Usage.

./FuzDrop protein_name.fasta protein_name.espritz

FuzDrop is available for both MacOSX and Linux.

Requirements.
1/ Sequence in fasta format.
- header is required
- only standard amino acids, no posttranslational modifications or gaps.

2/ Espritz disorder prediction file.
- extension .espritz
- same name as the .fasta (protein_name.fasta)

Note. Espritz is a standalone program, which can be downloaded from
https://protein.bio.unipd.it/downloads, specifying the program "Espritz".

Please run Espritz for the set of sequences before running FuzDrop. You need Espritz NMR
version, the fasta file must be present in the examples_fastas folder, where your espritz
program is.

Usage: perl espritz.pl your_protein.fasta N 1

FuzDrop Output.
The output file is automatically generated with extension _res.txt

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Example
Pos     Res     pDD     MBM     pDP
1       M       0.6387  0.4127  0.7877
2       S       0.6438  0.5903  0.7838
3       E       0.6387  0.6088  0.8029
4       Y       0.6438  0.6594  0.7731
5       I       0.6814  0.6539  0.7721
.
.
.
Liquid-liquid phase separation propensity p(LLPS) =     0.8981

Columns:
Pos: residue number in sequence
Res: amino acid type
pDD: propensity of disordered binding (from FuzPred)
MBM: multiplicity of binding modes
pDP: Droplet-promoting propensity per residue


Last line:
p(LLPS): probability of spontaneous liquid-liquid phase separation of the
protein
```