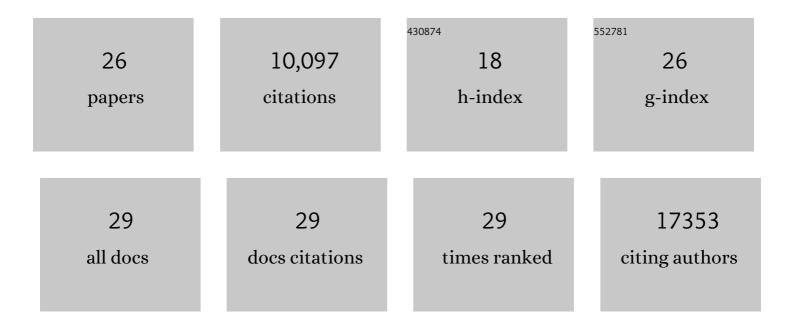
Gary C Hon

List of Publications by Year in descending order

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CARY C HON

#	Article	IF	CITATIONS
1	N6-methyladenosine-dependent regulation of messenger RNA stability. Nature, 2014, 505, 117-120.	27.8	3,138
2	Histone modifications at human enhancers reflect global cell-type-specific gene expression. Nature, 2009, 459, 108-112.	27.8	2,225
3	Base-Resolution Analysis of 5-Hydroxymethylcytosine in the Mammalian Genome. Cell, 2012, 149, 1368-1380.	28.9	912
4	Distinct Epigenomic Landscapes of Pluripotent and Lineage-Committed Human Cells. Cell Stem Cell, 2010, 6, 479-491.	11.1	747
5	Next-generation genomics: an integrative approach. Nature Reviews Genetics, 2010, 11, 476-486.	16.3	554
6	Global DNA hypomethylation coupled to repressive chromatin domain formation and gene silencing in breast cancer. Genome Research, 2012, 22, 246-258.	5.5	476
7	Blastocyst-like structures generated from human pluripotent stem cells. Nature, 2021, 591, 620-626.	27.8	275
8	Multiplexed Engineering and Analysis of Combinatorial Enhancer Activity in Single Cells. Molecular Cell, 2017, 66, 285-299.e5.	9.7	245
9	Tet-assisted bisulfite sequencing of 5-hydroxymethylcytosine. Nature Protocols, 2012, 7, 2159-2170.	12.0	236
10	In Situ Capture of Chromatin Interactions by Biotinylated dCas9. Cell, 2017, 170, 1028-1043.e19.	28.9	236
11	Identification of functionally distinct fibro-inflammatory and adipogenic stromal subpopulations in visceral adipose tissue of adult mice. ELife, 2018, 7, .	6.0	227
12	A Cellular Anatomy of the Normal Adult Human Prostate and Prostatic Urethra. Cell Reports, 2018, 25, 3530-3542.e5.	6.4	204
13	Predictive chromatin signatures in the mammalian genome. Human Molecular Genetics, 2009, 18, R195-R201.	2.9	196
14	SCINA: Semi-Supervised Analysis of Single Cells in Silico. Genes, 2019, 10, 531.	2.4	150
15	Identification and characterization of cellular heterogeneity within the developing renal interstitium. Development (Cambridge), 2020, 147, .	2.5	59
16	Tet-mediated covalent labelling of 5-methylcytosine for its genome-wide detection and sequencing. Nature Communications, 2013, 4, 1517.	12.8	48
17	Frequent sgRNA-barcode recombination in single-cell perturbation assays. PLoS ONE, 2018, 13, e0198635.	2.5	41
18	A single factor elicits multilineage reprogramming of astrocytes in the adult mouse striatum. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2107339119.	7.1	27

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#	Article	IF	CITATIONS
19	Tet-Assisted Bisulfite Sequencing (TAB-seq). Methods in Molecular Biology, 2018, 1708, 645-663.	0.9	23
20	Global Analysis of Enhancer Targets Reveals Convergent Enhancer-Driven Regulatory Modules. Cell Reports, 2019, 29, 2570-2578.e5.	6.4	20
21	Rational Reprogramming of Cellular States by Combinatorial Perturbation. Cell Reports, 2019, 27, 3486-3499.e6.	6.4	18
22	Using Gjd3-CreEGFP mice to examine atrioventricular node morphology and composition. Scientific Reports, 2019, 9, 2106.	3.3	10
23	FBA: feature barcoding analysis for single cell RNA-Seq. Bioinformatics, 2021, 37, 4266-4268.	4.1	9
24	Experimental and Computational Approaches for Single-Cell Enhancer Perturbation Assay. Methods in Molecular Biology, 2019, 1935, 203-221.	0.9	5
25	Computational identification of clonal cells in single-cell CRISPR screens. BMC Genomics, 2022, 23, 135.	2.8	4
26	Single-Cell Genomics: Catalyst for Cell Fate Engineering. Frontiers in Bioengineering and Biotechnology, 2021, 9, 748942.	4.1	1