Kalli Kappel

List of Publications by Year
in descending order

19 papers	2,556 citations	471509 17 h-index	794594 19 g-index
24 all docs	24 docs citations	24 times ranked	3516 citing authors

#	Article	IF	Citations
1	Learning cis-regulatory principles of ADAR-based RNA editing from CRISPR-mediated mutagenesis. Nature Communications, 2021, 12, 2165.	12.8	9
2	Cryo-EM structures of full-length Tetrahymena ribozyme at 3.1ÂÃ... resolution. Nature, 2021, 596, 603-607.	27.8	59
3	Macromolecular modeling and design in Rosetta: recent methods and frameworks. Nature Methods, 2020, 17, 665-680.	19.0	513
4	Distinct Conformational States Underlie Pausing during Initiation of HIV-1 Reverse Transcription. Journal of Molecular Biology, 2020, 432, 4499-4522.	4.2	5
5	Accelerated cryo-EM-guided determination of three-dimensional RNA-only structures. Nature Methods, 2020, 17, 699-707.	19.0	119
6	RNA 3D structure prediction guided by independent folding of homologous sequences. BMC Bioinformatics, 2019, 20, 512.	2.6	21
7	A unified mechanism for intron and exon definition and back-splicing. Nature, 2019, 573, 375-380.	27.8	114
8	A Quantitative and Predictive Model for RNA Binding by Human Pumilio Proteins. Molecular Cell, 2019, 74, 966-981.e18.	9.7	55
9	Blind tests of RNAâ€“protein binding affinity prediction. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 8336-8341.	7.1	21
10	Cryo-EM structure of a 40ÂkDa SAM-IV riboswitch RNA at 3.7â€‰Ã... resolution. Nature Communications, 2019, 10, 5511.	12.8	90
11	Sampling Native-like Structures of RNA-Protein Complexes through Rosetta Folding and Docking. Structure, 2019, 27, 140-151.e5.	3.3	34
12	Architecture of an HIV-1 reverse transcriptase initiation complex. Nature, 2018, 557, 118-122.	27.8	44
13	De novo computational RNA modeling into cryo-EM maps of large ribonucleoprotein complexes. Nature Methods, 2018, 15, 947-954.	19.0	45
14	RNA-Puzzles Round III: 3D RNA structure prediction of five riboswitches and one ribozyme. Rna, 2017, 23, 655-672.	3.5	158
15	The Rosetta All-Atom Energy Function for Macromolecular Modeling and Design. Journal of Chemical Theory and Computation, 2017, 13, 3031-3048.	5.3	1,032
16	Single-molecule FRET-Rosetta reveals RNA structural rearrangements during human telomerase catalysis. Rna, 2017, 23, 175-188.	3.5	23
17	Blind tests of RNA nearest-neighbor energy prediction. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 8430-8435.	7.1	29
18	Accelerated molecular dynamics simulations of ligand binding to a muscarinic G-protein-coupled receptor. Quarterly Reviews of Biophysics, 2015, 48, 479-487.	5.7	127

#	Article	IF	Citations
19	The binding mechanism, multiple binding modes, and allosteric regulation of Staphylococcus aureus Sortase A probed by molecular dynamics simulations. Protein Science, 2012, 21, 1858-1871.	7.6	36