

# Karissa Y Sanbonmatsu

## List of Publications by Year in descending order

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Version: 2024-02-01

64  
papers

4,226  
citations

117625

34  
h-index

114465

63  
g-index

68  
all docs

68  
docs citations

68  
times ranked

4285  
citing authors

#	ARTICLE	IF	CITATIONS
1	Getting to the bottom of lncRNA mechanism: structure–function relationships. <i>Mammalian Genome</i> , 2022, 33, 343-353.	2.2	15
2	Towards Molecular Mechanism in Long Non-coding RNAs: Linking Structure and Function. <i>Advances in Experimental Medicine and Biology</i> , 2022, 1363, 23-32.	1.6	1
3	Integrative structural studies of the SARS-CoV-2 spike protein during the fusion process (2022). <i>Current Research in Structural Biology</i> , 2022, , .	2.2	0
4	Hyper-swivel head domain motions are required for complete mRNA-tRNA translocation and ribosome resetting. <i>Nucleic Acids Research</i> , 2022, 50, 8302-8320.	14.5	3
5	Modeling the Influenza A NP-vRNA-Polymerase Complex in Atomic Detail. <i>Biomolecules</i> , 2021, 11, 124.	4.0	2
6	Chelated Magnesium Logic Gate Regulates Riboswitch Pseudoknot Formation. <i>Journal of Physical Chemistry B</i> , 2021, 125, 6479-6490.	2.6	9
7	Four-dimensional chromosome reconstruction elucidates the spatiotemporal reorganization of the mammalian X chromosome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	13
8	Zinc-finger protein CNBP alters the 3-D structure of lncRNA Braveheart in solution. <i>Nature Communications</i> , 2020, 11, 148.	12.8	53
9	Practical Considerations for Atomistic Structure Modeling with Cryo-EM Maps. <i>Journal of Chemical Information and Modeling</i> , 2020, 60, 2436-2442.	5.4	11
10	Elongation factor-Tu can repetitively engage aminoacyl-tRNA within the ribosome during the proofreading stage of tRNA selection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 3610-3620.	7.1	31
11	Elongation Factor Tu Switch I Element is a Gate for Aminoacyl-tRNA Selection. <i>Journal of Molecular Biology</i> , 2020, 432, 3064-3077.	4.2	11
12	Quantitative comparison between sub-millisecond time resolution single-molecule FRET measurements and 10-second molecular simulations of a biosensor protein. <i>PLoS Computational Biology</i> , 2020, 16, e1008293.	3.2	14
13	Cryo_fit: Democratization of flexible fitting for cryo-EM. <i>Journal of Structural Biology</i> , 2019, 208, 1-6.	2.8	30
14	Large-scale simulations of nucleoprotein complexes: ribosomes, nucleosomes, chromatin, chromosomes and CRISPR. <i>Current Opinion in Structural Biology</i> , 2019, 55, 104-113.	5.7	17
15	Scaling molecular dynamics beyond 100,000 processor cores for large-scale biophysical simulations. <i>Journal of Computational Chemistry</i> , 2019, 40, 1919-1930.	3.3	79
16	Stalking Structure in Plant Long Noncoding RNAs. <i>Methods in Molecular Biology</i> , 2019, 1933, 381-388.	0.9	2
17	Magnesium controls aptamer-expression platform switching in the SAM-I riboswitch. <i>Nucleic Acids Research</i> , 2019, 47, 3158-3170.	14.5	26
18	Tracking fluctuation hotspots on the yeast ribosome through the elongation cycle. <i>Nucleic Acids Research</i> , 2017, 45, 4958-4971.	14.5	17

