

Sample and Data Relationship Format for Proteomics (SDRF- Proteomics)

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Chapter 1. Status of this document

This document provides information to the proteomics community about a proposed standard for sample metadata annotations in public repositories called Sample and Data Relationship Format (SDRF)-Proteomics. Distribution is unlimited.

Version v1.1.0 - 2026-01

Chapter 2. Abstract

The Human Proteome Organisation (HUPO) Proteomics Standards Initiative (PSI) defines community standards for data representation in proteomics to facilitate data comparison, exchange, and verification. This document presents a specification for the Sample and Data Relationship Format (SDRF-Proteomics).

Further detailed information, including any updates to this document, implementations, and examples is available at [SDRF GitHub Repository](#). The official PSI web page for the document is: [HUPO-PSI SDRF](#).

Chapter 3. Motivation

Many resources have emerged that provide raw or integrated proteomics data in the public domain. If these are valuable individually, their integration through re-analysis represents a huge asset for the community [1].

Unfortunately, proteomics experimental design and sample related information are often missing in public repositories or stored in very diverse ways and formats. For example:

- The [CPTAC Consortium](#) provides for every dataset a set of Excel files with the information on [each sample](#) including tumor size, origin, but also how every sample is related to a specific raw file (e.g. instrument configuration parameters).
- As a resource routinely re-analysing public datasets, [ProteomicsDB](#) captures for each sample in the database a minimum number of properties to describe the sample and the related experimental protocol such as tissue, digestion method and instrument.

Such heterogeneity often prevents data interpretation, reproducibility, and integration of data from different resources. For every proteomics dataset we propose to capture at least three levels of metadata:

- (i) dataset description
- (ii) the sample metadata and data files acquisition metadata.
- (iii) The relation between the sample and the data files. The experimental design.

However, the information regarding the sample and its relation to the data files (**Figure 1**) is mostly missing in public repositories [1].

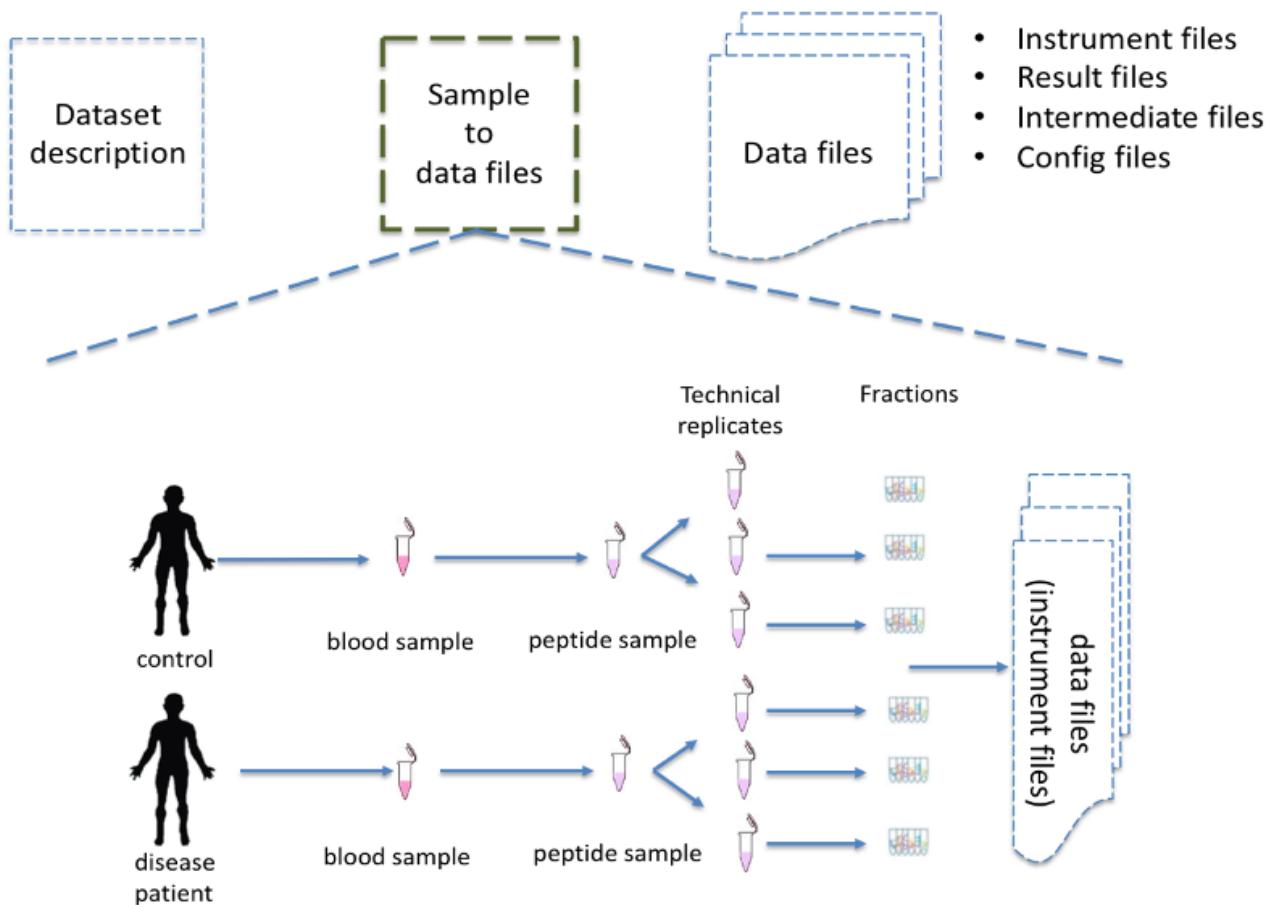


Figure 1: SDRF-Proteomics file format stores the information of the sample and its relation to the data files in the dataset. The file format includes not only information about the sample but also about how the data was acquired and processed.

Here, we introduced the Sample and Data Relationship Format (SDRF-Proteomics) to capture the sample metadata and its relation to the data files for proteomics experiments. The SDRF-Proteomics format is a tab-delimited file format that describes the sample characteristics and the relationships between samples and data files included in a dataset. SDRF-Proteomics is fully compatible with the SDRF file format part of [MAGE-TAB](#), enabling integration with transcriptomics metadata standards.

This specification, which is a community effort, aims to provide a standard for the proteomics community to annotate the sample metadata and its relation to the data files.

