



Product Specifications

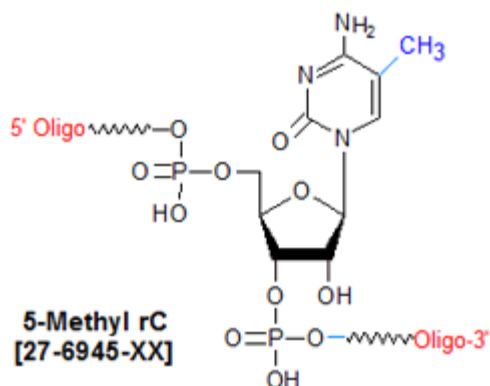
Custom Oligo Synthesis, antisense oligos, RNA oligos, chimeric oligos, Fluorescent dyes, Affinity Ligands, Spacers & Linkers, Duplex Stabilizers, Minor bases, labeled oligos, Molecular Beacons, siRNA, phosphonates Locked Nucleic Acids (LNA); 2'-5' linked Oligos

Oligo Modifications

For research use only. Not for use in diagnostic procedures for clinical purposes.

5-Me rC [5mrC]

Category	Epigenetics
Modification Code	5mrC
Reference Catalog Number	27-6945
5 Prime	Y
3 Prime	Y
Internal	Y
Molecular Weight(mw)	319.21



5-methyl cytosine (5-Me-rC) is a modified ribonucleotide which pairs with rG in an RNA duplex. 5-Me-rC forms a Watson-Crick base pair with rG in a normal manner. The presence of 5-Me-rC in cellular RNA is widespread, but its function is not well understood. 5-Me-rC has been observed in several base positions of eukaryotic and archaeal tRNA, most notably at positions 48/49, at the junction between the variable region and TphiC stem (1), suggesting an important structural role for it. The location of 5-Me-rC in rRNA from many organisms (bacterial to human) also appears to be fairly well-conserved, again hinting at an important structural role (2). Archaeal rRNA is an exception, however, as the number and location of 5-Me-rC is highly variable, complicating the picture (3,4). 5-Me-rRNA is found in the 5'-cap structure of mRNA, as well as in tRNA-like structures within other RNA molecules, such as viral RNA and SINE elements (5).

While there is a recognition that 5-methyl-rC plays a structural role in stabilizing tRNA, and appropriate binding of Mg²⁺ ions to it (6), little is known about how this modification's presence within tRNA and rRNA affects mRNA translation within the ribosome (2). Some evidence exists which suggests that the presence of 5-Me-rC, at least in yeast tRNA, is required to minimize translation errors, this is not definitive (7). In rRNA, its presence may assist with both tRNA recognition and peptidyl transfer (8).

One intriguing functional possibility for RNA methylation via 5-Me-rC is as a modulator of the innate human immune system. In one study, while a set of unmodified RNA strongly stimulated this system via Toll-like receptor activation, incorporation of 5-methyl-C into the oligos of this set dramatically reduced their stimulatory effect (9). These observations suggest that methylation interferes with the ability of the innate immune system to recognize RNA. Use of this principle may have therapeutic implications for a number of immune-system-related disorders.

The observation of RNA-dependent inheritance of certain phenotypes in mouse hints at a second possibility for RNA methylation: as a regulator of epigenetic inheritance patterns (10). The recent discovery that 5-Me-rC is widespread in both the coding and non-coding mRNA (esp. in the UTRs) of the human transcriptome supports this, and suggests that RNA methylation may play a much broader role in post-transcriptional control of cellular RNA than was previously believed (11), raising the possibility that RNA methylation may be critical to the ability of the cell to support various states of growth and differentiation.

References

1. Sprinzl, M., Vassilenko, K.S. Compilation of tRNA sequences and sequences of tRNA genes. *Nucleic Acids Res.* (2005), **33**: D139-D140.
2. Motorin, Y., Lyko, F., Helm, M. 5-methylcytosine in RNA: detection, enzymatic formation and biological functions. *Nucleic Acids Res.* (2010), **38**: 1415-1430.
3. Noon, K.R., Bruenger, E., McCloskey, J.A. Posttranscriptional modifications in 16S and 23S rRNAs of the archaeal hyperthermophile *Sulfolobus solfataricus*. *J. Bacteriol.* (1998), **180**: 2883-2888.
4. Kowalak, J.A., Bruenger, E., Crain, P.F., McCloskey, J.A. Identities and phylogenetic comparisons of posttranscriptional modifications in 16S ribosomal RNA from *Haloferax volcanii*. *J. Biol. Chem.* (2000), **275**: 24484-24489.
5. Sakamoto, K., Okada, N. 5-Methylcytidylic modification of in vitro transcript from the rat identifier sequence; evidence that the transcript forms a tRNA-like structure. *Nucleic Acids Res.* (1985), **13**: 7195-7206.
6. Chen, Y., Sierzputowska-Gracz, H., Guenther, R., Everett, K., Agris, P.F. 5-Methylcytidine is required for cooperative binding of Mg²⁺ and a conformational transition at the anticodon stem-loop of yeast phenylalanine tRNA. *Biochemistry* (1993), **32**: 10249-10253.
7. Wu, P., Brockenbrough, J.S., Paddy, M.R., Aris, J.P. NCL1, a novel gene for a non-essential nuclear protein in *Saccharomyces cerevisiae*. *Gene* (1998), **220**: 109-117.
8. Vicens, Q., Westhof, E. Crystal structure of paromomycin docked into the eubacterial ribosomal decoding A site. *Structure* (2001), **9**: 647-658.
9. Kariko, K., Buckstein, M., Ni, H., Weissman, D. Suppression of RNA recognition by Toll-like receptors: the impact of nucleoside modification and the evolutionary origin of RNA. *Immunity* (2005), **23**: 165-175.
10. Rassoulzadegan, M., Grandjean, V., Gounon, P., Vincent, S., Gillot, I., Cuzin, F. RNA-mediated non-mendelian inheritance of an epigenetic change in the mouse. *Nature* (2006), **441**: 469-474.
11. Squires, J.E., Hardip, R. Preiss T. Widespread occurrence of 5-methylcytosine in human coding and non-coding RNA. *Nucleic Acids Res.* (2012), **40**: 5023-5033.