activity in Peptide Bond Synthesis. <i>Science</i> , 2000, 289, 920-930.	6.0	2,045
3	DNA Polymerases: Structural Diversity and Common Mechanisms. <i>Journal of Biological Chemistry</i> , 1999, 274, 17395-17398.	1.6	741
4	Structure of catabolite gene activator protein at 2.9 Å... resolution suggests binding to left-handed B-DNA. <i>Nature</i> , 1981, 290, 744-749.	13.7	690
5	A mechanism for all polymerases. <i>Nature</i> , 1998, 391, 231-232.	13.7	557
6	Structure of the Replicating Complex of a Pol β Family DNA Polymerase. <i>Cell</i> , 2001, 105, 657-667.	13.5	547
7	The Structures of Four Macrolide Antibiotics Bound to the Large Ribosomal Subunit. <i>Molecular Cell</i> , 2002, 10, 117-128.	4.5	520
8	Insights into Editing from an Ile-tRNA Synthetase Structure with tRNA ^{Ile} and Mupirocin. <i>Science</i> , 1999, 285, 1074-1077.	6.0	425
9	Structures of MLSBK Antibiotics Bound to Mutated Large Ribosomal Subunits Provide a Structural Explanation for Resistance. <i>Cell</i> , 2005, 121, 257-270.	13.5	401
10	Structures of Five Antibiotics Bound at the Peptidyl Transferase Center of the Large Ribosomal Subunit. <i>Journal of Molecular Biology</i> , 2003, 330, 1061-1075.	2.0	372
11	A structural understanding of the dynamic ribosome machine. <i>Nature Reviews Molecular Cell Biology</i> , 2008, 9, 242-253.	16.1	364
12	Structure of Taq polymerase with DNA at the polymerase active site. <i>Nature</i> , 1996, 382, 278-281.	13.7	333
13	An induced-fit mechanism to promote peptide bond formation and exclude hydrolysis of peptidyl-tRNA. <i>Nature</i> , 2005, 438, 520-524.	13.7	326
14	The Structural Mechanism of Translocation and Helicase Activity in T7 RNA Polymerase. <i>Cell</i> , 2004, 116, 393-404.	13.5	310
15	Structural Basis for the Transition from Initiation to Elongation Transcription in T7 RNA Polymerase. <i>Science</i> , 2002, 298, 1387-1395.	6.0	309
16	Structural basis for initiation of transcription from an RNA polymerase- σ promoter complex. <i>Nature</i> , 1999, 399, 80-83.	13.7	295
17	Structural insights into peptide bond formation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 11670-11675.	3.3	267
18	Crystal Structure of the Oxazolidinone Antibiotic Linezolid Bound to the 50S Ribosomal Subunit. <i>Journal of Medicinal Chemistry</i> , 2008, 51, 3353-3356.	2.9	267

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19	Crystal structure of the site-specific recombinase ϕ 31 resolvase complexed with a 34 bp cleavage site. <i>Cell</i> , 1995, 82, 193-207.	13.5	259
20	RNA, the first macromolecular catalyst: the ribosome is a ribozyme. <i>Trends in Biochemical Sciences</i> , 2003, 28, 411-418.	3.7	255
21	Structural Insights into the Roles of Water and the 2'-OH of the P Site tRNA in the Peptidyl Transferase Reaction. <i>Molecular Cell</i> , 2005, 20, 437-448.	4.5	253
22	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, 17158-17163.	3.3	240
23	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.	3.6	224
24	Crystal Structures of the <i>E. coli</i> Transcription Initiation Complexes with a Complete Bubble. <i>Molecular Cell</i> , 2015, 58, 534-540.	4.5	220
25	Structural insights into the stabilization of MALAT1 noncoding RNA by a bipartite triple helix. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 633-640.	3.6	213
26	Formation of the First Peptide Bond: The Structure of EF-P Bound to the 70S Ribosome. <i>Science</i> , 2009, 325, 966-970.	6.0	201
27	Ribosome-Targeting Antibiotics: Modes of Action, Mechanisms of Resistance, and Implications for Drug Design. <i>Annual Review of Biochemistry</i> , 2018, 87, 451-478.	5.0	199