Chapter 4. The SDRF-Proteomics Format

The SDRF-Proteomics file format describes the sample characteristics and the relationships between samples and data files. The format is a tab-delimited file where each **ROW** corresponds to a relationship between a Sample and a Data file, each **COLUMN** corresponds to an attribute/property of the Sample, the Data file, or the Factor values, and the value in each **CELL** is the specific value of the property for a given Sample/Data file/Factor value.

The SDRF-Proteomics format contains three main sections:

- The first section contains the [sample metadata](#) using `characteristics[...]` columns (e.g., organism, disease)
- The second section contains the [data file metadata](#) using `comment[...]` columns (e.g., instrument, label)
- The third section contains the [factor values](#) using `factor_value[...]` columns to indicate variables under study

Each row links one sample to one data file. If you're new to SDRF-Proteomics, here's a minimal example to get you started:

source	char	char	char	char	char	assay	tech	com	com	com	com	com	com	com	com	com	fact
name	acte	acte	acte	acte	acte	y	nolo	men	men	men	men	men	men	men	men	men	or
	risti	risti	risti	risti	risti	nam	gy	t[proto	t[lab	t[ins	t[cle	t[fra	t[tec	t[dat	t[dat	valu	
	cs[o	cs[o	cs[d	cs[b	cs[e			mic	trum	ava	ctio	hnic	al	repli	a	e[di	
	rgan	rgan	isem	olo	gica			s	ent	ge	n	iden	repli	cate	file]	seas	
	ism]	ism	part]	isea	se]			data	age	age	nt	idene	al	cate]	e]	
								acq	uise	deta	ifi	repli	cate	repli	cate		
								uisit	ion	ils]	nt	ifi	cate	repli	cate		
								met	met	ils]	nt	ifi	cate	repli	cate		
								hod]	hod]	ils]	nt	ifi	cate	repli	cate		
sample_1	hom	liver	nor	1	run_1	proto	Data	label	Q	NT=	1	1	sample_1.ra	nor			
	o sapi		mal			profil	-dep	free	Exac	Tryp							
	ens					ing	ende	sam	tive	sin;A							
						by	nt	ple	HF	C=M							
						mas	acqu			S:10							
						spec	isitio			0125							
						trom	n			1							
						etry											

source name	characteristic	characteristic	characteristic	characteristic	assay name	technology type	com men t[proto	com men t[lab el]	com men t[instrument]	com men t[cle ave ge age nt datails]	com men t[fraction identifier]	com men t[technical replicate]	com men t[dataset file]	factor value[di sease]
sample_2	hom sapiens	liver	hepatocellular carcinoma	1	run_2	proteomic profiling by mass spectrometry	Data -dependent acquisition	label free sample	Q Exactive HF	NT= Trypsin;A C=M S:10 0125 1	1	1	sample_2.raw	hepatocellular carcinoma
sample_3	hom sapiens	not available	not available	1	run_3	proteomic profiling by mass spectrometry	Data -dependent acquisition	label free sample	Q Exactive HF	NT= Trypsin;A C=M S:10 0125 1	1	1	sample_3.raw	not available

Blue: Sample metadata | Green: Data file metadata | Orange: Factor values. Note: sample_3 demonstrates use of "not available" for unknown values.

NOTE

This minimal example shows a **mass spectrometry-based** proteomics experiment. For detailed requirements see the [MS-Proteomics template](#). For **affinity-based proteomics** (Olink, SomaScan), different columns are required - see the [Affinity-Proteomics template](#).

The SDRF-Proteomics format has the following core requirements:

- The SDRF file is a **tab-delimited format** where each row corresponds to a relationship between a Sample and a Data file.
- Each column **MUST** correspond to an attribute/property of the Sample or the Data file.

- Each cell value MUST be the property value for the corresponding Sample or Data file.
- The file MUST start with columns describing sample properties (e.g., organism, disease), followed by data file properties (e.g., label, fraction identifier, data file).
- Unknown values MUST be handled using reserved words: `not available` (value is unknown), `not applicable` (property doesn't apply), or `pooled` (value is a mixture from multiple samples).

For a step-by-step tutorial on creating your first SDRF file, see the [Quick Start Guide](#).

IMPORTANT

Throughout this specification, the keywords "MUST", "REQUIRED", "SHOULD", "RECOMMENDED", and "OPTIONAL" are interpreted as described in [RFC 2119](#).

4.1. Versioning

The SDRF-Proteomics specification uses [Semantic Versioning](#) (MAJOR.MINOR.PATCH). Version numbers are prefixed with "v" (e.g., v1.1.0). Changes are proposed via GitHub pull requests to the dev branch.

4.2. Format rules

- **Case sensitivity:** Text values are case-insensitive, but **column names are case-sensitive**. Use lowercase for all column names (e.g., `source name`, `characteristics[organism]`, `comment[label]`). Incorrect casing like `Source Name` or `Characteristics[organism]` will cause validation failures.
- **Space sensitivity:** The SDRF is sensitive to spaces in column names (`sourcename ↳ source name`). Column names must include appropriate spaces (e.g., `source name`, not `sourcename`) but must NOT have a space before the bracket (e.g., `characteristics[organism]`, not `characteristics [organism]`).
- **Column order:** The SDRF columns follows some structure; first the sample metadata columns in [Chapter 6](#); then the data file metadata columns in [Chapter 7](#); followed by the factor values columns in [Section 9.9](#).
- **Extension:** The extension of the SDRF file SHOULD be **sdrf.tsv (preferred)** or .txt.

4.3. Reserved words

There are general scenarios where cell values cannot be provided with actual data. The following reserved words MUST be used in these cases:

- **not available:** In some cases, the column is mandatory in the format, but for some samples the corresponding value is unknown or could not be determined. In those cases, users SHOULD use **not available**.
- **not applicable:** In some cases, the column is mandatory, but for some samples the corresponding value or concept does not apply. In those cases, users SHOULD use **not applicable**.
- **anonymized:** In some cases, the value exists but has been intentionally redacted for privacy protection (e.g., in clinical studies with de-identified patient data). In those cases, users SHOULD use

anonymized.

- **pooled:** In some cases, the sample is a pool of multiple samples (e.g., TMT reference channels), and the value cannot be represented as a single value. In those cases, users SHOULD use **pooled**.

