

Romain Koszul

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3873256/publications.pdf>

Version: 2024-02-01

68
papers

6,339
citations

147726

31
h-index

106281

65
g-index

91
all docs

91
docs citations

91
times ranked

7221
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome evolution in yeasts. <i>Nature</i> , 2004, 430, 35-44.	13.7	1,498
2	Total Synthesis of a Functional Designer Eukaryotic Chromosome. <i>Science</i> , 2014, 344, 55-58.	6.0	486
3	Genomic evidence for ameiotic evolution in the bdelloid rotifer <i>Adineta vaga</i> . <i>Nature</i> , 2013, 500, 453-457.	13.7	352
4	Multiscale Structuring of the <i>E. coli</i> Chromosome by Nucleoid-Associated and Condensin Proteins. <i>Cell</i> , 2018, 172, 771-783.e18.	13.5	285
5	Condensin- and Replication-Mediated Bacterial Chromosome Folding and Origin Condensation Revealed by Hi-C and Super-resolution Imaging. <i>Molecular Cell</i> , 2015, 59, 588-602.	4.5	245
6	Eucaryotic genome evolution through the spontaneous duplication of large chromosomal segments. <i>EMBO Journal</i> , 2004, 23, 234-243.	3.5	192
7	Normalization of a chromosomal contact map. <i>BMC Genomics</i> , 2012, 13, 436.	1.2	190
8	Deep functional analysis of synII, a 770-kilobase synthetic yeast chromosome. <i>Science</i> , 2017, 355, .	6.0	163
9	Segmental Duplications Arise from Pol32-Dependent Repair of Broken Forks through Two Alternative Replication-Based Mechanisms. <i>PLoS Genetics</i> , 2008, 4, e1000175.	1.5	161
10	Dynamic chromosome movements during meiosis: a way to eliminate unwanted connections?. <i>Trends in Cell Biology</i> , 2009, 19, 716-724.	3.6	158
11	Metagenomic chromosome conformation capture (meta3C) unveils the diversity of chromosome organization in microorganisms. <i>ELife</i> , 2014, 3, e03318.	2.8	154
12	A Predictive Computational Model of the Dynamic 3D Interphase Yeast Nucleus. <i>Current Biology</i> , 2012, 22, 1881-1890.	1.8	149
13	High-quality genome (re)assembly using chromosomal contact data. <i>Nature Communications</i> , 2014, 5, 5695.	5.8	142
14	Cohesins and condensins orchestrate the 4D dynamics of yeast chromosomes during the cell cycle. <i>EMBO Journal</i> , 2017, 36, 2684-2697.	3.5	137
15	A checkpoint control orchestrates the replication of the two chromosomes of <i>Vibrio cholerae</i> . <i>Science Advances</i> , 2016, 2, e1501914.	4.7	122
16	Csm4, in Collaboration with Ndj1, Mediates Telomere-Led Chromosome Dynamics and Recombination during Yeast Meiosis. <i>PLoS Genetics</i> , 2008, 4, e1000188.	1.5	117
17	3D organization of synthetic and scrambled chromosomes. <i>Science</i> , 2017, 355, .	6.0	116
18	Scaffolding bacterial genomes and probing host-virus interactions in gut microbiome by proximity ligation (chromosome capture) assay. <i>Science Advances</i> , 2017, 3, e1602105.	4.7	110

