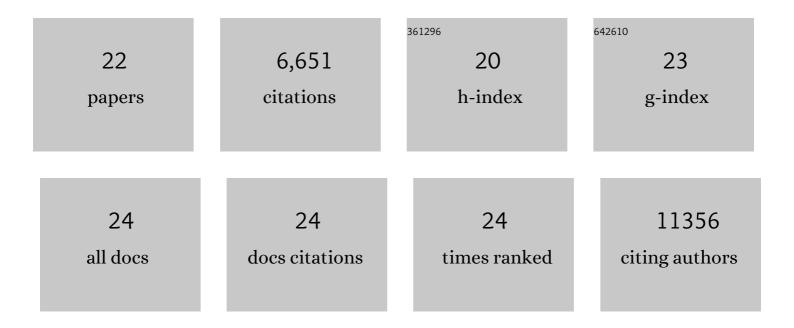
Serap Erkek

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Genomic basis for RNA alterations in cancer. Nature, 2020, 578, 129-136.	13.7	280
2	Identification and Analyses of Extra-Cranial and Cranial Rhabdoid Tumor Molecular Subgroups Reveal Tumors with Cytotoxic T Cell Infiltration. Cell Reports, 2019, 29, 2338-2354.e7.	2.9	74
3	InTAD: chromosome conformation guided analysis of enhancer target genes. BMC Bioinformatics, 2019, 20, 60.	1.2	14
4	Lsd1 as a therapeutic target in Gfi1-activated medulloblastoma. Nature Communications, 2019, 10, 332.	5.8	55
5	Comprehensive Analysis of Chromatin States in Atypical Teratoid/Rhabdoid Tumor Identifies Diverging Roles for SWI/SNF and Polycomb in Gene Regulation. Cancer Cell, 2019, 35, 95-110.e8.	7.7	65
6	Functional relevance of genes predicted to be affected by epigenetic alterations in atypical teratoid/rhabdoid tumors. Journal of Neuro-Oncology, 2019, 141, 43-55.	1.4	7
7	The landscape of genomic alterations across childhood cancers. Nature, 2018, 555, 321-327.	13.7	1,068
8	Therapeutic targeting of ependymoma as informed by oncogenic enhancer profiling. Nature, 2018, 553, 101-105.	13.7	170
9	Opposing Effects of CREBBP Mutations Govern the Phenotype of Rubinstein-Taybi Syndrome and Adult SHH Medulloblastoma. Developmental Cell, 2018, 44, 709-724.e6.	3.1	35
10	The whole-genome landscape of medulloblastoma subtypes. Nature, 2017, 547, 311-317.	13.7	787
11	Pan-cancer analysis of somatic copy-number alterations implicates IRS4 and IGF2 in enhancer hijacking. Nature Genetics, 2017, 49, 65-74.	9.4	326
12	Sperm is epigenetically programmed to regulate gene transcription in embryos. Genome Research, 2016, 26, 1034-1046.	2.4	109
13	Active medulloblastoma enhancers reveal subgroup-specific cellular origins. Nature, 2016, 530, 57-62.	13.7	318
14	Atypical Teratoid/Rhabdoid Tumors Are Comprised of Three Epigenetic Subgroups with Distinct Enhancer Landscapes. Cancer Cell, 2016, 29, 379-393.	7.7	438
15	Disruption of histone methylation in developing sperm impairs offspring health transgenerationally. Science, 2015, 350, aab2006.	6.0	426
16	Decoding the regulatory landscape of medulloblastoma using DNA methylation sequencing. Nature, 2014, 510, 537-541.	13.7	378
17	In utero undernourishment perturbs the adult sperm methylome and intergenerational metabolism. Science, 2014, 345, 1255903.	6.0	535
18	Enhancer hijacking activates GFI1 family oncogenes in medulloblastoma. Nature, 2014, 511, 428-434.	13.7	520

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#	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.	3.6	298
20	Genome-wide chromatin analysis in mature mouse and human spermatozoa. Nature Protocols, 2013, 8, 2449-2470.	5.5	76
21	Parental epigenetic control of embryogenesis: a balance between inheritance and reprogramming?. Current Opinion in Cell Biology, 2012, 24, 387-396.	2.6	34
22	Repressive and active histone methylation mark distinct promoters in human and mouse spermatozoa. Nature Structural and Molecular Biology, 2010, 17, 679-687.	3.6	610