Data Sheet (Cat.No.TMPY-01661)

TargetMol

METTL1 Protein, Human, Recombinant (His)

General Information

Synonyms:	methyltransferase like 1;TRMT8;TRM8;YDL201w;C12orf1
Protein Construction:	A DNA sequence encoding the human METTL1 (NP_005362.3) (Asp 32-Gln 265) was expressed, with a polyhistide tag at the N-terminus. Predicted N terminal: Met
Species:	Human
Expression Host:	E. coli
Accession:	Q9UBP6-1
Molecular Weight:	28 kDa (predicted); 30 kDa (reducing conditions)

QC Testing

Biological Activity:	Activity testing is in progress. It is theoretically active, but we cannot guarantee it. If you require protein activity, we recommend choosing the eukaryotic expression version first.
Purity:	> 95 % as determined by SDS-PAGE
Endotoxin:	Please contact us for more information.
Formulation:	Supplied as sterile 50 mM Tris, 0.5M NaCl, 20% glycerol, pH 8.0.

Preparation and Storage

Reconstitution:

A Certificate of Analysis (CoA) containing reconstitution instructions is included with the products. Please refer to the CoA for detailed information.

Stability & Storage:

It is recommended to store the product under sterile conditions at -20°C to -80°C. Samples are stable for up to 12 months. Please avoid multiple freeze-thaw cycles and store products in aliquots.

Actual storage temperature shall be subject to the COA.

Shipping:

Proteins are shipped with blue ice.

Protein Background

tRNA (guanine-N(7)-)-methyltransferase, also known as Methyltransferase-like protein 1, tRNA (m7G46)-methyltransferase and METTL1, is a nucleus protein that belongs to the methyltransferase superfamily and TrmB family. METTL1 gene has been identified by its sequence similarity to the yeast ORF YDL21w. The human cDNA and the genomic structure of METTL1 have been analyzed. The transcript contains 1292 nucleotides and codes for a protein of 276 amino acids. The METTL1 gene product shows high sequence similarities to putative proteins from mouse, Drosophila melanogaster, Arabidopsis thaliana, Caenorhabditis elegans, and yeast (39.8% identity between all six species). Computer analyses of the deduced protein sequence reveal two highly conserved amino acid motifs, one of which is typical for methyltransferases. Both motifs are also present in hypothetical proteins from eubacteria. Disruption of the homologous yeast ORF YDL21w shows that the gene is at least not essential for vegetative growth in Saccharomyces cerevisiae.

Reference

Bahr, A.et al., 1999, Genomics. 57 (3):424-8.
Wikman, H. et al., 2005,Genes Chromosomes Cancer. 42 (2):193-9.
Cartlidge, RA. et al., 2005, EMBO J. 24 (9):1696-705.