Hamish W King

List of Publications by Year in descending order

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HAMISH W/ KINC

#	Article	IF	CITATIONS
1	Hypoxic enhancement of exosome release by breast cancer cells. BMC Cancer, 2012, 12, 421.	2.6	821
2	Variant PRC1 Complex-Dependent H2A Ubiquitylation Drives PRC2 Recruitment and Polycomb Domain Formation. Cell, 2014, 157, 1445-1459.	28.9	613
3	Single-cell multi-omics analysis of the immune response in COVID-19. Nature Medicine, 2021, 27, 904-916.	30.7	452
4	Cell2location maps fine-grained cell types in spatial transcriptomics. Nature Biotechnology, 2022, 40, 661-671.	17.5	335
5	Cells of the human intestinal tract mapped across space and time. Nature, 2021, 597, 250-255.	27.8	266
6	Cross-tissue immune cell analysis reveals tissue-specific features in humans. Science, 2022, 376, eabl5197.	12.6	265
7	The pioneer factor OCT4 requires the chromatin remodeller BRG1 to support gene regulatory element function in mouse embryonic stem cells. ELife, 2017, 6, .	6.0	215
8	Synergy between Variant PRC1 Complexes Defines Polycomb-Mediated Gene Repression. Molecular Cell, 2019, 74, 1020-1036.e8.	9.7	200
9	Distinct microbial and immune niches of the human colon. Nature Immunology, 2020, 21, 343-353.	14.5	175
10	Single-cell analysis of human B cell maturation predicts how antibody class switching shapes selection dynamics. Science Immunology, 2021, 6, .	11.9	149
11	RYBP stimulates PRC1 to shape chromatin-based communication between Polycomb repressive complexes. ELife, 2016, 5, .	6.0	111
12	The SET1 Complex Selects Actively Transcribed Target Genes via Multivalent Interaction with CpG Island Chromatin. Cell Reports, 2017, 20, 2313-2327.	6.4	86
13	Protection of CpG islands from DNA methylation is DNA-encoded and evolutionarily conserved. Nucleic Acids Research, 2016, 44, 6693-6706.	14.5	80
14	Blood and immune development in human fetal bone marrow and Down syndrome. Nature, 2021, 598, 327-331.	27.8	73
15	Polycomb repressive complex 1 shapes the nucleosome landscape but not accessibility at target genes. Genome Research, 2018, 28, 1494-1507.	5.5	72
16	Exosomes and the kidney: Blaming the messenger. Nephrology, 2013, 18, 1-10.	1.6	68
17	Distinct contributions of DNA methylation and histone acetylation to the genomic occupancy of transcription factors. Genome Research, 2020, 30, 1393-1406.	5.5	41
18	Combinatorial Smad2/3 Activities Downstream of Nodal Signaling Maintain Embryonic/Extra-Embryonic Cell Identities during Lineage Priming. Cell Reports, 2018, 24, 1977-1985.e7.	6.4	31

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19	KDM2 proteins constrain transcription from CpG island gene promoters independently of their histone demethylase activity. Nucleic Acids Research, 2019, 47, 9005-9023.	14.5	26
20	Development of a Fish Cell Culture Model to Investigate the Impact of Fish Oil Replacement on Lipid Peroxidation. Lipids, 2011, 46, 753-764.	1.7	24
21	Integrated single-cell transcriptomics and epigenomics reveals strong germinal center–associated etiology of autoimmune risk loci. Science Immunology, 2021, 6, eabh3768.	11.9	19
22	PHGDH is required for germinal center formation and is a therapeutic target in MYC-driven lymphoma. Journal of Clinical Investigation, 2022, 132, .	8.2	14
23	The cation channel TRPM8 influences the differentiation and function of human monocytes. Journal of Leukocyte Biology, 2022, 112, 365-381.	3.3	11
24	Germs and germlines: how "public―B ell clones evolve in the gut. Immunology and Cell Biology, 2020, 98, 428-430.	2.3	1