

Traude H Beilharz

List of Publications by Year in descending order

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Version: 2024-02-01

70
papers

4,319
citations

117453

34
h-index

118652

62
g-index

74
all docs

74
docs citations

74
times ranked

6294
citing authors

#	ARTICLE	IF	CITATIONS
1	Multiple Cargo Binding Sites on the COPII Subunit Sec24p Ensure Capture of Diverse Membrane Proteins into Transport Vesicles. <i>Cell</i> , 2003, 114, 497-509.	13.5	461
2	Accessory subunits are integral for assembly and function of human mitochondrial complex I. <i>Nature</i> , 2016, 538, 123-126.	13.7	429
3	A protein complex containing Tho2, Hpr1, Mft1 and a novel protein, Thp2, connects transcription elongation with mitotic recombination in <i>Saccharomyces cerevisiae</i> . <i>EMBO Journal</i> , 2000, 19, 5824-5834.	3.5	267
4	Role for yeast inhibitor of apoptosis (IAP)-like proteins in cell division. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1999, 96, 10170-10175.	3.3	186
5	Dynamics of ribosome scanning and recycling revealed by translation complex profiling. <i>Nature</i> , 2016, 535, 570-574.	13.7	186
6	A Network of Multiple Regulatory Layers Shapes Gene Expression in Fission Yeast. <i>Molecular Cell</i> , 2007, 26, 145-155.	4.5	184
7	Glucose Homeostasis Is Important for Immune Cell Viability during <i>Candida</i> Challenge and Host Survival of Systemic Fungal Infection. <i>Cell Metabolism</i> , 2018, 27, 988-1006.e7.	7.2	162
8	Bipartite Signals Mediate Subcellular Targeting of Tail-anchored Membrane Proteins in <i>Saccharomyces cerevisiae</i> . <i>Journal of Biological Chemistry</i> , 2003, 278, 8219-8223.	1.6	156
9	Distinct Roles for the Hsp40 and Hsp90 Molecular Chaperones during Cystic Fibrosis Transmembrane Conductance Regulator Degradation in Yeast. <i>Molecular Biology of the Cell</i> , 2004, 15, 4787-4797.	0.9	149
10	Widespread use of poly(A) tail length control to accentuate expression of the yeast transcriptome. <i>Rna</i> , 2007, 13, 982-997.	1.6	122
11	Cell wall integrity is linked to mitochondria and phospholipid homeostasis in <i>Candida albicans</i> through the activity of the post-transcriptional regulator Ccr4-Pop2. <i>Molecular Microbiology</i> , 2011, 79, 968-989.	1.2	115
12	A SNARE required for retrograde transport to the endoplasmic reticulum. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 9873-9877.	3.3	91
13	microRNA-Mediated Messenger RNA Deadenylation Contributes to Translational Repression in Mammalian Cells. <i>PLoS ONE</i> , 2009, 4, e6783.	1.1	89
14	ePAT: A simple method to tag adenylated RNA to measure poly(A)-tail length and other 3' RACE applications. <i>Rna</i> , 2012, 18, 1289-1295.	1.6	87
15	CDK13 cooperates with CDK12 to control global RNA polymerase II processivity. <i>Science Advances</i> , 2020, 6, .	4.7	79
16	PAT-seq: a method to study the integration of 3'-UTR dynamics with gene expression in the eukaryotic transcriptome. <i>Rna</i> , 2015, 21, 1502-1510.	1.6	78
17	Targeting of tail-anchored proteins to yeast mitochondria in vivo. <i>FEBS Letters</i> , 1999, 451, 243-248.	1.3	66
18	Dissecting the Roles of Mitochondrial Complex I Intermediate Assembly Complex Factors in the Biogenesis of Complex I. <i>Cell Reports</i> , 2020, 31, 107541.	2.9	64

