Elena Evguenieva-Hackenberg

List of Publications by Year
in descending order

55 papers	1,718 citations	304743 22 h-index	289244 40 g-index
58 all docs	58 docs citations	58 times ranked	1429 citing authors

#	Article	IF	Citations
1	Riboregulation in bacteria: From general principles to novel mechanisms of the <i>trp</i> attenuator and its <scp>sRNA</scp> and peptide products. Wiley Interdisciplinary Reviews RNA, 2022, 13, e1696.	6.4	6
2	Bioinformatic prediction reveals posttranscriptional regulation of the chromosomal replication initiator gene <i>dnaA</i> by the attenuator sRNA rnTrpL in <i>Escherichia coli</i>. RNA Biology, 2021, 18, 1-15.	3.1	6
3	Reprograming of sRNA target specificity by the leader peptide peTrpL in response to antibiotic exposure. Nucleic Acids Research, 2021, 49, 2894-2915.	14.5	9
4	Editorial: RNA-Protein Interactions in mRNA Translation and Decay. Frontiers in Molecular Biosciences, 2021, 8, 803063.	3.5	0
5	Rapid Biophysical Characterization and NMR Spectroscopy Structural Analysis of Small Proteins from Bacteria and Archaea. ChemBioChem, 2020, 21, 1178-1187.	2.6	24
6	Similarities and differences between 6S RNAs from Bradyrhizobium japonicum and Sinorhizobium meliloti. Journal of Microbiology, 2020, 58, 945-956.	2.8	5
7	iCLIP analysis of RNA substrates of the archaeal exosome. BMC Genomics, 2020, 21, 797.	2.8	2
8	The Leader Peptide peTrpL Forms Antibiotic-Containing Ribonucleoprotein Complexes for Posttranscriptional Regulation of Multiresistance Genes. MBio, 2020, 11, .	4.1	10
9	Enzymatic Analysis of Reconstituted Archaeal Exosomes. Methods in Molecular Biology, 2020, 2062, 63-79.	0.9	0
10	Transcription attenuation-derived small RNA rnTrpL regulates tryptophan biosynthesis gene expression in trans. Nucleic Acids Research, 2019, 47, 6396-6410.	14.5	24
11	The SmAP1/2 proteins of the crenarchaeon Sulfolobus solfataricus interact with the exosome and stimulate A-rich tailing of transcripts. Nucleic Acids Research, 2017, 45, 7938-7949.	14.5	24
12	Nop5 interacts with the archaeal <scp>RNA</scp> exosome. FEBS Letters, 2017, 591, 4039-4048.	2.8	5
13	Conserved small mRNA with an unique, extended Shine-Dalgarno sequence. RNA Biology, 2017, 14, 1353-1363.	3.1	3
14	RNase E and RNase J are needed for S-adenosylmethionine homeostasis in Sinorhizobium meliloti. Microbiology (United Kingdom), 2017, 163, 570-583.	1.8	11
15	The Archaeal Exosome: Degradation and Tailing at the 3â€²-End of RNA. Nucleic Acids and Molecular Biology, 2017, , 115-128.	0.2	1
16	Small Open Reading Frames, Non-Coding RNAs and Repetitive Elements in Bradyrhizobium japonicum USDA 110. PLoS ONE, 2016, 11, e0165429.	2.5	9
17	Genome-wide transcription start site mapping of Bradyrhizobium japonicum grown free-living or in symbiosis â€" a rich resource to identify new transcripts, proteins and to study gene regulation. BMC Genomics, 2016, 17, 302.	2.8	70
18	The stress-related, rhizobial small RNA RcsR1 destabilizes the autoinducer synthase encoding mRNA<i>sinI</i>in<i>Sinorhizobium meliloti</i>. RNA Biology, 2016, 13, 486-499.	3.1	35

