

# Stewart Shuman

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/16672/publications.pdf>

Version: 2024-02-01

346  
papers

14,706  
citations

19657

61  
h-index

37204

96  
g-index

349  
all docs

349  
docs citations

349  
times ranked

8173  
citing authors

#	ARTICLE	IF	CITATIONS
1	Distinct Roles for CTD Ser-2 and Ser-5 Phosphorylation in the Recruitment and Allosteric Activation of Mammalian mRNA Capping Enzyme. <i>Molecular Cell</i> , 1999, 3, 405-411.	9.7	297
2	What messenger RNA capping tells us about eukaryotic evolution. <i>Nature Reviews Molecular Cell Biology</i> , 2002, 3, 619-625.	37.0	296
3	Friction and torque govern the relaxation of DNA supercoils by eukaryotic topoisomerase IB. <i>Nature</i> , 2005, 434, 671-674.	27.8	287
4	X-Ray Crystallography Reveals a Large Conformational Change during Guanyl Transfer by mRNA Capping Enzymes. <i>Cell</i> , 1997, 89, 545-553.	28.9	260
5	Structure, mechanism, and evolution of the mRNA capping apparatus. <i>Progress in Molecular Biology and Translational Science</i> , 2000, 66, 1-40.	1.9	252
6	Bacterial DNA repair by non-homologous end joining. <i>Nature Reviews Microbiology</i> , 2007, 5, 852-861.	28.6	245
7	Conservation of Structure and Mechanism between Eukaryotic Topoisomerase I and Site-Specific Recombinases. <i>Cell</i> , 1998, 92, 841-850.	28.9	235
8	RNA capping enzyme and DNA ligase: a superfamily of covalent nucleotidyl transferases. <i>Molecular Microbiology</i> , 1995, 17, 405-420.	2.5	227
9	The DExH protein NPH-II is a processive and directional motor for unwinding RNA. <i>Nature</i> , 2000, 403, 447-451.	27.8	209
10	Structure of an mRNA Capping Enzyme Bound to the Phosphorylated Carboxy-Terminal Domain of RNA Polymerase II. <i>Molecular Cell</i> , 2003, 11, 1549-1561.	9.7	192
11	Mechanism of nonhomologous end-joining in mycobacteria: a low-fidelity repair system driven by Ku, ligase D and ligase C. <i>Nature Structural and Molecular Biology</i> , 2005, 12, 304-312.	8.2	190
12	Division of labor among <i>Mycobacterium smegmatis</i> RNase H enzymes: RNase H1 activity of RnhA or RnhC is essential for growth whereas RnhB and RnhA guard against killing by hydrogen peroxide in stationary phase. <i>Nucleic Acids Research</i> , 2017, 45, 1-14.	14.5	183
13	The polynucleotide ligase and RNA capping enzyme superfamily of covalent nucleotidyltransferases. <i>Current Opinion in Structural Biology</i> , 2004, 14, 757-764.	5.7	167
14	Structure and mechanism of T4 polynucleotide kinase: an RNA repair enzyme. <i>EMBO Journal</i> , 2002, 21, 3873-3880.	7.8	162
15	Catalytic Mechanism of DNA Topoisomerase IB. <i>Molecular Cell</i> , 2000, 5, 1035-1041.	9.7	155
16	Crystal Structure of Eukaryotic DNA Ligase—Adenylate Illuminates the Mechanism of Nick Sensing and Strand Joining. <i>Molecular Cell</i> , 2000, 6, 1183-1193.	9.7	149
17	Modified Vaccinia Virus Ankara Triggers Type I IFN Production in Murine Conventional Dendritic Cells via a cGAS/STING-Mediated Cytosolic DNA-Sensing Pathway. <i>PLoS Pathogens</i> , 2014, 10, e1003989.	4.7	148
18	Site-Specific Ribonuclease Activity of Eukaryotic DNA Topoisomerase I. <i>Molecular Cell</i> , 1997, 1, 89-97.	9.7	147

#	ARTICLE	IF	CITATIONS
19	DNA Ligases: Progress and Prospects. <i>Journal of Biological Chemistry</i> , 2009, 284, 17365-17369.	3.4	146
20	Bacteriophage T4 RNA ligase 2 (gp24.1) exemplifies a family of RNA ligases found in all phylogenetic domains. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 12709-12714.	7.1	145
21	RtcB Is the RNA Ligase Component of an Escherichia coli RNA Repair Operon. <i>Journal of Biological Chemistry</i> , 2011, 286, 7727-7731.	3.4	143
22	Structure and Mechanism of Yeast RNA Triphosphatase. <i>Cell</i> , 1999, 99, 533-543.	28.9	140
23	Structure and Mechanism of mRNA Cap (Guanine-N7) Methyltransferase. <i>Molecular Cell</i> , 2004, 13, 77-89.	9.7	138
24	Structure-function analysis of the kinase-CPD domain of yeast tRNA ligase (Trl1) and requirements for complementation of tRNA splicing by a plant Trl1 homolog. <i>Nucleic Acids Research</i> , 2006, 34, 517-527.	14.5	137
25	Domain Structure and Mutational Analysis of T4 Polynucleotide Kinase. <i>Journal of Biological Chemistry</i> , 2001, 276, 26868-26874.	3.4	128
26	Biochemical and Genetic Analysis of the Four DNA Ligases of Mycobacteria. <i>Journal of Biological Chemistry</i> , 2004, 279, 20594-20606.	3.4	127
27	Tat Stimulates Cotranscriptional Capping of HIV mRNA. <i>Molecular Cell</i> , 2002, 10, 585-597.	9.7	125
28	Structure and Mechanism of RNA Ligase. <i>Structure</i> , 2004, 12, 327-339.	3.3	125
29	Interactions between Fission Yeast mRNA Capping Enzymes and Elongation Factor Spt5. <i>Journal of Biological Chemistry</i> , 2002, 277, 19639-19648.	3.4	122
30	Deciphering the RNA Polymerase II CTD Code in Fission Yeast. <i>Molecular Cell</i> , 2011, 43, 311-318.	9.7	109
31	Vaccinia DNA topoisomerase I: Single-turnover and steady-state kinetic analysis of the DNA strand cleavage and ligation reactions. <i>Biochemistry</i> , 1994, 33, 327-339.	2.5	107
32	Vaccinia virus DNA ligase: specificity, fidelity, and inhibition. <i>Biochemistry</i> , 1995, 34, 16138-16147.	2.5	106
33	The pathways and outcomes of mycobacterial NHEJ depend on the structure of the broken DNA ends. <i>Genes and Development</i> , 2008, 22, 512-527.	5.9	102
34	Intratumoral delivery of inactivated modified vaccinia virus Ankara (iMVA) induces systemic antitumor immunity via STING and Batf3-dependent dendritic cells. <i>Science Immunology</i> , 2017, 2, .	11.9	101
35	Mycobacteria exploit three genetically distinct DNA double-strand break repair pathways. <i>Molecular Microbiology</i> , 2011, 79, 316-330.	2.5	96
36	RNA ligase RtcB splices 3'-phosphate and 5'-OH ends via covalent RtcB-(histidinyI)-GMP and polynucleotide-(3'-pp(5'-G intermediates. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 6072-6077.	7.1	94

#	ARTICLE	IF	CITATIONS
37	Novel Mechanism of RNA Repair by RtcB via Sequential 2'-Cyclic Phosphodiesterase and 3'-Phosphate/5'-Hydroxyl Ligation Reactions. <i>Journal of Biological Chemistry</i> , 2011, 286, 43134-43143.	3.4	93
38	RtcB, a Novel RNA Ligase, Can Catalyze tRNA Splicing and HAC1 mRNA Splicing in Vivo. <i>Journal of Biological Chemistry</i> , 2011, 286, 30253-30257.	3.4	93
39	Vaccinia virus DNA topoisomerase: a model eukaryotic type IB enzyme. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 1998, 1400, 321-337.	2.4	86
40	Mutational analysis of Chlorella virus DNA ligase: catalytic roles of domain I and motif VI. <i>Nucleic Acids Research</i> , 1998, 26, 4618-4625.	14.5	85
41	Mycobacterial Nonhomologous End Joining Mediates Mutagenic Repair of Chromosomal Double-Strand DNA Breaks. <i>Journal of Bacteriology</i> , 2007, 189, 5237-5246.	2.2	84
42	AdnAB: a new DSB-resecting motor nuclease from mycobacteria. <i>Genes and Development</i> , 2009, 23, 1423-1437.	5.9	82
43	Last Stop on the Road to Repair: Structure of E. coli DNA Ligase Bound to Nicked DNA-Adenylate. <i>Molecular Cell</i> , 2007, 26, 257-271.	9.7	81
44	Genetic and Biochemical Analysis of the Functional Domains of Yeast tRNA Ligase. <i>Journal of Biological Chemistry</i> , 2003, 278, 43928-43938.	3.4	79
45	RNA Ligase Structures Reveal the Basis for RNA Specificity and Conformational Changes that Drive Ligation Forward. <i>Cell</i> , 2006, 127, 71-84.	28.9	78
46	Yeast and Viral RNA 5'-Triphosphatases Comprise a New Nucleoside Triphosphatase Family. <i>Journal of Biological Chemistry</i> , 1998, 273, 34151-34156.	3.4	77
47	RNA Substrate Specificity and Structure-guided Mutational Analysis of Bacteriophage T4 RNA Ligase 2. <i>Journal of Biological Chemistry</i> , 2004, 279, 31337-31347.	3.4	76
48	How an RNA Ligase Discriminates RNA versus DNA Damage. <i>Molecular Cell</i> , 2004, 16, 211-221.	9.7	76
49	The Structure of Fcp1, an Essential RNA Polymerase II CTD Phosphatase. <i>Molecular Cell</i> , 2008, 32, 478-490.	9.7	76
50	A poxvirus-like type IB topoisomerase family in bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 1853-1858.	7.1	75
51	Structural basis for nick recognition by a minimal pluripotent DNA ligase. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 770-778.	8.2	74
52	Characterization of Human, <i>Schizosaccharomyces pombe</i> , and <i>Candida albicans</i> mRNA Cap Methyltransferases and Complete Replacement of the Yeast Capping Apparatus by Mammalian Enzymes. <i>Journal of Biological Chemistry</i> , 1999, 274, 16553-16562.	3.4	73
53	RNA Repair: An Antidote to Cytotoxic Eukaryal RNA Damage. <i>Molecular Cell</i> , 2008, 31, 278-286.	9.7	71
54	Genetic, Physical, and Functional Interactions between the Triphosphatase and Guanylyltransferase Components of the Yeast mRNA Capping Apparatus. <i>Molecular and Cellular Biology</i> , 1998, 18, 5189-5198.	2.3	70