28	The structures of the anti-tuberculosis antibiotics viomycin and capreomycin bound to the 70S ribosome. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 289-293.	3.6	194
29	How Hibernation Factors RMF, HPF, and YfiA Turn Off Protein Synthesis. <i>Science</i> , 2012, 336, 915-918.	6.0	193
30	A proton wire to couple aminoacyl-tRNA accommodation and peptide-bond formation on the ribosome. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 787-793.	3.6	191
31	Crystal Structure of a DinB Lesion Bypass DNA Polymerase Catalytic Fragment Reveals a Classic Polymerase Catalytic Domain. <i>Molecular Cell</i> , 2001, 8, 427-437.	4.5	190
32	The initiation of mammalian protein synthesis and mRNA scanning mechanism. <i>Nature</i> , 2013, 500, 307-311.	13.7	163
33	The Mechanism of <i>E. coli</i> RNA Polymerase Regulation by ppGpp Is Suggested by the Structure of their Complex. <i>Molecular Cell</i> , 2013, 50, 430-436.	4.5	159
34	U2504 Determines the Species Specificity of the A-Site Cleft Antibiotics. <i>Journal of Molecular Biology</i> , 2009, 389, 146-156.	2.0	154
35	Poly(A) Tail Recognition by a Viral RNA Element Through Assembly of a Triple Helix. <i>Science</i> , 2010, 330, 1244-1247.	6.0	144
36	The mechanism of inhibition of protein synthesis by the proline-rich peptide oncocin. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 466-469.	3.6	144

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37	Structures of phi29 DNA polymerase complexed with substrate: the mechanism of translocation in B-family polymerases. <i>EMBO Journal</i> , 2007, 26, 3494-3505.	3.5	140
38	Structures of proline-rich peptides bound to the ribosome reveal a common mechanism of protein synthesis inhibition. <i>Nucleic Acids Research</i> , 2016, 44, 2439-2450.	6.5	132
39	The Structure of <i>T. aquaticus</i> DNA Polymerase III Is Distinct from Eukaryotic Replicative DNA Polymerases. <i>Cell</i> , 2006, 126, 893-904.	13.5	127
40	The crystal structure of the catalytic domain of the site-specific recombination enzyme ϕ 31 resolvase at 2.7 Å... resolution. <i>Cell</i> , 1990, 63, 1323-1329.	13.5	121
41	Mechanism of transfer RNA maturation by CCA-adding enzyme without using an oligonucleotide template. <i>Nature</i> , 2004, 430, 640-645.	13.7	120
42	Conformational Changes of Elongation Factor G on the Ribosome during tRNA Translocation. <i>Cell</i> , 2015, 160, 219-227.	13.5	117
43	Crystal Structures of the <i>Bacillus stearothermophilus</i> CCA-Adding Enzyme and Its Complexes with ATP or CTP. <i>Cell</i> , 2002, 111, 815-824.	13.5	115
44	Structure of a Synaptic ϕ 31 Resolvase Tetramer Covalently Linked to Two Cleaved DNAs. <i>Science</i> , 2005, 309, 1210-1215.	6.0	114
45	Structural Basis for the Rescue of Stalled Ribosomes: Structure of YaeJ Bound to the Ribosome. <i>Science</i> , 2012, 335, 1370-1372.	6.0	101
46	Polyspecific pyrrolysyl-tRNA synthetases from directed evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 16724-16729.	3.3	101
47	The Structure of a Transcribing T7 RNA Polymerase in Transition from Initiation to Elongation. <i>Science</i> , 2008, 322, 553-557.	6.0	98
48	Insights into the Replisome from the Structure of a Ternary Complex of the DNA Polymerase III β -Subunit. <i>Journal of Molecular Biology</i> , 2008, 382, 859-869.	2.0	85
49	Structures of deacylated tRNA mimics bound to the E site of the large ribosomal subunit. <i>Rna</i> , 2003, 9, 1345-1352.	1.6	81
50	Structures of <i>E. coli</i> σ ^S -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, 4051-4056.	3.3	80
