CSpritz - Accurate detection of protein disorder

Version 1.2

Title: PF3D7_0827400.fasta
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Status: finished

NB: *The data will be kept for* **two weeks**, *after which it will be* **deleted** *without further notice.*

Available files: (help)

Your input parameters:	HTML
Fasta sequences (amino, secondary structure, disorder, confidence):	TXT
Disorder plot:	PDF
Graph of PDB homologue(s) found::	PDF
Disorder Prediction (with disorder probability):	TXT
Protein statistics :	TXT

Disordered residues and stats: (help)

```
1        10        20        30        40        50        60
MRKESFLFFICTLNLLINSFFCYGGKVKKNKHLRNLLKTLTDRIETNDGENEYARLTQTPVINMNLEKTI
CCCHHHHHHHHHHHHHHHHHHCCCCCCCHHHHHHHHHHHHHHHHCCCCCCCHHHHHCCCCEEECCCCCEE
DDDDOOOOOOOOOOOOOOOOOOOODOOOOOOOOOOOOOOOOOOODDDDDOOOOOOOOOOOOOOOOOOOOO

71       80        90        100       110       120       130
FKTSLQDILVEPYAEKIKEIISKNNYEISKEKENLDEIRYYNDNLDKINNILIERENEKKKKKRKNIQLE
ECCCHHHHHHCCHHHHHHHHHHHHCCHHHHHHHHHHHHHHHCCCHHHHHHHHHHHHHHHHCCCCCCCCCCH
OOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOODOOOOOOOOOOOOOOOOOOOOOODDDDDDDDDDDDDDDOOO

141      150       160       170       180       190       200
NKLRNKYFHYLQDQDYGFSIFPVYKTFESNPLHFDNNIISSLLPHELLDKGILLNKQILENSEKILHYPE
HHHHHHHHHHCCCCCCCEEECEEEECCCCCCCCCCCHHHCCCHHHHHHCCCCCCCHHHCCCCCCEECCC
OOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOODDDOOOODDDDDD

211
RGDTLYEI
CCCCEECC
DDDDDDDD
```

Total amino acids:	218
Total % disorder:	18.34
Total no. of disordered regions > 30 amino acids:	0
Total no. of disordered regions > 50 amino acids:	0
Number of disordered segments:	7
Length distribution of segments (N to C terminal order):	4 1 5 1 12 3 14

Disordered segment motifs: (help)
2 ELM motif(s) in total found in disordered residues

SS Motif for disorder segment 1:
(start,end): (1,4)

Graph of Probability(helix, strand, coil)	PDF
Amino SS Probability(helix, strand, coil)	TXT

```
seq  : MRKE
S.S. : CCCH
alpha: 0135
beta : 0000
coil : 9854
```

Linear motif(s):

SS Motif for disorder segment 2:
(start,end): (46,50)

Graph of Probability(helix, strand, coil)	PDF
Amino SS Probability(helix, strand, coil)	TXT

```
seq  : TNDGE
S.S. : CCCCC
alpha: 11112
beta : 00000
coil : 78886
```

Linear motif(s):

SS Motif for disorder segment 3:
(start,end): (126,137)

Graph of Probability(helix, strand, coil)	PDF
Amino SS Probability(helix, strand, coil)	TXT

```
        126       135
seq  : ENEKKKKKRKNI
S.S. : HHHHHCCCCCCC
alpha: 877653222212
beta : 000000000000
coil : 111246666776
```

Linear motif(s):

SS Motif for disorder segment 4:
(start,end): (198,200)

Graph of Probability(helix, strand, coil)	PDF
Amino SS Probability(helix, strand, coil)	TXT

```
seq  : ILE
S.S. : HHC
alpha: 432
beta : 122
coil : 334
```

Linear motif(s):

SS Motif for disorder segment 5:
(start,end): (205,218)

Graph of Probability(helix, strand, coil)   PDF
Amino SS Probability(helix, strand, coil)   TXT

```
        205       214
seq  : ILHYPERGDTLYEI
S.S. : CEECCCCCCCEECC
alpha: 10000000011100
beta : 35431100035530
coil : 44468889853359
```

Linear motif(s):

residues (211,213)   **LIG_RGD = RGD**
residues (212,215)   **LIG_PDZ_3 = GDTL**

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