PeptideShakerCLI mzid generation

This document describes generation of mzid 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 mzid files. 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/sof
tware_searchGUI/PeptideShaker-1.16.11/PeptideShaker-1.16.11.jar eu.isas.peptidesh
aker.cmd.MzidCLI -in /projects/ptx_analysis/chughes/projects-current/test-project
/results-output/$i -output_file /projects/ptx_analysis/chughes/projects-current/t
est-project/mzid-output/$i.mzid -contact_first_name Christopher -contact_last_nam
e Hughes -contact_email "chughes@bcgsc.ca" -contact_address "Vancouver, BC, Canad
a" -organization_name "BC Cancer" -organization_email "chughes@bcgsc.ca" -organiz
ation_address "Vancouver, BC, Canada"; done
```