Stewart Shuman

List of Publications by Year
in descending order

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346 papers	14,706 citations	22548 61 h-index	42259 96 g-index
349 all docs	349 docs citations	349 times ranked	9185 citing authors

#	Article	IF	Citations
1	Cleavage-Polyadenylation Factor Cft1 and SPX Domain Proteins Are Agents of Inositol Pyrophosphate Toxicosis in Fission Yeast. MBio, 2022, 13, e0347621.	1.8	13
2	Fission yeast Duf89 and Duf8901 are cobalt/nickel-dependent phosphataseâ€“pyrophosphatases that act via a covalent aspartylâ€“phosphate intermediate. Journal of Biological Chemistry, 2022, 298, 101851.	1.6	1
3	Genetic screen for suppression of transcriptional interference reveals fission yeast 14â€“3â€“3 protein Rad24 as an antagonist of precocious Pol2 transcription termination. Nucleic Acids Research, 2022, 50, 803-819.	6.5	7
4	Structureâ€“activity relationships at a nucleobase-stacking tryptophan required for chemomechanical coupling in the DNA resecting motor-nuclease AdnAB. Nucleic Acids Research, 2022, 50, 952-961.	6.5	2
5	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. MBio, 2022, 13, e0103422.	1.8	13
6	Activity and substrate specificity of <i>Candida</i>, <i>Aspergillus</i>, and <i>Coccidioides</i> Tpt1: essential tRNA splicing enzymes and potential antifungal targets. Rna, 2021, 27, 616-627.	1.6	5
7	Structure of 3â€²-PO₄/5â€²-OH RNA ligase RtcB in complex with a 5â€²-OH oligonucleotide. Rna, 2021, 27, 584-590.	1.6	15
8	Transcriptional profiling of fission yeast RNA polymerase II CTD mutants. Rna, 2021, 27, 560-570.	1.6	8
9	Clutch mechanism of chemomechanical coupling in a DNA resecting motor nuclease. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, e2023955118.	3.3	6
10	Structure-function analysis of fission yeast cleavage and polyadenylation factor (CPF) subunit Ppn1 and its interactions with Dis2 and Swd22. PLoS Genetics, 2021, 17, e1009452.	1.5	5
11	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. Nucleic Acids Research, 2021, 49, 3876-3887.	6.5	4
12	NMR solution structures of Runella slithyformis RNA 2â€²-phosphotransferase Tpt1 provide insights into NAD+ binding and specificity. Nucleic Acids Research, 2021, 49, 9607-9624.	6.5	2
13	Structure and mechanism of <i>Mycobacterium smegmatis</i> polynucleotide phosphorylase. Rna, 2021, 27, 959-969.	1.6	8
14	Genetic screen for suppression of transcriptional interference identifies a gain-of-function mutation in Pol2 termination factor Seb1. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	10
15	<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 3â€²-PO4 and 3â€²-OH termini. Nucleic Acids Research, 2021, 49, 1023-1032.	6.5	0
16	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. Nucleic Acids Research, 2020, 48, 10739-10752.	6.5	16
17	Transcriptional interference at tandem lncRNA and protein-coding genes: an emerging theme in regulation of cellular nutrient homeostasis. Nucleic Acids Research, 2020, 48, 8243-8254.	6.5	38
18	Caveat mutator: alanine substitutions for conserved amino acids in RNA ligase elicit unexpected rearrangements of the active site for lysine adenylylation. Nucleic Acids Research, 2020, 48, 5603-5615.	6.5	1

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19	Substrate analogs that trap the 2â€²-phospho-ADP-ribosylated RNA intermediate of the Tpt1 (tRNA) Tj ETQq1 1 0.784314 rgBT /Overloc	1.6	3