Table 1. Reserved words for SDRF cell values

Term	Meaning	Example	Use Case
not available	Value exists but is unknown or could not be determined	characteristics[age] = not available	Patient age was not recorded in the study
not applicable	Value or concept does not apply to this sample	characteristics[age] = not applicable	Synthetic peptide library has no age
anonymized	Value exists but is redacted for privacy protection	characteristics[age] = anonymized	Clinical study with de-identified patient data
pooled	Value represents a mixture of multiple samples	characteristics[biological replicate] = pooled	TMT reference channel pooled from multiple replicates

4.4. SDRF file-level metadata

Since version 1.1.0, SDRF-Proteomics supports optional file-level metadata using header comments at the beginning of the file. These header comments provide information about the SDRF file itself, such as the format version, template used, and validation status. This approach is inspired by other omics formats such as VCF (Variant Call Format) file headers and is fully compatible with pandas and other tabular data processing tools.

Header comments MUST:

- Start with # (single hash) followed by a key-value pair
- Appear at the very beginning of the file, before the column header row
- Use the format `#key=value`

The following header fields are supported:

Key	Description	Example	Requirement	Ontology Term
<code>file_format</code>	Identifier for the file format	SDRF	RECO MMEN DED	PRIDE:0000831
<code>version</code>	SDRF-Proteomics specification version used	v1.1.0	RECO MMEN DED	NCIT:C25714

Key	Description	Example	Requirement	Ontology Term
<code>template</code>	Template declaration with version. Use one <code>#template</code> line per template. Format: <code>template_name,version=vX.Y.Z</code>	human,version=v1.1.0	OPTIONAL	PRIDE:0000832
<code>source</code>	Tool or origin that generated the file. Replaces per-row <code>comment[tool metadata]</code> column	lesSDRF v0.1.0	OPTIONAL	NCIT:C25683
<code>validation_hash</code>	Hash from validator certification	sha256:abc123...	OPTIONAL	PRIDE:0000834

Example of an SDRF file with header comments (simplified example showing only select columns; see [Chapter 9](#) for complete required columns):

```
#file_format=SDRF
#version=v1.1.0
#template=human,version=v1.1.0
#source=lesSDRF v0.1.0
source name characteristics[organism] characteristics[organism part]
characteristics[disease] assay name comment[data file]
sample_1 homo sapiens liver normal run_1 sample_1.raw
```

4.5. Specification structure

This document describes the main specification of SDRF-Proteomics, the structure of the specification ([Figure 2](#)), how to contribute, and extend the specification. SDRF-Proteomics uses a three-tier system for organizing metadata requirements:

- **The SDRF-Proteomics core specification:** This document contains the main specification, requirements and rules for the SDRF-Proteomics format. It also includes the notational conventions and the relationship to other specifications.
- **Templates:** All templates are organized in the `templates/` directory. This includes:
 - **Core templates** (organism-based): `human`, `vertebrates`, `invertebrates`, `plants`
 - **Specialized templates** (experiment-type): `cell-lines` (sample), `DDA acquisition` (data), `DIA acquisition` (data), `single-cell` (mixed), `affinity-proteomics` (data), `crosslinking` (data), `immunopeptidomics` (mixed), `metaproteomics` (mixed)

Each template has its own directory containing a detailed README.adoc with checklists and examples, plus a template file (`{name}-template.sdrf.tsv`) with column headers. See the [Templates](#) section.

[Logo] | [images/sdrf-guidelines-structure.png](#)

Figure 2: SDRF-Proteomics specification structure. The main specification defines the core rules and is extended by technology templates (ms-proteomics, affinity-proteomics), sample templates (human, vertebrates, etc.), and specialized experiment-type templates.

NOTE

The main specification is in the `sdrf-proteomics` directory. All templates are organized in `sdrf-proteomics/templates/`. Templates are extensions of the core specification and should follow all the rules and requirements in the main specification. Each template includes its own detailed documentation with checklists, examples, and annotation guidelines specific to that template type.

The official website for SDRF-Proteomics project is <https://github.com/bigbio/proteomics-metadata-standard>. New use cases, changes to the specification and examples can be added by using Pull requests or issues in GitHub to reach the bigbio team.

A set of examples and annotated projects from ProteomeXchange can be found here: <https://github.com/bigbio/proteomics-metadata-standard/tree/master/annotated-projects>

Multiple tools have been implemented to validate, annotate and convert SDRF-Proteomics files. The official validator of SDRF-Proteomics is sdrf-pipelines (Python - <https://github.com/bigbio/sdrf-pipelines>). This tool allows to validate an SDRF-Proteomics file. In addition, it allows converting SDRF to other popular pipelines and software configure files such as MaxQuant or OpenMS.

4.6. Table Column headers

Depending on each section the column headers (property names) will be prefixed with the following prefixes:

- `characteristics`: Sample metadata (e.g. `characteristics[organism]`)
- `comment`: Data file metadata (e.g. `comment[data file]`)
- `factor value`: Factor values properties (e.g. `factor value[disease]`)

Each property name MUST be a valid ontology term or a valid controlled vocabulary term. Each section will have some specific order for column headers.

NOTE

A list of all controlled vocabularies and ontologies supported are in the [Chapter 11](#) section. On each section we also provide a list of properties that are supported.

4.7. Table Cell values

The value for each property, (e.g. characteristics, comment, factor value) corresponding to each sample or data file can be represented in multiple ways.

- **Free Text (Human readable)**: In the free text representation, the value is provided as text without Ontology support (e.g. colon or providing accession numbers). This is only RECOMMENDED when the text inserted in the table is the exact name of an ontology/CV term in EFO. If the term is not in EFO, other ontologies can be used.

source name	characteristics[organism]
sample 1	homo sapiens

source name	characteristics[organism]
sample 2	homo sapiens

- **Ontology url (Computer readable):** Users can provide the corresponding URI (Uniform Resource Identifier) of the ontology/CV term as a value. This is recommended for enriched files where the user does not want to use intermediate tools to map from free text to ontology/CV terms.

source name	characteristics[organism]
Sample 1	http://purl.obolibrary.org/obo/NCBITaxon_9606
Sample 2	http://purl.obolibrary.org/obo/NCBITaxon_9606

- **Key=value representation (Human and Computer readable):** The current representation aims to provide a mechanism to represent the complete information of the ontology/CV term including Accession, Name and other additional properties. In the key=value pair representation, the Value of the property is represented as an Object with multiple properties, where the key is one of the properties of the object and the value is the corresponding value for the particular key. An example of key value pairs is post-translational modification (see [Protein Modifications](#)):

```
NT=Glu->pyro-Glu;MT=fixed;PP=Anywhere;AC=Unimod:27;TA=E
```

Chapter 5. Validating SDRF Files

The official validator for SDRF-Proteomics files is [sdrf-pipelines](#), a Python tool that checks your SDRF file for errors and compliance with the specification.

