

David Tollervey

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

253
papers

26,348
citations

92
h-index

157
g-index

278
ext. papers

29,027
ext. citations

13.6
avg, IF

7.16
L-index

#	Paper	IF	Citations
253	A disease-linked lncRNA mutation in RNase MRP inhibits ribosome synthesis.. <i>Nature Communications</i> , 2022 , 13, 649	17.4	2
252	NANOS2 is a sequence-specific mRNA-binding protein that promotes transcript degradation in spermatogonial stem cells. <i>Science</i> , 2021 , 24, 102762	6.1	2
251	Yeast Ssd1 is a non-enzymatic member of the RNase II family with an alternative RNA recognition site. <i>Nucleic Acids Research</i> , 2021 ,	20.1	2
250	Extended ncRNAs Interfere with Promoter Nucleosome Dynamics. <i>Trends in Genetics</i> , 2020 , 36, 637-639	8.5	1
249	Substrate specificity of the TRAMP nuclear surveillance complexes. <i>Nature Communications</i> , 2020 , 11, 3122	17.4	10
248	High density of unrepaired genomic ribonucleotides leads to Topoisomerase 1-mediated severe growth defects in absence of ribonucleotide reductase. <i>Nucleic Acids Research</i> , 2020 , 48, 4274-4297	20.1	1
247	Regulation of the RNAPII Pool Is Integral to the DNA Damage Response. <i>Cell</i> , 2020 , 180, 1245-1261.e21	56.2	51
246	Nascent Transcript Folding Plays a Major Role in Determining RNA Polymerase Elongation Rates. <i>Molecular Cell</i> , 2020 , 79, 488-503.e11	17.6	18
245	Integrative vectors for regulated expression of SARS-CoV-2 proteins implicated in RNA metabolism. <i>Wellcome Open Research</i> , 2020 , 5, 261	4.8	
244	Synergistic defects in pre-rRNA processing from mutations in the U3-specific protein Rrp9 and U3 snoRNA. <i>Nucleic Acids Research</i> , 2020 , 48, 3848-3868	20.1	7
243	Mapping Exosome-Substrate Interactions In Vivo by UV Cross-Linking. <i>Methods in Molecular Biology</i> , 2020 , 2062, 105-126	1.4	
242	Stress-Induced Translation Inhibition through Rapid Displacement of Scanning Initiation Factors. <i>Molecular Cell</i> , 2020 , 80, 470-484.e8	17.6	15
241	The expression of Rpb10, a small subunit common to RNA polymerases, is modulated by the R3H domain-containing Rbs1 protein and the Upf1 helicase. <i>Nucleic Acids Research</i> , 2020 , 48, 12252-12268	20.1	8
240	Defining the RNA interactome by total RNA-associated protein purification. <i>Molecular Systems Biology</i> , 2019 , 15, e8689	12.2	66
239	Molecular interactions between Hel2 and RNA supporting ribosome-associated quality control. <i>Nature Communications</i> , 2019 , 10, 563	17.4	16
238	High-Resolution, High-Throughput Analysis of Hfq-Binding Sites Using UV Crosslinking and Analysis of cDNA (CRAC). <i>Methods in Molecular Biology</i> , 2018 , 1737, 251-272	1.4	7
237	Ribosome maturation by the endoribonuclease YbeY stabilizes a type 3 secretion system transcript required for virulence of enterohemorrhagic. <i>Journal of Biological Chemistry</i> , 2018 , 293, 9006-9016	5.4	19

