

# Dong Wang

## List of Publications by Year in descending order

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Version: 2024-02-01

63  
papers

6,314  
citations

201674

27  
h-index

123424

61  
g-index

66  
all docs

66  
docs citations

66  
times ranked

9172  
citing authors

#	ARTICLE	IF	CITATIONS
1	RNA polymerase II trapped on a molecular treadmill: Structural basis of persistent transcriptional arrest by a minor groove DNA binder. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2114065119.	7.1	3
2	Cancer-cell-secreted miR-122 suppresses O-GlcNAcylation to promote skeletal muscle proteolysis. <i>Nature Cell Biology</i> , 2022, 24, 793-804.	10.3	29
3	The Cancer-Associated ATM R3008H Mutation Reveals the Link between ATM Activation and Its Exchange. <i>Cancer Research</i> , 2021, 81, 426-437.	0.9	7
4	Molecular basis of transcriptional pausing, stalling, and transcription-coupled repair initiation. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2021, 1864, 194659.	1.9	15
5	A comprehensive mechanism for 5-carboxylcytosine-induced transcriptional pausing revealed by Markov state models. <i>Journal of Biological Chemistry</i> , 2021, 296, 100735.	3.4	2
6	FATC Domain Deletion Compromises ATM Protein Stability, Blocks Lymphocyte Development, and Promotes Lymphomagenesis. <i>Journal of Immunology</i> , 2021, 206, 1228-1239.	0.8	3
7	Clofazimine broadly inhibits coronaviruses including SARS-CoV-2. <i>Nature</i> , 2021, 593, 418-423.	27.8	151
8	Opposite roles of transcription elongation factors Spt4/5 and Elf1 in RNA polymerase II transcription through B-form versus non-B DNA structures. <i>Nucleic Acids Research</i> , 2021, 49, 4944-4953.	14.5	8
9	Transcriptional processing of an unnatural base pair by eukaryotic RNA polymerase II. <i>Nature Chemical Biology</i> , 2021, 17, 906-914.	8.0	16
10	Strand-specific effect of Rad26 and TFIIIS in rescuing transcriptional arrest by CAG trinucleotide repeat slip-outs. <i>Nucleic Acids Research</i> , 2021, 49, 7618-7627.	14.5	3
11	Mechanism of Rad26-assisted rescue of stalled RNA polymerase II in transcription-coupled repair. <i>Nature Communications</i> , 2021, 12, 7001.	12.8	11
12	Cockayne syndrome B protein acts as an ATP-dependent processivity factor that helps RNA polymerase II overcome nucleosome barriers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 25486-25493.	7.1	26
13	A panorama of transcription-coupled repair in yeast chromatin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 20991-20993.	7.1	3
14	Using genetics to reveal protein structure. <i>Science</i> , 2020, 370, 1269-1270.	12.6	1
15	RNA sequencing by direct tagmentation of RNA/DNA hybrids. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 2886-2893.	7.1	86
16	RNA polymerase II stalls on oxidative DNA damage via a torsion-latch mechanism involving lone pair $\pi$ - $\pi$ and CH $\pi$ - $\pi$ interactions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 9338-9348.	7.1	26
17	3.1 $\text{\AA}$ ... structure of yeast RNA polymerase II elongation complex stalled at a cyclobutane pyrimidine dimer lesion solved using streptavidin affinity grids. <i>Journal of Structural Biology</i> , 2019, 207, 270-278.	2.8	27
18	Molecular basis of chromatin remodeling by Rhp26, a yeast CSB ortholog. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 6120-6129.	7.1	10