20	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/EXOâ€“POL enzyme. Nucleic Acids Research, 2020, 48, 3165-3180.	6.5	10
21	Genetic interactions and transcriptomics implicate fission yeast CTD prolyl isomerase Pin1 as an agent of RNA 3â€² processing and transcription termination that functions via its effects on CTD phosphatase Ssu72. Nucleic Acids Research, 2020, 48, 4811-4826.	6.5	14
22	Inactivation of fission yeast Erh1 de-represses <i>pho1</i> expression: evidence that Erh1 is a negative regulator of <i>prt</i> lncRNA termination. Rna, 2020, 26, 1334-1344.	1.6	6
23	Inositol pyrophosphates impact phosphate homeostasis via modulation of RNA 3â€² processing and transcription termination. Nucleic Acids Research, 2019, 47, 8452-8469.	6.5	38
24	Atomic structures of the RNA end-healing 5â€²-OH kinase and 2â€²,3â€²-cyclic phosphodiesterase domains of fungal tRNA ligase: conformational switches in the kinase upon binding of the GTP phosphate donor. Nucleic Acids Research, 2019, 47, 11826-11838.	6.5	4
25	Structure-Function Analysis of the Phosphoesterase Component of the Nucleic Acid End-Healing Enzyme Runella slithyformis HD-Pnk. Journal of Bacteriology, 2019, 201, .	1.0	0
26	NAD+-dependent RNA terminal 2â€² and 3â€² phosphomonoesterase activity of a subset of Tpt1 enzymes. Rna, 2019, 25, 783-792.	1.6	6
27	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. Molecular and Cellular Biology, 2019, 39, .	1.1	9
28	Activity and structure of Pseudomonas putida MPE, a manganese-dependent single-strand DNA endonuclease encoded in a nucleic acid repair gene cluster. Journal of Biological Chemistry, 2019, 294, 7931-7941.	1.6	9
29	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. Journal of Biological Chemistry, 2019, 294, 5094-5104.	1.6	16
30	RNA ligation precedes the retrotransposition of U6/LINE-1 chimeric RNA. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 20612-20622.	3.3	23
31	Structures and single-molecule analysis of bacterial motor nuclease AdnAB illuminate the mechanism of DNA double-strand break resection. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 24507-24516.	3.3	16
32	Structure of tRNA splicing enzyme Tpt1 illuminates the mechanism of RNA 2â€²-PO4 recognition and ADP-ribosylation. Nature Communications, 2019, 10, 218.	5.8	20
33	Structure and two-metal mechanism of fungal tRNA ligase. Nucleic Acids Research, 2019, 47, 1428-1439.	6.5	16
34	Domain Requirements and Genetic Interactions of the Mud1 Subunit of the Saccharomyces cerevisiae U1 snRNP. G3: Genes, Genomes, Genetics, 2019, 9, 145-151.	0.8	1
35	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. Journal of Biological Chemistry, 2018, 293, 4456-4467.	1.6	30
36	Defining essential elements and genetic interactions of the yeast Lsm2â€“8 ring and demonstration that essentiality of Lsm2â€“8 is bypassed via overexpression of U6 snRNA or the U6 snRNP subunit Prp24. Rna, 2018, 24, 853-864.	1.6	8

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37	Structure of mycobacterial 3â€²-to-5â€² RNA:DNA helicase Lhr bound to a ssDNA tracking strand highlights distinctive features of a novel family of bacterial helicases. Nucleic Acids Research, 2018, 46, 442-455.	6.5	11
38	The t⁶A modification acts as a positive determinant for the anticodon nuclease PrrC, and is distinctively nonessential in <i>Streptococcus mutans</i>. RNA Biology, 2018, 15, 508-517.	1.5	11
