

Novel Cytidine-Based Inhibitors of Orotidine-5'-Monophosphate Decarboxylase with an Unusual Twist

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Purity of the synthesized compounds:

Nucleoside purity was evaluated on a Water LC-MS system (Waters™ 2545 binary gradient module) equipped with a photodiode array detector using an X-Bridge C18 column (4.6 x 150 mm, 5 µm). The HPLC methods used for the purity assessment were Method A: (Isocratic conditions, 95% water with 0.05% TFA and 5% MeOH with 0.05% TFA, 10 min), Method B: (Isocratic conditions, 100% water with 0.05% TFA, 15 min). Nucleotide purity was evaluated on the same HPLC system using a Spherisorb C18 column (4.5 x 250 mm, 5µm). The HPLC methods used for the purity assessment were Method B: (Isocratic conditions, 100% water with 0.05% TFA, 10 min), Method C: (Gradient conditions, 100% water to 95% water and 5% AcCN with 0.05% TFA, 15 min). All HPLC solvents were filtered through membrane filters (47 mm GHP 0.45 µm, Pall Corporation). Injection samples were filtered using Pall Acrodisc ® Syringe filters 4 mm PTFE (0.2 µm).

Table S1. Purity Data.

Compound No	HPLC method	Retention time (min)	Purity
13	Method A	2.87	>99.9%
	Method B	2.68	>99.9%
15	Method A	3.93	>99.9%
	Method B	4.33	>99.9%
14	Method B	4.73	>99.9%
	Method C	4.77	>99.9%
27	Method B	4.76	>99.9%
	Method C	4.77	>99.9%

Semi preparatory Purification Method: Final compounds were purified on a Water HPLC using a semi-prep Spherisorb ODS2 C18 column (20 x150 mm, 4 ml/min). The HPLC method used for the purification was Method B: (Isocratic, 100% water with 0.05% TFA)

Table S2. UV spectra for compounds **14** and **27** after incubation in the crystallization buffer for 24 h at room temperature.