#	ARTICLE	IF	CITATIONS
55	RNA 5â€™-Triphosphatase, Nucleoside Triphosphatase, and Guanylyltransferase Activities of Baculovirus LEF-4 Protein. <i>Journal of Virology</i> , 1998, 72, 10020-10028.	3.4	70
56	Specificity and fidelity of strand joining by <i>Chlorella</i> virus DNA ligase. <i>Nucleic Acids Research</i> , 1998, 26, 3536-3541.	14.5	69
57	Mycobacterial UvrD1 Is a Ku-dependent DNA Helicase That Plays a Role in Multiple DNA Repair Events, Including Double-strand Break Repair. <i>Journal of Biological Chemistry</i> , 2007, 282, 15114-15125.	3.4	66
58	Portability and fidelity of RNA-repair systems. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 2788-2793.	7.1	65
59	Genetic and Biochemical Analysis of Yeast and Human Cap Trimethylguanosine Synthase. <i>Journal of Biological Chemistry</i> , 2008, 283, 31706-31718.	3.4	65
60	The Length, Phosphorylation State, and Primary Structure of the RNA Polymerase II Carboxyl-terminal Domain Dictate Interactions with mRNA Capping Enzymes. <i>Journal of Biological Chemistry</i> , 2001, 276, 28075-28082.	3.4	64
61	Mutational analysis defines the 5'-kinase and 3'-phosphatase active sites of T4 polynucleotide kinase. <i>Nucleic Acids Research</i> , 2002, 30, 1073-1080.	14.5	64
62	Mechanism of DNA transesterification by vaccinia topoisomerase: catalytic contributions of essential residues Arg-130, Gly-132, Tyr-136 and Lys-167. <i>Nucleic Acids Research</i> , 1997, 25, 3001-3008.	14.5	63
63	Stereochemical Outcome and Kinetic Effects of Rp- and Sp-Phosphorothioate Substitutions at the Cleavage Site of Vaccinia Type I DNA Topoisomerase. <i>Biochemistry</i> , 2000, 39, 5561-5572.	2.5	63
64	Proton Relay Mechanism of General Acid Catalysis by DNA Topoisomerase IB. <i>Journal of Biological Chemistry</i> , 2002, 277, 5711-5714.	3.4	62
65	Structure-Function Analysis of T4 RNA Ligase 2. <i>Journal of Biological Chemistry</i> , 2003, 278, 17601-17608.	3.4	62
66	Atomic structure and nonhomologous end-joining function of the polymerase component of bacterial DNA ligase D. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 1711-1716.	7.1	62
67	Characterization of the <i>Schizosaccharomyces pombe</i> Cdk9/Pch1 Protein Kinase. <i>Journal of Biological Chemistry</i> , 2003, 278, 43346-43356.	3.4	61
68	A Function of Yeast mRNA Cap Methyltransferase, Abd1, in Transcription by RNA Polymerase II. <i>Molecular Cell</i> , 2004, 13, 377-387.	9.7	61
69	Crystal Structure and Nonhomologous End-joining Function of the Ligase Component of <i>Mycobacterium</i> DNA Ligase D. <i>Journal of Biological Chemistry</i> , 2006, 281, 13412-13423.	3.4	61
70	A Phosphate-binding Histidine of Binuclear Metallophosphodiesterase Enzymes Is a Determinant of 2â€™,3â€™-Cyclic Nucleotide Phosphodiesterase Activity. <i>Journal of Biological Chemistry</i> , 2008, 283, 30942-30949.	3.4	60
71	Mutational Analysis of Vaccinia DNA Ligase Defines Residues Essential for Covalent Catalysis. <i>Virology</i> , 1995, 211, 73-83.	2.4	58
72	A Primer-dependent Polymerase Function of <i>Pseudomonas aeruginosa</i> ATP-dependent DNA Ligase (LigD). <i>Journal of Biological Chemistry</i> , 2005, 280, 418-427.	3.4	58

#	ARTICLE	IF	CITATIONS
73	Footprinting of Chlorella Virus DNA Ligase Bound at a Nick in Duplex DNA. <i>Journal of Biological Chemistry</i> , 1999, 274, 14032-14039.	3.4	57
74	NAD <sup>+</sup> -dependent DNA Ligase Encoded by a Eukaryotic Virus. <i>Journal of Biological Chemistry</i> , 2001, 276, 36100-36109.	3.4	57
75	Structure-function analysis of yeast RNA debranching enzyme (Dbr1), a manganese-dependent phosphodiesterase. <i>Nucleic Acids Research</i> , 2005, 33, 6349-6360.	14.5	57
76	Human RNA 5' kinase (hClp1) can function as a tRNA splicing enzyme in vivo. <i>Rna</i> , 2008, 14, 1737-1745.	3.5	57
77	Separable Functions of the Fission Yeast Spt5 Carboxyl-Terminal Domain (CTD) in Capping Enzyme Binding and Transcription Elongation Overlap with Those of the RNA Polymerase II CTD. <i>Molecular and Cellular Biology</i> , 2010, 30, 2353-2364.	2.3	57
78	Mechanism of RNA 2',3'-cyclic phosphate end healing by T4 polynucleotide kinase-phosphatase. <i>Nucleic Acids Research</i> , 2013, 41, 355-365.	14.5	57
79	Structure-Function Analysis of the mRNA Cap Methyltransferase of <i>Saccharomyces cerevisiae</i> . <i>Journal of Biological Chemistry</i> , 1997, 272, 14683-14689.	3.4	55
80	HIV-1 Tat Protein Interacts with Mammalian Capping Enzyme and Stimulates Capping of TAR RNA. <i>Journal of Biological Chemistry</i> , 2001, 276, 12959-12966.	3.4	55
81	Structure-function analysis of yeast tRNA ligase. <i>Rna</i> , 2005, 11, 966-975.	3.5	55
82	The Nucleoside Triphosphatase and Helicase Activities of Vaccinia Virus NPH-II Are Essential for Virus Replication. <i>Journal of Virology</i> , 1998, 72, 4729-4736.	3.4	55
83	Novel 3'-Ribonuclease and 3'-Phosphatase Activities of the Bacterial Non-homologous End-joining Protein, DNA Ligase D. <i>Journal of Biological Chemistry</i> , 2005, 280, 25973-25981.	3.4	54
84	Individual letters of the RNA polymerase II CTD code govern distinct gene expression programs in fission yeast. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 4185-4190.	7.1	53
85	Cyclin-Dependent Kinase 9 (Cdk9) of Fission Yeast Is Activated by the CDK-Activating Kinase Csk1, Overlaps Functionally with the TFIIF-Associated Kinase Mcs6, and Associates with the mRNA Cap Methyltransferase Pcm1 In Vivo. <i>Molecular and Cellular Biology</i> , 2006, 26, 777-788.	2.3	51
86	Mutational Analysis of 39 Residues of Vaccinia DNA Topoisomerase Identifies Lys-220, Arg-223, and Asn-228 as Important for Covalent Catalysis. <i>Journal of Biological Chemistry</i> , 1997, 272, 8263-8269.	3.4	50
87	Conserved Residues in Domain Ia Are Required for the Reaction of <i>Escherichia coli</i> DNA Ligase with NAD <sup>+</sup> . <i>Journal of Biological Chemistry</i> , 2002, 277, 9695-9700.	3.4	50
88	Histidine 265 Is Important for Covalent Catalysis by Vaccinia Topoisomerase and Is Conserved in All Eukaryotic Type I Enzymes. <i>Journal of Biological Chemistry</i> , 1997, 272, 3891-3896.	3.4	49
89	Bacterial Nonhomologous End Joining Ligases Preferentially Seal Breaks with a 3'-OH Monoribonucleotide. <i>Journal of Biological Chemistry</i> , 2008, 283, 8331-8339.	3.4	49
90	Structure-Function Analysis of Yeast mRNA Cap Methyltransferase and High-Copy Suppression of Conditional Mutants by AdoMet Synthase and the Ubiquitin Conjugating Enzyme Cdc34p. <i>Genetics</i> , 2000, 155, 1561-1576.	2.9	49

