

StratoMineR™

StratoMineR™ from [Core Life Analytics](#) helps scientists to independently analyze their high-content datasets. It guides users through a best-practice workflow, allowing them to easily explore their complex data and mine it for biological insight.

How it works

Export a text file with compound data from CDD Vault, and merge this with your high-content data in StratoMineR™ using the “Merge Metadata” function. Include the appropriate compound identifiers to ensure your results can easily be uploaded back into CDD Vault.

Run your data through the StratoMineR™ workflow, which allows you to preprocess your high-content data, perform data reduction, and identify hits based on phenotypic distance scores.

These phenotypic distance scores - a measure of how different the phenotype caused by a specific compound is from the negative control - can then be imported back into CDD Vault and added to the appropriate compounds using the compound identifier.