236	An RNA-dependent mechanism for transient expression of bacterial translocation filaments. <i>Nucleic Acids Research</i> , 2018 , 46, 3366-3381	20.1	14
235	Surveillance-ready transcription: nuclear RNA decay as a default fate. <i>Open Biology</i> , 2018 , 8,	7	34
234	HuD Is a Neural Translation Enhancer Acting on mTORC1-Responsive Genes and Counteracted by the Y3 Small Non-coding RNA. <i>Molecular Cell</i> , 2018 , 71, 256-270.e10	17.6	30
233	Mapping targets for small nucleolar RNAs in yeast. <i>Wellcome Open Research</i> , 2018 , 3, 120	4.8	9
232	Mapping targets for small nucleolar RNAs in yeast. <i>Wellcome Open Research</i> , 2018 , 3, 120	4.8	6
231	Tailing Off: PABP and CNOT Generate Cycles of mRNA Deadenylation. <i>Molecular Cell</i> , 2018 , 70, 987-988	17.6	4
230	Immunoprecipitation of RNA:DNA Hybrids from Budding Yeast. <i>Methods in Molecular Biology</i> , 2018 , 1703, 109-129	1.4	2
229	Transcriptome-Wide Analysis of Protein-RNA and RNA-RNA Interactions in Pathogenic Bacteria. <i>Methods in Enzymology</i> , 2018 , 612, 467-488	1.7	2
228	Small RNA interactome of pathogenic E. coli revealed through crosslinking of RNase E. <i>EMBO Journal</i> , 2017 , 36, 374-387	13	112
227	Nuclear RNA Decay Pathways Aid Rapid Remodeling of Gene Expression in Yeast. <i>Molecular Cell</i> , 2017 , 65, 787-800.e5	17.6	36
226	RNA Binding by Histone Methyltransferases Set1 and Set2. <i>Molecular and Cellular Biology</i> , 2017 , 37,	4.8	21
225	Transcription factor WilmsTumor 1 regulates developmental RNAs through 3'UTR interaction. <i>Genes and Development</i> , 2017 , 31, 347-352	12.6	30
224	RNA polymerase II stalling at pre-mRNA splice sites is enforced by ubiquitination of the catalytic subunit. <i>ELife</i> , 2017 , 6,	8.9	11
223	RNA substrate length as an indicator of exosome interactions. <i>Wellcome Open Research</i> , 2017 , 2, 34	4.8	5
222	Transcriptome-wide analysis of alternative routes for RNA substrates into the exosome complex. <i>PLoS Genetics</i> , 2017 , 13, e1006699	6	26
221	Identification of miRNA-Target RNA Interactions Using CLASH. <i>Methods in Molecular Biology</i> , 2016 , 1358, 229-51	1.4	7
220	Motoring toward pre-60S-ribosome export. <i>Nature Structural and Molecular Biology</i> , 2016 , 23, 3-4	17.6	3
219	VapCs of Mycobacterium tuberculosis cleave RNAs essential for translation. <i>Nucleic Acids Research</i> , 2016 , 44, 9860-9871	20.1	70

218	Strand-specific, high-resolution mapping of modified RNA polymerase II. <i>Molecular Systems Biology</i> , 2016 , 12, 874	12.2	40
217	Pre-40S ribosome biogenesis factor Tsr1 is an inactive structural mimic of translational GTPases. <i>Nature Communications</i> , 2016 , 7, 11789	17.4	29
216	Transcription by RNA polymerase III: insights into mechanism and regulation. <i>Biochemical Society Transactions</i> , 2016 , 44, 1367-1375	5.1	53
215	UtpA and UtpB chaperone nascent pre-ribosomal RNA and U3 snoRNA to initiate eukaryotic ribosome assembly. <i>Nature Communications</i> , 2016 , 7, 12090	17.4	43
214	Global analysis of transcriptionally engaged yeast RNA polymerase III reveals extended tRNA transcripts. <i>Genome Research</i> , 2016 , 26, 933-44	9.7	35
213	The PIN domain endonuclease Utp24 cleaves pre-ribosomal RNA at two coupled sites in yeast and humans. <i>Nucleic Acids Research</i> , 2016 , 44, 5399-409	20.1	41
212	Network of epistatic interactions within a yeast snoRNA. <i>Science</i> , 2016 , 352, 840-4	33.3	74
211	The DEAH-box helicase Dhr1 dissociates U3 from the pre-rRNA to promote formation of the central pseudoknot. <i>PLoS Biology</i> , 2015 , 13, e1002083	9.7	49
210	RNA surveillance and the exosome. <i>Rna</i> , 2015 , 21, 492-3	5.8	4
209	Cotranscriptional events in eukaryotic ribosome synthesis. <i>Wiley Interdisciplinary Reviews RNA</i> , 2015 , 6, 129-39	9.3	78
208	Loss of the Yeast SR Protein Npl3 Alters Gene Expression Due to Transcription Readthrough. <i>PLoS Genetics</i> , 2015 , 11, e1005735	6	11
207	Mapping the miRNA interactome by cross-linking ligation and sequencing of hybrids (CLASH). <i>Nature Protocols</i> , 2014 , 9, 711-28	18.8	96
206	A new system for naming ribosomal proteins. <i>Current Opinion in Structural Biology</i> , 2014 , 24, 165-9	8.1	365
205	Looking into the barrel of the RNA exosome. <i>Nature Structural and Molecular Biology</i> , 2014 , 21, 17-8	17.6	8
204	Coupled GTPase and remodelling ATPase activities form a checkpoint for ribosome export. <i>Nature</i> , 2014 , 505, 112-116	50.4	97
203	Lighting Up pre-mRNA recognition. <i>Molecular Cell</i> , 2014 , 55, 649-51	17.6	1
202	A network of assembly factors is involved in remodeling rRNA elements during preribosome maturation. <i>Journal of Cell Biology</i> , 2014 , 207, 481-98	7.3	38
201	Identification of bacteriophage-encoded anti-sRNAs in pathogenic Escherichia coli. <i>Molecular Cell</i> , 2014 , 55, 199-213	17.6	174

