

**Objective.**

LC-MS analysis of nucleosides from DNA and or RNA.

Chemicals and Tools	Vendor	Part#	Hazards/Notes
<ul style="list-style-type: none"><li>LC-MS grade methanol (MeOH)</li></ul>	Fisher	A456-4	(HPLC grade MeOH can be used)
<ul style="list-style-type: none"><li>Nucleoside Digestion Mix</li><li>Eppendorf tubes</li><li>Vortexer</li></ul>	NEB Eppendorf	M0649S 022431081	LoBind tubes

**Targeted analysis of nucleosides**

Nucleosides are measured using targeted LC-MS methods. The metabolites are separated using [hydrophilic interaction chromatography](#) (HILIC) and the mass to charge ratio (m/z) is measured in both positive and negative ionization modes— typically with mass accuracies  $\leq 2$  ppm. A library of >30 nucleoside standards (Refer to **Table 1**) are used for retention time validation. The PRC staff can measure other nucleosides if an authentic standard is provided by the user.

We recommend that 3 biological replicates ( $n \geq 3$ ) are prepared per condition. The recommended amount of RNA/DNA for sample preparation is 0.5-1 ug per sample – though this is dependent on the abundance of the nucleoside of interest.

	<b>Procedure.</b>	<i>Examples, Tricks &amp; Comments</i>
1	Cleanup DNA/RNA sample using phenol-chloroform extraction with ethanol precipitation, or a spin-column based cleanup kit like; Qiagen DNeasy Blood and tissue kit (e.g. 69504) or the Zymo Quick-DNA micro-prep kit (e.g. D3020).	<i>Step 1 is a general guideline. Prepare the samples as you see fit.</i>



<p>2</p>	<p><b><u>Digestion of (deoxy)ribonucleic acids:</u></b></p> <ul style="list-style-type: none"> <li>• (Optional): Spike in a known concentration of isotope-labeled internal standard (ISTD) to the RNA/DNA sample.</li> <li>• Digest 0.5-1ug RNA/DNA for 1 hour at 37°C using the NEB Nucleoside Digestion Mix<sup>1</sup>.</li> </ul> <p><sup>1</sup>You can digest the RNA using the NEB digest kit which can be found here: <a href="https://www.neb.com/products/m0649-nucleoside-digestion-mix#Product%20Information">https://www.neb.com/products/m0649-nucleoside-digestion-mix#Product%20Information</a> . The NEB kit suggests a 1 hour digestion time but we have had users incubate overnight with no issues.</p>	<p><i>Step 2 is also a guideline- other digestion methods can be used. We prefer this NEB kit due to the low% of glycerol and added salts.</i></p> <p><i>Isotopically labeled nucleosides can be ordered from Cambridge Isotopes and other vendors. These can be used for relative quantitation if a known concentration is spiked into the bio sample.</i></p>
<p>3</p>	<p><b><u>Extraction from digested nucleic acids:</u></b></p> <p>Pre-chill the MeOH at -20°C prior to extraction.</p> <ul style="list-style-type: none"> <li>• Cool the reaction mixture on ice and add cold MeOH (10X the reaction volume).</li> <li>• Vortex vigorously for 5-10 minutes followed by centrifugation (&gt;10,000 rpm or max speed) for 10 minutes.</li> <li>• Carefully remove supernatant into a pre-chilled Eppendorf tube.</li> </ul>	<p><i>Note. You can save the protein pellet to measure protein concentration for sample normalization or proteomic analysis.</i></p> <p><i>All steps must be performed on ice or at 4°C.</i></p>
<p>4</p>	<p>You can evaporate the methanol extracts using a temperature-controlled evaporator or speed vac and submit the dry pellet to the PRC. Note: You will likely not observe a pellet post digestion/extraction. The tube will look empty and that is okay. The dry pellet can be stored at -20°C or -80°C till submission.</p>	
<p>5</p>	<p>Fill out the metabolomics/lipidomics submission form.</p> <p><a href="https://www.rockefeller.edu/proteomics/uploads/www.rockefeller.edu/sites/216/2020/07/Metabolomics_submission_form_FY21.xlsx">https://www.rockefeller.edu/proteomics/uploads/www.rockefeller.edu/sites/216/2020/07/Metabolomics_submission_form_FY21.xlsx</a></p> <p>Please list which method/kits were used for oligonucleotide cleanup and digestion in the submission form.</p>	<p><i>Required information:</i></p> <ul style="list-style-type: none"> <li>• <i>Sample type/volume</i></li> <li>• <i>List of specific metabolites (or full profiling)</i></li> <li>• <i>ISTD composition/ concentration</i></li> <li>• <i>Cell treatment (e.g. labels, inhibitors, etc.)</i></li> </ul>

**Table 1.**

Nucleoside	Formula	HMDB ID	KEGG #
2-deoxyAdenosine	C10H13N5O3	HMDB0000101	C00559
5-deoxy-5-(methylthio)Adenosine	C11H15N5O3S	HMDB0001173	C00170
N6-methyl-deoxyAdenosine	C11H15N5O3		
2-deoxyGuanosine	C10H13N5O4	HMDB0000085	C00330
N2-ethyl-deoxyGuanosine	C12H17N5O4		
2-deoxyCytidine	C9H13N3O4	HMDB0000014	C00881
5-carboxy-deoxyCytidine	C10H13N3O6		
5-formyl-deoxyCytidine	C10H13N3O5		
5-methyl-deoxyCytidine	C10H15N3O4	HMDB0002224	C03592
5-hydroxy-methyl-deoxyCytidine	C10H15N3O5		
2-deoxyUridine	C9H12N2O5	HMDB0000012	C00526
2-deoxyInosine	C10H12N4O4	HMDB0000071	C05512
Thymidine	C10H14N2O5	HMDB0000273	C00214
1-methylAdenosine	C11H15N5O4	HMDB0003331	C02494
N6-methylAdenosine	C11H15N5O4	HMDB0004044	
Adenosine	C10H13N5O4	HMDB0000050	C00212
Guanosine	C10H13N5O5	HMDB0000133	C00387
1-methylGuanosine	C11H15N5O5	HMDB0001563	C04545
7-methylGuanosine	C11H15N5O5	HMDB0001107	
N2-methylGuanosine	C11H15N5O5	HMDB0005862	
2-O-methylGuanosine	C11H15N5O5		
8-hydroxyGuanosine	C10H13N5O6	HMDB0002044	
N2-N2-dimethylGuanosine	C12H17N5O5	HMDB0004824	
Cytidine	C9H13N3O5	HMDB0000089	C00475
3-methylCytidine	C10H15N3O5	HMDB0240577	
5-methylCytidine	C10H15N3O5	HMDB0000982	
2-O-methylCytidine	C10H15N3O5		
Uridine	C9H12N2O6	HMDB0000296	C00299
5-methylUridine	C10H14N2O6	HMDB0000884	
2-O-methylUridine	C10H14N2O6	HMDB0240328	
pseudoUridine	C9H12N2O6	HMDB0000767	C02067
Inosine	C10H12N4O5	HMDB0000195	C00294
Xanthosine	C10H12N4O6	HMDB0000299	C01762