Yoon Ki Kim

List of Publications by Year
in descending order

94 papers	5,893 citations	71102 41 h-index	79698 73 g-index
95 all docs	95 docs citations	95 times ranked	7352 citing authors

#	Article	IF	Citations
1	Mammalian Staufen1 Recruits Upf1 to Specific mRNA 3â€²UTRs so as to Elicit mRNA Decay. Cell, 2005, 120, 195-208.	28.9	438
2	Endoribonucleolytic Cleavage of m6A-Containing RNAs by RNase P/MRP Complex. Molecular Cell, 2019, 74, 494-507.e8.	9.7	371
3	The emerging role of RNA modifications in the regulation of mRNA stability. Experimental and Molecular Medicine, 2020, 52, 400-408.	7.7	259
4	Upf1 Phosphorylation Triggers Translational Repression during Nonsense-Mediated mRNA Decay. Cell, 2008, 133, 314-327.	28.9	251
5	Molecular Mechanisms Driving mRNA Degradation by m6A Modification. Trends in Genetics, 2020, 36, 177-188.	6.7	251
6	LIN28A Is a Suppressor of ER-Associated Translation in Embryonic Stem Cells. Cell, 2012, 151, 765-777.	28.9	208
7	Quantitative microarray profiling provides evidence against widespread coupling of alternative splicing with nonsense-mediated mRNA decay to control gene expression. Genes and Development, 2006, 20, 153-158.	5.9	192
8	Regulation of Multiple Core Spliceosomal Proteins by Alternative Splicing-Coupled Nonsense-Mediated mRNA Decay. Molecular and Cellular Biology, 2008, 28, 4320-4330.	2.3	183
9	Staufen1 regulates diverse classes of mammalian transcripts. EMBO Journal, 2007, 26, 2670-2681.	7.8	174
10	Protein-protein interaction among hnRNPs shuttling between nucleus and cytoplasm. Journal of Molecular Biology, 2000, 298, 395-405.	4.2	172
11	SMD and NMD are competitive pathways that contribute to myogenesis: effects on PAX3 and myogenin mRNAs. Genes and Development, 2009, 23, 54-66.	5.9	160
12	UPFront and center in RNA decay: UPF1 in nonsense-mediated mRNA decay and beyond. Rna, 2019, 25, 407-422.	3.5	152
13	Heterogeneous Nuclear Ribonucleoprotein L Interacts with the 3â€² Border of the Internal Ribosomal Entry Site of Hepatitis C Virus. Journal of Virology, 1998, 72, 8782-8788.	3.4	144
14	MG53-induced IRS-1 ubiquitination negatively regulates skeletal myogenesis and insulin signalling. Nature Communications, 2013, 4, 2354.	12.8	140
15	Human Proline-Rich Nuclear Receptor Coregulatory Protein 2 Mediates an Interaction between mRNA Surveillance Machinery and Decapping Complex. Molecular Cell, 2009, 33, 75-86.	9.7	138
16	Translation of Polioviral mRNA Is Inhibited by Cleavage of Polypyrimidine Tract-Binding Proteins Executed by Polioviral 3C pro. Journal of Virology, 2002, 76, 2529-2542.	3.4	132
17	CBP80 promotes interaction of Upf1 with Upf2 during nonsense-mediated mRNA decay in mammalian cells. Nature Structural and Molecular Biology, 2005, 12, 893-901.	8.2	130
18	Staufen1-Mediated mRNA Decay Functions in Adipogenesis. Molecular Cell, 2012, 46, 495-506.	9.7	93