Installation:

```
pip install sdrf-pipelines
```

Basic Validation:

```
# Validate an SDRF file
parse_sdrf validate-sdrf --sdrf_file your_file.sdrf.tsv

# Validate with a specific template
parse_sdrf validate-sdrf --sdrf_file your_file.sdrf.tsv --template human
```

For more information, visit: [sdrf-pipelines on GitHub](#)

Chapter 6. SDRF-Proteomics: Samples metadata

The Sample metadata section provides information about the samples of origin and their characteristics. Each sample contains a *source name* (unique identifier) and a set of *characteristics* columns. The first column of the file should be the *source name* and the following columns should be the characteristics of the sample. For example, for any proteomics experiment (human, vertebrate, cell line), the following characteristics should be provided:

- **source name:** Unique sample name (it can be present multiple times if the same sample is used several times in the same dataset)
- **characteristics[organism]:** The organism of the Sample of origin. Values MUST come from [NCBI Taxonomy](#).
- **characteristics[organism part]:** The part of organism's anatomy or substance arising from an organism from which the biomaterial was derived (e.g., liver). Values SHOULD come from [UBERON](#) or [BTO](#).
- **characteristics[disease]:** The disease under study in the Sample. Values SHOULD come from [MONDO](#), [EFO](#), or [DOID](#). For healthy/control samples, use [normal](#) ([PATO:0000461](#)) - see [Disease Annotation Guidelines](#).
- **characteristics[cell type]:** A cell type is a distinct morphological or functional form of cell (e.g., epithelial, glial). Values SHOULD come from [Cell Ontology \(CL\)](#) or [BTO](#).

Example:

source name	characteristics[organism]	characteristics[organism part]	characteristics[disease]	characteristics[cell type]
sample_treat	homo sapiens	liver	liver cancer	not available
sample_control	homo sapiens	liver	liver cancer	not available

NOTE

Additional characteristics can be added depending on the type of the experiment and sample. The [SDRF-Proteomics templates](#) defines a set of templates and checklists of properties that should be provided depending on the proteomics experiment. In the core guidelines and templates, main document of SDRF-Proteomics, we explain the major sample properties for different experiments. However, SDRF-Proteomics can be extended using guidelines for specific experiments.

IMPORTANT

Each characteristic name in the column header SHOULD be a CV term from the EFO ontology. For example, the header `characteristics[organism]` corresponds to the ontology term Organism. However the values could be from EFO or other ontologies. For example, we RECOMMEND to use MONDO for diseases because it has better coverage than EFO. For healthy samples, use [normal](#) ([PATO:0000461](#)) - see [Disease Annotation Guidelines](#).

IMPORTANT

Multiple values (columns) for the same `characteristics` term are allowed in SDRF-Proteomics (see [Section 8.1](#)). However, it is RECOMMENDED not to use the same column in the same file. If you have multiple phenotypes, you can

specify what it refers to or use another more specific term, e.g., "immunophenotype".

6.1. BioSamples database integration

[BioSamples](#) provides persistent identifiers for biological samples that enable cross-database linking [5]. Use the optional *characteristics[biosample accession number]* column to link samples to BioSamples entries (EBI format: SAMEA*, NCBI format: SAMN*).

Column: `characteristics[biosample accession number]`

Examples: `SAMN12345678` (NCBI), `SAMEA12345678` (EBI)

Example usage:

source name	characteristics[bio sample accession number]	characteristics[organism]	characteristics[organism part]	characteristics[disease]
sample_001	SAMN12345678	homo sapiens	liver	liver cancer
sample_002	SAMN12345679	homo sapiens	liver	normal
sample_003	SAMEA12345680	mus musculus	brain	normal

The BioSamples accession number enables connection to sample resources across databases, linking proteomics data with genomics, transcriptomics, and other omics datasets.

NOTE

BioSample accession numbers from NCBI follow the format `SAMNxxxxxxxxxx` and from EBI follow the format `SAMEAxxxxxxxxx`, where `x` represents digits. Either NCBI or EBI BioSample accession numbers can be used depending on where the sample is registered. The *characteristics[biosample accession number]* column is OPTIONAL, but when available, providing BioSample accession numbers is RECOMMENDED to enhance data integration and reusability. Users must first request BioSample accession numbers from the appropriate service (NCBI or EBI) before including them in their SDRF files.

6.2. Encoding sample technical and biological replicates

SDRF-Proteomics uses two columns to track replicates [4]:

- **characteristics[biological replicate]:** Identifies independent biological samples within each experimental condition (factor value group). Replicate numbers are assigned per condition, so if you have 2 cancer samples and 2 healthy samples, both groups would have biological replicates numbered 1 and 2.
- **comment[technical replicate]:** Identifies repeated measurements of the same sample (e.g., multiple LC-MS/MS injections)

IMPORTANT

Biological replicate numbering restarts for each experimental condition (factor value). For example, in a disease study with factor value[disease], the cancer samples would be numbered 1, 2, 3... and the normal samples would independently be numbered 1, 2, 3... This establishes the relationship between each sample and its experimental condition.

The following example shows 2 biological replicates, each with 2 fractions and 2 technical replicates:

source name	characteristics[biological replicate]	assay name	comment[label]	comment[fraction identifier]	comment[technical replicate]	comment[data file]
patient_001_sample	1	run_01	label free sample	1	1	P001_F1_TR 1.raw
patient_001_sample	1	run_02	label free sample	2	1	P001_F2_TR 1.raw
patient_001_sample	1	run_03	label free sample	1	2	P001_F1_TR 2.raw
patient_001_sample	1	run_04	label free sample	2	2	P001_F2_TR 2.raw
patient_002_sample	2	run_05	label free sample	1	1	P002_F1_TR 1.raw
patient_002_sample	2	run_06	label free sample	2	1	P002_F2_TR 1.raw
patient_002_sample	2	run_07	label free sample	1	2	P002_F1_TR 2.raw
patient_002_sample	2	run_08	label free sample	2	2	P002_F2_TR 2.raw

In this example:

- **Biological replicates:** `patient_001_sample` and `patient_002_sample` are different biological samples (different source names), annotated with `characteristics[biological replicate]` values 1 and 2
- **Technical replicates:** Each biological sample is measured twice (`comment[technical replicate] = 1 and 2`)
- **Fractions:** Each technical replicate has 2 fractions (`comment[fraction identifier] = 1 and 2`)

IMPORTANT

Both `characteristics[biological replicate]` and `comment[technical replicate]` columns are REQUIRED. When no replicates are performed in a study, set both columns to 1 (i.e., each sample is biological replicate 1 and technical replicate 1). For **pooled samples** (e.g., TMT reference channels), use `pooled` for biological replicate since these samples are mixtures of multiple replicates and assigning a specific replicate number would be misleading.