200	Hyb: a bioinformatics pipeline for the analysis of CLASH (crosslinking, ligation and sequencing of hybrids) data. <i>Methods</i> , 2014 , 65, 263-73	4.6	48
199	Kinetic analysis demonstrates a requirement for the Rat1 exonuclease in cotranscriptional pre-rRNA cleavage. <i>PLoS ONE</i> , 2014 , 9, e85703	3.7	19
198	Regulatory Aspects of rRNA Modification and Pre-rRNA Processing 2014 , 281-288		7
197	Integrity of SRP RNA is ensured by La and the nuclear RNA quality control machinery. <i>Nucleic Acids Research</i> , 2014 , 42, 10698-710	20.1	7
196	RNA mimicry by the fap7 adenylate kinase in ribosome biogenesis. <i>PLoS Biology</i> , 2014 , 12, e1001860	9.7	33
195	Genome-wide distribution of RNA-DNA hybrids identifies RNase H targets in tRNA genes, retrotransposons and mitochondria. <i>PLoS Genetics</i> , 2014 , 10, e1004716	6	140
194	Final pre-40S maturation depends on the functional integrity of the 60S subunit ribosomal protein L3. <i>PLoS Genetics</i> , 2014 , 10, e1004205	6	42
193	Rio1 mediates ATP-dependent final maturation of 40S ribosomal subunits. <i>Nucleic Acids Research</i> , 2014 , 42, 12189-99	20.1	61
192	Ki-67 is a PP1-interacting protein that organises the mitotic chromosome periphery. <i>ELife</i> , 2014 , 3, e016419	4.9	110
191	Threading the barrel of the RNA exosome. <i>Trends in Biochemical Sciences</i> , 2013 , 38, 485-93	10.3	87
190	Rrp5 binding at multiple sites coordinates pre-rRNA processing and assembly. <i>Molecular Cell</i> , 2013 , 52, 707-19	17.6	46
189	A transcriptome-wide atlas of RNP composition reveals diverse classes of mRNAs and lncRNAs. <i>Cell</i> , 2013 , 154, 996-1009	56.2	174
188	Mapping the human miRNA interactome by CLASH reveals frequent noncanonical binding. <i>Cell</i> , 2013 , 153, 654-65	56.2	880
187	Multiple RNA interactions position Mrd1 at the site of the small subunit pseudoknot within the 90S pre-ribosome. <i>Nucleic Acids Research</i> , 2013 , 41, 1178-90	20.1	18
186	Both endonucleolytic and exonucleolytic cleavage mediate ITS1 removal during human ribosomal RNA processing. <i>Journal of Cell Biology</i> , 2013 , 200, 577-88	7.3	94
185	Functions of Long Non-Coding RNAs in Non-mammalian Systems 2013 , 137-162		
184	Identification of RNA helicase target sites by UV cross-linking and analysis of cDNA. <i>Methods in Enzymology</i> , 2012 , 511, 275-88	1.7	43
183	Transcriptome-wide analysis of exosome targets. <i>Molecular Cell</i> , 2012 , 48, 422-33	17.6	145

