

# Gaofeng Cui

## List of Publications by Year in descending order

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31  
papers

1,647  
citations

471509

17  
h-index

434195

31  
g-index

32  
all docs

32  
docs citations

32  
times ranked

2426  
citing authors

#	ARTICLE	IF	CITATIONS
1	A novel missense HNRNPA1 variant in the PY-NLS domain in a patient with late-onset distal myopathy. <i>Neuromuscular Disorders</i> , 2022, 32, 521-526.	0.6	3
2	A rare germline CDKN2A variant (47T>G; p16-L16R) predisposes carriers to pancreatic cancer by reducing cell cycle inhibition. <i>Journal of Biological Chemistry</i> , 2021, 296, 100634.	3.4	2
3	Filamentous tangles with nemaline rods in MYH2 myopathy: a novel phenotype. <i>Acta Neuropathologica Communications</i> , 2021, 9, 79.	5.2	9
4	TIRR inhibits the 53BP1-p53 complex to alter cell-fate programs. <i>Molecular Cell</i> , 2021, 81, 2583-2595.e6.	9.7	16
5	ATM-phosphorylated SPOP contributes to 53BP1 exclusion from chromatin during DNA replication. <i>Science Advances</i> , 2021, 7, .	10.3	22
6	Mechanisms of BRCA1â€“BARD1 nucleosome recognition and ubiquitylation. <i>Nature</i> , 2021, 596, 438-443.	27.8	74
7	Cryo-EM reveals conformational flexibility in apo DNA polymerase Î¶. <i>Journal of Biological Chemistry</i> , 2021, 297, 100912.	3.4	5
8	SPOP mutation induces replication over-firing by impairing Geminin ubiquitination and triggers replication catastrophe upon ATR inhibition. <i>Nature Communications</i> , 2021, 12, 5779.	12.8	14
9	Structural Basis for the Interaction of Mutasome Assembly Factor REV1 with Ubiquitin. <i>Journal of Molecular Biology</i> , 2018, 430, 2042-2050.	4.2	6
10	Mechanism of 53BP1 activity regulation by RNA-binding TIRR and a designer protein. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 591-600.	8.2	32
11	TIRR regulates 53BP1 by masking its histone methyl-lysine binding function. <i>Nature</i> , 2017, 543, 211-216.	27.8	96
12	Mechanisms of Ubiquitin-Nucleosome Recognition and Regulation of 53BP1 Chromatin Recruitment by RNF168/169 and RAD18. <i>Molecular Cell</i> , 2017, 66, 473-487.e9.	9.7	66
13	PHF20 Readers Link Methylation of Histone H3K4 and p53 with H4K16 Acetylation. <i>Cell Reports</i> , 2016, 17, 1158-1170.	6.4	44
14	Methyllysine Recognition by the Royal Family Modules: Chromo, Tudor, MBT, Chromo Barrel, and PWWP Domains. , 2015, , 49-82.		3
15	Structural Plasticity of Methyllysine Recognition by the Tandem Tudor Domain of 53BP1. <i>Structure</i> , 2015, 23, 312-321.	3.3	32
16	An Acetyl-Methyl Switch Drives a Conformational Change in p53. <i>Structure</i> , 2015, 23, 322-331.	3.3	21
17	Identification of a Fragment-like Small Molecule Ligand for the Methyl-lysine Binding Protein, 53BP1. <i>ACS Chemical Biology</i> , 2015, 10, 1072-1081.	3.4	56
18	<sup>1</sup> H, <sup>15</sup> N and <sup>13</sup> C resonance assignments for the three LOTUS RNA binding domains of Tudor domain-containing protein TDRD7. <i>Biomolecular NMR Assignments</i> , 2013, 7, 79-83.	0.8	4

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19	Acetylation limits 53BP1 association with damaged chromatin to promote homologous recombination. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 317-325.	8.2	440
20	PHF20 is an effector protein of p53 double lysine methylation that stabilizes and activates p53. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 916-924.	8.2	89
21	The Potassium Channel Interacting Protein 3 (DREAM/KChIP3) Heterodimerizes with and Regulates Calmodulin Function. <i>Journal of Biological Chemistry</i> , 2012, 287, 39439-39448.	3.4	14
22	Structural basis for recognition of H3K56-acetylated histone H3â€“H4 by the chaperone Rtt106. <i>Nature</i> , 2012, 483, 104-107.	27.8	99
23	RNF8- and RNF168-dependent degradation of KDM4A/JMJD2A triggers 53BP1 recruitment to DNA damage sites. <i>EMBO Journal</i> , 2012, 31, 1865-1878.	7.8	302
24	Structural Basis of Ubiquitin Recognition by Translesion Synthesis DNA Polymerase Î¹. <i>Biochemistry</i> , 2010, 49, 10198-10207.	2.5	28
25	Structure and Novel Functional Mechanism of Drosophila SNF in Sex-Lethal Splicing. <i>PLoS ONE</i> , 2009, 4, e6890.	2.5	9
26	Preparation of Recombinant Peptides with Site- and Degree-Specific Lysine13C-Methylation. <i>Biochemistry</i> , 2009, 48, 3798-3800.	2.5	14
27	Solution structure and catalytic mechanism of human protein histidine phosphatase 1. <i>Biochemical Journal</i> , 2009, 418, 337-344.	3.7	21
28	Structural Basis for the Recognition of Methylated Histone H3K36 by the Eaf3 Subunit of Histone Deacetylase Complex Rpd3S. <i>Structure</i> , 2008, 16, 1740-1750.	3.3	84
29	Structure of a Second BRCT Domain Identified in the Nijmegen Breakage Syndrome Protein Nbs1 and its Function in an MDC1-Dependent Localization of Nbs1 to DNA Damage Sites. <i>Journal of Molecular Biology</i> , 2008, 381, 361-372.	4.2	29
30	1H, 13C, and 15N resonance assignments of human phosphohistidine phosphatase 1 (PHPT1). <i>Biomolecular NMR Assignments</i> , 2007, 1, 229-231.	0.8	1
31	Identification and Solution Structures of a Single Domain Biotin/Lipoyl Attachment Protein from <i>Bacillus subtilis</i> . <i>Journal of Biological Chemistry</i> , 2006, 281, 20598-20607.	3.4	11