51	Distinct tRNA Accommodation Intermediates Observed on the Ribosome with the Antibiotics Hygromycin A and A201A. <i>Molecular Cell</i> , 2015, 58, 832-844.	4.5	79
52	Structures of Normal Single-Stranded DNA and Deoxyribo-3 α -S-phosphorothiolates Bound to the 3 α -5 α Exonucleolytic Active Site of DNA Polymerase I from <i>Escherichia coli</i> . <i>Biochemistry</i> , 1999, 38, 696-704.	1.2	77
53	Visualizing polynucleotide polymerase machines at work. <i>EMBO Journal</i> , 2006, 25, 3458-3468.	3.5	76
54	A story with a good ending: tRNA 3 α -end maturation by CCA-adding enzymes. <i>Current Opinion in Structural Biology</i> , 2006, 16, 12-17.	2.6	75

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55	Mutations Outside the Anisomycin-Binding Site Can Make Ribosomes Drug-Resistant. <i>Journal of Molecular Biology</i> , 2008, 379, 505-519.	2.0	75
56	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, 13028-13033.	3.3	75
57	The structural changes of T7 RNA polymerase from transcription initiation to elongation. <i>Current Opinion in Structural Biology</i> , 2009, 19, 683-690.	2.6	74
58	Amicoumacin A Inhibits Translation by Stabilizing mRNA Interaction with the Ribosome. <i>Molecular Cell</i> , 2014, 56, 531-540.	4.5	73
59	Structural basis of bacterial transcription activation. <i>Science</i> , 2017, 358, 947-951.	6.0	71
60	Identification of Dihydrofuro[3,4- <i>d</i>]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.	2.9	70
61	Insights into RNA binding by the anticancer drug cisplatin from the crystal structure of cisplatin-modified ribosome. <i>Nucleic Acids Research</i> , 2016, 44, 4978-4987.	6.5	69
62	Crystal Structures of an Archaeal Class I CCA-Adding Enzyme and Its Nucleotide Complexes. <i>Molecular Cell</i> , 2003, 12, 1165-1172.	4.5	66
63	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, 4673-4678.	3.3	66
64	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.	2.6	59
65	Structural basis for potent and broad inhibition of HIV-1 RT by thiophene[3,2- <i>d</i>]pyrimidine non-nucleoside inhibitors. <i>ELife</i> , 2018, 7, .	2.8	57
66	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.	3.3	56
67	Structural basis for transcription reactivation by RapA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 2006-2010.	3.3	53
68	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, 5010-5014.	1.4	50
69	Implications of structures of synaptic tetramers of \hat{A} resolvase for the mechanism of recombination. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 10642-10647.	3.3	47
70	Crystal Structure of the Human Ribosome in Complex with DENR-MCT-1. <i>Cell Reports</i> , 2017, 20, 521-528.	2.9	47
71	The Structures of Antibiotics Bound to the E Site Region of the 50 S Ribosomal Subunit of <i>Haloarcula marismortui</i> : 13-Deoxytedanolid and Girodazole. <i>Journal of Molecular Biology</i> , 2007, 367, 1471-1479.	2.0	45
72	The Antibiotic Thermorubin Inhibits Protein Synthesis by Binding to Inter-Subunit Bridge B2a of the Ribosome. <i>Journal of Molecular Biology</i> , 2012, 416, 571-578.	2.0	42

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73	Negamycin Interferes with Decoding and Translocation by Simultaneous Interaction with rRNA and tRNA. <i>Molecular Cell</i> , 2014, 56, 541-550.	4.5	41
74	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.	1.8	39
75	Crystal structure of elongation factor 4 bound to a clockwise ratcheted ribosome. <i>Science</i> , 2014, 345, 684-687.	6.0	36
