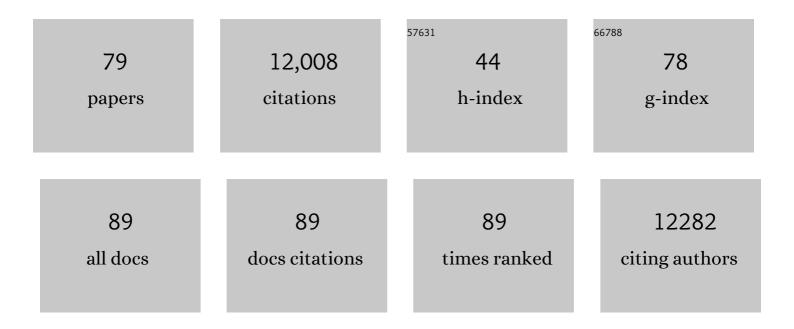
Leemor Joshua-Tor

List of Publications by Year in descending order

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LEEMOR LOSHUA-TOP

#	Article	IF	CITATIONS
1	Argonaute2 Is the Catalytic Engine of Mammalian RNAi. Science, 2004, 305, 1437-1441.	6.0	2,370
2	Crystal Structure of Argonaute and Its Implications for RISC Slicer Activity. Science, 2004, 305, 1434-1437.	6.0	1,283
3	Purified Argonaute2 and an siRNA form recombinant human RISC. Nature Structural and Molecular Biology, 2005, 12, 340-349.	3.6	658
4	Analysis of the C. elegans Argonaute Family Reveals that Distinct Argonautes Act Sequentially during RNAi. Cell, 2006, 127, 747-757.	13.5	576
5	The Structure of Human Argonaute-2 in Complex with miR-20a. Cell, 2012, 150, 100-110.	13.5	517
6	The crystal structure of the Argonaute2 PAZ domain reveals an RNA binding motif in RNAi effector complexes. Nature Structural and Molecular Biology, 2003, 10, 1026-1032.	3.6	487
7	Mechanism of DNA translocation in a replicative hexameric helicase. Nature, 2006, 442, 270-275.	13.7	472
8	Slicer and the Argonautes. Nature Chemical Biology, 2007, 3, 36-43.	3.9	410
9	A triple helix stabilizes the $3\hat{a}\in^2$ ends of long noncoding RNAs that lack poly(A) tails. Genes and Development, 2012, 26, 2392-2407.	2.7	375
10	Structural Basis for the EBA-175 Erythrocyte Invasion Pathway of the Malaria Parasite Plasmodium falciparum. Cell, 2005, 122, 183-193.	13.5	289
11	The structural biochemistry of Zucchini implicates it as a nuclease in piRNA biogenesis. Nature, 2012, 491, 279-283.	13.7	276
12	Xâ€ r ay crystal structures of the oxidized and reduced forms of the rubredoxin from the marine hyperthermophilic archaebacterium pyrococcus furiosus. Protein Science, 1992, 1, 1494-1507.	3.1	238
13	From guide to target: molecular insights into eukaryotic RNA-interference machinery. Nature Structural and Molecular Biology, 2015, 22, 20-28.	3.6	219
14	Strategies for protein coexpression in Escherichia coli. Nature Methods, 2006, 3, 55-64.	9.0	207
15	On helicases and other motor proteins. Current Opinion in Structural Biology, 2008, 18, 243-257.	2.6	189
16	Argonaute Slicing Is Required for Heterochromatic Silencing and Spreading. Science, 2006, 313, 1134-1137.	6.0	182
17	Conformational variability in structures of the nitrogenase iron proteins from Azotobacter vinelandii and Clostridium pasteurianum. Journal of Molecular Biology, 1998, 280, 669-685.	2.0	152
18	NSD3-Short Is an Adaptor Protein that Couples BRD4 to the CHD8 Chromatin Remodeler. Molecular Cell, 2015, 60, 847-859.	4.5	137

