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
MNMNLVLFISLICLFFGCSNKLYALRNVTRKSEPMSDKSFIVNRLISYKEEIDSQIKNFRKYYELPNEMD
CCHHHHHHHHHHHHHHHHHHHHHHHHCCCCCCCCCCCCCCCHHHHHHHHHHHHHHHHHCCCCCCCCCC
DDDDDDOOOOOOOOOOOOOOOOOOOODDDDDDDDDDDDDDDDOOOOOOOOOOOOODDDDDDDDDDDDDDDOOOOO

71       80        90        100       110       120       130
FELKELWDLVNIVSESQESQMKELFKFSHSLEQSKLSLFKMLSEYENRIDQLEYNIMEKKLYDPFIEKFI
HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHECCCCCCCHHCC
OOOOOOOOOOOOOOOODDDDDDDDDDOOOOOOOOOOOOOOOOOOOOODDOOOOOOOOOOOOOODOOOOOOO

141      150       160       170       180       190       200
YPISKYWLKIDFNNLRSYWKYENNKNDFSIIQANNISNINIPATILLLRHHKIINGYINVDIKPLFDDVK
CCCCEEEEEEHHHHHHHHHHHHCCCCCEEEEECCCCCCCCCCCHHHHHHHHCCEECCEEEEEEECCCCCHH
OOOOOOOOOOOOOOOOOOOOOOOODOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOODD

211      220       230       240       250       260       270
NLKQSSSGIIFDFVDYSNYRYIELAFINSDGIISVHQIVNGLGTKIVSKQVEADPNTFTTLTAEFLLNKI
HHHCCCCCEEEEEEECCCCCEEEEEEEECCCEEEEEEEEECCCCCEEEEEEEEECCCCCCEEEEEEECCCE
DDDDOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOODDDOOODDDDOOOOOOOOOOOOOOOO

281      290       300       310       320       330       340
NVFLNYKMIIEINITNQMIDINVGLFSKIGKAEFKNILSGNIDLEKLLSRKFVEFNEENISKVNMVNSYR
EEEEEEEEEEEEEEECCCCCCCEEEEECCCCHHHHHHHCCCCHHHHHHHHCCCCCCEEEEEEEECEE
OOOOOOOOOOOOOOOOOOOOODDDDDOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOO

351      360       370       380       390       400       410
FLNKMNIDNLGVYEIPYNYNKKDYDNFEDNIIDNVYAVPDSDSYYDDENITGWVKTNNINNNEFENNYIL
ECCCCCCCCCEEEEECCCCCCCCCCCHHHCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCEEE
OOOOOOOOOOOOOOOODDDDDOOOOOOOOOOOODDDDDDDOOOOODDDDDDDDDDDDDDDDDDDDOO

421      430       440       450       460       470       480
NKNINLIPSSCTNYNSSKNIFYLTEFIINNSSVHNWKITNEFGIQRIHFNNDYKKSIFKASLVYKHSTCN
CCCCCCCCCCCEEECCCCCEEEEEEEECCCCCCCCEEEEECCCCEEEEECCCCCCEECCEEEEECCCCC
OOOOOOOOOOODDDOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOO

491      500       510       520       530       540       550
SVTISSYIKLEYNSEAGLIFRYENINNMYILIISTNTKEILLKKIINDIPTIIKSKYIHNINTYQRHHLL
CEEEEEEEEEECCCCEEEEEEECCCCCEEEEEEECCCCEEEEEECCCCEEEEEEEEEECCCCCEEEEE
OOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOO

561      570       580       590       600       610       620
INDQGQNGHISIFLNNIKIFSINNEHFYKSSFYGLYVQSGYATFDTFQIEAHKKNFNAININK
EECCCCCCEEEEEEECCEEEEEECCCCCCCCCEEEEEEECCCCCCCHHHHHHHCCCCCCCCCC
OOOOOOOOOOOOOOOOOOOOOOOOOOODDDDDOOOOOOOOOOOOOODDDDDDDDDDDDDDD
```

Total amino acids:	623
Total % disorder:	18.94
Total no. of disordered regions > 30 amino acids:	0
Total no. of disordered regions > 50 amino acids:	0
Number of disordered segments:	17
Length distribution of segments (N to C terminal order):	6 15 13 10 2 1 1 6 3 4 5 5 7 19 3 5 13

Disordered segment motifs: (help)

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

SS Motif for disorder segment 1:
(start,end): (1,6)

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

Linear motif(s):

