

# Ryuichiro Nakato

## List of Publications by Year in descending order

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Version: 2024-02-01

53  
papers

3,586  
citations

201575

27  
h-index

182361

51  
g-index

63  
all docs

63  
docs citations

63  
times ranked

6336  
citing authors

#	ARTICLE	IF	CITATIONS
1	Highly rigid H3.1/H3.2â€“H3K9me3 domains set a barrier for cell fate reprogramming in trophoblast stem cells. <i>Genes and Development</i> , 2022, 36, 84-102.	2.7	10
2	PHOSPHATE exporter XPR1/SLC53A1 is required for the tumorigenicity of epithelial ovarian cancer. <i>Cancer Science</i> , 2022, 113, 2034-2043.	1.7	7
3	CRISPR/Cas9 Screening for Identification of Genes Required for the Growth of Ovarian Clear Cell Carcinoma Cells. <i>Current Issues in Molecular Biology</i> , 2022, 44, 1587-1596.	1.0	0
4	Cohesin-dependent chromosome loop extrusion is limited by transcription and stalled replication forks. <i>Science Advances</i> , 2022, 8, .	4.7	28
5	Large-scale multi-omics analysis suggests specific roles for intragenic cohesin in transcriptional regulation. <i>Nature Communications</i> , 2022, 13, .	5.8	7
6	Methods for CHIP-seq analysis: A practical workflow and advanced applications. <i>Methods</i> , 2021, 187, 44-53.	1.9	114
7	Codependency and mutual exclusivity for gene community detection from sparse single-cell transcriptome data. <i>Nucleic Acids Research</i> , 2021, 49, e104-e104.	6.5	3
8	OUP accepted manuscript. <i>Briefings in Bioinformatics</i> , 2021, , .	3.2	8
9	The splicing factor DHX38/PRP16 is required for ovarian clear cell carcinoma tumorigenesis, as revealed by a CRISPRâ€“Cas9 screen. <i>FEBS Open Bio</i> , 2021, , .	1.0	3
10	Phi-C: deciphering Hi-C data into polymer dynamics. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa020.	1.5	33
11	Toward understanding the dynamic state of 3D genome. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 2259-2269.	1.9	6
12	Paternal restraint stress affects offspring metabolism via ATF-2 dependent mechanisms in <i>Drosophila melanogaster</i> germ cells. <i>Communications Biology</i> , 2020, 3, 208.	2.0	16
13	Tet2 and Tet3 in B cells are required to repress CD86 and prevent autoimmunity. <i>Nature Immunology</i> , 2020, 21, 950-961.	7.0	55
14	Missense Mutations in NKAP Cause a Disorder of Transcriptional Regulation Characterized by Marfanoid Habitus and Cognitive Impairment. <i>American Journal of Human Genetics</i> , 2019, 105, 987-995.	2.6	11
15	Cux2 refines the forelimb field by controlling expression of <i>Raldh2</i> and <i>Hox</i> genes. <i>Biology Open</i> , 2019, 8, .	0.6	6
16	The novel lnc <i>RNA</i> <i>CALIC</i> upregulates <i>AXL</i> to promote colon cancer metastasis. <i>EMBO Reports</i> , 2019, 20, e47052.	2.0	29
17	Comprehensive epigenome characterization reveals diverse transcriptional regulation across human vascular endothelial cells. <i>Epigenetics and Chromatin</i> , 2019, 12, 77.	1.8	34
18	Combined Loss of JMJD1A and JMJD1B Reveals Critical Roles for H3K9 Demethylation in the Maintenance of Embryonic Stem Cells and Early Embryogenesis. <i>Stem Cell Reports</i> , 2018, 10, 1340-1354.	2.3	23