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19	Identification and Characterization of a Class of MALAT1-like Genomic Loci. <i>Cell Reports</i> , 2017, 19, 1723-1738.	6.4	55
20	Tools for the cryo-EM gold rush: going from the cryo-EM map to the atomistic model. <i>Bioscience Reports</i> , 2017, 37, .	2.4	18
21	Cooperation between Magnesium and Metabolite Controls Collapse of the SAM-I Riboswitch. <i>Biophysical Journal</i> , 2017, 113, 348-359.	0.5	20
22	Stringent Nucleotide Recognition by the Ribosome at the Middle Codon Position. <i>Molecules</i> , 2017, 22, 1427.	3.8	5
23	A magnesium-induced triplex pre-organizes the SAM-II riboswitch. <i>PLoS Computational Biology</i> , 2017, 13, e1005406.	3.2	24
24	Mesoscale Modeling Reveals Hierarchical Looping of Chromatin Fibers Near Gene Regulatory Elements. <i>Journal of Physical Chemistry B</i> , 2016, 120, 8642-8653.	2.6	40
25	A G-Rich Motif in the lncRNA Braveheart Interacts with a Zinc-Finger Transcription Factor to Specify the Cardiovascular Lineage. <i>Molecular Cell</i> , 2016, 64, 37-50.	9.7	133
26	COOLAIR Antisense RNAs Form Evolutionarily Conserved Elaborate Secondary Structures. <i>Cell Reports</i> , 2016, 16, 3087-3096.	6.4	132
27	Towards structural classification of long non-coding RNAs. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2016, 1859, 41-45.	1.9	29
28	Functional and Structural Analysis of a Highly-Expressed <i>Yersinia pestis</i> Small RNA following Infection of Cultured Macrophages. <i>PLoS ONE</i> , 2016, 11, e0168915.	2.5	9
29	Generalized Manning Condensation Model Captures the RNA Ion Atmosphere. <i>Physical Review Letters</i> , 2015, 114, 258105.	7.8	69
30	Using Molecular Simulation to Model High-Resolution Cryo-EM Reconstructions. <i>Methods in Enzymology</i> , 2015, 558, 497-514.	1.0	21
31	Cryo-EM of Ribosomal 80S Complexes with Termination Factors Reveals the Translocated Cricket Paralysis Virus IRES. <i>Molecular Cell</i> , 2015, 57, 422-432.	9.7	82
32	Tunable Riboregulator Switches for Post-transcriptional Control of Gene Expression. <i>ACS Synthetic Biology</i> , 2015, 4, 1326-1334.	3.8	22
33	Integrating Molecular Dynamics Simulations with Chemical Probing Experiments Using SHAPE-FIT. <i>Methods in Enzymology</i> , 2015, 553, 215-234.	1.0	14
34	Reduced Model Captures Mg <sup>2+</sup> -RNA Interaction Free Energy of Riboswitches. <i>Biophysical Journal</i> , 2014, 106, 1508-1519.	0.5	46
35	Cryo-EM structure of the small subunit of the mammalian mitochondrial ribosome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 7284-7289.	7.1	72
36	Flipping through the Genetic Code: New Developments in Discrimination between Cognate and Near-Cognate tRNAs and the Effect of Antibiotics. <i>Journal of Molecular Biology</i> , 2014, 426, 3197-3200.	4.2	6