```
seq   : MNMNLV
S.S.  : CCHHHH
alpha : 016789
beta  : 000000
coil  : 983100
```

SS Motif for disorder segment 2:
(start,end): (25,39)

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

```
         25        34
 seq  : LRNVTRKSEPMSDKS
 S.S. : HHHHCCCCCCCCCCC
 alpha: 887543211111100
 beta : 000000000000000
 coil : 012346778788888
```

Linear motif(s):

SS Motif for disorder segment 3:
(start,end): (53,65)

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

```
        53        62
 seq  : DSQIKNFRKYYEL
 S.S. : HHHHHHHHCCCCC
 alpha: 7777654332110
 beta : 1111122223331
 coil : 0000112344457
```

Linear motif(s):

SS Motif for disorder segment 4:
(start,end): (86,95)

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

```
 seq  : SQESQMKELF
 S.S. : HHHHHHHHHH
 alpha: 6899888888
 beta : 0000000000
 coil : 3100111111
```

Linear motif(s):

residues (92,95)   LIG_CYCLIN_1 = KELF

SS Motif for disorder segment 5:
(start,end): (209,214)

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

```
 seq  : VKNLKQ
 S.S. : HHHHHC
 alpha: 677654
 beta : 000001
 coil : 322234
```

Linear motif(s):

SS Motif for disorder segment 6:
(start,end): (256,258)

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

```
 seq  : IVS
 S.S. : EEE
 alpha: 111
 beta : 665
 coil : 122
```

Linear motif(s):

SS Motif for disorder segment 7:
(start,end): (262,265)

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

```
 seq  : EADP
 S.S. : EECC
 alpha: 0001
 beta : 6520
 coil : 2478
```

Linear motif(s):

SS Motif for disorder segment 8:
(start,end): (303,307)

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

```
 seq  : VGLFS
 S.S. : EEEEE
 alpha: 00000
 beta : 66775
 coil : 32223
```

Linear motif(s):

SS Motif for disorder segment 9:
(start,end): (371,375)

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

```
 seq  : KKDYD
 S.S. : CCCCC
 alpha: 00000
 beta : 01110
 coil : 88778
```

Linear motif(s):

SS Motif for disorder segment 10:
(start,end): (388,394)

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

```
 seq  : VPDSDSY
 S.S. : CCCCCCC
 alpha: 0001111
 beta : 1000012
 coil : 8887765
```

Linear motif(s):

SS Motif for disorder segment 11:
(start,end): (400,418)

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

```
        400        409
seq  : ITGWVKTNNINNNEFENNY
S.S. : CCCCCCCCCCCCCCCCCCE
alpha: 1111110000000122222
beta : 2223321121000000135
coil : 5665567777888876642
```

Linear motif(s):

___

SS Motif for disorder segment 12:
(start,end): (432,434)

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

```
seq  : TNY
S.S. : EEE
alpha: 110
beta : 454
coil : 434
```

Linear motif(s):

___

SS Motif for disorder segment 13:
(start,end): (592,596)

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

```
seq  : FYGLY
S.S. : EEEEE
alpha: 00000
beta : 58999
coil : 41000
```

Linear motif(s):

___

SS Motif for disorder segment 14:
(start,end): (611,623)

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

```
        611        620
seq  : AHKKNFNAININK
S.S. : HHHCCCCCCCCCC
alpha: 6554444432100
beta : 1000001122110
coil : 2344554445689
```

Linear motif(s):

residues (613,621)   **LIG_MAPK_1 = KKNFNAINI**

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