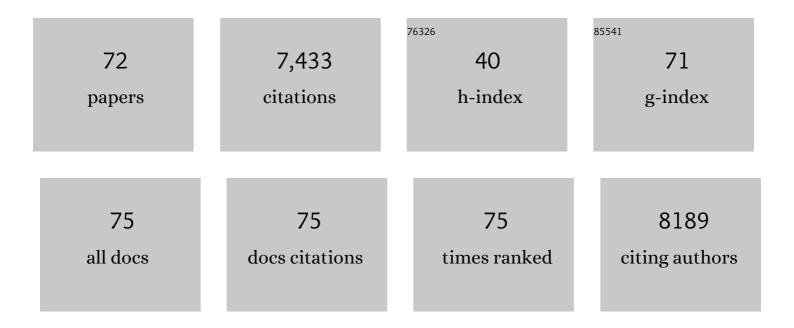
Markus T Bohnsack

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Exportin 5 is a RanGTP-dependent dsRNA-binding protein that mediates nuclear export of pre-miRNAs. Rna, 2004, 10, 185-191.	3.5	1,125
2	Human METTL16 is a <i>N</i> ⁶ â€methyladenosine (m ⁶ A) methyltransferase that targets preâ€mRNAs and various nonâ€coding RNAs. EMBO Reports, 2017, 18, 2004-2014.	4.5	481
3	Tuning the ribosome: The influence of rRNA modification on eukaryotic ribosome biogenesis and function. RNA Biology, 2017, 14, 1138-1152.	3.1	479
4	The box C/D and H/ACA snoRNPs: key players in the modification, processing and the dynamic folding of ribosomal RNA. Wiley Interdisciplinary Reviews RNA, 2012, 3, 397-414.	6.4	388
5	The human 18S rRNA m6A methyltransferase METTL5 is stabilized by TRMT112. Nucleic Acids Research, 2019, 47, 7719-7733.	14.5	312
6	Eukaryotic 5-methylcytosine (m5C) RNA Methyltransferases: Mechanisms, Cellular Functions, and Links to Disease. Genes, 2019, 10, 102.	2.4	291
7	The 5S RNP Couples p53 Homeostasis to Ribosome Biogenesis and Nucleolar Stress. Cell Reports, 2013, 5, 237-247.	6.4	244
8	A centriole- and RanGTP-independent spindle assembly pathway in meiosis I of vertebrate oocytes. Journal of Cell Biology, 2007, 176, 295-305.	5.2	219
9	Exp5 exports eEF1A via tRNA from nuclei and synergizes with other transport pathways to confine translation to the cytoplasm. EMBO Journal, 2002, 21, 6205-6215.	7.8	203
10	<scp>NSUN</scp> 3 and <scp>ABH</scp> 1 modify the wobble position of mtâ€ŧ <scp>RNA</scp> ^{Met} to expand codon recognition in mitochondrial translation. EMBO Journal, 2016, 35, 2104-2119.	7.8	197
11	Changes in m6A RNA methylation contribute to heart failure progression by modulating translation. European Journal of Heart Failure, 2020, 22, 54-66.	7.1	193
12	A selective block of nuclear actin export stabilizes the giant nuclei of Xenopus oocytes. Nature Cell Biology, 2006, 8, 257-263.	10.3	180
13	The m ⁶ A reader protein YTHDC2 interacts with the small ribosomal subunit and the 5′–3′ exoribonuclease XRN1. Rna, 2018, 24, 1339-1350.	3.5	171
14	Uncovering the assembly pathway of human ribosomes and its emerging links to disease. EMBO Journal, 2019, 38, e100278.	7.8	157
15	Prp43 Bound at Different Sites on the Pre-rRNA Performs Distinct Functions in Ribosome Synthesis. Molecular Cell, 2009, 36, 583-592.	9.7	152
16	NSUN6 is a human RNA methyltransferase that catalyzes formation of m ⁵ C72 in specific tRNAs. Rna, 2015, 21, 1532-1543.	3.5	144
17	DExD/H-box RNA helicases in ribosome biogenesis. RNA Biology, 2013, 10, 4-18.	3.1	110
18	The Bowen–Conradi syndrome protein Nep1 (Emg1) has a dual role in eukaryotic ribosome biogenesis, as an essential assembly factor and in the methylation of ΰ1191 in yeast 18S rRNA. Nucleic Acids Research, 2011, 39, 1526-1537.	14.5	108

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19	NuSAP, a Mitotic RanGTP Target That Stabilizes and Cross-links Microtubules. Molecular Biology of the Cell, 2006, 17, 2646-2660.	2.1	107
20	The mitochondrial epitranscriptome: the roles of RNA modifications in mitochondrial translation and human disease. Cellular and Molecular Life Sciences, 2018, 75, 241-260.	5.4	103