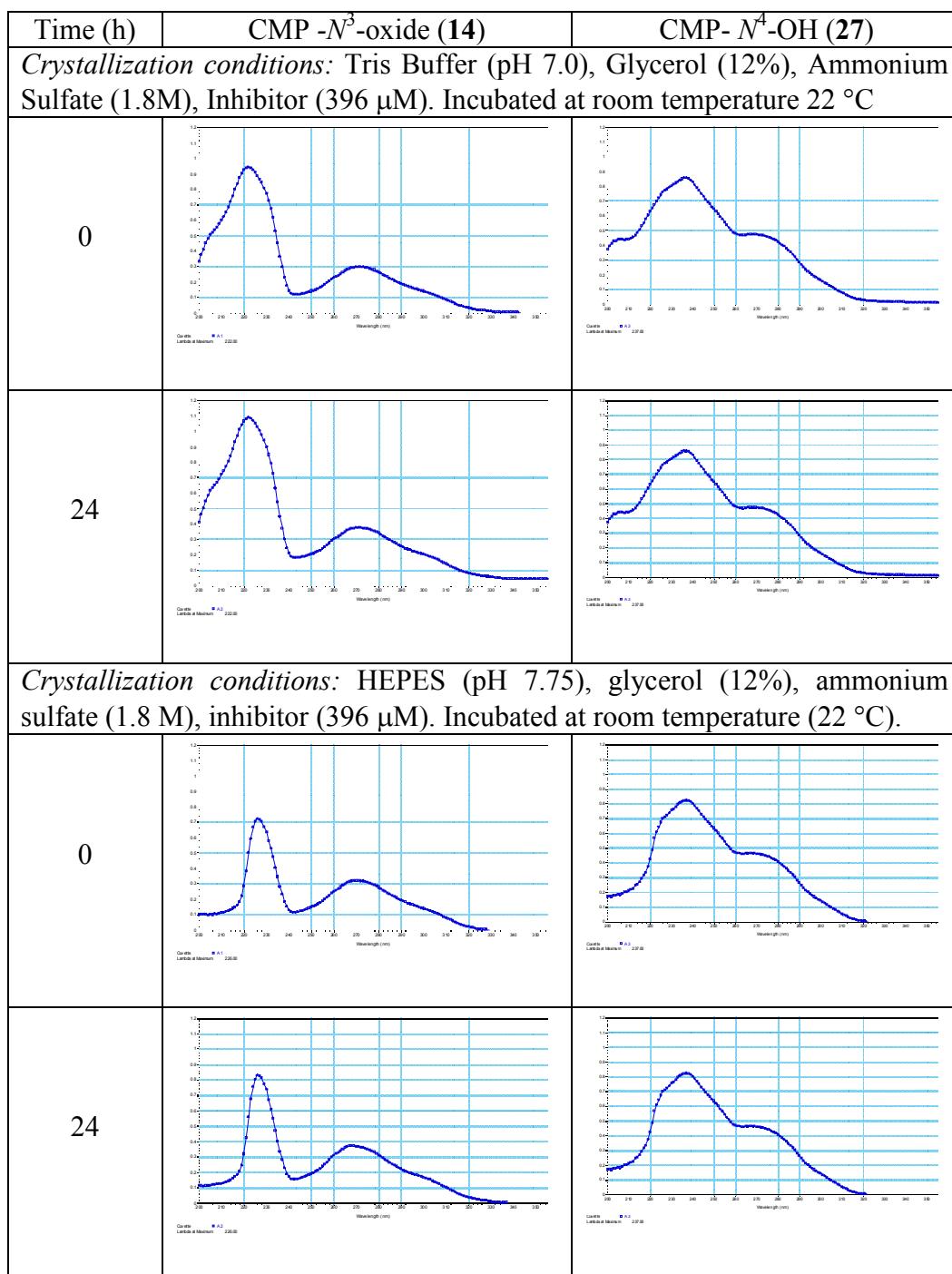


Table S3. Diffraction and refinement data for co-crystal complexes of compound **14** and **27** with *Hs* ODCase .

Diffraction Data	Human ODCase + Compound 14	Human ODCase + Compound 27
Space Group	P2 ₁	P2 ₁
Unit cell axes [Å]	a=69.3 b=61.8 c=70.5	a=69.8 b=61.6 c=71.4
Unit cell angle [°]	$\alpha=90 \beta=112.9 \gamma=90$	$\alpha=90 \beta=112.1 \gamma=90$
Resolution [Å]	1.75 [1.80 – 1.75]	1.90 [1.95 – 1.90]
Measured reflections	216201 [1.75]	179171 [1.90]
Unique reflections	53542	50390
Completeness [%]	92.7	98.4
Rsym	0.029	0.038
Refinement Statistics		
Resolution [Å]	65.0 – 1.75	66.0 – 1.90
Protein atoms	3962	4048
Water molecules	304	190
Reflections used for	50805	42064
R _{cryst} [%]	16.1	19.0
R _{free} [%]	18.5	22.3
RMSD Bond Length [Å]	0.016	0.026
RMSD Bond Angle [°]	1.6	2.1
Average B-factor [Å]	17.9	28.5
Ramachandran plot		
Residues in allowed regions [%]	96.74	95.98
Residues in generously allowed regions [%]	2.65	3.59
Residues in not allowed regions [%]	0.61	0.42

Figure S1. IR Spectrum for Cyd-*N*³-oxide (**13**).

