

# Updates to MISO, the open-source NGS LIMS project

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## Abstract

MISO ("Managing Information for Sequencing Operations") is a freely available open-source LIMS for recording next-generation sequencing (NGS) metadata for sequencing centres. Based on the common objects (projects, samples, libraries, pools and runs etc.) from the European Bioinformatics Institute (EBI) Sequence Read Archive schemas, MISO stores relevant metadata for typical lab workflows and automatically tracks run information from common NGS platforms (e.g. Illumina GA, HiSeq and MiSeq, Roche 454, ABI SOLiD and PacBio RS). MISO can also initiate HPC job submission for initial analysis and QC of sequencing data, and automatically generates public repository data submission schemas. Because MISO is modular, and it is designed to be extensible and customisable, MISO can be used by both large centres characterised by high-throughput data production and smaller scale laboratories with constrained expenditure for IT solutions.

We present the recent highlighted updates of MISO: Plate support (e.g. 96-well and 384-well), new visualisations in reporting, entity groups (i.e. grouping of objects for easier project management, such as sample groups), more flexible barcode printing, sequencing run QC analysis reporting and visualisation, support for traditional Excel/ODF/CSV input and output for bulk data import and export, continued support of new NGS platforms, and a new workflow system for customised lab processes.