21	WBSCR22/Merm1 is required for late nuclear pre-ribosomal RNA processing and mediates N ⁷ -methylation of G1639 in human 18S rRNA. Rna, 2015, 21, 180-187.	3.5	102
22	Exportin 7 defines a novel general nuclear export pathway. EMBO Journal, 2004, 23, 3227-3236.	7.8	96
23	Zebrafish survival motor neuron mutants exhibit presynaptic neuromuscular junction defects. Human Molecular Genetics, 2009, 18, 3615-3625.	2.9	93
24	Modifications in small nuclear RNAs and their roles in spliceosome assembly and function. Biological Chemistry, 2018, 399, 1265-1276.	2.5	92
25	Unravelling the Mechanisms of RNA Helicase Regulation. Trends in Biochemical Sciences, 2018, 43, 237-250.	7.5	89
26	The evolution of the ribosome biogenesis pathway from a yeast perspective. Nucleic Acids Research, 2014, 42, 1509-1523.	14.5	87
27	Functional and Phylogenetic Properties of the Pore-forming Î ² -Barrel Transporters of the Omp85 Family. Journal of Biological Chemistry, 2007, 282, 1882-1890.	3.4	74
28	40S Ribosome Biogenesis Co-Factors Are Essential for Gametophyte and Embryo Development. PLoS ONE, 2013, 8, e54084.	2.5	74
29	Quantitative analysis of snoRNA association with preâ€ribosomes and release of snR30 by Rok1 helicase. EMBO Reports, 2008, 9, 1230-1236.	4.5	72
30	atBRX1-1 and atBRX1-2 are involved in an alternative rRNA processing pathway in <i>Arabidopsis thaliana</i> . Rna, 2015, 21, 415-425.	3.5	68
31	Structural and functional analysis of the archaeal endonuclease Nob1. Nucleic Acids Research, 2012, 40, 3259-3274.	14.5	64
32	The association of late-acting snoRNPs with human pre-ribosomal complexes requires the RNA helicase DDX21. Nucleic Acids Research, 2015, 43, 553-564.	14.5	64
33	The roles of SSU processome components and surveillance factors in the initial processing of human ribosomal RNA. Rna, 2014, 20, 540-550.	3.5	61
34	Identification of RNA Helicase Target Sites by UV Cross-Linking and Analysis of cDNA. Methods in Enzymology, 2012, 511, 275-288.	1.0	56
35	The yeast ribosome synthesis factor Emg1 is a novel member of the superfamily of alpha/beta knot fold methyltransferases. Nucleic Acids Research, 2007, 36, 629-639.	14.5	54
36	The G-patch protein NF-κB-repressing factor mediates the recruitment of the exonuclease XRN2 and activation of the RNA helicase DHX15 in human ribosome biogenesis. Nucleic Acids Research, 2017, 45, gkx013.	14.5	54

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37	Nucleocytoplasmic Transport of RNAs and RNA–Protein Complexes. Journal of Molecular Biology, 2016, 428, 2040-2059.	4.2	52
38	A novel translational control mechanism involving RNA structures within coding sequences. Genome Research, 2017, 27, 95-106.	5.5	48
39	The human RNA helicase DHX37 is required for release of the U3 snoRNP from pre-ribosomal particles. RNA Biology, 2019, 16, 54-68.	3.1	46
40	A pre-ribosomal RNA interaction network involving snoRNAs and the Rok1 helicase. Rna, 2014, 20, 1173-1182.	3.5	45
41	The 60S associated ribosome biogenesis factor <scp>LSG</scp> 1â€2 is required for 40S maturation in <i>Arabidopsis thaliana</i> . Plant Journal, 2014, 80, 1043-1056.	5.7	43
42	An inÂvitro system to silence mitochondrial gene expression. Cell, 2021, 184, 5824-5837.e15.	28.9	40
