

Elizabeth J Grayhack

List of Publications by Year in descending order

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42
papers

3,517
citations

186265

28
h-index

289244

40
g-index

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45
docs citations

45
times ranked

3716
citing authors

#	ARTICLE	IF	CITATIONS
1	Frameshifting at collided ribosomes is modulated by elongation factor eEF3 and by integrated stress response regulators Gcn1 and Gcn20. <i>Rna</i> , 2022, 28, 320-339.	3.5	13
2	Conservation of location of several specific inhibitory codon pairs in the <i>Saccharomyces sensu stricto</i> yeasts reveals translational selection. <i>Nucleic Acids Research</i> , 2019, 47, 1164-1177.	14.5	15
3	Multi-protein bridging factor 1(Mbf1), Rps3 and Asc1 prevent stalled ribosomes from frameshifting. <i>ELife</i> , 2018, 7, .	6.0	37
4	Synonymous Codons: Choose Wisely for Expression. <i>Trends in Genetics</i> , 2017, 33, 283-297.	6.7	161
5	A genome wide dosage suppressor network reveals genomic robustness. <i>Nucleic Acids Research</i> , 2017, 45, 255-270.	14.5	13
6	Adjacent Codons Act in Concert to Modulate Translation Efficiency in Yeast. <i>Cell</i> , 2016, 166, 679-690.	28.9	180
7	RNA-ID, a Powerful Tool for Identifying and Characterizing Regulatory Sequences. <i>Methods in Enzymology</i> , 2016, 572, 237-253.	1.0	1
8	Functional profiling in <i>Streptococcus mutans</i> : construction and examination of a genomic collection of gene deletion mutants. <i>Molecular Oral Microbiology</i> , 2015, 30, 474-495.	2.7	37
9	Asc1, homolog of human RACK1, prevents frameshifting in yeast by ribosomes stalled at CGA codon repeats. <i>Rna</i> , 2015, 21, 935-945.	3.5	68
10	Identification of the determinants of tRNA function and susceptibility to rapid tRNA decay by high-throughput in vivo analysis. <i>Genes and Development</i> , 2014, 28, 1721-1732.	5.9	58
11	The Structure of Yeast Glutamyl-tRNA Synthetase and Modeling of Its Interaction with tRNA. <i>Journal of Molecular Biology</i> , 2013, 425, 2480-2493.	4.2	13
12	Translation of CGA codon repeats in yeast involves quality control components and ribosomal protein L1. <i>Rna</i> , 2013, 19, 1208-1217.	3.5	100
13	Structural conservation of an ancient tRNA sensor in eukaryotic glutamyl-tRNA synthetase. <i>Nucleic Acids Research</i> , 2012, 40, 3723-3731.	14.5	14
14	RNA-ID, a highly sensitive and robust method to identify <i>cis</i> -regulatory sequences using superfolder GFP and a fluorescence-based assay. <i>Rna</i> , 2012, 18, 2335-2344.	3.5	22
15	Control of translation efficiency in yeast by codon-anticodon interactions. <i>Rna</i> , 2010, 16, 2516-2528.	3.5	143
16	Heterologous expression of L. major proteins in <i>S. cerevisiae</i> : a test of solubility, purity, and gene recoding. <i>Journal of Structural and Functional Genomics</i> , 2009, 10, 233-247.	1.2	43
17	Identification of yeast tRNA Um ₄₄ 2 ^O -methyltransferase (Trm44) and demonstration of a Trm44 role in sustaining levels of specific tRNA ^{Ser} species. <i>Rna</i> , 2008, 14, 158-169.	3.5	77
18	Identification and Analysis of tRNAs That Are Degraded in <i>Saccharomyces cerevisiae</i> Due To Lack of Modifications. <i>Methods in Enzymology</i> , 2008, 449, 221-237.	1.0	16