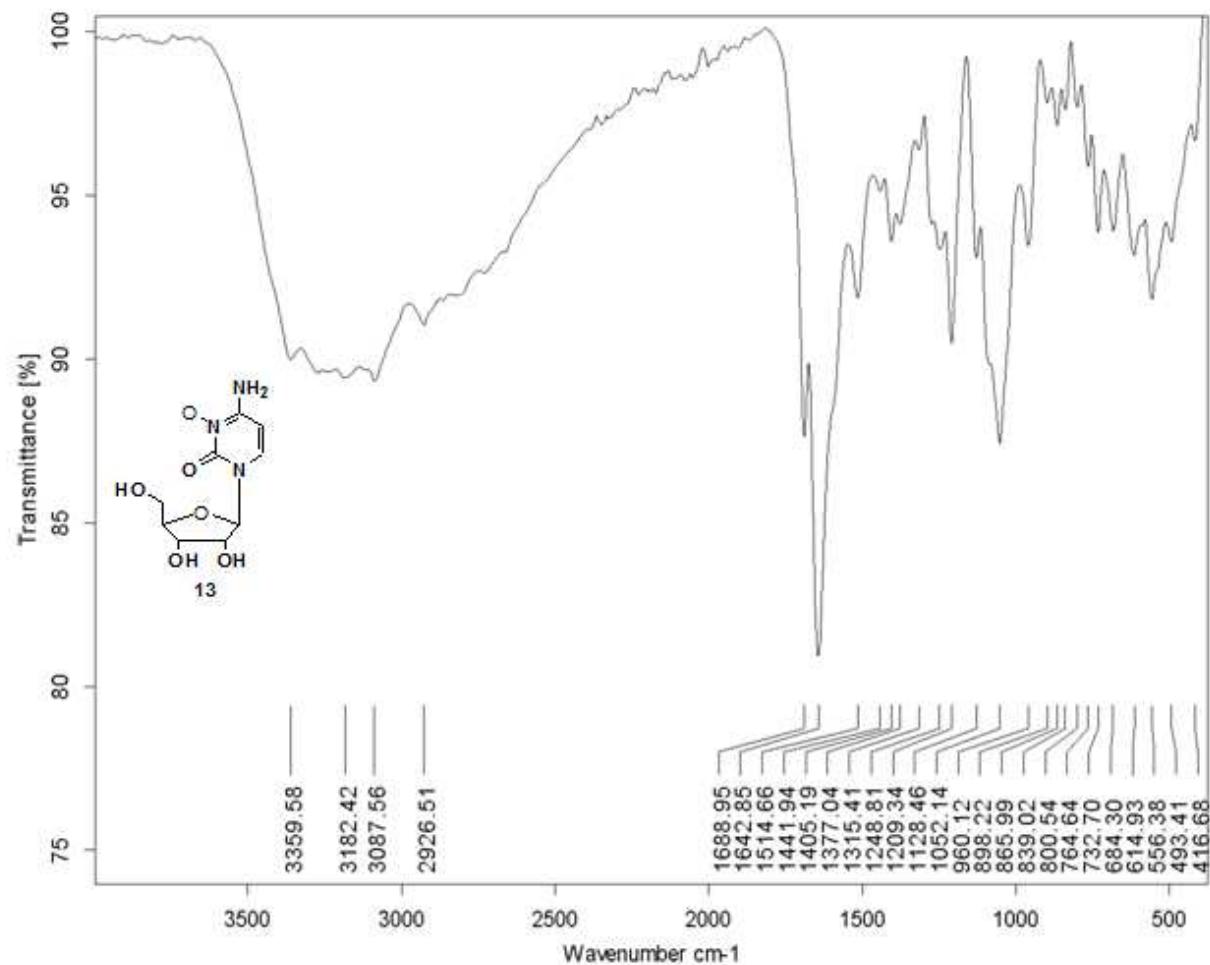


Figure S2. IR Spectrum for Cyd-*N*⁴-OH (**15**).

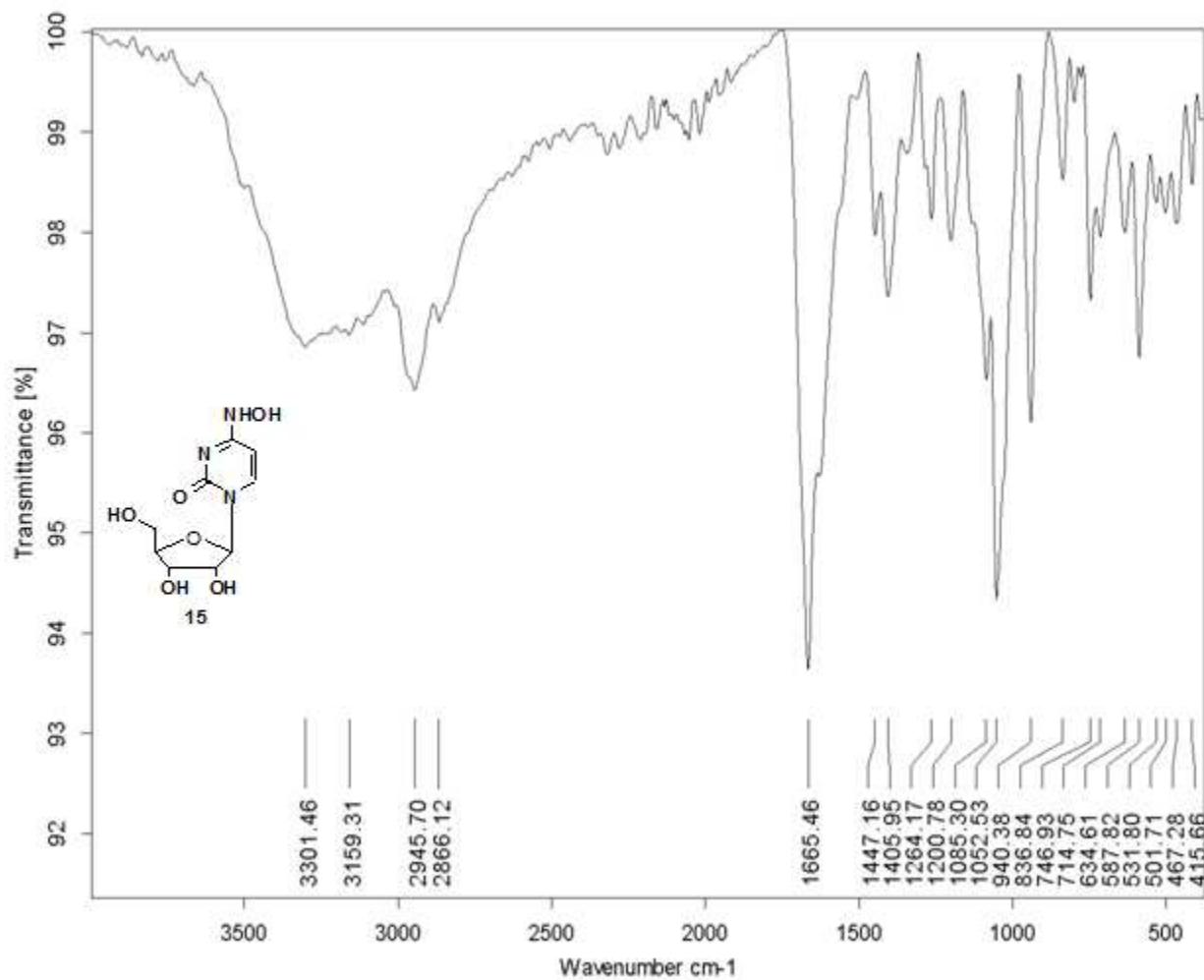


Figure S3. IR Spectrum for CMP- N^3 -oxide (**15**).