182	An RNA reset button. <i>Molecular Cell</i> , 2012 , 45, 435-6	17.6	2
181	Structure of the pre-60S ribosomal subunit with nuclear export factor Arx1 bound at the exit tunnel. <i>Nature Structural and Molecular Biology</i> , 2012 , 19, 1234-41	17.6	92
180	Proofreading of pre-40S ribosome maturation by a translation initiation factor and 60S subunits. <i>Nature Structural and Molecular Biology</i> , 2012 , 19, 744-53	17.6	134
179	Kinetic analysis of pre-ribosome structure in vivo. <i>Rna</i> , 2012 , 18, 2187-200	5.8	21
178	Brr2p-mediated conformational rearrangements in the spliceosome during activation and substrate repositioning. <i>Genes and Development</i> , 2012 , 26, 2408-21	12.6	60
177	Murine cytomegalovirus encodes a miR-27 inhibitor disguised as a target. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 279-84	11.5	100
176	Box C/D snoRNP catalysed methylation is aided by additional pre-rRNA base-pairing. <i>EMBO Journal</i> , 2011 , 30, 2420-30	13	50
175	The nuclear RNA polymerase II surveillance system targets polymerase III transcripts. <i>EMBO Journal</i> , 2011 , 30, 1790-803	13	141
174	RNA in pieces. <i>Trends in Genetics</i> , 2011 , 27, 422-32	8.5	109
173	Cross-linking, ligation, and sequencing of hybrids reveals RNA-RNA interactions in yeast. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 10010-5	11.5	212
172	Distinguishing the roles of Topoisomerases I and II in relief of transcription-induced torsional stress in yeast rRNA genes. <i>Molecular and Cellular Biology</i> , 2011 , 31, 482-94	4.8	75
171	Repeat expansion in the budding yeast ribosomal DNA can occur independently of the canonical homologous recombination machinery. <i>Nucleic Acids Research</i> , 2011 , 39, 8778-91	20.1	33
170	The nuclear RNA polymerase II surveillance system targets polymerase III transcripts. <i>EMBO Journal</i> , 2011 , 30, 2982-2982	13	1
169	A cluster of ribosome synthesis factors regulate pre-rRNA folding and 5.8S rRNA maturation by the Rat1 exonuclease. <i>EMBO Journal</i> , 2011 , 30, 4006-19	13	135
168	Finding the exosome. <i>Advances in Experimental Medicine and Biology</i> , 2011 , 702, 1-8	3.6	3
167	Cracking pre-40S ribosomal subunit structure by systematic analyses of RNA-protein cross-linking. <i>EMBO Journal</i> , 2010 , 29, 2026-36	13	108
166	Apparent non-canonical trans-splicing is generated by reverse transcriptase in vitro. <i>Nature Precedings</i> , 2010 ,		3
165	Apparent non-canonical trans-splicing is generated by reverse transcriptase in vitro. <i>PLoS ONE</i> , 2010 , 5, e12271	3.7	106