#	ARTICLE	IF	CITATIONS
91	Vaccinia DNA Topoisomerase I: Kinetic Evidence for General Acid-Base Catalysis and a Conformational Step. <i>Biochemistry</i> , 1994, 33, 15449-15458.	2.5	47
92	Mutational Analysis of Bacteriophage T4 RNA Ligase 1. <i>Journal of Biological Chemistry</i> , 2003, 278, 29454-29462.	3.4	47
93	Transcription of lncRNA prt, clustered prt RNA sites for Mmi1 binding, and RNA polymerase II CTD phospho-sites govern the repression of pho1 gene expression under phosphate-replete conditions in fission yeast. <i>Rna</i> , 2016, 22, 1011-1025.	3.5	47
94	Domain Requirements for DNA Unwinding by Mycobacterial UvrD2, an Essential DNA Helicase. <i>Biochemistry</i> , 2008, 47, 9355-9364.	2.5	46
95	The sequential 2',3'-cyclic phosphodiesterase and 3'-phosphate/5'-OH ligation steps of the RtcB RNA splicing pathway are GTP-dependent. <i>Nucleic Acids Research</i> , 2012, 40, 8558-8567.	14.5	46
96	Mammalian 2',3'-cyclic nucleotide phosphodiesterase (CNP) can function as a tRNA splicing enzyme in vivo. <i>Rna</i> , 2008, 14, 204-210.	3.5	45
97	The PAF Complex and Prf1/Rtf1 Delineate Distinct Cdk9-Dependent Pathways Regulating Transcription Elongation in Fission Yeast. <i>PLoS Genetics</i> , 2013, 9, e1004029.	3.5	45
98	Proteolytic Footprinting of Vaccinia Topoisomerase Bound to DNA. <i>Journal of Biological Chemistry</i> , 1995, 270, 11636-11645.	3.4	44
99	Mutational Analyses of Yeast RNA Triphosphatases Highlight a Common Mechanism of Metal-dependent NTP Hydrolysis and a Means of Targeting Enzymes to Pre-mRNAs in Vivo by Fusion to the Guanylyltransferase Component of the Capping Apparatus. <i>Journal of Biological Chemistry</i> , 1999, 274, 28865-28874.	3.4	44
100	Structure-Function Analysis of the Active Site Tunnel of Yeast RNA Triphosphatase. <i>Journal of Biological Chemistry</i> , 2001, 276, 17261-17266.	3.4	42
101	An end-healing enzyme from <i>Clostridium thermocellum</i> with 5' kinase, 2',3' phosphatase, and adenylyltransferase activities. <i>Rna</i> , 2005, 11, 1271-1280.	3.5	42
102	A Conserved Domain of Yeast RNA Triphosphatase Flanking the Catalytic Core Regulates Self-association and Interaction with the Guanylyltransferase Component of the mRNA Capping Apparatus. <i>Journal of Biological Chemistry</i> , 1999, 274, 22668-22678.	3.4	41
103	Characterization of Mimivirus DNA Topoisomerase IB Suggests Horizontal Gene Transfer between Eukaryal Viruses and Bacteria. <i>Journal of Virology</i> , 2006, 80, 314-321.	3.4	41
104	Punctuation and syntax of the RNA polymerase II CTD code in fission yeast. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 18024-18029.	7.1	41
105	Crystal Structure of Vaccinia Virus mRNA Capping Enzyme Provides Insights into the Mechanism and Evolution of the Capping Apparatus. <i>Structure</i> , 2014, 22, 452-465.	3.3	41
106	Role of nucleotidyltransferase motifs I, III and IV in the catalysis of phosphodiester bond formation by <i>Chlorella</i> virus DNA ligase. <i>Nucleic Acids Research</i> , 2002, 30, 903-911.	14.5	40
107	Specificity and Mechanism of RNA Cap Guanine-N2 Methyltransferase (Tgs1). <i>Journal of Biological Chemistry</i> , 2005, 280, 4021-4024.	3.4	40
108	Characterization of a Trifunctional Mimivirus mRNA Capping Enzyme and Crystal Structure of the RNA Triphosphatase Domain. <i>Structure</i> , 2008, 16, 501-512.	3.3	40

#	ARTICLE	IF	CITATIONS
109	How an mRNA capping enzyme reads distinct RNA polymerase II and Spt5 CTD phosphorylation codes. <i>Genes and Development</i> , 2014, 28, 1323-1336.	5.9	40
110	Peptide inhibitors of DNA cleavage by tyrosine recombinases and topoisomerases. <i>Journal of Molecular Biology</i> , 2000, 299, 1203-1216.	4.2	39
111	Characterization of the mRNA Capping Apparatus of the Microsporidian Parasite <i>Encephalitozoon cuniculi</i> . <i>Journal of Biological Chemistry</i> , 2002, 277, 96-103.	3.4	39
112	Guarding the Genome. <i>Molecular Cell</i> , 2003, 12, 199-208.	9.7	39
113	Characterization of a Baculovirus Enzyme with RNA Ligase, Polynucleotide 5' Kinase, and Polynucleotide 3' Phosphatase Activities. <i>Journal of Biological Chemistry</i> , 2004, 279, 18220-18231.	3.4	38
114	Characterization of three mycobacterial DinB (DNA polymerase IV) paralogs highlights DinB2 as naturally adept at ribonucleotide incorporation. <i>Nucleic Acids Research</i> , 2014, 42, 11056-11070.	14.5	38
115	Inositol pyrophosphates impact phosphate homeostasis via modulation of RNA processing and transcription termination. <i>Nucleic Acids Research</i> , 2019, 47, 8452-8469.	14.5	38
116	Transcriptional interference at tandem lncRNA and protein-coding genes: an emerging theme in regulation of cellular nutrient homeostasis. <i>Nucleic Acids Research</i> , 2020, 48, 8243-8254.	14.5	38
117	Requirements for noncovalent binding of vaccinia topoisomerase I to duplex DNA. <i>Nucleic Acids Research</i> , 1994, 22, 5360-5365.	14.5	37
118	Characterization of <i>Agrobacterium tumefaciens</i> DNA ligases C and D. <i>Nucleic Acids Research</i> , 2007, 35, 3631-3645.	14.5	37
119	Mutational Analysis of the Guanylyltransferase Component of Mammalian mRNA Capping Enzyme. <i>Biochemistry</i> , 2003, 42, 8240-8249.	2.5	36
120	Characterization of a Thermophilic ATP-Dependent DNA Ligase from the Euryarchaeon <i>Pyrococcus horikoshii</i> . <i>Journal of Bacteriology</i> , 2005, 187, 6902-6908.	2.2	36
121	<i>Encephalitozoon cuniculi</i> mRNA Cap (Guanine N-7) Methyltransferase. <i>Journal of Biological Chemistry</i> , 2005, 280, 20404-20412.	3.4	36
122	Gap Filling Activities of <i>Pseudomonas</i> DNA Ligase D (LigD) Polymerase and Functional Interactions of LigD with the DNA End-binding Ku Protein. <i>Journal of Biological Chemistry</i> , 2010, 285, 4815-4825.	3.4	36
123	Rewriting the rules for end joining via enzymatic splicing of DNA 3'-PO <sub>4</sub> and 5'-OH ends. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 20437-20442.	7.1	36
124	<i>Chlorella</i> Virus RNA Triphosphatase. <i>Journal of Biological Chemistry</i> , 2002, 277, 15317-15324.	3.4	35
125	<i>Mycobacterium smegmatis</i> DinB2 misincorporates deoxyribonucleotides and ribonucleotides during templated synthesis and lesion bypass. <i>Nucleic Acids Research</i> , 2014, 42, 12722-12734.	14.5	35
126	A dual role for mycobacterial RecO in RecA-dependent homologous recombination and RecA-independent single-strand annealing. <i>Nucleic Acids Research</i> , 2013, 41, 2284-2295.	14.5	34



#	ARTICLE	IF	CITATIONS
127	Remote Phosphate Contacts Trigger Assembly of the Active Site of DNA Topoisomerase IB. <i>Structure</i> , 2004, 12, 31-40.	3.3	33
128	RNA polymerase II CTD interactome with 3' processing and termination factors in fission yeast and its impact on phosphate homeostasis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E10652-E10661.	7.1	33
129	NAD <sup>+</sup> -dependent synthesis of a 5'-phospho-ADP-ribosylated RNA/DNA cap by RNA 2'-phosphotransferase Tpt1. <i>Nucleic Acids Research</i> , 2018, 46, 9617-9624.	14.5	33
130	Vaccinia Virus mRNA (Guanine-7-)Methyltransferase: Mutational Effects on Cap Methylation and AdoHcy-Dependent Photo-Cross-Linking of the Cap to the Methyl Acceptor Site. <i>Biochemistry</i> , 1996, 35, 6900-6910.	2.5	32
131	An essential surface motif (WAQKW) of yeast RNA triphosphatase mediates formation of the mRNA capping enzyme complex with RNA guanylyltransferase. <i>Nucleic Acids Research</i> , 1999, 27, 4671-4678.	14.5	32
132	Characterization of the mRNA Capping Apparatus of <i>Candida albicans</i> . <i>Journal of Biological Chemistry</i> , 2001, 276, 1857-1864.	3.4	32
133	An RNA Ligase from <i>Deinococcus radiodurans</i> . <i>Journal of Biological Chemistry</i> , 2004, 279, 50654-50661.	3.4	32
134	Mechanistic Plasticity of DNA Topoisomerase IB: Phosphate Electrostatics Dictate the Need for a Catalytic Arginine. <i>Structure</i> , 2005, 13, 513-520.	3.3	32
135	Structure-function analysis of the yeast NAD <sup>+</sup> -dependent tRNA 2'-phosphotransferase Tpt1. <i>Rna</i> , 2005, 11, 107-113.	3.5	32
136	Essential Constituents of the 3'-Phosphoesterase Domain of Bacterial DNA Ligase D, a Nonhomologous End-joining Enzyme. <i>Journal of Biological Chemistry</i> , 2005, 280, 33707-33715.	3.4	32
137	Mutational Analysis of <i>Encephalitozoon cuniculi</i> mRNA Cap (Guanine-N7) Methyltransferase, Structure of the Enzyme Bound to Sinefungin, and Evidence That Cap Methyltransferase Is the Target of Sinefungin's Antifungal Activity. <i>Journal of Biological Chemistry</i> , 2006, 281, 35904-35913.	3.4	32
138	Structure-function analysis of Plasmodium RNA triphosphatase and description of a triphosphate tunnel metalloenzyme superfamily that includes Cet1-like RNA triphosphatases and CYTH proteins. <i>Rna</i> , 2006, 12, 1468-1474.	3.5	32
139	Mutational Analysis of <i>Mycobacterium</i> UvrD1 Identifies Functional Groups Required for ATP Hydrolysis, DNA Unwinding, and Chemomechanical Coupling. <i>Biochemistry</i> , 2009, 48, 4019-4030.	2.5	32
140	An essential role for trimethylguanosine RNA caps in <i>Saccharomyces cerevisiae</i> meiosis and their requirement for splicing of SAE3 and PCH2 meiotic pre-mRNAs. <i>Nucleic Acids Research</i> , 2011, 39, 5633-5646.	14.5	32
141	A kinetic framework for tRNA ligase and enforcement of a 2'-phosphate requirement for ligation highlights the design logic of an RNA repair machine. <i>Rna</i> , 2013, 19, 659-669.	3.5	32
142	2'-Phosphate cyclase activity of RtcA: a potential rationale for the operon organization of RtcA with an RNA repair ligase RtcB in <i>Escherichia coli</i> and other bacterial taxa. <i>Rna</i> , 2013, 19, 1355-1362.	3.5	32
143	RNA polymerase II CTD phospho-sites Ser5 and Ser7 govern phosphate homeostasis in fission yeast. <i>Rna</i> , 2015, 21, 1770-1780.	3.5	32
144	Analysis of the DNA joining repertoire of <i>Chlorella</i> virus DNA ligase and a new crystal structure of the ligase-adenylate intermediate. <i>Nucleic Acids Research</i> , 2003, 31, 5090-5100.	14.5	31