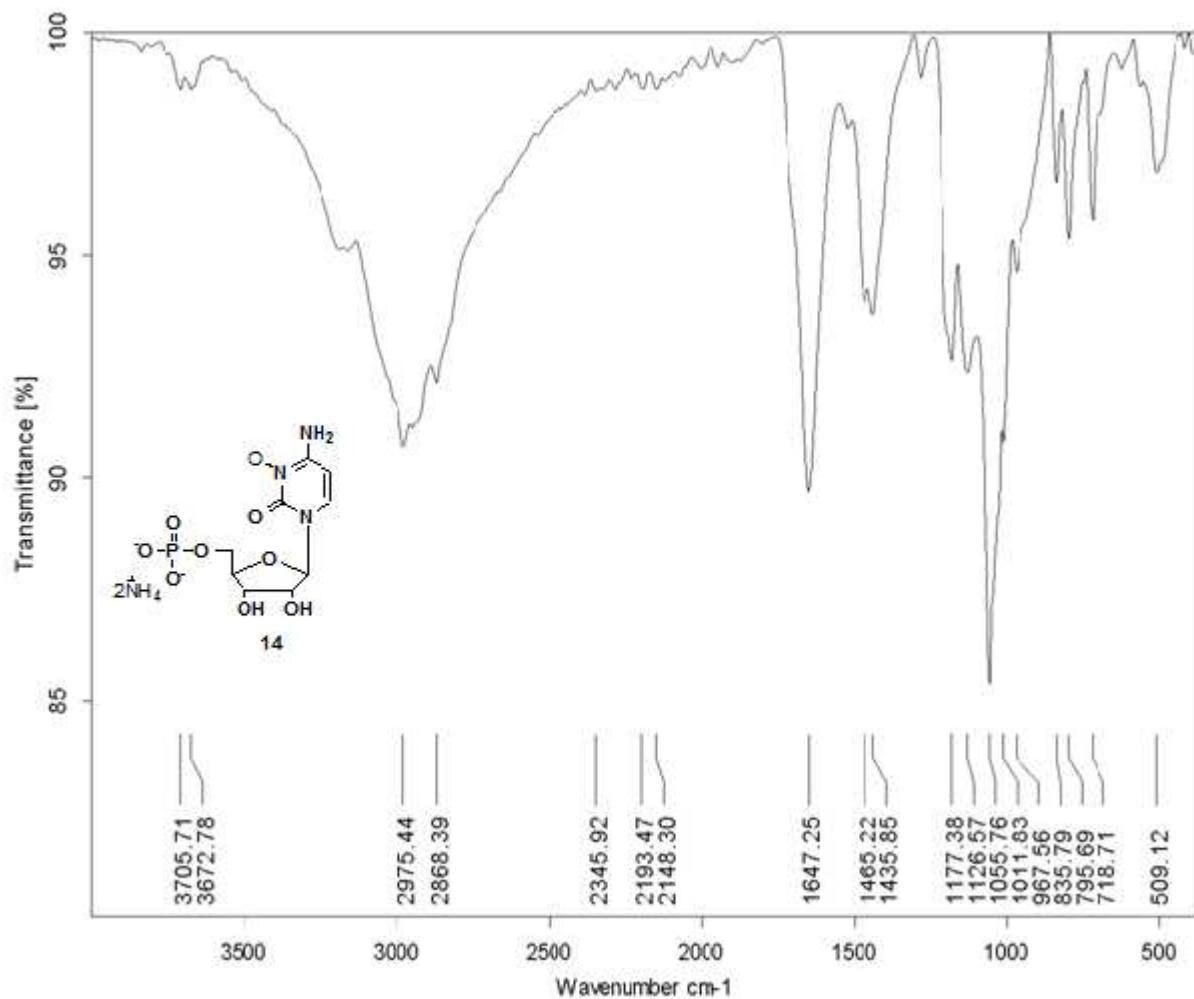


Figure S4. IR Spectrum for CMP- N^4 -OH (27).

