Rick Russell

List of Publications by Year
in descending order

59 papers	3,746 citations	201674 27 h-index	144013 57 g-index
61 all docs	61 docs citations	61 times ranked	3222 citing authors

#	Article	IF	Citations
1	A Single-Molecule Study of RNA Catalysis and Folding. Science, 2000, 288, 2048-2051.	12.6	696
2	DMS footprinting of structured RNAs and RNAâ€“protein complexes. Nature Protocols, 2007, 2, 2608-2623.	12.0	235
3	Kinetic Basis for DNA Target Specificity of CRISPR-Cas12a. Molecular Cell, 2018, 71, 816-824.e3.	9.7	225
4	Exploring the folding landscape of a structured RNA. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 155-160.	7.1	222
5	Rapid compaction during RNA folding. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 4266-4271.	7.1	207
6	RNA Helicase Proteins as Chaperones and Remodelers. Annual Review of Biochemistry, 2014, 83, 697-725.	11.1	207
7	DEADâ€box proteins as RNA helicases and chaperones. Wiley Interdisciplinary Reviews RNA, 2011, 2, 135-152.	6.4	135
8	DEAD-box proteins can completely separate an RNA duplex using a single ATP. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 20203-20208.	7.1	119
9	Kinetic redistribution of native and misfolded RNAs by a DEAD-box chaperone. Nature, 2007, 449, 1014-1018.	27.8	109
10	New pathways in folding of the Tetrahymena group I RNA enzyme. Journal of Molecular Biology, 1999, 291, 1155-1167.	4.2	105
11	RNA misfolding and the action of chaperones. Frontiers in Bioscience - Landmark, 2008, 13, 1.	3.0	104
12	Probing the folding landscape of the Tetrahymena ribozyme: commitment to form the native conformation is late in the folding pathway. Journal of Molecular Biology, 2001, 308, 839-851.	4.2	97
13	Small angle X-ray scattering reveals a compact intermediate in RNA folding. Nature Structural Biology, 2000, 7, 367-370.	9.7	96
14	Nonspecific binding to structured RNA and preferential unwinding of an exposed helix by the CYT-19 protein, a DEAD-box RNA chaperone. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 16698-16703.	7.1	93
15	The Paradoxical Behavior of a Highly Structured Misfolded Intermediate in RNA Folding. Journal of Molecular Biology, 2006, 363, 531-544.	4.2	92
16	Distinct RNA-unwinding mechanisms of DEAD-box and DEAH-box RNA helicase proteins in remodeling structured RNAs and RNPs. Biochemical Society Transactions, 2017, 45, 1313-1321.	3.4	77
17	Toward a molecular understanding of RNA remodeling by DEAD-box proteins. RNA Biology, 2013, 10, 44-55.	3.1	74
18	Probing the Mechanisms of DEAD-Box Proteins as General RNA Chaperones: The C-Terminal Domain of CYT-19 Mediates General Recognition of RNAâ€. Biochemistry, 2007, 46, 3013-3022.	2.5	69

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19	Solution structures of DEAD-box RNA chaperones reveal conformational changes and nucleic acid tethering by a basic tail. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 12254-12259.	7.1	66
20	Do DEAD-Box Proteins Promote Group II Intron Splicing without Unwinding RNA?. Molecular Cell, 2007, 28, 159-166.	9.7	61
21	Visualization of local DNA unwinding by Mre11/Rad50/Nbs1 using single-molecule FRET. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 18868-18873.	7.1	55
22	Visualizing the formation of an RNA folding intermediate through a fast highly modular secondary structure switch. Nature Communications, 2016, 7, ncomms11768.	12.8	50
23	Structural specificity conferred by a group I RNA peripheral element. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 10176-10181.	7.1	43
24	Roles of DEAD-box proteins in RNA and RNP Folding. RNA Biology, 2010, 7, 667-676.	3.1	40
25	The G-quadruplex (G4) resolvase DHX36 efficiently and specifically disrupts DNA G4s via a translocation-based helicase mechanism. Journal of Biological Chemistry, 2018, 293, 1924-1932.	3.4	31
26	ATP-Dependent Roles of the DEAD-Box Protein Mss116p in Group II Intron Splicing In Vitro and In Vivo. Journal of Molecular Biology, 2011, 411, 661-679.	4.2	30
27	Inhibition of CRISPR-Cas12a DNA targeting by nucleosomes and chromatin. Science Advances, 2021, 7, .	10.3	30
28	Specificity from steric restrictions in the guanosine binding pocket of a group I ribozyme. Rna, 1999, 5, 158-166.	3.5	29
29	Multiple Unfolding Events during Native Folding of the Tetrahymena Group I Ribozyme. Journal of Molecular Biology, 2010, 400, 1067-1077.	4.2	29
30	The Azoarcus Group I Intron Ribozyme Misfolds and Is Accelerated for Refolding by ATP-dependent RNA Chaperone Proteins. Journal of Biological Chemistry, 2011, 286, 37304-37312.	3.4	28
31	DEAD-box protein CYT-19 is activated by exposed helices in a group I intron RNA. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E2928-36.	7.1	23
32	Deletion of the P5abc Peripheral Element Accelerates Early and Late Folding Steps of the Tetrahymena Group I Ribozyme. Biochemistry, 2007, 46, 4951-4961.	2.5	20
33	Catalytic Activity as a Probe of Native RNA Folding. Methods in Enzymology, 2009, 468, 195-218.	1.0	20
34	The Long-Range P3 Helix of the Tetrahymena Ribozyme Is Disrupted during Folding between the Native and Misfolded Conformations. Journal of Molecular Biology, 2013, 425, 2670-2686.	4.2	20
35	Hidden Structural Modules in a Cooperative RNA Folding Transition. Cell Reports, 2018, 22, 3240-3250.	6.4	20
36	Zeptomole detection of DNA nanoparticles by single-molecule fluorescence with magnetic field-directed localization. Analytical Biochemistry, 2012, 431, 40-47.	2.4	18

