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
MRKNIILVAYICFIYMRAKCEALKINNILNKSYFAIISNYNNNNNNNIKHINHINGQGKHINKSSHNKGG
CCCHHHHHHHHHHHHHHHHHHHHHHHHCCCHHHHHCCCCCCCCCCCHHHHCCCCCCCCCCCCCCCCCCCCC
OOOOOOOOOOOOOOOOOOOOODOOODOOOOOOOOOOOOODDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD
```
```
71        80        90        100       110       120       130
ILNNEVLKKPGKENKKLKENVPKDIKEHVSEISKENKFLHFENNKKISINPLFQSLCKKVSVSETCLYNI
CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCHEEHCCCCEEECCHHHHHHHHCCCCHHHHHHHH
DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDOOOOOOOOOOOOOOOOOOOOOOOODDOOOOOOOOOO
```
```
141       150       160       170       180       190       200
QKFYSEVNYMNLKNKNPKDNKYFCGVLYGKYERDEFVKVEHVFFSMNKTEQGYDEKYLLHSEDRKRADQL
HHHHHHHHHHCCCCCCCCCCCEEEEEEEEEEECCCCEEEEEEEEEECCCCCCCCCCHHHHCCCCHHHHHHH
OOOOOOOOOOOOODDOOOOOOOOOOOOOOOOOOOOOOODOOOOOOOOOOOOOOOOOOOODDDDDDDD
```
```
211       220       230       240       250       260       270
AKMLNLEVVGFLYAYPDIGVDLNMSNKKQKHFIKLNKKMKTLNDEENEIFIPMGGKEVLLSIMLMWQIRR
HHHHHHHHHEECCCCCCCCHHHHHHHHHHHHHHHHHCCCCCCCEEECCCCHHHHHHHHHHHHHHHH
DDDDOOOOOOOOOOOOOOOOOODDDDDDDDDOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOO
```
```
281       290       300       310       320       330       340
QSKIVEEKNGKAYAHMNKNKNNDSHNDDHNDGHNDGHNHNSDDTNFIEENSDQHNNGNIKKKKKNETIKFK
CCCEEECCCCCCHHCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
ODDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD
```
```
351       360       370       380       390       400       410
NVKKKNKTKQGKKNMNIKPFITLSIGMNKNNESIIVEAYEMNYDLLKLIKHDMVKDINKQNSILQFEKND
CCCCCCCCCCCCCCCCCEEEECCCCCCCCCEEEEHHHHHHHHHHHHHHHHHHHHHHCCHHHHHCCC
DDDDDDDDDDDDDDDOOOOODOOOOOOODDDOOOOOOOOOOOOOOOOOOOOOOOOOOOOOODDDDDDDD
```
```
421       430       440       450       460       470       480
KDKEIKIKTFDSEIDIMNELYLKCKNNILIKKIEIKKIDILFCVNNIPIFSHKGNYNYFFPYPTNTNYYY
CCCCEEEECCCHHHHHHHHHHHHHHCCCCEEEEEEEEEEEEEEEECCCCEECCCCCCCEECCCCCCCHHHH
DDDDOOOOOOOOOOOOOOOOOOOOOOOOOODDDDDDDDDOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOO
```
```
491       500       510       520       530       540       550
ILQTFNHMIKALHNKSDIVHIFRDFNFLFFLTNIFSIKHDLPYFCNAVKDVNNSVDIPDHYLHILQNLSN
HHHHHHHHHHHCCCCCHHHHHHHHHHHHHHHHHHCHCCCCCHHHHHHHHCCCCCCCCHHHHHHHHHHH
OOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOODOOOOOOOOOOOOOOOOODDD
```
```
561
NANMLN
CCCCCC
DDDDDD
```

Total amino acids:	566
Total % disorder:	37.27
Total no. of disordered regions > 30 amino acids:	2
Total no. of disordered regions > 50 amino acids:	2
Number of disordered segments:	15
Length distribution of segments (N to C terminal order):	1 1 64 2 2 1 12 9 84 1 3 12 9 1 9

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

SS Motif for disorder segment 1:
(start,end): (40,103)

```
      40        49        59        69        79        89        99
seq  : YNNNNNNNIKHINHINGQGKHINKSSHNKGGILNNEVLKKPGKENKKLKENVPKDIKEHVSEIS
S.S. : CCCCCCCCCHHHHCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCHHHH
alpha: 2222222234454432211122101111100111123210012333344321133444444322
beta : 0000000012111110000122100000001221011000000000000000000100000
coil : 677777764333445677764568877788866776567888656555556876544445566
```

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

Linear motif(s):

residues (40,43)   **LIG_SH2_GRB2 = YNNN**
residues (74,77)   **LIG_PDZ_3 = NEVL**

residues (81,85)	LIG_APCC_KENbox_2 = GKENK
residues (87,91)	LIG_APCC_KENbox_2 = LKENV
residues (88,91)	LIG_PDZ_3 = KENV
residues (96,99)	LIG_PDZ_3 = KEHV

SS Motif for disorder segment 2:
(start,end): (203,214)

```
        203       212
 seq  : DRKRADQLAKML
 S.S. : HHHHHHHHHHHH
 alpha: 588999999997
 beta : 000000000000
 coil : 411000000002
```

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

Linear motif(s):

residues (207,210)   LIG_PDZ_3 = ADQL

SS Motif for disorder segment 3:
(start,end): (234,242)

```
 seq  : MSNKKQKHF
 S.S. : HHHHHHHHH
 alpha: 666666667
 beta : 000000001
 coil : 233223321
```

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): (282,365)

```
        282       291       301       311       321       331       341
 seq  : SKIVEEKNGKAYAHMNKNKNNDSHNDDHNDGHNDGHNHNSDDTNFIEENSDQHNNGNIKKKKNETIKFKN
 S.S. : CCEEECCCCCCHHCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
 alpha: 2111111123443211100111111111111111111122333221123221112122222233333
 beta : 0244420001221110000000000000000000000000001233210000000001111001111111
 coil : 6643468875333467888888888888888888888887888765333577766688766666666555445
        352       361
 seq  : VKKKNKTKQGKKNM
 S.S. : CCCCCCCCCCCCCC
 alpha: 33221111111221
 beta : 11110001011211
 coil : 55567777776567
```

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

Linear motif(s):

residues (322,328)   LIG_FHA_1 = DDTNFIE
residues (340,349)   LIG_MAPK_1 = KKKKNETIKF
residues (344,347)   LIG_PDZ_3 = NETI

SS Motif for disorder segment 5:
(start,end): (379,381)

```
 seq  : KNN
 S.S. : CCC
 alpha: 001
 beta : 000
 coil : 888
```

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): (413,424)

```
        413       422
 seq  : ILQFEKNDKDKE
 S.S. : HHHHHCCCCCCC
 alpha: 444444321111
 beta : 233321000013
 coil : 212234677765
```

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): (452,460)

```
 seq  : KIEIKKIDI
 S.S. : EEEEEEEEE
 alpha: 100000000
 beta : 677766668
 coil : 222122221
```

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): (558,566)

```
 seq  : LSNNANMLN
 S.S. : HHHCCCCCC
 alpha: 655444320
 beta : 000000000
 coil : 344555679
```

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

Linear motif(s):

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