

# Judith B Zaugg

## List of Publications by Year in descending order

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Version: 2024-02-01

34  
papers

2,935  
citations

331670

21  
h-index

395702

33  
g-index

57  
all docs

57  
docs citations

57  
times ranked

5807  
citing authors

#	ARTICLE	IF	CITATIONS
1	CDK7/12/13 inhibition targets an oscillating leukemia stem cell network and synergizes with venetoclax in acute myeloid leukemia. <i>EMBO Molecular Medicine</i> , 2022, 14, e14990.	6.9	14
2	Glucose Metabolism and Aging of Hematopoietic Stem and Progenitor Cells. <i>International Journal of Molecular Sciences</i> , 2022, 23, 3028.	4.1	6
3	Integrative Single-Cell RNA-Seq and ATAC-Seq Analysis of Human Developmental Hematopoiesis. <i>Cell Stem Cell</i> , 2021, 28, 472-487.e7.	11.1	184
4	<i>Plasmodium falciparum</i> malaria drives epigenetic reprogramming of human monocytes toward a regulatory phenotype. <i>PLoS Pathogens</i> , 2021, 17, e1009430.	4.7	40
5	Donor cell memory confers a metastable state of directly converted cells. <i>Cell Stem Cell</i> , 2021, 28, 1291-1306.e10.	11.1	5
6	Hotspot DNMT3A mutations in clonal hematopoiesis and acute myeloid leukemia sensitize cells to azacytidine via viral mimicry response. <i>Nature Cancer</i> , 2021, 2, 527-544.	13.2	37
7	Enhancers in disease: molecular basis and emerging treatment strategies. <i>Trends in Molecular Medicine</i> , 2021, 27, 1060-1073.	6.7	84
8	Transcription factors: Bridge between cell signaling and gene regulation. <i>Proteomics</i> , 2021, 21, e2000034.	2.2	79
9	Genome-wide quantification of transcription factor binding at single-DNA-molecule resolution using methyl-transferase footprinting. <i>Nature Protocols</i> , 2021, 16, 5673-5706.	12.0	6
10	Mechanistic insights into transcription factor cooperativity and its impact on protein-phenotype interactions. <i>Nature Communications</i> , 2020, 11, 124.	12.8	54
11	Landscape of cohesin-mediated chromatin loops in the human genome. <i>Nature</i> , 2020, 583, 737-743.	27.8	134
12	How Has the COVID-19 Pandemic Changed How You Will Approach Research and Lab Work in the Future?. <i>Cell Systems</i> , 2020, 11, 550-554.	6.2	0
13	Genomic Rewiring of SOX2 Chromatin Interaction Network during Differentiation of ESCs to Postmitotic Neurons. <i>Cell Systems</i> , 2020, 10, 480-494.e8.	6.2	25
14	Lysine 4 of histone H3.3 is required for embryonic stem cell differentiation, histone enrichment at regulatory regions and transcription accuracy. <i>Nature Genetics</i> , 2020, 52, 273-282.	21.4	37
15	Remodeling of active endothelial enhancers is associated with aberrant gene-regulatory networks in pulmonary arterial hypertension. <i>Nature Communications</i> , 2020, 11, 1673.	12.8	60
16	Predictive features of gene expression variation reveal mechanistic link with differential expression. <i>Molecular Systems Biology</i> , 2020, 16, e9539.	7.2	42
17	Hepatic leukemia factor is a novel leukemic stem cell regulator in DNMT3A, NPM1, and FLT3-ITD triple-mutated AML. <i>Blood</i> , 2019, 134, 263-276.	1.4	41
18	TET2 binding to enhancers facilitates transcription factor recruitment in hematopoietic cells. <i>Genome Research</i> , 2019, 29, 564-575.	5.5	66

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19	Quantification of Differential Transcription Factor Activity and Multiomics-Based Classification into Activators and Repressors: diffTF. <i>Cell Reports</i> , 2019, 29, 3147-3159.e12.	6.4	84
20	Cell-specific proteome analyses of human bone marrow reveal molecular features of age-dependent functional decline. <i>Nature Communications</i> , 2018, 9, 4004.	12.8	71
21	Structure meets function: How chromatin organisation conveys functionality. <i>Current Opinion in Systems Biology</i> , 2017, 1, 129-136.	2.6	23
22	CTCF-Mediated Chromatin Loops between Promoter and Gene Body Regulate Alternative Splicing across Individuals. <i>Cell Systems</i> , 2017, 5, 628-637.e6.	6.2	80
23	Haplotype-specific MAPT exon 3 expression regulated by common intronic polymorphisms associated with Parkinsonian disorders. <i>Molecular Neurodegeneration</i> , 2017, 12, 79.	10.8	13
24	Backmasking in the yeast genome: encoding overlapping information for protein-coding and RNA degradation. <i>Nucleic Acids Research</i> , 2016, 44, 8065-8072.	14.5	15
25	Data-driven hypothesis weighting increases detection power in genome-scale multiple testing. <i>Nature Methods</i> , 2016, 13, 577-580.	19.0	483
26	SNPhood: investigate, quantify and visualise the epigenomic neighbourhood of SNPs using NGS data. <i>Bioinformatics</i> , 2016, 32, 2359-2360.	4.1	5
27	Influence of the bleaching interval on the luminosity of long-term discolored enamel-dentin discs. <i>Clinical Oral Investigations</i> , 2016, 20, 451-458.	3.0	6
28	Genetic Control of Chromatin States in Humans Involves Local and Distal Chromosomal Interactions. <i>Cell</i> , 2015, 162, 1051-1065.	28.9	304
29	Role of histone modifications and early termination in pervasive transcription and antisense-mediated gene silencing in yeast. <i>Nucleic Acids Research</i> , 2014, 42, 4348-4362.	14.5	50
30	Extensive Variation in Chromatin States Across Humans. <i>Science</i> , 2013, 342, 750-752.	12.6	338
31	A genomic model of condition-specific nucleosome behavior explains transcriptional activity in yeast. <i>Genome Research</i> , 2012, 22, 84-94.	5.5	48
32	Gene Loops Enhance Transcriptional Directionality. <i>Science</i> , 2012, 338, 671-675.	12.6	219
33	Structure Determination of a Flexible Cyclic Peptide Based on NMR and MD Simulation 3<i>J</i>â€œCoupling. <i>ChemPhysChem</i> , 2010, 11, 830-835.	2.1	13
34	Bacterial adaptation through distributed sensing of metabolic fluxes. <i>Molecular Systems Biology</i> , 2010, 6, 355.	7.2	224