Kristoffer Vitting-Seerup

List of Publications by Year
in descending order

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Version: 2024-02-01

28 papers	2,653 citations	430874 18 h-index	552781 26 g-index
36 all docs	36 docs citations	36 times ranked	5251 citing authors

#	Article	IF	Citations
1	Target isoforms are an overlooked challenge and opportunity in chimeric antigen receptor cell therapy. Immunotherapy Advances, 2022, 2, .	3.0	7
2	Editorial: Alternative Splicing in Health and Disease. Frontiers in Molecular Biosciences, 2022, 9, 878668.	3.5	0
3	PTBP1 promotes hematopoietic stem cell maintenance and red blood cell development by ensuring sufficient availability of ribosomal constituents. Cell Reports, 2022, 39, 110793.	6.4	3
4	The RNA m6A Reader YTHDF2 Maintains Oncogene Expression and Is a Targetable Dependency in Glioblastoma Stem Cells. Cancer Discovery, 2021, 11, 480-499.	9.4	218
5	Plasma IL-8 and ICOSLG as prognostic biomarkers in glioblastoma. Neuro-Oncology Advances, 2021, 3, vdab072.	0.7	4
6	Perspective: targeting VEGF-A and YKL-40 in glioblastoma â€“ matter matters. Cell Cycle, 2021, 20, 702-715.	2.6	6
7	Personalized B cell response to the <i>Lactobacillus rhamnosus GG</i> probiotic in healthy human subjects: a randomized trial. Gut Microbes, 2020, 12, 1854639.	9.8	5
8	Mutant CEBPA directly drives the expression of the targetable tumor-promoting factor CD73 in AML. Science Advances, 2019, 5, eaaw4304.	10.3	28
9	CAGEfightR: analysis of 5â€²-end data using R/Bioconductor. BMC Bioinformatics, 2019, 20, 487.	2.6	59
10	A Functional Link between Nuclear RNA Decay and Transcriptional Control Mediated by the Polycomb Repressive Complex 2. Cell Reports, 2019, 29, 1800-1811.e6.	6.4	32
11	IsoformSwitchAnalyzeR: analysis of changes in genome-wide patterns of alternative splicing and its functional consequences. Bioinformatics, 2019, 35, 4469-4471.	4.1	189
12	Astrogliogenesis in human fetal brain: complex spatiotemporal immunoreactivity patterns of <scp>GFAP</scp>, S100, <scp>AQP</scp>4 and <scp>YKL</scp>â€40. Journal of Anatomy, 2019, 235, 590-615.	1.5	37
13	Targeting glioma stemâ€like cell survival and chemoresistance through inhibition of lysineâ€specific histone demethylase <scp>KDM</scp>2B. Molecular Oncology, 2018, 12, 406-420.	4.6	56
14	Loss-of-function variants in ADCY3 increase risk of obesity and type 2 diabetes. Nature Genetics, 2018, 50, 172-174.	21.4	156
15	Characterization of the enhancer and promoter landscape of inflammatory bowel disease from human colon biopsies. Nature Communications, 2018, 9, 1661.	12.8	78
16	The Landscape of Isoform Switches in Human Cancers. Molecular Cancer Research, 2017, 15, 1206-1220.	3.4	208
17	Identification of Gene Transcription Start Sites and Enhancers Responding to Pulmonary Carbon Nanotube Exposure <i>in Vivo</i>. ACS Nano, 2017, 11, 3597-3613.	14.6	23
18	An integrated expression atlas of miRNAs and their promoters in human and mouse. Nature Biotechnology, 2017, 35, 872-878.	17.5	456

#	ARTICLE	IF	CITATIONS
19	Transcriptional changes induced by bevacizumab combination therapy in responding and non-responding recurrent glioblastoma patients. BMC Cancer, 2017, 17, 278.	2.6	16
20	On-the-fly selection of cell-specific enhancers, genes, miRNAs and proteins across the human body using SlideBase. Database: the Journal of Biological Databases and Curation, 2016, 2016, .	3.0	24
21	Identification of a Nuclear Exosome Decay Pathway for Processed Transcripts. Molecular Cell, 2016, 64, 520-533.	9.7	209
22	UPF2-Dependent Nonsense-Mediated mRNA Decay Pathway Is Essential for Spermatogenesis by Selectively Eliminating Longer 3'UTR Transcripts. PLoS Genetics, 2016, 12, e1005863.	3.5	94
23	Transcribed enhancers lead waves of coordinated transcription in transitioning mammalian cells. Science, 2015, 347, 1010-1014.	12.6	517
24	Amplification of pico-scale DNA mediated by bacterial carrier DNA for small-cell-number transcription factor ChIP-seq. BMC Genomics, 2015, 16, 46.	2.8	27
25	UBL5 is essential for preâ€‹<scp>mRNA</scp> splicing and sister chromatid cohesion in human cells. EMBO Reports, 2014, 15, 956-964.	4.5	41
26	spliceR: an R package for classification of alternative splicing and prediction of coding potential from RNA-seq data. BMC Bioinformatics, 2014, 15, 81.	2.6	100
27	Significance of Calcium Binding, Tyrosine Phosphorylation, and Lysine Trimethylation for the Essential Function of Calmodulin in Vertebrate Cells Analyzed in a Novel Gene Replacement System. Journal of Biological Chemistry, 2012, 287, 18173-18181.	3.4	18
28	satuRn:ÂScalable analysis of differential transcript usageÂfor bulk and single-cell RNA-sequencing applications. F1000Research, 0, 10, 374.	1.6	17