

Gary LeRoy

List of Publications by Year in descending order

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Version: 2024-02-01

23
papers

2,913
citations

394421
19
h-index

642732
23
g-index

26
all docs

26
docs citations

26
times ranked

4570
citing authors

#	ARTICLE	IF	CITATIONS
1	CRISPR and biochemical screens identify MAZ as a cofactor in CTCF-mediated insulation at Hox clusters. <i>Nature Genetics</i> , 2022, 54, 202-212.	21.4	37
2	RNA-Mediated Feedback Control of Transcriptional Condensates. <i>Cell</i> , 2021, 184, 207-225.e24.	28.9	324
3	An Esrrb and Nanog Cell Fate Regulatory Module Controlled by Feed Forward Loop Interactions. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 630067.	3.7	8
4	The H3K36me2 writer-reader dependency in H3K27M-DIPG. <i>Science Advances</i> , 2021, 7, .	10.3	20
5	MeCP2 links heterochromatin condensates and neurodevelopmental disease. <i>Nature</i> , 2020, 586, 440-444.	27.8	112
6	Automethylation of PRC2 promotes H3K27 methylation and is impaired in H3K27M pediatric glioma. <i>Genes and Development</i> , 2019, 33, 1428-1440.	5.9	75
7	LEDGF and HDGF2 relieve the nucleosome-induced barrier to transcription in differentiated cells. <i>Science Advances</i> , 2019, 5, eaay3068.	10.3	61
8	Distinct Stimulatory Mechanisms Regulate the Catalytic Activity of Polycomb Repressive Complex 2. <i>Molecular Cell</i> , 2018, 70, 435-448.e5.	9.7	90
9	Allosteric Activation Dictates PRC2 Activity Independent of Its Recruitment to Chromatin. <i>Molecular Cell</i> , 2018, 70, 422-434.e6.	9.7	100
10	Multiple modes of PRC2 inhibition elicit global chromatin alterations in H3K27M pediatric glioma. <i>Science Advances</i> , 2018, 4, eaau5935.	10.3	126
11	Capturing the Onset of PRC2-Mediated Repressive Domain Formation. <i>Molecular Cell</i> , 2018, 70, 1149-1162.e5.	9.7	222
12	Low-Grade Astrocytoma Mutations in IDH1, P53, and ATRX Cooperate to Block Differentiation of Human Neural Stem Cells via Repression of SOX2. <i>Cell Reports</i> , 2017, 21, 1267-1280.	6.4	95
13	Identification of Nidogen 1 as a lung metastasis protein through secretome analysis. <i>Genes and Development</i> , 2017, 31, 1439-1455.	5.9	41
14	Chromatin Starts to Come Clean. <i>Molecular Cell</i> , 2016, 64, 439-441.	9.7	2
15	Proteogenomics analysis reveals specific genomic orientations of distal regulatory regions composed by non-canonical histone variants. <i>Epigenetics and Chromatin</i> , 2015, 8, 13.	3.9	10
16	BRD4 assists elongation of both coding and enhancer RNAs by interacting with acetylated histones. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 1047-1057.	8.2	247
17	Chromatin proteins captured by ChIPâ€‘mass spectrometry are linked to dosage compensation in <i>Drosophila</i> . <i>Nature Structural and Molecular Biology</i> , 2013, 20, 202-209.	8.2	100
18	Proteogenomic characterization and mapping of nucleosomes decoded by Brd and HP1 proteins. <i>Genome Biology</i> , 2012, 13, R68.	9.6	81

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19	Heterochromatin Protein 1 Is Extensively Decorated with Histone Code-like Post-translational Modifications. Molecular and Cellular Proteomics, 2009, 8, 2432-2442.	3.8	88
20	The Double Bromodomain Proteins Brd2 and Brd3 Couple Histone Acetylation to Transcription. Molecular Cell, 2008, 30, 51-60.	9.7	321
21	Nucleolin Is Required for RNA Polymerase I Transcription In Vivo. Molecular and Cellular Biology, 2007, 27, 937-948.	2.3	109
22	Identification of RecQL1 as a Holliday junction processing enzyme in human cell lines. Nucleic Acids Research, 2005, 33, 6251-6257.	14.5	52
23	FACT, a Factor that Facilitates Transcript Elongation through Nucleosomes. Cell, 1998, 92, 105-116.	28.9	587