MIDAS CORE sample parameters 5\_2025

Protein Sample Submission Parameters (default):

**Protein concentration:** 200 - 500 μM.  
**Protein volume:** Two 160 μL aliquots, snap-frozen, provided in 1.5 mL tubes.  
**Protein buffer:** 25 mM HEPES pH 7.4, 100 mM NaCl.  
**Sample tube identification:** Please print and label the sample tubes with your full name, email, user sample ID, and sample submission date. Please use printable cryogenic labels for -80°C storage.

**Protein affinity tag:**If your protein contains an affinity tag or fusion protein other than 6xHis (e.g. GST, MBP, etc.) that has not been removed, we require that the fusion protein be provided as an equal molar sample to the target protein to control for off-target interactions. Please contact us for questions.

**Sample billing:** Please reach out to Kevin Hicks ([kevin.hicks@health.utah.edu](mailto:kevin.hicks@health.utah.edu)) for billing purposes.