

# Gary C Hon

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5137772/publications.pdf>

Version: 2024-02-01

26  
papers

10,097  
citations

430874

18  
h-index

552781

26  
g-index

29  
all docs

29  
docs citations

29  
times ranked

17353  
citing authors

#	ARTICLE	IF	CITATIONS
1	Computational identification of clonal cells in single-cell CRISPR screens. BMC Genomics, 2022, 23, 135.	2.8	4
2	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
3	Blastocyst-like structures generated from human pluripotent stem cells. Nature, 2021, 591, 620-626.	27.8	275
4	FBA: feature barcoding analysis for single cell RNA-Seq. Bioinformatics, 2021, 37, 4266-4268.	4.1	9
5	Single-Cell Genomics: Catalyst for Cell Fate Engineering. Frontiers in Bioengineering and Biotechnology, 2021, 9, 748942.	4.1	1
6	Identification and characterization of cellular heterogeneity within the developing renal interstitium. Development (Cambridge), 2020, 147, .	2.5	59
7	SCINA: Semi-Supervised Analysis of Single Cells in Silico. Genes, 2019, 10, 531.	2.4	150
8	Rational Reprogramming of Cellular States by Combinatorial Perturbation. Cell Reports, 2019, 27, 3486-3499.e6.	6.4	18
9	Experimental and Computational Approaches for Single-Cell Enhancer Perturbation Assay. Methods in Molecular Biology, 2019, 1935, 203-221.	0.9	5
10	Using Cjd3-CreEGFP mice to examine atrioventricular node morphology and composition. Scientific Reports, 2019, 9, 2106.	3.3	10
11	Global Analysis of Enhancer Targets Reveals Convergent Enhancer-Driven Regulatory Modules. Cell Reports, 2019, 29, 2570-2578.e5.	6.4	20
12	Tet-Assisted Bisulfite Sequencing (TAB-seq). Methods in Molecular Biology, 2018, 1708, 645-663.	0.9	23
13	A Cellular Anatomy of the Normal Adult Human Prostate and Prostatic Urethra. Cell Reports, 2018, 25, 3530-3542.e5.	6.4	204
14	Frequent sgRNA-barcode recombination in single-cell perturbation assays. PLoS ONE, 2018, 13, e0198635.	2.5	41
15	Identification of functionally distinct fibro-inflammatory and adipogenic stromal subpopulations in visceral adipose tissue of adult mice. ELife, 2018, 7, .	6.0	227
16	Multiplexed Engineering and Analysis of Combinatorial Enhancer Activity in Single Cells. Molecular Cell, 2017, 66, 285-299.e5.	9.7	245
17	In Situ Capture of Chromatin Interactions by Biotinylated dCas9. Cell, 2017, 170, 1028-1043.e19.	28.9	236
18	N6-methyladenosine-dependent regulation of messenger RNA stability. Nature, 2014, 505, 117-120.	27.8	3,138

#	ARTICLE	IF	CITATIONS
19	Tet-mediated covalent labelling of 5-methylcytosine for its genome-wide detection and sequencing. Nature Communications, 2013, 4, 1517.	12.8	48
20	Tet-assisted bisulfite sequencing of 5-hydroxymethylcytosine. Nature Protocols, 2012, 7, 2159-2170.	12.0	236
21	Base-Resolution Analysis of 5-Hydroxymethylcytosine in the Mammalian Genome. Cell, 2012, 149, 1368-1380.	28.9	912
22	Global DNA hypomethylation coupled to repressive chromatin domain formation and gene silencing in breast cancer. Genome Research, 2012, 22, 246-258.	5.5	476
23	Next-generation genomics: an integrative approach. Nature Reviews Genetics, 2010, 11, 476-486.	16.3	554
24	Distinct Epigenomic Landscapes of Pluripotent and Lineage-Committed Human Cells. Cell Stem Cell, 2010, 6, 479-491.	11.1	747
25	Predictive chromatin signatures in the mammalian genome. Human Molecular Genetics, 2009, 18, R195-R201.	2.9	196
26	Histone modifications at human enhancers reflect global cell-type-specific gene expression. Nature, 2009, 459, 108-112.	27.8	2,225