## Krzysztof Ginalski

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/1215309/publications.pdf

Version: 2024-02-01

39 papers 2,337 citations

331259 21 h-index 288905 40 g-index

44 all docs

44 docs citations

times ranked

44

4068 citing authors

| #  | Article  | IF  | CITATIONS |
|----|--|-----|-----------|
| 1  | Nucleotide-resolution DNA double-strand break mapping by next-generation sequencing. Nature Methods, 2013, 10, 361-365.  | 9.0 | 409       |
| 2  | Comprehensive Mapping of Histone Modifications at DNA Double-Strand Breaks Deciphers Repair Pathway Chromatin Signatures. Molecular Cell, 2018, 72, 250-262.e6.                                      | 4.5 | 232       |
| 3  | Genome-wide mapping of long-range contacts unveils clustering of DNA double-strand breaks at damaged active genes. Nature Structural and Molecular Biology, 2017, 24, 353-361.                       | 3.6 | 221       |
| 4  | Fungal lifestyle reflected in serine protease repertoire. Scientific Reports, 2017, 7, 9147.   | 1.6 | 120       |
| 5  | Topoisomerase 1 prevents replication stress at R-loop-enriched transcription termination sites. Nature Communications, 2020, 11, 3940.   | 5.8 | 105       |
| 6  | A specialized histone H1 variant is required for adaptive responses to complex abiotic stress and related DNA methylation in Arabidopsis. Plant Physiology, 2015, 169, pp.00493.2015.                | 2.3 | 101       |
| 7  | Strategies for Achieving High Sequencing Accuracy for Low Diversity Samples and Avoiding Sample Bleeding Using Illumina Platform. PLoS ONE, 2015, 10, e0120520.                                      | 1.1 | 98        |
| 8  | 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        |
| 9  | Comprehensive classification of the PIN domain-like superfamily. Nucleic Acids Research, 2017, 45, 6995-7020.  | 6.5 | 78        |
| 10 | Cut-and-Paste Transposons in Fungi with Diverse Lifestyles. Genome Biology and Evolution, 2017, 9, 3463-3477.  | 1.1 | 77        |
| 11 | FAM46 proteins are novel eukaryotic non-canonical poly(A) polymerases. Nucleic Acids Research, 2016, 44, 3534-3548.  | 6.5 | 60        |
| 12 | Transposable elements contribute to fungal genes and impact fungal lifestyle. Scientific Reports, 2019, 9, 4307.   | 1.6 | 59        |
| 13 | Unfolding the mechanism of the AAA+ unfoldase VAT by a combined cryo-EM, solution NMR study.<br>Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E4190-9. | 3.3 | 55        |
| 14 | Dbf4 recruitment by forkhead transcription factors defines an upstream rate-limiting step in determining origin firing timing. Genes and Development, 2017, 31, 2405-2415.                           | 2.7 | 53        |
| 15 | MRX Increases Chromatin Accessibility at Stalled Replication Forks to Promote Nascent DNA Resection and Cohesin Loading. Molecular Cell, 2020, 77, 395-410.e3.                                       | 4.5 | 49        |
| 16 | Mec1 Is Activated at the Onset of Normal S Phase by Low-dNTP Pools Impeding DNA Replication. Molecular Cell, 2020, 78, 396-410.e4.   | 4.5 | 48        |
| 17 | Comparative genomic analysis of Staphylococcus lugdunensis shows a closed pan-genome and multiple barriers to horizontal gene transfer. BMC Genomics, 2018, 19, 621.                                 | 1.2 | 42        |
| 18 | qDSB-Seq is a general method for genome-wide quantification of DNA double-strand breaks using sequencing. Nature Communications, 2019, 10, 2313.   | 5.8 | 40        |

