Sander Granneman

List of Publications by Year in Descending Order

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	The role of RNA-binding proteins in mediating adaptive responses in Gram-positive bacteria. *FEBS Journal*, **2021**,	5.7	5
62	diffBUM-HMM: a robust statistical modeling approach for detecting RNA flexibility changes in high-throughput structure probing data. *Genome Biology*, **2021**, 22, 165	18.3	2
61	Radical genome remodelling accompanied the emergence of a novel host-restricted bacterial pathogen. *PLoS Pathogens*, **2021**, 17, e1009606	7.6	4
60	The mRNA derived MalH sRNA contributes to alternative carbon source utilization by tuning maltoporin expression in E. coli. *RNA Biology*, **2021**, 18, 914-931	4.8	3
59	Puf6 primes 60S pre-ribosome nuclear export at low temperature. *Nature Communications*, **2021**, 12, 4696	17.4	5
58	Monitoring Protein-RNA Interaction Dynamics in vivo at High Temporal Resolution using ⁴CRAC. *Journal of Visualized Experiments*, **2020**,	1.6	2
57	Hfq CLASH uncovers sRNA-target interaction networks linked to nutrient availability adaptation. *ELife*, **2020**, 9,	8.9	30
56	Purification of cross-linked RNA-protein complexes by phenol-toluol extraction. *Nature Communications*, **2019**, 10, 990	17.4	94
55	Probing the RNA-Binding Proteome from Yeast to Man: Major Advances and Challenges. *Methods in Molecular Biology*, **2019**, 2049, 213-231	1.4	1
54	Maturation of the 90S pre-ribosome requires Mrd1 dependent U3 snoRNA and 35S pre-rRNA structural rearrangements. *Nucleic Acids Research*, **2018**, 46, 3692-3706	20.1	6
53	High-Resolution, High-Throughput Analysis of Hfq-Binding Sites Using UV Crosslinking and Analysis of cDNA (CRAC). *Methods in Molecular Biology*, **2018**, 1737, 251-272	1.4	7
52	An RNA-dependent mechanism for transient expression of bacterial translocation filaments. *Nucleic Acids Research*, **2018**, 46, 3366-3381	20.1	14
51	High-throughput RNA structure probing reveals critical folding events during early 60S ribosome assembly in yeast. *Nature Communications*, **2017**, 8, 714	17.4	23
50	Specialized box C/D snoRNPs act as antisense guides to target RNA base acetylation. *PLoS Genetics*, **2017**, 13, e1006804	6	55
49	RNA-binding activity of TRIM25 is mediated by its PRY/SPRY domain and is required for ubiquitination. *BMC Biology*, **2017**, 15, 105	7.3	80
48	Kinetic CRAC uncovers a role for Nab3 in determining gene expression profiles during stress. *Nature Communications*, **2017**, 8, 12	17.4	49
47	Robust statistical modeling improves sensitivity of high-throughput RNA structure probing experiments. *Nature Methods*, **2017**, 14, 83-89	21.6	22

46   The Nrd1-like protein Seb1 coordinates cotranscriptional 3′end processing and polyadenylation site selection. *Genes and Development*, **2016**, 30, 1558-72   12.6   35

45   The DEAH-box helicase Dhr1 dissociates U3 from the pre-rRNA to promote formation of the central pseudoknot. *PLoS Biology*, **2015**, 13, e1002083   9.7   49

44   Cell populations can use aneuploidy to survive telomerase insufficiency. *Nature Communications*, **2015**, 6, 8664   17.4   28

43   Loss of the Yeast SR Protein Npl3 Alters Gene Expression Due to Transcription Readthrough. *PLoS Genetics*, **2015**, 11, e1005735   6   11

42   Regulation of mRNA Levels by Decay-Promoting Introns that Recruit the Exosome Specificity Factor Mmi1. *Cell Reports*, **2015**, 13, 2504-2515   10.6   44

41   Transcriptome-wide RNA processing kinetics revealed using extremely short 4tU labeling. *Genome Biology*, **2015**, 16, 282   18.3   37

40   Coupled GTPase and remodelling ATPase activities form a checkpoint for ribosome export. *Nature*, **2014**, 505, 112-116   50.4   97

39   A network of assembly factors is involved in remodeling rRNA elements during preribosome maturation. *Journal of Cell Biology*, **2014**, 207, 481-98   7.3   38

38   Identification of bacteriophage-encoded anti-sRNAs in pathogenic Escherichia coli. *Molecular Cell*, **2014**, 55, 199-213   17.6   174

37   Rio1 mediates ATP-dependent final maturation of 40S ribosomal subunits. *Nucleic Acids Research*, **2014**, 42, 12189-99   20.1   61

36   Snapshots of pre-rRNA structural flexibility reveal eukaryotic 40S assembly dynamics at nucleotide resolution. *Nucleic Acids Research*, **2014**, 42, 12138-54   20.1   68

35   PAR-CLIP data indicate that Nrd1-Nab3-dependent transcription termination regulates expression of hundreds of protein coding genes in yeast. *Genome Biology*, **2014**, 15, R8   18.3   114

34   Rrp5 binding at multiple sites coordinates pre-rRNA processing and assembly. *Molecular Cell*, **2013**, 52, 707-19   17.6   46

33   Spliceosome-mediated decay (SMD) regulates expression of nonintronic genes in budding yeast. *Genes and Development*, **2013**, 27, 2025-38   12.6   37

