Karissa Y Sanbonmatsu

List of Publications by Year
in descending order

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	Head swivel on the ribosome facilitates translocation by means of intra-subunit tRNA hybrid sites. Nature, 2010, 468, 713-716.	27.8	336
2	SMOG@ctbp: simplified deployment of structure-based models in GROMACS. Nucleic Acids Research, 2010, 38, W657-W661.	14.5	291
3	Simulating movement of tRNA into the ribosome during decoding. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 15854-15859.	7.1	260
4	Structure of Met-enkephalin in explicit aqueous solution using replica exchange molecular dynamics. Proteins: Structure, Function and Bioinformatics, 2002, 46, 225-234.	2.6	254
5	Structural architecture of the human long non-coding RNA, steroid receptor RNA activator. Nucleic Acids Research, 2012, 40, 5034-5051.	14.5	237
6	Accommodation of aminoacyl-tRNA into the ribosome involves reversible excursions along multiple pathways. Rna, 2010, 16, 1196-1204.	3.5	174
7	Free State Conformational Sampling of the SAM-I Riboswitch Aptamer Domain. Structure, 2010, 18, 787-797.	3.3	167
8	A G-Rich Motif in the lncRNA Braveheart Interacts with a Zinc-Finger Transcription Factor to Specify the Cardiovascular Lineage. Molecular Cell, 2016, 64, 37-50.	9.7	133
9	COOLAIR Antisense RNAs Form Evolutionarily Conserved Elaborate Secondary Structures. Cell Reports, 2016, 16, 3087-3096.	6.4	132
10	Regulation of the Mammalian Elongation Cycle by Subunit Rolling: A Eukaryotic-Specific Ribosome Rearrangement. Cell, 2014, 158, 121-131.	28.9	125
11	Rise of the RNA Machines: Exploring the Structure of Long Non-Coding RNAs. Journal of Molecular Biology, 2013, 425, 3731-3746.	4.2	124
12	Sizing up long non-coding RNAs: Do lncRNAs have secondary and tertiary structure?. Bioarchitecture, 2012, 2, 189-199.	1.5	121
13	Magnesium Fluctuations Modulate RNA Dynamics in the SAM-I Riboswitch. Journal of the American Chemical Society, 2012, 134, 12043-12053.	13.7	91
14	Excited states of ribosome translocation revealed through integrative molecular modeling. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 18943-18948.	7.1	89
15	Tackling Structures of Long Noncoding RNAs. International Journal of Molecular Sciences, 2013, 14, 23672-23684.	4.1	84
16	Cryo-EM of Ribosomal 80S Complexes with Termination Factors Reveals the Translocated Cricket Paralysis Virus IRES. Molecular Cell, 2015, 57, 422-432.	9.7	82
17	Connecting the Kinetics and Energy Landscape of tRNA Translocation on the Ribosome. PLoS Computational Biology, 2013, 9, e1003003.	3.2	79
18	Scaling molecular dynamics beyond 100,000 processor cores for large‐scale biophysical simulations. Journal of Computational Chemistry, 2019, 40, 1919-1930.	3.3	79

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19	Cryo-EM structure of the small subunit of the mammalian mitochondrial ribosome. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 7284-7289.	7.1	72
20	Functional Role of the Sarcinâ€"Ricin Loop of the 23S rRNA in the Elongation Cycle of Protein Synthesis. Journal of Molecular Biology, 2012, 419, 125-138.	4.2	70
21	Generalized Manning Condensation Model Captures the RNA Ion Atmosphere. Physical Review Letters, 2015, 114, 258105.	7.8	69
22	Stochastic Gating and Drugâ€"Ribosome Interactions. Journal of Molecular Biology, 2009, 386, 648-661.	4.2	66
23	Computational studies of molecular machines: the ribosome. Current Opinion in Structural Biology, 2012, 22, 168-174.	5.7	66
24	Understanding Discrimination by the Ribosome: Stability Testing and Groove Measurement of Codonâ€"Anticodon Pairs. Journal of Molecular Biology, 2003, 328, 33-47.	4.2	65
25	The expression platform and the aptamer: cooperativity between Mg2+ and ligand in the SAM-I riboswitch. Nucleic Acids Research, 2013, 41, 1922-1935.	14.5	57
26	3S: Shotgun secondary structure determination of long non-coding RNAs. Methods, 2013, 63, 170-177.	3.8	56
27	Identification and Characterization of a Class of MALAT1-like Genomic Loci. Cell Reports, 2017, 19, 1723-1738.	6.4	55
28	Zinc-finger protein CNBP alters the 3-D structure of lncRNA Braveheart in solution. Nature Communications, 2020, 11, 148.	12.8	53
29	Energy landscape ofÂtheÂribosomal decoding center. Biochimie, 2006, 88, 1053-1059.	2.6	49
30	Connecting Energy Landscapes with Experimental Rates for Aminoacyl-tRNA Accommodation in the Ribosome. Journal of the American Chemical Society, 2010, 132, 13170-13171.	13.7	48
31	Reduced Model Captures Mg2+-RNA Interaction Free Energy of Riboswitches. Biophysical Journal, 2014, 106, 1508-1519.	0.5	46
32	Mesoscale Modeling Reveals Hierarchical Looping of Chromatin Fibers Near Gene Regulatory Elements. Journal of Physical Chemistry B, 2016, 120, 8642-8653.	2.6	40
33	Tertiary contacts control switching of the SAM-I riboswitch. Nucleic Acids Research, 2011, 39, 2416-2431.	14.5	39
34	Key Intermolecular Interactions in the <i>E. coli</i> 70S Ribosome Revealed by Coarse-Grained Analysis. Journal of the American Chemical Society, 2011, 133, 16828-16838.	13.7	38
35	Consensus among flexible fitting approaches improves the interpretation of cryo-EM data. Journal of Structural Biology, 2012, 177, 561-570.	2.8	38
36	Alignment/misalignment hypothesis forÂtRNA selection byÂtheÂribosome. Biochimie, 2006, 88, 1075-1089.	2.6	35