Some examples with explicit annotation of the biological replicates can be found here:

- <https://github.com/bigbio/proteomics-metadata-standard/blob/c3a56b076ef381280dfcb0140d2520126ace53ff/annotated-projects/PXD006401/PXD006401.sdrf.tsv>

6.3. Pooled samples

When multiple samples are pooled into one (e.g., TMT/iTRAQ reference channels for normalization), use the *characteristics[pooled sample]* column to indicate pooling status. Allowed values:

- **not pooled**: Regular individual samples
- **pooled**: Sample is pooled but individual sources are unknown
- **SN=sample1;SN=sample2;...:** Lists source names of pooled samples when known

Example:

source name	characteristics[pooled sample]	characteristics[organism]	characteristics[age]	comment[label]	comment[data file]
sample_1	not pooled	homo sapiens	45Y	TMT126	file01.raw
sample_2	not pooled	homo sapiens	52Y	TMT127N	file01.raw
pooled_ref	SN=sample_1;SN=sample_2	homo sapiens	pooled	TMT131C	file01.raw

TIP

For pooled samples, use **pooled** for individual-specific fields (biological replicate, age, sex) to indicate a mixture rather than a single sample.

6.4. Sample Metadata Guidelines

For detailed guidance on annotating sample metadata, refer to the following conventions documents:

- [Sample Metadata Guidelines](#) - Detailed guidelines for age, sex, disease, organism part, cell type, developmental stage, spiked-in samples, and other sample characteristics
- [Human Sample Metadata Guidelines](#) - Human-specific metadata including disease staging, treatment history, demographics, and lifestyle factors

Chapter 7. SDRF-Proteomics: data files metadata

The connection between samples and data files is done using properties annotated with the `comment` prefix. All properties referring to a data file (e.g., MS run file) are annotated with the category `comment`. This differentiates data file properties from sample properties (characteristics).

7.1. CV Term Format for Data File Metadata

For data file metadata (`comment` columns) that reference ontology terms, use the structured format:
`NT={term name};AC={accession}`

Examples: `NT=HCD;AC=PRIDE:0000590`, `NT=Orbitrap;AC=MS:1000484`

This format enables automated validation and software extraction from raw files. Sample metadata (characteristics) can use simple term names since they are typically human-annotated.

The following properties MUST be provided for each data file in **mass spectrometry-based proteomics** experiments. For **affinity-based proteomics** (Olink, SomaScan), see the [Affinity-Proteomics template](#) for different required columns.

Column	Requirement	Description	Ontology
<code>assay_name</code>	REQUIRED	Unique identifier for an MS run/data file	Free text
<code>technology_type</code>	REQUIRED	Technology used to capture the data	Fixed values
<code>comment[proteomics data acquisition method]</code>	REQUIRED	DDA, DIA, PRM, SRM	PRIDE:0000659
<code>comment[label]</code>	REQUIRED	Label applied to sample (or "label free sample")	PRIDE - Labels
<code>comment[instrument]</code>	REQUIRED	Mass spectrometer model	PSI-MS - Instruments
<code>comment[cleavage agent details]</code>	REQUIRED	Enzyme information (use "not applicable" for top-down/undigested samples)	PSI-MS - Cleavage agents
<code>comment[fraction identifier]</code>	REQUIRED	Fraction number (1 if not fractionated)	Integer
<code>comment[technical replicate]</code>	REQUIRED	Technical replicate number (1 if none)	Integer
<code>comment[data file]</code>	REQUIRED	Name of the raw file	Free text

Example:

source name	assay name	technology type	comment[proteomics data acquisition method]	comment[label]	comment[instrument]	comment[data file]
sample_1	sample1_ru_n1	proteomic profiling by mass spectrometry	data-dependent acquisition	label free sample	Q Exactive HF	sample1.raw

7.2. Sample Preparation and Fragmentation (MS-based only)

NOTE

This section applies to **mass spectrometry-based proteomics** experiments only. For affinity-based proteomics, these properties do not apply.

For detailed documentation of sample preparation and MS/MS fragmentation properties, see the [MS-Proteomics Template](#):

- **Sample preparation:** depletion, reduction reagent, alkylation reagent
- **Fractionation:** fractionation method (used with `comment[fraction identifier]`)
- **Fragmentation:** collision energy, dissociation method

7.3. Proteomics data acquisition method

Proteomics data acquisition method can happen in multiple ways: Data Dependent Acquisition (DDA), Data Independent Acquisition (DIA), and targeted approaches. The SDRF-Proteomics file format REQUIRES capturing the method used for the data acquisition in the `comment[proteomics data acquisition method]` column. The values MUST be children of the PRIDE ontology term [proteomics data acquisition method \(PRIDE:0000659\)](#). The following values are commonly used:

- data-dependent acquisition
- data-independent acquisition
 - diaPASEF
 - SWATH MS
- parallel reaction monitoring
- selected reaction monitoring

IMPORTANT

The `comment[proteomics data acquisition method]` column is REQUIRED for all mass spectrometry-based SDRF files. This field must be explicitly specified and cannot be omitted or assumed.

You can find an example of a DIA experiment in the following link: [DIA example](#)

TIP

For DIA experiments, additional properties like MS1 scan range can be captured. See [DIA Scan Window Limits](#) in the MS-Proteomics Template.

7.4. MS-Proteomics Template

For detailed guidance on data file metadata, refer to the conventions document:

- [MS-Proteomics Template](#) - Detailed guidelines for labels, instruments, modifications, cleavage agents, mass tolerances, RAW file URLs, and other data file properties

Chapter 8. Additional SDRF Rules

8.1. Column Cardinality

Some columns can appear multiple times for the same sample. The cardinality rules are:

- **Single (1):** Column appears exactly once per sample (e.g., `characteristics[biological replicate]`)
- **Multiple (*):** Column can appear multiple times (e.g., `comment[modification parameters]` can specify multiple post-translational modifications)

Example of multiple `comment[modification parameters]` columns:

source name	characteristics[...]	comment[modification parameters]	comment[modification parameters]	...
sample-1	...	NT=Carbamidomethyl;AC=UNIMOD:4;TA=C;MT=fixed;PP=Anywhere	NT=Oxidation;AC=UNIMOD:5;TA=M;MT=variable;PP=Anywhere	...

8.2. Row Uniqueness Requirements

SDRF files must satisfy specific uniqueness constraints to ensure data integrity and enable proper indexing by analysis tools.