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19	Structural and biochemical analysis of DNA lesion-induced RNA polymerase II arrest. <i>Methods</i> , 2019, 159-160, 29-34.	3.8	6
20	8-Oxo-guanine DNA damage induces transcription errors by escaping two distinct fidelity control checkpoints of RNA polymerase II. <i>Journal of Biological Chemistry</i> , 2019, 294, 4924-4933.	3.4	9
21	Intrinsic cleavage of RNA polymerase II adopts a nucleobase-independent mechanism assisted by transcript phosphate. <i>Nature Catalysis</i> , 2019, 2, 228-235.	34.4	13
22	Structural basis of transcriptional stalling and bypass of abasic DNA lesion by RNA polymerase II. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E2538-E2545.	7.1	31
23	Identification of H3K4me1-associated proteins at mammalian enhancers. <i>Nature Genetics</i> , 2018, 50, 73-82.	21.4	177
24	Structural basis of DNA lesion recognition for eukaryotic transcription-coupled nucleotide excision repair. <i>DNA Repair</i> , 2018, 71, 43-55.	2.8	41
25	Structural basis of RNA polymerase I stalling at UV light-induced DNA damage. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 8972-8977.	7.1	27
26	Mechanism of transcription-coupled DNA modification recognition. <i>Cell and Bioscience</i> , 2017, 7, 9.	4.8	12
27	Epigenetic DNA Modification <sup>6</sup> -Methyladenine Causes Site-Specific RNA Polymerase II Transcriptional Pausing. <i>Journal of the American Chemical Society</i> , 2017, 139, 14436-14442.	13.7	35
28	Mechanism of DNA alkylation-induced transcriptional stalling, lesion bypass, and mutagenesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E7082-E7091.	7.1	31
29	Structural basis for the initiation of eukaryotic transcription-coupled DNA repair. <i>Nature</i> , 2017, 551, 653-657.	27.8	151
30	Kinase-dead ATM protein is highly oncogenic and can be preferentially targeted by Topo-isomerase I inhibitors. <i>ELife</i> , 2016, 5, .	6.0	38
31	Bridge helix bending promotes RNA polymerase II backtracking through a critical and conserved threonine residue. <i>Nature Communications</i> , 2016, 7, 11244.	12.8	77
32	RNA polymerase II senses obstruction in the DNA minor groove via a conserved sensor motif. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 12426-12431.	7.1	25
33	Functional interplay between NTP leaving group and base pair recognition during RNA polymerase II nucleotide incorporation revealed by methylene substitution. <i>Nucleic Acids Research</i> , 2016, 44, 3820-3828.	14.5	4
34	RNA polymerase II acts as a selective sensor for DNA lesions and endogenous DNA modifications. <i>Transcription</i> , 2016, 7, 57-62.	3.1	10
35	Elucidation of the Dynamics of Transcription Elongation by RNA Polymerase II using Kinetic Network Models. <i>Accounts of Chemical Research</i> , 2016, 49, 687-694.	15.6	49
36	Structural Model of RNA Polymerase II Elongation Complex with Complete Transcription Bubble Reveals NTP Entry Routes. <i>PLoS Computational Biology</i> , 2015, 11, e1004354.	3.2	15

