

Argyris Papantonis

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1221382/publications.pdf>

Version: 2024-02-01

67
papers

3,011
citations

201575

27
h-index

197736

49
g-index

77
all docs

77
docs citations

77
times ranked

4047
citing authors

#	ARTICLE	IF	CITATIONS
1	Functional organization of RNA polymerase II in nuclear subcompartments. <i>Current Opinion in Cell Biology</i> , 2022, 74, 88-96.	2.6	20
2	Escape from senescence: revisiting cancer therapeutic strategies. <i>Molecular and Cellular Oncology</i> , 2022, 9, 2030158.	0.3	6
3	CRISPR-Cas9-mediated induction of large chromosomal inversions in human bronchial epithelial cells. <i>STAR Protocols</i> , 2022, 3, 101257.	0.5	4
4	Microgravity-induced stress mechanisms in human stem cell-derived cardiomyocytes. <i>IScience</i> , 2022, 25, 104577.	1.9	12
5	Isolation methodology is essential to the evaluation of the extracellular vesicle component of the senescence-associated secretory phenotype. <i>Journal of Extracellular Vesicles</i> , 2021, 10, e12041.	5.5	11
6	DNA methylation changes during long-term in vitro cell culture are caused by epigenetic drift. <i>Communications Biology</i> , 2021, 4, 598.	2.0	27
7	Overarching control of autophagy and DNA damage response by CHD6 revealed by modeling a rare human pathology. <i>Nature Communications</i> , 2021, 12, 3014.	5.8	16
8	HMGBl coordinates SASP-related chromatin folding and RNA homeostasis on the path to senescence. <i>Molecular Systems Biology</i> , 2021, 17, e9760.	3.2	31
9	HMGs as rheostats of chromosomal structure and cell proliferation. <i>Trends in Genetics</i> , 2021, 37, 986-994.	2.9	5
10	RNA polymerase II transcription compartments: from multivalent chromatin binding to liquid droplet formation?. <i>Nature Reviews Molecular Cell Biology</i> , 2021, 22, 645-646.	16.1	15
11	Human brain organoids assemble functionally integrated bilateral optic vesicles. <i>Cell Stem Cell</i> , 2021, 28, 1740-1757.e8.	5.2	77
12	Cilium induction triggers differentiation of glioma stem cells. <i>Cell Reports</i> , 2021, 36, 109656.	2.9	24
13	RNA polymerase II is required for spatial chromatin reorganization following exit from mitosis. <i>Science Advances</i> , 2021, 7, eabg8205.	4.7	70
14	Monitoring the Levels of Cellular NF- κ B Activation States. <i>Cancers</i> , 2021, 13, 5351.	1.7	15
15	Cohesin puts a break on distal homology hunt. <i>Nature Cell Biology</i> , 2021, 23, 1112-1114.	4.6	0
16	TNF- α -producing macrophages determine subtype identity and prognosis via AP1 enhancer reprogramming in pancreatic cancer. <i>Nature Cancer</i> , 2021, 2, 1185-1203.	5.7	46
17	A recurrent chromosomal inversion suffices for driving escape from oncogene-induced senescence via subTAD reorganization. <i>Molecular Cell</i> , 2021, 81, 4907-4923.e8.	4.5	28
18	iHi-C 2.0: A simple approach for mapping native spatial chromatin organisation from low cell numbers. <i>Methods</i> , 2020, 170, 33-37.	1.9	6

