

# Terrence S Furey

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/261462/publications.pdf>

Version: 2024-02-01

92  
papers

70,467  
citations

61857

43  
h-index

54797

84  
g-index

101  
all docs

101  
docs citations

101  
times ranked

76889  
citing authors

#	ARTICLE	IF	CITATIONS
1	Initial sequencing and analysis of the human genome. <i>Nature</i> , 2001, 409, 860-921.	13.7	21,074
2	An integrated encyclopedia of DNA elements in the human genome. <i>Nature</i> , 2012, 489, 57-74.	13.7	15,516
3	The Human Genome Browser at UCSC. <i>Genome Research</i> , 2002, 12, 996-1006.	2.4	8,776
4	Initial sequencing and comparative analysis of the mouse genome. <i>Nature</i> , 2002, 420, 520-562.	13.7	6,819
5	The accessible chromatin landscape of the human genome. <i>Nature</i> , 2012, 489, 75-82.	13.7	2,434
6	The UCSC Table Browser data retrieval tool. <i>Nucleic Acids Research</i> , 2004, 32, 493D-496.	6.5	2,074
7	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. <i>Nature</i> , 2004, 428, 493-521.	13.7	1,943
8	The Human Genome Browser at UCSC. <i>Genome Research</i> , 2002, 12, 996-1006.	2.4	1,472
9	The UCSC Genome Browser Database. <i>Nucleic Acids Research</i> , 2003, 31, 51-54.	6.5	1,460
10	High-Resolution Mapping and Characterization of Open Chromatin across the Genome. <i>Cell</i> , 2008, 132, 311-322.	13.5	1,246
11	A physical map of the human genome. <i>Nature</i> , 2001, 409, 934-941.	13.7	865
12	ChIP-seq and beyond: new and improved methodologies to detect and characterize protein-DNA interactions. <i>Nature Reviews Genetics</i> , 2012, 13, 840-852.	7.7	692
13	The Status, Quality, and Expansion of the NIH Full-Length cDNA Project: The Mammalian Gene Collection (MGC). <i>Genome Research</i> , 2004, 14, 2121-2127.	2.4	486
14	Comparative Recombination Rates in the Rat, Mouse, and Human Genomes. <i>Genome Research</i> , 2004, 14, 528-538.	2.4	452
15	Open chromatin defined by DNaseI and FAIRE identifies regulatory elements that shape cell-type identity. <i>Genome Research</i> , 2011, 21, 1757-1767.	2.4	449
16	F-Seq: a feature density estimator for high-throughput sequence tags. <i>Bioinformatics</i> , 2008, 24, 2537-2538.	1.8	336
17	Heritable Individual-Specific and Allele-Specific Chromatin Signatures in Humans. <i>Science</i> , 2010, 328, 235-239.	6.0	304
18	Integration of cytogenetic landmarks into the draft sequence of the human genome. <i>Nature</i> , 2001, 409, 953-958.	13.7	302