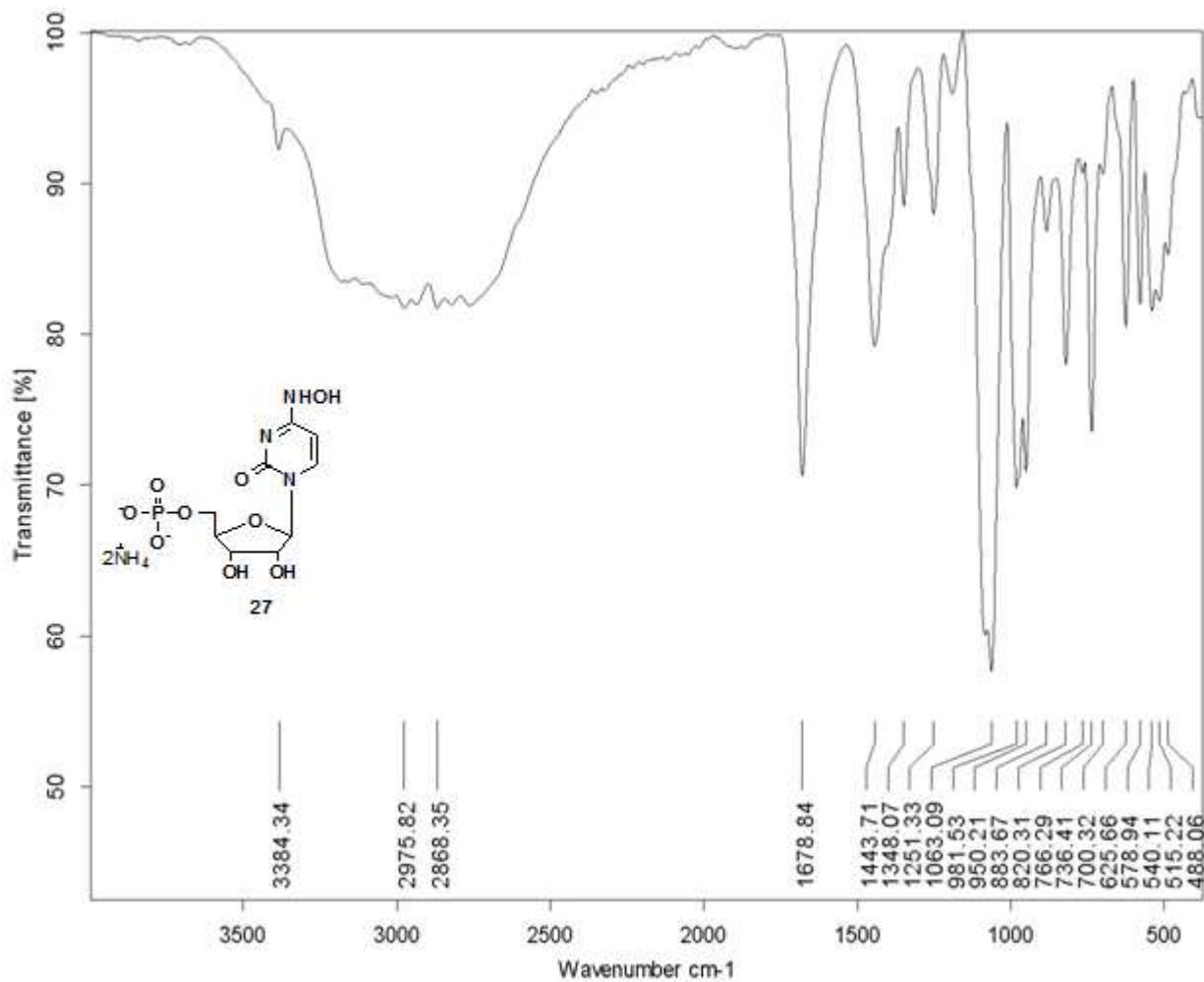


Figure S5. ^1H NMR spectrum for compound **13**.