#	ARTICLE	IF	CITATIONS
145	Yeast-like mRNA Capping Apparatus in <i>Giardia lamblia</i> . <i>Journal of Biological Chemistry</i> , 2005, 280, 12077-12086.	3.4	31
146	Distinct Enzymic Functional Groups Are Required for the Phosphomonoesterase and Phosphodiesterase Activities of <i>Clostridium thermocellum</i> Polynucleotide Kinase/Phosphatase. <i>Journal of Biological Chemistry</i> , 2006, 281, 19251-19259.	3.4	31
147	Characterization of the 2',3' cyclic phosphodiesterase activities of <i>Clostridium thermocellum</i> polynucleotide kinase-phosphatase and bacteriophage $\lambda$ phosphatase. <i>Nucleic Acids Research</i> , 2007, 35, 7721-7732.	14.5	31
148	Composition of yeast snRNPs and snoRNPs in the absence of trimethylguanosine caps reveals nuclear cap binding protein as a gained U1 component implicated in the cold-sensitivity of tgs1 <sup>Δ</sup> cells. <i>Nucleic Acids Research</i> , 2011, 39, 6715-6728.	14.5	31
149	RNA capping: progress and prospects. <i>Rna</i> , 2015, 21, 735-737.	3.5	31
150	Factor-dependent Release of Nascent RNA by Ternary Complexes of <i>Vaccinia</i> RNA Polymerase. <i>Journal of Biological Chemistry</i> , 1996, 271, 19556-19562.	3.4	30
151	Nucleotide Misincorporation, 3'-Mismatch Extension, and Responses to Abasic Sites and DNA Adducts by the Polymerase Component of Bacterial DNA Ligase D. <i>Journal of Biological Chemistry</i> , 2006, 281, 25026-25040.	3.4	30
152	Bacterial Hen1 is a 3' terminal RNA ribose 2'-O-methyltransferase component of a bacterial RNA repair cassette. <i>Rna</i> , 2010, 16, 316-323.	3.5	30
153	A long noncoding (lnc)RNA governs expression of the phosphate transporter Pho84 in fission yeast and has cascading effects on the flanking prt lncRNA and pho1 genes. <i>Journal of Biological Chemistry</i> , 2018, 293, 4456-4467.	3.4	30
154	Ligation of RNA-Containing Duplexes by <i>Vaccinia</i> DNA Ligase. <i>Biochemistry</i> , 1997, 36, 9073-9079.	2.5	29
155	RNA Triphosphatase Component of the mRNA Capping Apparatus of <i>Paramecium bursaria</i> Chlorella Virus 1. <i>Journal of Virology</i> , 2001, 75, 1744-1750.	3.4	29
156	<i>Schizosaccharomyces pombe</i> Carboxyl-terminal Domain (CTD) Phosphatase Fcp1. <i>Journal of Biological Chemistry</i> , 2004, 279, 10892-10900.	3.4	29
157	Substrate Specificity and Structure-Function Analysis of the 3'-Phosphoesterase Component of the Bacterial NHEJ Protein, DNA Ligase D. <i>Journal of Biological Chemistry</i> , 2006, 281, 13873-13881.	3.4	29
158	Biochemical and genetic analysis of RNA cap guanine-N2 methyltransferases from <i>Giardia lamblia</i> and <i>Schizosaccharomyces pombe</i> . <i>Nucleic Acids Research</i> , 2007, 35, 1411-1420.	14.5	29
159	Double Strand Break Unwinding and Resection by the Mycobacterial Helicase-Nuclease AdnAB in the Presence of Single Strand DNA-binding Protein (SSB). <i>Journal of Biological Chemistry</i> , 2010, 285, 34319-34329.	3.4	29
160	Characterization of the Mycobacterial AdnAB DNA Motor Provides Insights into the Evolution of Bacterial Motor-Nuclease Machines. <i>Journal of Biological Chemistry</i> , 2010, 285, 2632-2641.	3.4	29
161	A Yeast-Based Genetic System for Functional Analysis of Viral mRNA Capping Enzymes. <i>Journal of Virology</i> , 2000, 74, 5486-5494.	3.4	28
162	Role of Nucleotidyl Transferase Motif V in Strand Joining by <i>Chlorella</i> Virus DNA Ligase. <i>Journal of Biological Chemistry</i> , 2002, 277, 9661-9667.	3.4	28

#	ARTICLE	IF	CITATIONS
163	Characterization of mimivirus NAD <sup>+</sup> -dependent DNA ligase. <i>Virology</i> , 2006, 353, 133-143.	2.4	28
164	Novel Triphosphate Phosphohydrolase Activity of <i>Clostridium thermocellum</i> TTM, a Member of the Triphosphate Tunnel Metalloenzyme Superfamily. <i>Journal of Biological Chemistry</i> , 2007, 282, 11941-11949.	3.4	28
165	Characterization of a thermostable archaeal polynucleotide kinase homologous to human Clp1. <i>Rna</i> , 2009, 15, 923-931.	3.5	28
166	Structure of bacterial LigD 3 <sup>â€²</sup> -phosphoesterase unveils a DNA repair superfamily. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 12822-12827.	7.1	28
167	A Catalytic Domain of Eukaryotic DNA Topoisomerase I. <i>Journal of Biological Chemistry</i> , 1998, 273, 11589-11595.	3.4	27
168	<i>Trypanosoma brucei</i> RNA Triphosphatase. <i>Journal of Biological Chemistry</i> , 2001, 276, 46182-46186.	3.4	27
169	RNA 3 <sup>â€²</sup> -Phosphate Cyclase (RtcA) Catalyzes Ligase-like Adenylation of DNA and RNA 5 <sup>â€²</sup> -Monophosphate Ends. <i>Journal of Biological Chemistry</i> , 2011, 286, 4117-4122.	3.4	27
170	Mutations Within a Conserved Region of <i>Vaccinia</i> Topoisomerase Affect the DNA Cleavage-Religation Equilibrium. <i>Journal of Molecular Biology</i> , 1996, 263, 181-195.	4.2	26
171	Mechanism of the phosphatase component of <i>Clostridium thermocellum</i> polynucleotide kinase-phosphatase. <i>Rna</i> , 2006, 12, 73-82.	3.5	26
172	The C-terminal domain of T4 RNA ligase 1 confers specificity for tRNA repair. <i>Rna</i> , 2007, 13, 1235-1244.	3.5	26
173	Structure and mechanism of the 2',3' phosphatase component of the bacterial Pnkp-Hen1 RNA repair system. <i>Nucleic Acids Research</i> , 2013, 41, 5864-5873.	14.5	26
174	Poly(A) site choice and Pol2 CTD Serine-5 status govern lncRNA control of phosphate-responsive <i>tgp1</i> gene expression in fission yeast. <i>Rna</i> , 2018, 24, 237-250.	3.5	26
175	Structure-Function Analysis of <i>Trypanosoma brucei</i> RNA Triphosphatase and Evidence for a Two-metal Mechanism. <i>Journal of Biological Chemistry</i> , 2003, 278, 50843-50852.	3.4	25
176	Determinants of Nam8-dependent splicing of meiotic pre-mRNAs. <i>Nucleic Acids Research</i> , 2011, 39, 3427-3445.	14.5	25
177	An ATPase Component of the Transcription Elongation Complex Is Required for Factor-dependent Transcription Termination by <i>Vaccinia</i> RNA Polymerase. <i>Journal of Biological Chemistry</i> , 1996, 271, 29386-29392.	3.4	24
178	Recombinogenic Flap Ligation Pathway for Intrinsic Repair of Topoisomerase IB-Induced Double-Strand Breaks. <i>Molecular and Cellular Biology</i> , 2000, 20, 8059-8068.	2.3	24
179	Yeast-Based Genetic System for Functional Analysis of Poxvirus mRNA Cap Methyltransferase. <i>Journal of Virology</i> , 2003, 77, 7300-7307.	3.4	24
180	Characterization of Polynucleotide Kinase/Phosphatase Enzymes from Mycobacteriophages Omega and Cjw1 and Vibriophage KVP40. <i>Journal of Biological Chemistry</i> , 2004, 279, 26358-26369.	3.4	24

