

Chul-Hwan Lee

List of Publications by Year in descending order

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Version: 2024-02-01

26
papers

1,414
citations

516215

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32
all docs

32
docs citations

32
times ranked

1832
citing authors

#	ARTICLE	IF	CITATIONS
1	Capturing the Onset of PRC2-Mediated Repressive Domain Formation. <i>Molecular Cell</i> , 2018, 70, 1149-1162.e5.	4.5	222
2	PRC2 is high maintenance. <i>Genes and Development</i> , 2019, 33, 903-935.	2.7	197
3	Multiple modes of PRC2 inhibition elicit global chromatin alterations in H3K27M pediatric glioma. <i>Science Advances</i> , 2018, 4, eaau5935.	4.7	126
4	H1 histones control the epigenetic landscape by local chromatin compaction. <i>Nature</i> , 2021, 589, 293-298.	13.7	101
5	Allosteric Activation Dictates PRC2 Activity Independent of Its Recruitment to Chromatin. <i>Molecular Cell</i> , 2018, 70, 422-434.e6.	4.5	100
6	Distinct Stimulatory Mechanisms Regulate the Catalytic Activity of Polycomb Repressive Complex 2. <i>Molecular Cell</i> , 2018, 70, 435-448.e5.	4.5	90
7	Automethylation of PRC2 promotes H3K27 methylation and is impaired in H3K27M pediatric glioma. <i>Genes and Development</i> , 2019, 33, 1428-1440.	2.7	75
8	Dna2 on the road to Okazaki fragment processing and genome stability in eukaryotes. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2010, 45, 71-96.	2.3	71
9	LEDGF and HDGF2 relieve the nucleosome-induced barrier to transcription in differentiated cells. <i>Science Advances</i> , 2019, 5, eaay3068.	4.7	61
10	Structures of monomeric and dimeric PRC2:EZH1 reveal flexible modules involved in chromatin compaction. <i>Nature Communications</i> , 2021, 12, 714.	5.8	54
11	Chromatin Remodelers Fine-Tune H3K36me-Directed Deacetylation of Neighbor Nucleosomes by Rpd3S. <i>Molecular Cell</i> , 2013, 52, 255-263.	4.5	52
12	Multivalent di-nucleosome recognition enables the Rpd3S histone deacetylase complex to tolerate decreased H3K36 methylation levels. <i>EMBO Journal</i> , 2012, 31, 3564-3574.	3.5	49
13	Nucleosome Contact Triggers Conformational Changes of Rpd3S Driving High-Affinity H3K36me Nucleosome Engagement. <i>Cell Reports</i> , 2015, 10, 204-215.	2.9	46
14	The MPH1 Gene of <i>Saccharomyces cerevisiae</i> Functions in Okazaki Fragment Processing. <i>Journal of Biological Chemistry</i> , 2009, 284, 10376-10386.	1.6	25
15	Genetic and functional interactions between Mus81-Mms4 and Rad27. <i>Nucleic Acids Research</i> , 2010, 38, 7611-7625.	6.5	23
16	Homodimeric PHD Domain-containing Rco1 Subunit Constitutes a Critical Interaction Hub within the Rpd3S Histone Deacetylase Complex. <i>Journal of Biological Chemistry</i> , 2016, 291, 5428-5438.	1.6	20
17	Rad52/Rad59-dependent Recombination as a Means to Rectify Faulty Okazaki Fragment Processing. <i>Journal of Biological Chemistry</i> , 2014, 289, 15064-15079.	1.6	18
18	Human Replication Factor C Stimulates Flap Endonuclease 1. <i>Journal of Biological Chemistry</i> , 2009, 284, 10387-10399.	1.6	15

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19	The N-terminal 45-kDa Domain of Dna2 Endonuclease/Helicase Targets the Enzyme to Secondary Structure DNA. <i>Journal of Biological Chemistry</i> , 2013, 288, 9468-9481.	1.6	14
20	Involvement of Vts1, a structure-specific RNA-binding protein, in Okazaki fragment processing in yeast. <i>Nucleic Acids Research</i> , 2010, 38, 1583-1595.	6.5	10
21	The Trans-autostimulatory Activity of Rad27 Suppresses dna2 Defects in Okazaki Fragment Processing. <i>Journal of Biological Chemistry</i> , 2012, 287, 8675-8687.	1.6	8
22	Biochemical studies of the <i>Saccharomyces cerevisiae</i> Mph1 helicase on junction-containing DNA structures. <i>Nucleic Acids Research</i> , 2012, 40, 2089-2106.	6.5	7
23	Analysis of subunit assembly and function of the <i>Saccharomyces cerevisiae</i> RNase H2 complex. <i>FEBS Journal</i> , 2011, 278, 4927-4942.	2.2	6
24	GSK-3 β Homolog Rim11 and the Histone Deacetylase Complex Ume6-Sin3-Rpd3 Are Involved in Replication Stress Response Caused by Defects in Dna2. <i>Genetics</i> , 2017, 206, 829-842.	1.2	4
25	Physical and functional interactions between nucleosomes and Rad27, a critical component of <sc>DNA</sc> processing during <sc>DNA</sc> metabolism. <i>FEBS Journal</i> , 2016, 283, 4247-4262.	2.2	3
26	Lagging Strand Synthesis and Genomic Stability. , 0, , .		0