164	Loss of Topoisomerase I leads to R-loop-mediated transcriptional blocks during ribosomal RNA synthesis. <i>Genes and Development</i> , 2010 , 24, 1546-58	12.6	301
163	RiboSys, a high-resolution, quantitative approach to measure the in vivo kinetics of pre-mRNA splicing and 3Rend processing in <i>Saccharomyces cerevisiae</i> . <i>Rna</i> , 2010 , 16, 2570-80	5.8	41
162	The final step in 5.8S rRNA processing is cytoplasmic in <i>Saccharomyces cerevisiae</i> . <i>Molecular and Cellular Biology</i> , 2010 , 30, 976-84	4.8	56
161	Yeast pre-rRNA processing and modification occur cotranscriptionally. <i>Molecular Cell</i> , 2010 , 37, 809-20	17.6	217
160	RNA helicase Prp43 and its co-factor Pfa1 promote 20 to 18 S rRNA processing catalyzed by the endonuclease Nob1. <i>Journal of Biological Chemistry</i> , 2009 , 284, 35079-91	5.4	142
159	The N-terminal PIN domain of the exosome subunit Rrp44 harbors endonuclease activity and tethers Rrp44 to the yeast core exosome. <i>Nucleic Acids Research</i> , 2009 , 37, 1127-40	20.1	182
158	An endoribonuclease functionally linked to perinuclear mRNP quality control associates with the nuclear pore complexes. <i>PLoS Biology</i> , 2009 , 7, e8	9.7	47
157	Coding-sequence determinants of gene expression in <i>Escherichia coli</i> . <i>Science</i> , 2009 , 324, 255-8	33.3	1011
156	The many pathways of RNA degradation. <i>Cell</i> , 2009 , 136, 763-76	56.2	768
155	Prp43 bound at different sites on the pre-rRNA performs distinct functions in ribosome synthesis. <i>Molecular Cell</i> , 2009 , 36, 583-92	17.6	128
154	Rrp17p is a eukaryotic exonuclease required for 5Rend processing of Pre-60S ribosomal RNA. <i>Molecular Cell</i> , 2009 , 36, 768-81	17.6	64
153	Identification of protein binding sites on U3 snoRNA and pre-rRNA by UV cross-linking and high-throughput analysis of cDNAs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 9613-8	11.5	259
152	Quantitative analysis of snoRNA association with pre-ribosomes and release of snR30 by Rok1 helicase. <i>EMBO Reports</i> , 2008 , 9, 1230-6	6.5	64
151	Efficient termination of transcription by RNA polymerase I requires the 5Rexonuclease Rat1 in yeast. <i>Genes and Development</i> , 2008 , 22, 1069-81	12.6	83
150	A ncRNA modulates histone modification and mRNA induction in the yeast GAL gene cluster. <i>Molecular Cell</i> , 2008 , 32, 685-95	17.6	232
149	The nuclear RNA surveillance machinery: the link between ncRNAs and genome structure in budding yeast?. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2008 , 1779, 239-46	6	67
148	The mRNA encoding the yeast ARE-binding protein Cth2 is generated by a novel 3Rend processing pathway. <i>Nucleic Acids Research</i> , 2008 , 36, 3075-84	20.1	35
147	Inactivation of cleavage factor I components Rna14p and Rna15p induces sequestration of small nucleolar ribonucleoproteins at discrete sites in the nucleus. <i>Molecular Biology of the Cell</i> , 2008 , 19, 1499-508	3.5	7

146	A yeast exosome cofactor, Mpp6, functions in RNA surveillance and in the degradation of noncoding RNA transcripts. <i>Molecular and Cellular Biology</i> , 2008 , 28, 5446-57	4.8	75
145	Modelling co-transcriptional cleavage in the synthesis of yeast pre-rRNA. <i>Theoretical Computer Science</i> , 2008 , 408, 41-54	1.1	5
144	The yeast ribosome synthesis factor Emg1 is a novel member of the superfamily of alpha/beta knot fold methyltransferases. <i>Nucleic Acids Research</i> , 2008 , 36, 629-39	20.1	45
143	Imaging the migrating border cell cluster in living <i>Drosophila</i> egg chambers. <i>Developmental Dynamics</i> , 2007 , 236, 2818-24	2.9	13
142	Trf4 targets ncRNAs from telomeric and rDNA spacer regions and functions in rDNA copy number control. <i>EMBO Journal</i> , 2007 , 26, 4996-5006	13	146
141	Building ribosomes: even more expensive than expected?. <i>Current Biology</i> , 2007 , 17, R415-7	6.3	31
140	Yeast Rrp14p is required for ribosomal subunit synthesis and for correct positioning of the mitotic spindle during mitosis. <i>Nucleic Acids Research</i> , 2007 , 35, 1354-66	20.1	34
139	Roles of the HEAT repeat proteins Utp10 and Utp20 in 40S ribosome maturation. <i>Rna</i> , 2007 , 13, 1516-27	5.8	37
138	Nop9 is an RNA binding protein present in pre-40S ribosomes and required for 18S rRNA synthesis in yeast. <i>Rna</i> , 2007 , 13, 2165-74	5.8	46
137	Depletion of the yeast nuclear exosome subunit Rrp6 results in accumulation of polyadenylated RNAs in a discrete domain within the nucleolus. <i>Molecular and Cellular Biology</i> , 2007 , 27, 4157-65	4.8	41
136	The exosome subunit Rrp44 plays a direct role in RNA substrate recognition. <i>Molecular Cell</i> , 2007 , 27, 324-331	17.6	125
135	Modelling Yeast Pre-rRNA Processing. <i>Lecture Notes in Computer Science</i> , 2007 , 32-47	0.9	1
134	FLIPing heterokaryons to analyze nucleo-cytoplasmic shuttling of yeast proteins. <i>Rna</i> , 2006 , 12, 921-30	5.8	11
133	Ribosomal RNA 2006 ,		1
132	Microarray detection of novel nuclear RNA substrates for the exosome. <i>Yeast</i> , 2006 , 23, 439-54	3.4	61
131	Formation and nuclear export of preribosomes are functionally linked to the small-ubiquitin-related modifier pathway. <i>Traffic</i> , 2006 , 7, 1311-21	5.7	70
130	Molecular biology: RNA lost in translation. <i>Nature</i> , 2006 , 440, 425-6	50.4	27
129	RNA-quality control by the exosome. <i>Nature Reviews Molecular Cell Biology</i> , 2006 , 7, 529-39	48.7	513