#	ARTICLE	IF	CITATIONS
181	Crystal Structure of a Bacterial Type IB DNA Topoisomerase Reveals a Preassembled Active Site in the Absence of DNA. <i>Journal of Biological Chemistry</i> , 2006, 281, 6030-6037.	3.4	24
182	Structure and two-metal mechanism of a eukaryal nick-sealing RNA ligase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 13868-13873.	7.1	24
183	Polynucleotide Ligase Activity of Eukaryotic Topoisomerase I. <i>Molecular Cell</i> , 1998, 1, 741-748.	9.7	23
184	Crystal Structure of Baculovirus RNA Triphosphatase Complexed with Phosphate. <i>Journal of Biological Chemistry</i> , 2005, 280, 17848-17856.	3.4	23
185	Mutational analyses of trimethylguanosine synthase (Tgs1) and Mud2: Proteins implicated in pre-mRNA splicing. <i>Rna</i> , 2010, 16, 1018-1031.	3.5	23
186	The adenylyltransferase domain of bacterial Pnkp defines a unique RNA ligase family. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 2296-2301.	7.1	23
187	Genetic interactions of hypomorphic mutations in the m <sup>7</sup> G cap-binding pocket of yeast nuclear cap binding complex: An essential role for Cbc2 in meiosis via splicing of <i>MER3</i> pre-mRNA. <i>Rna</i> , 2012, 18, 1996-2011.	3.5	23
188	Defining the DNA Binding Site Recognized by the Fission Yeast Zn <sub>2</sub> Cys <sub>6</sub> Transcription Factor Pho7 and Its Role in Phosphate Homeostasis. <i>MBio</i> , 2017, 8, .	4.1	23
189	RNA ligation precedes the retrotransposition of U6/LINE-1 chimeric RNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 20612-20622.	7.1	23
190	Defining the Active Site of <i>Schizosaccharomyces pombe</i> C-terminal Domain Phosphatase Fcp1. <i>Journal of Biological Chemistry</i> , 2003, 278, 13627-13632.	3.4	22
191	Dual Mechanisms whereby a Broken RNA End Assists the Catalysis of Its Repair by T4 RNA Ligase 2. <i>Journal of Biological Chemistry</i> , 2005, 280, 23484-23489.	3.4	22
192	Reprogramming the tRNA-splicing activity of a bacterial RNA repair enzyme. <i>Nucleic Acids Research</i> , 2007, 35, 3624-3630.	14.5	22
193	<i>Mycobacterium smegmatis</i> SftH exemplifies a distinctive clade of superfamily II DNA-dependent ATPases with 3 <sup>â€²</sup> to 5 <sup>â€²</sup> translocase and helicase activities. <i>Nucleic Acids Research</i> , 2012, 40, 7465-7475.	14.5	22
194	Characterization of <i>Mycobacterium smegmatis</i> PolD2 and PolD1 as RNA/DNA Polymerases Homologous to the POL Domain of Bacterial DNA Ligase D. <i>Biochemistry</i> , 2012, 51, 10147-10158.	2.5	22
195	Crystal structure, mutational analysis and RNA-dependent ATPase activity of the yeast DEAD-box pre-mRNA splicing factor Prp28. <i>Nucleic Acids Research</i> , 2014, 42, 12885-12898.	14.5	22
196	Kinetic mechanism and fidelity of nick sealing by <i>Escherichia coli</i> NAD <sup>+</sup> -dependent DNA ligase (LigA). <i>Nucleic Acids Research</i> , 2016, 44, 2298-2309.	14.5	22
197	Characterization of a DNA Topoisomerase Encoded by <i>Amsacta moorei</i> Entomopoxvirus. <i>Virology</i> , 1997, 230, 197-206.	2.4	21
198	Site-Specific DNA Transesterification by Vaccinia Topoisomerase: A Role of Specific Phosphates and Nucleosides. <i>Biochemistry</i> , 1999, 38, 16599-16612.	2.5	21

#	ARTICLE	IF	CITATIONS
199	Mutational Analysis of Baculovirus Capping Enzyme Lef4 Delineates an Autonomous Triphosphatase Domain and Structural Determinants of Divalent Cation Specificity. <i>Journal of Biological Chemistry</i> , 2001, 276, 45522-45529.	3.4	21
200	Mapping the triphosphatase active site of baculovirus mRNA capping enzyme LEF4 and evidence for a two-metal mechanism. <i>Nucleic Acids Research</i> , 2003, 31, 1455-1463.	14.5	21
201	Structure-activity relationships in <i>Kluyveromyces lactis</i> $\hat{A}$ -toxin, a eukaryal tRNA anticodon nuclease. <i>Rna</i> , 2009, 15, 1036-1044.	3.5	21
202	Functional interaction of Rpb1 and Spt5 C-terminal domains in co-transcriptional histone modification. <i>Nucleic Acids Research</i> , 2015, 43, gkv837.	14.5	21
203	Biochemical Characterization of <i>Mycobacterium smegmatis</i> RnhC (MSMEG_4305), a Bifunctional Enzyme Composed of Autonomous N-Terminal Type I RNase H and C-Terminal Acid Phosphatase Domains. <i>Journal of Bacteriology</i> , 2015, 197, 2489-2498.	2.2	21
204	Mapping the active site of vaccinia virus RNA triphosphatase. <i>Virology</i> , 2003, 309, 125-134.	2.4	20
205	Structure-guided Mutational Analysis of the Nucleotidyltransferase Domain of <i>Escherichia coli</i> NAD <sup>+</sup> -dependent DNA Ligase (LigA). <i>Journal of Biological Chemistry</i> , 2005, 280, 12137-12144.	3.4	20
206	Structure-guided mutational analysis of T4 RNA ligase 1. <i>Rna</i> , 2006, 12, 2126-2134.	3.5	20
207	Characterization of a mimivirus RNA cap guanine-N2 methyltransferase. <i>Rna</i> , 2009, 15, 666-674.	3.5	20
208	Structure and mechanism of <i>E. coli</i> RNA 2',3'-cyclic phosphodiesterase. <i>Rna</i> , 2014, 20, 1697-1705.	3.5	20
209	Structural basis for recognition of intron branchpoint RNA by yeast Msl5 and selective effects of interfacial mutations on splicing of yeast pre-mRNAs. <i>Rna</i> , 2015, 21, 401-414.	3.5	20
210	Structure of tRNA splicing enzyme Tpt1 illuminates the mechanism of RNA 2'-PO <sub>4</sub> recognition and ADP-ribosylation. <i>Nature Communications</i> , 2019, 10, 218.	12.8	20
211	Structure-guided Mutational Analysis of the OB, HhH, and BRCT Domains of <i>Escherichia coli</i> DNA Ligase. <i>Journal of Biological Chemistry</i> , 2008, 283, 23343-23352.	3.4	19
212	Structure of the RNA 3'-Phosphate Cyclase-Adenylate Intermediate Illuminates Nucleotide Specificity and Covalent Nucleotidyl Transfer. <i>Structure</i> , 2010, 18, 449-457.	3.3	19
213	Structure-function analysis and genetic interactions of the yeast branchpoint binding protein Msl5. <i>Nucleic Acids Research</i> , 2012, 40, 4539-4552.	14.5	19
214	<i>Mycobacterium smegmatis</i> Lhr Is a DNA-dependent ATPase and a 3'-to-5' DNA Translocase and Helicase That Prefers to Unwind 3'-Tailed RNA:DNA Hybrids. <i>Journal of Biological Chemistry</i> , 2013, 288, 14125-14134.	3.4	19
215	Two-step mechanism and step-arrest mutants of <i>Runella slithyformis</i> NAD <sup>+</sup> -dependent tRNA 2'-phosphotransferase Tpt1. <i>Rna</i> , 2018, 24, 1144-1157.	3.5	19
216	<i>Melanoplus sanguinipes</i> Entomopoxvirus DNA Topoisomerase: Site-Specific DNA Transesterification and Effects of 5'-Bridging Phosphorothiolates. <i>Virology</i> , 1999, 264, 441-451.	2.4	18

