Paul A Khavari

List of Publications by Year
in descending order

83 papers	15,714 citations	36203 51 h-index	62479 80 g-index
97 all docs	97 docs citations	97 times ranked	24038 citing authors

#	Article	IF	Citations
1	Super-resolved spatial transcriptomics by deep data fusion. Nature Biotechnology, 2022, 40, 476-479.	9.4	61
2	Abstract PR016: The spatial landscape of clonal somatic mutations in benign and malignant tissue. Cancer Research, 2022, 82, PR016-PR016.	0.4	0
3	Targeted Proteomic Approaches for Proteome-Wide Characterizations of the AMP-Binding Capacities of Kinases. Journal of Proteome Research, 2022, 21, 2063-2070.	1.8	3
4	easyCLIP analysis of RNA-protein interactions incorporating absolute quantification. Nature Communications, 2021, 12, 1569.	5.8	26
5	Integrating single-cell and spatial transcriptomics to elucidate intercellular tissue dynamics. Nature Reviews Genetics, 2021, 22, 627-644.	7.7	423
6	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.	4.6	188
7	Mutant collagen COL11A1 enhances cancerous invasion. Oncogene, 2021, 40, 6299-6307.	2.6	20
8	The proximal proteome of 17 SARS-CoV-2 proteins links to disrupted antiviral signaling and host translation. PLoS Pathogens, 2021, 17, e1009412.	2.1	27
9	The dynamic, combinatorial cis-regulatory lexicon of epidermal differentiation. Nature Genetics, 2021, 53, 1564-1576.	9.4	45
10	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.	1.4	21
11	Structural modularity of the XIST ribonucleoprotein complex. Nature Communications, 2020, 11, 6163.	5.8	53
12	Multimodal Analysis of Composition and Spatial Architecture in Human Squamous Cell Carcinoma. Cell, 2020, 182, 497-514.e22.	13.5	508
13	Genome-wide meta-analysis identifies eight new susceptibility loci for cutaneous squamous cell carcinoma. Nature Communications, 2020, 11, 820.	5.8	30
14	Spen links RNA-mediated endogenous retrovirus silencing and X chromosome inactivation. ELife, 2020, 9, .	2.8	33
15	KRAS regulation by small non-coding RNAs and SNARE proteins. Nature Communications, 2019, 10, 5118.	5.8	17
16	HiChIRP reveals RNA-associated chromosome conformation. Nature Methods, 2019, 16, 489-492.	9.0	70
17	Impact of a patient-derived hepatitis C viral RNA genome with a mutated microRNA binding site. PLoS Pathogens, 2019, 15, e1007467.	2.1	13
18	Methods to study RNA–protein interactions. Nature Methods, 2019, 16, 225-234.	9.0	244

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19	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.	1.6	26
20	Coupled Single-Cell CRISPR Screening and Epigenomic Profiling Reveals Causal Gene Regulatory Networks. Cell, 2019, 176, 361-376.e17.	13.5	215
21	The Functional Proximal Proteome of Oncogenic Ras Includes mTORC2. Molecular Cell, 2019, 73, 830-844.e12.	4.5	104
22	Ras functional proximity proteomics establishes mTORC2 as new direct ras effector. Oncotarget, 2019, 10, 5126-5135.	0.8	6
23	Cancer-Associated Long Noncoding RNA SMRT-2 Controls Epidermal Differentiation. Journal of Investigative Dermatology, 2018, 138, 1445-1449.	0.3	13
24	Transcript-indexed ATAC-seq for precision immune profiling. Nature Medicine, 2018, 24, 580-590.	15.2	124
25	RNA–protein interaction detection in living cells. Nature Methods, 2018, 15, 207-212.	9.0	234
26	Retinoic acid and BMP4 cooperate with p63 to alter chromatin dynamics during surface epithelial commitment. Nature Genetics, 2018, 50, 1658-1665.	9.4	47
27	The functions and unique features of long intergenic non-coding RNA. Nature Reviews Molecular Cell Biology, 2018, 19, 143-157.	16.1	968
28	Enhancer connectome in primary human cells identifies target genes of disease-associated DNA elements. Nature Genetics, 2017, 49, 1602-1612.	9.4	419
29	CSNK1a1 Regulates PRMT1 to Maintain the Progenitor State in Self-Renewing Somatic Tissue. Developmental Cell, 2017, 43, 227-239.e5.	3.1	48
30	Lineage-specific dynamic and pre-established enhancer–promoter contacts cooperate in terminal differentiation. Nature Genetics, 2017, 49, 1522-1528.	9.4	255
31	Research Techniques Made Simple: Emerging Methods to Elucidate Protein Interactions through Spatial Proximity. Journal of Investigative Dermatology, 2017, 137, e197-e203.	0.3	10
32	An improved ATAC-seq protocol reduces background and enables interrogation of frozen tissues. Nature Methods, 2017, 14, 959-962.	9.0	1,653
33	Novel lincRNA SLINKY is a prognostic biomarker in kidney cancer. Oncotarget, 2017, 8, 18657-18669.	0.8	21
34	irCLIP platform for efficient characterization of protein–RNA interactions. Nature Methods, 2016, 13, 489-492.	9.0	222
35	Factors That May Promote an Effective Local Research Environment. Journal of Investigative Dermatology, 2016, 136, 1529-1531.	0.3	1
36	HiChIP: efficient and sensitive analysis of protein-directed genome architecture. Nature Methods, 2016, 13, 919-922.	9.0	853