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37	Elongation factor-Tu can repetitively engage aminoacyl-tRNA within the ribosome during the proofreading stage of tRNA selection. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 3610-3620.	7.1	31
38	Cryo_fit: Democratization of flexible fitting for cryo-EM. Journal of Structural Biology, 2019, 208, 1-6.	2.8	30
39	Simulating movement of tRNA through the ribosome during hybrid-state formation. Journal of Chemical Physics, 2013, 139, 121919.	3.0	29
40	Towards structural classification of long non-coding RNAs. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2016, 1859, 41-45.	1.9	29
41	Magnesium controls aptamer-expression platform switching in the SAM-I riboswitch. Nucleic Acids Research, 2019, 47, 3158-3170.	14.5	26
42	A magnesium-induced triplex pre-organizes the SAM-II riboswitch. PLoS Computational Biology, 2017, 13, e1005406.	3.2	24
43	Tunable Riboregulator Switches for Post-transcriptional Control of Gene Expression. ACS Synthetic Biology, 2015, 4, 1326-1334.	3.8	22
44	Using Molecular Simulation to Model High-Resolution Cryo-EM Reconstructions. Methods in Enzymology, 2015, 558, 497-514.	1.0	21
45	Cooperation between Magnesium and Metabolite Controls Collapse of the SAM-I Riboswitch. Biophysical Journal, 2017, 113, 348-359.	0.5	20
46	Tools for the cryo-EM gold rush: going from the cryo-EM map to the atomistic model. Bioscience Reports, 2017, 37, .	2.4	18
47	Tracking fluctuation hotspots on the yeast ribosome through the elongation cycle. Nucleic Acids Research, 2017, 45, 4958-4971.	14.5	17
48	Large-scale simulations of nucleoprotein complexes: ribosomes, nucleosomes, chromatin, chromosomes and CRISPR. Current Opinion in Structural Biology, 2019, 55, 104-113.	5.7	17
49	Getting to the bottom of lncRNA mechanism: structure–function relationships. Mammalian Genome, 2022, 33, 343-353.	2.2	15
50	Integrating Molecular Dynamics Simulations with Chemical Probing Experiments Using SHAPE-FIT. Methods in Enzymology, 2015, 553, 215-234.	1.0	14
51	Quantitative comparison between sub-millisecond time resolution single-molecule FRET measurements and 10-second molecular simulations of a biosensor protein. PLoS Computational Biology, 2020, 16, e1008293.	3.2	14
52	Four-dimensional chromosome reconstruction elucidates the spatiotemporal reorganization of the mammalian X chromosome. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	13
53	Practical Considerations for Atomistic Structure Modeling with Cryo-EM Maps. Journal of Chemical Information and Modeling, 2020, 60, 2436-2442.	5.4	11
54	Elongation Factor Tu Switch I Element is a Gate for Aminoacyl-tRNA Selection. Journal of Molecular Biology, 2020, 432, 3064-3077.	4.2	11

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55	Chelated Magnesium Logic Gate Regulates Riboswitch Pseudoknot Formation. Journal of Physical Chemistry B, 2021, 125, 6479-6490.	2.6	9
56	Functional and Structural Analysis of a Highly-Expressed Yersinia pestis Small RNA following Infection of Cultured Macrophages. PLoS ONE, 2016, 11, e0168915.	2.5	9
57	Dynamics of riboswitches: Molecular simulations. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2014, 1839, 1046-1050.	1.9	7
58	Flipping through the Genetic Code: New Developments in Discrimination between Cognate and Near-Cognate tRNAs and the Effect of Antibiotics. Journal of Molecular Biology, 2014, 426, 3197-3200.	4.2	6
59	Stringent Nucleotide Recognition by the Ribosome at the Middle Codon Position. Molecules, 2017, 22, 1427.	3.8	5
60	Hyper-swivel head domain motions are required for complete mRNA-tRNA translocation and ribosome resetting. Nucleic Acids Research, 2022, 50, 8302-8320.	14.5	3
61	Stalking Structure in Plant Long Noncoding RNAs. Methods in Molecular Biology, 2019, 1933, 381-388.	0.9	2
62	Modeling the Influenza A NP-vRNA-Polymerase Complex in Atomic Detail. Biomolecules, 2021, 11, 124.	4.0	2
63	Towards Molecular Mechanism in Long Non-coding RNAs: Linking Structure and Function. Advances in Experimental Medicine and Biology, 2022, 1363, 23-32.	1.6	1
64	Integrative structural studies of the SARS-CoV-2 spike protein during the fusion process (2022). Current Research in Structural Biology, 2022, , .	2.2	0