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19	A new MIF4G domain-containing protein, CTIF, directs nuclear cap-binding protein CBP80/20-dependent translation. Genes and Development, 2009, 23, 2033-2045.	5.9	91
20	Cell-surface Receptor for Complement Component C1q (gC1qR) Is a Key Regulator for Lamellipodia Formation and Cancer Metastasis. Journal of Biological Chemistry, 2011, 286, 23093-23101.	3.4	81
21	SMG5â€“PNRC2 is functionally dominant compared with SMG5â€“SMG7 in mammalian nonsense-mediated mRNA decay. Nucleic Acids Research, 2013, 41, 1319-1328.	14.5	77
22	Polypyrimidine tract-binding protein interacts with HnRNP L. FEBS Letters, 1998, 425, 401-406.	2.8	75
23	E2 of Hepatitis C Virus Inhibits Apoptosis. Journal of Immunology, 2005, 175, 8226-8235.	0.8	69
24	Long-range RNA-RNA interaction between the 5' nontranslated region and the core-coding sequences of hepatitis C virus modulates the IRES-dependent translation. Rna, 2003, 9, 599-606.	3.5	67
25	Polypyrimidine tract-binding protein inhibits translation of bip mRNA. Journal of Molecular Biology, 2000, 304, 119-133.	4.2	65
26	Nonsense-Mediated mRNA Decay Factors, UPF1 and UPF3, Contribute to Plant Defense. Plant and Cell Physiology, 2011, 52, 2147-2156.	3.1	64
27	eIF4AIII enhances translation of nuclear cap-binding complexâ€“bound mRNAs by promoting disruption of secondary structures in 5â€²UTR. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E4577-86.	7.1	62
28	Insights into degradation mechanism of N-end rule substrates by p62/SQSTM1 autophagy adapter. Nature Communications, 2018, 9, 3291.	12.8	62
29	Structural Basis of the PNRC2-Mediated Link between mRNA Surveillance and Decapping. Structure, 2012, 20, 2025-2037.	3.3	59
30	Insights into autophagosome maturation revealed by the structures of ATG5 with its interacting partners. Autophagy, 2015, 11, 75-87.	9.1	59
31	RNA surveillance via nonsense-mediated mRNA decay is crucial for longevity in daf-2/insulin/IGF-1 mutant C. elegans. Nature Communications, 2017, 8, 14749.	12.8	59
32	Domains I and II in the 5â€² Nontranslated Region of the HCV Genome Are Required for RNA Replication. Biochemical and Biophysical Research Communications, 2002, 290, 105-112.	2.1	58
33	A high-resolution temporal atlas of the SARS-CoV-2 translatome and transcriptome. Nature Communications, 2021, 12, 5120.	12.8	57
34	The regulatory impact of RNA-binding proteins on microRNA targeting. Nature Communications, 2021, 12, 5057.	12.8	54
35	Failsafe nonsense-mediated mRNA decay does not detectably target eIF4E-bound mRNA. Nature Structural and Molecular Biology, 2007, 14, 974-979.	8.2	53
36	Glucocorticoid receptor interacts with PNRC2 in a ligand-dependent manner to recruit UPF1 for rapid mRNA degradation. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E1540-9.	7.1	53

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37	La protein is required for efficient translation driven by encephalomyocarditis virus internal ribosomal entry site. Journal of General Virology, 1999, 80, 3159-3166.	2.9	52
38	Continuous heat shock enhances translational initiation directed by internal ribosomal entry site. Biochemical and Biophysical Research Communications, 2002, 297, 224-231.	2.1	51
39	Selective Translational Repression of Truncated Proteins from Frameshift Mutation-Derived mRNAs in Tumors. PLoS Biology, 2007, 5, e109.	5.6	50
40	Opposite functions of HIF-Î± isoforms in VEGF induction by TGF-Î²1 under non-hypoxic conditions. Oncogene, 2011, 30, 1213-1228.	5.9	50
41	DLK regulates a distinctive transcriptional regeneration program after peripheral nerve injury. Neurobiology of Disease, 2019, 127, 178-192.	4.4	49
42	microRNA/Argonaute 2 regulates nonsenseâ€mediated messenger RNA decay. EMBO Reports, 2010, 11, 380-386.	4.5	47
43	Translation Initiation on mRNAs Bound by Nuclear Cap-binding Protein Complex CBP80/20 Requires Interaction between CBP80/20-dependent Translation Initiation Factor and Eukaryotic Translation Initiation Factor 3g. Journal of Biological Chemistry, 2012, 287, 18500-18509.	3.4	45
44	Identification and molecular characterization of cellular factors required for glucocorticoid receptor-mediated mRNA decay. Genes and Development, 2016, 30, 2093-2105.	5.9	41
45	LC3B is an RNA-binding protein to trigger rapid mRNA degradation during autophagy. Nature Communications, 2022, 13, 1436.	12.8	39
46	eIF4A3 Phosphorylation by CDKs Affects NMD during the Cell Cycle. Cell Reports, 2019, 26, 2126-2139.e9.	6.4	36
47	Emerging functions of circular RNA in aging. Trends in Genetics, 2021, 37, 819-829.	6.7	36
48	When a ribosome encounters a premature termination codon. BMB Reports, 2013, 46, 9-16.	2.4	36
49	A multifunctional protein EWS regulates the expression of Drosha and microRNAs. Cell Death and Differentiation, 2014, 21, 136-145.	11.2	34
50	Misfolded polypeptides are selectively recognized and transported toward aggresomes by a CED complex. Nature Communications, 2017, 8, 15730.	12.8	34
51	The mRNP remodeling mediated by UPF1 promotes rapid degradation of replication-dependent histone mRNA. Nucleic Acids Research, 2014, 42, 9334-9349.	14.5	32
52	Exon junction complex enhances translation of spliced mRNAs at multiple steps. Biochemical and Biophysical Research Communications, 2009, 384, 334-340.	2.1	30
53	Quantitative proteome analysis of ageâ€related changes in mouse gastrocnemius muscle using m<scp>TRAQ</scp>. Proteomics, 2014, 14, 121-132.	2.2	30
54	Rapid degradation of replication-dependent histone mRNAs largely occurs on mRNAs bound by nuclear cap-binding proteins 80 and 20. Nucleic Acids Research, 2013, 41, 1307-1318.	14.5	29

