List of Publications by Year in descending order

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ΡΑΙΙΙ Δ ΚΗΛΥΛΡΙ

#	Article	IF	CITATIONS
1	An improved ATAC-seq protocol reduces background and enables interrogation of frozen tissues. Nature Methods, 2017, 14, 959-962.	19.0	1,653
2	The functions and unique features of long intergenic non-coding RNA. Nature Reviews Molecular Cell Biology, 2018, 19, 143-157.	37.0	968
3	HiChIP: efficient and sensitive analysis of protein-directed genome architecture. Nature Methods, 2016, 13, 919-922.	19.0	853
4	Control of somatic tissue differentiation by the long non-coding RNA TINCR. Nature, 2013, 493, 231-235.	27.8	810
5	Nucleosome disruption and enhancement of activator binding by a human SW1/SNF complex. Nature, 1994, 370, 477-481.	27.8	744
6	BRG1 contains a conserved domain of the SWI2/SNF2 family necessary for normal mitotic growth and transcription. Nature, 1993, 366, 170-174.	27.8	625
7	Advances in skin grafting and treatment of cutaneous wounds. Science, 2014, 346, 941-945.	12.6	609
8	NF-κB blockade and oncogenic Ras trigger invasive human epidermal neoplasia. Nature, 2003, 421, 639-643.	27.8	537
9	Multimodal Analysis of Composition and Spatial Architecture in Human Squamous Cell Carcinoma. Cell, 2020, 182, 497-514.e22.	28.9	508
10	Integrating single-cell and spatial transcriptomics to elucidate intercellular tissue dynamics. Nature Reviews Genetics, 2021, 22, 627-644.	16.3	423
11	Enhancer connectome in primary human cells identifies target genes of disease-associated DNA elements. Nature Genetics, 2017, 49, 1602-1612.	21.4	419
12	p63 regulates proliferation and differentiation of developmentally mature keratinocytes. Genes and Development, 2006, 20, 3185-3197.	5.9	412
13	DNMT1 maintains progenitor function in self-renewing somatic tissue. Nature, 2010, 463, 563-567.	27.8	407
14	Suppression of progenitor differentiation requires the long noncoding RNA ANCR. Genes and Development, 2012, 26, 338-343.	5.9	391
15	Lineage-specific dynamic and pre-established enhancer–promoter contacts cooperate in terminal differentiation. Nature Genetics, 2017, 49, 1522-1528.	21.4	255
16	Methods to study RNA–protein interactions. Nature Methods, 2019, 16, 225-234.	19.0	244
17	Genomic analysis of mycosis fungoides and Sézary syndrome identifies recurrent alterations in TNFR2. Nature Genetics, 2015, 47, 1056-1060.	21.4	242
18	Control of differentiation in a self-renewing mammalian tissue by the histone demethylase JMJD3. Genes and Development, 2008, 22, 1865-1870.	5.9	239

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19	RNA–protein interaction detection in living cells. Nature Methods, 2018, 15, 207-212.	19.0	234
20	irCLIP platform for efficient characterization of protein–RNA interactions. Nature Methods, 2016, 13, 489-492.	19.0	222
21	Coupled Single-Cell CRISPR Screening and Epigenomic Profiling Reveals Causal Gene Regulatory Networks. Cell, 2019, 176, 361-376.e17.	28.9	215
22	ZNF750 Is a p63 Target Gene that Induces KLF4 to Drive Terminal Epidermal Differentiation. Developmental Cell, 2012, 22, 669-677.	7.0	198
23	CDK4 coexpression with Ras generates malignant human epidermal tumorigenesis. Nature Medicine, 2002, 8, 1105-1114.	30.7	190
24	Invasive three-dimensional organotypic neoplasia from multiple normal human epithelia. Nature Medicine, 2010, 16, 1450-1455.	30.7	190
25	SARS-CoV-2 B.1.1.7 and B.1.351 spike variants bind human ACE2 with increased affinity. Lancet Infectious Diseases, The, 2021, 21, 1070.	9.1	188
26	IQGAP1 scaffold-kinase interaction blockade selectively targets RAS-MAP kinase–driven tumors. Nature Medicine, 2013, 19, 626-630.	30.7	173
27	A LncRNA-MAF:MAFB Transcription Factor Network Regulates Epidermal Differentiation. Developmental Cell, 2015, 32, 693-706.	7.0	172
28	Immunization via hair follicles by topical application of naked DNA to normal skin. Nature Biotechnology, 1999, 17, 870-872.	17.5	169
29	Corrective gene transfer in the human skin disorder lamellar ichthyosis. Nature Medicine, 1996, 2, 1263-1267.	30.7	167
30	Safety and Wound Outcomes Following Genetically Corrected Autologous Epidermal Grafts in Patients With Recessive Dystrophic Epidermolysis Bullosa. JAMA - Journal of the American Medical Association, 2016, 316, 1808.	7.4	161
31	Quantitative analysis of mammalian translation initiation sites by <scp>FACS</scp> â€seq. Molecular Systems Biology, 2014, 10, 748.	7.2	158
32	Sonic Hedgehog Opposes Epithelial Cell Cycle Arrest. Journal of Cell Biology, 1999, 147, 71-76.	5.2	144
33	The noncoding RNAs SNORD50A and SNORD50B bind K-Ras and are recurrently deleted in human cancer. Nature Genetics, 2016, 48, 53-58.	21.4	143
34	A novel ATAC-seq approach reveals lineage-specific reinforcement of the open chromatin landscape via cooperation between BAF and p63. Genome Biology, 2015, 16, 284.	8.8	135
35	Mek1/2 MAPK Kinases Are Essential for Mammalian Development, Homeostasis, and Raf-Induced Hyperplasia. Developmental Cell, 2007, 12, 615-629.	7.0	132
36	Recurrent point mutations in the kinetochore gene KNSTRN in cutaneous squamous cell carcinoma. Nature Genetics, 2014, 46, 1060-1062.	21.4	125