#	ARTICLE	IF	CITATIONS
19	The 3D folding of metazoan genomes correlates with the association of similar repetitive elements. <i>Nucleic Acids Research</i> , 2016, 44, 245-255.	6.5	90
20	Dynamic Processing of Displacement Loops during Recombinational DNA Repair. <i>Molecular Cell</i> , 2019, 73, 1255-1266.e4.	4.5	84
21	Regulation of Cohesin-Mediated Chromosome Folding by Eco1 and Other Partners. <i>Molecular Cell</i> , 2020, 77, 1279-1293.e4.	4.5	80
22	Spatial reorganization of telomeres in long-lived quiescent cells. <i>Genome Biology</i> , 2015, 16, 206.	3.8	75
23	Evidence for actin dual role in regulating chromosome organization and dynamics in yeast. <i>Journal of Cell Science</i> , 2016, 129, 681-92.	1.2	73
24	The complete mitochondrial genome sequence of the pathogenic yeast <i>Candida (Torulopsis) glabrata</i> . <i>FEBS Letters</i> , 2003, 534, 39-48.	1.3	68
25	Computer vision for pattern detection in chromosome contact maps. <i>Nature Communications</i> , 2020, 11, 5795.	5.8	64
26	Chromosome organization by a conserved condensin-ParB system in the actinobacterium <i>Corynebacterium glutamicum</i> . <i>Nature Communications</i> , 2020, 11, 1485.	5.8	64
27	Characterizing meiotic chromosomes' structure and pairing using a designer sequence optimized for Hi-C. <i>Molecular Systems Biology</i> , 2018, 14, e8293.	3.2	63
28	MetaHiC phage-bacteria infection network reveals active cycling phages of the healthy human gut. <i>ELife</i> , 2021, 10, .	2.8	57
29	Tridimensional infiltration of DNA viruses into the host genome shows preferential contact with active chromatin. <i>Nature Communications</i> , 2018, 9, 4268.	5.8	51
30	Stability of Large Segmental Duplications in the Yeast Genome. <i>Genetics</i> , 2006, 172, 2211-2222.	1.2	50
31	FACT mediates cohesin function on chromatin. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 970-979.	3.6	43
32	Cohesin regulates homology search during recombinational DNA repair. <i>Nature Cell Biology</i> , 2021, 23, 1176-1186.	4.6	43
33	Euryarchaeal genomes are folded into SMC-dependent loops and domains, but lack transcription-mediated compartmentalization. <i>Molecular Cell</i> , 2021, 81, 459-472.e10.	4.5	42
34	Contact genomics: scaffolding and phasing (meta)genomes using chromosome 3D physical signatures. <i>FEBS Letters</i> , 2015, 589, 2966-2974.	1.3	41
35	instaGRAAL: chromosome-level quality scaffolding of genomes using a proximity ligation-based scaffold. <i>Genome Biology</i> , 2020, 21, 148.	3.8	38
36	Filling annotation gaps in yeast genomes using genome-wide contact maps. <i>Bioinformatics</i> , 2014, 30, 2105-2113.	1.8	36

#	ARTICLE	IF	CITATIONS
37	A prominent role for segmental duplications in modeling Eukaryotic genomes. <i>Comptes Rendus - Biologies</i> , 2009, 332, 254-266.	0.1	31
38	Proximity ligation scaffolding and comparison of two <i>Trichoderma reesei</i> strains genomes. <i>Biotechnology for Biofuels</i> , 2017, 10, 151.	6.2	31
39	Smc3 acetylation, Pds5 and Scc2 control the translocase activity that establishes cohesin-dependent chromatin loops. <i>Nature Structural and Molecular Biology</i> , 2022, 29, 575-585.	3.6	31
40	Chromosome-level genome assembly reveals homologous chromosomes and recombination in asexual rotifer <i>Adineta vaga</i> . <i>Science Advances</i> , 2021, 7, eabg4216.	4.7	30
41	Chromosomal scale assembly of parasitic wasp genome reveals symbiotic virus colonization. <i>Communications Biology</i> , 2021, 4, 104.	2.0	27
42	Condensin-Mediated Chromosome Folding and Internal Telomeres Drive Dicentric Severing by Cytokinesis. <i>Molecular Cell</i> , 2019, 75, 131-144.e3.	4.5	24
43	Metagenome Analysis Exploiting High-Throughput Chromosome Conformation Capture (3C) Data. <i>Trends in Genetics</i> , 2015, 31, 673-682.	2.9	22
44	MetaTOR: A Computational Pipeline to Recover High-Quality Metagenomic Bins From Mammalian Gut Proximity-Ligation (meta3C) Libraries. <i>Frontiers in Genetics</i> , 2019, 10, 753.	1.1	22
45	Serpentine: a flexible 2D binning method for differential Hi-C analysis. <i>Bioinformatics</i> , 2020, 36, 3645-3651.	1.8	19
46	Purification of G ₁ daughter cells from different <i>Saccharomycetes</i> species through an optimized centrifugal elutriation procedure. <i>Yeast</i> , 2014, 31, 159-166.	0.8	18
47	Extended sister-chromosome catenation leads to massive reorganization of the <i>E. coli</i> genome. <i>Nucleic Acids Research</i> , 2022, 50, 2635-2650.	6.5	18
48	Genome-wide replication landscape of <i>Candida glabrata</i> . <i>BMC Biology</i> , 2015, 13, 69.	1.7	16
49	Sir3 mediates long-range chromosome interactions in budding yeast. <i>Genome Research</i> , 2021, 31, 411-425.	2.4	16
50	Generation and Analysis of Chromosomal Contact Maps of Yeast Species. <i>Methods in Molecular Biology</i> , 2016, 1361, 227-245.	0.4	16
51	A Proximity Ligation-Based Method for Quantitative Measurement of D-Loop Extension in <i>S. cerevisiae</i> . <i>Methods in Enzymology</i> , 2018, 601, 27-44.	0.4	15
52	The Centenary of Janssens's Chiasmotype Theory. <i>Genetics</i> , 2012, 191, 309-317.	1.2	14
53	Kinetic Signature of Cooperativity in the Irreversible Collapse of a Polymer. <i>Physical Review Letters</i> , 2018, 121, 057801.	2.9	14
54	La Theorie de la Chiasmotypie. <i>Genetics</i> , 2012, 191, 319-346.	1.2	10

