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
MEERKWSYIMVSVIFYLCYFFYFLTYSYEIIFLFQTKIDYIVFCLLFITSLFSIYFCSKGLKYICTFLIT
CCCCCHHHHHHHHHHHHHHHHHHHHHHHHHHCCHHHHHEHHHHHHHHHHHHHHHHHHHHHHHEEEEEE
DDDDDOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOO


71        80        90        100       110       120       130
IISLIEIYEYTNNIPKDLYDEEFLKLFLLVRLFSAVNLVVFLYLHIKNLKNIKDEKLNNDKDSTIQSVAE
EEEHHHHHCCCCCCCCCCCHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHCCCCCCCEEEEEC
OOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOODDDDDDDDDDDDDDDDDDDD


141       150       160       170       180       190       200
PTNTTTENNHNQNNNHNNNNIHNNNHNNNHNNNNIHNNNHNDPCNNHNDPCNNYYKNQDNFLKSNTVTYS
CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDOOODDDDDDDDDDDDD


211       220       230       240       250       260       270
HNNLFKENIPHVHQHTGIITSKTLPQENIYVLKHVSIPIFEKEIINKDTNISHMYEMQTNDSFNHYQVNN
CCCCCCCCCCCCCCCCCCCCCCCCCCCEEEEEEEEEECEEEEHHCCCCCCCHHHHCCCCCCCCCEEEEEC
DDDDDDDDDDDDDDDDDDDDDDDOOOOODOOOOOOOOOOOODOOODDDDDDDDDDDDDOOODDD


281       290       300       310       320       330       340
LSSSNNINDNKITEPITTHNLNKNNNAYTNHIIQNNHVPNYTYEHPKGLQYYPGNFHTHNMGNNIQ
CCCCCCCCCCCCCCCCCCCCCCCCCCCCCHHHCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDOOOOOOODDDDDDDDDDDDDDDDDDDDDDDDDDDDDD
```

Total amino acids:	346
Total % disorder:	56.35
Total no. of disordered regions > 30 amino acids:	3
Total no. of disordered regions > 50 amino acids:	1
Number of disordered segments:	8
Length distribution of segments (N to C terminal order):	5 74 38 1 1 14 30 32

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

SS Motif for disorder segment 1:
(start,end): (1,5)

```
seq   : MEERK
S.S.  : CCCCC
alpha : 01224
beta  : 00000
coil  : 98765
```

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): (122,195)

```
        122       131       141       151       161       171       181
seq   : IKDEKLNNDKDSTIQSVAEPTNTTTENNHNQNNNHNNNNIHNNNHNNNHNNNNIHNNNHNDPCNNHNDPC
S.S.  : HHHHHCCCCCCCEEEEECCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
alpha : 65666531110000000000011222222222222222223332222222223333321100111100022
beta  : 00000000000135665432100111111111111011221111111111112222110000000000
coil  : 34333367888863223467887655566556666666654456666666655554345678877788876

seq   : NNYY
S.S.  : CCCC
alpha : 2222
beta  : 0112
coil  : 6654
```

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

Linear motif(s):

residues (124,127)	LIG_PDZ_3 = DEKL
residues (135,141)	LIG_SH3_3 = IQSVAEP
residues (142,148)	LIG_FHA_2 = TNTTTEN

SS Motif for disorder segment 3:
(start,end): (199,236)

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

```
        199       208       218       228
seq  : DNFLKSNTVTYSHNNLFKENIPHVHQHTGIITSKTLPQ
S.S. : CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
alpha: 22332210001122233321001211100000000000
beta : 00111112333200122322112222222331000002
coil : 66555676555667543345775555567567888886
```

Linear motif(s):

residues (215,219)
LIG_APCC_KENbox_2 = FKENI
residues (216,219)   LIG_PDZ_3 = KENI
residues (224,230)   LIG_FHA_1 =
QHTGIIT
residues (232,235)   LIG_CYCLIN_1 =
KTLP

SS Motif for disorder segment 4:
(start,end): (261,274)

```
        261       270
seq  : ISHMYEMQTNDSFN
S.S. : CCCHHHHCCCCCCC
alpha: 23334333211111
beta : 11223322110011
coil : 54432234577766
```

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

Linear motif(s):

residues (265,268)   LIG_SH2_STAT3 =
YEMQ

SS Motif for disorder segment 5:
(start,end): (278,307)

```
        278       287       297
seq  : VNNLSSSNNINDNKITEPITTHNLNKNNNA
S.S. : EECCCCCCCCCCCCCCCCCCCCCCCCCCCCC
alpha: 21111111111100000011112221122
beta : 54211100121002333232221100001
coil : 23567777767786566665555566667775
```

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

Linear motif(s):

residues (291,297)   LIG_FHA_1 =
KITEPIT
residues (293,296)   LIG_PDZ_3 = TEPI

SS Motif for disorder segment 6:
(start,end): (315,346)

```
        315       324       334       344
seq  : NNHVPNYTYEHPKGLQYYPGNFHTHNMGNNIQ
S.S. : CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
alpha: 21000000000001000001111111111100
beta : 10111123321001233210122211000110
coil : 5777876556888765568876666778879
```

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

Linear motif(s):

residues (321,324)   LIG_SH2_STAT5 =
YTYE
residues (323,326)   LIG_SH2_SRC =
YEHP
residues (327,331)   LIG_CYCLIN_1 =
KGLQY