128	Hrr25-dependent phosphorylation state regulates organization of the pre-40S subunit. <i>Nature</i> , 2006 , 441, 651-5	50.4	169
127	Surveillance of nuclear-restricted pre-ribosomes within a subnucleolar region of <i>Saccharomyces cerevisiae</i> . <i>EMBO Journal</i> , 2006 , 25, 1534-46	13	112
126	Yeast Trf5p is a nuclear poly(A) polymerase. <i>EMBO Reports</i> , 2006 , 7, 205-11	6.5	136
125	The Putative RNA Helicase Dbp4p Is Required for Release of the U14 snoRNA from Preribosomes in <i>Saccharomyces cerevisiae</i> . <i>Molecular Cell</i> , 2005 , 20, 53-64	17.6	75
124	Sen34p depletion blocks tRNA splicing in vivo and delays rRNA processing. <i>Biochemical and Biophysical Research Communications</i> , 2005 , 337, 89-94	3.4	24
123	RNA degradation by the exosome is promoted by a nuclear polyadenylation complex. <i>Cell</i> , 2005 , 121, 713-24	56.2	700
122	Crosstalk between RNA metabolic pathways: an RNOMICS approach. <i>Nature Reviews Molecular Cell Biology</i> , 2005 , 6, 423-9	48.7	7
121	Functional link between ribosome formation and biogenesis of iron-sulfur proteins. <i>EMBO Journal</i> , 2005 , 24, 580-8	13	133
120	Nop53p is required for late 60S ribosome subunit maturation and nuclear export in yeast. <i>Rna</i> , 2005 , 11, 1215-24	5.8	34
119	A nuclear surveillance pathway for mRNAs with defective polyadenylation. <i>Molecular and Cellular Biology</i> , 2005 , 25, 9996-10004	4.8	89
118	The Noc proteins involved in ribosome synthesis and export contain divergent HEAT repeats. <i>Rna</i> , 2004 , 10, 351-4	5.8	11
117	PIN domain of Nob1p is required for D-site cleavage in 20S pre-rRNA. <i>Rna</i> , 2004 , 10, 1698-701	5.8	96
116	Rea1, a dynein-related nuclear AAA-ATPase, is involved in late rRNA processing and nuclear export of 60 S subunits. <i>Journal of Biological Chemistry</i> , 2004 , 279, 55411-8	5.4	57
115	A pre-ribosome-associated HEAT-repeat protein is required for export of both ribosomal subunits. <i>Genes and Development</i> , 2004 , 18, 196-209	12.6	93
114	A Surfeit of Factors: Why is Ribosome Assembly So Much More Complicated in Eukaryotes than Bacteria?. <i>RNA Biology</i> , 2004 , 1, 9-14	4.8	55
113	The ScavengerRm7GpppX pyrophosphatase activity of Dcs1 modulates nutrient-induced responses in yeast. <i>Nucleic Acids Research</i> , 2004 , 32, 3590-600	20.1	33
112	A pre-ribosome with a tadpole-like structure functions in ATP-dependent maturation of 60S subunits. <i>Molecular Cell</i> , 2004 , 15, 295-301	17.6	61
111	Ribosome synthesis meets the cell cycle. <i>Current Opinion in Microbiology</i> , 2004 , 7, 631-7	7.9	116