#	ARTICLE	IF	CITATIONS
19	The DNA sequence and biology of human chromosome 19. <i>Nature</i> , 2004, 428, 529-535.	13.7	298
20	High-resolution genome-wide in vivo footprinting of diverse transcription factors in human cells. <i>Genome Research</i> , 2011, 21, 456-464.	2.4	286
21	Covariation in Frequencies of Substitution, Deletion, Transposition, and Recombination During Eutherian Evolution. <i>Genome Research</i> , 2003, 13, 13-26.	2.4	263
22	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. <i>Nature Communications</i> , 2016, 7, 10495.	5.8	245
23	The DNA sequence of human chromosome 7. <i>Nature</i> , 2003, 424, 157-164.	13.7	236
24	Patterns of regulatory activity across diverse human cell types predict tissue identity, transcription factor binding, and long-range interactions. <i>Genome Research</i> , 2013, 23, 777-788.	2.4	203
25	Identification and Characterization of Cell Type-Specific and Ubiquitous Chromatin Regulatory Structures in the Human Genome. <i>PLoS Genetics</i> , 2007, 3, e136.	1.5	196
26	Global Epigenomic Analysis of Primary Human Pancreatic Islets Provides Insights into Type 2 Diabetes Susceptibility Loci. <i>Cell Metabolism</i> , 2010, 12, 443-455.	7.2	190
27	The structure and evolution of centromeric transition regions within the human genome. <i>Nature</i> , 2004, 430, 857-864.	13.7	179
28	Variation in chromatin accessibility in human kidney cancer links H3K36 methyltransferase loss with widespread RNA processing defects. <i>Genome Research</i> , 2014, 24, 241-250.	2.4	160
29	Extensive Evolutionary Changes in Regulatory Element Activity during Human Origins Are Associated with Altered Gene Expression and Positive Selection. <i>PLoS Genetics</i> , 2012, 8, e1002789.	1.5	135
30	Cell-type specific and combinatorial usage of diverse transcription factors revealed by genome-wide binding studies in multiple human cells. <i>Genome Research</i> , 2012, 22, 9-24.	2.4	119
31	Dynamics of the epigenetic landscape during erythroid differentiation after GATA1 restoration. <i>Genome Research</i> , 2011, 21, 1659-1671.	2.4	110
32	Both Noncoding and Protein-Coding RNAs Contribute to Gene Expression Evolution in the Primate Brain. <i>Genome Biology and Evolution</i> , 2010, 2, 67-79.	1.1	103
33	Integrating genetic and gene expression evidence into genome-wide association analysis of gene sets. <i>Genome Research</i> , 2012, 22, 386-397.	2.4	90
34	Molecular classification of Crohn's disease reveals two clinically relevant subtypes. <i>Gut</i> , 2018, 67, 36-42.	6.1	89
35	Generation and annotation of the DNA sequences of human chromosomes 2 and 4. <i>Nature</i> , 2005, 434, 724-731.	13.7	85
36	Evidence of Influence of Genomic DNA Sequence on Human X Chromosome Inactivation. <i>PLoS Computational Biology</i> , 2006, 2, e113.	1.5	84

#	ARTICLE	IF	CITATIONS
37	Genomic dissection of conserved transcriptional regulation in intestinal epithelial cells. <i>PLoS Biology</i> , 2017, 15, e2002054.	2.6	80
38	Integration of the cytogenetic map with the draft human genome sequence. <i>Human Molecular Genetics</i> , 2003, 12, 1037-1044.	1.4	79
39	MicroRNAs Classify Different Disease Behavior Phenotypes of Crohn's Disease and May Have Prognostic Utility. <i>Inflammatory Bowel Diseases</i> , 2015, 21, 2178-2187.	0.9	68
40	Chromatin accessibility reveals insights into androgen receptor activation and transcriptional specificity. <i>Genome Biology</i> , 2012, 13, R88.	13.9	65
41	Redefining the IBDs using genome-scale molecular phenotyping. <i>Nature Reviews Gastroenterology and Hepatology</i> , 2019, 16, 296-311.	8.2	62
42	GSAASeqSP: A Toolset for Gene Set Association Analysis of RNA-Seq Data. <i>Scientific Reports</i> , 2014, 4, 6347.	1.6	53
43	Genetics Driving Epigenetics. <i>Science</i> , 2013, 342, 705-706.	6.0	47
44	A hidden Markov random field-based Bayesian method for the detection of long-range chromosomal interactions in Hi-C data. <i>Bioinformatics</i> , 2016, 32, 650-656.	1.8	47
45	Adipose Tissue Gene Expression Associations Reveal Hundreds of Candidate Genes for Cardiometabolic Traits. <i>American Journal of Human Genetics</i> , 2019, 105, 773-787.	2.6	45
46	A computational screen for site selective A-to-I editing detects novel sites in neuron specific Hu proteins. <i>BMC Bioinformatics</i> , 2010, 11, 6.	1.2	35
47	Integrative QTL analysis of gene expression and chromatin accessibility identifies multi-tissue patterns of genetic regulation. <i>PLoS Genetics</i> , 2020, 16, e1008537.	1.5	35
48	Identifying and Characterizing Regulatory Sequences in the Human Genome with Chromatin Accessibility Assays. <i>Genes</i> , 2012, 3, 651-670.	1.0	33
49	PROMOTER REGION-BASED CLASSIFICATION OF GENES. , 2000, , 151-63.		33
50	DeFCoM: analysis and modeling of transcription factor binding sites using a motif-centric genomic footprinter. <i>Bioinformatics</i> , 2017, 33, 956-963.	1.8	30
51	Alterations to chromatin in intestinal macrophages link IL-10 deficiency to inappropriate inflammatory responses. <i>European Journal of Immunology</i> , 2016, 46, 1912-1925.	1.6	30
52	Allele-specific and heritable chromatin signatures in humans. <i>Human Molecular Genetics</i> , 2010, 19, R204-R209.	1.4	28
53	Analysis of Human mRNAs With the Reference Genome Sequence Reveals Potential Errors, Polymorphisms, and RNA Editing. <i>Genome Research</i> , 2004, 14, 2034-2040.	2.4	26
54	Genomic sweeping for hypermethylated genes. <i>Bioinformatics</i> , 2007, 23, 281-288.	1.8	22