#	ARTICLE	IF	CITATIONS
55	Generation of a Metagenomics Proximity Ligation 3C Library of a Mammalian Gut Microbiota. <i>Methods in Enzymology</i> , 2018, 612, 183-195.	0.4	7
56	Generation of gene-level resolution chromosome contact maps in bacteria and archaea. <i>STAR Protocols</i> , 2021, 2, 100512.	0.5	7
57	Normalization of Chromosome Contact Maps: Matrix Balancing and Visualization. <i>Methods in Molecular Biology</i> , 2022, 2301, 1-15.	0.4	6
58	Real-Time Imaging of Meiotic Chromosomes in <i>Saccharomyces cerevisiae</i> . <i>Methods in Molecular Biology</i> , 2009, 558, 81-89.	0.4	6
59	Crosstalk between Hepatitis B Virus and the 3D Genome Structure. <i>Viruses</i> , 2022, 14, 445.	1.5	6
60	Beyond the bounds of evolution: Synthetic chromosomes – How and what for?. <i>Comptes Rendus - Biologies</i> , 2016, 339, 324-328.	0.1	5
61	Chromosome-level genome assembly and annotation of two lineages of the ant <i>Cataglyphis hispanica</i> : stepping stones towards genomic studies of hybridogenesis and thermal adaptation in desert ants. , 0, 2, .		5
62	Filling the gap: Micro-C accesses the nucleosomal fiber at 100–1000 bp resolution. <i>Genome Biology</i> , 2015, 16, 169.	3.8	4
63	Closed and High-Quality Bacterial Genome Sequences of the Oligo-Mouse-Microbiota Community. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	4
64	A deep dive into genome assemblies of non-vertebrate animals. , 0, 2, .		4
65	Generation and Analysis of Chromosomal Contact Maps of Bacteria. <i>Methods in Molecular Biology</i> , 2017, 1624, 75-84.	0.4	3
66	Metagenomes Binning Using Proximity-Ligation Data. <i>Methods in Molecular Biology</i> , 2022, 2301, 163-181.	0.4	3
67	Functional Partition of a Bacterial Chromosome Through the Interplay of Nucleoid Associated Proteins and Condensin. <i>SSRN Electronic Journal</i> , 0, , .	0.4	1
68	Perspectives on Chromosome Organization. <i>Journal of Molecular Biology</i> , 2020, 432, 635-637.	2.0	0