#	ARTICLE	IF	CITATIONS
217	Benzo[a]pyrene-dG Adduct Interference Illuminates the Interface of Vaccinia Topoisomerase with the DNA Minor Groove. <i>Journal of Biological Chemistry</i> , 2003, 278, 9905-9911.	3.4	18
218	Poxvirus mRNA Cap Methyltransferase. <i>Journal of Biological Chemistry</i> , 2006, 281, 18953-18960.	3.4	18
219	Structure–function analysis of the 3 <sup>â€²</sup> phosphatase component of T4 polynucleotide kinase/phosphatase. <i>Virology</i> , 2007, 366, 126-136.	2.4	18
220	Structure and mechanism of the polynucleotide kinase component of the bacterial Pnkp-Hen1 RNA repair system. <i>Rna</i> , 2012, 18, 2277-2286.	3.5	18
221	Determinants of the cytotoxicity of PrrC anticodon nuclease and its amelioration by tRNA repair. <i>Rna</i> , 2012, 18, 145-154.	3.5	18
222	A fungal anticodon nuclease ribotoxin exploits a secondary cleavage site to evade tRNA repair. <i>Rna</i> , 2012, 18, 1716-1724.	3.5	18
223	Structure-function analysis of the Yhc1 subunit of yeast U1 snRNP and genetic interactions of Yhc1 with Mud2, Nam8, Mud1, Tgs1, U1 snRNA, Smd3 and Prp28. <i>Nucleic Acids Research</i> , 2014, 42, 4697-4711.	14.5	18
224	Distinctive kinetics and substrate specificities of plant and fungal tRNA ligases. <i>Rna</i> , 2014, 20, 462-473.	3.5	18
225	Structure–function analysis and genetic interactions of the Yhc1, Smd3, Smb, and Snp1 subunits of yeast U1 snRNP and genetic interactions of Smd3 with U2 snRNP subunit Lea1. <i>Rna</i> , 2015, 21, 1173-1186.	3.5	18
226	Structure–function analysis and genetic interactions of the Luc7 subunit of the <i>Saccharomyces cerevisiae</i> U1 snRNP. <i>Rna</i> , 2016, 22, 1302-1310.	3.5	18
227	DNA Strand Transfer Catalyzed by Vaccinia Topoisomerase: A Peroxidolysis and Hydroxylaminolysis of the Covalent Protein–DNA Intermediate. <i>Biochemistry</i> , 2000, 39, 6422-6432.	2.5	17
228	Individual Nucleotide Bases, Not Base Pairs, Are Critical for Triggering Site-specific DNA Cleavage by Vaccinia Topoisomerase. <i>Journal of Biological Chemistry</i> , 2004, 279, 39718-39726.	3.4	17
229	Determinants of eukaryal cell killing by the bacterial ribotoxin PrrC. <i>Nucleic Acids Research</i> , 2011, 39, 687-700.	14.5	17
230	Structures of bacterial polynucleotide kinase in a Michaelis complex with GTP•Mg <sup>2+</sup> and 5'-OH oligonucleotide and a product complex with GDP•Mg <sup>2+</sup> and 5'-PO <sub>4</sub> oligonucleotide reveal a mechanism of general acid-base catalysis and the determinants of phosphoacceptor recognition. <i>Nucleic Acids Research</i> , 2014, 42, 1152-1161.	14.5	17
231	Characterization of a novel eukaryal nick-sealing RNA ligase from <i>Naegleria gruberi</i> . <i>Rna</i> , 2015, 21, 824-832.	3.5	17
232	Homologous recombination mediated by the mycobacterial AdnAB helicase without end resection by the AdnAB nucleases. <i>Nucleic Acids Research</i> , 2017, 45, 762-774.	14.5	17
233	RNA triphosphatase is essential in <i>Schizosaccharomyces pombe</i> and <i>Candida albicans</i> . <i>BMC Microbiology</i> , 2001, 1, 29.	3.3	16
234	An Essential Function of <i>Saccharomyces cerevisiae</i> RNA Triphosphatase Cet1 Is to Stabilize RNA Guanylyltransferase Ceg1 against Thermal Inactivation. <i>Journal of Biological Chemistry</i> , 2001, 276, 36116-36124.	3.4	16

#	ARTICLE	IF	CITATIONS
235	Homodimeric Quaternary Structure Is Required for the in Vivo Function and Thermal Stability of <i>Saccharomyces cerevisiae</i> and <i>Schizosaccharomyces pombe</i> RNA Triphosphatases. <i>Journal of Biological Chemistry</i> , 2003, 278, 30487-30496.	3.4	16
236	Transcriptional Networking Cap-tures the 7SK RNA 5â€²-Î²-Methyltransferase. <i>Molecular Cell</i> , 2007, 27, 517-519.	9.7	16
237	Chemical and Traditional Mutagenesis of <i>Vaccinia</i> DNA Topoisomerase Provides Insights to Cleavage Site Recognition and Transesterification Chemistry. <i>Journal of Biological Chemistry</i> , 2008, 283, 16093-16103.	3.4	16
238	Dynamics of phosphodiester synthesis by DNA ligase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 6894-6899.	7.1	16
239	Characterization of the <i>Schizosaccharomyces pombe</i> Spt5-Spt4 complex. <i>Rna</i> , 2009, 15, 1241-1250.	3.5	16
240	Structure-activity relationships in human RNA 3â€²-phosphate cyclase. <i>Rna</i> , 2009, 15, 1865-1874.	3.5	16
241	Impact of DNA 3'pp5'G capping on repair reactions at DNA 3' ends. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 11317-11322.	7.1	16
242	Structure, Mechanism, and Specificity of a Eukaryal tRNA Restriction Enzyme Involved in Self-Nonself Discrimination. <i>Cell Reports</i> , 2014, 7, 339-347.	6.4	16
243	RecF and RecR Play Critical Roles in the Homologous Recombination and Single-Strand Annealing Pathways of <i>Mycobacteria</i> . <i>Journal of Bacteriology</i> , 2015, 197, 3121-3132.	2.2	16
244	Nanomolar Inhibitors of <i>Trypanosoma brucei</i> RNA Triphosphatase. <i>MBio</i> , 2016, 7, e00058-16.	4.1	16
245	Characterization of Lhr-Core DNA helicase and manganese-dependent DNA nuclease components of a bacterial gene cluster encoding nucleic acid repair enzymes. <i>Journal of Biological Chemistry</i> , 2018, 293, 17491-17504.	3.4	16
246	Structures of ATP-bound DNA ligase D in a closed domain conformation reveal a network of amino acid and metal contacts to the ATP phosphates. <i>Journal of Biological Chemistry</i> , 2019, 294, 5094-5104.	3.4	16
247	Structures and single-molecule analysis of bacterial motor nuclease AdnAB illuminate the mechanism of DNA double-strand break resection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 24507-24516.	7.1	16
248	Structure and two-metal mechanism of fungal tRNA ligase. <i>Nucleic Acids Research</i> , 2019, 47, 1428-1439.	14.5	16
249	A genetic screen for suppressors of hyper-repression of the fission yeast PHO regulon by Pol2 CTD mutation T4A implicates inositol 1-pyrophosphates as agonists of precocious lncRNA transcription termination. <i>Nucleic Acids Research</i> , 2020, 48, 10739-10752.	14.5	16
250	Mutational Analysis of <i>Vaccinia</i> Virus Nucleoside Triphosphate Phosphohydrolase I, a DNA-Dependent ATPase of the DEXH Box Family. <i>Journal of Virology</i> , 1999, 73, 1302-1308.	3.4	16
251	<i>Deinococcus radiodurans</i> RNA ligase D exemplifies a novel ligase clade with a distinctive N-terminal module that is important for 5'-PO4 nick sealing and ligase adenylation but dispensable for phosphodiester formation at an adenylylated nick. <i>Nucleic Acids Research</i> , 2007, 35, 839-849.	14.5	15
252	Polyphosphatase Activity of CthTTM, a Bacterial Triphosphate Tunnel Metalloenzyme. <i>Journal of Biological Chemistry</i> , 2008, 283, 31047-31057.	3.4	15

#	ARTICLE	IF	CITATIONS
253	Structure-function analysis of vaccinia virus mRNA cap (guanine-N7) methyltransferase. <i>Rna</i> , 2008, 14, 696-705.	3.5	15
254	Parallel analysis of ribonucleotide-dependent deletions produced by yeast Top1 <i>in vitro</i> and <i>in vivo</i> . <i>Nucleic Acids Research</i> , 2016, 44, 7714-7721.	14.5	15
255	Distinct Contributions of Enzymic Functional Groups to the 2',3'-Cyclic Phosphodiesterase, 3'-Phosphate Guanylylation, and 3'-ppG/5'-OH Ligation Steps of the Escherichia coli RtcB Nucleic Acid Splicing Pathway. <i>Journal of Bacteriology</i> , 2016, 198, 1294-1304.	2.2	15
256	Two-metal versus one-metal mechanisms of lysine adenylation by ATP-dependent and NAD <sup>+</sup> -dependent polynucleotide ligases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 2592-2597.	7.1	15
257	Structure of 3'-PO <sub>4</sub> /5'-OH RNA ligase RtcB in complex with a 5'-OH oligonucleotide. <i>Rna</i> , 2021, 27, 584-590.	3.5	15
258	Elongation Properties of Vaccinia Virus RNA Polymerase: Pausing, Slippage, 3' End Addition, and Termination Site Choice. <i>Biochemistry</i> , 1997, 36, 15892-15899.	2.5	14
259	Genetic analysis of poxvirus mRNA cap methyltransferase: Suppression of conditional mutations in the stimulatory D12 subunit by second-site mutations in the catalytic D1 subunit. <i>Virology</i> , 2006, 352, 145-156.	2.4	14
260	Kinetic mechanism of nick sealing by T4 RNA ligase 2 and effects of 3'-OH base mismatches and damaged base lesions. <i>Rna</i> , 2013, 19, 1840-1847.	3.5	14
261	Structure-function analysis of the 5' end of yeast U1 snRNA highlights genetic interactions with the Msl5-Mud2 branchpoint-binding complex and other spliceosome assembly factors. <i>Nucleic Acids Research</i> , 2013, 41, 7485-7500.	14.5	14
262	Effects of 3'-OH and 5'-PO <sub>4</sub> 4 Base Mismatches and Damaged Base Lesions on the Fidelity of Nick Sealing by <i>Deinococcus radiodurans</i> RNA Ligase. <i>Journal of Bacteriology</i> , 2014, 196, 1704-1712.	2.2	14
263	Genetic interactions and transcriptomics implicate fission yeast CTD prolyl isomerase Pin1 as an agent of RNA 3' processing and transcription termination that functions via its effects on CTD phosphatase Ssu72. <i>Nucleic Acids Research</i> , 2020, 48, 4811-4826.	14.5	14
264	Kinetic Analysis of DNA Strand Joining by Chlorella Virus DNA Ligase and the Role of Nucleotidyltransferase Motif VI in Ligase Adenylation. <i>Journal of Biological Chemistry</i> , 2012, 287, 28609-28618.	3.4	13
265	Characterization of 3'-Phosphate RNA Ligase Paralogs RtcB1, RtcB2, and RtcB3 from <i>Myxococcus xanthus</i> Highlights DNA and RNA 5'-Phosphate Capping Activity of RtcB3. <i>Journal of Bacteriology</i> , 2015, 197, 3616-3624.	2.2	13
266	Genetic and structural analysis of the essential fission yeast RNA polymerase II CTD phosphatase Fcp1. <i>Rna</i> , 2015, 21, 1135-1146.	3.5	13
267	Characterization of the tRNA ligases of pathogenic fungi <i>Aspergillus fumigatus</i> and <i>Coccidioides immitis</i> . <i>Rna</i> , 2016, 22, 1500-1509.	3.5	13
268	Distinctive structural basis for DNA recognition by the fission yeast Zn <sup>2+</sup> Cys <sub>6</sub> transcription factor Pho7 and its role in phosphate homeostasis. <i>Nucleic Acids Research</i> , 2018, 46, 11262-11273.	14.5	13
269	Cleavage-Polyadenylation Factor Cft1 and SPX Domain Proteins Are Agents of Inositol Pyrophosphate Toxicosis in Fission Yeast. <i>MBio</i> , 2022, 13, e0347621.	4.1	13
270	Activities and Structure-Function Analysis of Fission Yeast Inositol Pyrophosphate (IPP) Kinase-Pyrophosphatase Asp1 and Its Impact on Regulation of <i>pho1</i> Gene Expression. <i>MBio</i> , 2022, 13, e0103422.	4.1	13