#	ARTICLE	IF	CITATIONS
55	DNase-seq predicts regions of rotational nucleosome stability across diverse human cell types. <i>Genome Research</i> , 2013, 23, 1118-1129.	2.4	22
56	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. <i>Environmental Health Perspectives</i> , 2017, 125, 107006.	2.8	22
57	Tissue- and strain-specific effects of a genotoxic carcinogen 1,3-butadiene on chromatin and transcription. <i>Mammalian Genome</i> , 2018, 29, 153-167.	1.0	21
58	A genome-wide analysis of open chromatin in human tracheal epithelial cells reveals novel candidate regulatory elements for lung function. <i>Thorax</i> , 2012, 67, 385-391.	2.7	20
59	Colonic epithelial miR-31 associates with the development of Crohn's phenotypes. <i>JCI Insight</i> , 2018, 3, .	2.3	20
60	Comparison of human (and other) genome browsers. <i>Human Genomics</i> , 2006, 2, 266.	1.4	18
61	A Genome-Wide Analysis of Open Chromatin in Human Epididymis Epithelial Cells Reveals Candidate Regulatory Elements for Genes Coordinating Epididymal Function1. <i>Biology of Reproduction</i> , 2013, 89, 104.	1.2	18
62	Correcting nucleotide-specific biases in high-throughput sequencing data. <i>BMC Bioinformatics</i> , 2017, 18, 357.	1.2	18
63	Analysis of Complex Disease Association and Linkage Studies Using the University of California Santa Cruz Genome Browser. <i>Circulation: Cardiovascular Genetics</i> , 2009, 2, 199-204.	5.1	17
64	Genome-wide sequence and functional analysis of early replicating DNA in normal human fibroblasts. <i>BMC Genomics</i> , 2006, 7, 301.	1.2	15
65	DNaseI hypersensitivity at gene-poor, FSH dystrophy-linked 4q35.2. <i>Nucleic Acids Research</i> , 2009, 37, 7381-7393.	6.5	15
66	Novel Distal eQTL Analysis Demonstrates Effect of Population Genetic Architecture on Detecting and Interpreting Associations. <i>Genetics</i> , 2014, 198, 879-893.	1.2	14
67	Increased colonic expression of ACE2 associates with poor prognosis in Crohn's disease. <i>Scientific Reports</i> , 2021, 11, 13533.	1.6	14
68	Removing reference mapping biases using limited or no genotype data identifies allelic differences in protein binding at disease-associated loci. <i>BMC Medical Genomics</i> , 2015, 8, 43.	0.7	13
69	Subcutaneous adipose tissue splice quantitative trait loci reveal differences in isoform usage associated with cardiometabolic traits. <i>American Journal of Human Genetics</i> , 2022, 109, 66-80.	2.6	13
70	Decreased Colonic Activin Receptor-Like Kinase 1 Disrupts Epithelial Barrier Integrity in Patients With Crohn's Disease. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2020, 10, 779-796.	2.3	12
71	Single-Cell Analysis Reveals Unexpected Cellular Changes and Transposon Expression Signatures in the Colonic Epithelium of Treatment-Naïve Adult Crohn's Disease Patients. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2022, 13, 1717-1740.	2.3	12
72	Mutational Signatures of De-Differentiation in Functional Non-Coding Regions of Melanoma Genomes. <i>PLoS Genetics</i> , 2012, 8, e1002871.	1.5	11