39	Poly(A) site choice and Pol2 CTD Serine-5 status govern lncRNA control of phosphate-responsive <i>tgp1</i> gene expression in fission yeast. Rna, 2018, 24, 237-250.	1.6	26
40	Characterization of Lhr-Core DNA helicase and manganese- dependent DNA nuclease components of a bacterial gene cluster encoding nucleic acid repair enzymes. Journal of Biological Chemistry, 2018, 293, 17491-17504.	1.6	16
41	Crystal structure and mutational analysis of Mycobacterium smegmatis FenA highlight active site amino acids and three metal ions essential for flap endonuclease and 5â€² exonuclease activities. Nucleic Acids Research, 2018, 46, 4164-4175.	6.5	9
42	RNA polymerase II CTD interactome with 3â€² processing and termination factors in fission yeast and its impact on phosphate homeostasis. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E10652-E10661.	3.3	33
43	Distinctive structural basis for DNA recognition by the fission yeast Zn2Cys6 transcription factor Pho7 and its role in phosphate homeostasis. Nucleic Acids Research, 2018, 46, 11262-11273.	6.5	13
44	NAD+-dependent synthesis of a 5â€²-phospho-ADP-ribosylated RNA/DNA cap by RNA 2â€²-phosphotransferase Tpt1. Nucleic Acids Research, 2018, 46, 9617-9624.	6.5	33
45	Deinococcus radiodurans HD-Pnk, a Nucleic Acid End-Healing Enzyme, Abets Resistance to Killing by Ionizing Radiation and Mitomycin C. Journal of Bacteriology, 2018, 200, .	1.0	4
46	Two-step mechanism and step-arrest mutants of <i>Runella slithyformis</i> NAD⁺-dependent tRNA 2â€²-phosphotransferase Tpt1. Rna, 2018, 24, 1144-1157.	1.6	19
47	Two-metal versus one-metal mechanisms of lysine adenylylation by ATP-dependent and NAD+-dependent polynucleotide ligases. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 2592-2597.	3.3	15
48	Characterization of DNA Binding by the Isolated N-Terminal Domain of Vaccinia Virus DNA Topoisomerase IB. Biochemistry, 2017, 56, 3307-3317.	1.2	4
49	Intratumoral delivery of inactivated modified vaccinia virus Ankara (iMVA) induces systemic antitumor immunity via STING and Batf3-dependent dendritic cells. Science Immunology, 2017, 2, .	5.6	101
50	The DNA Repair Repertoire of Mycobacterium smegmatis FenA Includes the Incision of DNA 5â€² Flaps and the Removal of 5â€² Adenylylated Products of Aborted Nick Ligation. Journal of Bacteriology, 2017, 199, .	1.0	8
51	Characterization of Runella slithyformis HD-Pnk, a Bifunctional DNA/RNA End-Healing Enzyme Composed of an N-Terminal 2â€²,3â€²-Phosphoesterase HD Domain and a C-Terminal 5â€²-OH Polynucleotide Kinase Domain. Journal of Bacteriology, 2017, 199, .	1.0	6
52	Deletion of the<i>rnl</i>gene encoding a nick-sealing RNA ligase sensitizes<i>Deinococcus radiodurans</i>to ionizing radiation. Nucleic Acids Research, 2017, 45, gkx038.	6.5	9
53	Will the circle be unbroken: specific mutations in the yeast Sm protein ring expose a requirement for assembly factor Brr1, a homolog of Gemin2. Rna, 2017, 23, 420-430.	1.6	9
54	Defining the DNA Binding Site Recognized by the Fission Yeast Zn ₂ Cys ₆ Transcription Factor Pho7 and Its Role in Phosphate Homeostasis. MBio, 2017, 8, .	1.8	23

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55	Structural basis for the GTP specificity of the RNA kinase domain of fungal tRNA ligase. Nucleic Acids Research, 2017, 45, 12945-12953.	6.5	12
