

Serap Erkek

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/10407999/publications.pdf>

Version: 2024-02-01

22
papers

6,651
citations

361413

20
h-index

642732

23
g-index

24
all docs

24
docs citations

24
times ranked

11356
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomic basis for RNA alterations in cancer. <i>Nature</i> , 2020, 578, 129-136.	27.8	280
2	Identification and Analyses of Extra-Cranial and Cranial Rhabdoid Tumor Molecular Subgroups Reveal Tumors with Cytotoxic T Cell Infiltration. <i>Cell Reports</i> , 2019, 29, 2338-2354.e7.	6.4	74
3	InTAD: chromosome conformation guided analysis of enhancer target genes. <i>BMC Bioinformatics</i> , 2019, 20, 60.	2.6	14
4	Lsd1 as a therapeutic target in Gfi1-activated medulloblastoma. <i>Nature Communications</i> , 2019, 10, 332.	12.8	55
5	Comprehensive Analysis of Chromatin States in Atypical Teratoid/Rhabdoid Tumor Identifies Diverging Roles for SWI/SNF and Polycomb in Gene Regulation. <i>Cancer Cell</i> , 2019, 35, 95-110.e8.	16.8	65
6	Functional relevance of genes predicted to be affected by epigenetic alterations in atypical teratoid/rhabdoid tumors. <i>Journal of Neuro-Oncology</i> , 2019, 141, 43-55.	2.9	7
7	The landscape of genomic alterations across childhood cancers. <i>Nature</i> , 2018, 555, 321-327.	27.8	1,068
8	Therapeutic targeting of ependymoma as informed by oncogenic enhancer profiling. <i>Nature</i> , 2018, 553, 101-105.	27.8	170
9	Opposing Effects of CREBBP Mutations Govern the Phenotype of Rubinstein-Taybi Syndrome and Adult SHH Medulloblastoma. <i>Developmental Cell</i> , 2018, 44, 709-724.e6.	7.0	35
10	The whole-genome landscape of medulloblastoma subtypes. <i>Nature</i> , 2017, 547, 311-317.	27.8	787
11	Pan-cancer analysis of somatic copy-number alterations implicates IRS4 and IGF2 in enhancer hijacking. <i>Nature Genetics</i> , 2017, 49, 65-74.	21.4	326
12	Sperm is epigenetically programmed to regulate gene transcription in embryos. <i>Genome Research</i> , 2016, 26, 1034-1046.	5.5	109
13	Active medulloblastoma enhancers reveal subgroup-specific cellular origins. <i>Nature</i> , 2016, 530, 57-62.	27.8	318
14	Atypical Teratoid/Rhabdoid Tumors Are Comprised of Three Epigenetic Subgroups with Distinct Enhancer Landscapes. <i>Cancer Cell</i> , 2016, 29, 379-393.	16.8	438
15	Disruption of histone methylation in developing sperm impairs offspring health transgenerationally. <i>Science</i> , 2015, 350, aab2006.	12.6	426
16	Decoding the regulatory landscape of medulloblastoma using DNA methylation sequencing. <i>Nature</i> , 2014, 510, 537-541.	27.8	378
17	In utero undernourishment perturbs the adult sperm methylome and intergenerational metabolism. <i>Science</i> , 2014, 345, 1255903.	12.6	535
18	Enhancer hijacking activates GF11 family oncogenes in medulloblastoma. <i>Nature</i> , 2014, 511, 428-434.	27.8	520

#	ARTICLE	IF	CITATIONS
19	Molecular determinants of nucleosome retention at CpG-rich sequences in mouse spermatozoa. Nature Structural and Molecular Biology, 2013, 20, 868-875.	8.2	298
20	Genome-wide chromatin analysis in mature mouse and human spermatozoa. Nature Protocols, 2013, 8, 2449-2470.	12.0	76
21	Parental epigenetic control of embryogenesis: a balance between inheritance and reprogramming?. Current Opinion in Cell Biology, 2012, 24, 387-396.	5.4	34
22	Repressive and active histone methylation mark distinct promoters in human and mouse spermatozoa. Nature Structural and Molecular Biology, 2010, 17, 679-687.	8.2	610