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37	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.	3.8	161
38	7SK-BAF axis controls pervasive transcription at enhancers. Nature Structural and Molecular Biology, 2016, 23, 231-238.	3.6	92
39	The noncoding RNAs SNORD50A and SNORD50B bind K-Ras and are recurrently deleted in human cancer. Nature Genetics, 2016, 48, 53-58.	9.4	143
40	RAC1 activation drives pathologic interactions between the epidermis and immune cells. Journal of Clinical Investigation, 2016, 126, 2661-2677.	3.9	48
41	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.	3.8	135
42	CALML5 is a ZNF750- and TINCR-induced protein that binds stratifin to regulate epidermal differentiation. Genes and Development, 2015, 29, 2225-2230.	2.7	61
43	Dissecting noncoding and pathogen RNAâ€"protein interactomes. Rna, 2015, 21, 135-143.	1.6	71
44	A LncRNA-MAF:MAFB Transcription Factor Network Regulates Epidermal Differentiation. Developmental Cell, 2015, 32, 693-706.	3.1	172
45	Genomic analysis of mycosis fungoides and SÃ©zary syndrome identifies recurrent alterations in TNFR2. Nature Genetics, 2015, 47, 1056-1060.	9.4	242
46	Network Analysis Identifies Mitochondrial Regulation of Epidermal Differentiation by MPZL3 and FDXR. Developmental Cell, 2015, 35, 444-457.	3.1	50
47	Activating HRAS Mutation in Nevus Spilus. Journal of Investigative Dermatology, 2014, 134, 1766-1768.	0.3	31
48	Advances in skin grafting and treatment of cutaneous wounds. Science, 2014, 346, 941-945.	6.0	609
49	Quantitative analysis of mammalian translation initiation sites by <scp>FACS</scp>â€seq. Molecular Systems Biology, 2014, 10, 748.	3.2	158
50	Recurrent point mutations in the kinetochore gene KNSTRN in cutaneous squamous cell carcinoma. Nature Genetics, 2014, 46, 1060-1062.	9.4	125
51	Dicer-microRNA-Myc circuit promotes transcription of hundreds of long noncoding RNAs. Nature Structural and Molecular Biology, 2014, 21, 585-590.	3.6	90
52	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.	2.7	122
53	Enhancer-targeted genome editing selectively blocks innate resistance to oncokinase inhibition. Genome Research, 2014, 24, 751-760.	2.4	67
54	Inhibiting Oncogenic RAS in Multiple Myeloma By Targeting Scaffold-ERK Interactions. Blood, 2014, 124, 2089-2089.	0.6	0