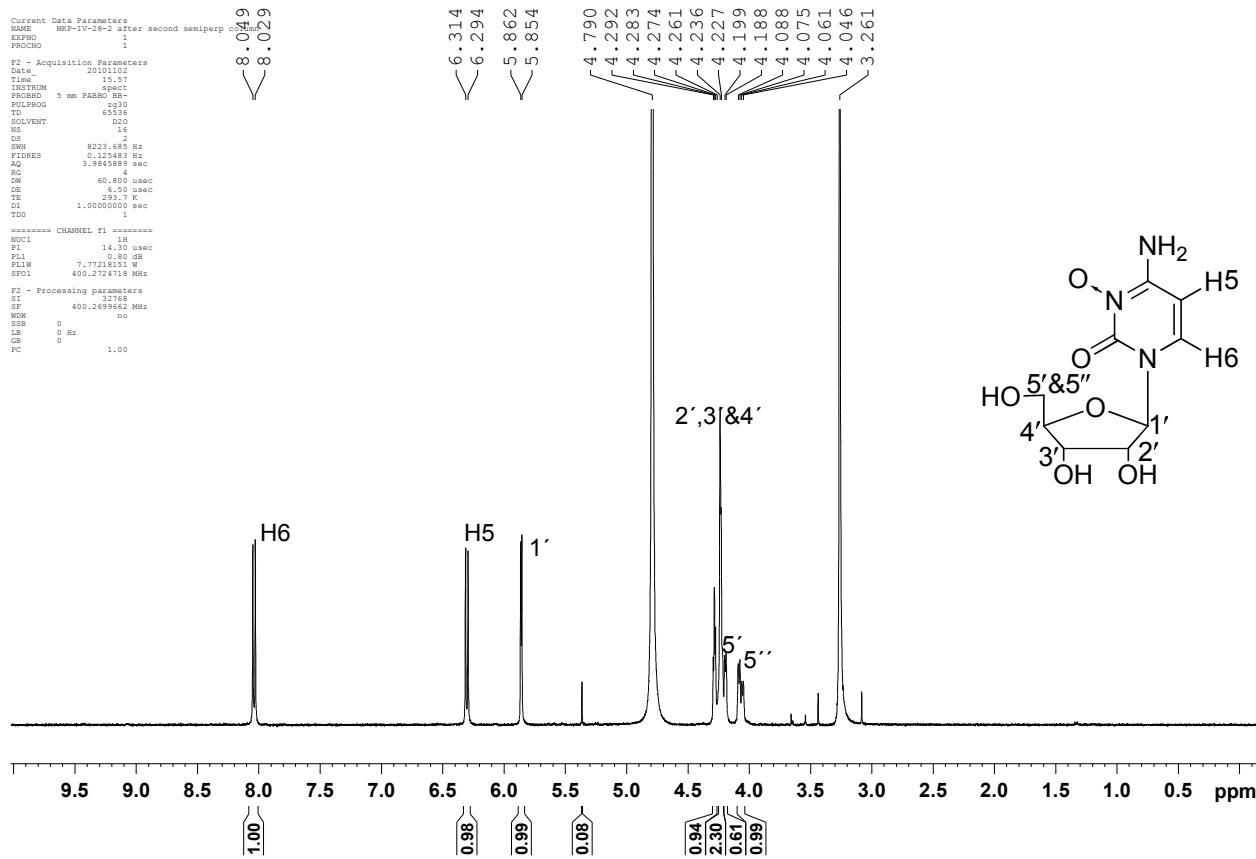


Figure S6. ^1H NMR spectrum for compound **15**.

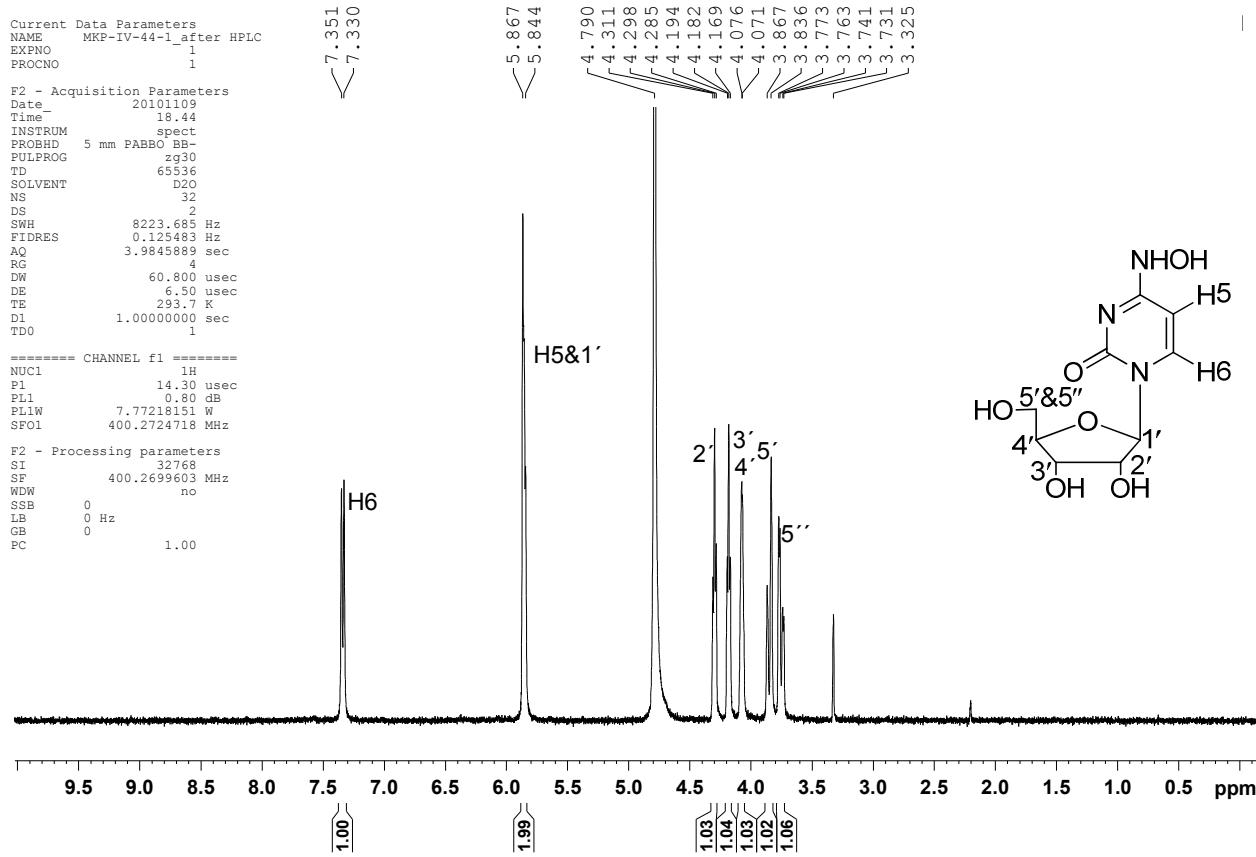


Figure S7. ^1H NMR spectrum for compound 14.

