Terrence S Furey

List of Publications by Year
in descending order

92 papers	70,467 citations	71004 43 h-index	62345 84 g-index
101 all docs	101 docs citations	101 times ranked	85594 citing authors

#	Article	IF	Citations
1	Integrative analysis reveals mouse strain-dependent responses to acute ozone exposure associated with airway macrophage transcriptional activity. American Journal of Physiology - Lung Cellular and Molecular Physiology, 2022, 322, L33-L49.	1.3	7
2	Subcutaneous adipose tissue splice quantitative trait loci reveal differences in isoform usage associated with cardiometabolic traits. American Journal of Human Genetics, 2022, 109, 66-80.	2.6	13
3	Single-Cell Analysis Reveals Unexpected Cellular Changes and Transposon Expression Signatures in the Colonic Epithelium of Treatment-NaÃ¯ve Adult Crohnâ€™s Disease Patients. Cellular and Molecular Gastroenterology and Hepatology, 2022, 13, 1717-1740.	2.3	12
4	BET Protein Inhibition Regulates Macrophage Chromatin Accessibility and Microbiota-Dependent Colitis. Frontiers in Immunology, 2022, 13, 856966.	2.2	4
5	Increased colonic expression of ACE2 associates with poor prognosis in Crohnâ€™s disease. Scientific Reports, 2021, 11, 13533.	1.6	14
6	A machine learning approach identifies 5-ASA and ulcerative colitis as being linked with higher COVID-19 mortality in patients with IBD. Scientific Reports, 2021, 11, 16522.	1.6	9
7	Crohnâ€™s Disease Differentially Affects Region-Specific Composition and Aerotolerance Profiles of Mucosally Adherent Bacteria. Inflammatory Bowel Diseases, 2020, 26, 1843-1855.	0.9	9
8	Decreased Colonic Activin Receptor-Like Kinase 1 Disrupts Epithelial Barrier Integrity in Patients With Crohnâ€™s Disease. Cellular and Molecular Gastroenterology and Hepatology, 2020, 10, 779-796.	2.3	12
9	Integrative QTL analysis of gene expression and chromatin accessibility identifies multi-tissue patterns of genetic regulation. PLoS Genetics, 2020, 16, e1008537.	1.5	35
10	Title is missing!. , 2020, 16, e1008537.		0
11	Title is missing!. , 2020, 16, e1008537.		0
12	Title is missing!. , 2020, 16, e1008537.		0
13	Title is missing!. , 2020, 16, e1008537.		0
14	Adipose Tissue Gene Expression Associations Reveal Hundreds of Candidate Genes for Cardiometabolic Traits. American Journal of Human Genetics, 2019, 105, 773-787.	2.6	45
15	Redefining the IBDs using genome-scale molecular phenotyping. Nature Reviews Gastroenterology and Hepatology, 2019, 16, 296-311.	8.2	62
16	Tissue- and strain-specific effects of a genotoxic carcinogen 1,3-butadiene on chromatin and transcription. Mammalian Genome, 2018, 29, 153-167.	1.0	21
17	Molecular classification of Crohn's disease reveals two clinically relevant subtypes. Gut, 2018, 67, 36-42.	6.1	89
18	Colonic epithelial miR-31 associates with the development of Crohnâ€™s phenotypes. JCI Insight, 2018, 3, .	2.3	20

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19	DeFCoM: analysis and modeling of transcription factor binding sites using a motif-centric genomic footprinter. Bioinformatics, 2017, 33, 956-963.	1.8	30
20	Genetic and epigenetic determinants of inter-individual variability in responses to toxicants. Current Opinion in Toxicology, 2017, 6, 50-59.	2.6	11
21	Correcting nucleotide-specific biases in high-throughput sequencing data. BMC Bioinformatics, 2017, 18, 357.	1.2	18
22	Variation in DNA-Damage Responses to an Inhalational Carcinogen (1,3-Butadiene) in Relation to Strain-Specific Differences in Chromatin Accessibility and Gene Transcription Profiles in C57BL/6J and CAST/EiJ Mice. Environmental Health Perspectives, 2017, 125, 107006.	2.8	22
23	Genomic dissection of conserved transcriptional regulation in intestinal epithelial cells. PLoS Biology, 2017, 15, e2002054.	2.6	80
24	P-193â€ƒA Distinct Microbiome Signature Characterizes Patients with Penetrating and Fistulizing CrohnÊ¼s Disease. Inflammatory Bowel Diseases, 2016, 22, S67-S68.	0.9	1
25	Alterations to chromatin in intestinal macrophages link ILâ€10 deficiency to inappropriate inflammatory responses. European Journal of Immunology, 2016, 46, 1912-1925.	1.6	30
26	O-004â€ƒAnalysis of Chromatin and Transcriptional Profiles in CrohnÊ¼s Disease Reveals Molecular Subclasses and Highlights Functional Regulatory Regions Implicated in Disease. Inflammatory Bowel Diseases, 2016, 22, S1-S2.	0.9	1
27	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. Nature Communications, 2016, 7, 10495.	5.8	245
28	A hidden Markov random field-based Bayesian method for the detection of long-range chromosomal interactions in Hi-C data. Bioinformatics, 2016, 32, 650-656.	1.8	47
29	MicroRNAs Classify Different Disease Behavior Phenotypes of CrohnÊ¼s Disease and May Have Prognostic Utility. Inflammatory Bowel Diseases, 2015, 21, 2178-2187.	0.9	68
30	Removing reference mapping biases using limited or no genotype data identifies allelic differences in protein binding at disease-associated loci. BMC Medical Genomics, 2015, 8, 43.	0.7	13
31	Chromatin Accessibility Mapping Identifies Mediators of Basal Transcription and Retinoid-Induced Repression of OTX2 in Medulloblastoma. PLoS ONE, 2014, 9, e107156.	1.1	8
32	O-020â€ƒIL-10 Dependent Changes in Chromatin Accessibility Drive Altered Transcriptional Responses to the Enteric Microbiota in Lamina Propria Macrophages. Inflammatory Bowel Diseases, 2014, 20, S11-S14.	0.9	0
33	Novel Distal eQTL Analysis Demonstrates Effect of Population Genetic Architecture on Detecting and Interpreting Associations. Genetics, 2014, 198, 879-893.	1.2	14
34	Variation in chromatin accessibility in human kidney cancer links H3K36 methyltransferase loss with widespread RNA processing defects. Genome Research, 2014, 24, 241-250.	2.4	160
35	Tu1927 Genetically Driven Chromatin Organization Identifies Regulatory SNPs Associated With Crohn's Disease. Gastroenterology, 2014, 146, S-874.	0.6	0
36	GSAASeqSP: A Toolset for Gene Set Association Analysis of RNA-Seq Data. Scientific Reports, 2014, 4, 6347.	1.6	53

