

# Portable Proteomics Pipeline (P3)

## Use Case: PrideID

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### Pride ID

This is a use case/manual for a P3 pipeline with files retrieved from Pride database.

1. Make sure Docker engine is installed and running.

```
docker ps
```

2. Download a sample p3.config and MSGFDB\_Mods.txt file and put it to a directory. e.g.

```
cd ~/Desktop/PXD001468
ls
```

If other PrideID is desired, change the PRIDEID option on the p3.config. Ensure that the corresponding PrideID have the required files (\*.fasta, \*.mzml, etc.).

3. Download / update p3 from Dockerhub, and run the image.

```
docker pull kristiyanto/p3
docker run --rm -v ~/Desktop:/root/data kristiyanto/p3
```

if necessary, another image can be run simultaneously (in a different terminal windows).

4. Once processes completed, the directory will be populated with:

- Mass Spectrometry files downloaded from Pride repository (\*.mzid, \*.mzml)
- Peptide Sequence file (\*.fasta)
- MSGF+ output files (\*.mzid, \*.canon, \*.revCat.cnlcp, \*.revCat.csarr, \*.revCat.cseq)
- Output table (\*.txt)
- Output file as R objects (\*.rda)