Error-level constraint (validation fails): The combination of `source name + assay name + comment[label]` MUST be unique across all rows in the SDRF file. If two rows have identical values for all three columns, validation will fail with an error. This constraint ensures that each sample-run-label combination can be uniquely identified.

Warning-level constraint (validation warns): The combination of `source name + assay name` SHOULD be unique across all rows. Non-unique combinations will generate a warning during validation. This constraint helps identify potential issues where the same sample appears to have multiple entries for the same MS run without distinguishing labels.

Assay name uniqueness: Each distinct MS run/data file MUST have exactly one globally unique `assay name`, and no two different data files may share an assay name. To ensure uniqueness, it is RECOMMENDED to incorporate sample-specific information in assay names, such as sample IDs or replicate numbers (e.g., "sample1_run1", "sample1_run2", "patient001_fraction01").

NOTE For multiplexed experiments (e.g., TMT, iTRAQ), multiple SDRF rows will share the same `assay name` because multiple samples are analyzed in a single MS run. In these cases, the `comment[label]` column distinguishes between different samples within the same run, and the combination of `source name + assay name + comment[label]` remains unique.

Example of valid multiplexed experiment:

source name	...	assay name	comment[label]	...	comment[data file]
sample_A	...	TMT_batch1_ru n1	TMT126	...	batch1_run1.ra w
sample_B	...	TMT_batch1_ru n1	TMT127N	...	batch1_run1.ra w
sample_C	...	TMT_batch1_ru n1	TMT127C	...	batch1_run1.ra w
sample_D	...	TMT_batch1_ru n1	TMT128N	...	batch1_run1.ra w

In this example, all four rows share the same `assay name` and `comment[data file]` because they represent different samples multiplexed in a single MS run. The combination of `source name + assay name + comment[label]` is unique for each row.

Chapter 9. Templates

9.1. What is a Template?

A **template** in SDRF-Proteomics is a predefined set of metadata columns (both required and recommended) that ensures consistent and complete annotation for a specific type of experiment or sample. Templates serve the same purpose as **metadata checklists**, **minimum information standards** (like MIAPE), or **validation schemas** in other data standards—they define what information must be captured to make a dataset FAIR (Findable, Accessible, Interoperable, Reusable).

Each template includes both **sample metadata** (characteristics columns describing the biological sample) and **data file metadata** (comment columns describing the MS data files)—everything needed to create a complete, validated SDRF file.

9.2. Template Layered Architecture

Templates in SDRF-Proteomics follow a **layered architecture** that separates concerns:

Layer	Purpose	Templates	Valid Alone?
BASE	Internal construction artifact with shared columns (not user-facing)	<code>base</code> (internal only)	No - never use directly
TECHNOLOGY	Minimum valid templates for data acquisition	ms-proteomics , affinity-proteomics	Yes - these are the minimum valid SDRFs
SAMPLE	Organism-specific sample metadata	human , vertebrates , invertebrates , plants	No - must combine with TECHNOLOGY
EXPERIMENT	Experiment-specific columns	cell-lines , single-cell , crosslinking , dda-acquisition , dia-acquisition	No - must combine with TECHNOLOGY

TIP

The **base** template is an internal construction artifact that should never be used directly by users. Start with a **technology template** instead: [ms-proteomics](#) for mass spectrometry experiments or [affinity-proteomics](#) for Olink/SomaScan experiments. All columns defined in the **sample metadata** and **data file metadata** sections are inherited by these technology templates.

Key concepts:

- **Technology templates** ([ms-proteomics](#) or [affinity-proteomics](#)) are **required** - you must use exactly one
- **Sample templates** ([human](#), [vertebrates](#), etc.) are **recommended** but optional
- **Experiment templates** provide additional methodology-specific columns

- Templates can be **extended**: add custom columns beyond the template requirements for study-specific metadata

When combining templates, include all required columns from each applicable template. The validator will check compliance with all specified templates.

9.3. Template Inheritance

Templates form a layered inheritance hierarchy. Child templates inherit all columns and validators from parent templates and can add new columns or strengthen requirements.

```

base (CONSTRUCTION ARTIFACT - not valid alone)
  ↗ Shared columns: source name, organism, organism part,
  ↗           biological replicate, assay name, technology type,
  ↗           instrument, technical replicate, data file
  ↗
  ↗ ms-proteomics (MINIMUM VALID for MS proteomics)
    ↗   ↗ Adds: acquisition method, cleavage agent, label, fraction identifier
    ↗   ↗
    ↗   ↗ dda-acquisition (extends ms-proteomics with DDA-specific columns)
    ↗   ↗ dia-acquisition (extends ms-proteomics with DIA-specific columns)
    ↗   ↗ crosslinking (extends ms-proteomics with XL-MS columns)
    ↗   ↗ single-cell (extends ms-proteomics with SCP columns)
    ↗   ↗ immunopeptidomics (extends ms-proteomics with MHC-MS columns)
    ↗
  ↗ affinity-proteomics (MINIMUM VALID for affinity proteomics)
    ↗   ↗ Adds: instrument, panel name, quantification unit, sample type
    ↗   ↗
    ↗   ↗ olink (extends affinity-proteomics with Olink-specific columns)
    ↗   ↗ somascan (extends affinity-proteomics with SomaScan-specific columns)

Sample templates (combine with TECHNOLOGY templates):
  ↗ human (adds: disease, age, sex, ancestry)
  ↗ vertebrates (adds: disease, developmental stage, strain)
  ↗ invertebrates (adds: disease, developmental stage, genotype)
  ↗ plants (adds: disease, developmental stage, growth conditions)

Experiment templates (organism-agnostic):
  ↗ cell-lines (adds: cell line name, Cellosaurus ID, passage number)

```

Inheritance rules:

1. Child templates inherit all columns from parent templates
2. Child templates may add new columns
3. Child templates may promote **optional** → **recommended** → **required**
4. Child templates **must not** weaken requirements (e.g., **required** → **optional**)
5. Multiple templates can be combined (e.g., **ms-proteomics + human + crosslinking**)

Column requirement levels in templates:

Each column in a template has one of three requirement levels:

- **REQUIRED:** The column **MUST** appear in the SDRF file. Validation will fail if this column is missing. Template header files (.sdrf.tsv) always include these columns.
- **RECOMMENDED:** The column **SHOULD** appear in the SDRF file when applicable to the experiment. These columns are included in template header files and validation will generate warnings if missing.
- **OPTIONAL:** The column **MAY** be included if relevant to the study. These columns are NOT included in template header files but are documented in the template checklist. Users can add them as needed.