43	Protein cofactor competition regulates the action of a multifunctional RNA helicase in different pathways. RNA Biology, 2016, 13, 320-330.	3.1	39
44	<i>N</i> ⁶ â€Methyladenosineâ€Sensitive RNAâ€Cleaving Deoxyribozymes. Angewandte Chemie - International Edition, 2018, 57, 15117-15121.	13.8	39
45	Xpo7 is a broad-spectrum exportin and a nuclear import receptor. Journal of Cell Biology, 2018, 217, 2329-2340.	5.2	39
46	Regulation of DEAH-box RNA helicases by G-patch proteins. Biological Chemistry, 2021, 402, 561-579.	2.5	39
47	The evolution of protein targeting and translocation systems. Biochimica Et Biophysica Acta - Molecular Cell Research, 2010, 1803, 1115-1130.	4.1	38
48	The mRNA encoding the yeast ARE-binding protein Cth2 is generated by a novel 3′ processing pathway. Nucleic Acids Research, 2008, 36, 3075-3084.	14.5	36
49	Effects of the Bowen-Conradi syndrome mutation in EMG1 on its nuclear import, stability and nucleolar recruitment. Human Molecular Genetics, 2016, 25, ddw351.	2.9	36
50	Exportin T and Exportin 5: tRNA and miRNA biogenesis – and beyond. Biological Chemistry, 2012, 393, 599-604.	2.5	32
51	RNA helicases mediate structural transitions and compositional changes in pre-ribosomal complexes. Nature Communications, 2018, 9, 5383.	12.8	30
52	RNA helicase-mediated regulation of snoRNP dynamics on pre-ribosomes and rRNA 2′- <i>O</i> -methylation. Nucleic Acids Research, 2021, 49, 4066-4084.	14.5	26
53	Transitions of gene expression induced by shortâ€ŧerm blue light. Plant Biology, 2011, 13, 349-361.	3.8	23
54	The human box C/D snoRNA U3 is a miRNA source and miR-U3 regulates expression of sortin nexin 27. Nucleic Acids Research, 2020, 48, 8074-8089.	14.5	20

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55	DEAD-box RNA helicase Dbp4/DDX10 is an enhancer of $\hat{I}\pm$ -synuclein toxicity and oligomerization. PLoS Genetics, 2021, 17, e1009407.	3.5	19
56	Association of snR190 snoRNA chaperone with early pre-60S particles is regulated by the RNA helicase Dbp7 in yeast. Nature Communications, 2021, 12, 6153.	12.8	19
57	The RNA helicase Dbp7 promotes domain V/VI compaction and stabilization of inter-domain interactions during early 60S assembly. Nature Communications, 2021, 12, 6152.	12.8	19
58	The RNA methyltransferase METTL8 installs m3C32 in mitochondrial tRNAsThr/Ser(UCN) to optimise tRNA structure and mitochondrial translation. Nature Communications, 2022, 13, 209.	12.8	19
59	The functional domains of the chloroplast unusual positioning protein 1. Plant Science, 2011, 180, 650-654.	3.6	16
60	The DExD box ATPase DDX55 is recruited to domain IV of the 28S ribosomal RNA by its C-terminal region. RNA Biology, 2021, 18, 1124-1135.	3.1	15
61	The interaction of DNA repair factors ASCC2 and ASCC3 is affected by somatic cancer mutations. Nature Communications, 2020, 11, 5535.	12.8	12
62	Crosslinking Methods to Identify RNA Methyltransferase Targets In Vivo. Methods in Molecular Biology, 2017, 1562, 269-281.	0.9	11
63	N 6 â€Methyladenosineâ€Sensitive RNAâ€Cleaving Deoxyribozymes. Angewandte Chemie, 2018, 130, 15337-15	3410	11
