Jeff Coller

List of Publications by Year in Descending Order

49 papers	4,887 citations	26 h-index	69 g-index
91 ext. papers	6,099 ext. citations	17.3 avg, IF	6.25 L-index

#	Paper	IF	Citations
49	Suppression of premature transcription termination leads to reduced mRNA isoform diversity and neurodegeneration.. *Neuron*, **2022**,	13.9	2
48	Codon optimality-mediated mRNA degradation: Linking translational elongation to mRNA stability.. *Molecular Cell*, **2022**, 82, 1467-1476	17.6	0
47	Roles of mRNA poly(A) tails in regulation of eukaryotic gene expression. *Nature Reviews Molecular Cell Biology*, **2021**,	48.7	14
46	Codon and amino acid content are associated with mRNA stability in mammalian cells. *PLoS ONE*, **2020**, 15, e0228730	3.7	19
45	Quantitative tRNA-sequencing uncovers metazoan tissue-specific tRNA regulation. *Nature Communications*, **2020**, 11, 4104	17.4	29
44	The Ccr4-Not complex monitors the translating ribosome for codon optimality. *Science*, **2020**, 368,	33.3	59
43	Codon optimality, bias and usage in translation and mRNA decay. *Nature Reviews Molecular Cell Biology*, **2018**, 19, 20-30	48.7	275
42	Translation elongation and mRNA stability are coupled through the ribosomal A-site. *Rna*, **2018**, 24, 1377-1389	5.1	26
41	Attenuated Codon Optimality Contributes to Neural-Specific mRNA Decay in Drosophila. *Cell Reports*, **2018**, 24, 1704-1712	10.6	25
40	mRNA Deadenylation Is Coupled to Translation Rates by the Differential Activities of Ccr4-Not Nucleases. *Molecular Cell*, **2018**, 70, 1089-1100.e8	17.6	100
39	Structural and molecular mechanisms for the control of eukaryotic 5T3TmRNA decay. *Nature Structural and Molecular Biology*, **2018**, 25, 1077-1085	17.6	58
38	Short poly(A) tails are a conserved feature of highly expressed genes. *Nature Structural and Molecular Biology*, **2017**, 24, 1057-1063	17.6	106
37	The DEAD-Box Protein Dhh1p Couples mRNA Decay and Translation by Monitoring Codon Optimality. *Cell*, **2016**, 167, 122-132.e9	56.2	148
36	A Universal Code for mRNA Stability?. *Trends in Genetics*, **2016**, 32, 687-688	8.5	12
35	mRNA decapping in 3D. *Nature Structural and Molecular Biology*, **2016**, 23, 954-956	17.6	5
34	The deadenylase components Not2p, Not3p, and Not5p promote mRNA decapping. *Rna*, **2016**, 22, 709-21	5.8	21
33	Cotranslational microRNA mediated messenger RNA destabilization. *ELife*, **2016**, 5,	8.9	23

32	Codon optimality is a major determinant of mRNA stability. *Cell*, **2015**, 160, 1111-24	56.2	485
31	Pausing on Polyribosomes: Make Way for Elongation in Translational Control. *Cell*, **2015**, 163, 292-300	56.2	111
30	A Method that Will Captivate U. *Molecular Cell*, **2015**, 59, 716-7	17.6	2
29	Caps and tales. *Rna*, **2015**, 21, 588-9	5.8	
28	KLF15 Establishes the Landscape of Diurnal Expression in the Heart. *Cell Reports*, **2015**, 13, 2368-2375	10.6	51
27	Translation of small open reading frames within unannotated RNA transcripts in Saccharomyces cerevisiae. *Cell Reports*, **2014**, 7, 1858-66	10.6	119
26	PAN-orama: three convergent views of a eukaryotic deadenylase. *Nature Structural and Molecular Biology*, **2014**, 21, 577-8	17.6	1
25	RNA in unexpected places: long non-coding RNA functions in diverse cellular contexts. *Nature Reviews Molecular Cell Biology*, **2013**, 14, 699-712	48.7	1047
24	The DHH1/RCKp54 family of helicases: an ancient family of proteins that promote translational silencing. *Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms*, **2013**, 1829, 817-23	6	46
23	Polysome analysis for determining mRNA and ribosome association in Saccharomyces cerevisiae. *Methods in Enzymology*, **2013**, 530, 193-206	1.7	2
22	Method for measuring mRNA decay rate in Saccharomyces cerevisiae. *Methods in Enzymology*, **2013**, 530, 137-55	1.7	3
21	Control of mRNA metabolism by deadenylation. *FASEB Journal*, **2013**, 27, 325.1	0.9	
20	Decapping of long noncoding RNAs regulates inducible genes. *Molecular Cell*, **2012**, 45, 279-91	17.6	111
19	What comes first: translational repression or mRNA degradation? The deepening mystery of microRNA function. *Cell Research*, **2012**, 22, 1322-4	24.7	64
18	XRN1: A Major 5Tto 3TExoribonuclease in Eukaryotic Cells. *The Enzymes*, **2012**, 31, 97-114	2.3	11
17	The DEAD-box protein Dhh1 promotes decapping by slowing ribosome movement. *PLoS Biology*, **2012**, 10, e1001342	9.7	109
16	A quantitative assay for measuring mRNA decapping by splinted ligation reverse transcription polymerase chain reaction: qSL-RT-PCR. *Rna*, **2011**, 17, 535-43	5.8	19
15	A novel origin for granulovacuolar degeneration in aging and Alzheimer‘s disease: parallels to stress granules. *Laboratory Investigation*, **2011**, 91, 1777-86	5.9	37

14	Nonsense-mediated mRNA decapping occurs on polyribosomes in Saccharomyces cerevisiae. *Nature Structural and Molecular Biology*, **2010**, 17, 244-7	17.6	63
13	Alternate endings: a new story for mRNA decapping. *Molecular Cell*, **2010**, 40, 349-50	17.6	2
12	Co-translational mRNA decay in Saccharomyces cerevisiae. *Nature*, **2009**, 461, 225-9	50.4	247
11	Methods to determine mRNA half-life in Saccharomyces cerevisiae. *Methods in Enzymology*, **2008**, 448, 267-84	1.7	25
10	Tethered function assays: an adaptable approach to study RNA regulatory proteins. *Methods in Enzymology*, **2007**, 429, 299-321	1.7	36
9	Microtubule disruption stimulates P-body formation. *Rna*, **2007**, 13, 493-502	5.8	64
8	Staufen- and FMRP-containing neuronal RNPs are structurally and functionally related to somatic P bodies. *Neuron*, **2006**, 52, 997-1009	13.9	295
7	General translational repression by activators of mRNA decapping. *Cell*, **2005**, 122, 875-86	56.2	489
6	Crystal structure and functional analysis of DEAD-box protein Dhh1p. *Rna*, **2005**, 11, 1258-70	5.8	97
5	The yeast Apq12 protein affects nucleocytoplasmic mRNA transport. *Rna*, **2004**, 10, 1352-8	5.8	16
4	Eukaryotic mRNA decapping. *Annual Review of Biochemistry*, **2004**, 73, 861-90	29.1	397
3	Codon Usage and Amino Acid Identity Are Major Determinants of MRNA Stability in Humans. *SSRN Electronic Journal*,	1	1
2	Ccr4 and Pop2 control poly(A) tail length in Saccharomyces cerevisiae		5
1	The Ccr4-Not complex monitors the translating ribosome for codon optimality		2