

Richard S Sandstrom

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4002734/publications.pdf>

Version: 2024-02-01

53
papers

54,512
citations

76326

40
h-index

161849

54
g-index

63
all docs

63
docs citations

63
times ranked

67490
citing authors

#	ARTICLE	IF	CITATIONS
1	An integrated encyclopedia of DNA elements in the human genome. <i>Nature</i> , 2012, 489, 57-74.	27.8	15,516
2	Comprehensive Mapping of Long-Range Interactions Reveals Folding Principles of the Human Genome. <i>Science</i> , 2009, 326, 289-293.	12.6	7,170
3	Integrative analysis of 111 reference human epigenomes. <i>Nature</i> , 2015, 518, 317-330.	27.8	5,653
4	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. <i>Nature</i> , 2007, 447, 799-816.	27.8	4,709
5	Genetic effects on gene expression across human tissues. <i>Nature</i> , 2017, 550, 204-213.	27.8	3,500
6	Systematic Localization of Common Disease-Associated Variation in Regulatory DNA. <i>Science</i> , 2012, 337, 1190-1195.	12.6	3,129
7	The accessible chromatin landscape of the human genome. <i>Nature</i> , 2012, 489, 75-82.	27.8	2,434
8	A comparative encyclopedia of DNA elements in the mouse genome. <i>Nature</i> , 2014, 515, 355-364.	27.8	1,444
9	BEDOPS: high-performance genomic feature operations. <i>Bioinformatics</i> , 2012, 28, 1919-1920.	4.1	840
10	Comprehensive analysis of the chromatin landscape in <i>Drosophila melanogaster</i> . <i>Nature</i> , 2011, 471, 480-485.	27.8	781
11	An expansive human regulatory lexicon encoded in transcription factor footprints. <i>Nature</i> , 2012, 489, 83-90.	27.8	715
12	Resolving the complexity of the human genome using single-molecule sequencing. <i>Nature</i> , 2015, 517, 608-611.	27.8	714
13	Global mapping of protein-DNA interactions in vivo by digital genomic footprinting. <i>Nature Methods</i> , 2009, 6, 283-289.	19.0	533
14	Sequencing newly replicated DNA reveals widespread plasticity in human replication timing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 139-144.	7.1	497
15	Dynamic landscape and regulation of RNA editing in mammals. <i>Nature</i> , 2017, 550, 249-254.	27.8	495
16	Widespread plasticity in CTCF occupancy linked to DNA methylation. <i>Genome Research</i> , 2012, 22, 1680-1688.	5.5	494
17	Cell-of-origin chromatin organization shapes the mutational landscape of cancer. <i>Nature</i> , 2015, 518, 360-364.	27.8	491
18	Circuitry and Dynamics of Human Transcription Factor Regulatory Networks. <i>Cell</i> , 2012, 150, 1274-1286.	28.9	451

#	ARTICLE	IF	CITATIONS
19	Foxp3 Exploits a Pre-Existent Enhancer Landscape for Regulatory T Cell Lineage Specification. <i>Cell</i> , 2012, 151, 153-166.	28.9	411
20	An encyclopedia of mouse DNA elements (Mouse ENCODE). <i>Genome Biology</i> , 2012, 13, 418.	9.6	410
21	Native Elongating Transcript Sequencing Reveals Human Transcriptional Activity at Nucleotide Resolution. <i>Cell</i> , 2015, 161, 541-554.	28.9	342
22	Developmental Fate and Cellular Maturity Encoded in Human Regulatory DNA Landscapes. <i>Cell</i> , 2013, 154, 888-903.	28.9	329
23	A Temporal Chromatin Signature in Human Embryonic Stem Cells Identifies Regulators of Cardiac Development. <i>Cell</i> , 2012, 151, 221-232.	28.9	306
24	Domains of genome-wide gene expression dysregulation in Downâ€™s syndrome. <i>Nature</i> , 2014, 508, 345-350.	27.8	298
25	Mapping and Dynamics of Regulatory DNA and Transcription Factor Networks in <i>A. thaliana</i> . <i>Cell Reports</i> , 2014, 8, 2015-2030.	6.4	249
26	Genome Sequencing of Autism-Affected Families Reveals Disruption of Putative Noncoding Regulatory DNA. <i>American Journal of Human Genetics</i> , 2016, 98, 58-74.	6.2	248
27	Mouse regulatory DNA landscapes reveal global principles of cis-regulatory evolution. <i>Science</i> , 2014, 346, 1007-1012.	12.6	244
28	Global reference mapping of human transcription factor footprints. <i>Nature</i> , 2020, 583, 729-736.	27.8	228
29	Conservation of trans-acting circuitry during mammalian regulatory evolution. <i>Nature</i> , 2014, 515, 365-370.	27.8	211
30	Index and biological spectrum of human DNase I hypersensitive sites. <i>Nature</i> , 2020, 584, 244-251.	27.8	207
31	Large-scale identification of sequence variants influencing human transcription factor occupancy in vivo. <i>Nature Genetics</i> , 2015, 47, 1393-1401.	21.4	202
32	Dynamic reprogramming of chromatin accessibility during <i>Drosophila</i> embryo development. <i>Genome Biology</i> , 2011, 12, R43.	9.6	174
33	Probing DNA shape and methylation state on a genomic scale with DNase I. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 6376-6381.	7.1	151
34	CCCTC-Binding Factor and the Transcription Factor T-bet Orchestrate T Helper 1 Cell-Specific Structure and Function at the Interferon- γ Locus. <i>Immunity</i> , 2009, 31, 551-564.	14.3	129
35	Zebrafish globin switching occurs in two developmental stages and is controlled by the LCR. <i>Developmental Biology</i> , 2012, 366, 185-194.	2.0	122
36	DNase Iâ€™hypersensitive exons colocalize with promoters and distal regulatory elements. <i>Nature Genetics</i> , 2013, 45, 852-859.	21.4	112

