CSpritz - Accurate detection of protein disorder

Version 1.2

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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
MKILNLILLSIIFLKYYHVCCISTREILRDKRNEFQRYCEFIINEKNLVDNNEKIVNNSIRTYKYYMEKG
CCHHHHHHHHHHHCCCCEEEEECHHHHHHHHHHHHHHHHHHHCCCCCCCCCCCHHCCCCCHHHHHHHHCC
OOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOODOOOODOOOOOOOOOOOOOOOOOOOO

71        80        90        100       110       120       130
IKEIVAIFIFDDLNITKARELGILNKADHELNISNIPKNIQNIYPLDEINSFSDLIYKERKLFSFETEYS
CCEEEEEEEEECCCCCCHHHHCCCCCHHCCCCCHCCCCCHHCCCCCCCHHHCHHHHHHHHHHHHHCECCCCC
OOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOO

141       150       160       170       180       190       200
VTNYVFTKFVFHVKITEENDEEIMFLMINNELNMKQKNLEIIKKTDEYNGNNNMPSVNSNSVNLYQKHPQ
CCEEEEEEEEEEEEEEECCCHHHHHHHHHHHHHHCCCCCCEEEECCCCCCCCCCCCCCCCCCCCCHHCCCHH
OOOOODDDDDDDOOOODDDDOOOOOOOOOOOOOODDOOOODOOOOOODDDDDDDDDDOOOOOOOOOOOOO

211       220       230       240       250       260       270
AFVQFIGAIIGIATLVSSISGAVSGISSIFSSRPAPTPPEFLGDEKSKLSKYETGKKEVEKKDKKKKYYQ
HHHHHHHHHHHHHHHHHHHHHHHHEECCCCCCCCCCCCCCCCCHCCCCCCCCCCCCCCCCCCCCCCCCCCCC
OOOOOOOOOOOOOOOOOOOOOOOOOOODDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD

281       290       300       310
EEDDVYDYDEYYDDEYYDDKYYDDEYYDDEYYDDY
CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD
```

Total amino acids:	315
Total % disorder:	32.69
Total no. of disordered regions > 30 amino acids:	1
Total no. of disordered regions > 50 amino acids:	1
Number of disordered segments:	8
Length distribution of segments (N to C terminal order):	1 1 7 4 2 1 10 77

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

SS Motif for disorder segment 1:
(start,end): (146,152)

```
seq  : FTKFVFH
S.S. : EEEEEEE
alpha: 1111000
beta : 7777887
coil : 0011112
```

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

Linear motif(s):

SS Motif for disorder segment 2:
(start,end): (157,160)

```
seq  : EEND
S.S. : CCCH
alpha: 0006
beta : 3100
coil : 6893
```

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

Linear motif(s):

SS Motif for disorder segment 3:
(start,end): (188,197)

```
seq  : YNGNNNMPSV
S.S. : CCCCCCCCCC
alpha: 2111110112
beta : 0000000011
coil : 6788788776
```

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

Linear motif(s):

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

SS Motif for disorder segment 4:
(start,end): (239,315)

```
        239     248     258     268     278     288     298
seq  : IFSSRPAPTPPEFLGDEKSKLSKYETGKKEVEKKDKKKKYYQEEDDVYDYDEYYDDEYYDDKYYDDEYYD
S.S. : CCCCCCCCCCCHCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
alpha: 3210000000344211222100111100011111111111222222222233332223322222223322
beta : 2210000000001100000100232100122110000011111000110000110000000000000000
coil : 4578999999644677666788545688766677888776666666666665566665677766776567

seq  : DEYYDDY
S.S. : CCCCCCC
alpha: 2332100
beta : 0000000
coil : 6656799
```

Linear motif(s):

residues (243,249)   **LIG_SH3_3 = RPAPTPP**

residues (244,249)   **LIG_WW_4 = PAPTPP**

residues (245,251)   **LIG_FHA_2 = APTPPEF**

residues (249,252)   **LIG_PDZ_3 = PEFL**

residues (282,285)   **LIG_PDZ_3 = EDDV**

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