56	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. Nucleic Acids Research, 2017, 45, 1-14.	6.5	183
57	Homologous recombination mediated by the mycobacterial AdnAB helicase without end resection by the AdnAB nucleases. Nucleic Acids Research, 2017, 45, 762-774.	6.5	17
58	Parallel analysis of ribonucleotide-dependent deletions produced by yeast Top1<i>in vitro</i>and<i>in vivo</i>. Nucleic Acids Research, 2016, 44, 7714-7721.	6.5	15
59	Structureâ€"function analysis and genetic interactions of the Luc7 subunit of the <i>Saccharomyces cerevisiae</i> U1 snRNP. Rna, 2016, 22, 1302-1310.	1.6	18
60	Structureâ€"function analysis and genetic interactions of the SmG, SmE, and SmF subunits of the yeast Sm protein ring. Rna, 2016, 22, 1320-1328.	1.6	9
61	Distinct Contributions of Enzymic Functional Groups to the 2â€²,3â€²-Cyclic Phosphodiesterase, 3â€²-Phosphate Guanylylation, and 3â€²-ppG/5â€²-OH Ligation Steps of the Escherichia coli RtcB Nucleic Acid Splicing Pathway. Journal of Bacteriology, 2016, 198, 1294-1304.	1.0	15
62	Characterization of the tRNA ligases of pathogenic fungi <i>Aspergillus fumigatus</i> and <i>Coccidioides immitis</i>. Rna, 2016, 22, 1500-1509.	1.6	13
63	Mechanistic insights into the manganese-dependent phosphodiesterase activity of yeast Dbr1 with bis-<i>p</i>-nitrophenylphosphate and branched RNA substrates. Rna, 2016, 22, 1819-1827.	1.6	11
64	Phospho-site mutants of the RNA Polymerase II C-terminal domain alter subtelomeric gene expression and chromatin modification state in fission yeast. Nucleic Acids Research, 2016, 44, gkw603.	6.5	9
65	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. Rna, 2016, 22, 1011-1025.	1.6	47
66	Kinetic mechanism and fidelity of nick sealing by<i>Escherichia coli</i>NAD⁺-dependent DNA ligase (LigA). Nucleic Acids Research, 2016, 44, 2298-2309.	6.5	22
67	Nanomolar Inhibitors of Trypanosoma brucei RNA Triphosphatase. MBio, 2016, 7, e00058-16.	1.8	16
68	Crystal Structure and Biochemical Characterization of a Mycobacterium smegmatis AAA-Type Nucleoside Triphosphatase Phosphohydrolase (Msm0858). Journal of Bacteriology, 2016, 198, 1521-1533.	1.0	8
69	Characterization of 3â€²-Phosphate RNA Ligase Paralogs RtcB1, RtcB2, and RtcB3 from Myxococcus xanthus Highlights DNA and RNA 5â€²-Phosphate Capping Activity of RtcB3. Journal of Bacteriology, 2015, 197, 3616-3624.	1.0	13
70	Characterization of a novel eukaryal nick-sealing RNA ligase from <i>Naegleria gruberi</i>. Rna, 2015, 21, 824-832.	1.6	17
71	Genetic and structural analysis of the essential fission yeast RNA polymerase II CTD phosphatase Fcp1. Rna, 2015, 21, 1135-1146.	1.6	13
72	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. G3: Genes, Genomes, Genetics, 2015, 5, 1361-1370.	0.8	7

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73	Structure and two-metal mechanism of a eukaryal nick-sealing RNA ligase. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 13868-13873.	3.3	24
74	Effects of DNA3â€²pp5â€²G capping on 3â€² end repair reactions and of an embedded pyrophosphate-linked guanylate on ribonucleotide surveillance. Nucleic Acids Research, 2015, 43, 3197-3207.	6.5	5
75	DNA3â€²pp5â€²G de-capping activity of aprataxin: effect of cap nucleoside analogs and structural basis for guanosine recognition. Nucleic Acids Research, 2015, 43, 6075-6083.	6.5	3