#	ARTICLE	IF	CITATIONS
271	Importance of Homodimerization for the in Vivo Function of Yeast RNA Triphosphatase. <i>Journal of Biological Chemistry</i> , 2001, 276, 14996-15002.	3.4	12
272	Site-specific DNA Transesterification by Vaccinia Topoisomerase. <i>Journal of Biological Chemistry</i> , 2003, 278, 42170-42177.	3.4	12
273	Structure-Function Analysis of the OB and Latch Domains of Chlorella Virus DNA Ligase. <i>Journal of Biological Chemistry</i> , 2011, 286, 22642-22652.	3.4	12
274	Structural basis for the GTP specificity of the RNA kinase domain of fungal tRNA ligase. <i>Nucleic Acids Research</i> , 2017, 45, 12945-12953.	14.5	12
275	Mutational Analysis of 26 Residues of Vaccinia DNA Topoisomerase Identifies Ser-204 as Important for DNA Binding and Cleavage. <i>Biochemistry</i> , 1997, 36, 7944-7950.	2.5	11
276	Solution NMR Studies of Chlorella Virus DNA Ligase-adenylate. <i>Journal of Molecular Biology</i> , 2010, 395, 291-308.	4.2	11
277	<i>Mycobacterium smegmatis</i> RqlH defines a novel clade of bacterial RecQ-like DNA helicases with ATP-dependent 3' to 5' translocase and duplex unwinding activities. <i>Nucleic Acids Research</i> , 2012, 40, 4604-4614.	14.5	11
278	Structure-function relations in the NTPase domain of the antiviral tRNA ribotoxin Escherichia coli PrrC. <i>Virology</i> , 2012, 427, 144-150.	2.4	11
279	Fission yeast RNA triphosphatase reads an Spt5 CTD code. <i>Rna</i> , 2015, 21, 113-123.	3.5	11
280	Mechanistic insights into the manganese-dependent phosphodiesterase activity of yeast Dbr1 with bis- <i>p</i> -nitrophenylphosphate and branched RNA substrates. <i>Rna</i> , 2016, 22, 1819-1827.	3.5	11
281	Structure of mycobacterial 3' to 5' RNA:DNA helicase Lhr bound to a ssDNA tracking strand highlights distinctive features of a novel family of bacterial helicases. <i>Nucleic Acids Research</i> , 2018, 46, 442-455.	14.5	11
282	The t <sup>6</sup> A modification acts as a positive determinant for the anticodon nuclease PrrC, and is distinctively nonessential in <i>Streptococcus mutans</i> . <i>RNA Biology</i> , 2018, 15, 508-517.	3.1	11
283	Functional Groups Required for the Stability of Yeast RNA Triphosphatase in Vitro and in Vivo. <i>Journal of Biological Chemistry</i> , 2001, 276, 30514-30520.	3.4	10
284	Sinefungin resistance of <i>Saccharomyces cerevisiae</i> arising from sam3 mutations that inactivate the AdoMet transporter or from increased expression of AdoMet synthase plus mRNA cap guanine-N7 methyltransferase. <i>Nucleic Acids Research</i> , 2007, 35, 6895-6903.	14.5	10
285	Structures of RNA 3'-phosphate cyclase bound to ATP reveal the mechanism of nucleotidyl transfer and metal-assisted catalysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 21034-21039.	7.1	10
286	Functional Dissection of the DNA Interface of the Nucleotidyltransferase Domain of Chlorella Virus DNA Ligase. <i>Journal of Biological Chemistry</i> , 2011, 286, 13314-13326.	3.4	10
287	Structural and Biochemical Analysis of the Phosphate Donor Specificity of the Polynucleotide Kinase Component of the Bacterial Pnkp-Hen1 RNA Repair System. <i>Biochemistry</i> , 2013, 52, 4734-4743.	2.5	10
288	Distinctive Effects of Domain Deletions on the Manganese-Dependent DNA Polymerase and DNA Phosphorylase Activities of <i>Mycobacterium smegmatis</i> Polynucleotide Phosphorylase. <i>Biochemistry</i> , 2013, 52, 2967-2981.	2.5	10

#	ARTICLE	IF	CITATIONS
289	Mycobacterium smegmatis HelY Is an RNA-Activated ATPase/dATPase and 3' to 5' Helicase That Unwinds 3'-Tailed RNA Duplexes and RNA:DNA Hybrids. <i>Journal of Bacteriology</i> , 2015, 197, 3057-3065.	2.2	10
290	Mycobacterial DNA polymerase I: activities and crystal structures of the POL domain as apoenzyme and in complex with a DNA primer-template and of the full-length FEN/EXO POL enzyme. <i>Nucleic Acids Research</i> , 2020, 48, 3165-3180.	14.5	10
291	Genetic screen for suppression of transcriptional interference identifies a gain-of-function mutation in Pol2 termination factor Seb1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	10
292	Effect of 2'-5' Phosphodiesterases on DNA Transesterification by Vaccinia Topoisomerase. <i>Journal of Biological Chemistry</i> , 2001, 276, 20907-20912.	3.4	9
293	Nonpolar Nucleobase Analogs Illuminate Requirements for Site-specific DNA Cleavage by Vaccinia Topoisomerase. <i>Journal of Biological Chemistry</i> , 2006, 281, 35914-35921.	3.4	9
294	Substrate specificity and mutational analysis of <i>Kluyveromyces lactis</i> $\beta$ -toxin, a eukaryal tRNA anticodon nuclease. <i>Rna</i> , 2011, 17, 1336-1343.	3.5	9
295	Structures and activities of archaeal members of the LigD phosphoesterase DNA repair enzyme superfamily. <i>Nucleic Acids Research</i> , 2011, 39, 3310-3320.	14.5	9
296	Structure-function analysis and genetic interactions of the SmG, SmE, and SmF subunits of the yeast Sm protein ring. <i>Rna</i> , 2016, 22, 1320-1328.	3.5	9
297	Phospho-site mutants of the RNA Polymerase II C-terminal domain alter subtelomeric gene expression and chromatin modification state in fission yeast. <i>Nucleic Acids Research</i> , 2016, 44, gkw603.	14.5	9
298	Deletion of the <i>rnl</i> gene encoding a nick-sealing RNA ligase sensitizes <i>Deinococcus radiodurans</i> to ionizing radiation. <i>Nucleic Acids Research</i> , 2017, 45, gkx038.	14.5	9
299	Will the circle be unbroken: specific mutations in the yeast Sm protein ring expose a requirement for assembly factor Brr1, a homolog of Gemin2. <i>Rna</i> , 2017, 23, 420-430.	3.5	9
300	Crystal structure and mutational analysis of Mycobacterium smegmatis FenA highlight active site amino acids and three metal ions essential for flap endonuclease and 5' exonuclease activities. <i>Nucleic Acids Research</i> , 2018, 46, 4164-4175.	14.5	9
301	Structure of Fission Yeast Transcription Factor Pho7 Bound to <i>pho1</i> Promoter DNA and Effect of Pho7 Mutations on DNA Binding and Phosphate Homeostasis. <i>Molecular and Cellular Biology</i> , 2019, 39, .	2.3	9
302	Activity and structure of Pseudomonas putida MPE, a manganese-dependent single-strand DNA endonuclease encoded in a nucleic acid repair gene cluster. <i>Journal of Biological Chemistry</i> , 2019, 294, 7931-7941.	3.4	9
303	Vaccinia Topoisomerase Mutants Illuminate Conformational Changes during Closure of the Protein Clamp and Assembly of a Functional Active Site. <i>Journal of Biological Chemistry</i> , 2001, 276, 36091-36099.	3.4	8
304	Mutational analysis of vaccinia virus mRNA cap (guanine-N7) methyltransferase reveals essential contributions of the N-terminal peptide that closes over the active site. <i>Rna</i> , 2008, 14, 2297-2304.	3.5	8
305	Structure-guided Mutational Analysis of the Nucleotidyltransferase Domain of Escherichia coli DNA Ligase (LigA). <i>Journal of Biological Chemistry</i> , 2009, 284, 8486-8494.	3.4	8
306	Crystal Structure and Biochemical Characterization of a Mycobacterium smegmatis AAA-Type Nucleoside Triphosphatase Phosphohydrolase (Msm0858). <i>Journal of Bacteriology</i> , 2016, 198, 1521-1533.	2.2	8

