Convertible Bases Introduction

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Convertible Bases Design Protocols

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Convertible Bases Applications

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References

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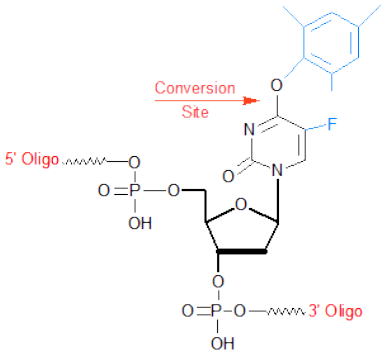
Modificaton Code List

Modification	Code	Catalog Number
Convertible 5-F-dC (TMP-5-F-dU)	[5-F-dC]	26-6607
Convertible dA (O6-Phenyl-deoxy Inosine)	[O6-Phenyl-dI]	26-6921
Convertible dG (2-Fluoro deoxy inosine)	[2-FdI]	26-6671
Convertible dU & dC (O4 Triazolyl dU)	[O4-Tri-dU]	26-6608
N6-Methyl rA (m6A)	[m6A]	27-6601

Convertible 5-F-dC

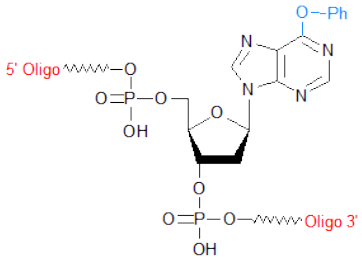
Category	Convertible Bases
Modification Code	5-F-dC
Reference Catalog Number	26-6607
5 Prime	Y
3 Prime	Y
Internal	Y
Molecular Weight(mw)	307.8



TMP-F-dU (Convertible 5-F-dC)
[26-6607-XX]

Convertible dA (O6-Phenyl-dI)

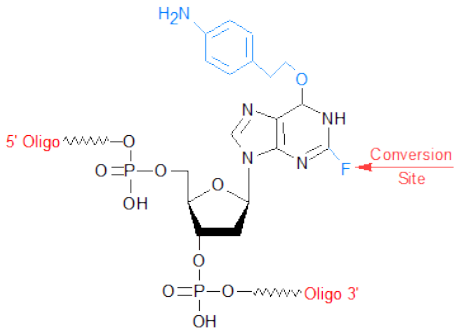
Category	Others
Modification Code	O6-Phenyl-dI
Reference Catalog Number	26-6921
5 Prime	Y
3 Prime	Y
Internal	Y
Molecular Weight(mw)	830.92



O6-Phenyl-dI (Convertible dA)
[26-6921-XX]

Convertible dG (2-F-dI)

Category	Minor Bases
Modification Code	2-FdI
Reference Catalog Number	26-6671
5 Prime	Y
3 Prime	Y
Internal	Y
Molecular Weight(mw)	332.18



2-F-dI (Convertible dG)
[26-6671-XX]

Gene Link supplies Convertible modified oligos protected with oligo bound to CPG solid support or can conjugate the convertible site to user specified ligand.

2-Fluoro-deoxyinosine (2-F-dI) is classified as a convertible dG nucleotide. After incorporation into an oligo, reaction of the 2-fluorine on the inosine base with a primary amine displaces the fluorine atom, and converts the nucleotide into a N2-substituted dG. Oligos containing 2-F-dI modifications are useful precursors in studies requiring cross-linking, at G position(s), between oligos, or between an oligo and an enzyme. For example, 2-F-dI modified oligos have been reacted with disulfide-containing diamines (1) or thiopropylamines (2) in order to subsequently form disulfide-crosslinked DNA duplexes. Such oligos have also been reacted with bis-(3-aminopropyl)disulfide dihydrochloride, and the disulfide-containing oligo intermediate coupled to a short-lived HIV-1 reverse transcriptase kinetic intermediate to form stable enzyme-oligo complexes. The ability to synthesize such complexes have enabled deeper study of the DNA translocation mechanism of HIV-1 RT (3).

In order to minimize the possibility of unwanted side reactions with the exocyclic amines of other bases of the oligo, it must be fully protected and still attached to the synthesis solid support when reacted with the primary amine. Consequently, for customers ordering 2-F-dI-modified oligonucleotides, Gene Link supplies the oligo attached to a solid support for subsequent conversion to the appropriate N2-modified dG by the enduser.
See examples below of Convertible dG (2-Fluoro deoxy inosine) to various amino derivatives.

Protocol for conversion of 2-FI (convertible G) to the appropriate N2-modified dG.