#	ARTICLE	IF	CITATIONS
19	Genome folding and refolding in differentiation and cellular senescence. <i>Current Opinion in Cell Biology</i> , 2020, 67, 56-63.	2.6	3
20	Spatial genome architecture and the emergence of malignancy. <i>Human Molecular Genetics</i> , 2020, 29, R197-R204.	1.4	6
21	Redundant and specific roles of cohesin STAG subunits in chromatin looping and transcriptional control. <i>Genome Research</i> , 2020, 30, 515-527.	2.4	54
22	Distinct IL-1 β -responsive enhancers promote acute and coordinated changes in chromatin topology in a hierarchical manner. <i>EMBO Journal</i> , 2020, 39, e101533.	3.5	25
23	<i>GemC1</i> is a critical switch for neural stem cell generation in the postnatal brain. <i>Glia</i> , 2019, 67, 2360-2373.	2.5	23
24	Technologies to study spatial genome organization: beyond 3C. <i>Briefings in Functional Genomics</i> , 2019, 18, 395-401.	1.3	4
25	Modes of phase separation affecting chromatin regulation. <i>Open Biology</i> , 2019, 9, 190167.	1.5	30
26	Organizing Principles for the Spatial Folding of Chromosomes. , 2019, , 107-130.		0
27	Spatial Chromosome Folding and Active Transcription Drive DNA Fragility and Formation of Oncogenic MLL Translocations. <i>Molecular Cell</i> , 2019, 75, 267-283.e12.	4.5	104
28	GemC1 governs multiciliogenesis through direct interaction and transcriptional regulation of p73. <i>Journal of Cell Science</i> , 2019, 132, .	1.2	27
29	Loss of genomic integrity induced by lysosphingolipid imbalance drives ageing in the heart. <i>EMBO Reports</i> , 2019, 20, .	2.0	26
30	yIncT Defines a Class of Divergently Transcribed lncRNAs and Safeguards the T-mediated Mesodermal Commitment of Human PSCs. <i>Cell Stem Cell</i> , 2019, 24, 318-327.e8.	5.2	44
31	Transcription Factories as Spatial and Functional Organization Nodes. , 2018, , 283-296.		1
32	Detecting Circular RNAs by RNA Fluorescence In Situ Hybridization. <i>Methods in Molecular Biology</i> , 2018, 1724, 69-75.	0.4	43
33	Shaping epigenetic memory via genomic bookmarking. <i>Nucleic Acids Research</i> , 2018, 46, 83-93.	6.5	73
34	HMGB2 Loss upon Senescence Entry Disrupts Genomic Organization and Induces CTCF Clustering across Cell Types. <i>Molecular Cell</i> , 2018, 70, 730-744.e6.	4.5	164
35	Forces driving the three-dimensional folding of eukaryotic genomes. <i>Molecular Systems Biology</i> , 2018, 14, e8214.	3.2	75
36	Senescence-associated DNA methylation is stochastically acquired in subpopulations of mesenchymal stem cells. <i>Aging Cell</i> , 2017, 16, 183-191.	3.0	70

