

Experimental Metadata Specifications:

SWATH-DIA Proteomics Assay

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

LINCS Field Name	Definition	Importance
PROTEOMICS_SWATHDIA_Type	Overall description of DIA window design strategy	1
PROTEOMICS_SWATHDIA_Multiplexing	Description of multiplexing strategy	1
PROTEOMICS_SWATHDIA_Deconvolution_Software	Method used to deconvolved overlapped or MSX scans	1
PROTEOMICS_SWATHDIA_Internal_Standards_Present	Whether internal standards are present	1
PROTEOMICS_SWATHDIA_Internal_Standards_Type	The nature of the internal standards	2
PROTEOMICS_SWATHDIA_Internal_Standards_Sequence	File containing the peptide sequences of the standard used	2
PROTEOMICS_SWATHDIA_Internal_Standards_Labeled	Whether internal standards are labeled in some manner	2
PROTEOMICS_SWATHDIA_Internal_Standards_Label_Type	How internal standards are labeled if present	2
PROTEOMICS_SWATHDIA_Precursor_Dwell_Time	Method by which the desired amount of precursor ions are accumulated	1
PROTEOMICS_SWATHDIA_Precursor_Dwell_Time_Target	For methods that use TIME, the duration in ms	2
PROTEOMICS_SWATHDIA_Precursor_Maximum_Dwell_Time	For methods that use ION_CURRENT_TARGET gating, the maximum ion accumulation time (ms)	2
PROTEOMICS_SWATHDIA_Number_of_Windows	Number of total SWATH/DIA windows in the assay, or NA for randomized MSX	1
PROTEOMICS_SWATHDIA_Window_Table	Systematic table of analytes targeted; this table would be blank for randomized MSX	2