Jian Yan

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/3001950/publications.pdf

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25	5,370	18	27
papers	citations	h-index	g-index
35	35	35	10973 citing authors
all docs	docs citations	times ranked	

#	Article	IF	Citations
1	PELO facilitates PLK1-induced the ubiquitination and degradation of Smad4 and promotes the progression of prostate cancer. Oncogene, 2022, 41, 2945-2957.	2.6	8
2	Pancreatic progenitor epigenome maps prioritize type 2 diabetes risk genes with roles in development. ELife, $2021,10,$.	2.8	15
3	An atlas of the binding specificities of transcription factors in Pseudomonas aeruginosa directs prediction of novel regulators in virulence. ELife, 2021, 10, .	2.8	21
4	Directed Evolution of an Enhanced POU Reprogramming Factor for Cell Fate Engineering. Molecular Biology and Evolution, 2021, 38, 2854-2868.	3.5	11
5	Systematic analysis of binding of transcription factors to noncoding variants. Nature, 2021, 591, 147-151.	13.7	89
6	A compendium of DNA-binding specificities of transcription factors in Pseudomonas syringae. Nature Communications, 2020, 11, 4947.	5.8	19
7	CRISPR-assisted detection of RNA–protein interactions in living cells. Nature Methods, 2020, 17, 685-688.	9.0	82
8	An array of 60,000 antibodies for proteome-scale antibody generation and target discovery. Science Advances, 2020, 6, eaax2271.	4.7	22
9	Pancreatic islet chromatin accessibility and conformation reveals distal enhancer networks of type 2 diabetes risk. Nature Communications, 2019, 10, 2078.	5.8	82
10	Super-enhancers in transcriptional regulation and genome organization. Nucleic Acids Research, 2019, 47, 11481-11496.	6.5	85
11	Histone H3 lysine 4 monomethylation modulates long-range chromatin interactions at enhancers. Cell Research, 2018, 28, 204-220.	5.7	131
12	A Scalable Epitope Tagging Approach for High Throughput ChIP-Seq Analysis. ACS Synthetic Biology, 2017, 6, 1034-1042.	1.9	19
13	The non-coding variant rs1800734 enhances DCLK3 expression through long-range interaction and promotes colorectal cancer progression. Nature Communications, 2017, 8, 14418.	5.8	48
14	Impact of cytosine methylation on DNA binding specificities of human transcription factors. Science, 2017, 356, .	6.0	912
15	Mice deficient of Myc super-enhancer region reveal differential control mechanism between normal and pathological growth. ELife, 2017, 6, .	2.8	52
16	ERBB3 -rs2292239 as primary type 1 diabetes association locus among non- HLA genes in Chinese. Meta Gene, 2016, 9, 120-123.	0.3	14
17	A prostate cancer susceptibility allele at 6q22 increases RFX6 expression by modulating HOXB13 chromatin binding. Nature Genetics, 2014, 46, 126-135.	9.4	182
18	Transcription Factor Binding in Human Cells Occurs in Dense Clusters Formed around Cohesin Anchor Sites. Cell, 2013, 154, 801-813.	13.5	327

#	Article	IF	Citations
19	DNA-Binding Specificities of Human Transcription Factors. Cell, 2013, 152, 327-339.	13.5	1,085
20	Characterization of the colorectal cancer–associated enhancer MYC-335 at 8q24: the role of rs67491583. Cancer Genetics, 2012, 205, 25-33.	0.2	24
21	Mice Lacking a <i>Myc</i> Enhancer That Includes Human SNP rs6983267 Are Resistant to Intestinal Tumors. Science, 2012, 338, 1360-1363.	6.0	200
22	<i>MED12</i> , the <i>Mediator Complex Subunit 12</i> Gene, Is Mutated at High Frequency in Uterine Leiomyomas. Science, 2011, 334, 252-255.	6.0	547
23	Genome-wide analysis of ETS-family DNA-binding in vitro and in vivo. EMBO Journal, 2010, 29, 2147-2160.	3.5	497
24	Multiplexed massively parallel SELEX for characterization of human transcription factor binding specificities. Genome Research, 2010, 20, 861-873.	2.4	382
25	The common colorectal cancer predisposition SNP rs6983267 at chromosome 8q24 confers potential to enhanced Wnt signaling. Nature Genetics, 2009, 41, 885-890.	9.4	463