#	ARTICLE	IF	CITATIONS
73	Genetic and epigenetic determinants of inter-individual variability in responses to toxicants. <i>Current Opinion in Toxicology</i> , 2017, 6, 50-59.	2.6	11
74	Crohn's Disease Differentially Affects Region-Specific Composition and Aerotolerance Profiles of Mucosally Adherent Bacteria. <i>Inflammatory Bowel Diseases</i> , 2020, 26, 1843-1855.	0.9	9
75	A machine learning approach identifies 5-ASA and ulcerative colitis as being linked with higher COVID-19 mortality in patients with IBD. <i>Scientific Reports</i> , 2021, 11, 16522.	1.6	9
76	Chromatin Accessibility Mapping Identifies Mediators of Basal Transcription and Retinoid-Induced Repression of OTX2 in Medulloblastoma. <i>PLoS ONE</i> , 2014, 9, e107156.	1.1	8
77	A general integrative genomic feature transcription factor binding site prediction method applied to analysis of USF1 binding in cardiovascular disease. <i>Human Genomics</i> , 2009, 3, 221.	1.4	7
78	Integrative analysis reveals mouse strain-dependent responses to acute ozone exposure associated with airway macrophage transcriptional activity. <i>American Journal of Physiology - Lung Cellular and Molecular Physiology</i> , 2022, 322, L33-L49.	1.3	7
79	High-resolution mapping studies of chromatin and gene regulatory elements. <i>Epigenomics</i> , 2009, 1, 319-329.	1.0	5
80	A Predictive Framework for Integrating Disparate Genomic Data Types Using Sample-Specific Gene Set Enrichment Analysis and Multi-Task Learning. <i>PLoS ONE</i> , 2012, 7, e44635.	1.1	5
81	BET Protein Inhibition Regulates Macrophage Chromatin Accessibility and Microbiota-Dependent Colitis. <i>Frontiers in Immunology</i> , 2022, 13, 856966.	2.2	4
82	Global Epigenomic Analysis of Primary Human Pancreatic Islets Provides Insights into Type 2 Diabetes Susceptibility Loci. <i>Cell Metabolism</i> , 2010, 12, 683.	7.2	1
83	P-193 A Distinct Microbiome Signature Characterizes Patients with Penetrating and Fistulizing Crohn's Disease. <i>Inflammatory Bowel Diseases</i> , 2016, 22, S67-S68.	0.9	1
84	O-004 Analysis of Chromatin and Transcriptional Profiles in Crohn's Disease Reveals Molecular Subclasses and Highlights Functional Regulatory Regions Implicated in Disease. <i>Inflammatory Bowel Diseases</i> , 2016, 22, S1-S2.	0.9	1
85	O-020 IL-10 Dependent Changes in Chromatin Accessibility Drive Altered Transcriptional Responses to the Enteric Microbiota in Lamina Propria Macrophages. <i>Inflammatory Bowel Diseases</i> , 2014, 20, S11-S14.	0.9	0
86	Tu1927 Genetically Driven Chromatin Organization Identifies Regulatory SNPs Associated With Crohn's Disease. <i>Gastroenterology</i> , 2014, 146, S-874.	0.6	0
87	Identification and characterization of cell type-specific and ubiquitous chromatin regulatory structures in the human genome. <i>PLoS Genetics</i> , 2005, preprint, e136.	1.5	0
88	Abstract B44: Chromatin structure impacts androgen receptor transcriptional specificity in prostate cancer cell lines. , 2009, , .		0
89	Title is missing!. , 2020, 16, e1008537.		0
90	Title is missing!. , 2020, 16, e1008537.		0

#	ARTICLE	IF	CITATIONS
91	Title is missing!. , 2020, 16, e1008537.		0
92	Title is missing!. , 2020, 16, e1008537.		0