

Product datasheet

m6A RNA Methylation Assay Kit (Colorimetric) ab185912

[52 References](#) [2 Images](#)

Overview

Product name	m6A RNA Methylation Assay Kit (Colorimetric)
Detection method	Colorimetric
Assay type	Quantitative
Sensitivity	0.01 ng
Range	10 ng/ml - 500 ng/ml
Assay time	3h 45m

Product overview The m6A RNA Methylation Quantification Kit (Colorimetric) (ab185912) is a complete set of optimized buffers and reagents to colorimetrically quantify methylated N6-methyladenosine (m6A) in RNA. It is suitable for a direct detection of m6A RNA methylation status using total RNA isolated from any species such as mammals, plants, fungi, bacteria, and viruses.

Be aware that m6A is present in mRNA and ribosomal RNA, and this kit detects m6A in total RNA, ie. both mRNA and ribosomal RNA and any other RNA containing m6A.

The amount of RNA for each assay can be 100 ng - 300 ng. For optimal quantification, the input RNA amount should be 200 ng, as the abundance of m6A is generally less than 0.1% of total RNA.

Chinese protocol available. See Protocols section below.

Notes N6-methyladenosine (m6A) is the most common and abundant modification in RNA molecules present in eukaryotes. The m6A modification is catalyzed by a methyltransferase complex METTL3 and removed by the recently discovered m6A RNA demethylases FTO and ALKBH5, which catalyze m6A demethylation in an α -ketoglutarate (α -KG)- and Fe²⁺-dependent manner. It was shown that METTL3, FTO, and ALKBH5 play important roles in many biological processes, ranging from development and metabolism to fertility. m6A accounts for more than 80% of all RNA base methylations and exists in various species. m6A is mainly distributed in mRNA and also occurs in non-coding RNA such as tRNA, rRNA, and snRNA. The relative abundance of m6A in mRNA transcripts has been shown to affect RNA metabolism processes such as splicing, nuclear export, translation ability and stability, and RNA transcription. Abnormal m6A methylation levels induced by defects in m6A RNA methylase and demethylase could lead to dysfunction of RNA and diseases. For example, abnormally low levels of m6A in target mRNAs due to increased FTO activity in patients with FTO mutations, through an as-yet undefined pathway, contributes to the

onset of obesity and related diseases. The dynamic and reversible chemical m6A modification in RNA may also serve as a novel epigenetic marker of profound biological significance. Therefore, more useful information for a better understanding of m6A RNA methylation levels and distribution on RNA transcripts could benefit diagnostics and therapeutics of disease.

Platform Microplate reader

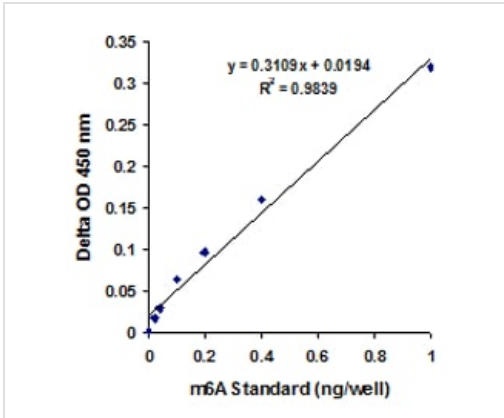
Properties

Storage instructions Please refer to protocols.

Components	48 tests	96 tests
10X Wash Buffer	1 x 14ml	1 x 28ml
8-Well Assay Strips (with Frame)	1 x 6 units	1 x 12 units
Binding Solution	1 x 5ml	1 x 10ml
Capture Antibody	1 x 5 μ l	1 x 10 μ l
Detection Antibody	1 x 6 μ l	1 x 12 μ l
Developer Solution	1 x 5ml	1 x 10ml
Enhancer Solution	1 x 5 μ l	1 x 10 μ l
Negative Control	1 x 10 μ l	1 x 20 μ l
Positive Control	1 x 10 μ l	1 x 20 μ l
Stop Solution	1 x 5ml	1 x 10ml

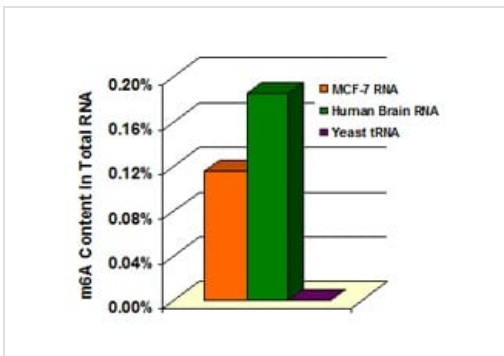
Relevance N6-Methyladenosine (m6A) is an abundant modification found in mRNA, tRNA, snRNA, as well as long non-coding RNA, in all species. RNA adenosine methylation is catalyzed by a multicomponent complex composed of METTL3/MT-A70, METTL14, and WTAP in mammals. METTL3 & METTL14 are responsible for the methyltransferase activity of the complex, and WTAP mediates substrate recruitment.

Images



m6A Standard curve

m6A standard control was added into the assay wells at different concentrations and then measured with the m6A RNA Methylation Quantification Kit (Colorimetric).



Quantification of m6A RNA methylation

Quantification of m6A RNA methylation in different samples. 200 ng of RNA isolated from different tissues or cells were added into the assay wells and the m6A contained in RNA was measured using the m6A RNA Methylation Quantification Kit (Colorimetric).

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