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19	Crystal structure of a conserved protease that binds DNA: the bleomycin hydrolase, Gal6. Science, 1995, 269, 945-950.	6.0	135
20	The Making of a Slicer: Activation of Human Argonaute-1. Cell Reports, 2013, 3, 1901-1909.	2.9	129
21	Mechanism of Dis3l2 substrate recognition in the Lin28–let-7 pathway. Nature, 2014, 514, 252-256.	13.7	110
22	SARS-CoV-2 neutralizing antibody responses are more robust in patients with severe disease. Emerging Microbes and Infections, 2020, 9, 2091-2093.	3.0	109
23	The three-dimensional structure of a DNA duplex containing looped-out bases. Nature, 1988, 334, 82-84.	13.7	103
24	High-Affinity Binding of Chp1 Chromodomain to K9 Methylated Histone H3 Is Required to Establish Centromeric Heterochromatin. Molecular Cell, 2009, 34, 36-46.	4.5	103
25	Eukaryotic Argonautes come into focus. Trends in Biochemical Sciences, 2013, 38, 263-271.	3.7	96
26	Three-dimensional structures of bulge-containing DNA fragments. Journal of Molecular Biology, 1992, 225, 397-431.	2.0	94
27	Argonautes confront new small RNAs. Current Opinion in Chemical Biology, 2007, 11, 569-577.	2.8	89
28	PTEN Functions by Recruitment to Cytoplasmic Vesicles. Molecular Cell, 2015, 58, 255-268.	4.5	89
29	Multivalent Recruitment of Human Argonaute by GW182. Molecular Cell, 2017, 67, 646-658.e3.	4.5	81
30	Crystal structure of apaf-1 caspase recruitment domain: an α-helical greek key fold for apoptotic signaling 1 1Edited by D. C. Rees. Journal of Molecular Biology, 1999, 293, 439-447.	2.0	80
31	Crystal Structure of the DNA Binding Domain of the Replication Initiation Protein E1 from Papillomavirus. Molecular Cell, 2000, 6, 149-158.	4.5	80
32	FUS Regulates Activity of MicroRNA-Mediated Gene Silencing. Molecular Cell, 2018, 69, 787-801.e8.	4.5	76
33	Ancestral Roles of Small RNAs: An Ago-Centric Perspective. Cold Spring Harbor Perspectives in Biology, 2011, 3, a003772-a003772.	2.3	75
34	Crystal structures of two intermediates in the assembly of the papillomavirus replication initiation complex. EMBO Journal, 2002, 21, 1487-1496.	3.5	68
35	Argonaute and RNA — getting into the groove. Current Opinion in Structural Biology, 2006, 16, 5-11.	2.6	63
36	Crystal structure of human bleomycin hydrolase, a self-compartmentalizing cysteine protease. Structure, 1999, 7, 619-627.	1.6	62

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37	On-Enzyme Refolding Permits Small RNA and tRNA Surveillance by the CCA-Adding Enzyme. Cell, 2015, 160, 644-658.	13.5	61
38	Dynamic look at DNA unwinding by a replicative helicase. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E827-35.	3.3	60
39	siRNA carrying an (E)-vinylphosphonate moiety at the 5Î,, end of the guide strand augments gene silencing by enhanced binding to human Argonaute-2. Nucleic Acids Research, 2017, 45, 3528-3536.	6.5	59
40	The Unusual Active Site of Gal6/Bleomycin Hydrolase Can Act as a Carboxypeptidase, Aminopeptidase, and Peptide Ligase. Cell, 1998, 93, 103-109.	13.5	56
41	The Argonautes. Cold Spring Harbor Symposia on Quantitative Biology, 2006, 71, 67-72.	2.0	54
42	High-resolution cryo-EM structures of outbreak strain human norovirus shells reveal size variations. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 12828-12832.	3.3	53
43	ELTA: Enzymatic Labeling of Terminal ADP-Ribose. Molecular Cell, 2019, 73, 845-856.e5.	4.5	52
44	Decoding the 5′ nucleotide bias of PIWI-interacting RNAs. Nature Communications, 2019, 10, 828.	5.8	51
45	Comparison of the Xâ€ray structure of native rubredoxin from pyrococcus furiosus with the NMR structure of the zincâ€substituted protein. Protein Science, 1992, 1, 1522-1525.	3.1	47
46	NADP Regulates the Yeast <i>GAL</i> Induction System. Science, 2008, 319, 1090-1092.	6.0	47
47	Chd5 Requires PHD-Mediated Histone 3 Binding for Tumor Suppression. Cell Reports, 2013, 3, 92-102.	2.9	47
48	Crystal structure of the DNA binding domain of the replication initiation protein E1 from papillomavirus. Molecular Cell, 2000, 6, 149-58.	4.5	47
49	Multi-domain utilization by TUT4 and TUT7 in control of let-7 biogenesis. Nature Structural and Molecular Biology, 2017, 24, 658-665.	3.6	44
50	Structure of the active form of human origin recognition complex and its ATPase motor module. ELife, 2017, 6, .	2.8	44
51	The Gal3p transducer of the <i>GAL</i> regulon interacts with the Gal80p repressor in its ligand-induced closed conformation. Genes and Development, 2012, 26, 294-303.	2.7	42
52	Harnessing insulin- and leptin-induced oxidation of PTP1B for therapeutic development. Nature Communications, 2018, 9, 283.	5.8	39
53	The Chp1–Tas3 core is a multifunctional platform critical for gene silencing by RITS. Nature Structural and Molecular Biology, 2011, 18, 1351-1357.	3.6	38
54	Noncysteinyl Coordination to the [4Fe-4S]2+Cluster of the DNA Repair Adenine Glycosylase MutY Introduced via Site-Directed Mutagenesis. Structural Characterization of an Unusual Histidinyl-Coordinated Clusterâ€,‡. Biochemistry, 2002, 41, 3931-3942.	1.2	37

