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
MKLSLVIFCIVIIFFKENISVKIKTNDTAIFDINKVLQKKLAVLYRKGNKLNNYFFSYIEKNGKNNKCYR
CCCEEEEEEHHHHHHCCCCCEEEECCCCEEEHHHHHHHHHHHHHHHHCCHHHHHHHHHHCCCCCCCHHH
DOOOOODDDDDDDDDDDDDDDDDDDOOOOOOOODDDDDDDDDDDDOOOOOOOOOODDDDDDDDOOOO

71        80        90        100       110       120       130
YIQEALYDPNIQIMKNEVMKSFNYSKDILKKTFHDIINKLFLYIKNVFLKKYFVFFLLYLINFNCDTLAS
HHHHHCCCCHHHHHHHHHHHHCHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHCCCCCCHHHHHC
OOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOO

141       150       160       170       180       190       200
QMNDPYILNNYNLELNASPSMYNLKYEEIGIPISNSTVKGWLIKPTKKSNKLFLLLHGYNSNRQACLFFL
CCCCHHHHCCCCCCCCCCCCHCCCCEEEEEECCCCCCCCEEEEECCCCCCEEEEEECCCCCCHHHHHHHH
OOOOOOOOOOOOODOOOOOOOOOOOOOOOOOOOOODOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOO

211       220       230       240       250       260       270
NILKNLNIHNDTTIFIPDMKNFNERGVDDIYNILSYFKDNMGLNEVNIYTQSSTNLLVLLLSKHYKNKIA
HHHHHCCCCCCCCEEECCCHCCCCCCHHHHHHHHHHHHHCCCCCEEEEEECCHHHHHHHHHHHHCCCC
OOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOO

281       290       300       310       320       330       340
NKSKEKFIKTIIPYSTDKNKNKNTENIIYIDKYIFDSPIFNLHKTINMHFNLSDIDKKLNEERMKNKQEI
CCCCCCCCCCCCCCCCCCCCCCCCCCEEEEEEEECCCCHHHHHHHHHCCCCCHHHHHHHHHHHHCCC
DDDDDDOOOOOOODDDDDDDDDOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOODDDDDDDDDDDDD

351       360       370       380       390       400       410
NLHDKKSIMNYFLSFCMWLLNNQLKGHLYDYDFNKIITENDINTSNIYILHPLNDNISLLNILSQEVKEN
CCCCHHHHHHHHHHHHHHHHHCCCCCCHCHHHHHHHCCCCCCCCEEEEECCCCCCHHHHHHHHHHC
DOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOODOO

421       430       440       450       460       470
RRFPLKNIYIFKNGKHANIYGSAKREYSLIVKRILKGFNILDFLYYIPLRSRFSSLPF
CCCCCCCEEEEECCCCCCCCCCHHHHHHHHHHHHCCCHHHHHHCCCCCCCCCCCC
OOOOOOOOOOOOOOODDDOOOOOOOOOOOOOOOOOOOOOOOOOODDDDDDDDDD
```

Total amino acids:	478
Total % disorder:	18.41
Total no. of disordered regions > 30 amino acids:	0
Total no. of disordered regions > 50 amino acids:	0
Number of disordered segments:	12
Length distribution of segments (N to C terminal order):	1 21 13 8 1 1 6 9 14 1 3 10

Disordered segment motifs: (help)

4 ELM motif(s) in total found in disordered residues

SS Motif for disorder segment 1:
(start,end): (7,27)

```
        7         16        26
seq  : IFCIVIIFFKENISVKIKTND
S.S. : EEEHHHHHHCCCCCEEEECCC
alpha: 334455443332100000000
beta : 554444432211235776300
coil : 001000113445663213698
```

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

Linear motif(s):

residues (15,19) LIG_APCC_KENbox_2 = FKENI
residues (16,19) LIG_PDZ_3 = KENI

SS Motif for disorder segment 2:
(start,end): (36,48)

```
        36        45
seq  : VLQKKLAVLYRKG
S.S. : HHHHHHHHHHHC
alpha: 9999999998743
beta : 0000000000000
coil : 0000000001246
```

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

Linear motif(s):

residues (39,43) LIG_CYCLIN_1 = KKLAV

SS Motif for disorder segment 3:
(start,end): (59,66)

```
seq  : IEKNGKNN
S.S. : HHCCCCCC
alpha: 65310011
beta : 11100000
coil : 12479888
```

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

Linear motif(s):

SS Motif for disorder segment 4:
(start,end): (281,286)

```
seq  : NKSKEK
S.S. : CCCCCC
alpha: 111233
beta : 101100
coil : 777655
```

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

Linear motif(s):

SS Motif for disorder segment 5:
(start,end): (294,302)

```
seq  : YSTDKNKNK
S.S. : CCCCCCCCC
alpha: 000022212
beta : 210000001
coil : 678876676
```

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

Linear motif(s):

SS Motif for disorder segment 6:
(start,end): (338,351)

```
        338      347
seq  : KLNEERMKNKQEIN
S.S. : HHHHHHHHHHCCCC
alpha: 76578876554333
beta : 00000000000000
coil : 12321122345666
```

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

Linear motif(s):

SS Motif for disorder segment 7:
(start,end): (437,439)

```
seq  : ANI
S.S. : CCC
alpha: 011
beta : 433
coil : 444
```

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

Linear motif(s):

SS Motif for disorder segment 8:
(start,end): (469,478)

```
seq  : LRSRFSSLPF
S.S. : CCCCCCCCCC
alpha: 3333221000
beta : 0000000000
coil : 6556677899
```

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

Linear motif(s):

residues (472,477) LIG_14-3-3_1 = RFSSLP

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