

Richard I Sherwood

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1162178/publications.pdf>

Version: 2024-02-01

25
papers

1,568
citations

759233

12
h-index

713466

21
g-index

29
all docs

29
docs citations

29
times ranked

3144
citing authors

#	ARTICLE	IF	CITATIONS
1	Discovery of directional and nondirectional pioneer transcription factors by modeling DNase profile magnitude and shape. <i>Nature Biotechnology</i> , 2014, 32, 171-178.	17.5	415
2	Predictable and precise template-free CRISPR editing of pathogenic variants. <i>Nature</i> , 2018, 563, 646-651.	27.8	414
3	High-throughput mapping of regulatory DNA. <i>Nature Biotechnology</i> , 2016, 34, 167-174.	17.5	217
4	Gata6 potently initiates reprogramming of pluripotent and differentiated cells to extraembryonic endoderm stem cells. <i>Genes and Development</i> , 2015, 29, 1239-1255.	5.9	120
5	Wnt signaling specifies and patterns intestinal endoderm. <i>Mechanisms of Development</i> , 2011, 128, 387-400.	1.7	94
6	Cloning-free CRISPR. <i>Stem Cell Reports</i> , 2015, 5, 908-917.	4.8	53
7	Prostaglandin E2 Regulates Liver versus Pancreas Cell-Fate Decisions and Endodermal Outgrowth. <i>Developmental Cell</i> , 2014, 28, 423-437.	7.0	43
8	Cas9 Functionally Opens Chromatin. <i>PLoS ONE</i> , 2016, 11, e0152683.	2.5	34
9	Peptide fusion improves prime editing efficiency. <i>Nature Communications</i> , 2022, 13, .	12.8	27
10	A synergistic DNA logic predicts genome-wide chromatin accessibility. <i>Genome Research</i> , 2016, 26, 1430-1440.	5.5	18
11	A CRISPR view of gene regulation. <i>Current Opinion in Systems Biology</i> , 2017, 1, 1-8.	2.6	16
12	Dam mutants provide improved sensitivity and spatial resolution for profiling transcription factor binding. <i>Epigenetics and Chromatin</i> , 2019, 12, 36.	3.9	16
13	Identification of determinants of differential chromatin accessibility through a massively parallel genome-integrated reporter assay. <i>Genome Research</i> , 2020, 30, 1468-1480.	5.5	16
14	Small molecule inhibition of ATM kinase increases CRISPR-Cas9 1-bp insertion frequency. <i>Nature Communications</i> , 2021, 12, 5111.	12.8	15
15	Chemogenetic System Demonstrates That Cas9 Longevity Impacts Genome Editing Outcomes. <i>ACS Central Science</i> , 2020, 6, 2228-2237.	11.3	14
16	Comprehensive Mapping of Key Regulatory Networks that Drive Oncogene Expression. <i>Cell Reports</i> , 2020, 33, 108426.	6.4	14
17	A Multiplexed Barcodelet Single-Cell RNA-Seq Approach Elucidates Combinatorial Signaling Pathways that Drive ESC Differentiation. <i>Cell Stem Cell</i> , 2020, 26, 938-950.e6.	11.1	12
18	Using CRISPR to understand and manipulate gene regulation. <i>Development (Cambridge)</i> , 2021, 148, .	2.5	9

#	ARTICLE	IF	CITATIONS
19	Machine learning based CRISPR gRNA design for therapeutic exon skipping. PLoS Computational Biology, 2021, 17, e1008605.	3.2	7
20	A High-Throughput Genome-Integrated Assay Reveals Spatial Dependencies Governing Tcf7l2 Binding. Cell Systems, 2020, 11, 315-327.e5.	6.2	2
21	Detection of gene cis-regulatory element perturbations in single-cell transcriptomes. PLoS Computational Biology, 2021, 17, e1008789.	3.2	0
22	Machine learning based CRISPR gRNA design for therapeutic exon skipping. , 2021, 17, e1008605.		0
23	Machine learning based CRISPR gRNA design for therapeutic exon skipping. , 2021, 17, e1008605.		0
24	Machine learning based CRISPR gRNA design for therapeutic exon skipping. , 2021, 17, e1008605.		0
25	Machine learning based CRISPR gRNA design for therapeutic exon skipping. , 2021, 17, e1008605.		0