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37	Genetics Driving Epigenetics. Science, 2013, 342, 705-706.	6.0	47
38	Patterns of regulatory activity across diverse human cell types predict tissue identity, transcription factor binding, and long-range interactions. Genome Research, 2013, 23, 777-788.	2.4	203
39	A Genome-Wide Analysis of Open Chromatin in Human Epididymis Epithelial Cells Reveals Candidate Regulatory Elements for Genes Coordinating Epididymal Function1. Biology of Reproduction, 2013, 89, 104.	1.2	18
40	DNase-seq predicts regions of rotational nucleosome stability across diverse human cell types. Genome Research, 2013, 23, 1118-1129.	2.4	22
41	Extensive Evolutionary Changes in Regulatory Element Activity during Human Origins Are Associated with Altered Gene Expression and Positive Selection. PLoS Genetics, 2012, 8, e1002789.	1.5	135
42	A genome-wide analysis of open chromatin in human tracheal epithelial cells reveals novel candidate regulatory elements for lung function. Thorax, 2012, 67, 385-391.	2.7	20
43	Integrating genetic and gene expression evidence into genome-wide association analysis of gene sets. Genome Research, 2012, 22, 386-397.	2.4	90
44	Cell-type specific and combinatorial usage of diverse transcription factors revealed by genome-wide binding studies in multiple human cells. Genome Research, 2012, 22, 9-24.	2.4	119
45	Chromatin accessibility reveals insights into androgen receptor activation and transcriptional specificity. Genome Biology, 2012, 13, R88.	13.9	65
46	An integrated encyclopedia of DNA elements in the human genome. Nature, 2012, 489, 57-74.	13.7	15,516
47	ChIPâ€“seq and beyond: new and improved methodologies to detect and characterize proteinâ€“DNA interactions. Nature Reviews Genetics, 2012, 13, 840-852.	7.7	692
48	The accessible chromatin landscape of the human genome. Nature, 2012, 489, 75-82.	13.7	2,434
49	Mutational Signatures of De-Differentiation in Functional Non-Coding Regions of Melanoma Genomes. PLoS Genetics, 2012, 8, e1002871.	1.5	11
50	Identifying and Characterizing Regulatory Sequences in the Human Genome with Chromatin Accessibility Assays. Genes, 2012, 3, 651-670.	1.0	33
51	A Predictive Framework for Integrating Disparate Genomic Data Types Using Sample-Specific Gene Set Enrichment Analysis and Multi-Task Learning. PLoS ONE, 2012, 7, e44635.	1.1	5
52	High-resolution genome-wide in vivo footprinting of diverse transcription factors in human cells. Genome Research, 2011, 21, 456-464.	2.4	286
53	Open chromatin defined by DNaseI and FAIRE identifies regulatory elements that shape cell-type identity. Genome Research, 2011, 21, 1757-1767.	2.4	449
54	Dynamics of the epigenetic landscape during erythroid differentiation after GATA1 restoration. Genome Research, 2011, 21, 1659-1671.	2.4	110

