

Krzysztof Ginalski

List of Publications by Year in descending order

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Version: 2024-02-01

39
papers

2,337
citations

331259

21
h-index

288905

40
g-index

44
all docs

44
docs citations

44
times ranked

4068
citing authors

#	ARTICLE	IF	CITATIONS
1	A Role for the Mre11-Rad50-Xrs2 Complex in Gene Expression and Chromosome Organization. <i>Molecular Cell</i> , 2021, 81, 183-197.e6.	4.5	15
2	High-resolution, ultrasensitive and quantitative DNA double-strand break labeling in eukaryotic cells using i-BLESS. <i>Nature Protocols</i> , 2021, 16, 1034-1061.	5.5	3
3	Recombinant immunotoxin targeting GPC3 is cytotoxic to H466 small cell lung cancer cells. <i>Oncology Letters</i> , 2021, 21, 222.	0.8	4
4	MRX Increases Chromatin Accessibility at Stalled Replication Forks to Promote Nascent DNA Resection and Cohesin Loading. <i>Molecular Cell</i> , 2020, 77, 395-410.e3.	4.5	49
5	Topoisomerase 1 prevents replication stress at R-loop-enriched transcription termination sites. <i>Nature Communications</i> , 2020, 11, 3940.	5.8	105
6	Mec1 Is Activated at the Onset of Normal S Phase by Low-dNTP Pools Impeding DNA Replication. <i>Molecular Cell</i> , 2020, 78, 396-410.e4.	4.5	48
7	Poly-Saturated Dolichols from Filamentous Fungi Modulate Activity of Dolichol-Dependent Glycosyltransferase and Physical Properties of Membranes. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3043.	1.8	8
8	qDSB-Seq is a general method for genome-wide quantification of DNA double-strand breaks using sequencing. <i>Nature Communications</i> , 2019, 10, 2313.	5.8	40
9	Transposable elements contribute to fungal genes and impact fungal lifestyle. <i>Scientific Reports</i> , 2019, 9, 4307.	1.6	59
10	Overactive BRCA1 Affects Presenilin 1 in Induced Pluripotent Stem Cell-Derived Neurons in Alzheimer's Disease. <i>Journal of Alzheimer's Disease</i> , 2018, 62, 175-202.	1.2	36
11	Structural, Biochemical, and Evolutionary Characterizations of Glyoxylate/Hydroxypyruvate Reductases Show Their Division into Two Distinct Subfamilies. <i>Biochemistry</i> , 2018, 57, 963-977.	1.2	12
12	Predicting double-strand DNA breaks using epigenome marks or DNA at kilobase resolution. <i>Genome Biology</i> , 2018, 19, 34.	3.8	26
13	Classification, substrate specificity and structural features of D-2-hydroxyacid dehydrogenases: 2HADH knowledgebase. <i>BMC Evolutionary Biology</i> , 2018, 18, 199.	3.2	21
14	Predicting proteome dynamics using gene expression data. <i>Scientific Reports</i> , 2018, 8, 13866.	1.6	19
15	Comprehensive Mapping of Histone Modifications at DNA Double-Strand Breaks Deciphers Repair Pathway Chromatin Signatures. <i>Molecular Cell</i> , 2018, 72, 250-262.e6.	4.5	232
16	Exome scale map of genetic alterations promoting metastasis in colorectal cancer. <i>BMC Genetics</i> , 2018, 19, 85.	2.7	22
17	i-BLESS is an ultra-sensitive method for detection of DNA double-strand breaks. <i>Communications Biology</i> , 2018, 1, 181.	2.0	37
18	Hypermethylation of TRIM59 and KLF14 Influences Cell Death Signaling in Familial Alzheimer's Disease. <i>Oxidative Medicine and Cellular Longevity</i> , 2018, 2018, 1-11.	1.9	23

