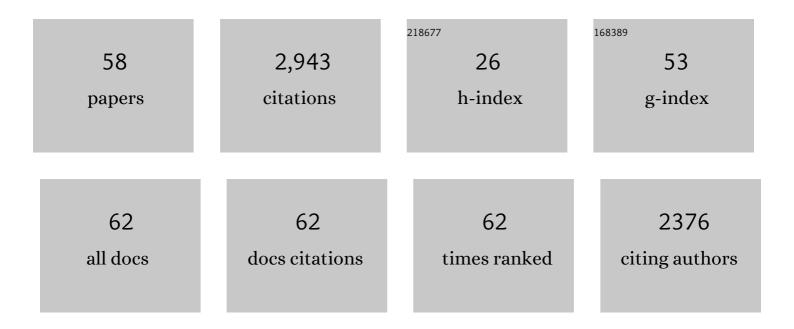


## List of Publications by Year in descending order

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HONCL

#	Article	IF	CITATIONS
1	Structural principles of CRISPR-Cas enzymes used in nucleic acid detection. Journal of Structural Biology, 2022, 214, 107838.	2.8	8
2	Structural and biochemical characterization of in vivo assembled Lactococcus lactis CRISPR-Csm complex. Communications Biology, 2022, 5, 279.	4.4	9
3	"X―marks the spot: Mining the gold in CasX for gene editing. Molecular Cell, 2022, 82, 1083-1085.	9.7	0
4	CryoEM structures of pseudouridine-free ribosome suggest impacts of chemical modifications on ribosome conformations. Structure, 2022, 30, 983-992.e5.	3.3	14
5	Artificial intelligence-assisted cryoEM structure of Bfr2-Lcp5 complex observed in the yeast small subunit processome. Communications Biology, 2022, 5, .	4.4	1
6	Virus detection via programmable Type III-A CRISPR-Cas systems. Nature Communications, 2021, 12, 5653.	12.8	40
7	The molecular basis for recognition of 5′-NNNCC-3′ PAM and its methylation state by Acidothermus cellulolyticus Cas9. Nature Communications, 2020, 11, 6346.	12.8	15
8	Directed evolution studies of a thermophilic Type II-C Cas9. Methods in Enzymology, 2019, 616, 265-288.	1.0	9
9	Yeast R2TP Interacts with Extended Termini of Client Protein Nop58p. Scientific Reports, 2019, 9, 20228.	3.3	5
10	Phosphate Lock Residues of <i>Acidothermus cellulolyticus</i> Cas9 Are Critical to Its Substrate Specificity. ACS Synthetic Biology, 2018, 7, 2908-2917.	3.8	7
11	The multistructural forms of box C/D ribonucleoprotein particles. Rna, 2018, 24, 1625-1633.	3.5	31
12	The Impact of DNA Topology and Guide Length on Target Selection by a Cytosine-Specific Cas9. ACS Synthetic Biology, 2017, 6, 1103-1113.	3.8	27
13	Cas6 processes tight and relaxed repeat RNA via multiple mechanisms: A hypothesis. BioEssays, 2017, 39, 1700019.	2.5	13
14	Pih1p-Tah1p Puts a Lid on Hexameric AAA+ ATPases Rvb1/2p. Structure, 2017, 25, 1519-1529.e4.	3.3	22
15	A Non-Stem-Loop CRISPR RNA Is Processed by Dual Binding Cas6. Structure, 2016, 24, 547-554.	3.3	24
16	Structure Principles of CRISPR-Cas Surveillance and Effector Complexes. Annual Review of Biophysics, 2015, 44, 229-255.	10.0	21
17	Inhibition of cGAS DNA Sensing by a Herpesvirus Virion Protein. Cell Host and Microbe, 2015, 18, 333-344.	11.0	223
18	Structural Principles of CRISPR RNA Processing. Structure, 2015, 23, 13-20.	3.3	43

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19	Essential Structural and Functional Roles of the Cmr4 Subunit in RNA Cleavage by the Cmr CRISPR-Cas Complex. Cell Reports, 2014, 9, 1610-1617.	6.4	57
20	Staphylococcus epidermidis Csm1 is a 3'-5' exonuclease. Nucleic Acids Research, 2014, 42, 1129-1138.	14.5	34
21	Target RNA capture and cleavage by the Cmr type III-B CRISPR–Cas effector complex. Genes and Development, 2014, 28, 2432-2443.	5.9	104
22	Co-Expression and Co-Purification of Archaeal and Eukaryal Box C/D RNPs. PLoS ONE, 2014, 9, e103096.	2.5	14
23	Structure of an RNA Silencing Complex of the CRISPR-Cas Immune System. Molecular Cell, 2013, 52, 146-152.	9.7	117
24	Recognition and Cleavage of a Nonstructured CRISPR RNA by Its Processing Endoribonuclease Cas6. Structure, 2013, 21, 385-393.	3.3	47
25	Structure of the Cmr2-Cmr3 Subcomplex of the Cmr RNA Silencing Complex. Structure, 2013, 21, 376-384.	3.3	42
26	The impact of CRISPR repeat sequence on structures of a Cas6 protein–RNA complex. Protein Science, 2012, 21, 405-417.	7.6	31
27	The mysterious RAMP proteins and their roles in small RNAâ€based immunity. Protein Science, 2012, 21, 463-470.	7.6	19
28	Structure of the Cmr2 Subunit of the CRISPR-Cas RNA Silencing Complex. Structure, 2012, 20, 545-553.	3.3	69
29	Structures of ribonucleoprotein particle modification enzymes. Quarterly Reviews of Biophysics, 2011, 44, 95-122.	5.7	20
30	Interaction of the Cas6 Riboendonuclease with CRISPR RNAs: Recognition and Cleavage. Structure, 2011, 19, 257-264.	3.3	154
31	Structural and functional evidence of high specificity of Cbf5 for ACA trinucleotide. Rna, 2011, 17, 244-250.	3.5	13
32	Functional and Structural Impact of Target Uridine Substitutions on the H/ACA Ribonucleoprotein Particle Pseudouridine Synthase,. Biochemistry, 2010, 49, 6276-6281.	2.5	19
33	Structural Basis for Substrate Placement by an Archaeal Box C/D Ribonucleoprotein Particle. Molecular Cell, 2010, 39, 939-949.	9.7	59
34	Glycosidic Bond Conformation Preference Plays a Pivotal Role in Catalysis of RNA Pseudouridylation: A Combined Simulation and Structural Study. Journal of Molecular Biology, 2010, 401, 690-695.	4.2	11
35	Crystal structure and assembly of the functional Nanoarchaeum equitans tRNA splicing endonuclease. Nucleic Acids Research, 2009, 37, 5793-5802.	14.5	25
36	Structure of a functional ribonucleoprotein pseudouridine synthase bound to a substrate RNA. Nature Structural and Molecular Biology, 2009, 16, 740-746.	8.2	77