NOTE

When a column is marked as RECOMMENDED or OPTIONAL, it means users should evaluate whether the column applies to their specific experiment. For example, `characteristics[cell_line]` is RECOMMENDED in the immunopeptidomics template because cell lines are commonly used, but tissue samples may use `not applicable`.

TIP

For developers and maintainers: For detailed information on YAML template structure, validators, and LinkML schema, see the [Template Definitions Guidelines](#).

9.4. Specifying Templates in File Headers

When declaring templates in the `#template` header field, follow these rules:

Rule 1: Only list leaf templates - parent templates are implied

Since child templates inherit from parents, you only need to list the most specific (leaf) template. The parent is automatically implied:

```
# CORRECT: crosslinking inherits from ms-proteomics
#template=crosslinking,version=v1.0.0

# INCORRECT: don't list parent when child is present
#template=ms-proteomics,version=v1.1.0
#template=crosslinking,version=v1.0.0
```

Rule 2: List templates from different branches

When combining templates from different branches of the hierarchy (e.g., organism + experiment), list each on its own line with its version:

```
# Human sample with crosslinking experiment
# - human is from the SAMPLE branch
# - crosslinking is from the EXPERIMENT branch (inherits ms-proteomics)
#template=human,version=v1.1.0
#template=crosslinking,version=v1.0.0
```

Rule 3: Independent versioning

Each template is declared on its own line with its version, allowing templates to evolve independently:

```
# Each template declares its own version
#template=human,version=v1.2.0
#template=crosslinking,version=v1.0.0
#template=phosphoproteomics,version=v1.1.0
```

Common examples:

Experiment Type	Templates	Header
Human MS proteomics	human (inherits ms-proteomics)	#template=human,version=v1.1.0
Mouse MS proteomics	vertebrates (inherits ms-proteomics)	#template=vertebrates,version=v1.1.0
Non-organism-specific MS	ms-proteomics only	#template=ms-proteomics,version=v1.1.0
Human crosslinking	human + crosslinking	#template=human,version=v1.1.0 + #template=crosslinking,version=v1.0.0
Recombinant protein crosslinking	crosslinking only (no organism template)	#template=crosslinking,version=v1.0.0
Human Olink	human + olink	#template=human,version=v1.1.0 + #template=olink,version=v1.0.0
Human DIA with cell lines	human + dia-acquisition + cell-lines	#template=human,version=v1.1.0 + #template=dia-acquisition,version=v1.0.0 + #template=cell-lines,version=v1.0.0

9.5. Choosing Templates

First, determine your proteomics technology and select the appropriate technology template:

Template	Use For	Documentation	Valid Alone?
MS-Proteomics	All mass spectrometry-based proteomics (DDA, DIA, SRM/MRM/PRM)	Full documentation	Yes - minimum for MS
Affinity-Proteomics	Affinity-based proteomics (Olink, SomaScan)	Full documentation	Yes - minimum for affinity

9.6. Core Templates

Add the appropriate sample template based on your sample organism:

Template	Use For	Key Additional Columns	Documentation
Human	Human clinical samples	disease, age, sex, ancestry category, individual	Full documentation
Vertebrates	Mouse, rat, zebrafish, other vertebrates	disease, developmental stage, strain/breed, sex	Full documentation
Invertebrates	Drosophila, C. elegans, insects	disease, developmental stage, strain/breed, genotype	Full documentation
Plants	Arabidopsis, crops, other plants	disease, developmental stage, strain/breed, growth conditions, treatment	Full documentation

For detailed explanations of each column, see [sample metadata](#) for sample properties and [data file metadata](#) for data file properties.

NOTE

The [characteristics\[cell type\]](#) column is RECOMMENDED across all templates when the cell type is known or can be determined. Use [not available](#) if the cell type cannot be determined (e.g., whole tissue samples, mixed cell populations). For cell line experiments, use the cell-lines template which provides more specific guidance.

9.7. Experiment-Type Templates

In addition to sample templates, SDRF-Proteomics provides specialized experiment-type templates. These templates extend the core templates with methodology-specific columns.

- **DDA Acquisition:** Data-dependent acquisition experiments. Includes columns for dissociation method, collision energy, fractionation method, modification parameters, and mass tolerances.
- **DIA Acquisition:** Data-independent acquisition experiments. Includes columns for scan window limits, isolation window width, DIA method, and spectral library information.
- **Cell Lines:** Experiments using cell line samples. Includes Cellosaurus integration for cell line identification.
- **Single-Cell Proteomics:** Single-cell proteomics experiments. Includes columns for cell isolation method, carrier proteome, and single-cell identifiers.
- **Immunopeptidomics:** MHC peptide immunopeptidomics. Includes columns for MHC class, HLA typing, and enrichment methods.
- **Crosslinking MS:** Cross-linking mass spectrometry experiments. Includes columns for crosslinking reagents and enrichment methods.

- **Metaproteomics:** Environmental and microbiome proteomics. Includes columns for environmental sample type and geographic location.
- **Affinity Proteomics:** Affinity-based proteomics (Olink, SomaScan). Includes columns specific to these platforms.

The template files can be downloaded from the [templates](#) folder.

9.8. Extending a Template

Templates define the minimum required and recommended columns for a given experiment type. However, SDRF-Proteomics is designed to be **extensible**:

1. **Add experiment-type templates:** If your experiment type has a specialized template (DDA, DIA, cell-lines, etc.), add it to your base configuration. See [Experiment-Type Templates](#) above.
2. **Add custom columns:** You can add any additional columns to capture study-specific metadata beyond what templates define. This section provides guidance on adding custom columns.