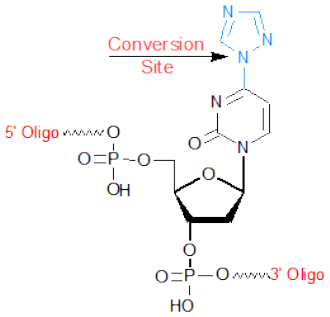
References

1. Erlanson, D.A.; Chen, L.; Verdine, G.L. DNA Methylation through a Locally Unpaired Intermediate. *J. Am. Chem. Soc.* (1993), **115**: 12583-12584. 2. Erlanson, D.A.; Glover, J.N.M.; Verdine, G.L. Disulfide Cross-linking as a Mechanistic Probe for the B<-->Z Transition in DNA. *J. Am. Chem. Soc.* (1997), **119**: 6927-6928.

3. Sarafianos, S.G.; et al. Trapping HIV-1 Reverse Transcriptase Before and After Translocation on DNA. *J. Biol. Chem.* (2003), **278**: 16280-16288.

Convertible dU & dC

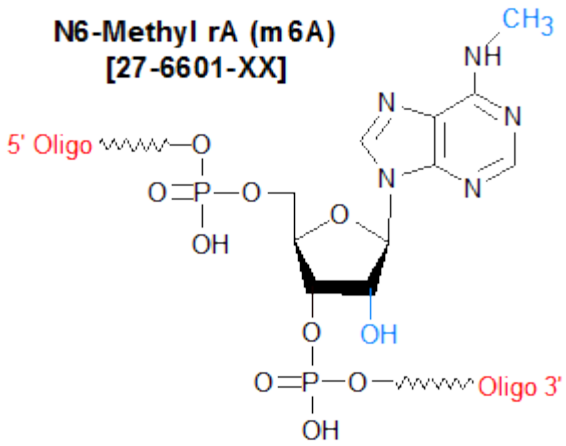
Category	Convertible Bases
Modification Code	O4-Tri-dU
Reference Catalog Number	26-6608
5 Prime	Y
3 Prime	Y
Internal	Y
Molecular Weight(mw)	289.18



O4-Triazolyl-dU (Convertible dU and dC)
[26-6608-XX]

N6-Methyl rA (m6A)

Category	Epigenetics
Modification Code	m6A
Reference Catalog Number	27-6601
5 Prime	Y
3 Prime	Y
Internal	Y
Molecular Weight(mw)	343.23



N6-methyl-riboadenosine (N6-methyl rA; m6A) is a common, fairly abundant RNA modification found in the mRNA of most eukaryotes (1,2); it has also been observed in tRNA, rRNA snRNA and in long non-coding RNA (3). While the biological importance of this modification remains poorly understood, results from a number of research studies suggest that regulation of m6A levels in mRNA may have significant effects on subsequent gene expression. The modification mainly appears in exons, 3'-UTRs and near stop codons. Within 3'-UTRs, N6-methyl-rA is associated with miRNA binding sites (4). The modification itself is catalyzed by a N6-methyl-rA methyltransferase complex that contains the METTL3 subunit (5). Silencing this methyltransferase dramatically affects N6-methyl-A cellular levels, gene expression and alternative RNA splicing patterns (6). The FTO and ALKBH5 genes, implicated in obesity risk, encode two different N6-methyl-rA demethylases; silencing of FTO with siRNA results in increased levels of N6-methyl-rA in poly(A) RNA (6), while FTO overexpression results in decreased levels (4). Moreover, modulation of the activities of these three enzymes can alter the expression of thousands of genes at the cellular level. This suggests that N6-methyl-rA plays an important role in RNA metabolism and as an epigenetic marker (7). **References**

1. Tuck, M.T. The formation of internal 6-methyladenine residues in eucaryotic messenger RNA. *Int. J. Biochem.* (1992), **24**: 379-386.
2. Jia, G., Fu, Y., He, G. Reversible RNA adenosine methylation in biological regulation. *Trends Genet.* (2013), **29**: 108-115.
3. Pan, T. N6-methyl-adenosine modification in messenger and long non-coding RNA. *Trends Biochem. Sci.* (2013), **38**: 204-209.
4. Meyer, K.D., Saletore, Y., Zumbo, P., Elemento, O. Mason, C.E., Jaffrey, S.R. Comprehensive Analysis of mRNA Methylation Reveals Enrichment in 3' UTRs and near Stop Codons. *Cell* (2012), **149**: 1635-1646.
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6. Dominissini, D., Moshitch-Moshkovitz, S., Schwartz, S., Salmon-Divon, M., Ungar, L., Osenberg, S., Cesarkas, K., Jacob-Hirsch, J., Amariglio, N., Kupiec, M., Sorek, R., Rechavi, G. Topology of the human and mouse m6A RNA methylomes revealed by m6A-seq.

Nature (2112), **485**: 201-206.
7. Niu, Y., Zhao, X., Wu, Y.S., Li, M.M., Wang, X.J., Yang, Y.G. N6-methyl-adenosine (m6A) in RNA: an old modification with a novel epigenetic function. *Genom. Proteom. Bioinform.* (2013), **11**: 8-17.