76	The Antibiotics Dityromycin and GE82832 Bind Protein S12 and Block EF-G-Catalyzed Translocation. <i>Cell Reports</i> , 2014, 6, 357-365.	2.9	36
77	Structural insights into NusG regulating transcription elongation. <i>Nucleic Acids Research</i> , 2017, 45, 968-974.	6.5	33
78	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, 955-958.	1.3	32
79	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, 165-172.	2.0	31
80	How the CCA-Adding Enzyme Selects Adenine over Cytosine at Position 76 of tRNA. <i>Science</i> , 2010, 330, 937-940.	6.0	29
81	RNA stabilization by a poly(A) tail 3' end binding pocket and other modes of poly(A)-RNA interaction. <i>Science</i> , 2021, 371, .	6.0	29
82	Crystal structure of an intermediate of rotating dimers within the synaptic tetramer of the G-segment invertase. <i>Nucleic Acids Research</i> , 2013, 41, 2673-2682.	6.5	24
83	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, 4994-4999.	3.3	19
84	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.	3.3	19
85	Elements of ribosomal drug resistance and specificity. <i>Current Opinion in Structural Biology</i> , 2012, 22, 750-758.	2.6	17
86	Structure of the PolIII β -c-DNA Complex Suggests an Atomic Model of the Replisome. <i>Structure</i> , 2013, 21, 658-664.	1.6	15
87	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.	0.3	13
88	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.	2.0	13
89	A structure-based kinetic model of transcription. <i>Transcription</i> , 2017, 8, 1-8.	1.7	11
90	Protomer Structure of Oligomeric Enzymes: Symmetry and Allosteric Interactions in Yeast Hexokinase. <i>Biochemical Society Transactions</i> , 1977, 5, 620-623.	1.6	5

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91	The Structures of Four Macrolide Antibiotics Bound to the Large Ribosomal Subunit. journal of hand surgery Asian-Pacific volume, The, 2020, , 525-536.	0.2	5
92	The Structure of Yeast Hexokinase and its Complexes with Substrates. Biochemical Society Transactions, 1974, 2, 52-54.	1.6	4
93	Collecting Butterflies and the Protein Structure Initiative: The Right Questions?. Structure, 2007, 15, 1523-1524.	1.6	4
94	Perspectives on the ribosome. Philosophical Transactions of the Royal Society B: Biological Sciences, 2017, 372, 20160537.	1.8	4
95	Structural Insights into Transcription Initiation from De Novo RNA Synthesis to Transitioning into Elongation. IScience, 2020, 23, 101445.	1.9	4
96	Molecular dynamics analysis of Mg ²⁺ -dependent cleavage of a pistol ribozyme reveals a fail-safe secondary ion for catalysis. Journal of Computational Chemistry, 2020, 41, 1345-1352.	1.5	4
97	Exploiting large non-isomorphous differences for phase determination of a G-segment invertase-DNA complex. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 685-693.	2.5	4
98	Structural Insights into the Functions of the Large Ribosomal Subunit, a Major Antibiotic Target. Keio Journal of Medicine, 2008, 57, 1-14.	0.5	4
99	Crystal structure of the C-terminal domain of DENR. Computational and Structural Biotechnology Journal, 2020, 18, 696-704.	1.9	3
100	Antimicrobial peptides targeting bacterial ribosome. Oncotarget, 2015, 6, 18744-18745.	0.8	3
101	Structure of DNA Polymerase I Klenow Fragment Bound to Duplex DNA. journal of hand surgery Asian-Pacific volume, The, 2020, , 270-273.	0.2	3
102	Frederic M. Richards (1925-2009). Science, 2009, 323, 1181-1181.	6.0	2
103	Crystal Structure of the Large Ribosomal Subunit at 5-Angstrom Resolution. , 0, , 11-20.		1
104	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.	0.2	1