#	ARTICLE	IF	CITATIONS
307	The DNA Repair Repertoire of <i>Mycobacterium smegmatis</i> FenA Includes the Incision of DNA 5' Flaps and the Removal of 5' Adenylylated Products of Aborted Nick Ligation. <i>Journal of Bacteriology</i> , 2017, 199, .	2.2	8
308	Defining essential elements and genetic interactions of the yeast Lsm28 ring and demonstration that essentiality of Lsm28 is bypassed via overexpression of U6 snRNA or the U6 snRNP subunit Prp24. <i>Rna</i> , 2018, 24, 853-864.	3.5	8
309	Transcriptional profiling of fission yeast RNA polymerase II CTD mutants. <i>Rna</i> , 2021, 27, 560-570.	3.5	8
310	Structure and mechanism of <i>Mycobacterium smegmatis</i> polynucleotide phosphorylase. <i>Rna</i> , 2021, 27, 959-969.	3.5	8
311	Effects of Alanine Cluster Mutations in the D12 Subunit of Vaccinia Virus mRNA (Guanine-N7) Methyltransferase. <i>Virology</i> , 2001, 287, 40-48.	2.4	7
312	Defining the Mer1 and Nam8 meiotic splicing regulons by cDNA rescue. <i>Rna</i> , 2011, 17, 1648-1654.	3.5	7
313	Structural insights to the metal specificity of an archaeal member of the LigD 3'-phosphoesterase DNA repair enzyme family. <i>Nucleic Acids Research</i> , 2012, 40, 828-836.	14.5	7
314	Solution structure and DNA-binding properties of the phosphoesterase domain of DNA ligase D. <i>Nucleic Acids Research</i> , 2012, 40, 2076-2088.	14.5	7
315	Discrimination of RNA from DNA by Polynucleotide Phosphorylase. <i>Biochemistry</i> , 2013, 52, 6702-6711.	2.5	7
316	Two Routes to Genetic Suppression of RNA Trimethylguanosine Cap Deficiency via C-Terminal Truncation of U1 snRNP Subunit Snp1 or Overexpression of RNA Polymerase Subunit Rpo26. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 1361-1370.	1.8	7
317	Genetic screen for suppression of transcriptional interference reveals fission yeast 14-3-3 protein Rad24 as an antagonist of precocious Pol2 transcription termination. <i>Nucleic Acids Research</i> , 2022, 50, 803-819.	14.5	7
318	Deletions at the Carboxyl Terminus of Vaccinia DNA Topoisomerase Affect DNA Binding and Enhance Distributivity in DNA Relaxation. <i>Biochemistry</i> , 1997, 36, 3909-3916.	2.5	6
319	Vaccinia topoisomerase mutants illuminate roles for Phe59, Gly73, Gln69 and Phe215. <i>Virology</i> , 2007, 359, 466-476.	2.4	6
320	Mutational analysis of the 5'-OH oligonucleotide phosphate acceptor site of T4 polynucleotide kinase. <i>Nucleic Acids Research</i> , 2010, 38, 1304-1311.	14.5	6
321	Characterization of <i>Runella slithyformis</i> HD-Pnk, a Bifunctional DNA/RNA End-Healing Enzyme Composed of an N-Terminal 2',3'-Phosphoesterase HD Domain and a C-Terminal 5'-OH Polynucleotide Kinase Domain. <i>Journal of Bacteriology</i> , 2017, 199, .	2.2	6
322	NAD <sup>+</sup> -dependent RNA terminal 2' and 3' phosphomonoesterase activity of a subset of Tpt1 enzymes. <i>Rna</i> , 2019, 25, 783-792.	3.5	6
323	Clutch mechanism of chemomechanical coupling in a DNA resecting motor nuclease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, e202395118.	7.1	6
324	Inactivation of fission yeast Erh1 de-represses <i>pho1</i> expression: evidence that Erh1 is a negative regulator of <i>prt</i> lncRNA termination. <i>Rna</i> , 2020, 26, 1334-1344.	3.5	6

#	ARTICLE	IF	CITATIONS
325	DNA strand transfer catalyzed by vaccinia topoisomerase: ligation of DNAs containing a 3' mononucleotide overhang. <i>Nucleic Acids Research</i> , 2000, 28, 1893-1898.	14.5	5
326	Effects of DNA 3'pp5'G capping on 3' end repair reactions and of an embedded pyrophosphate-linked guanylate on ribonucleotide surveillance. <i>Nucleic Acids Research</i> , 2015, 43, 3197-3207.	14.5	5
327	Activity and substrate specificity of <i>Candida</i> , <i>Aspergillus</i> , and <i>Coccidioides</i> Tpt1: essential tRNA splicing enzymes and potential antifungal targets. <i>Rna</i> , 2021, 27, 616-627.	3.5	5
328	Structure-function analysis of fission yeast cleavage and polyadenylation factor (CPF) subunit Ppn1 and its interactions with Dis2 and Swd22. <i>PLoS Genetics</i> , 2021, 17, e1009452.	3.5	5
329	Box H/ACA snoRNAs are preferred substrates for the trimethylguanosine synthase in the divergent unicellular eukaryote <i>Trichomonas vaginalis</i> . <i>Rna</i> , 2012, 18, 1656-1665.	3.5	4
330	Characterization of DNA Binding by the Isolated N-Terminal Domain of Vaccinia Virus DNA Topoisomerase IB. <i>Biochemistry</i> , 2017, 56, 3307-3317.	2.5	4
331	<i>Deinococcus radiodurans</i> HD-Pnk, a Nucleic Acid End-Healing Enzyme, Abets Resistance to Killing by Ionizing Radiation and Mitomycin C. <i>Journal of Bacteriology</i> , 2018, 200, .	2.2	4
332	Atomic structures of the RNA end-healing 5'-OH kinase and 2',3'-cyclic phosphodiesterase domains of fungal tRNA ligase: conformational switches in the kinase upon binding of the GTP phosphate donor. <i>Nucleic Acids Research</i> , 2019, 47, 11826-11838.	14.5	4
333	Oligomeric quaternary structure of <i>Escherichia coli</i> and <i>Mycobacterium smegmatis</i> Lhr helicases is nucleated by a novel C-terminal domain composed of five winged-helix modules. <i>Nucleic Acids Research</i> , 2021, 49, 3876-3887.	14.5	4
334	Chemical Mutagenesis of Vaccinia DNA Topoisomerase Lysine 167 Provides Insights to the Catalysis of DNA Transesterification. <i>Biochemistry</i> , 2013, 52, 984-991.	2.5	3
335	Structures of Bacterial Polynucleotide Kinase in a Michaelis Complex with Nucleoside Triphosphate (NTP)-Mg <sup>2+</sup> and 5'-OH RNA and a Mixed Substrate-Product Complex with NTP-Mg <sup>2+</sup> and a 5'-Phosphorylated Oligonucleotide. <i>Journal of Bacteriology</i> , 2014, 196, 4285-4292.	2.2	3
336	DNA 3'pp5'G de-capping activity of aprataxin: effect of cap nucleoside analogs and structural basis for guanosine recognition. <i>Nucleic Acids Research</i> , 2015, 43, 6075-6083.	14.5	3
337	Substrate analogs that trap the 2'-phospho-ADP-ribosylated RNA intermediate of the Tpt1 (tRNA) Tj ETQq1 1 0.784314 rgBT /Over	3.5	3
338	Sequence-specific 1HN, 13C, and 15N backbone resonance assignments of the 34kDa <i>Paramecium bursaria</i> <i>Chlorella virus 1</i> (PBCV1) DNA ligase. <i>Biomolecular NMR Assignments</i> , 2009, 3, 77-80.	0.8	2
339	Sequence-specific 1H, 13C and 15N assignments of the phosphoesterase (PE) domain of <i>Pseudomonas aeruginosa</i> DNA ligase D (LigD). <i>Biomolecular NMR Assignments</i> , 2011, 5, 151-155.	0.8	2
340	NMR solution structures of <i>Runella slithyformis</i> RNA 2'-phosphotransferase Tpt1 provide insights into NAD <sup>+</sup> binding and specificity. <i>Nucleic Acids Research</i> , 2021, 49, 9607-9624.	14.5	2
341	Structure-activity relationships at a nucleobase-stacking tryptophan required for chemomechanical coupling in the DNA resecting motor-nuclease AdnAB. <i>Nucleic Acids Research</i> , 2022, 50, 952-961.	14.5	2
342	Domain Requirements and Genetic Interactions of the Mud1 Subunit of the <i>Saccharomyces cerevisiae</i> U1 snRNP. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 145-151.	1.8	1

#	ARTICLE	IF	CITATIONS
343	Caveat mutator: alanine substitutions for conserved amino acids in RNA ligase elicit unexpected rearrangements of the active site for lysine adenylylation. <i>Nucleic Acids Research</i> , 2020, 48, 5603-5615.	14.5	1
344	Fission yeast Duf89 and Duf8901 are cobalt/nickel-dependent phosphatase–pyrophosphatases that act via a covalent aspartyl–phosphate intermediate. <i>Journal of Biological Chemistry</i> , 2022, 298, 101851.	3.4	1
345	Structure-Function Analysis of the Phosphoesterase Component of the Nucleic Acid End-Healing Enzyme <i>Runella slithyformis</i> HD-Pnk. <i>Journal of Bacteriology</i> , 2019, 201, .	2.2	0
346	<i>Pseudomonas putida</i> MPE, a manganese-dependent endonuclease of the binuclear metallophosphoesterase superfamily, incises single-strand DNA in two orientations to yield a mixture of 3'-PO <sub>4</sub> and 3'-OH termini. <i>Nucleic Acids Research</i> , 2021, 49, 1023-1032.	14.5	0