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37	Unveiling substrate RNA binding to H/ACA RNPs: one side fits all. Current Opinion in Structural Biology, 2008, 18, 78-85.	5.7	24
38	Determination of Proteinâ^'RNA Interaction Sites in the Cbf5-H/ACA Guide RNA Complex by Mass Spectrometric Protein Footprinting. Biochemistry, 2008, 47, 1500-1510.	2.5	12
39	Long-distance placement of substrate RNA by H/ACA proteins. Rna, 2008, 14, 2086-2094.	3.5	22
40	Cas6 is an endoribonuclease that generates guide RNAs for invader defense in prokaryotes. Genes and Development, 2008, 22, 3489-3496.	5.9	495
41	'In-line attack' conformational effect plays a modest role in an enzyme-catalyzed RNA cleavage: a free energy simulation study. Nucleic Acids Research, 2007, 35, 4001-4006.	14.5	24
42	Achieving Specific RNA Cleavage Activity by an Inactive Splicing Endonuclease Subunit Through Engineered Oligomerization. Journal of Molecular Biology, 2007, 366, 642-649.	4.2	5
43	Alternative Conformations of the Archaeal Nop56/58-Fibrillarin Complex Imply Flexibility in Box C/D RNPs. Journal of Molecular Biology, 2007, 371, 1141-1150.	4.2	36
44	Protein-RNA contacts at crystal packing surfaces. Proteins: Structure, Function and Bioinformatics, 2007, 67, 121-127.	2.6	12
45	Substrate RNA positioning in the archaeal H/ACA ribonucleoprotein complex. Nature Structural and Molecular Biology, 2007, 14, 1189-1195.	8.2	57
46	Complexes of tRNA and maturation enzymes: shaping up for translation. Current Opinion in Structural Biology, 2007, 17, 293-301.	5.7	25
47	RNA Recognition and Cleavage by a Splicing Endonuclease. Science, 2006, 312, 906-910.	12.6	102
48	Crystal Structure of a Cbf5-Nop10-Gar1 Complex and Implications in RNA-Guided Pseudouridylation and Dyskeratosis Congenita. Molecular Cell, 2006, 21, 249-260.	9.7	152
49	Cleavage of pre-tRNAs by the splicing endonuclease requires a composite active site. Nature, 2006, 441, 375-377.	27.8	64
50	The heteromeric Nanoarchaeum equitans splicing endonuclease cleaves noncanonical bulge-helix-bulge motifs of joined tRNA halves. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 17934-17939.	7.1	71
51	Structural Characterization of the Catalytic Subunit of a Novel RNA Splicing Endonuclease. Journal of Molecular Biology, 2005, 353, 952-960.	4.2	28
52	Structural comparison of yeast snoRNP and spliceosomal protein Snu13p with its homologs. Biochemical and Biophysical Research Communications, 2005, 333, 550-554.	2.1	20
53	Structural and Thermodynamic Evidence for a Stabilizing Role of Nop5p in S-Adenosyl-L-methionine Binding to Fibrillarin. Journal of Biological Chemistry, 2004, 279, 41822-41829.	3.4	28
54	Molecular Basis of Box C/D RNA-Protein Interactions. Structure, 2004, 12, 807-818.	3.3	158

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55	Structure determination of a truncated dimeric splicing endonuclease in pseudo-face-centered space groupP21212. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 447-452.	2.5	5
56	Structure and function of archaeal box C/D sRNP core proteins. Nature Structural and Molecular Biology, 2003, 10, 256-263.	8.2	113
57	Crystal structure of a dimeric archaeal splicing endonuclease. Journal of Molecular Biology, 2000, 302, 639-648.	4.2	46
58	Crystallization and Preliminary X-Ray Analysis of Borrelia burgdorferi Outer Surface Protein A (OspA) Complexed with a Murine Monoclonal Antibody Fab Fragment. Journal of Structural Biology, 1995, 115, 335-337.	2.8	16