Supporting information for

Synthesis and characterization of modified nucleotides in the 970 hairpin loop of *Escherichia coli* 16S ribosomal RNA

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Figure S1. Characterization of helix 31 analogues by MALDI-TOF mass spectrometric analysis.



Figure S2. Confirmation of nucleosides present in the synthetic oligos obtained by digestion of ECh31UNMOD (**A**), ECh31WT (**B**) and ECh31M2G (**C**) RNAs with P1 nuclease and treatment of resulting nucleotides with calf intestinal phosphatase were analyzed by reverse-phase HPLC on a Supelco C18 column. Approximately 0.5 OD of RNA were digested and 0.25 OD were injected for each analysis. A linear gradient in 0.1 M TEAA buffer, pH 6.0 from 0 to 30% methanol over 17 min at a flow rate of 1 mL/min was employed. The retention times of the nucleosides were confirmed by injection of authentic standards (D) with a deviation of <0.5% (C = 6.71 min, U = 9.62 min, m⁵C = 12.77, G = 16.19 min, m²G = 19.42 min, A = 19.95 min).



Figure S3. The UV melting profiles representing the melting transitions of four RNAs are shown. AU0-AU4 represent profiles corresponding to different dilutions of each RNA taken in 15 mM NaCl, 20 mM sodium cacodylate, 0.5 mM Na₂EDTA at pH 7.0.



NaCl buffer = 15 mM NaCl, 20 mM sodium cacodylate, 0.5 mM Na₂EDTA at pH 7.0

KCl buffer = 15 mM KCl, 20 mM cacodylic acid, 20 mM Tris [basic form], 0.5 mM Na₂EDTA at pH 7.0

Mg buffer = 25 mM cacodylic acid, 25 mM Tris [basic form], 30 mM KCl, 70 mM NH_4Cl , 3 mM $MgCl_2$ at pH 7.0

Figure S4. CD spectra of the ECh31WT RNA construct acquired in Na⁺, K⁺, and Mg²⁺ containing buffers.



Figure S5. Representative normalized UV melting curves of the ECh31WT RNA taken in Na⁺ (15 mM NaCl, 20 mM sodium cacodylate, 0.5 mM Na₂EDTA at pH 7.0) and K⁺ (15 mM KCl, 20 mM cacodylic acid, 20 mM Tris [basic form], 0.5 mM Na₂EDTA, pH 7.0) buffers (A), AU0-AU4 representing the profiles corresponding to different dilutions of ECh31WT RNA taken in K⁺ buffer (B), Thermodynamics of the ECh31WT RNA in Na⁺ and K⁺ buffers (C).

NMR characterization for 2-N-Methyl-6-O-(diphenylcarbamoyl)guanosine [5].

¹H NMR (DMSO- d^6 , 400 MHz) 2.81 (d, 3H), 3.51-3.56 (m, 1H), 3.61-3.66 (m, 1H), 3.90 (m, 1H), 4.02 (q, 1H), 4.15 (br.d, 1H), 4.62 (br.s, 1H), 4.99 (br.s, 1H), 5.21 (d, J = 4.8 Hz, 1H), 5.48 (d, J = 5.6 Hz, 1H), 5.82 (d, J = 5.6 Hz, 1H), 7.28-7.32 (m, 4H), 7.4-7.44 (m, 6H), 8.19 (s, 1H); ¹³C NMR (DMSO- d^6 , 400 MHz) 28.3, 61.5, 70.5, 73.1, 85.5, 116.4, 127.1, 129.4, 140.9, 141.8, 150.4, 155.6, 155.9, 159.6







0505040548 35 (1.834) Cm (33:39-8:15x1.500)

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493.2

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2-N-Methyl-6-O-(diphenylcarbamoyl)guanosine [5].









Supplementary scheme. Synthesis of 5'-O-DMT-2'-O-TOM-6-O-DPC-2-N-methylguanosine phosphoramidite **8**: (i) DMTCl, DMAP, pyridine, room temperature, 24 h; (ii) a) *tert*-Bu₂SnCl₂, *i*Pr₂NEt, dichloroethane, 70 °C, 15 min; b) TOMCl, room temperature, 3 h; (iii) 2-cyanoethyldiisopropylphosphoramidochloridite, *i*Pr₂NEt, dichloromethane, room temperature, 2 h.

NMR characterization for 5'-O-(4,4'-Dimethoxytrityl)-2-*N*-methyl-6-O-(diphenylcarbamoyl)guanosine [**6**].

