

SF-RAD Metadata Specifications for:

RNA-seq Results

Importance 1: Required, 0: Optional

SF-RAD Field Name	Definition	Importance
sample_id	Code for sample identification	1
maquant_yn	Was the sample quantified	1
maquant_assay_kit	Assay kit used for RNA quantitation	1
maquant_date_of_quant	Date of quantitation	0
maquant_sample_ul	Volume of sample used for quantitation, uL	0
maquant_dilution_concentration	Concentration of the sample in the assay tube, QF value in ng/mL	1
maquant_concentration	Concentration of the sample in ng/mL	1
ma_libprep_user	Name of the technician performing the library prep	0
ma_libprep_industry	Facility performing the RNA NGS Library Prep	0
ma_libprep_date_of_prep	Date of library prep	0
ma_libprep_rRNA_depletion	Ribosomal RNA depletion performed on sample	0
ma_libprep_rRNA_depletion_kit	Ribosomal RNA depletion kit	0
ma_libprep_kit	Name of the RNA NGS Library Prep kit used	1
ma_libprep_protocol_version	RNA Library prep protocol version - derived from protocols.io	0
ma_libprep_primer_version	ARTIC specific primer version	0
ma_libprep_index_1	Index kit used during protocol	0
ma_libprep_index_2	Index kit used during protocol	0
ma_libprep_input_volume	Input/Starting RNA volume, uL	1
ma_libprep_elution_volume	Elution volume, uL	1
ma_seq_industry	Facility performing the RNA NGS Library Prep	0
ma_seq_machine_model	Instrument used for NGS	0
ma_seq_machine_serial_number	Serial number of the NGS device	0
ma_seq_runid	Run ID for sequencing run	1
ma_seq_date	Date of sequencing	0
ma_seq_user	Name of the technician performing the library prep	0
ma_seq_protocol	Protocol used for the run	1
ma_seq_flowcell	Flowcell name/identifier	0
ma_seq_lane	Flowcell lane	0
ma_seq_yield_mbases	Yield, total number of bases sequenced per sequencing run or per lane	1
ma_seq_raw_reads	Raw reads	1
ma_seq_pf_reads	PF reads	0