

Sander Granneman

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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.

63

papers

3,957

citations

37

h-index

62

g-index

70

ext. papers

4,628

ext. citations

12.7

avg, IF

5.32

L-index

#	Paper	IF	Citations
63	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
62	The apoptosis-promoting factor TIA-1 is a regulator of alternative pre-mRNA splicing. <i>Molecular Cell</i> , 2000 , 6, 1089-98	17.6	221
61	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
60	RNA polymerase I transcription and pre-rRNA processing are linked by specific SSU processome components. <i>Genes and Development</i> , 2004 , 18, 2506-17	12.6	193
59	Ribosome biogenesis: of knobs and RNA processing. <i>Experimental Cell Research</i> , 2004 , 296, 43-50	4.2	186
58	Identification of bacteriophage-encoded anti-sRNAs in pathogenic Escherichia coli. <i>Molecular Cell</i> , 2014 , 55, 199-213	17.6	174
57	The nuclear RNA polymerase II surveillance system targets polymerase III transcripts. <i>EMBO Journal</i> , 2011 , 30, 1790-803	13	141
56	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
55	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
54	The small-subunit processome is a ribosome assembly intermediate. <i>Eukaryotic Cell</i> , 2004 , 3, 1619-26		134
53	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
52	PAR-CLIP data indicate that Nrd1-Nab3-dependent transcription termination regulates expression of hundreds of protein coding genes in yeast. <i>Genome Biology</i> , 2014 , 15, R8	18.3	114
51	Cracking pre-40S ribosomal subunit structure by systematic analyses of RNA-protein cross-linking. <i>EMBO Journal</i> , 2010 , 29, 2026-36	13	108
50	Coupled GTPase and remodelling ATPase activities form a checkpoint for ribosome export. <i>Nature</i> , 2014 , 505, 112-116	50.4	97
49	Crosstalk in gene expression: coupling and co-regulation of rDNA transcription, pre-ribosome assembly and pre-rRNA processing. <i>Current Opinion in Cell Biology</i> , 2005 , 17, 281-6	9	95
48	Purification of cross-linked RNA-protein complexes by phenol-toluol extraction. <i>Nature Communications</i> , 2019 , 10, 990	17.4	94
47	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

46	The putative NTPase Fap7 mediates cytoplasmic 20S pre-rRNA processing through a direct interaction with Rps14. <i>Molecular and Cellular Biology</i> , 2005 , 25, 10352-64	4.8	81
45	RNA-binding activity of TRIM25 is mediated by its PRY/SPRY domain and is required for ubiquitination. <i>BMC Biology</i> , 2017 , 15, 105	7.3	80
44	The PINc domain protein Utp24, a putative nuclease, is required for the early cleavage steps in 18S rRNA maturation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 9464-9	11.5	72
43	Snapshots of pre-rRNA structural flexibility reveal eukaryotic 40S assembly dynamics at nucleotide resolution. <i>Nucleic Acids Research</i> , 2014 , 42, 12138-54	20.1	68
42	Rio1 mediates ATP-dependent final maturation of 40S ribosomal subunits. <i>Nucleic Acids Research</i> , 2014 , 42, 12189-99	20.1	61
41	The human Imp3 and Imp4 proteins form a ternary complex with hMpp10, which only interacts with the U3 snoRNA in 60-80S ribonucleoprotein complexes. <i>Nucleic Acids Research</i> , 2003 , 31, 1877-87	20.1	61
40	Specialized box C/D snoRNPs act as antisense guides to target RNA base acetylation. <i>PLoS Genetics</i> , 2017 , 13, e1006804	6	55
39	Comprehensive mutational analysis of yeast DEXD/H box RNA helicases involved in large ribosomal subunit biogenesis. <i>Molecular and Cellular Biology</i> , 2006 , 26, 1195-208	4.8	55
38	Box C/D snoRNP catalysed methylation is aided by additional pre-rRNA base-pairing. <i>EMBO Journal</i> , 2011 , 30, 2420-30	13	50
37	The nucleolar protein Esf2 interacts directly with the DEXD/H box RNA helicase, Dbp8, to stimulate ATP hydrolysis. <i>Nucleic Acids Research</i> , 2006 , 34, 3189-99	20.1	50
36	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
35	Kinetic CRAC uncovers a role for Nab3 in determining gene expression profiles during stress. <i>Nature Communications</i> , 2017 , 8, 12	17.4	49
34	Rrp5 binding at multiple sites coordinates pre-rRNA processing and assembly. <i>Molecular Cell</i> , 2013 , 52, 707-19	17.6	46
33	Comprehensive mutational analysis of yeast DEXD/H box RNA helicases required for small ribosomal subunit synthesis. <i>Molecular and Cellular Biology</i> , 2006 , 26, 1183-94	4.8	46
32	Regulation of mRNA Levels by Decay-Promoting Introns that Recruit the Exosome Specificity Factor Mmi1. <i>Cell Reports</i> , 2015 , 13, 2504-2515	10.6	44
31	The roles of Rrp5p in the synthesis of yeast 18S and 5.8S rRNA can be functionally and physically separated. <i>Rna</i> , 1999 , 5, 779-93	5.8	44
30	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
29	The hU3-55K protein requires 15.5K binding to the box B/C motif as well as flanking RNA elements for its association with the U3 small nucleolar RNA in Vitro. <i>Journal of Biological Chemistry</i> , 2002 , 277, 48490-500	5.4	39

