Patrick Linder

List of Publications by Year
in descending order

28 papers	1,698 citations	516710 16 h-index	642732 23 g-index
28 all docs	28 docs citations	28 times ranked	2646 citing authors

#	Article	IF	Citations
1	From unwinding to clamping â€" the DEAD box RNA helicase family. Nature Reviews Molecular Cell Biology, 2011, 12, 505-516.	37.0	886
2	Looking back on the birth of DEAD-box RNA helicases. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2013, 1829, 750-755.	1.9	108
3	Decay-Initiating Endoribonucleolytic Cleavage by RNase Y Is Kept under Tight Control via Sequence Preference and Sub-cellular Localisation. PLoS Genetics, 2015, 11, e1005577.	3.5	76
4	Bacterial versatility requires DEAD-box RNA helicases. FEMS Microbiology Reviews, 2015, 39, 392-412.	8.6	69
5	Transcriptome-Wide Analyses of 5â€²-Ends in RNase J Mutants of a Gram-Positive Pathogen Reveal a Role in RNA Maturation, Regulation and Degradation. PLoS Genetics, 2014, 10, e1004207.	3.5	65
6	The CshA DEAD-box RNA helicase is important for quorum sensing control in<i>Staphylococcus aureus</i>. RNA Biology, 2013, 10, 157-165.	3.1	60
7	Bent out of Shape: RNA Unwinding by the DEAD-Box Helicase Vasa. Cell, 2006, 125, 219-221.	28.9	56
8	<i>Staphylococcus aureus</i>, phagocyte NADPH oxidase and chronic granulomatous disease. FEMS Microbiology Reviews, 2017, 41, fuw042.	8.6	56
9	The C-terminal region of the RNA helicase CshA is required for the interaction with the degradosome and turnover of bulk RNA in the opportunistic pathogen<i>Staphylococcus aureus</i>. RNA Biology, 2015, 12, 658-674.	3.1	49
10	TSS-EMOTE, a refined protocol for a more complete and less biased global mapping of transcription start sites in bacterial pathogens. BMC Genomics, 2016, 17, 849.	2.8	37
11	New Range of Vectors with a Stringent 5-Fluoroorotic Acid-Based Counterselection System for Generating Mutants by Allelic Replacement in Staphylococcus aureus. Applied and Environmental Microbiology, 2012, 78, 3846-3854.	3.1	36
12	An Essential Factor for High Mg2+ Tolerance of Staphylococcus aureus. Frontiers in Microbiology, 2016, 7, 1888.	3.5	35
13	mRNA Export: RNP Remodeling by DEAD-Box Proteins. Current Biology, 2008, 18, R297-R299.	3.9	29
14	Happy Birthday: 25 Years of DEAD-Box Proteins. Methods in Molecular Biology, 2015, 1259, 17-33.	0.9	25
15	RNA helicases in bacteria. Current Opinion in Microbiology, 2016, 30, 58-66.	5.1	21
16	RNA helicases in RNA decay. Biochemical Society Transactions, 2018, 46, 163-172.	3.4	20
17	Both exo- and endo-nucleolytic activities of RNase J1 from Staphylococcus aureus are manganese dependent and active on triphosphorylated 5â€²-ends. RNA Biology, 2017, 14, 1431-1443.	3.1	19
18	Happy Birthday: 30 Years of RNA Helicases. Methods in Molecular Biology, 2021, 2209, 17-34.	0.9	18

#	Article	IF	Citations
19	Genetic screens reveal novel major and minor players in magnesium homeostasis of Staphylococcus aureus. PLoS Genetics, 2019, 15, e1008336.	3.5	16
20	The DEAD-box RNA helicase CshA is required for fatty acid homeostasis in Staphylococcus aureus. PLoS Genetics, 2020, 16, e1008779.	3.5	5
21	RNase J1 and J2 Are Host-Encoded Factors for Plasmid Replication. Frontiers in Microbiology, 2021, 12, 586886.	3.5	5
22	BiOutils: an interface to connect university laboratories with microbiology classes in schools. FEMS Microbiology Letters, 2015, 362, fnv171.	1.8	4
23	Preface. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2013, 1829, 749.	1.9	3
24	RNA metabolism in Staphylococcus aureus virulence. Swiss Medical Weekly, 2017, 147, w14527.	1.6	0
25	The DEAD-box RNA helicase CshA is required for fatty acid homeostasis in Staphylococcus aureus. , 2020, 16, e1008779.		0
26	The DEAD-box RNA helicase CshA is required for fatty acid homeostasis in Staphylococcus aureus. , 2020, 16, e1008779.		0
27	The DEAD-box RNA helicase CshA is required for fatty acid homeostasis in Staphylococcus aureus. , 2020, 16, e1008779.		0
28	The DEAD-box RNA helicase CshA is required for fatty acid homeostasis in Staphylococcus aureus. , 2020, 16, e1008779.		0