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19	Sensitive and robust assessment of ChIP-seq read distribution using a strand-shift profile. <i>Bioinformatics</i> , 2018, 34, 2356-2363.	1.8	21
20	Statistical Analysis and Quality Assessment of ChIP-seq Data with DROMPA. <i>Methods in Molecular Biology</i> , 2018, 1672, 631-643.	0.4	5
21	Recent advances in ChIP-seq analysis: from quality management to whole-genome annotation. <i>Briefings in Bioinformatics</i> , 2017, 18, bbw023.	3.2	107
22	Decreased cohesin in the brain leads to defective synapse development and anxiety-related behavior. <i>Journal of Experimental Medicine</i> , 2017, 214, 1431-1452.	4.2	44
23	Two Components of Aversive Memory in <i>Drosophila</i> , Anesthesia-Sensitive and Anesthesia-Resistant Memory, Require Distinct Domains Within the Rgl1 Small GTPase. <i>Journal of Neuroscience</i> , 2017, 37, 5496-5510.	1.7	8
24	The HSF1- $\alpha$ -PARP1 complex facilitates DNA repair and promotes mammary tumorigenesis. <i>Nature Communications</i> , 2017, 8, 1638.	5.8	57
25	MRG15-mediated tethering of PALB2 to unperturbed chromatin protects active genes from genotoxic stress. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 7671-7676.	3.3	45
26	Genome-Wide Target Analyses of Otx2 Homeoprotein in Postnatal Cortex. <i>Frontiers in Neuroscience</i> , 2017, 11, 307.	1.4	25
27	Assembly of Slx4 signaling complexes behind $\alpha$ -DNA replication forks. <i>EMBO Journal</i> , 2015, 34, 2182-2197.	3.5	40
28	Replication-Coupled PCNA Unloading by the Elg1 Complex Occurs Genome-wide and Requires Okazaki Fragment Ligation. <i>Cell Reports</i> , 2015, 12, 774-787.	2.9	100
29	Condensin targets and reduces unwound DNA structures associated with transcription in mitotic chromosome condensation. <i>Nature Communications</i> , 2015, 6, 7815.	5.8	100
30	Esco1 Acetylates Cohesin via a Mechanism Different from That of Esco2. <i>Current Biology</i> , 2015, 25, 1694-1706.	1.8	74
31	Germline gain-of-function mutations in AFF4 cause a developmental syndrome functionally linking the super elongation complex and cohesin. <i>Nature Genetics</i> , 2015, 47, 338-344.	9.4	109
32	The Deubiquitinating Enzyme USP7 Regulates Androgen Receptor Activity by Modulating Its Binding to Chromatin. <i>Journal of Biological Chemistry</i> , 2015, 290, 21713-21723.	1.6	50
33	ATF1 Modulates the Heat Shock Response by Regulating the Stress-Inducible Heat Shock Factor 1 Transcription Complex. <i>Molecular and Cellular Biology</i> , 2015, 35, 11-25.	1.1	50
34	A Cohesin-Independent Role for NIPBL at Promoters Provides Insights in CdLS. <i>PLoS Genetics</i> , 2014, 10, e1004153.	1.5	123
35	The Chromosomal Association of the Smc5/6 Complex Depends on Cohesion and Predicts the Level of Sister Chromatid Entanglement. <i>PLoS Genetics</i> , 2014, 10, e1004680.	1.5	60
36	Smc5/6-mediated regulation of replication progression contributes to chromosome assembly during mitosis in human cells. <i>Molecular Biology of the Cell</i> , 2014, 25, 302-317.	0.9	61

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37	The dynamics of genome replication using deep sequencing. <i>Nucleic Acids Research</i> , 2014, 42, e3-e3.	6.5	113
38	Dimeric combinations of MafB, cFos and cJun control the apoptosis-survival balance in limb morphogenesis. <i>Development (Cambridge)</i> , 2014, 141, 2885-2894.	1.2	27
39	BRCA2 Coordinates the Activities of Cell-Cycle Kinases to Promote Genome Stability. <i>Cell Reports</i> , 2014, 7, 1547-1559.	2.9	49
40	Histone Variants Enriched in Oocytes Enhance Reprogramming to Induced Pluripotent Stem Cells. <i>Cell Stem Cell</i> , 2014, 14, 217-227.	5.2	130
41	Chromatin Immunoprecipitation Protocol for Mammalian Cells. <i>Methods in Molecular Biology</i> , 2014, 1164, 33-38.	0.4	16
42	Recurrent mutations in multiple components of the cohesin complex in myeloid neoplasms. <i>Nature Genetics</i> , 2013, 45, 1232-1237.	9.4	334
43	Eukaryotic Replisome Components Cooperate to Process Histones During Chromosome Replication. <i>Cell Reports</i> , 2013, 3, 892-904.	2.9	157
44	PRDM14 Ensures Naive Pluripotency through Dual Regulation of Signaling and Epigenetic Pathways in Mouse Embryonic Stem Cells. <i>Cell Stem Cell</i> , 2013, 12, 368-382.	5.2	266
45	<sc>DROMPA</sc>: easy to handle peak calling and visualization software for the computational analysis and validation of ChIP-seq data. <i>Genes To Cells</i> , 2013, 18, 589-601.	0.5	67
46	Telomere-binding protein Taz1 controls global replication timing through its localization near late replication origins in fission yeast. <i>Genes and Development</i> , 2012, 26, 2050-2062.	2.7	68
47	HDAC8 mutations in Cornelia de Lange syndrome affect the cohesin acetylation cycle. <i>Nature</i> , 2012, 489, 313-317.	13.7	488
48	Replisome Stability at Defective DNA Replication Forks Is Independent of S Phase Checkpoint Kinases. <i>Molecular Cell</i> , 2012, 45, 696-704.	4.5	140
49	The Inheritance of Histone Modifications Depends upon the Location in the Chromosome in <i>Saccharomyces cerevisiae</i> . <i>PLoS ONE</i> , 2011, 6, e28980.	1.1	2
50	Origin Association of Sld3, Sld7, and Cdc45 Proteins Is a Key Step for Determination of Origin-Firing Timing. <i>Current Biology</i> , 2011, 21, 2055-2063.	1.8	232
51	Cgaln: fast and space-efficient whole-genome alignment. <i>BMC Bioinformatics</i> , 2010, 11, 224.	1.2	14
52	Methods and application of genomic sequence alignment and alignment between genomic sequence and transcripts. <i>Journal of Animal Genetics</i> , 2008, 36, 177-183.	0.1	0
53	A NOVEL METHOD FOR REDUCING COMPUTATIONAL COMPLEXITY OF WHOLE GENOME SEQUENCE ALIGNMENT. , 2007, , .		1