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19	Comparative genomic analysis of <i>Staphylococcus lugdunensis</i> shows a closed pan-genome and multiple barriers to horizontal gene transfer. <i>BMC Genomics</i> , 2018, 19, 621.	1.2	42
20	Ssb1 and Ssb2 cooperate to regulate mouse hematopoietic stem and progenitor cells by resolving replicative stress. <i>Blood</i> , 2017, 129, 2479-2492.	0.6	18
21	Genome-wide mapping of long-range contacts unveils clustering of DNA double-strand breaks at damaged active genes. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 353-361.	3.6	221
22	Comprehensive classification of the PIN domain-like superfamily. <i>Nucleic Acids Research</i> , 2017, 45, 6995-7020.	6.5	78
23	Phylogeny-Based Systematization of Arabidopsis Proteins with Histone H1 Globular Domain. <i>Plant Physiology</i> , 2017, 174, 27-34.	2.3	28
24	Biochemical and structural bioinformatics studies of fungal CutA nucleotidyltransferases explain their unusual specificity toward CTP and increased tendency for cytidine incorporation at the 3'-terminal positions of synthesized tails. <i>Rna</i> , 2017, 23, 1902-1926.	1.6	7
25	Systematic classification of the His-Me finger superfamily. <i>Nucleic Acids Research</i> , 2017, 45, 11479-11494.	6.5	22
26	Fungal lifestyle reflected in serine protease repertoire. <i>Scientific Reports</i> , 2017, 7, 9147.	1.6	120
27	A heterozygous mutation in GOT1 is associated with familial macro-aspartate aminotransferase. <i>Journal of Hepatology</i> , 2017, 67, 1026-1030.	1.8	18
28	Dbf4 recruitment by forkhead transcription factors defines an upstream rate-limiting step in determining origin firing timing. <i>Genes and Development</i> , 2017, 31, 2405-2415.	2.7	53
29	Cut-and-Paste Transposons in Fungi with Diverse Lifestyles. <i>Genome Biology and Evolution</i> , 2017, 9, 3463-3477.	1.1	77
30	Towards Engineering Novel PE-Based Immunotoxins by Targeting Them to the Nucleus. <i>Toxins</i> , 2016, 8, 321.	1.5	12
31	Diverse cap-binding properties of <i>Drosophila</i> eIF4E isoforms. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2016, 1864, 1292-1303.	1.1	4
32	FAM46 proteins are novel eukaryotic non-canonical poly(A) polymerases. <i>Nucleic Acids Research</i> , 2016, 44, 3534-3548.	6.5	60
33	Unfolding the mechanism of the AAA+ unfoldase VAT by a combined cryo-EM, solution NMR study. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E4190-9.	3.3	55
34	Histone H1 Variants in Arabidopsis Are Subject to Numerous Post-Translational Modifications, Both Conserved and Previously Unknown in Histones, Suggesting Complex Functions of H1 in Plants. <i>PLoS ONE</i> , 2016, 11, e0147908.	1.1	36
35	Strategies for Achieving High Sequencing Accuracy for Low Diversity Samples and Avoiding Sample Bleeding Using Illumina Platform. <i>PLoS ONE</i> , 2015, 10, e0120520.	1.1	98
36	A specialized histone H1 variant is required for adaptive responses to complex abiotic stress and related DNA methylation in Arabidopsis. <i>Plant Physiology</i> , 2015, 169, pp.00493.2015.	2.3	101

#	ARTICLE	IF	CITATIONS
37	Probabilistic Approach to Predicting Substrate Specificity of Methyltransferases. PLoS Computational Biology, 2014, 10, e1003514.	1.5	19
38	The Histone Deacetylases Sir2 and Rpd3 Act on Ribosomal DNA to Control the Replication Program in Budding Yeast. Molecular Cell, 2014, 54, 691-697.	4.5	95
39	Nucleotide-resolution DNA double-strand break mapping by next-generation sequencing. Nature Methods, 2013, 10, 361-365.	9.0	409