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19	Alternative polyadenylation in the regulation and dysregulation of gene expression. <i>Seminars in Cell and Developmental Biology</i> , 2018, 75, 61-69.	2.3	59
20	Ccr4 contributes to tolerance of replication stress through control of CRT1 mRNA poly(A) tail length. <i>Journal of Cell Science</i> , 2006, 119, 5178-5192.	1.2	57
21	Mitochondrial Sorting and Assembly Machinery Subunit Sam37 in <i>Candida albicans</i> : Insight into the Roles of Mitochondria in Fitness, Cell Wall Integrity, and Virulence. <i>Eukaryotic Cell</i> , 2012, 11, 532-544.	3.4	57
22	Probing the closed-loop model of mRNA translation in living cells. <i>RNA Biology</i> , 2015, 12, 248-254.	1.5	54
23	In vivo mutation of pre-mRNA processing factor 8 (Prpf8) affects transcript splicing, cell survival and myeloid differentiation. <i>FEBS Letters</i> , 2013, 587, 2150-2157.	1.3	52
24	LIN-41 and OMA Ribonucleoprotein Complexes Mediate a Translational Repression-to-Activation Switch Controlling Oocyte Meiotic Maturation and the Oocyte-to-Embryo Transition in <i>Caenorhabditis elegans</i> . <i>Genetics</i> , 2017, 206, 2007-2039.	1.2	52
25	Translational profiling: The genome-wide measure of the nascent proteome. <i>Briefings in Functional Genomics & Proteomics</i> , 2004, 3, 103-111.	3.8	50
26	Integral membrane proteins in the mitochondrial outer membrane of <i>Saccharomyces cerevisiae</i> . <i>FEBS Journal</i> , 2006, 273, 1507-1515.	2.2	50
27	The Functions of Mediator in <i>Candida albicans</i> Support a Role in Shaping Species-Specific Gene Expression. <i>PLoS Genetics</i> , 2012, 8, e1002613.	1.5	50
28	piRNAs and Aubergine cooperate with Wispy poly(A) polymerase to stabilize mRNAs in the germ plasm. <i>Nature Communications</i> , 2017, 8, 1305.	5.8	49
29	A conserved proline residue is present in the transmembrane-spanning domain of Tom7 and other tail-anchored protein subunits of the TOM translocase. <i>FEBS Letters</i> , 2002, 514, 347-350.	1.3	44
30	SRSF3 promotes pluripotency through Nanog mRNA export and coordination of the pluripotency gene expression program. <i>ELife</i> , 2018, 7, .	2.8	44
31	Methods to Analyze MicroRNA-Mediated Control of mRNA Translation. <i>Methods in Enzymology</i> , 2007, 431, 83-111.	0.4	43
32	Translation complex profile sequencing to study the in vivo dynamics of mRNA-ribosome interactions during translation initiation, elongation and termination. <i>Nature Protocols</i> , 2017, 12, 697-731.	5.5	43
33	Topconfects: a package for confident effect sizes in differential expression analysis provides a more biologically useful ranked gene list. <i>Genome Biology</i> , 2019, 20, 67.	3.8	43
34	Introns Regulate Gene Expression in <i>Cryptococcus neoformans</i> in a Pab2p Dependent Pathway. <i>PLoS Genetics</i> , 2013, 9, e1003686.	1.5	39
35	A Metabolic Checkpoint for the Yeast-to-Hyphae Developmental Switch Regulated by Endogenous Nitric Oxide Signaling. <i>Cell Reports</i> , 2018, 25, 2244-2258.e7.	2.9	37
36	Transcriptional Profiling of a Yeast Colony Provides New Insight into the Heterogeneity of Multicellular Fungal Communities. <i>PLoS ONE</i> , 2012, 7, e46243.	1.1	34

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37	<i>ifet-1</i> is a broad scale translational repressor required for normal P granule formation in <i>C. elegans</i> . <i>Journal of Cell Science</i> , 2013, 126, 850-9.	1.2	32
38	Mft52, an Acid-bristle Protein in the Cytosol That Delivers Precursor Proteins to Yeast Mitochondria. <i>Journal of Biological Chemistry</i> , 1997, 272, 5320-5325.	1.6	31
39	Integration of Posttranscriptional Gene Networks into Metabolic Adaptation and Biofilm Maturation in <i>Candida albicans</i> . <i>PLoS Genetics</i> , 2015, 11, e1005590.	1.5	31
40	miR-222 isoforms are differentially regulated by type-I interferon. <i>Rna</i> , 2018, 24, 332-341.	1.6	31
41	A model system for mitochondrial biogenesis reveals evolutionary rewiring of protein import and membrane assembly pathways. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E3358-66.	3.3	30
42	Coordination of Cell Cycle Progression and Mitotic Spindle Assembly Involves Histone H3 Lysine 4 Methylation by Set1/COMPASS. <i>Genetics</i> , 2017, 205, 185-199.	1.2	28
43	FGF13 promotes metastasis of triple-negative breast cancer. <i>International Journal of Cancer</i> , 2020, 147, 230-243.	2.3	24
44	The Ccr4-Pop2-NOT mRNA Deadenylase Contributes to Septin Organization in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2009, 182, 955-966.	1.2	23
45	mRNA isoform diversity can obscure detection of miRNA-mediated control of translation. <i>Rna</i> , 2011, 17, 1025-1031.	1.6	23
46	Functional and genomic characterization of a xenograft model system for the study of metastasis in triple-negative breast cancer. <i>DMM Disease Models and Mechanisms</i> , 2018, 11, .	1.2	23
47	POS-1 Promotes Endo-mesoderm Development by Inhibiting the Cytoplasmic Polyadenylation of <i>neg-1</i> mRNA. <i>Developmental Cell</i> , 2015, 34, 108-118.	3.1	22
48	A Toxic Fusion Protein Accumulating between the Mitochondrial Membranes Inhibits Protein Assembly in Vivo. <i>Journal of Biological Chemistry</i> , 1998, 273, 35268-35272.	1.6	20
49	Transcriptome-wide measurement of mRNA polyadenylation state. <i>Methods</i> , 2009, 48, 294-300.	1.9	20
50	Role of miRNAs and alternative mRNA 3'-end cleavage and polyadenylation of their mRNA targets in cardiomyocyte hypertrophy. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2016, 1859, 744-756.	0.9	19
51	The YEATS Domain Histone Crotonylation Readers Control Virulence-Related Biology of a Major Human Pathogen. <i>Cell Reports</i> , 2020, 31, 107528.	2.9	19
52	Requirement for cleavage factor II _m in the control of alternative polyadenylation in breast cancer cells. <i>Rna</i> , 2020, 26, 969-981.	1.6	18
53	miRNA Effects on mRNA Closed-Loop Formation During Translation Initiation. <i>Progress in Molecular and Subcellular Biology</i> , 2010, 50, 99-112.	0.9	14
54	The mitochondrial protein targeting suppressor (<i>mts1</i>) mutation maps to the mRNA-binding domain of Npl3p and affects translation on cytoplasmic polysomes. <i>Molecular Microbiology</i> , 2002, 35, 1277-1285.	1.2	9