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|----|--|-----|-----------|
| 19 | i-BLESS is an ultra-sensitive method for detection of DNA double-strand breaks. Communications Biology, 2018, 1, 181.  | 2.0 | 37        |
| 20 | Overactive BRCA1 Affects Presenilin 1 in Induced Pluripotent Stem Cell-Derived Neurons in Alzheimer's Disease. Journal of Alzheimer's Disease, 2018, 62, 175-202.  | 1.2 | 36        |
| 21 | 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. PLoS ONE, 2016, 11, e0147908.  | 1.1 | 36        |
| 22 | Phylogeny-Based Systematization of Arabidopsis Proteins with Histone H1 Globular Domain. Plant Physiology, 2017, 174, 27-34.   | 2.3 | 28        |
| 23 | Predicting double-strand DNA breaks using epigenome marks or DNA at kilobase resolution. Genome<br>Biology, 2018, 19, 34.  | 3.8 | 26        |
| 24 | Hypermethylation of TRIM59 and KLF14 Influences Cell Death Signaling in Familial Alzheimer's Disease.<br>Oxidative Medicine and Cellular Longevity, 2018, 2018, 1-11.  | 1.9 | 23        |
| 25 | Systematic classification of the His-Me finger superfamily. Nucleic Acids Research, 2017, 45, 11479-11494.   | 6.5 | 22        |
| 26 | Exome scale map of genetic alterations promoting metastasis in colorectal cancer. BMC Genetics, 2018, 19, 85.  | 2.7 | 22        |
| 27 | Classification, substrate specificity and structural features of D-2-hydroxyacid dehydrogenases: 2HADH knowledgebase. BMC Evolutionary Biology, 2018, 18, 199.   | 3.2 | 21        |
| 28 | Probabilistic Approach to Predicting Substrate Specificity of Methyltransferases. PLoS Computational Biology, 2014, 10, e1003514.  | 1.5 | 19        |
| 29 | Predicting proteome dynamics using gene expression data. Scientific Reports, 2018, 8, 13866.   | 1.6 | 19        |
| 30 | Ssb1 and Ssb2 cooperate to regulate mouse hematopoietic stem and progenitor cells by resolving replicative stress. Blood, 2017, 129, 2479-2492.  | 0.6 | 18        |
| 31 | A heterozygous mutation in GOT1 is associated with familial macro-aspartate aminotransferase. Journal of Hepatology, 2017, 67, 1026-1030.  | 1.8 | 18        |
| 32 | A Role for the Mre11-Rad50-Xrs2 Complex in Gene Expression and Chromosome Organization. Molecular Cell, 2021, 81, 183-197.e6.  | 4.5 | 15        |
| 33 | Towards Engineering Novel PE-Based Immunotoxins by Targeting Them to the Nucleus. Toxins, 2016, 8, 321.  | 1.5 | 12        |
| 34 | Structural, Biochemical, and Evolutionary Characterizations of Glyoxylate/Hydroxypyruvate Reductases Show Their Division into Two Distinct Subfamilies. Biochemistry, 2018, 57, 963-977.   | 1.2 | 12        |
| 35 | Poly-Saturated Dolichols from Filamentous Fungi Modulate Activity of Dolichol-Dependent Glycosyltransferase and Physical Properties of Membranes. International Journal of Molecular Sciences, 2019, 20, 3043.   | 1.8 | 8         |
| 36 | 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. Rna, 2017, 23, 1902-1926. | 1.6 | 7         |

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|----|---|-----|-----------|
| 37 | Diverse cap-binding properties of Drosophila elF4E isoforms. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2016, 1864, 1292-1303.                | 1.1 | 4         |
| 38 | Recombinant immunotoxin targeting GPC3 is cytotoxic to H466 small cell lung cancer cells. Oncology Letters, 2021, 21, 222.                                  | 0.8 | 4         |
| 39 | High-resolution, ultrasensitive and quantitative DNA double-strand break labeling in eukaryotic cells using i-BLESS. Nature Protocols, 2021, 16, 1034-1061. | 5.5 | 3         |