Peter C Scacheri

List of Publications by Year
in descending order

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47 papers	4,680 citations	172207 29 h-index	197535 49 g-index
52 all docs	52 docs citations	52 times ranked	10251 citing authors

#	Article	IF	Citations
1	Chromatin Mechanisms Driving Cancer. Cold Spring Harbor Perspectives in Biology, 2022, 14, a040956.	2.3	9
2	Convergence of case-specific epigenetic alterations identify a confluence of genetic vulnerabilities tied to opioid overdose. Molecular Psychiatry, 2022, 27, 2158-2170.	4.1	9
3	Beyond GWAS of Colorectal Cancer: Evidence of Interaction with Alcohol Consumption and Putative Causal Variant for the 10q24.2 Region. Cancer Epidemiology Biomarkers and Prevention, 2022, 31, 1077-1089.	1.1	6
4	Genetic architectures of proximal and distal colorectal cancer are partly distinct. Gut, 2021, 70, 1325-1334.	6.1	44
5	CHD7 promotes neural progenitor differentiation in embryonic stem cells via altered chromatin accessibility and nascent gene expression. Scientific Reports, 2020, 10, 17445.	1.6	23
6	Robust Hi-C Maps of Enhancer-Promoter Interactions Reveal the Function of Non-coding Genome in Neural Development and Diseases. Molecular Cell, 2020, 79, 521-534.e15.	4.5	110
7	Cell Type-Specific Intralocus Interactions Reveal Oligodendrocyte Mechanisms in MS. Cell, 2020, 181, 382-395.e21.	13.5	39
8	Chemotherapy-Induced Distal Enhancers Drive Transcriptional Programs to Maintain the Chemoresistant State in Ovarian Cancer. Cancer Research, 2019, 79, 4599-4611.	0.4	39
9	A miRNA-Mediated Approach to Dissect the Complexity of Tumor-Initiating Cell Function and Identify miRNA-Targeting Drugs. Stem Cell Reports, 2019, 12, 122-134.	2.3	8
10	Chromatin landscapes reveal developmentally encoded transcriptional states that define human glioblastoma. Journal of Experimental Medicine, 2019, 216, 1071-1090.	4.2	89
11	Genetic variant predictors of gene expression provide new insight into risk of colorectal cancer. Human Genetics, 2019, 138, 307-326.	1.8	44
12	Functional Enhancers Shape Extrachromosomal Oncogene Amplifications. Cell, 2019, 179, 1330-1341.e13.	13.5	206
13	Discovery of common and rare genetic risk variants for colorectal cancer. Nature Genetics, 2019, 51, 76-87.	9.4	377
14	Ex vivo screen identifies CDK12 as a metastatic vulnerability in osteosarcoma. Journal of Clinical Investigation, 2019, 129, 4377-4392.	3.9	34
15	Mismatch repair-signature mutations activate gene enhancers across human colorectal cancer epigenomes. ELife, 2019, 8, .	2.8	19
16	Targeting Epigenetics to Prevent Obesity Promoted Cancers. Cancer Prevention Research, 2018, 11, 125-128.	0.7	10
17	PRC2 Is Dispensablein Vivofor Î²-Catenin-Mediated Repression of Chondrogenesis in the Mouse Embryonic Cranial Mesenchyme. G3: Genes, Genomes, Genetics, 2018, 8, 491-503.	0.8	15
18	Therapeutic targeting of ependymoma as informed by oncogenic enhancer profiling. Nature, 2018, 553, 101-105.	13.7	170