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37	Transcript-indexed ATAC-seq for precision immune profiling. Nature Medicine, 2018, 24, 580-590.	30.7	124
38	ZNF750 interacts with KLF4 and RCOR1, KDM1A, and CTBP1/2 chromatin regulators to repress epidermal progenitor genes and induce differentiation genes. Genes and Development, 2014, 28, 2013-2026.	5.9	122
39	The Functional Proximal Proteome of Oncogenic Ras Includes mTORC2. Molecular Cell, 2019, 73, 830-844.e12.	9.7	104
40	ACTL6a Enforces the Epidermal Progenitor State by Suppressing SWI/SNF-Dependent Induction of KLF4. Cell Stem Cell, 2013, 12, 193-203.	11.1	97
41	Genetic pathways in disorders of epidermal differentiation. Trends in Genetics, 2013, 29, 31-40.	6.7	92
42	7SK-BAF axis controls pervasive transcription at enhancers. Nature Structural and Molecular Biology, 2016, 23, 231-238.	8.2	92
43	Dicer-microRNA-Myc circuit promotes transcription of hundreds of long noncoding RNAs. Nature Structural and Molecular Biology, 2014, 21, 585-590.	8.2	90
44	Long-Term Type VII Collagen Restoration to Human Epidermolysis Bullosa Skin Tissue. Human Gene Therapy, 2010, 21, 1299-1310.	2.7	80
45	Modeling Inducible Human Tissue Neoplasia Identifies an Extracellular Matrix Interaction Network Involved in Cancer Progression. Cancer Cell, 2009, 15, 477-488.	16.8	79
46	Dissecting noncoding and pathogen RNA–protein interactomes. Rna, 2015, 21, 135-143.	3.5	71
47	HiChIRP reveals RNA-associated chromosome conformation. Nature Methods, 2019, 16, 489-492.	19.0	70
48	Enhancer-targeted genome editing selectively blocks innate resistance to oncokinase inhibition. Genome Research, 2014, 24, 751-760.	5.5	67
49	CALML5 is a ZNF750- and TINCR-induced protein that binds stratifin to regulate epidermal differentiation. Genes and Development, 2015, 29, 2225-2230.	5.9	61
50	Super-resolved spatial transcriptomics by deep data fusion. Nature Biotechnology, 2022, 40, 476-479.	17.5	61
51	Mosaic Activating RAS Mutations in Nevus Sebaceus and Nevus Sebaceus Syndrome. Journal of Investigative Dermatology, 2013, 133, 824-827.	0.7	55
52	Structural modularity of the XIST ribonucleoprotein complex. Nature Communications, 2020, 11, 6163.	12.8	53
53	Sustainable Systemic Delivery via a Single Injection of Lentivirus into Human Skin Tissue. Human Gene Therapy, 2001, 12, 1551-1558.	2.7	50
54	Network Analysis Identifies Mitochondrial Regulation of Epidermal Differentiation by MPZL3 and FDXR. Developmental Cell, 2015, 35, 444-457.	7.0	50