32   Multiple RNA interactions position Mrd1 at the site of the small subunit pseudoknot within the 90S pre-ribosome. *Nucleic Acids Research*, **2013**, 41, 1178-90   20.1   18

31   Identification of RNA helicase target sites by UV cross-linking and analysis of cDNA. *Methods in Enzymology*, **2012**, 511, 275-88   1.7   43

30   Structure of the pre-60S ribosomal subunit with nuclear export factor Arx1 bound at the exit tunnel. *Nature Structural and Molecular Biology*, **2012**, 19, 1234-41   17.6   92

29   Proofreading of pre-40S ribosome maturation by a translation initiation factor and 60S subunits. *Nature Structural and Molecular Biology*, **2012**, 19, 744-53   17.6   134

28	Box C/D snoRNP catalysed methylation is aided by additional pre-rRNA base-pairing. *EMBO Journal*, **2011**, 30, 2420-30	13	50
27	The nuclear RNA polymerase II surveillance system targets polymerase III transcripts. *EMBO Journal*, **2011**, 30, 1790-803	13	141
26	Cross-linking, ligation, and sequencing of hybrids reveals RNA-RNA interactions in yeast. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108, 10010-5	11.5	212
25	The nuclear RNA polymerase II surveillance system targets polymerase III transcripts. *EMBO Journal*, **2011**, 30, 2982-2982	13	1
24	A cluster of ribosome synthesis factors regulate pre-rRNA folding and 5.8S rRNA maturation by the Rat1 exonuclease. *EMBO Journal*, **2011**, 30, 4006-19	13	135
23	Cracking pre-40S ribosomal subunit structure by systematic analyses of RNA-protein cross-linking. *EMBO Journal*, **2010**, 29, 2026-36	13	108
22	Prp43 bound at different sites on the pre-rRNA performs distinct functions in ribosome synthesis. *Molecular Cell*, **2009**, 36, 583-92	17.6	128
21	Identification of protein binding sites on U3 snoRNA and pre-rRNA by UV cross-linking and high-throughput analysis of cDNAs. *Proceedings of the National Academy of Sciences of the United States of America*, **2009**, 106, 9613-8	11.5	259
20	Building ribosomes: even more expensive than expected?. *Current Biology*, **2007**, 17, R415-7	6.3	31
19	The nucleolar protein Esf2 interacts directly with the DExD/H box RNA helicase, Dbp8, to stimulate ATP hydrolysis. *Nucleic Acids Research*, **2006**, 34, 3189-99	20.1	50
18	The PINc domain protein Utp24, a putative nuclease, is required for the early cleavage steps in 18S rRNA maturation. *Proceedings of the National Academy of Sciences of the United States of America*, **2006**, 103, 9464-9	11.5	72
17	Comprehensive mutational analysis of yeast DEXD/H box RNA helicases required for small ribosomal subunit synthesis. *Molecular and Cellular Biology*, **2006**, 26, 1183-94	4.8	46
16	Comprehensive mutational analysis of yeast DEXD/H box RNA helicases involved in large ribosomal subunit biogenesis. *Molecular and Cellular Biology*, **2006**, 26, 1195-208	4.8	55
15	Crosstalk in gene expression: coupling and co-regulation of rDNA transcription, pre-ribosome assembly and pre-rRNA processing. *Current Opinion in Cell Biology*, **2005**, 17, 281-6	9	95
14	The putative NTPase Fap7 mediates cytoplasmic 20S pre-rRNA processing through a direct interaction with Rps14. *Molecular and Cellular Biology*, **2005**, 25, 10352-64	4.8	81
13	Role of pre-rRNA base pairing and 80S complex formation in subnucleolar localization of the U3 snoRNP. *Molecular and Cellular Biology*, **2004**, 24, 8600-10	4.8	37
12	The small-subunit processome is a ribosome assembly intermediate. *Eukaryotic Cell*, **2004**, 3, 1619-26		134
11	RNA polymerase I transcription and pre-rRNA processing are linked by specific SSU processome components. *Genes and Development*, **2004**, 18, 2506-17	12.6	193

LIST OF PUBLICATIONS

10	Ribosome biogenesis: of knobs and RNA processing. *Experimental Cell Research*, **2004**, 296, 43-50	4.2	186
9	The human Imp3 and Imp4 proteins form a ternary complex with hMpp10, which only interacts with the U3 snoRNA in 60-80S ribonucleoprotein complexes. *Nucleic Acids Research*, **2003**, 31, 1877-87	20.1	61
8	Probing the yeast proteome for RNA-processing factors. *Genome Biology*, **2003**, 4, 229	18.3	2
7	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. *Journal of Biological Chemistry*, **2002**, 277, 48490-500	5.4	39
6	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. *Nucleic Acids Research*, **2000**, 28, 3462-71	20.1	38
5	The apoptosis-promoting factor TIA-1 is a regulator of alternative pre-mRNA splicing. *Molecular Cell*, **2000**, 6, 1089-98	17.6	221
4	The roles of Rrp5p in the synthesis of yeast 18S and 5.8S rRNA can be functionally and physically separated. *Rna*, **1999**, 5, 779-93	5.8	44
3	Hfq CLASH uncovers sRNA-target interaction networks involved in adaptation to nutrient availability		1
2	Differential BUM-HMM: a robust statistical modelling approach for detecting RNA flexibility changes in high-throughput structure probing data		1
1	Purification of Cross-linked RNA-Protein Complexes by Phenol-Toluol Extraction		3