Supporting Information

2-(4-Tolylsulfonyl)ethoxymethyl(TEM) - A New 2'-OH Protecting Group For Solid Support RNA Synthesis

Chuanzheng Zhou, Dmytro Honcharenko and Jyoti Chattopadhyaya* Department of Bioorganic Chemistry, Box 581, Biomedical Center, Uppsala University, S-751 23 Uppsala, Sweden

jyoti@boc.uu.se

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General Experimental Methods

Chromatographic separations were performed on Merck G60 silica gel. Thin layer chromatography (TLC) was performed on Merck pre-coated silica gel 60 F_{254} glass-backed plates. ¹H NMR spectra were recorded at 270 MHz, using TMS (0.0 ppm) as internal standards. ¹³C NMR spectra were recorded at 67.9 MHz, using the central peak of CDCl₃ (76.9 ppm) as an internal standard. ³¹P NMR spectra were recorded at 109.4 MHz using 85% phosphoric acid as external standard. Chemical shifts are reported in ppm (δ scale). The $\delta_{C2'}$, $\delta_{C3'}$, $\delta_{H1'}$, $\delta_{H2'}$, $\delta_{H3'}$ are assigned according to H-H cosy and C-H cosy. MALDI-TOF mass spectra were recorded in positive ion mode. For oligo-RNAs, the mass spectrometer was externally calibrated with standard oligonucleotide using 3-HAP and ammonium citrate as co-matrix. For other compounds, the mass spectrometer was externally calibrated with peptide mixture using THPA and ammonium citrate as matrix.

	function	reagents	Time (s)
1	coupling	0.1 M amidite in $CH_3CN + 0.25M$ ETT in	120
		CH ₃ CN	
2	capping	0.1 M Ac ₂ O in THF + N-Methyl-	15
		imidazole/THF/Pyridine	
3	oxidation	0.02 M I ₂ in THF-H ₂ O-Pyridine (7:1:2)	8
4	deblocking	3% DCA in CH ₂ Cl ₂	98

Table S1. Synthetic cycle and reagen





Figure S1.2. HPLC profiles of crude products. HPLC conditions: A) ON1. AE HPLC, 0-40 min, buffer A \rightarrow A/B 2/8. B) ON 2. anion exchange column, 0-60 min, buffer A/B form 6/4 to2/8. ON 3 and ON 4 : RP column, 0-40 min, buffer C \rightarrow C/D 8/2.

MS spectra of synthesized oligo-RNAs.



Figure S1.3. MALDI-TOF MS spectrum of ON 1.



Figure S1.4. MALDI-TOF MS spectrum of ON 2.



Figure S1.5. MALDI-TOF MS spectrum of ON 3.



Figure S1.6. MALDI-TOF MS spectrum of ON 4.



Figure S1.7. MALDI-TOF MS spectrum of ON 5.



Figure S1.8. MALDI-TOF MS spectrum of ON 6.



Figure S1.9. MALDI-TOF MS spectrums of ON 7.



Figure S1.10. MALDI-TOF MS spectrums of ON 8...



Figure S1.11. MALDI-TOF MS spectrums of ON 9.



Figure S1.12. MALDI-TOF MS spectrums of ON 10.



Figure S1.13. MALDI-TOF MS spectrums of ON 11.



Figure S1.14. MALDI-TOF MS spectrums of ON 12.



³¹P and ¹H NMR spectra of phosphoramidite.

Figure S2.1. ³¹P NMR spectrum of uridine phosphoramidite.



Figure S2.2. ¹H NMR spectrum of uridine phosphoramidite.



Figure S2.3. ³¹P NMR spectrum of cytidine phosphoramidite.



Figure S2.4. ¹H NMR spectrum of cytidine phosphoramidite.



Figure S2.5. ³¹P NMR spectrum of adenosine phosphoramidite.



Figure S2.6. ¹H NMR spectrum of adenosine phosphoramidite.



Figure S2.7. ³¹P NMR spectrum of guanosine phosphoramidite.



Figure S2.8. ¹H NMR spectrum of guanosine phosphoramidite.





Figure S2.9. ¹H and ¹³C NMR spectra of 5'-*O*-DMTr-2'-TEM uridine.



Figure S2.10. ¹H and ¹³C NMR spectra of 5'-*O*-DMTr-2'-TEM cytidine.



Figure S2.11. ¹H and ¹³C NMR spectra of 5'-*O*-DMTr-2'-TEM adenosine.



Figure S2.12. ¹H and ¹³C NMR spectra of 5'-O-DMTr-2'-TEM guanosine.

HPLC profiles of crude ON 3 and 4 under different unblocking conditions.



