Judith B Zaugg

List of Publications by Year
in descending order

34 papers	2,935 citations	331259 21 h-index	395343 33 g-index
57 all docs	57 docs citations	57 times ranked	5807 citing authors

#	Article	IF	Citations
1	Data-driven hypothesis weighting increases detection power in genome-scale multiple testing. Nature Methods, 2016, 13, 577-580.	9.0	483
2	Extensive Variation in Chromatin States Across Humans. Science, 2013, 342, 750-752.	6.0	338
3	Genetic Control of Chromatin States in Humans Involves Local and Distal Chromosomal Interactions. Cell, 2015, 162, 1051-1065.	13.5	304
4	Bacterial adaptation through distributed sensing of metabolic fluxes. Molecular Systems Biology, 2010, 6, 355.	3.2	224
5	Gene Loops Enhance Transcriptional Directionality. Science, 2012, 338, 671-675.	6.0	219
6	Integrative Single-Cell RNA-Seq and ATAC-Seq Analysis of Human Developmental Hematopoiesis. Cell Stem Cell, 2021, 28, 472-487.e7.	5.2	184
7	Landscape of cohesin-mediated chromatin loops in the human genome. Nature, 2020, 583, 737-743.	13.7	134
8	Quantification of Differential Transcription Factor Activity and Multiomics-Based Classification into Activators and Repressors: diffTF. Cell Reports, 2019, 29, 3147-3159.e12.	2.9	84
9	Enhancers in disease: molecular basis and emerging treatment strategies. Trends in Molecular Medicine, 2021, 27, 1060-1073.	3.5	84
10	CTCF-Mediated Chromatin Loops between Promoter and Gene Body Regulate Alternative Splicing across Individuals. Cell Systems, 2017, 5, 628-637.e6.	2.9	80
11	Transcription factors: Bridge between cell signaling and gene regulation. Proteomics, 2021, 21, e2000034.	1.3	79
12	Cell-specific proteome analyses of human bone marrow reveal molecular features of age-dependent functional decline. Nature Communications, 2018, 9, 4004.	5.8	71
13	TET2 binding to enhancers facilitates transcription factor recruitment in hematopoietic cells. Genome Research, 2019, 29, 564-575.	2.4	66
14	Remodeling of active endothelial enhancers is associated with aberrant gene-regulatory networks in pulmonary arterial hypertension. Nature Communications, 2020, 11, 1673.	5.8	60
15	Mechanistic insights into transcription factor cooperativity and its impact on protein-phenotype interactions. Nature Communications, 2020, 11, 124.	5.8	54
16	Role of histone modifications and early termination in pervasive transcription and antisense-mediated gene silencing in yeast. Nucleic Acids Research, 2014, 42, 4348-4362.	6.5	50
17	A genomic model of condition-specific nucleosome behavior explains transcriptional activity in yeast. Genome Research, 2012, 22, 84-94.	2.4	48
18	Predictive features of gene expression variation reveal mechanistic link with differential expression. Molecular Systems Biology, 2020, 16, e9539.	3.2	42

#	Article	IF	Citations
19	Hepatic leukemia factor is a novel leukemic stem cell regulator in DNMT3A, NPM1, and FLT3-ITD triple-mutated AML. Blood, 2019, 134, 263-276.	0.6	41
20	Plasmodium falciparum malaria drives epigenetic reprogramming of human monocytes toward a regulatory phenotype. PLoS Pathogens, 2021, 17, e1009430.	2.1	40
21	Lysine 4 of histone H3.3 is required for embryonic stem cell differentiation, histone enrichment at regulatory regions and transcription accuracy. Nature Genetics, 2020, 52, 273-282.	9.4	37
22	Hotspot DNMT3A mutations in clonal hematopoiesis and acute myeloid leukemia sensitize cells to azacytidine via viral mimicry response. Nature Cancer, 2021, 2, 527-544.	5.7	37
23	Genomic Rewiring of SOX2 Chromatin Interaction Network during Differentiation of ESCs to Postmitotic Neurons. Cell Systems, 2020, 10, 480-494.e8.	2.9	25
24	Structure meets function: How chromatin organisation conveys functionality. Current Opinion in Systems Biology, 2017, 1, 129-136.	1.3	23
25	Backmasking in the yeast genome: encoding overlapping information for protein-coding and RNA degradation. Nucleic Acids Research, 2016, 44, 8065-8072.	6.5	15
26	CDK7/12/13 inhibition targets an oscillating leukemia stem cell network and synergizes with venetoclax in acute myeloid leukemia. EMBO Molecular Medicine, 2022, 14, e14990.	3.3	14
27	Structure Determination of a Flexible Cyclic Peptide Based on NMR and MD Simulation 3$\langle i\rangle J\langle /i\rangle$â€Coupling. ChemPhysChem, 2010, 11, 830-835.	1.0	13
28	Haplotype-specific MAPT exon 3 expression regulated by common intronic polymorphisms associated with Parkinsonian disorders. Molecular Neurodegeneration, 2017, 12, 79.	4.4	13
29	Influence of the bleaching interval on the luminosity of long-term discolored enamel-dentin discs. Clinical Oral Investigations, 2016, 20, 451-458.	1.4	6
30	Genome-wide quantification of transcription factor binding at single-DNA-molecule resolution using methyl-transferase footprinting. Nature Protocols, 2021, 16, 5673-5706.	5.5	6
31	Glucose Metabolism and Aging of Hematopoietic Stem and Progenitor Cells. International Journal of Molecular Sciences, 2022, 23, 3028.	1.8	6
32	SNPhood: investigate, quantify and visualise the epigenomic neighbourhood of SNPs using NGS data. Bioinformatics, 2016, 32, 2359-2360.	1.8	5
33	Donor cell memory confers a metastable state of directly converted cells. Cell Stem Cell, 2021, 28, 1291-1306.e10.	5.2	5
34	How Has the COVID-19 Pandemic Changed How You Will Approach Research and Lab Work in the Future?. Cell Systems, 2020, 11, 550-554.	2.9	0