

# Kevin Huang

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

20  
papers

1,532  
citations

15  
h-index

30  
g-index

30  
ext. papers

1,903  
ext. citations

9.6  
avg, IF

4.14  
L-index

#	Paper	IF	Citations
20	Single-cell analysis of nonhuman primate preimplantation development in comparison to humans and mice. <i>Developmental Dynamics</i> , <b>2021</b> , 250, 974-985	2.9	3
19	Recent advances in preimplantation genetic diagnosis and screening. <i>Journal of Assisted Reproduction and Genetics</i> , <b>2016</b> , 33, 1129-34	3.4	18
18	Low CD38 Identifies Progenitor-like Inflammation-Associated Luminal Cells that Can Initiate Human Prostate Cancer and Predict Poor Outcome. <i>Cell Reports</i> , <b>2016</b> , 17, 2596-2606	10.6	67
17	Single-cell RNA-seq reveals distinct injury responses in different types of DRG sensory neurons. <i>Scientific Reports</i> , <b>2016</b> , 6, 31851	4.9	73
16	Simultaneous profiling of transcriptome and DNA methylome from a single cell. <i>Genome Biology</i> , <b>2016</b> , 17, 88	18.3	169
15	Reversible Regulation of Promoter and Enhancer Histone Landscape by DNA Methylation in Mouse Embryonic Stem Cells. <i>Cell Reports</i> , <b>2016</b> , 17, 289-302	10.6	65
14	Diagnostic value of maspin in distinguishing adenocarcinoma from benign biliary epithelium on endoscopic bile duct biopsy. <i>Human Pathology</i> , <b>2015</b> , 46, 1647-54	3.7	15
13	The naive state of human pluripotent stem cells: a synthesis of stem cell and preimplantation embryo transcriptome analyses. <i>Cell Stem Cell</i> , <b>2014</b> , 15, 410-415	18	117
12	A panel of CpG methylation sites distinguishes human embryonic stem cells and induced pluripotent stem cells. <i>Stem Cell Reports</i> , <b>2014</b> , 2, 36-43	8	30
11	Integrated analysis of DNA methylation and RNA transcriptome during in vitro differentiation of human pluripotent stem cells into retinal pigment epithelial cells. <i>PLoS ONE</i> , <b>2014</b> , 9, e91416	3.7	18
10	Selective demethylation and altered gene expression are associated with ICF syndrome in human-induced pluripotent stem cells and mesenchymal stem cells. <i>Human Molecular Genetics</i> , <b>2014</b> , 23, 6448-57	5.6	20
9	Recent Advances in Studying of Copy Number Variation and Gene Expression <b>2014</b> , 1		5
8	Genetic programs in human and mouse early embryos revealed by single-cell RNA sequencing. <i>Nature</i> , <b>2013</b> , 500, 593-7	50.4	622
7	Identification of novel molecular markers through transcriptomic analysis in human fetal and adult corneal endothelial cells. <i>Human Molecular Genetics</i> , <b>2013</b> , 22, 1271-9	5.6	47
6	Identification of miRNA signatures during the differentiation of hESCs into retinal pigment epithelial cells. <i>PLoS ONE</i> , <b>2012</b> , 7, e37224	3.7	25
5	Epigenetic modifications in distinction: histone versus DNA methylation in ESCs. <i>Cell Stem Cell</i> , <b>2011</b> , 8, 604-5	18	5
4	Functional modules distinguish human induced pluripotent stem cells from embryonic stem cells. <i>Stem Cells and Development</i> , <b>2011</b> , 20, 1937-50	4.4	25

3	Molecular signature of primary retinal pigment epithelium and stem-cell-derived RPE cells. <i>Human Molecular Genetics</i> , <b>2010</b> , 19, 4229-38	5.6	152
2	DNA methylation in cell differentiation and reprogramming: an emerging systematic view. <i>Regenerative Medicine</i> , <b>2010</b> , 5, 531-44	2.5	54
1	X-chromosome dosage compensation dynamics in human early embryos		2