9.8.1. When to Add Custom Columns

Add custom columns when your experiment requires metadata that is:

- Not covered by existing templates but important for data interpretation
- Specific to your experimental design or technology
- Required for cross-study integration or data reuse
- Needed to comply with domain-specific standards (e.g., clinical trials, environmental studies)

9.8.2. Rules for Custom Columns

1. Use appropriate column prefixes:

- `characteristics[...]` - For sample-related metadata (properties of the biological material)
- `comment[...]` - For technical or protocol-related metadata (data acquisition, processing)
- `factor value[...]` - For experimental variables (see [Section 9.9](#))

2. Follow naming conventions:

- Use lowercase for column names inside brackets
- Column names (text inside brackets) MUST be valid ontology terms - free text is not allowed
- Use specific ontology terms (e.g., `characteristics[tumor grading]` from NCIT, not `characteristics[grade]`)
- Search the [EBI Ontology Lookup Service \(OLS\)](#) to find appropriate ontology terms for your column names

3. Use controlled vocabularies for cell values:

- Reference existing ontologies (EFO, MONDO, UBERON, etc.) for cell values when available

- For cell values, ontology terms are recommended but free text is allowed when the exact term exists in EFO
- For new terms, follow the key=value format if ontology reference is needed

9.8.3. Common Additional Columns

Beyond template requirements, many commonly used columns can enhance your SDRF file. For a comprehensive list of additional columns for sample metadata (treatment, time point, dose, BMI, smoking status, etc.) and data metadata (sample preparation, enrichment method, etc.), see:

- [Common Additional Columns](#) in the Sample Metadata Guidelines
- [SDRF Terms Reference](#) for a comprehensive list of commonly used terms

9.8.4. Example: Adding Study-Specific Columns

For a drug treatment time-course study, you might add columns beyond the template requirements:

source name	characteristics[organism]	characteristics[disease]	characteristics[treatment]	characteristics[time point]	characteristics[dose]	...	factor value[treatment]	factor value[time point]
sample_c trl_0h	homo sapiens	normal	vehicle control	0h	not applicable	...	vehicle control	0h
sample_d rug_24h	homo sapiens	normal	dexamethasone	24h	100 nM	...	dexamethasone	24h

TIP

When adding custom columns, you MUST use valid ontology terms for column names. Check the [SDRF Terms Reference](#) and [EBI Ontology Lookup Service \(OLS\)](#) to find existing ontology terms that match your metadata needs. Free text column names are not allowed - each column name must be backed by an ontology term.

9.9. Contributing New Templates

To contribute to template development or propose a new template:

1. Open an [issue on GitHub](#) describing the experiment type
2. Discuss requirements with the community
3. Submit a pull request following the established template structure

Chapter 10. Factor Values (Study Variables)

Factor values identify the experimental variables being studied - the conditions you want to compare in your analysis. They highlight which sample characteristics are the focus of your experiment.

10.1. Column Format

```
factor value[{variable name}]
```

10.2. When to Use Factor Values

Use factor values to indicate:

- The primary variable(s) under investigation
- Conditions being compared (e.g., disease vs. normal, treated vs. untreated)
- Variables that define experimental groups

NOTE

Use `normal` (not "control") in the disease field for healthy samples. "Control" is an experimental design concept, not a disease state. See [Disease Annotation Guidelines](#) for details.

10.3. Rules

- Factor value columns SHOULD appear after all characteristics and comment columns
- Multiple factor values can be used when studying multiple variables
- The value in a factor value column typically mirrors a characteristics column value

10.4. Example

In an experiment comparing tumor vs. normal tissue across different cancer stages:

source name	...	characteristics[disease]	characteristics[disease staging]	...	factor value[disease]	factor value[disease staging]
tumor_sample_1	...	breast carcinoma	stage II	...	breast carcinoma	stage II
normal_sample_1	...	normal	not applicable	...	normal	not applicable
tumor_sample_2	...	breast carcinoma	stage III	...	breast carcinoma	stage III

In this example, both `disease` and `disease staging` are factor values because the experiment aims to compare expression differences between disease states and across cancer stages.

Chapter 11. Ontologies and Controlled Vocabularies

SDRF-Proteomics uses ontologies and controlled vocabularies (CVs) to standardize metadata values. The following ontologies are supported:

Category	Ontology/CV	Description	Notes
General Purpose			
General	Experimental Factor Ontology (EFO)	General experimental metadata	
General	PATO	Phenotype and Trait Ontology	
General	NCI Thesaurus (NCIT)	Biomedical terminology	
General	PRIDE Controlled Vocabulary	Proteomics-specific terms	
Organism and Taxonomy			
Taxonomy	NCBI Taxonomy (NCBITaxon)	Organism classification	
Anatomy and Cell Types			
Anatomy	UBERON	Cross-species anatomy ontology	
Cell Type	Cell Ontology (CL)	Cell type classification	
Anatomy	BRENDA Tissue Ontology (BTO)	Tissues and cell lines	
Anatomy	Plant Ontology (PO)	Plant anatomy and development	For plant samples
Anatomy	FlyBase Anatomy (FBbt)	Drosophila anatomy	For Drosophila samples
Anatomy	WormBase Anatomy (WBbt)	C. elegans anatomy	For C. elegans samples
Anatomy	Zebrafish Anatomy (ZFA)	Zebrafish anatomy and development	For zebrafish samples
Disease (see Disease Annotation Guidelines)			
Disease	Mondo Disease Ontology (MONDO)	Unified disease ontology	RECOMMENDED
Disease	Experimental Factor Ontology (EFO)	Disease terms from EFO	
Healthy samples	Phenotype And Trait Ontology (PATO)	Use normal (PATO:0000461) for healthy samples	
Cell Lines			
Cell Lines	Cellosaurus	Cell line knowledge resource	RECOMMENDED

Category	Ontology/CV	Description	Notes
Cell Lines	Cell Line Ontology (CLO)	Cell line ontology	
Mass Spectrometry and Proteomics			
MS/Proteomics	PSI Mass Spectrometry CV (PSI-MS)	Instruments, methods, parameters	
Modifications	Unimod	Protein modifications database	
Modifications	PSI-MOD CV	Protein modifications ontology	
Other			
Chemistry	ChEBI	Chemical Entities of Biological Interest	
Environment	Environment Ontology (ENVO)	Environmental sample classification	For metaproteomics
Ancestry	Human Ancestry Ontology (HANCESTRO)	Human ancestry categories	For human samples

Chapter 12. Examples of Annotated Datasets

The following table provides links to example SDRF files for different experiment types. Click "View in Explorer" to open the SDRF file in the interactive viewer.

Experiment Type	Dataset	Description	View	Source
Label-free	PXD008934	Human proteome label-free quantification	View in Explorer	GitHub
TMT	PXD017710	TMT-labeled quantitative proteomics	View in Explorer	GitHub
SILAC	PXD000612	SILAC-based quantification	View in Explorer	GitHub
DIA	PXD018830	Data-independent acquisition	View in Explorer	GitHub
Phosphoproteomics	PXD000759	PTM enrichment study	View in Explorer	GitHub
Cell lines	PXD001819	Cell line proteomics	View in Explorer	GitHub

TIP

Use the [SDRF Explorer](#) to browse all {total_datasets}+ annotated datasets with filtering, statistics, and interactive viewing.

A comprehensive collection of annotated projects is available at: [Annotated Projects Repository](#)

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