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55	Heritable Individual-Specific and Allele-Specific Chromatin Signatures in Humans. Science, 2010, 328, 235-239.	6.0	304
56	A computational screen for site selective A-to-I editing detects novel sites in neuron specific Hu proteins. BMC Bioinformatics, 2010, 11, 6.	1.2	35
57	Allele-specific and heritable chromatin signatures in humans. Human Molecular Genetics, 2010, 19, R204-R209.	1.4	28
58	Both Noncoding and Protein-Coding RNAs Contribute to Gene Expression Evolution in the Primate Brain. Genome Biology and Evolution, 2010, 2, 67-79.	1.1	103
59	Global Epigenomic Analysis of Primary Human Pancreatic Islets Provides Insights into Type 2 Diabetes Susceptibility Loci. Cell Metabolism, 2010, 12, 443-455.	7.2	190
60	Global Epigenomic Analysis of Primary Human Pancreatic Islets Provides Insights into Type 2 Diabetes Susceptibility Loci. Cell Metabolism, 2010, 12, 683.	7.2	1
61	DNaseI hypersensitivity at gene-poor, FSH dystrophy-linked 4q35.2. Nucleic Acids Research, 2009, 37, 7381-7393.	6.5	15
62	Analysis of Complex Disease Association and Linkage Studies Using the University of California Santa Cruz Genome Browser. Circulation: Cardiovascular Genetics, 2009, 2, 199-204.	5.1	17
63	High-resolution mapping studies of chromatin and gene regulatory elements. Epigenomics, 2009, 1, 319-329.	1.0	5
64	A general integrative genomic feature transcription factor binding site prediction method applied to analysis of USF1 binding in cardiovascular disease. Human Genomics, 2009, 3, 221.	1.4	7
65	Abstract B44: Chromatin structure impacts androgen receptor transcriptional specificity in prostate cancer cell lines. , 2009, , .		0
66	High-Resolution Mapping andÂCharacterization of Open Chromatin across the Genome. Cell, 2008, 132, 311-322.	13.5	1,246
67	F-Seq: a feature density estimator for high-throughput sequence tags. Bioinformatics, 2008, 24, 2537-2538.	1.8	336
68	Identification and Characterization of Cell Typeâ€“Specific and Ubiquitous Chromatin Regulatory Structures in the Human Genome. PLoS Genetics, 2007, 3, e136.	1.5	196
69	Genomic sweeping for hypermethylated genes. Bioinformatics, 2007, 23, 281-288.	1.8	22
70	Comparison of human (and other) genome browsers. Human Genomics, 2006, 2, 266.	1.4	18
71	Genome-wide sequence and functional analysis of early replicating DNA in normal human fibroblasts. BMC Genomics, 2006, 7, 301.	1.2	15
72	Evidence of Influence of Genomic DNA Sequence on Human X Chromosome Inactivation. PLoS Computational Biology, 2006, 2, e113.	1.5	84

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73	Generation and annotation of the DNA sequences of human chromosomes 2 and 4. Nature, 2005, 434, 724-731.	13.7	85
74	Identification and characterization of cell type-specific and ubiquitous chromatin regulatory structures in the human genome. PLoS Genetics, 2005, preprint, e136.	1.5	0
75	Comparative Recombination Rates in the Rat, Mouse, and Human Genomes. Genome Research, 2004, 14, 528-538.	2.4	452
76	Analysis of Human mRNAs With the Reference Genome Sequence Reveals Potential Errors, Polymorphisms, and RNA Editing. Genome Research, 2004, 14, 2034-2040.	2.4	26
77	The Status, Quality, and Expansion of the NIH Full-Length cDNA Project: The Mammalian Gene Collection (MGC). Genome Research, 2004, 14, 2121-2127.	2.4	486
78	The DNA sequence and biology of human chromosome 19. Nature, 2004, 428, 529-535.	13.7	298
79	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. Nature, 2004, 428, 493-521.	13.7	1,943
80	The structure and evolution of centromeric transition regions within the human genome. Nature, 2004, 430, 857-864.	13.7	179
81	The UCSC Table Browser data retrieval tool. Nucleic Acids Research, 2004, 32, 493D-496.	6.5	2,074
82	The UCSC Genome Browser Database. Nucleic Acids Research, 2003, 31, 51-54.	6.5	1,460
83	The DNA sequence of human chromosome 7. Nature, 2003, 424, 157-164.	13.7	236
84	Covariation in Frequencies of Substitution, Deletion, Transposition, and Recombination During Eutherian Evolution. Genome Research, 2003, 13, 13-26.	2.4	263
85	Integration of the cytogenetic map with the draft human genome sequence. Human Molecular Genetics, 2003, 12, 1037-1044.	1.4	79
86	The Human Genome Browser at UCSC. Genome Research, 2002, 12, 996-1006.	2.4	8,776
87	Initial sequencing and comparative analysis of the mouse genome. Nature, 2002, 420, 520-562.	13.7	6,319
88	The Human Genome Browser at UCSC. Genome Research, 2002, 12, 996-1006.	2.4	1,472
89	A physical map of the human genome. Nature, 2001, 409, 934-941.	13.7	865
90	Initial sequencing and analysis of the human genome. Nature, 2001, 409, 860-921.	13.7	21,074

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91	Integration of cytogenetic landmarks into the draft sequence of the human genome. Nature, 2001, 409, 953-958.	13.7	302
92	PROMOTER REGION-BASED CLASSIFICATION OF GENES. , 2000, , 151-63.		33