#	ARTICLE	IF	CITATIONS
37	Cutting a Long Intron Short: Recursive Splicing and Its Implications. <i>Frontiers in Physiology</i> , 2016, 7, 598.	1.3	26
38	Exploiting native forces to capture chromosome conformation in mammalian cell nuclei. <i>Molecular Systems Biology</i> , 2016, 12, 891.	3.2	52
39	GARLIC: a bioinformatic toolkit for aetiologically connecting diseases and cell type-specific regulatory maps. <i>Human Molecular Genetics</i> , 2016, 26, ddw423.	1.4	1
40	Binding of nuclear factor $\hat{\text{I}}^{\text{B}}$ to noncanonical consensus sites reveals its multimodal role during the early inflammatory response. <i>Genome Research</i> , 2016, 26, 1478-1489.	2.4	43
41	Isolation of the protein and RNA content of active sites of transcription from mammalian cells. <i>Nature Protocols</i> , 2016, 11, 553-565.	5.5	20
42	Contribution of 3D Chromatin Architecture to the Maintenance of Pluripotency. <i>Current Stem Cell Reports</i> , 2015, 1, 170-175.	0.7	2
43	Splicing of many human genes involves sites embedded within introns. <i>Nucleic Acids Research</i> , 2015, 43, 4721-4732.	6.5	31
44	Dissecting the nascent human transcriptome by analysing the RNA content of transcription factories. <i>Nucleic Acids Research</i> , 2015, 43, e95-e95.	6.5	28
45	Exon Skipping Is Correlated with Exon Circularization. <i>Journal of Molecular Biology</i> , 2015, 427, 2414-2417.	2.0	308
46	Chorion Genes: A Landscape of Their Evolution, Structure, and Regulation. <i>Annual Review of Entomology</i> , 2015, 60, 177-194.	5.7	40
47	TNF $\hat{\text{I}}^{\text{B}}$ signalling primes chromatin for NF- $\hat{\text{I}}^{\text{B}}$ binding and induces rapid and widespread nucleosome repositioning. <i>Genome Biology</i> , 2014, 15, 536.	3.8	45
48	Transcription as a force partitioning the eukaryotic genome. <i>Biological Chemistry</i> , 2014, 395, 1301-1305.	1.2	10
49	The 4-D landscape of the inflammatory response. <i>Epigenetics and Chromatin</i> , 2013, 6, .	1.8	0
50	Nonspecific bridging-induced attraction drives clustering of DNA-binding proteins and genome organization. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E3605-11.	3.3	219
51	Transcription Factories: Genome Organization and Gene Regulation. <i>Chemical Reviews</i> , 2013, 113, 8683-8705.	23.0	218
52	Promoter type influences transcriptional topography by targeting genes to distinct nucleoplasmic sites. <i>Journal of Cell Science</i> , 2013, 126, 2052-9.	1.2	12
53	Space exploration by the promoter of a long human gene during one transcription cycle. <i>Nucleic Acids Research</i> , 2013, 41, 2216-2227.	6.5	26
54	TNF $\hat{\text{I}}^{\text{B}}$ signals through specialized factories where responsive coding and miRNA genes are transcribed. <i>EMBO Journal</i> , 2012, 31, 4404-4414.	3.5	122

#	ARTICLE	IF	CITATIONS
55	Enhancers and silencers: an integrated and simple model for their function. <i>Epigenetics and Chromatin</i> , 2012, 5, 1.	1.8	119
56	Dynamic Reconfiguration of Long Human Genes during One Transcription Cycle. <i>Molecular and Cellular Biology</i> , 2012, 32, 2738-2747.	1.1	37
57	The proteomes of transcription factories containing RNA polymerases I, II or III. <i>Nature Methods</i> , 2011, 8, 963-968.	9.0	74
58	Fixing the model for transcription. <i>Transcription</i> , 2011, 2, 41-44.	1.7	37
59	Genome architecture and the role of transcription. <i>Current Opinion in Cell Biology</i> , 2010, 22, 271-276.	2.6	46
60	Modeling bidirectional transcription using silkmoth chorion gene promoters. <i>Organogenesis</i> , 2010, 6, 54-58.	0.4	6
61	Active RNA Polymerases: Mobile or Immobile Molecular Machines?. <i>PLoS Biology</i> , 2010, 8, e1000419.	2.6	84
62	A wave of nascent transcription on activated human genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 18357-18361.	3.3	145
63	A modified chromatin-immunoprecipitation protocol for silkmoth ovarian follicular cells reveals C/EBP and GATA binding modes on an early chorion gene promoter. <i>Molecular Biology Reports</i> , 2009, 36, 733-736.	1.0	9
64	CHD1 Assumes a Central Role during Follicle Development. <i>Journal of Molecular Biology</i> , 2008, 383, 957-969.	2.0	6
65	Chorion gene activation and repression is dependent on BmC/EBP expression and binding to cognate cis-elements. <i>Biochemical and Biophysical Research Communications</i> , 2008, 369, 905-909.	1.0	12
66	Architectural factor HMGA induces promoter bending and recruits C/EBP and GATA during silkmoth chorion gene regulation. <i>Biochemical Journal</i> , 2008, 416, 85-97.	1.7	12
67	DNA Methylation Changes Upon Senescence are Strand-Specific and Reflect Chromatin Conformation. <i>SSRN Electronic Journal</i> , 0, , .	0.4	2