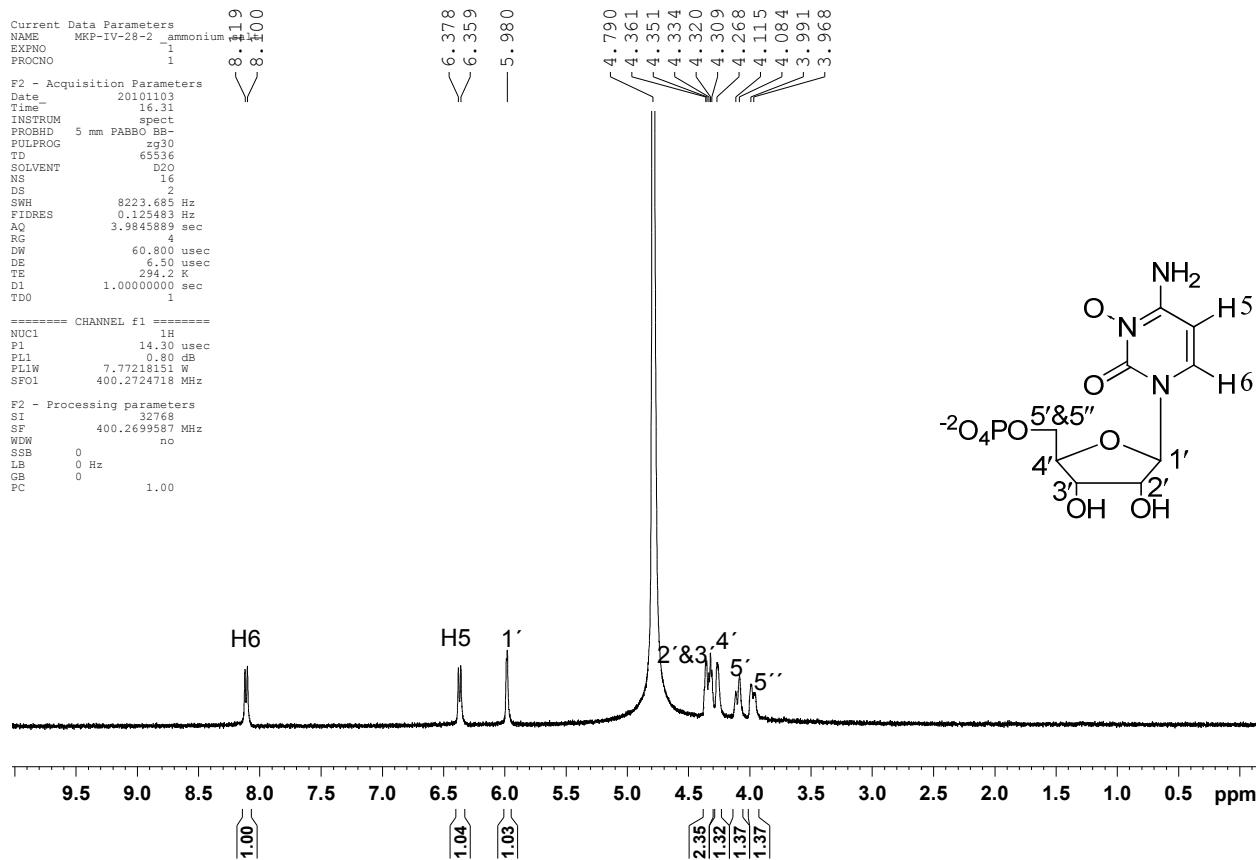


Figure S8. ^1H NMR spectrum for compound 27.