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55	Genomic Profiling of a Human Organotypic Model of AEC Syndrome Reveals ZNF750 as an Essential Downstream Target of Mutant TP63. American Journal of Human Genetics, 2012, 91, 435-443.	6.2	49
56	CSNK1a1 Regulates PRMT1 to Maintain the Progenitor State in Self-Renewing Somatic Tissue. Developmental Cell, 2017, 43, 227-239.e5.	7.0	48
57	RAC1 activation drives pathologic interactions between the epidermis and immune cells. Journal of Clinical Investigation, 2016, 126, 2661-2677.	8.2	48
58	Retinoic acid and BMP4 cooperate with p63 to alter chromatin dynamics during surface epithelial commitment. Nature Genetics, 2018, 50, 1658-1665.	21.4	47
59	Tumor Necrosis Factor Receptor 1/c-Jun-NH2-Kinase Signaling Promotes Human Neoplasia. Cancer Research, 2007, 67, 3827-3834.	0.9	46
60	The dynamic, combinatorial cis-regulatory lexicon of epidermal differentiation. Nature Genetics, 2021, 53, 1564-1576.	21.4	45
61	Identification of proteins binding coding and non-coding human RNAs using protein microarrays. BMC Genomics, 2012, 13, 633.	2.8	35
62	Spen links RNA-mediated endogenous retrovirus silencing and X chromosome inactivation. ELife, 2020, 9, .	6.0	33
63	Activating HRAS Mutation in Nevus Spilus. Journal of Investigative Dermatology, 2014, 134, 1766-1768.	0.7	31
64	Genome-wide meta-analysis identifies eight new susceptibility loci for cutaneous squamous cell carcinoma. Nature Communications, 2020, 11, 820.	12.8	30
65	The proximal proteome of 17 SARS-CoV-2 proteins links to disrupted antiviral signaling and host translation. PLoS Pathogens, 2021, 17, e1009412.	4.7	27
66	Profiling of rotavirus 3′UTR-binding proteins reveals the ATP synthase subunit ATP5B as a host factor that supports late-stage virus replication. Journal of Biological Chemistry, 2019, 294, 5993-6006.	3.4	26
67	easyCLIP analysis of RNA-protein interactions incorporating absolute quantification. Nature Communications, 2021, 12, 1569.	12.8	26
68	Novel lincRNA SLINKY is a prognostic biomarker in kidney cancer. Oncotarget, 2017, 8, 18657-18669.	1.8	21
69	Genetic and genomic studies of pathogenic EXOSC2 mutations in the newly described disease SHRF implicate the autophagy pathway in disease pathogenesis. Human Molecular Genetics, 2020, 29, 541-553.	2.9	21
70	Omni-ATAC-seq: Improved ATAC-seq protocol. Protocol Exchange, 0, , .	0.3	21
71	Impact of Laminin 5 β3 Gene versus Protein Replacement on Gene Expression Patterns in Junctional Epidermolysis Bullosa. Human Gene Therapy, 2001, 12, 1443-1448.	2.7	20
72	Mutant collagen COL11A1 enhances cancerous invasion. Oncogene, 2021, 40, 6299-6307.	5.9	20

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73	KRAS regulation by small non-coding RNAs and SNARE proteins. Nature Communications, 2019, 10, 5118.	12.8	17
74	Cancer-Associated Long Noncoding RNA SMRT-2 Controls Epidermal Differentiation. Journal of Investigative Dermatology, 2018, 138, 1445-1449.	0.7	13
75	Impact of a patient-derived hepatitis C viral RNA genome with a mutated microRNA binding site. PLoS Pathogens, 2019, 15, e1007467.	4.7	13
76	Research Techniques Made Simple: Emerging Methods to Elucidate Protein Interactions through Spatial Proximity. Journal of Investigative Dermatology, 2017, 137, e197-e203.	0.7	10
77	Ras functional proximity proteomics establishes mTORC2 as new direct ras effector. Oncotarget, 2019, 10, 5126-5135.	1.8	6
78	Targeted Proteomic Approaches for Proteome-Wide Characterizations of the AMP-Binding Capacities of Kinases. Journal of Proteome Research, 2022, 21, 2063-2070.	3.7	3
79	RNA-Protein Interaction Detection (RaPID). Protocol Exchange, O, , .	0.3	2
80	Factors That May Promote an Effective Local Research Environment. Journal of Investigative Dermatology, 2016, 136, 1529-1531.	0.7	1
81	HiChIRP: RNA-centric chromatin conformation. Protocol Exchange, 0, , .	0.3	1
82	Inhibiting Oncogenic RAS in Multiple Myeloma By Targeting Scaffold-ERK Interactions. Blood, 2014, 124, 2089-2089.	1.4	0
83	Abstract PR016: The spatial landscape of clonal somatic mutations in benign and malignant tissue. Cancer Research. 2022. 82. PR016-PR016.	0.9	0