

Configure ChIP-Seq Analysis Data

UGENE integrates the [Cistrome workflow](#) for analysis of ChIP-Seq data. The workflow requires reference data to be present in the UGENE data folder. Reference data for human are provided in the [NGS package](#) and in the Online Installer. To configure them manually download the data from the "[Download UGENE and components](#)" page and unpack to the "cistrome" folder inside the UGENE data folder.

Note that RScript [external tool](#) should also be provided.