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55	Genetic pathways in disorders of epidermal differentiation. Trends in Genetics, 2013, 29, 31-40.	2.9	92
56	Control of somatic tissue differentiation by the long non-coding RNA TINCR. Nature, 2013, 493, 231-235.	13.7	810
57	ACTL6a Enforces the Epidermal Progenitor State by Suppressing SWI/SNF-Dependent Induction of KLF4. Cell Stem Cell, 2013, 12, 193-203.	5.2	97
58	IQGAP1 scaffold-kinase interaction blockade selectively targets RAS-MAP kinaseâ€"driven tumors. Nature Medicine, 2013, 19, 626-630.	15.2	173
59	Mosaic Activating RAS Mutations in Nevus Sebaceus and Nevus Sebaceus Syndrome. Journal of Investigative Dermatology, 2013, 133, 824-827.	0.3	55
60	Suppression of progenitor differentiation requires the long noncoding RNA ANCR. Genes and Development, 2012, 26, 338-343.	2.7	391
61	ZNF750 Is a p63 Target Gene that Induces KLF4 to Drive Terminal Epidermal Differentiation. Developmental Cell, 2012, 22, 669-677.	3.1	198
62	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.	2.6	49
63	Identification of proteins binding coding and non-coding human RNAs using protein microarrays. BMC Genomics, 2012, 13, 633.	1.2	35
64	DNMT1 maintains progenitor function in self-renewing somatic tissue. Nature, 2010, 463, 563-567.	13.7	407
65	Invasive three-dimensional organotypic neoplasia from multiple normal human epithelia. Nature Medicine, 2010, 16, 1450-1455.	15.2	190
66	Long-Term Type VII Collagen Restoration to Human Epidermolysis Bullosa Skin Tissue. Human Gene Therapy, 2010, 21, 1299-1310.	1.4	80
67	Modeling Inducible Human Tissue Neoplasia Identifies an Extracellular Matrix Interaction Network Involved in Cancer Progression. Cancer Cell, 2009, 15, 477-488.	7.7	79
68	Control of differentiation in a self-renewing mammalian tissue by the histone demethylase JMJD3. Genes and Development, 2008, 22, 1865-1870.	2.7	239
69	Tumor Necrosis Factor Receptor 1/c-Jun-NH2-Kinase Signaling Promotes Human Neoplasia. Cancer Research, 2007, 67, 3827-3834.	0.4	46
70	Mek1/2 MAPK Kinases Are Essential for Mammalian Development, Homeostasis, and Raf-Induced Hyperplasia. Developmental Cell, 2007, 12, 615-629.	3.1	132
71	p63 regulates proliferation and differentiation of developmentally mature keratinocytes. Genes and Development, 2006, 20, 3185-3197.	2.7	412
72	NF-κB blockade and oncogenic Ras trigger invasive human epidermal neoplasia. Nature, 2003, 421, 639-643.	13.7	537

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73	CDK4 coexpression with Ras generates malignant human epidermal tumorigenesis. Nature Medicine, 2002, 8, 1105-1114.	15.2	190
74	Sustainable Systemic Delivery via a Single Injection of Lentivirus into Human Skin Tissue. Human Gene Therapy, 2001, 12, 1551-1558.	1.4	50
75	Impact of Laminin 5 Î²3 Gene versus Protein Replacement on Gene Expression Patterns in Junctional Epidermolysis Bullosa. Human Gene Therapy, 2001, 12, 1443-1448.	1.4	20
76	Sonic Hedgehog Opposes Epithelial Cell Cycle Arrest. Journal of Cell Biology, 1999, 147, 71-76.	2.3	144
77	Immunization via hair follicles by topical application of naked DNA to normal skin. Nature Biotechnology, 1999, 17, 870-872.	9.4	169
78	Corrective gene transfer in the human skin disorder lamellar ichthyosis. Nature Medicine, 1996, 2, 1263-1267.	15.2	167
79	Nucleosome disruption and enhancement of activator binding by a human SW1/SNF complex. Nature, 1994, 370, 477-481.	13.7	744
80	BRG1 contains a conserved domain of the SWI2/SNF2 family necessary for normal mitotic growth and transcription. Nature, 1993, 366, 170-174.	13.7	625
81	Omni-ATAC-seq: Improved ATAC-seq protocol. Protocol Exchange, 0, , .	0.3	21
82	RNA-Protein Interaction Detection (RaPID). Protocol Exchange, 0, , .	0.3	2
83	HiChIRP: RNA-centric chromatin conformation. Protocol Exchange, 0, , .	0.3	1