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37	Regulation of the Mammalian Elongation Cycle by Subunit Rolling: A Eukaryotic-Specific Ribosome Rearrangement. <i>Cell</i> , 2014, 158, 121-131.	28.9	125
38	Dynamics of riboswitches: Molecular simulations. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2014, 1839, 1046-1050.	1.9	7
39	3S: Shotgun secondary structure determination of long non-coding RNAs. <i>Methods</i> , 2013, 63, 170-177.	3.8	56
40	Tackling Structures of Long Noncoding RNAs. <i>International Journal of Molecular Sciences</i> , 2013, 14, 23672-23684.	4.1	84
41	Simulating movement of tRNA through the ribosome during hybrid-state formation. <i>Journal of Chemical Physics</i> , 2013, 139, 121919.	3.0	29
42	Rise of the RNA Machines: Exploring the Structure of Long Non-Coding RNAs. <i>Journal of Molecular Biology</i> , 2013, 425, 3731-3746.	4.2	124
43	The expression platform and the aptamer: cooperativity between Mg <sup>2+</sup> and ligand in the SAM-I riboswitch. <i>Nucleic Acids Research</i> , 2013, 41, 1922-1935.	14.5	57
44	Connecting the Kinetics and Energy Landscape of tRNA Translocation on the Ribosome. <i>PLoS Computational Biology</i> , 2013, 9, e1003003.	3.2	79
45	Structural architecture of the human long non-coding RNA, steroid receptor RNA activator. <i>Nucleic Acids Research</i> , 2012, 40, 5034-5051.	14.5	237
46	Sizing up long non-coding RNAs: Do lncRNAs have secondary and tertiary structure?. <i>Bioarchitecture</i> , 2012, 2, 189-199.	1.5	121
47	Magnesium Fluctuations Modulate RNA Dynamics in the SAM-I Riboswitch. <i>Journal of the American Chemical Society</i> , 2012, 134, 12043-12053.	13.7	91
48	Functional Role of the Sarcinâ€“Ricin Loop of the 23S rRNA in the Elongation Cycle of Protein Synthesis. <i>Journal of Molecular Biology</i> , 2012, 419, 125-138.	4.2	70
49	Consensus among flexible fitting approaches improves the interpretation of cryo-EM data. <i>Journal of Structural Biology</i> , 2012, 177, 561-570.	2.8	38
50	Computational studies of molecular machines: the ribosome. <i>Current Opinion in Structural Biology</i> , 2012, 22, 168-174.	5.7	66
51	Key Intermolecular Interactions in the <i>E. coli</i> 70S Ribosome Revealed by Coarse-Grained Analysis. <i>Journal of the American Chemical Society</i> , 2011, 133, 16828-16838.	13.7	38
52	Excited states of ribosome translocation revealed through integrative molecular modeling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 18943-18948.	7.1	89
53	Tertiary contacts control switching of the SAM-I riboswitch. <i>Nucleic Acids Research</i> , 2011, 39, 2416-2431.	14.5	39
54	Free State Conformational Sampling of the SAM-I Riboswitch Aptamer Domain. <i>Structure</i> , 2010, 18, 787-797.	3.3	167

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55	Head swivel on the ribosome facilitates translocation by means of intra-subunit tRNA hybrid sites. <i>Nature</i> , 2010, 468, 713-716.	27.8	336
56	SMOG@ctbp: simplified deployment of structure-based models in GROMACS. <i>Nucleic Acids Research</i> , 2010, 38, W657-W661.	14.5	291
57	Accommodation of aminoacyl-tRNA into the ribosome involves reversible excursions along multiple pathways. <i>Rna</i> , 2010, 16, 1196-1204.	3.5	174
58	Connecting Energy Landscapes with Experimental Rates for Aminoacyl-tRNA Accommodation in the Ribosome. <i>Journal of the American Chemical Society</i> , 2010, 132, 13170-13171.	13.7	48
59	Stochastic Gating and Drug-Ribosome Interactions. <i>Journal of Molecular Biology</i> , 2009, 386, 648-661.	4.2	66
60	Energy landscape of the ribosomal decoding center. <i>Biochimie</i> , 2006, 88, 1053-1059.	2.6	49
61	Alignment/misalignment hypothesis for tRNA selection by the ribosome. <i>Biochimie</i> , 2006, 88, 1075-1089.	2.6	35
62	Simulating movement of tRNA into the ribosome during decoding. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 15854-15859.	7.1	260
63	Understanding Discrimination by the Ribosome: Stability Testing and Groove Measurement of Codon-Anticodon Pairs. <i>Journal of Molecular Biology</i> , 2003, 328, 33-47.	4.2	65
64	Structure of Met-enkephalin in explicit aqueous solution using replica exchange molecular dynamics. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 46, 225-234.	2.6	254