28	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
27	Interaction of the U3-55k protein with U3 snoRNA is mediated by the box B/C motif of U3 and the WD repeats of U3-55k. <i>Nucleic Acids Research</i> , 2000 , 28, 3462-71	20.1	38
26	Transcriptome-wide RNA processing kinetics revealed using extremely short 4tU labeling. <i>Genome Biology</i> , 2015 , 16, 282	18.3	37
25	Spliceosome-mediated decay (SMD) regulates expression of nonintronic genes in budding yeast. <i>Genes and Development</i> , 2013 , 27, 2025-38	12.6	37
24	Role of pre-rRNA base pairing and 80S complex formation in subnucleolar localization of the U3 snoRNP. <i>Molecular and Cellular Biology</i> , 2004 , 24, 8600-10	4.8	37
23	The Nrd1-like protein Seb1 coordinates cotranscriptional 3'end processing and polyadenylation site selection. <i>Genes and Development</i> , 2016 , 30, 1558-72	12.6	35
22	Building ribosomes: even more expensive than expected?. <i>Current Biology</i> , 2007 , 17, R415-7	6.3	31
21	Hfq CLASH uncovers sRNA-target interaction networks linked to nutrient availability adaptation. <i>ELife</i> , 2020 , 9,	8.9	30
20	Cell populations can use aneuploidy to survive telomerase insufficiency. <i>Nature Communications</i> , 2015 , 6, 8664	17.4	28
19	High-throughput RNA structure probing reveals critical folding events during early 60S ribosome assembly in yeast. <i>Nature Communications</i> , 2017 , 8, 714	17.4	23
18	Robust statistical modeling improves sensitivity of high-throughput RNA structure probing experiments. <i>Nature Methods</i> , 2017 , 14, 83-89	21.6	22
17	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
16	An RNA-dependent mechanism for transient expression of bacterial translocation filaments. <i>Nucleic Acids Research</i> , 2018 , 46, 3366-3381	20.1	14
15	Loss of the Yeast SR Protein Npl3 Alters Gene Expression Due to Transcription Readthrough. <i>PLoS Genetics</i> , 2015 , 11, e1005735	6	11
14	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
13	Maturation of the 90S pre-ribosome requires Mrd1 dependent U3 snoRNA and 35S pre-rRNA structural rearrangements. <i>Nucleic Acids Research</i> , 2018 , 46, 3692-3706	20.1	6
12	The role of RNA-binding proteins in mediating adaptive responses in Gram-positive bacteria. <i>FEBS Journal</i> , 2021 ,	5.7	5
11	Puf6 primes 60S pre-ribosome nuclear export at low temperature. <i>Nature Communications</i> , 2021 , 12, 4696	17.4	5

10	Radical genome remodelling accompanied the emergence of a novel host-restricted bacterial pathogen. <i>PLoS Pathogens</i> , 2021 , 17, e1009606	7.6	4
9	Purification of Cross-linked RNA-Protein Complexes by Phenol-Toluol Extraction		3
8	The mRNA derived MalH sRNA contributes to alternative carbon source utilization by tuning maltoporin expression in <i>E. coli</i> . <i>RNA Biology</i> , 2021 , 18, 914-931	4.8	3
7	Monitoring Protein-RNA Interaction Dynamics in vivo at High Temporal Resolution using μ RAC. <i>Journal of Visualized Experiments</i> , 2020 ,	1.6	2
6	Probing the yeast proteome for RNA-processing factors. <i>Genome Biology</i> , 2003 , 4, 229	18.3	2
5	diffBUM-HMM: a robust statistical modeling approach for detecting RNA flexibility changes in high-throughput structure probing data. <i>Genome Biology</i> , 2021 , 22, 165	18.3	2
4	The nuclear RNA polymerase II surveillance system targets polymerase III transcripts. <i>EMBO Journal</i> , 2011 , 30, 2982-2982	13	1
3	Hfq CLASH uncovers sRNA-target interaction networks involved in adaptation to nutrient availability		1
2	Probing the RNA-Binding Proteome from Yeast to Man: Major Advances and Challenges. <i>Methods in Molecular Biology</i> , 2019 , 2049, 213-231	1.4	1
1	Differential BUM-HMM: a robust statistical modelling approach for detecting RNA flexibility changes in high-throughput structure probing data		1