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55	OCA-T1 and OCA-T2 are coactivators of POU2F3 in the tuft cell lineage. Nature, 2022, 607, 169-175.	13.7	35
56	Structurally modulated codelivery of siRNA and Argonaute 2 for enhanced RNA interference. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E2696-E2705.	3.3	34
57	A structural snapshot of base-pair opening in DNA. Proceedings of the National Academy of Sciences of the United States of America, 1999, 96, 11809-11814.	3.3	33
58	Conformational substates in different crystal forms of the photoactive yellow protein—Correlation with theoretical and experimental flexibility. Protein Science, 2000, 9, 64-72.	3.1	31
59	Essential Dynamics from NMR Clusters: Dynamic Properties of the Myb DNA-Binding Domain and a Hinge-Bending Enhancing Variant. Methods, 1998, 14, 318-328.	1.9	30
60	Crystal Structure of Carboxypeptidase A Complexed with d-Cysteine at 1.75 Ã â^' Inhibitor-Induced Conformational Changes,. Biochemistry, 2000, 39, 10082-10089.	1.2	27
61	The DNA-binding Domain of Human Papillomavirus Type 18 E1. Journal of Biological Chemistry, 2004, 279, 3733-3742.	1.6	27
62	Rapid generation of drug-resistance alleles at endogenous loci using CRISPR-Cas9 indel mutagenesis. PLoS ONE, 2017, 12, e0172177.	1.1	25
63	CRL4-like Clr4 complex in <i>Schizosaccharomyces pombe</i> depends on an exposed surface of Dos1 for heterochromatin silencing. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 1795-1800.	3.3	21
64	The dynamic nature of the human origin recognition complex revealed through five cryoEM structures. ELife, 2020, 9, .	2.8	20
65	The coming of age of DMA crystallography. Current Opinion in Structural Biology, 1993, 3, 323-335.	2.6	18
66	Argonaute MID domain takes centre stage. EMBO Reports, 2010, 11, 564-565.	2.0	18
67	Evolution of DNA replication origin specification and gene silencing mechanisms. Nature Communications, 2020, 11, 5175.	5.8	16
68	Selective chemical inactivation of AAA proteins reveals distinct functions of proteasomal ATPases. Chemistry and Biology, 2001, 8, 941-950.	6.2	14
69	Structure of the photoactive yellow protein reconstituted with caffeic acid at 1.16â€Ã resolution. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 585-590.	2.5	13
70	A structural view of the initiators for chromosome replication. Current Opinion in Structural Biology, 2018, 53, 131-139.	2.6	13
71	Engineering Photocycle Dynamics. Journal of Biological Chemistry, 2002, 277, 6463-6468.	1.6	12
72	Asterix/Gtsf1 links tRNAs and piRNA silencing of retrotransposons. Cell Reports, 2021, 34, 108914.	2.9	12

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73	Mutagenesis and crystallographic studies of the catalytic residues of the papain family protease bleomycin hydrolase: new insights into active-site structure. Biochemical Journal, 2007, 401, 421-428.	1.7	11
74	Target binding triggers hierarchical phosphorylation of human Argonaute-2 to promote target release. ELife, 0, 11, .	2.8	11
75	A Structural Model For Sequence-Specific Proflavin-DNA Interactions DuringIn VitroFrameshift Mutagenesis. Journal of Biomolecular Structure and Dynamics, 1992, 10, 317-331.	2.0	7
76	Developmental roles and molecular mechanisms of Asterix/GTSF1. Wiley Interdisciplinary Reviews RNA, 2022, 13, e1716.	3.2	6
77	siRNAs at RISC. Structure, 2004, 12, 1120-1122.	1.6	5
78	The Structure of Human Argonaute-2 in Complex with miR-20a. Cell, 2012, 150, 233.	13.5	4
79	Structural Basis for the EBA-175 Erythrocyte Invasion Pathway of the Malaria Parasite Plasmodium falciparum. Cell, 2005, 122, 485.	13.5	1