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55	Translation initiation mediated by nuclear cap-binding protein complex. BMB Reports, 2017, 50, 186-193.	2.4	28
56	Iron increases translation initiation directed by internal ribosome entry site of hepatitis C virus. Virus Genes, 2008, 37, 154-160.	1.6	25
57	Crosstalk between translation and the aggresomeâ€“autophagy pathway. Autophagy, 2018, 14, 1-3.	9.1	23
58	SMG1 regulates adipogenesis via targeting of staufen1-mediated mRNA decay. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2013, 1829, 1276-1287.	1.9	22
59	UPF1 promotes rapid degradation of m6A-containing RNAs. Cell Reports, 2022, 39, 110861.	6.4	22
60	Ago2/miRISC-mediated inhibition of CBP80/20-dependent translation and thereby abrogation of nonsense-mediated mRNA decay require the cap-associating activity of Ago2. FEBS Letters, 2011, 585, 2682-2687.	2.8	20
61	Nonsense-mediated mRNA decay factor UPF1 promotes aggresome formation. Nature Communications, 2020, 11, 3106.	12.8	20
62	Pioneer round of translation occurs during serum starvation. Biochemical and Biophysical Research Communications, 2007, 362, 145-151.	2.1	18
63	Staufen1 and UPF1 exert opposite actions on the replacement of the nuclear cap-binding complex by eIF4E at the 5â€² end of mRNAs. Nucleic Acids Research, 2019, 47, 9313-9328.	14.5	18
64	Reinvestigation of Aminoacyl-TRNA Synthetase Core Complex by Affinity Purification-Mass Spectrometry Reveals TARSL2 as a Potential Member of the Complex. PLoS ONE, 2013, 8, e81734.	2.5	18
65	Comparative analysis of the transcriptome of injured nerve segments reveals spatiotemporal responses to neural damage in mice. Journal of Comparative Neurology, 2018, 526, 1195-1208.	1.6	17
66	TAZ links exercise to mitochondrial biogenesis via mitochondrial transcription factor A. Nature Communications, 2022, 13, 653.	12.8	16
67	Pioneer round of translation mediated by nuclear capâ€binding proteins CBP80/20 occurs during prolonged hypoxia. FEBS Letters, 2007, 581, 5158-5164.	2.8	15
68	Nonsenseâ€mediated translational repression involves exon junction complex downstream of premature translation termination codon. FEBS Letters, 2010, 584, 795-800.	2.8	15
69	The upstream open reading frame of cyclin-dependent kinase inhibitor 1A mRNA negatively regulates translation of the downstream main open reading frame. Biochemical and Biophysical Research Communications, 2012, 424, 469-475.	2.1	15
70	A new function of glucocorticoid receptor: regulation of mRNA stability. BMB Reports, 2015, 48, 367-368.	2.4	15
71	UPF1: From mRNA Surveillance to Protein Quality Control. Biomedicines, 2021, 9, 995.	3.2	15
72	Ectopic expression of eIF4E-transporter triggers the movement of eIF4E into P-bodies, inhibiting steady-state translation but not the pioneer round of translation. Biochemical and Biophysical Research Communications, 2008, 369, 1160-1165.	2.1	14

