

Benedikt S Nilges

List of Publications by Year in descending order

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Version: 2024-02-01

9
papers

370
citations

1163117

8
h-index

1588992

8
g-index

10
all docs

10
docs citations

10
times ranked

564
citing authors

#	ARTICLE	IF	CITATIONS
1	Humans and other commonly used model organisms are resistant to cycloheximide-mediated biases in ribosome profiling experiments. <i>Nature Communications</i> , 2021, 12, 5094.	12.8	21
2	PDCD4 controls the G1/S-phase transition in a telomerase-immortalized epithelial cell line and affects the expression level and translation of multiple mRNAs. <i>Scientific Reports</i> , 2020, 10, 2758.	3.3	9
3	Enzymatic or In Vivo Installation of Propargyl Groups in Combination with Click Chemistry for the Enrichment and Detection of Methyltransferase Target Sites in RNA. <i>Angewandte Chemie - International Edition</i> , 2018, 57, 6342-6346.	13.8	82
4	Enzymatischer oder In-vivo-Einbau von Propargylgruppen in Kombination mit Klick-Chemie zur Anreicherung und Detektion von Methyltransferase-Zielsequenzen in RNA. <i>Angewandte Chemie</i> , 2018, 130, 6451-6455.	2.0	19
5	The dual methyltransferase METTL13 targets N terminus and Lys55 of eEF1A and modulates codon-specific translation rates. <i>Nature Communications</i> , 2018, 9, 3411.	12.8	81
6	Innentitelbild: Enzymatischer oder In vivo Einbau von Propargylgruppen in Kombination mit Klick-Chemie zur Anreicherung und Detektion von Methyltransferase-Zielsequenzen in RNA (<i>Angew. Chem.</i> 21/2018). <i>Angewandte Chemie</i> , 2018, 130, 6064-6064.	2.0	0
7	The novel lysine specific methyltransferase METTL21B affects mRNA translation through inducible and dynamic methylation of Lys-165 in human eukaryotic elongation factor 1 alpha (eEF1A). <i>Nucleic Acids Research</i> , 2017, 45, gkx002.	14.5	64
8	Methylation of human eukaryotic elongation factor alpha (eEF1A) by a member of a novel protein lysine methyltransferase family modulates mRNA translation. <i>Nucleic Acids Research</i> , 2017, 45, 8239-8254.	14.5	44
9	Dual randomization of oligonucleotides to reduce the bias in ribosome-profiling libraries. <i>Methods</i> , 2016, 107, 89-97.	3.8	50