

Experimental Metadata Specifications:

Targeted Proteomics Assay

Importance 1: Required, 2: Required if available, 3: Optional

LINCS Field Name	Definition	Importance
PROTEOMICS_TARGETED_Internal_Standards_Present	Whether internal standards are used	1
PROTEOMICS_TARGETED_Internal_Standards_Type	The nature of the internal standards	2
PROTEOMICS_TARGETED_Internal_Standards_Sequence	Link to the file containing the peptide sequences of the standard used	2
PROTEOMICS_TARGETED_Internal_Standards_Labeled	Whether internal standards are labeled in some manner	2
PROTEOMICS_TARGETED_Internal_Standards_Label_Type	How internal standards are labeled if present	2
PROTEOMICS_TARGETED_Internal_Standards_as_Triggers	If internal standards are used to trigger acquisition of other analytes	2
PROTEOMICS_TARGETED_Discrete_Transitions	If transitions to be monitored are pre-selected, enforced by hardware	1
PROTEOMICS_TARGETED_Analytes_Scheduled	Whether individual analytes are scheduled	1
PROTEOMICS_TARGETED_Precursor_Gating	Method by which the desired amount of precursor ions are accumulated	1
PROTEOMICS_TARGETED_Precursor_Gating_Target	For methods that use 'ion current target' gating, the target value	2
PROTEOMICS_TARGETED_Precursor_Maximum_Dwell_Time	For methods that use 'ion current target' gating, the maximum ion accumulation time (ms)	2
PROTEOMICS_TARGETED_Isolation_Width	Width of precursor selection window, in m/z	1
PROTEOMICS_TARGETED_Isolation_Offset	Offset of center of precursor window from target m/z in table	1
PROTEOMICS_TARGETED_Mass_Analyzer_Bandpass_Width	For assays with discrete transitions, describes the width of Q3 or equivalent in m/z; NA for PRM assays	2
PROTEOMICS_TARGETED_Number_of_Targets	Number of total analytes (including stds) in the assay	1
PROTEOMICS_TARGETED_Target_Table	Systematic table of analytes targeted	2