Figure S3.1



Result Table - Calculation Method Uncal

Peak	Reten.	Area [mV s]	Height [mV]	W05 [min.]	Area [%]	Height [%]
NO.	4 607	191,1781	18.272	0.193	0.671	2.236
- 1	4.007	276 1546	30,350	0.133	0.969	3,714
4	4,000	923 5623	100.948	0.127	2.889	12.352
5	5.360	133 8423	14.279	0.153	0.470	1.747
4	5.807	93 1497	7,603	0.200	0.292	0.930
5	6.307	207 7748	20.489	0.233	1.045	2.507
6	6.587	297.7740	6 946	0.187	0.301	0.850
7	7.033	85.7459	0.940	0 313	0.686	1.091
8	8.813	195.4707	30 317	0.360	2.595	3.710
9	10.133	139.0019	2 371	1 147	0.650	0.413
10	11.133	185.4109	2 494	0 460	0.371	0,426
11	13.393	105.8221	34 111	0.267	2 203	4,174
12	14.500	627.8841	34.111	0.353	0 903	1.343
13	15,540	257.4576	10.975	0.303	0.914	1 691
14	16.673	260.5721	13.820	0.233	0.602	0 801
15	19.540	171.5488	6.547	0.375	0.002	1 338
16	20.287	251.4269	10.935	0.340	1 330	1 329
17	21.933	381.4677	10.857	0.380	1.330	1.920
18	22.907	591.8062	14.839	0.573	2.076	1.010
19	23.940	1211.0865	39.540	0.627	4.249	4.838
20	24.953	2540.6790	48.059	0.847	8,913	5.881
21	27.393	676.7945	20,289	0.520	2.374	2.463
22	28.440	553.6175	10.867	0.820	1.942	1.330
23	31.240	618.4824	15.207	0.553	2.170	1.861
24	32.980	13853.6421	279.492	0.713	48.603	34,199
25	34.593	1664.5863	28.437	0.760	5.840	3.480
26	37.033	932.4753	10.491	1.473	3.271	1.284
27	39.000	531.7612	12.042	0.640	1.866	1.473
28	40,90	260.8153	5.768	0.60	0.915	0.704
0	Total	28503,9167	817.252	2	12.2.3.1.5.	a the second

Figure S3.2



Figure S3.3.



Figure S3.4.



	Result	Table	÷	Calculation	Method	Uncal	
en	. Area			Height	W05	Area	
÷						Law all the	

Peak No.	Reten. time	Area [mV.s]	Height [mV]	W05 [min.]	Area [%]	Height	
1	5.300	256.5522	10.717	0.293	1.543	2.796	
2	7.913	1234.1828	50.494	0.320	7.424	13,172	
3	9.980	166.2121	3.894	0.373	1.000	1.016	
4	11.860	521.3368	27.197	0.240	3,136	7.095	
5	13.187	79.9868	2.484	0.613	0.481	0.648	
6	14.147	258.5239	11.434	0.333	1.555	2,983	
7	16,200	59.7749	1.872	0.307	0,360	0.488	
8	16.687	164.2585	7.021	0.353	0.988	1.831	
9	17.473	184.6807	6.721	0.420	1.111	1.753	
10	19.167	223.6841	7.214	0.440	1.346	1.882	
11	19.873	487.3455	13.348	0,600	2,932	3,482	
12	20.993	1502.3377	52.872	0.460	9.037	13.792	
13	21.600	1358.7590	37.439	0.513	8,174	9.766	
14	24.053	795.0137	11,139	1.307	4.782	2,906	
15	25.207	499.0604	10.124	0.733	3,002	2.641	
16	27.853	293.8092	4.952	1.027	1.767	1,292	
17	29.973	4630.5768	69.620	0.920	27.855	18.161	
18	33.127	221.1330	3.510	1,173	1.330	0.916	
19	35.520	682.3452	10.232	1.213	4,105	2.669	
20	37.213	254.6058	4.749	1.033	1.532	1,239	
21	39.233	809.6426	15.604	0.933	4.870	4.071	
22	40.813	1940.0089	20.713	1.647	11.670	5.401	
	Total	16623.8304	383.352				

0

Figure S3.5.



Figure S3.6.

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Result Table - Calculation Method Uncal

Figure S3.7.



Figure S3.8.



Result Table - Calculation Method Uncal

Peak No.	Reten. time	Area [mV.s]	Height [mV]	W05 [min.]	Area [%]	Height [%]
1	4.460	49.3355	1.687	0.667	0.168	0.299
2	5.247	70.6843	9.199	0.120	0.241	1.633
3	6.193	30.5340	1.813	0.220	0.104	0.322
4	8.187	566.2155	29.502	0.287	1.933	5.238
5	11.227	95.2518	5.294	0.267	0.325	0.940
6	12.553	542.5773	23.343	0.313	1.852	4.144
7	15.480	186.3593	5.769	0.340	0.636	1.024
8	17.740	655.1728	34.227	0.287	2.237	6.077
9	18.520	1098.3316	40.831	0.387	3.749	7.249
10	19.507	1531.9080	57.470	0.320	5.230	10,203
11	21.120	1984.5500	58.380	0.680	6.775	10.365
12	21,593	1317.5156	47.590	0.480	4.498	8.449
13	22.593	1564.6360	22.671	1.260	5.341	4.025
14	26.027	1451.1175	17.059	1.113	4.954	3.029
15	26.960	1323.0817	16.398	1.653	4.517	2.911
16	30.613	14383.5893	170.569	0.880	49.102	30.282
17	32.607	2316.0542	18.949	2.427	7,906	3.364
18	36.847	126.2726	2.516	0.680	0.432	0.446
	Total	29293.1870	563.268			



Figure S3.9.





S32



Figure S3.11.



Figure S4. RNase H digestion of 15 mer DNA/RNA duplex. Lanes 1 - 8 represent digestion of RNA after 0, 2, 5, 10, 15, 25, 40, 60 min of incubation with enzyme. Conditions of cleavage reactions: pure RNA (0.1 μ M) or crude RNA (0.1 μ M) and complementary DNA (1 μ M) in buffer containing 20 mM Tris-HCl (pH 8.0), 20 mM KCl, 10 mM MgCl₂ and 0.1 mM DTT at 21 °C; 0.06 U of RNase H in a total reaction volume of 30 μ L.