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19	Positively selected enhancer elements endow osteosarcoma cells with metastatic competence. Nature Medicine, 2018, 24, 176-185.	15.2	126
20	Enhancers: bridging the gap between gene control and human disease. Human Molecular Genetics, 2018, 27, R219-R227.	1.4	51
21	Enhancer mapping uncovers phenotypic heterogeneity and evolution in patients with luminal breast cancer. Nature Medicine, 2018, 24, 1469-1480.	15.2	98
22	CHD7 represses the retinoic acid synthesis enzyme ALDH1A3 during inner ear development. JCI Insight, 2018, 3, .	2.3	27
23	Hotspots of aberrant enhancer activity punctuate the colorectal cancer epigenome. Nature Communications, 2017, 8, 14400.	5.8	93
24	iPSC Reprogramming Is Not Just an Open and Shut Case. Cell Stem Cell, 2017, 21, 711-712.	5.2	1
25	Transcription elongation factors represent in vivo cancer dependencies in glioblastoma. Nature, 2017, 547, 355-359.	13.7	156
26	Transcriptome-wide identification of mRNAs and lincRNAs associated with trastuzumab-resistance in HER2-positive breast cancer. Oncotarget, 2016, 7, 53230-53244.	0.8	30
27	Upregulation of Glucose-Regulated Protein 78 in Metastatic Cancer Cells Is Necessary for Lung Metastasis Progression. Neoplasia, 2016, 18, 699-710.	2.3	41
28	Modeling disease risk through analysis of physical interactions between genetic variants within chromatin regulatory circuitry. Nature Genetics, 2016, 48, 1313-1320.	9.4	57
29	mTOR Inhibition Mitigates Enhanced mRNA Translation Associated with the Metastatic Phenotype of Osteosarcoma Cells In Vivo. Clinical Cancer Research, 2016, 22, 6129-6141.	3.2	23
30	A Germline Variant on Chromosome 4q31.1 Associates with Susceptibility to Developing Colon Cancer Metastasis. PLoS ONE, 2016, 11, e0146435.	1.1	2
31	Mutations in the noncoding genome. Current Opinion in Pediatrics, 2015, 27, 659-664.	1.0	52
32	ZNF143 provides sequence specificity to secure chromatin interactions at gene promoters. Nature Communications, 2015, 6, 6186.	5.8	173
33	â€œPEAR-ingâ€•Genomic and Epigenomic Analyses for Cancer Gene Discovery. Cancer Discovery, 2015, 5, 1018-1020.	7.7	1
34	Enhancer variants: evaluating functions in common disease. Genome Medicine, 2014, 6, 85.	3.6	195
35	Combinatorial effects of multiple enhancer variants in linkage disequilibrium dictate levels of gene expression to confer susceptibility to common traits. Genome Research, 2014, 24, 1-13.	2.4	326
36	Epigenomic Comparison Reveals Activation of â€œSeedâ€•Enhancers during Transition from Naive to Primed Pluripotency. Cell Stem Cell, 2014, 14, 854-863.	5.2	137

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37	Knockdown of fbxl10/kdm2bb rescues chd7 morphant phenotype in a zebrafish model of CHARGE syndrome. Developmental Biology, 2013, 382, 57-69.	0.9	34
38	The Chromatin Fingerprint of Gene Enhancer Elements. Journal of Biological Chemistry, 2012, 287, 30888-30896.	1.6	77
39	Epigenomic Enhancer Profiling Defines a Signature of Colon Cancer. Science, 2012, 336, 736-739.	6.0	304
40	Otitis Media in a New Mouse Model for CHARGE Syndrome with a Deletion in the Chd7 Gene. PLoS ONE, 2012, 7, e34944.	1.1	23
41	Epigenetic signatures distinguish multiple classes of enhancers with distinct cellular functions. Genome Research, 2011, 21, 1273-1283.	2.4	487
42	Molecular and phenotypic aspects of CHD7 mutation in CHARGE syndrome. American Journal of Medical Genetics, Part A, 2010, 152A, 674-686.	0.7	265
43	CHD7 functions in the nucleolus as a positive regulator of ribosomal RNA biogenesis. Human Molecular Genetics, 2010, 19, 3491-3501.	1.4	91
44	Mutations in the CHD7 Gene: The Experience of a Commercial Laboratory. Genetic Testing and Molecular Biomarkers, 2010, 14, 881-891.	0.3	46
45	CHD7 Targets Active Gene Enhancer Elements to Modulate ES Cell-Specific Gene Expression. PLoS Genetics, 2010, 6, e1001023.	1.5	213
46	Genomic distribution of CHD7 on chromatin tracks H3K4 methylation patterns. Genome Research, 2009, 19, 590-601.	2.4	210
47	[14] Statistics for ChIPâ€chip and DNase Hypersensitivity Experiments on NimbleGen Arrays. Methods in Enzymology, 2006, 411, 270-282.	0.4	83