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
```

in this case, `p3.config` must have the following fields:

```
REPO = PRIDE
PRIDEID = (e.g: PXD001468)
RUN_MSGF = (e.g: YES)
METHOD = (e.g: SPECTRUM_COUNT)
```

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