

Richard S Sandstrom

List of Publications by Year in descending order

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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 | 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 |
| 2 | Global reference mapping of human transcription factor footprints. <i>Nature</i> , 2020, 583, 729-736. | 27.8 | 228 |
| 3 | Index and biological spectrum of human DNase I hypersensitive sites. <i>Nature</i> , 2020, 584, 244-251. | 27.8 | 207 |
| 4 | 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 |
| 5 | Integrated epigenomic profiling reveals endogenous retrovirus reactivation in renal cell carcinoma. <i>EBioMedicine</i> , 2019, 41, 427-442. | 6.1 | 26 |
| 6 | 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 |
| 7 | 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 |
| 8 | The birth of a human-specific neural gene by incomplete duplication and gene fusion. <i>Genome Biology</i> , 2017, 18, 49. | 8.8 | 39 |
| 9 | Dynamic landscape and regulation of RNA editing in mammals. <i>Nature</i> , 2017, 550, 249-254. | 27.8 | 495 |
| 10 | Genetic effects on gene expression across human tissues. <i>Nature</i> , 2017, 550, 204-213. | 27.8 | 3,500 |
| 11 | 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 |
| 12 | 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 |
| 13 | 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 |
| 14 | 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 |
| 15 | 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 |
| 16 | Integrative analysis of 111 reference human epigenomes. <i>Nature</i> , 2015, 518, 317-330. | 27.8 | 5,653 |
| 17 | Cell-of-origin chromatin organization shapes the mutational landscape of cancer. <i>Nature</i> , 2015, 518, 360-364. | 27.8 | 491 |
| 18 | Native Elongating Transcript Sequencing Reveals Human Transcriptional Activity at Nucleotide Resolution. <i>Cell</i> , 2015, 161, 541-554. | 28.9 | 342 |

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|----|---|------|-----------|
| 19 | Genome-wide comparative analysis reveals human-mouse regulatory landscape and evolution. <i>BMC Genomics</i> , 2015, 16, 87. | 2.8 | 62 |
| 20 | Large-scale identification of sequence variants influencing human transcription factor occupancy in vivo. <i>Nature Genetics</i> , 2015, 47, 1393-1401. | 21.4 | 202 |
| 21 | Resolving the complexity of the human genome using single-molecule sequencing. <i>Nature</i> , 2015, 517, 608-611. | 27.8 | 714 |
| 22 | 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 |
| 23 | 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 |
| 24 | 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 |
| 25 | Domains of genome-wide gene expression dysregulation in Downâ€™s syndrome. <i>Nature</i> , 2014, 508, 345-350. | 27.8 | 298 |
| 26 | Coupling transcription factor occupancy to nucleosome architecture with DNase-FLASH. <i>Nature Methods</i> , 2014, 11, 66-72. | 19.0 | 58 |
| 27 | Conservation of trans-acting circuitry during mammalian regulatory evolution. <i>Nature</i> , 2014, 515, 365-370. | 27.8 | 211 |
| 28 | A comparative encyclopedia of DNA elements in the mouse genome. <i>Nature</i> , 2014, 515, 355-364. | 27.8 | 1,444 |
| 29 | Mouse regulatory DNA landscapes reveal global principles of cis-regulatory evolution. <i>Science</i> , 2014, 346, 1007-1012. | 12.6 | 244 |
| 30 | 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 |
| 31 | Developmental Fate and Cellular Maturity Encoded in Human Regulatory DNA Landscapes. <i>Cell</i> , 2013, 154, 888-903. | 28.9 | 329 |
| 32 | Comprehensive characterization of erythroid-specific enhancers in the genomic regions of human KrÄ¶ppel-like factors. <i>BMC Genomics</i> , 2013, 14, 587. | 2.8 | 32 |
| 33 | DNase Iâ€™-hypersensitive exons colocalize with promoters and distal regulatory elements. <i>Nature Genetics</i> , 2013, 45, 852-859. | 21.4 | 112 |
| 34 | 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 |
| 35 | Widespread plasticity in CTCF occupancy linked to DNA methylation. <i>Genome Research</i> , 2012, 22, 1680-1688. | 5.5 | 494 |
| 36 | An encyclopedia of mouse DNA elements (Mouse ENCODE). <i>Genome Biology</i> , 2012, 13, 418. | 9.6 | 410 |

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|----|---|------|-----------|
| 37 | BEDOPS: high-performance genomic feature operations. <i>Bioinformatics</i> , 2012, 28, 1919-1920. | 4.1 | 840 |
| 38 | Foxp3 Exploits a Pre-Existent Enhancer Landscape for Regulatory T Cell Lineage Specification. <i>Cell</i> , 2012, 151, 153-166. | 28.9 | 411 |
| 39 | An integrated encyclopedia of DNA elements in the human genome. <i>Nature</i> , 2012, 489, 57-74. | 27.8 | 15,516 |
| 40 | An expansive human regulatory lexicon encoded in transcription factor footprints. <i>Nature</i> , 2012, 489, 83-90. | 27.8 | 715 |
| 41 | Systematic Localization of Common Disease-Associated Variation in Regulatory DNA. <i>Science</i> , 2012, 337, 1190-1195. | 12.6 | 3,129 |
| 42 | Circuitry and Dynamics of Human Transcription Factor Regulatory Networks. <i>Cell</i> , 2012, 150, 1274-1286. | 28.9 | 451 |
| 43 | A Temporal Chromatin Signature in Human Embryonic Stem Cells Identifies Regulators of Cardiac Development. <i>Cell</i> , 2012, 151, 221-232. | 28.9 | 306 |
| 44 | The accessible chromatin landscape of the human genome. <i>Nature</i> , 2012, 489, 75-82. | 27.8 | 2,434 |
| 45 | 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 |
| 46 | Dynamic reprogramming of chromatin accessibility during <i>Drosophila</i> embryo development. <i>Genome Biology</i> , 2011, 12, R43. | 9.6 | 174 |
| 47 | Comprehensive analysis of the chromatin landscape in <i>Drosophila melanogaster</i> . <i>Nature</i> , 2011, 471, 480-485. | 27.8 | 781 |
| 48 | Late-replicating heterochromatin is characterized by decreased cytosine methylation in the human genome. <i>Genome Research</i> , 2011, 21, 1833-1840. | 5.5 | 38 |
| 49 | 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 |
| 50 | CCCTC-Binding Factor and the Transcription Factor T-bet Orchestrate T Helper 1 Cell-Specific Structure and Function at the Interferon- β Locus. <i>Immunity</i> , 2009, 31, 551-564. | 14.3 | 129 |
| 51 | Global mapping of protein-DNA interactions in vivo by digital genomic footprinting. <i>Nature Methods</i> , 2009, 6, 283-289. | 19.0 | 533 |
| 52 | Comprehensive Mapping of Long-Range Interactions Reveals Folding Principles of the Human Genome. <i>Science</i> , 2009, 326, 289-293. | 12.6 | 7,170 |
| 53 | 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 |