105	The Structural Basis of Ribosome Activity in Peptide Bond Synthesis. journal of hand surgery Asian-Pacific volume, The, 2020, , 501-511.	0.2	1
106	The roles of RNA in the peptidyl transferase reaction and its inhibition by antibiotics. FASEB Journal, 2006, 20, A422.	0.2	0
107	Structural basis for base discrimination by RB69 DNA polymerase. FASEB Journal, 2008, 22, 593.2.	0.2	0
108	Crystallization of Escherichia coli 70S Ribosome in complex with tRNAs. FASEB Journal, 2012, 26, 550.1.	0.2	0

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109	Crystal Structure of a CAP-DNA Complex: The DNA Is Bent by 90°. journal of hand surgery Asian-Pacific volume, The, 2020, , 210-216.	0.2	0
110	Structural Insights into the Roles of Water and the 2'-OH Hydroxyl of the P Site tRNA in the Peptidyl Transferase Reaction. journal of hand surgery Asian-Pacific volume, The, 2020, , 557-568.	0.2	0
111	DNA Polymerases: Structural Diversity and Common Mechanisms. journal of hand surgery Asian-Pacific volume, The, 2020, , 318-321.	0.2	0
112	The Structural Mechanism of Translocation and Helicase Activity in T7 RNA Polymerase. journal of hand surgery Asian-Pacific volume, The, 2020, , 342-353.	0.2	0
113	Structural basis for initiation of transcription from an RNA polymerase-promoter complex. journal of hand surgery Asian-Pacific volume, The, 2020, , 297-300.	0.2	0
114	Revisiting the structures of several antibiotics bound to the bacterial ribosome. journal of hand surgery Asian-Pacific volume, The, 2020, , 589-594.	0.2	0
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.	0.2	0
116	Structure of Catabolite Gene Activator Protein at 2.9-Å... Resolution. journal of hand surgery Asian-Pacific volume, The, 2020, , 187-193.	0.2	0
117	Crystal structure of <i>Thermus aquaticus</i> DNA polymerase. journal of hand surgery Asian-Pacific volume, The, 2020, , 288-292.	0.2	0
118	Structure of <i>Taq</i> polymerase with DNA at the polymerase active site. journal of hand surgery Asian-Pacific volume, The, 2020, , 293-296.	0.2	0
119	Structural basis for the 3'→5' exonuclease activity of <i>Escherichia coli</i> DNA polymerase I: a two metal ion mechanism. journal of hand surgery Asian-Pacific volume, The, 2020, , 245-253.	0.2	0
120	Structure of a Complex Between Yeast Hexokinase A and Glucose. journal of hand surgery Asian-Pacific volume, The, 2020, , 108-127.	0.2	0
121	A general two-metal-ion mechanism for catalytic RNA. journal of hand surgery Asian-Pacific volume, The, 2020, , 597-601.	0.2	0
122	Structure of a Complex of Catabolite Gene Activator Protein and Cyclic AMP Refined at 2.5 Å... Resolution. journal of hand surgery Asian-Pacific volume, The, 2020, , 194-209.	0.2	0
123	Structure of a Synaptic λ Resolvase Tetramer Covalently Linked to Two Cleaved DNAs. journal of hand surgery Asian-Pacific volume, The, 2020, , 447-452.	0.2	0
124	Glucose-induced conformational change in yeast hexokinase. journal of hand surgery Asian-Pacific volume, The, 2020, , 65-69.	0.2	0
125	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.	0.2	0
126	Structural Basis for Transfer RNA Aminoacylation by <i>Escherichia coli</i> Glutamyl-tRNA Synthetase. journal of hand surgery Asian-Pacific volume, The, 2020, , 401-414.	0.2	0

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127	Structure of a Complex Between Yeast Hexokinase A and Glucose. journal of hand surgery Asian-Pacific volume, The, 2020, , 81-107.	0.2	0
128	The Hexameric Helicase DnaB Adopts a Nonplanar Conformation during Translocation. journal of hand surgery Asian-Pacific volume, The, 2020, , 365-375.	0.2	0