

Georges Mer

List of Publications by Year in descending order

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Version: 2024-02-01

44
papers

4,316
citations

201674

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233421

45
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docs citations

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times ranked

5343
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	Ubiquitin Phosphorylation at Thr12 Modulates the DNA Damage Response. <i>Molecular Cell</i> , 2020, 80, 423-436.e9.	9.7	38
10	Vesicular Stomatitis Virus Encoding a Destabilized Tumor Antigen Improves Activation of Anti-tumor T Cell Responses. <i>Molecular Therapy</i> , 2020, 28, 2540-2552.	8.2	4
11	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
12	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
13	TIRR regulates 53BP1 by masking its histone methyl-lysine binding function. <i>Nature</i> , 2017, 543, 211-216.	27.8	96
14	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
15	Genomic analysis reveals frequent <i>TRAF7</i> mutations in intraneural perineuriomas. <i>Annals of Neurology</i> , 2017, 81, 316-321.	5.3	53
16	A New BRCT Binding Mode in TopBP1-BLM Helicase Interaction. <i>Structure</i> , 2017, 25, 1471-1472.	3.3	2
17	Stabilization of Nucleosomes by Histone Tails and by FACT Revealed by spFRET Microscopy. <i>Cancers</i> , 2017, 9, 3.	3.7	38
18	PHF20 Readers Link Methylation of Histone H3K4 and p53 with H4K16 Acetylation. <i>Cell Reports</i> , 2016, 17, 1158-1170.	6.4	44

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19	Cyclin A2 is an RNA binding protein that controls <i>Mre11</i> mRNA translation. <i>Science</i> , 2016, 353, 1549-1552.	12.6	64
20	Structural Plasticity of Methyllysine Recognition by the Tandem Tudor Domain of 53BP1. <i>Structure</i> , 2015, 23, 312-321.	3.3	32
21	An Acetyl-Methyl Switch Drives a Conformational Change in p53. <i>Structure</i> , 2015, 23, 322-331.	3.3	21
22	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
23	Defects of mutant DNMT1 are linked to a spectrum of neurological disorders. <i>Brain</i> , 2015, 138, 845-861.	7.6	94
24	¹ H, ¹⁵ N and ¹³ 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
25	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
26	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
27	Molecular Basis for the Association of Microcephalin (MCPH1) Protein with the Cell Division Cycle Protein 27 (Cdc27) Subunit of the Anaphase-promoting Complex. <i>Journal of Biological Chemistry</i> , 2012, 287, 2854-2862.	3.4	24
28	Dual recognition of phosphoserine and phosphotyrosine in histone variant H2A.X by DNA damage response protein MCPH1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 14381-14386.	7.1	60
29	Structural basis for recognition of H3K56-acetylated histone H3-H4 by the chaperone Rtt106. <i>Nature</i> , 2012, 483, 104-107.	27.8	99
30	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
31	Structure and Histone Binding Properties of the Vps75-Rtt109 Chaperone-Lysine Acetyltransferase Complex. <i>Journal of Biological Chemistry</i> , 2011, 286, 15625-15629.	3.4	34
32	Molecular Basis for the Association of Human E4B U Box Ubiquitin Ligase with E2-Conjugating Enzymes UbcH5c and Ubc4. <i>Structure</i> , 2010, 18, 955-965.	3.3	45
33	Structural Basis of Ubiquitin Recognition by Translesion Synthesis DNA Polymerase η . <i>Biochemistry</i> , 2010, 49, 10198-10207.	2.5	28
34	Celastrol Inhibits Hsp90 Chaperoning of Steroid Receptors by Inducing Fibrillization of the Co-chaperone p23. <i>Journal of Biological Chemistry</i> , 2010, 285, 4224-4231.	3.4	83
35	Preparation of Recombinant Peptides with Site- and Degree-Specific Lysine ¹³ C-Methylation. <i>Biochemistry</i> , 2009, 48, 3798-3800.	2.5	14
36	Distinct binding modes specify the recognition of methylated histones H3K4 and H4K20 by JMJD2A-tudor. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 109-111.	8.2	183

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37	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
38	Structural Basis for the Methylation State-Specific Recognition of Histone H4-K20 by 53BP1 and Crb2 in DNA Repair. <i>Cell</i> , 2006, 127, 1361-1373.	28.9	883
39	The Tandem BRCT Domain of 53BP1 Is Not Required for Its Repair Function. <i>Journal of Biological Chemistry</i> , 2006, 281, 38472-38477.	3.4	71
40	Structural Basis of BACH1 Phosphopeptide Recognition by BRCA1 Tandem BRCT Domains. <i>Structure</i> , 2004, 12, 1137-1146.	3.3	87
41	The BRCT Domain Is a Phospho-Protein Binding Domain. <i>Science</i> , 2003, 302, 639-642.	12.6	770
42	Solution structure and dynamics of yeast elongin C in complex with a von hippel-lindau peptide 1 Edited by M. F. Summers. <i>Journal of Molecular Biology</i> , 2001, 312, 177-186.	4.2	30
43	Structural Basis for the Recognition of DNA Repair Proteins UNG2, XPA, and RAD52 by Replication Factor RPA. <i>Cell</i> , 2000, 103, 449-456.	28.9	234
44	Structural Dynamics of PMP-D2: An Experimental and Theoretical Study. <i>The Journal of Physical Chemistry</i> , 1996, 100, 2667-2674.	2.9	15