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73	LSM12-EPAC1 defines a neuroprotective pathway that sustains the nucleocytoplasmic RAN gradient. PLoS Biology, 2020, 18, e3001002.	5.6	12
74	Nonâ€structural protein 1 of influenza viruses inhibits rapid mRNA degradation mediated by doubleâ€stranded RNAâ€binding protein, staufen1. FEBS Letters, 2013, 587, 2118-2124.	2.8	10
75	Increased ribosomal protein levels and protein synthesis in the striatal synaptosome of Shank3-overexpressing transgenic mice. Molecular Brain, 2021, 14, 39.	2.6	10
76	Translation mediated by the nuclear cap-binding complex is confined to the perinuclear region via a CTIFâ€"DDX19B interaction. Nucleic Acids Research, 2021, 49, 8261-8276.	14.5	10
77	UXT chaperone prevents proteotoxicity by acting as an autophagy adaptor for p62-dependent aggrephagy. Nature Communications, 2021, 12, 1955.	12.8	9
78	Hepatitis C virus NS2 protein activates cellular cyclic AMP-dependent pathways. Biochemical and Biophysical Research Communications, 2007, 356, 948-954.	2.1	8
79	TRIM28 functions as a negative regulator of aggresome formation. Autophagy, 2021, 17, 4231-4248.	9.1	7
80	HuR stabilizes a polyadenylated form of replicationâ€dependent histone mRNAs under stress conditions. FASEB Journal, 2019, 33, 2680-2693.	0.5	6
81	AU-rich elementâ€"mediated mRNA decay via the butyrate response factor 1 controls cellular levels of polyadenylated replication-dependent histone mRNAs. Journal of Biological Chemistry, 2019, 294, 7558-7565.	3.4	3
82	The position of the target site for engineered nucleases improves the aberrant mRNA clearance in in vivo genome editing. Scientific Reports, 2020, 10, 4173.	3.3	3
83	The pioneer round of translation ensures proper targeting of ER and mitochondrial proteins. Nucleic Acids Research, 2021, 49, 12517-12534.	14.5	3
84	Single polysome analysis of mRNP. Biochemical and Biophysical Research Communications, 2022, 618, 73-78.	2.1	2
85	Editorial : RNA at the heart of gene expression: Special issue of BMB Reports 2017. BMB Reports, 2017, 50, 157-157.	2.4	0
86	LSM12-EPAC1 defines a neuroprotective pathway that sustains the nucleocytoplasmic RAN gradient. , 2020, 18, e3001002.		0
87	LSM12-EPAC1 defines a neuroprotective pathway that sustains the nucleocytoplasmic RAN gradient. , 2020, 18, e3001002.		0
88	LSM12-EPAC1 defines a neuroprotective pathway that sustains the nucleocytoplasmic RAN gradient. , 2020, 18, e3001002.		0
89	LSM12-EPAC1 defines a neuroprotective pathway that sustains the nucleocytoplasmic RAN gradient. , 2020, 18, e3001002.		0
90	LSM12-EPAC1 defines a neuroprotective pathway that sustains the nucleocytoplasmic RAN gradient. , 2020, 18, e3001002.		0

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91	LSM12-EPAC1 defines a neuroprotective pathway that sustains the nucleocytoplasmic RAN gradient. , 2020, 18, e3001002.		0
92	LSM12-EPAC1 defines a neuroprotective pathway that sustains the nucleocytoplasmic RAN gradient. , 2020, 18, e3001002.		0
93	LSM12-EPAC1 defines a neuroprotective pathway that sustains the nucleocytoplasmic RAN gradient. , 2020, 18, e3001002.		0
94	Resolving m6A epitranscriptome with stoichiometry. Trends in Genetics, 2022, , .	6.7	0