76	Functional interaction of Rpb1 and Spt5 C-terminal domains in co-transcriptional histone modification. Nucleic Acids Research, 2015, 43, gkv837.	6.5	21
77	Structural basis for recognition of intron branchpoint RNA by yeast Msl5 and selective effects of interfacial mutations on splicing of yeast pre-mRNAs. Rna, 2015, 21, 401-414.	1.6	20
78	RecF and RecR Play Critical Roles in the Homologous Recombination and Single-Strand Annealing Pathways of Mycobacteria. Journal of Bacteriology, 2015, 197, 3121-3132.	1.0	16
79	Mycobacterium smegmatis HelY Is an RNA-Activated ATPase/dATPase and 3â€²-to-5â€² Helicase That Unwinds 3â€²-Tailed RNA Duplexes and RNA:DNA Hybrids. Journal of Bacteriology, 2015, 197, 3057-3065.	1.0	10
80	Fission yeast RNA triphosphatase reads an Spt5 CTD code. Rna, 2015, 21, 113-123.	1.6	11
81	Structureâ€“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. Rna, 2015, 21, 1173-1186.	1.6	18
82	Biochemical Characterization of Mycobacterium smegmatis RnhC (MSMEG_4305), a Bifunctional Enzyme Composed of Autonomous N-Terminal Type I RNase H and C-Terminal Acid Phosphatase Domains. Journal of Bacteriology, 2015, 197, 2489-2498.	1.0	21
83	RNA capping: progress and prospects. Rna, 2015, 21, 735-737.	1.6	31
84	RNA polymerase II CTD phospho-sites Ser5 and Ser7 govern phosphate homeostasis in fission yeast. Rna, 2015, 21, 1770-1780.	1.6	32
85	Individual letters of the RNA polymerase II CTD code govern distinct gene expression programs in fission yeast. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 4185-4190.	3.3	53
86	Structures of Bacterial Polynucleotide Kinase in a Michaelis Complex with Nucleoside Triphosphate (NTP)-Mg ²⁺ and 5â€²-OH RNA and a Mixed Substrate-Product Complex with NTP-Mg ²⁺ and a 5â€²-Phosphorylated Oligonucleotide. Journal of Bacteriology, 2014, 196, 4285-4292.	1.0	3
87	Modified Vaccinia Virus Ankara Triggers Type I IFN Production in Murine Conventional Dendritic Cells via a cGAS/STING-Mediated Cytosolic DNA-Sensing Pathway. PLoS Pathogens, 2014, 10, e1003989.	2.1	148
88	Structure and mechanism of <i>E. coli</i> RNA 2â€²,3â€²-cyclic phosphodiesterase. Rna, 2014, 20, 1697-1705.	1.6	20
89	Crystal structure, mutational analysis and RNA-dependent ATPase activity of the yeast DEAD-box pre-mRNA splicing factor Prp28. Nucleic Acids Research, 2014, 42, 12885-12898.	6.5	22
90	Effects of 3â€²-OH and 5â€²-PO 4 Base Mispairs and Damaged Base Lesions on the Fidelity of Nick Sealing by Deinococcus radiodurans RNA Ligase. Journal of Bacteriology, 2014, 196, 1704-1712.	1.0	14

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91	Mycobacterium smegmatis DinB2 misincorporates deoxyribonucleotides and ribonucleotides during templated synthesis and lesion bypass. Nucleic Acids Research, 2014, 42, 12722-12734.	6.5	35
92	Structures of bacterial polynucleotide kinase in a Michaelis complex with GTP*Mg2+ and 5'-OH oligonucleotide and a product complex with GDP*Mg2+ and 5'-PO4 oligonucleotide reveal a mechanism of general acid-base catalysis and the determinants of phosphoacceptor recognition. Nucleic Acids Research, 2014, 42, 1152-1161.	6.5	17
93	Impact of DNA3'pp5'G capping on repair reactions at DNA 3' ends. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 11317-11322.	3.3	16
94	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. Nucleic Acids Research, 2014, 42, 4697-4711.	6.5	18