¹H NMR (CD₃OD, 400 MHz) 2.71 (br.s, 1H), 2.98-3.03 (q, 1H), 3.21 (d, *J* = 3.2 Hz, 3H), 3.25-3.27 (m, 1H), 3.29-3.32 (m, 1H), 3.60 (d, *J* = 4.8 Hz, 6H), 3.66 (m, 1H), 4.07-4.10 (m, 1H), 4.45 (m, 1H), 4.83 (m, 1H), 5.87 (d, *J* = 4.8 Hz, 1H), 6.64-6.69 (m, 5H), 7.05-7.38 (m, 18H), 8.0 (s, 1H); ¹³C NMR ((CD₃)₂SO, 500 MHz) 28.8, 55.6, 72.2, 74.9, 82.3, 85.3, 87.7, 113.8, 114.0, 126.3, 127.8, 128.5, 128.7, 129.1, 129.2, 129.3, 129.9, 130.2, 130.4, 131.2, 141.2, 149.2, 159.9







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5'-O-(4,4'-Dimethoxytrityl)-2-N-methyl-6-O-(diphenylcarbamoyl)guanosine [6]



795.7

NMR characterization for 5'-O-(4,4'-Dimethoxytrityl)-2'-O-[[(triisopropylsilyl)oxy]methyl]-2-*N*-methyl-6-O-(diphenylcarbamoyl)guanosine [**7**].

¹H NMR (CD₃OD, 400 MHz) 0.89-1.05 (m, 18H), 1.25-1.3 (m, 3H), 2.79-2.8 (m, 7H), 3.1 (s, 1H), 3.3-3.5 (m, 2H), 3.70 (d, *J* = 4.8 Hz, 3H), 4.15-4.25 (m, 1H), 4.65-4.7 (m, 1H), 4.85 (s, 2H), 5.05-5.15 (m, 1H), 6.1 (d, *J* = 5 Hz, 1H), 6.79-6.83 (m, 5H), 7.17-7.5 (m, 18H), 8.05 (s, 1H)

proton spectrum

Pulse Sequence: s2pul

5'-O-(4,4'-Dimethoxytrityl)-2'-O-[[(triisopropylsilyl)oxy]methyl]-2-N-methyl-6-O-(diphenylcarbamoyl) guanosine [7].











5'-O-(4,4'-Dimethoxytrityl)-2'-O-[[(triisopropylsilyl)oxy]methyl]-2-N-methyl-6-O-(diphenylcarbamoyl) guanosine 3'-(2-cyanoethyl diisopropylphosphoramidite) [8].





Pulse Sequence: s2pul

W

151.138

5'-O-(4,4'-Dimethoxytrityl)-2'-O-[[(triisopropylsilyl)oxy]methyl]-2-N-methyl-6-O-(diphenylcarbamoyl) guanosine 3'-(2-cyanoethyl diisopropylphosphoramidite) [8].



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155	150	145	140	135	130	S22 125	120	115	110	105	ppm

0609272559 108 (1.996) Cm (108:124-13:57x1.500)



Elemental Composition Report

Single Mass Analysis

Tolerance = 8.0 PPM / DBE: min = -1.5, max = 50.0 Element prediction: Off Number of isotope peaks used for i-FIT = 3

Monoisotopic Mass, Even Electron Ions

1096 formula(e) evaluated with 3 results within limits (up to 50 best isotopic matches for each mass) Elements Used:

C: 0-66 H: 0-1000 N: 0-8 O: 0-10 23Na: 0-1 Si: 0-1 P: 0-1

Chow- Dinuka Abeydeera DA-i-244 LCT0246 mw1180 4uL meoh Shay 2008-07b.pro

2008_1212_0246b 14 (0.301) Cm (11:20-(1:6+26:36)x3.000)

LCT Premier 12-Dec-2008 14:48:58 1: TOF MS ES+ 4.25e+004

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		1206.5515		206.5515	1219.5358	221.5438	1233	55441235.55	1246.5406		
0	1190.0	1200.0		1210.0	1220.0		1230.0	124	0.0		- m/z
Minimum: Maximum:		5.0	8.0	-1.5 50.0							
Mass	Calc. Mass	mDa	PPM	DBE	i⊢FIT	i-FIT	(Norm)	Formula			
1181.5634	1181.5637	-0.3	-0.3	26.5	25.0	0.5		C62 H83	N8 P	010	
	1181.5661	-2.7	-2.3	29.5	25.7	1.2		C64 H82	N8	010	Si
	1181.5605	2.9	2.5	31.5 S24	26.6	2.2		C66 H79 23Na P	N8	09	

5'-O-(4,4'-Dimethoxytrityl)-2'-O-[[(triisopropylsilyl)oxy]methyl]-2-N-methyl-6-O-(diphenylcarbamoyl) guanosine 3'-(2-cyanoethyl diisopropylphosphoramidite) [8].

C-NPh2

CH3

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