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37	Mechanism of RNA polymerase II bypass of oxidative cyclopurine DNA lesions. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E410-9.	7.1	38
38	Impact of template backbone heterogeneity on RNA polymerase II transcription. Nucleic Acids Research, 2015, 43, 2232-2241.	14.5	15
39	Molecular basis for 5-carboxycytosine recognition by RNA polymerase II elongation complex. Nature, 2015, 523, 621-625.	27.8	141
40	RNA polymerase II transcriptional fidelity control and its functional interplay with DNA modifications. Critical Reviews in Biochemistry and Molecular Biology, 2015, 50, 503-519.	5.2	25
41	Strand-specific (asymmetric) contribution of phosphodiester linkages on RNA polymerase II transcriptional efficiency and fidelity. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E3269-76.	7.1	8
42	Regulation of the Rhp26 <sup>ERCC6/CSB</sup> chromatin remodeler by a novel conserved leucine latch motif. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 18566-18571.	7.1	22
43	Dissecting the chemical interactions and substrate structural signatures governing RNA polymerase II trigger loop closure by synthetic nucleic acid analogues. Nucleic Acids Research, 2014, 42, 5863-5870.	14.5	17
44	Millisecond dynamics of RNA polymerase II translocation at atomic resolution. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 7665-7670.	7.1	127
45	Molecular basis of transcriptional fidelity and DNA lesion-induced transcriptional mutagenesis. DNA Repair, 2014, 19, 71-83.	2.8	28
46	Pyrene-Based Quantitative Detection of the 5-Formylcytosine Loci Symmetry in the CpG Duplex Content during TET-Dependent Demethylation. Angewandte Chemie - International Edition, 2014, 53, 11223-11227.	13.8	35
47	A chemical probe targets DNA 5-formylcytosine sites and inhibits TDG excision, polymerases bypass, and gene expression. Chemical Science, 2014, 5, 567-574.	7.4	29
48	Molecular Dynamics Simulation Study of Conformational Changes of Transcription Factor TFIIIS during RNA Polymerase II Transcriptional Arrest and Reactivation. PLoS ONE, 2014, 9, e97975.	2.5	10
49	Mechanisms of RNA polymerase II processing of DNA lesions formed by novel monofunctional platinum anticancer drugs (560.11). FASEB Journal, 2014, 28, .	0.5	0
50	Structural and chemical perspectives of RNA polymerase II transcriptional fidelity (939.5). FASEB Journal, 2014, 28, .	0.5	0
51	Understanding the Molecular Basis of RNA Polymerase II Transcription. Israel Journal of Chemistry, 2013, 53, 442-449.	2.3	11
52	Effect of a Monofunctional Phenanthriplatin-DNA Adduct on RNA Polymerase II Transcriptional Fidelity and Translesion Synthesis. Journal of the American Chemical Society, 2013, 135, 13054-13061.	13.7	67
53	Innenteilbild: A Chemical Perspective on Transcriptional Fidelity: Dominant Contributions of Sugar Integrity Revealed by Unlocked Nucleic Acids (Angew. Chem. 47/2013). Angewandte Chemie, 2013, 125, 12418-12418.	2.0	0
54	A Chemical Perspective on Transcriptional Fidelity: Dominant Contributions of Sugar Integrity Revealed by Unlocked Nucleic Acids. Angewandte Chemie - International Edition, 2013, 52, 12341-12345.	13.8	14

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55	Dynamics of Pyrophosphate Ion Release and Its Coupled Trigger Loop Motion from Closed to Open State in RNA Polymerase II. <i>Journal of the American Chemical Society</i> , 2012, 134, 2399-2406.	13.7	118
56	5-formylcytosine and 5-carboxylcytosine reduce the rate and substrate specificity of RNA polymerase II transcription. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 831-833.	8.2	204
57	Dissecting Chemical Interactions Governing RNA Polymerase II Transcriptional Fidelity. <i>Journal of the American Chemical Society</i> , 2012, 134, 8231-8240.	13.7	34
58	RNA polymerase II trigger loop residues stabilize and position the incoming nucleotide triphosphate in transcription. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 15745-15750.	7.1	70
59	X-ray structure and mechanism of RNA polymerase II stalled at an antineoplastic monofunctional platinum-DNA adduct. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 9584-9589.	7.1	116
60	Structural Basis of Transcription: Backtracked RNA Polymerase II at 3.4 Angstrom Resolution. <i>Science</i> , 2009, 324, 1203-1206.	12.6	225
61	Structural Basis of Transcription: Role of the Trigger Loop in Substrate Specificity and Catalysis. <i>Cell</i> , 2006, 127, 941-954.	28.9	421
62	Cellular processing of platinum anticancer drugs. <i>Nature Reviews Drug Discovery</i> , 2005, 4, 307-320.	46.4	3,194
63	Transcription-coupled and DNA damage-dependent ubiquitination of RNA polymerase II in vitro. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 4239-4244.	7.1	162