

SF-RAD Metadata Specifications for:

Extraction

Importance 1: Required, 0: Optional

SF-RAD Field Name	Definition	Importance
extraction_run_id	Unique identifier for the extraction run	0
approach	Defines manual or automated extraction	0
machine_model	Maker and model of extraction instrument	0
machine_serial_number	Serial number of instrument	0
software_name	Instrument software name	0
software_version	Version of software	0
machine_protocol_name	Name of the run protocol for the instrument run	0
manual_protocol_name	Protocol name for manual runs	0
chemical_principle	Type of extraction performed - e.g. phenol chloroform	0
format	plate format or tube format	0
commercially_performed	commercial kit or in-house approach, e.g. kit or phenol/chloro	0
commercial_kit	Consumables kit name	0
assay_date	Date performed	0
user	User name running extraction	0
manifest_file_name	File (.csv or .tsv) name containing sample manifest	0
sop_name	SOP name	0
output_sample_type	class of sample extracted, RNA, total NA etc.	0
concentrate_id	identifier of the concentrate utilized for nucleic acid extraction with the appropriate zz annotation (start)(OGSR = (-17), CFAR = (-18), WCM = (-40))	0
extractant_id	identifier of the nucleic acid resulting from extraction with the appropriate zz annotation (finish) (OGSR = (-32), CFAR = (-21), WCM = (-41))	0
plate_id	individual plate identifier - relates to RNA extraction id but not the same	0
well_position_row	Position of the sample on the plate, row	0
well_position_column	Position of the sample on the plate, column	0
separation_on_magnet_time	Amount of time the concentrate was incubated on a magnet to separate beads from solution	0
sample_class	expt or standard or neg etc	0
input_amount_ul	amount of concentrate starting material (uL)	1
elution_volume_1	First / only elution volume (uL) (elution information now in SharkeySummaryTable file)	1
elution_buffer	Vehicle sample is in	0
spikein_1_type	type/name of spike utilized in extractant	0
spikein_1_conc_cp_ul	concentration (cp/uL) of spike used in extractant	0
spikein_1_amount_ul	amount of spike used in extractant (uL)	0
spikein_2_type	type/name of second spike utilized in extractant	0
spikein_2_conc_cp_ul	concentration (cp/uL) of second spike used in extractant	0
spikein_2_amount_ul	amount of second spike used in extractant (uL)	0
elution_concentration	NA concentration ng/uL on platform A	0
quantification_platform	Platform used for quantification of elution A	0
pre_ext_storage_time	The approximate average duration of time between when samples are concentrated (if concentrated) and when they are extracted	0
pre_ext_storage_temp	The storage temperature of samples after concentration (if concentrated) and prior to extraction	0