95	Characterization of three mycobacterial DinB (DNA polymerase IV) paralogs highlights DinB2 as naturally adept at ribonucleotide incorporation. Nucleic Acids Research, 2014, 42, 11056-11070.	6.5	38
96	Crystal Structure of Vaccinia Virus mRNA Capping Enzyme Provides Insights into the Mechanism and Evolution of the Capping Apparatus. Structure, 2014, 22, 452-465.	1.6	41
97	Distinctive kinetics and substrate specificities of plant and fungal tRNA ligases. Rna, 2014, 20, 462-473.	1.6	18
98	How an mRNA capping enzyme reads distinct RNA polymerase II and Spt5 CTD phosphorylation codes. Genes and Development, 2014, 28, 1323-1336.	2.7	40
99	Structure, Mechanism, and Specificity of a Eukaryal tRNA Restriction Enzyme Involved in Self-Nonself Discrimination. Cell Reports, 2014, 7, 339-347.	2.9	16
100	Rewriting the rules for end joining via enzymatic splicing of DNA 3'-PO4 and 5'-OH ends. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 20437-20442.	3.3	36
101	Kinetic mechanism of nick sealing by T4 RNA ligase 2 and effects of 3â€²-OH base mispairs and damaged base lesions. Rna, 2013, 19, 1840-1847.	1.6	14
102	Mechanism of RNA 2â€²,3â€²-cyclic phosphate end healing by T4 polynucleotide kinaseâ€“phosphatase. Nucleic Acids Research, 2013, 41, 355-365.	6.5	57
103	Structural and Biochemical Analysis of the Phosphate Donor Specificity of the Polynucleotide Kinase Component of the Bacterial Pnkpâ€¢Hen1 RNA Repair System. Biochemistry, 2013, 52, 4734-4743.	1.2	10
104	Discrimination of RNA from DNA by Polynucleotide Phosphorylase. Biochemistry, 2013, 52, 6702-6711.	1.2	7
105	Chemical Mutagenesis of Vaccinia DNA Topoisomerase Lysine 167 Provides Insights to the Catalysis of DNA Transesterification. Biochemistry, 2013, 52, 984-991.	1.2	3
106	Distinctive Effects of Domain Deletions on the Manganese-Dependent DNA Polymerase and DNA Phosphorylase Activities of <i>Mycobacterium smegmatis</i> Polynucleotide Phosphorylase. Biochemistry, 2013, 52, 2967-2981.	1.2	10
107	A dual role for mycobacterial RecO in RecA-dependent homologous recombination and RecA-independent single-strand annealing. Nucleic Acids Research, 2013, 41, 2284-2295.	6.5	34
108	Structure-function analysis of the 5â€² end of yeast U1 snRNA highlights genetic interactions with the Msl5â€¢Mud2 branchpoint-binding complex and other spliceosome assembly factors. Nucleic Acids Research, 2013, 41, 7485-7500.	6.5	14

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109	The PAF Complex and Prf1/Rtf1 Delineate Distinct Cdk9-Dependent Pathways Regulating Transcription Elongation in Fission Yeast. PLoS Genetics, 2013, 9, e1004029.	1.5	45
110	Structure and mechanism of the 2',3' phosphatase component of the bacterial Pnkp-Hen1 RNA repair system. Nucleic Acids Research, 2013, 41, 5864-5873.	6.5	26
111	A kinetic framework for tRNA ligase and enforcement of a 2â€²-phosphate requirement for ligation highlights the design logic of an RNA repair machine. Rna, 2013, 19, 659-669.	1.6	32
112	2â€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. Rna, 2013, 19, 1355-1362.	1.6	32
113	Mycobacterium smegmatis Lhr Is a DNA-dependent ATPase and a 3â€²-to-5â€² DNA Translocase and Helicase That Prefers to Unwind 3â€²-Tailed RNA:DNA Hybrids. Journal of Biological Chemistry, 2013, 288, 14125-14134.	1.6	19