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19	Riboregulation in plant-associated Î±-proteobacteria. RNA Biology, 2014, 11, 550-562.	3.1	43
20	Structure and function of the archaeal exosome. Wiley Interdisciplinary Reviews RNA, 2014, 5, 623-635.	6.4	29
21	Archaeal DnaG contains a conserved N-terminal RNA-binding domain and enables tailing of rRNA by the exosome. Nucleic Acids Research, 2014, 42, 12691-12706.	14.5	16
22	RNase E Affects the Expression of the Acyl-Homoserine Lactone Synthase Gene <i>sinI</i> in Sinorhizobium meliloti. Journal of Bacteriology, 2014, 196, 1435-1447.	2.2	34
23	Homoserine Lactones Influence the Reaction of Plants to Rhizobia. International Journal of Molecular Sciences, 2013, 14, 17122-17146.	4.1	77
24	Attack from both ends: mRNA degradation in the crenarchaeon <i>Sulfolobus solfataricus</i>. Biochemical Society Transactions, 2013, 41, 379-383.	3.4	11
25	The archaeal DnaG protein needs Csl4 for binding to the exosome and enhances its interaction with adenine-rich RNAs. RNA Biology, 2013, 10, 415-424.	3.1	13
26	Small RNAs of theBradyrhizobium/Rhodopseudomonaslineage and their analysis. RNA Biology, 2012, 9, 47-58.	3.1	41
27	Heterogeneous complexes of the RNA exosome in Sulfolobus solfataricus. Biochimie, 2012, 94, 1578-1587.	2.6	24
28	New aspects of RNA processing in prokaryotes. Current Opinion in Microbiology, 2011, 14, 587-592.	5.1	49
29	Subcellular localization of RNA degrading proteins and protein complexes in prokaryotes. RNA Biology, 2011, 8, 49-54.	3.1	21
30	A genome-wide survey of sRNAs in the symbiotic nitrogen-fixing alpha-proteobacterium Sinorhizobium meliloti. BMC Genomics, 2010, 11, 245.	2.8	104
31	The archaeal exosome localizes to the membrane. FEBS Letters, 2010, 584, 2791-2795.	2.8	18
32	The evolutionarily conserved subunits Rrp4 and Csl4 confer different substrate specificities to the archaeal exosome. FEBS Letters, 2010, 584, 2931-2936.	2.8	24
33	The Archaeal Exosome. Advances in Experimental Medicine and Biology, 2010, 702, 29-38.	1.6	10
34	The archaeal exosome. Advances in Experimental Medicine and Biology, 2010, 702, 29-38.	1.6	3
35	RNase J is involved in the 5â€²â€end maturation of 16S rRNA and 23S rRNA in <i>Sinorhizobium meliloti</i>. FEBS Letters, 2009, 583, 2339-2342.	2.8	39
36	Expression of small RNAs in Rhizobiales and protection of a small RNA and its degradation products by Hfq in Sinorhizobium meliloti. Biochemical and Biophysical Research Communications, 2009, 390, 331-336.	2.1	35

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37	Chapter 7 RNA Degradation in Archaea and Gramâ€Negative Bacteria Different from Escherichia coli. Progress in Molecular Biology and Translational Science, 2009, 85, 275-317.	1.7	41
38	Rrp4 and Csl4 Are Needed for Efficient Degradation but Not for Polyadenylation of Synthetic and Natural RNA by the Archaeal Exosome. Biochemistry, 2008, 47, 13158-13168.	2.5	29
39	Chapter 19 In Vivo and In Vitro Studies of RNA Degrading Activities in Archaea. Methods in Enzymology, 2008, 447, 381-416.	1.0	8
40	Characterization of native and reconstituted exosome complexes from the hyperthermophilic archaeon Sulfolobus solfataricus. Molecular Microbiology, 2006, 62, 1076-1089.	2.5	51
41	Bacterial ribosomal RNA in pieces. Molecular Microbiology, 2005, 57, 318-325.	2.5	62
42	The archaeal exosome core is a hexameric ring structure with three catalytic subunits. Nature Structural and Molecular Biology, 2005, 12, 575-581.	8.2	198
43	RNA polyadenylation in Archaea: not observed in Haloferax while the exosome polynucleotidylates RNA in Sulfolobus. EMBO Reports, 2005, 6, 1188-1193.	4.5	82
44	Exoribonuclease R Interacts with Endoribonuclease E and an RNA Helicase in the Psychrotrophic Bacterium Pseudomonas syringae Lz4W. Journal of Biological Chemistry, 2005, 280, 14572-14578.	3.4	114
45	Temperature-dependent processing of the cspA mRNA in Rhodobacter capsulatus. Microbiology (United) Tj ETQq1 1 0.784314 rgBT /Ov	1.8	8
46	An exosomeâ€like complex in Sulfolobus solfataricus. EMBO Reports, 2003, 4, 889-893.	4.5	128
47	Atypical Processing in Domain III of 23S rRNA of Rhizobium leguminosarum ATCC 10004 T at a Position Homologous to an rRNA Fragmentation Site in Protozoa. Journal of Bacteriology, 2002, 184, 3176-3185.	2.2	5
48	Dehydrogenases from All Three Domains of Life Cleave RNA. Journal of Biological Chemistry, 2002, 277, 46145-46150.	3.4	43
49	RNase E is involved in 5â€²-end 23S rRNA processing in Î±-Proteobacteria. Biochemical and Biophysical Research Communications, 2002, 299, 780-786.	2.1	9
50	One functional subunit is sufficient for catalytic activity and substrate specificity of <i>Escherichia coli</i> endoribonuclease III artificial heterodimers. FEBS Letters, 2002, 518, 93-96.	2.8	17
51	Both N-terminal catalytic and C-terminal RNA binding domain contribute to substrate specificity and cleavage site selection of RNase III. FEBS Letters, 2001, 509, 53-58.	2.8	10
52	RNase III Processing of Intervening Sequences Found in Helix 9 of 23S rRNA in the Alpha Subclass of <i>Proteobacteria</i>. Journal of Bacteriology, 2000, 182, 4719-4729.	2.2	43
53	RNase E Enzymes from Rhodobacter capsulatus and Escherichia coli Differ in Context- and Sequence-Dependent In Vivo Cleavage within the Polycistronic puf mRNA. Journal of Bacteriology, 1999, 181, 7621-7625.	2.2	9
54	Random and Repetitive Primer Amplified Polymorphic DNA Analysis of Five Soil and Two Clinical Isolates of Rahnella aquatilis. Systematic and Applied Microbiology, 1995, 18, 425-438.	2.8	19

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55	RNA Processing. , 0, , 158-174.		3