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19	Degradation of several hypomodified mature tRNA species in <i>Saccharomyces cerevisiae</i> is mediated by Met22 and the 5' and 3' exonucleases Rat1 and Xrn1. <i>Genes and Development</i> , 2008, 22, 1369-1380.	5.9	228
20	Structural Genomics of Pathogenic Protozoa: an Overview. <i>Methods in Molecular Biology</i> , 2008, 426, 497-513.	0.9	38
21	The use of <i>Saccharomyces cerevisiae</i> proteomic libraries to identify RNA-modifying proteins. <i>Methods in Molecular Biology</i> , 2008, 488, 383-393.	0.9	2
22	A novel tRNA degradation pathway that acts on mature tRNA. <i>FASEB Journal</i> , 2008, 22, 994.2.	0.5	0
23	The 2'-O-methyltransferase responsible for modification of yeast tRNA at position 4. <i>Rna</i> , 2007, 13, 404-413.	3.5	45
24	Blocking S-adenosylmethionine synthesis in yeast allows selenomethionine incorporation and multiwavelength anomalous dispersion phasing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 6678-6683.	7.1	45
25	Characteristics Affecting Expression and Solubilization of Yeast Membrane Proteins. <i>Journal of Molecular Biology</i> , 2007, 365, 621-636.	4.2	43
26	Identification and Characterization of Modification Enzymes by Biochemical Analysis of the Proteome. <i>Methods in Enzymology</i> , 2007, 425, 139-152.	1.0	3
27	Proteome-Scale Analysis of Biochemical Activity. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2006, 41, 315-327.	5.2	13
28	Rapid tRNA Decay Can Result from Lack of Nonessential Modifications. <i>Molecular Cell</i> , 2006, 21, 87-96.	9.7	409
29	Pseudouridylation of yeast U2 snRNA is catalyzed by either an RNA-guided or RNA-independent mechanism. <i>EMBO Journal</i> , 2005, 24, 2403-2413.	7.8	73
30	tRNA m7G methyltransferase Trm8p/Trm82p: Evidence linking activity to a growth phenotype and implicating Trm82p in maintaining levels of active Trm8p. <i>Rna</i> , 2005, 11, 821-830.	3.5	96
31	Biochemical and genetic analysis of the yeast proteome with a movable ORF collection. <i>Genes and Development</i> , 2005, 19, 2816-2826.	5.9	443
32	Depletion of <i>Saccharomyces cerevisiae</i> tRNA ^{His} Guanylyltransferase Thg1p Leads to Uncharged tRNA ^{His} with Additional m5C. <i>Molecular and Cellular Biology</i> , 2005, 25, 8191-8201.	2.3	87
33	A Facile Method for High-throughput Co-expression of Protein Pairs. <i>Molecular and Cellular Proteomics</i> , 2004, 3, 934-938.	3.8	105
34	The essential transcription factor Reb1p interacts with the CLB2 UAS outside of the G2/M control region. <i>Nucleic Acids Research</i> , 2003, 31, 4597-4607.	14.5	12
35	Biochemical genomics approach to map activities to genes activities to gene. <i>Methods in Enzymology</i> , 2002, 350, 546-559.	1.0	31
36	Genomic analysis of biochemical function. <i>Current Opinion in Chemical Biology</i> , 2001, 5, 34-39.	6.1	22

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37	A Biochemical Genomics Approach for Identifying Genes by the Activity of Their Products. <i>Science</i> , 1999, 286, 1153-1155.	12.6	408
38	Multiple Phosphorylated Forms of the <i>Saccharomyces cerevisiae</i> Mcm1 Protein Include an Isoform Induced in Response to High Salt Concentrations. <i>Molecular and Cellular Biology</i> , 1997, 17, 819-832.	2.3	59
39	A library of yeast genomic MCM1 binding sites contains genes involved in cell cycle control, cell wall and membrane structure, and metabolism. <i>Molecular and Cellular Biology</i> , 1994, 14, 348-359.	2.3	40
40	Transcription antitermination by phage lambda gene Q protein requires a DNA segment spanning the RNA start site.. <i>Genes and Development</i> , 1987, 1, 217-226.	5.9	47
41	Phage lambda gene Q antiterminator recognizes RNA polymerase near the promoter and accelerates it through a pause site. <i>Cell</i> , 1985, 42, 259-269.	28.9	174
42	The phage λ Q gene product: Activity of a transcription antiterminator in vitro. <i>Cell</i> , 1982, 30, 637-648.	28.9	81