createMSDB

→ input

INPUT/sample list.csv

output →

OUTPUT/{project_name,test_data}/tmp/MSDB.RData

scoringAndFiltering

→ input

INPUT/sample_list.csv

OUTPUT/{project_name}/tmp/MSDB.RData

output →

OUTPUT/{project_name,test_data}/tmp/allPSMs.RData
OUTPUT/{project_name,test_data}/tmp/allPSMs_Delta.RData

removeSynErrors

→ input

OUTPUT/{project_name}/tmp/allPSMs.RData

output →

OUTPUT/{project_name,test_data}/tmp/extractedPSMs.RData

mapping

→ input

OUTPUT/{project_name}/tmp/allPSMs_Delta.RData

OUTPUT/{project_name}/tmp/extractedPSMs.RData

output →

OUTPUT/{project_name,test_data}/ProteasomeDB.csv
OUTPUT/{project_name,test_data}/tmp/DeltaPeptides.csv

output_statistics

input

OUTPUT/{project_name}/ProteasomeDB.csv

output →

OUTPUT/{project_name,test_data}/DB_stats.pdf
OUTPUT/{project_name,test_data}/length_distributions.pdf
OUTPUT/{project_name,test_data}/number_of_products.pdf

all

→ input

OUTPUT/test_data/DB_stats.pdf

OUTPUT/test_data/ProteasomeDB.csv