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55	Disruption of Iron Homeostasis and Mitochondrial Metabolism Are Promising Targets to Inhibit <i>Candida auris</i> . <i>Microbiology Spectrum</i> , 2022, 10, e0010022.	1.2	9
56	The mRNA Decay Pathway Regulates the Expression of the Flo11 Adhesin and Biofilm Formation in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2012, 191, 1387-1391.	1.2	8
57	Epitope-tagged yeast strains reveal promoter driven changes to 3' end formation and convergent antisense-transcription from common 3' UTRs. <i>Nucleic Acids Research</i> , 2016, 44, 377-386.	6.5	8
58	Annexin A1 Is Required for Efficient Tumor Initiation and Cancer Stem Cell Maintenance in a Model of Human Breast Cancer. <i>Cancers</i> , 2021, 13, 1154.	1.7	7
59	The protein encoded by the MFT1 gene is a targeting factor for mitochondrial precursor proteins, and not a core ribosomal protein. <i>FEBS Letters</i> , 1997, 407, 220-224.	1.3	5
60	The Detection and Bioinformatic Analysis of Alternative 3' UTR Isoforms as Potential Cancer Biomarkers. <i>International Journal of Molecular Sciences</i> , 2021, 22, 5322.	1.8	5
61	Genetic and pharmacological evidence for kinetic competition between alternative poly(A) sites in yeast. <i>ELife</i> , 2021, 10, .	2.8	5
62	PAT-Seq: A Method for Simultaneous Quantitation of Gene Expression, Poly(A)-Site Selection and Poly(A)-Length Distribution in Yeast Transcriptomes. <i>Methods in Molecular Biology</i> , 2019, 2049, 141-164.	0.4	5
63	Polyadenylation State Microarray (PASTA) Analysis. <i>Methods in Molecular Biology</i> , 2011, 759, 133-148.	0.4	4
64	Yeast hEST1A/B (SMG5/6)-Like Proteins Contribute to Environment-Sensing Adaptive Gene Expression Responses. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 1649-1659.	0.8	4
65	3'-UTRs and the Control of Protein Expression in Space and Time. <i>Advances in Experimental Medicine and Biology</i> , 2019, 1203, 133-148.	0.8	4
66	Understanding the regulation of coding and noncoding transcription in cell populations. <i>Current Genetics</i> , 2016, 62, 317-319.	0.8	3
67	Using Klenow-Mediated Extension to Measure Poly(A)-Tail Length and Position in the Transcriptome. <i>Methods in Molecular Biology</i> , 2014, 1125, 25-42.	0.4	2
68	Seeking a Role for Translational Control by Alternative Polyadenylation in <i>Saccharomyces cerevisiae</i> . <i>Microorganisms</i> , 2021, 9, 1885.	1.6	1
69	A novel cause of DKC1 related bone marrow failure: Partial deletion of the 3' untranslated region. <i>EJHaem</i> , 2021, 2, 157-166.	0.4	1
70	Probing connectivity between transcriptional and post-transcriptional gene networks. <i>Microbiology Australia</i> , 2011, 32, 166.	0.1	0