

PeptideShakerCLI reports generation

This document describes generation of reports output using PeptideShakerCLI.

Required software

1. Download PeptideShaker from <http://compomics.github.io/projects/peptide-shaker.html> if not already done.

Protocol

1. Navigate to the directory where you have stored your .cpsx files generated by PeptideShakerCLI.
2. Generate the reports. The -Xmx command here specifies the amount of available RAM. Alter based on your system.

```
for i in *.cpsx; do java -Xmx400g -cp /projects/ptx_analysis/chughes/software/software_searchGUI/PeptideShaker-1.16.11/PeptideShaker-1.16.11.jar eu.isas.peptideshaker.cmd.ReportCLI -in /projects/ptx_analysis/chughes/projects-current/test-project/results-output/$i -out_reports /projects/ptx_analysis/chughes/projects-current/test-project/reports-output/ -reports 0,3,5,7; done
```

3. This command will generate the certificate of analysis, default peptide spectral match, default peptide, and default protein text outputs. If you desire other outputs, specify in the -reports command.
4. If the reports command throws an error before generating any reports, re-run peptideshaker for the file where it throws the error and retry making the report.