

High-Resolution Mapping Reveals a Conserved, Widespread Program in Yeast Meiosis

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Citation Report

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2	Transcriptome-Wide Mapping of Pseudouridines: Pseudouridine Synthases Modify Specific mRNAs in <i>S. cerevisiae</i> . PLoS ONE, 2014, 9, e110799.	1.1	305
3	FTO-dependent demethylation of N6-methyladenosine regulates mRNA splicing and is required for adipogenesis. Cell Research, 2014, 24, 1403-1419.	5.7	869
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5	Reading RNA methylation codes through methyl-specific binding proteins. RNA Biology, 2014, 11, 669-672.	1.5	99
6	Transcriptome-wide N ⁶ -methyladenosine profiling of rice callus and leaf reveals the presence of tissue-specific competitors involved in selective mRNA modification. RNA Biology, 2014, 11, 1180-1188.	1.5	126
7	Crystal structure of the YTH domain of YTHDF2 reveals mechanism for recognition of N6-methyladenosine. Cell Research, 2014, 24, 1493-1496.	5.7	266
8	Methyltransferases modulate RNA stability in embryonic stem cells. Nature Cell Biology, 2014, 16, 129-131.	4.6	44
9	Molecular basis for the recognition of methylated adenines in RNA by the eukaryotic YTH domain. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 13834-13839.	3.3	186
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18	m6A RNA Modification Controls Cell Fate Transition in Mammalian Embryonic Stem Cells. Cell Stem Cell, 2014, 15, 707-719.	5.2	990

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