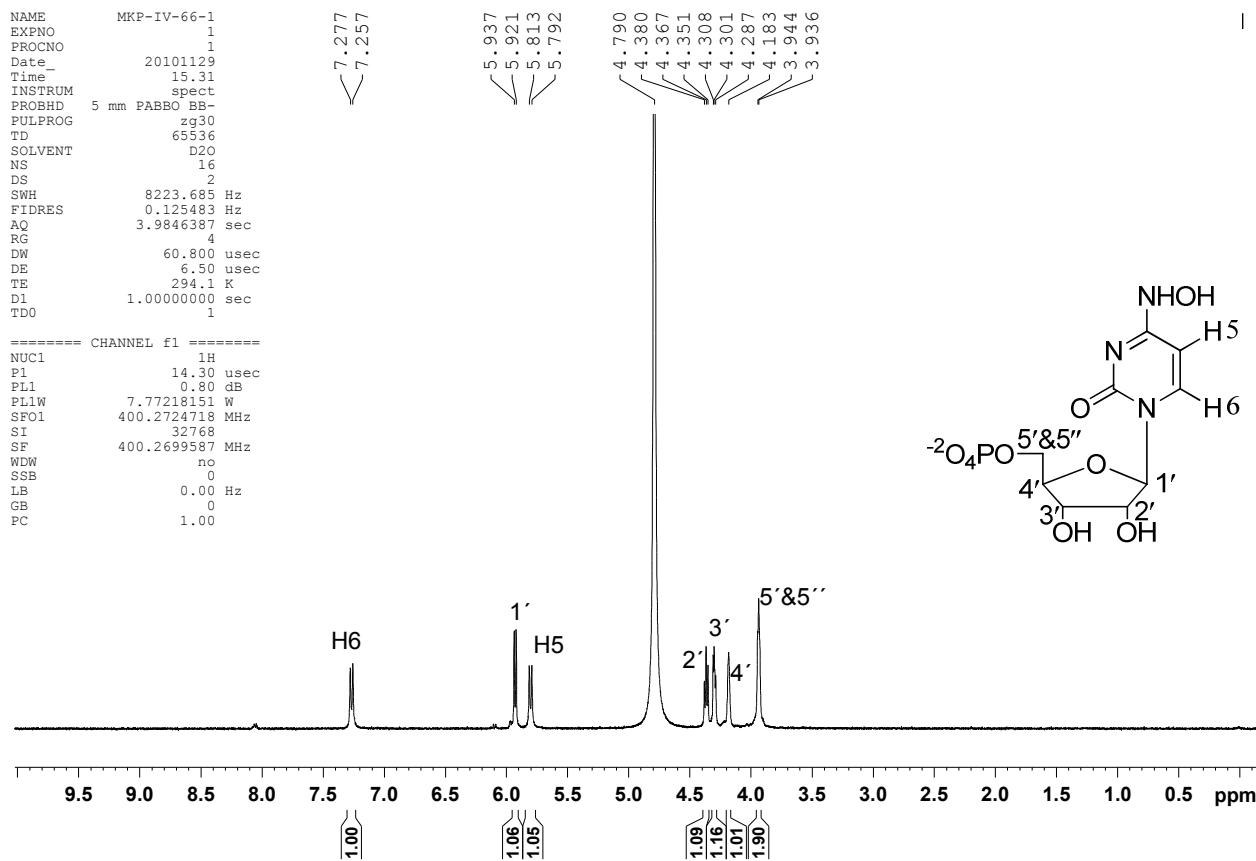


Figure S9. Mass spectrum for compound 27.

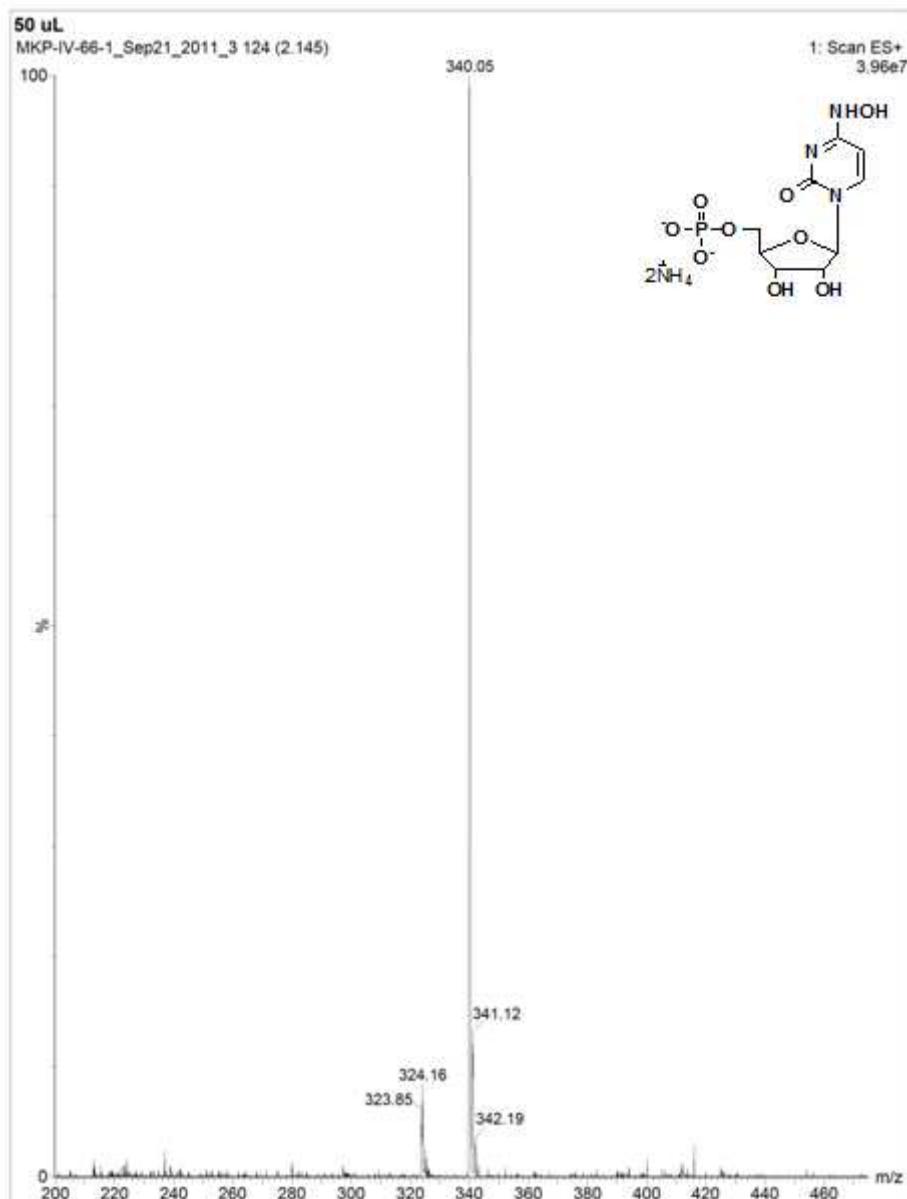


Figure S10. Mass spectrum for compound 15.