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37	DEAD-Box Helicase Proteins Disrupt RNA Tertiary Structure Through Helix Capture. PLoS Biology, 2014, 12, e1001981.	5.6	18
38	Template-switching mechanism of a group II intron-encoded reverse transcriptase and its implications for biological function and RNA-Seq. Journal of Biological Chemistry, 2019, 294, 19764-19784.	3.4	18
39	Organization of DNA Partners and Strand Exchange Mechanisms during Flp Site-Specific Recombination Analyzed by Difference Topology, Single Molecule FRET and Single Molecule TPM. Journal of Molecular Biology, 2014, 426, 793-815.	4.2	17
40	The DEAD-Box Protein CYT-19 Uses Arginine Residues in Its C-Tail To Tether RNA Substrates. Biochemistry, 2017, 56, 3571-3578.	2.5	16
41	Folding Pathways of the Tetrahymena Ribozyme. Journal of Molecular Biology, 2014, 426, 2300-2312.	4.2	15
42	RNA Structural Modules Control the Rate and Pathway of RNA Folding and Assembly. Journal of Molecular Biology, 2016, 428, 3972-3985.	4.2	14
43	Structural basis for template switching by a group II intronâ€“encoded non-LTR-retroelement reverse transcriptase. Journal of Biological Chemistry, 2021, 297, 100971.	3.4	13
44	A Dual-Mode Single-Molecule Fluorescence Assay for the Detection of Expanded CGG Repeats in Fragile X Syndrome. Molecular Biotechnology, 2013, 53, 19-28.	2.4	10
45	ATP utilization by a DEAD-box protein during refolding of a misfolded group I intron ribozyme. Journal of Biological Chemistry, 2021, 296, 100132.	3.4	8
46	Direct Measurement of Interhelical DNA Repulsion and Attraction by Quantitative Cross-Linking. Journal of the American Chemical Society, 2022, 144, 1718-1728.	13.7	8
47	RNA Catalysis as a Probe for Chaperone Activity of DEAD-Box Helicases. Methods in Enzymology, 2012, 511, 111-130.	1.0	6
48	Unwinding the Mechanisms of a DEAD-Box RNA Helicase in Cancer. Journal of Molecular Biology, 2015, 427, 1797-1800.	4.2	6
49	Hexapeptides That Inhibit Processing of Branched DNA Structures Induce a Dynamic Ensemble of Holliday Junction Conformations. Journal of Biological Chemistry, 2015, 290, 22734-22746.	3.4	6
50	The DHX36-specific-motif (DSM) enhances specificity by accelerating recruitment of DNA G-quadruplex structures. Biological Chemistry, 2021, 402, 593-604.	2.5	5
51	How to Kinetically Dissect an RNA Machine. Biochemistry, 2021, 60, 3485-3490.	2.5	3
52	Chance, Destiny, and the Inner Workings of ClpXP. Cell, 2014, 158, 479-480.	28.9	2
53	Key Points to Consider When Studying RNA Remodeling by Proteins. Methods in Molecular Biology, 2021, 2209, 1-16.	0.9	2
54	Key Points to Consider When Studying RNA Remodeling by Proteins. Methods in Molecular Biology, 2015, 1259, 1-16.	0.9	1

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55	A tweak and a peek: How Cas9 pries open double-stranded DNA to check its sequence. Nature Structural and Molecular Biology, 2022, 29, 286-288.	8.2	1
56	Kinetics measurements of G-quadruplex binding and unfolding by helicases. Methods, 2022, 204, 1-13.	3.8	1
57	Measurement of ATP utilization in RNA unwinding and RNA chaperone activities by DEAD-box helicase proteins. Methods in Enzymology, 2022, , .	1.0	1
58	Reflections on 20 years of RNA folding, dynamics, and structure. Rna, 2015, 21, 723-724.	3.5	0
59	RNA chaperone activity of DEADâ€box â€˜helicaseâ€™ proteins. FASEB Journal, 2013, 27, 96.3.	0.5	0