114	Structural insights to the metal specificity of an archaeal member of the LigD 3â€²-phosphoesterase DNA repair enzyme family. Nucleic Acids Research, 2012, 40, 828-836.	6.5	7
115	Box H/ACA snoRNAs are preferred substrates for the trimethylguanosine synthase in the divergent unicellular eukaryote <i>Trichomonas vaginalis</i>. Rna, 2012, 18, 1656-1665.	1.6	4
116	Mycobacterium smegmatis SftH exemplifies a distinctive clade of superfamily II DNA-dependent ATPases with 3â€² to 5â€² translocase and helicase activities. Nucleic Acids Research, 2012, 40, 7465-7475.	6.5	22
117	Structure and mechanism of the polynucleotide kinase component of the bacterial Pnkp-Hen1 RNA repair system. Rna, 2012, 18, 2277-2286.	1.6	18
118	Kinetic Analysis of DNA Strand Joining by Chlorella Virus DNA Ligase and the Role of Nucleotidyltransferase Motif VI in Ligase Adenylylation. Journal of Biological Chemistry, 2012, 287, 28609-28618.	1.6	13
119	RNA ligase RtcB splices 3â€²-phosphate and 5â€²-OH ends via covalent RtcB-(histidinyl)-GMP and polynucleotide-(3â€²)pp(5â€²)G intermediates. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 6072-6077.	3.3	94
120	Determinants of the cytotoxicity of PrrC anticodon nuclease and its amelioration by tRNA repair. Rna, 2012, 18, 145-154.	1.6	18
121	The adenylyltransferase domain of bacterial Pnkp defines a unique RNA ligase family. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 2296-2301.	3.3	23
122	Mycobacterium smegmatis RqlH defines a novel clade of bacterial RecQ-like DNA helicases with ATP-dependent 3â€²â€“5â€² translocase and duplex unwinding activities. Nucleic Acids Research, 2012, 40, 4604-4614.	6.5	11
123	Solution structure and DNA-binding properties of the phosphoesterase domain of DNA ligase D. Nucleic Acids Research, 2012, 40, 2076-2088.	6.5	7
124	A fungal anticodon nuclease ribotoxin exploits a secondary cleavage site to evade tRNA repair. Rna, 2012, 18, 1716-1724.	1.6	18
125	Genetic interactions of hypomorphic mutations in the m⁷G cap-binding pocket of yeast nuclear cap binding complex: An essential role for Cbc2 in meiosis via splicing of <i>MER3</i> pre-mRNA. Rna, 2012, 18, 1996-2011.	1.6	23
126	Structureâ€“function analysis and genetic interactions of the yeast branchpoint binding protein Msl5. Nucleic Acids Research, 2012, 40, 4539-4552.	6.5	19

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127	The sequential 2',3'-cyclic phosphodiesterase and 3'-phosphate/5'-OH ligation steps of the RtcB RNA splicing pathway are GTP-dependent. Nucleic Acids Research, 2012, 40, 8558-8567.	6.5	46
128	Punctuation and syntax of the RNA polymerase II CTD code in fission yeast. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 18024-18029.	3.3	41
129	Characterization of <i>Mycobacterium smegmatis</i> PolD2 and PolD1 as RNA/DNA Polymerases Homologous to the POL Domain of Bacterial DNA Ligase D. Biochemistry, 2012, 51, 10147-10158.	1.2	22
130	Structureâ€“function relations in the NTPase domain of the antiviral tRNA ribotoxin Escherichia coli PrrC. Virology, 2012, 427, 144-150.	1.1	11
131	Deciphering the RNA Polymerase II CTD Code in Fission Yeast. Molecular Cell, 2011, 43, 311-318.	4.5	109
132	Mycobacteria exploit three genetically distinct DNA doubleâ€•strand break repair pathways. Molecular Microbiology, 2011, 79, 316-330.	1.2	96
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