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	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
2	Macromolecular modeling and design in Rosetta: recent methods and frameworks. Nature Methods, 2020, 17, 665-680.	19.0	513
3	RNA-Puzzles Round III: 3D RNA structure prediction of five riboswitches and one ribozyme. Rna, 2017, 23, 655-672.	3.5	158
4	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
5	Accelerated cryo-EM-guided determination of three-dimensional RNA-only structures. Nature Methods, 2020, 17, 699-707.	19.0	119
6	A unified mechanism for intron and exon definition and back-splicing. Nature, 2019, 573, 375-380.	27.8	114
7	Cryo-EM structure of a 40 kDa SAM-IV riboswitch RNA at 3.7 Å resolution. Nature Communications, 2019, 10, 5511.	12.8	90
8	Cryo-EM structures of full-length Tetrahymena ribozyme at 3.1 Å resolution. Nature, 2021, 596, 603-607.	27.8	59
9	A Quantitative and Predictive Model for RNA Binding by Human Pumilio Proteins. Molecular Cell, 2019, 74, 966-981.e18.	9.7	55
10	De novo computational RNA modeling into cryo-EM maps of large ribonucleoprotein complexes. Nature Methods, 2018, 15, 947-954.	19.0	45
11	Architecture of an HIV-1 reverse transcriptase initiation complex. Nature, 2018, 557, 118-122.	27.8	44
12	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
13	Sampling Native-like Structures of RNA-Protein Complexes through Rosetta Folding and Docking. Structure, 2019, 27, 140-151.e5.	3.3	34
14	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
15	Single-molecule FRET-Rosetta reveals RNA structural rearrangements during human telomerase catalysis. Rna, 2017, 23, 175-188.	3.5	23
16	RNA 3D structure prediction guided by independent folding of homologous sequences. BMC Bioinformatics, 2019, 20, 512.	2.6	21
17	Blind tests of RNA–protein binding affinity prediction. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 8336-8341.	7.1	21
18	Learning cis-regulatory principles of ADAR-based RNA editing from CRISPR-mediated mutagenesis. Nature Communications, 2021, 12, 2165.	12.8	9

#	Article	IF	Citations
19	Distinct Conformational States Underlie Pausing during Initiation of HIV-1 Reverse Transcription. Journal of Molecular Biology, 2020, 432, 4499-4522.	4.2	5