pWALTZ use instructions

1-The pWALTZ executable file (pwaltz2.7) can be freely used for academic purposes. Incorporation into commercial products is restricted.

2- The pWALTZ executable runs on Linux.

3- Typical pWALTZ usage:

pwaltz2.7 fasta_file

where fasta_file is a .txt file containing the protein sequences in fasta-format (run the test.txt file as example)

The output includes the name of positive sequences, their 21 residues amyloid-cores and their associated scores. Negative sequences are not shown (see the output test.txt as an example)

4- pWALTZ is aimed for the detection and discrimination of prion forming domains (PFDs) in intrinsically disordered Q/N-rich regions. Therefore, it is recommended that you check whether your sequences are enriched in those polar residues and predicted as disordered (i. e. using Foldindex at bip.weizmann.ac.il/fldbin/findex), before pWALTZ analysis.

5- If you use pWALTZ please cite: Sabate R., Rousseau F., Schymkowitz J. and Ventura S. *PLoS Comp. Biol.* (2014).