#	ARTICLE	IF	CITATIONS
37	Genome-wide comparative analysis reveals human-mouse regulatory landscape and evolution. <i>BMC Genomics</i> , 2015, 16, 87.	2.8	62
38	DNase I hypersensitivity analysis of the mouse brain and retina identifies region-specific regulatory elements. <i>Epigenetics and Chromatin</i> , 2015, 8, 8.	3.9	60
39	Coupling transcription factor occupancy to nucleosome architecture with DNase-FLASH. <i>Nature Methods</i> , 2014, 11, 66-72.	19.0	58
40	Epigenetic Regulation by Chromatin Activation Mark H3K4me3 in Primate Progenitor Cells within Adult Neurogenic Niche. <i>Scientific Reports</i> , 2015, 4, 5371.	3.3	45
41	The birth of a human-specific neural gene by incomplete duplication and gene fusion. <i>Genome Biology</i> , 2017, 18, 49.	8.8	39
42	Late-replicating heterochromatin is characterized by decreased cytosine methylation in the human genome. <i>Genome Research</i> , 2011, 21, 1833-1840.	5.5	38
43	DNase I hypersensitivity mapping, genomic footprinting, and transcription factor networks in plants. <i>Current Plant Biology</i> , 2015, 3-4, 40-47.	4.7	33
44	Comprehensive characterization of erythroid-specific enhancers in the genomic regions of human KrÄ¼ppel-like factors. <i>BMC Genomics</i> , 2013, 14, 587.	2.8	32
45	Molecular targets of chromatin repressive mark H3K9me3 in primate progenitor cells within adult neurogenic niches. <i>Frontiers in Genetics</i> , 2014, 5, 252.	2.3	32
46	Functionally and Phenotypically Distinct Subpopulations of Marrow Stromal Cells Are Fibroblast in Origin and Induce Different Fates in Peripheral Blood Monocytes. <i>Stem Cells and Development</i> , 2014, 23, 729-740.	2.1	30
47	Integrated Functional Genomic Analysis Enables Annotation of Kidney Genome-Wide Association Study Loci. <i>Journal of the American Society of Nephrology: JASN</i> , 2019, 30, 421-441.	6.1	27
48	Integrated epigenomic profiling reveals endogenous retrovirus reactivation in renal cell carcinoma. <i>EBioMedicine</i> , 2019, 41, 427-442.	6.1	26
49	Cross-species analyses unravel the complexity of H3K27me3 and H4K20me3 in the context of neural stem progenitor cells. <i>Neuroepigenetics</i> , 2016, 6, 10-25.	2.8	18
50	Mapping and Dynamics of Regulatory DNA in Maturing <i>Arabidopsis thaliana</i> Siliques. <i>Frontiers in Plant Science</i> , 2019, 10, 1434.	3.6	13
51	A genome-wide map of adeno-associated virusâ€‘mediated human gene targeting. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 969-975.	8.2	12
52	Global Regulatory DNA Potentiation by SMARCA4 Propagates to Selective Gene Expression Programs via Domain-Level Remodeling. <i>Cell Reports</i> , 2020, 31, 107676.	6.4	8
53	Inaccessible LCG Promoters Act as Safeguards to Restrict T Cell Development to Appropriate Notch Signaling Environments. <i>Stem Cell Reports</i> , 2021, 16, 717-726.	4.8	0