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	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
2	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
3	Kinetics measurements of G-quadruplex binding and unfolding by helicases. Methods, 2022, 204, 1-13.	3.8	1
4	Measurement of ATP utilization in RNA unwinding and RNA chaperone activities by DEAD-box helicase proteins. Methods in Enzymology, 2022, , .	1.0	1
5	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
6	Inhibition of CRISPR-Cas12a DNA targeting by nucleosomes and chromatin. Science Advances, 2021, 7, .	10.3	30
7	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
8	How to Kinetically Dissect an RNA Machine. Biochemistry, 2021, 60, 3485-3490.	2.5	3
9	The DHX36-specific-motif (DSM) enhances specificity by accelerating recruitment of DNA G-quadruplex structures. Biological Chemistry, 2021, 402, 593-604.	2.5	5
10	Key Points to Consider When Studying RNA Remodeling by Proteins. Methods in Molecular Biology, 2021, 2209, 1-16.	0.9	2
11	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
12	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
13	Hidden Structural Modules in a Cooperative RNA Folding Transition. Cell Reports, 2018, 22, 3240-3250.	6.4	20
14	Kinetic Basis for DNA Target Specificity of CRISPR-Cas12a. Molecular Cell, 2018, 71, 816-824.e3.	9.7	225
15	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
16	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
17	Visualizing the formation of an RNA folding intermediate through a fast highly modular secondary structure switch. Nature Communications, 2016, 7, ncomms11768.	12.8	50
18	RNA Structural Modules Control the Rate and Pathway of RNA Folding and Assembly. Journal of Molecular Biology, 2016, 428, 3972-3985.	4.2	14

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19	Reflections on 20 years of RNA folding, dynamics, and structure. Rna, 2015, 21, 723-724.	3.5	0
20	Unwinding the Mechanisms of a DEAD-Box RNA Helicase in Cancer. Journal of Molecular Biology, 2015, 427, 1797-1800.	4.2	6
21	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
22	Key Points to Consider When Studying RNA Remodeling by Proteins. Methods in Molecular Biology, 2015, 1259, 1-16.	0.9	1
23	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
24	DEAD-Box Helicase Proteins Disrupt RNA Tertiary Structure Through Helix Capture. PLoS Biology, 2014, 12, e1001981.	5.6	18
25	Folding Pathways of the Tetrahymena Ribozyme. Journal of Molecular Biology, 2014, 426, 2300-2312.	4.2	15
26	RNA Helicase Proteins as Chaperones and Remodelers. Annual Review of Biochemistry, 2014, 83, 697-725.	11.1	207
27	Chance, Destiny, and the Inner Workings of ClpXP. Cell, 2014, 158, 479-480.	28.9	2
28	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
29	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
30	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
31	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
32	Toward a molecular understanding of RNA remodeling by DEAD-box proteins. RNA Biology, 2013, 10, 44-55.	3.1	74
33	RNA chaperone activity of DEADâ€box â€˜helicaseâ€™ proteins. FASEB Journal, 2013, 27, 96.3.	0.5	0
34	RNA Catalysis as a Probe for Chaperone Activity of DEAD-Box Helicases. Methods in Enzymology, 2012, 511, 111-130.	1.0	6
35	Zeptomole detection of DNA nanoparticles by single-molecule fluorescence with magnetic field-directed localization. Analytical Biochemistry, 2012, 431, 40-47.	2.4	18
36	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

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37	DEADâ€box proteins as RNA helicases and chaperones. Wiley Interdisciplinary Reviews RNA, 2011, 2, 135-152.	6.4	135
38	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
39	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
40	Roles of DEAD-box proteins in RNA and RNP Folding. RNA Biology, 2010, 7, 667-676.	3.1	40
41	Multiple Unfolding Events during Native Folding of the Tetrahymena Group I Ribozyme. Journal of Molecular Biology, 2010, 400, 1067-1077.	4.2	29
42	Catalytic Activity as a Probe of Native RNA Folding. Methods in Enzymology, 2009, 468, 195-218.	1.0	20
43	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
44	RNA misfolding and the action of chaperones. Frontiers in Bioscience - Landmark, 2008, 13, 1.	3.0	104
45	Do DEAD-Box Proteins Promote Group II Intron Splicing without Unwinding RNA?. Molecular Cell, 2007, 28, 159-166.	9.7	61
46	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
47	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
48	DMS footprinting of structured RNAs and RNAâ€“protein complexes. Nature Protocols, 2007, 2, 2608-2623.	12.0	235
49	Kinetic redistribution of native and misfolded RNAs by a DEAD-box chaperone. Nature, 2007, 449, 1014-1018.	27.8	109
50	The Paradoxical Behavior of a Highly Structured Misfolded Intermediate in RNA Folding. Journal of Molecular Biology, 2006, 363, 531-544.	4.2	92
51	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
52	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
53	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
54	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

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55	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
56	Small angle X-ray scattering reveals a compact intermediate in RNA folding. Nature Structural Biology, 2000, 7, 367-370.	9.7	96
57	A Single-Molecule Study of RNA Catalysis and Folding. Science, 2000, 288, 2048-2051.	12.6	696
58	Specificity from steric restrictions in the guanosine binding pocket of a group I ribozyme. Rna, 1999, 5, 158-166.	3.5	29
59	New pathways in folding of the Tetrahymena group I RNA enzyme. Journal of Molecular Biology, 1999, 291, 1155-1167.	4.2	105