64	Tracing Eukaryotic Ribosome Biogenesis Factors Into the Archaeal Domain Sheds Light on the Evolution of Functional Complexity. Frontiers in Microbiology, 2021, 12, 739000.	3.5	11
65	Roles and dynamics of 3-methylcytidine in cellular RNAs. Trends in Biochemical Sciences, 2022, 47, 596-608.	7.5	11
66	RNA-Binding Proteins Chaperone Ribonucleoprotein Complex Assembly to Solve the RNA-Folding Problem. Cell, 2019, 179, 1248-1250.	28.9	9
67	Sgd1 is an MIF4G domain-containing cofactor of the RNA helicase Fal1 and associates with the 5' domain of the 18S rRNA sequence. RNA Biology, 2020, 17, 539-553.	3.1	8
68	Pol5 is required for recycling of small subunit biogenesis factors and for formation of the peptide exit tunnel of the large ribosomal subunit. Nucleic Acids Research, 2019, 48, 405-420.	14.5	7
69	Backbone and side chain NMR resonance assignments for an archaeal homolog of the endonuclease Nob1 involved in ribosome biogenesis. Biomolecular NMR Assignments, 2012, 6, 47-50.	0.8	4
70	How RNA modification allows non-conventional decoding in mitochondria. Cell Cycle, 2017, 16, 145-146.	2.6	4
71	In Vitro Assays for RNA Methyltransferase Activity. Methods in Molecular Biology, 2017, 1562, 259-268.	0.9	2

 $Titelbild: <i>N</i>⁶â \in Methyladenosine a \in Sensitive RNA a \in Cleaving Deoxyribozymes (Angew. Chem.) Ti_{2.0} Q o g rgBT / Over the sensitive RNA a \in Cleaving Deoxyribozymes (Angew. Chem.) Ti_{2.0} Q o g rgBT / Over the sensitive RNA a \in Cleaving Deoxyribozymes (Angew. Chem.) Ti_{2.0} Q o g rgBT / Over the sensitive RNA a \in Cleaving Deoxyribozymes (Angew. Chem.) Ti_{2.0} Q o g rgBT / Over the sensitive RNA a \in Cleaving Deoxyribozymes (Angew. Chem.) Ti_{2.0} Q o g rgBT / Over the sensitive RNA a \in Cleaving Deoxyribozymes (Angew. Chem.) Ti_{2.0} Q o g rgBT / Over the sensitive RNA a \in Cleaving Deoxyribozymes (Angew. Chem.) Ti_{2.0} Q o g rgBT / Over the sensitive RNA a \in Cleaving Deoxyribozymes (Angew. Chem.) Ti_{2.0} Q o g rgBT / Over the sensitive RNA a \in Cleaving Deoxyribozymes (Angew. Chem.) Ti_{2.0} Q o g rgBT / Over the sensitive RNA a \in Cleaving Deoxyribozymes (Angew. Chem.) Ti_{2.0} Q o g rgBT / Over the sensitive RNA a \in Cleaving Deoxyribozymes (Angew. Chem.) Ti_{2.0} Q o g rgBT / Over the sensitive RNA a \in Cleaving Deoxyribozymes (Angew. Chem.) Ti_{2.0} Q o g rgBT / Over the sensitive RNA a \in Cleaving Deoxyribozymes (Angew. Chem.) Ti_{2.0} Q o g rgBT / Over the sensitive RNA a \in Cleaving Deoxyribozymes (Angew. Chem.) Ti_{2.0} Q o g rgBT / Over the sensitive RNA a \in Cleaving Deoxyribozymes (Angew. Chem.) Ti_{2.0} Q o g rgBT / Over the sensitive RNA a \in Cleaving Deoxyribozymes (Angew. Chem.) Ti_{2.0} Q o g rgBT / Over the sensitive RNA a \in Cleaving Deoxyribozymes (Angew. Chem.) Ti_{2.0} Q o g rgBT / Over the sensitive RNA a \in Cleaving Deoxyribozymes (Angew. Chem.) Ti_{2.0} Q o g rgBT / Over the sensitive RNA a \in Cleaving Deoxyribozymes (Angew. Chem.) Ti_{2.0} Q o g rgBT / Over the sensitive RNA a \in Cleaving Deoxyribozymes (Angew. Chem.) Ti_{2.0} Q o g rgBT / Over the sensitive RNA a (Angew. Chem.) Ti_{2.0} Q o g rgBT / Over the sensitive RNA a (Angew. Chem.) Ti_{2.0} Q o g rgBT / Over the sensitive RNA a (Angew. Chem.) Ti_{2.0} Q o g rgBT / Over the sensitive RNA a (Angew. Chem.) Ti_{2.0} Q o$