110	Nuclear pre-mRNA decapping and 5Rdegradation in yeast require the Lsm2-8p complex. <i>Molecular and Cellular Biology</i> , 2004 , 24, 9646-57	4.8	53
109	A surfeit of factors: why is ribosome assembly so much more complicated in eukaryotes than bacteria?. <i>RNA Biology</i> , 2004 , 1, 10-5	4.8	54
108	Cic1p/Nsa3p is required for synthesis and nuclear export of 60S ribosomal subunits. <i>Rna</i> , 2003 , 9, 1431-65.8	6.5	32
107	The path from nucleolar 90S to cytoplasmic 40S pre-ribosomes. <i>EMBO Journal</i> , 2003 , 22, 1370-80	13	237
106	Formation and nuclear export of tRNA, rRNA and mRNA is regulated by the ubiquitin ligase Rsp5p. <i>EMBO Reports</i> , 2003 , 4, 1156-62	6.5	63
105	Yeast Nop15p is an RNA-binding protein required for pre-rRNA processing and cytokinesis. <i>EMBO Journal</i> , 2003 , 22, 6573-83	13	56
104	Lsm Proteins are required for normal processing and stability of ribosomal RNAs. <i>Journal of Biological Chemistry</i> , 2003 , 278, 2147-56	5.4	63
103	A complex pathway for 3Rprocessing of the yeast U3 snoRNA. <i>Nucleic Acids Research</i> , 2003 , 31, 6788-97	20.1	36
102	An NMD pathway in yeast involving accelerated deadenylation and exosome-mediated 3R->5R degradation. <i>Molecular Cell</i> , 2003 , 11, 1405-13	17.6	166
101	Nob1p is required for cleavage of the 3Rend of 18S rRNA. <i>Molecular and Cellular Biology</i> , 2003 , 23, 1798-807	4.8	122
100	Rrp47p is an exosome-associated protein required for the 3Rprocessing of stable RNAs. <i>Molecular and Cellular Biology</i> , 2003 , 23, 6982-92	4.8	134
99	Fibrillarin is essential for early development and required for accumulation of an intron-encoded small nucleolar RNA in the mouse. <i>Molecular and Cellular Biology</i> , 2003 , 23, 8519-27	4.8	76
98	3Rprocessing of yeast tRNATrp precedes 5Rprocessing. <i>Rna</i> , 2003 , 9, 202-8	5.8	31
97	Yeast Pescadillo is required for multiple activities during 60S ribosomal subunit synthesis. <i>Rna</i> , 2002 , 8, 626-36	5.8	61
96	Making ribosomes. <i>Current Opinion in Cell Biology</i> , 2002 , 14, 313-8	9	428
95	60S pre-ribosome formation viewed from assembly in the nucleolus until export to the cytoplasm. <i>EMBO Journal</i> , 2002 , 21, 5539-47	13	281
94	Lsm proteins are required for normal processing of pre-tRNAs and their efficient association with La-homologous protein Lhp1p. <i>Molecular and Cellular Biology</i> , 2002 , 22, 5248-56	4.8	56
93	Ssf1p prevents premature processing of an early pre-60S ribosomal particle. <i>Molecular Cell</i> , 2002 , 9, 341-51.6	5.16	148

92	Processing of 3' extended read-through transcripts by the exosome can generate functional mRNAs. <i>Molecular Cell</i> , 2002 , 9, 1285-96	17.6	138
91	90S pre-ribosomes include the 35S pre-rRNA, the U3 snoRNP, and 40S subunit processing factors but predominantly lack 60S synthesis factors. <i>Molecular Cell</i> , 2002 , 10, 105-15	17.6	395
90	Rlp7p is associated with 60S preribosomes, restricted to the granular component of the nucleolus, and required for pre-rRNA processing. <i>Journal of Cell Biology</i> , 2002 , 157, 941-51	7.3	66
89	Naf1 p is a box H/ACA snoRNP assembly factor. <i>Rna</i> , 2002 , 8, 1502-14	5.8	60
88	Ribosomal RNA 2001 ,		3
87	A nuclear AAA-type ATPase (Rix7p) is required for biogenesis and nuclear export of 60S ribosomal subunits. <i>EMBO Journal</i> , 2001 , 20, 3695-704	13	73
86	Box C/D small nucleolar RNA trafficking involves small nucleolar RNP proteins, nucleolar factors and a novel nuclear domain. <i>EMBO Journal</i> , 2001 , 20, 5480-90	13	88
85	The function and synthesis of ribosomes. <i>Nature Reviews Molecular Cell Biology</i> , 2001 , 2, 514-20	48.7	139
84	mRNA turnover. <i>Current Opinion in Cell Biology</i> , 2001 , 13, 320-5	9	139
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2	Stress-induced translation inhibition through rapid displacement of scanning initiation factors	2
1	Yeast Ssd1 is a non-enzymatic member of the RNase II family with an alternative RNA recognition interface	1