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
MTFYKKGYRKLFIHFNNNVIIKHNFSTLDINRGSLKKKQTKEKFEEVWKNIIRKKYIKKIVDIFEIEEEK
CCCCCCCCCCEEEECCCCCEEECCCCCCCCCCCCCCCCCCCHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH
DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD

71        80        90        100       110       120       130
KKKKKKDYYVNVDLYDKHKKCNNHNKYRKIDENVKGIHLVDGSKKNIQNDEYTCDDNQIVDPPRTCYFVV
CCCCCCCEEEECCCCCCCCCCCCCCCCCCCCCCCCCCCCCEEECCCCCCCCCCCCCCCCCCCCCCCEEEEE
DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDOOOOOODD

141       150       160       170       180       190       200
GSEGVGKKFIIEKAKEIFVNSPHNVQYGDCHNSEMKKNKKKKKNIFFEYDFKEMNDIINFSMKIYTLEYC
CCCCCCCHHHHHHCHHEEECCCCCCCCCCCCCCHHHCCCCCCCCEEEEECCHHCCCCCCCCEEEEHHHHH
DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDOOOOOOOODDDOOOOOOOOOOOOOOOO

211       220       230       240       250       260       270
LRYTLLKELNDDIIHNYINLKDIYDNMIYKDNINKSYNMLSRWRDFFIHIYENPQLYDYFNEKDLKEINN
HHHHHHHHHHHHCCCCCHHHHHHHHHHCCCCCCCCCHHHHHHHHHHHHHHCCCCHHHHCCHHHHHHHHH
OOOOODDDDDDOOODOOOODOOOOOOOOOOODDDDDDDDDDOOOOOOOOOOOOOOOODDDOOOOOOOOOOO

281       290       300       310       320       330       340
YQIMIKENKYNYETWYAFLEILLKKLKVKAFCNYFNHFSAYLYFFKMLGDYEEYDYYKKNTNNILINYTN
HHHHHHCCCCHHHHHHHHHHHHHHHCHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHCCCCCEEEECCC
OOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOODDDDDDDDDDOOOODDDDOOOO

351       360       370       380       390       400       410
GKFIYTYFLYILGNLQHIYNYNFFFLFYNFHLFLLSTQPIKDFNFFVNFLKQNIYSHTYCFPMVIHAIKN
CHHHHHHHHHHHHHHHHCCCCEEEEEEEEECEEEEECCCCCCCCHHHHHHHHHHHHCCCCCCCCCEEEHHHH
OOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOODOOOOOOOOOOOOO

421       430       440       450       460       470       480
LEIMKSIFMYNNIIIKWIRDKHVVNQTKSKHIEKAQHNDLYLKKIQCNPNIKNINNKNKNNSNNNMCFSK
HHHHHHHHHHCCEEEEEEECCCCCCCCCCCCCHHHHHCCCCCHHCCCCCCCCCCCCHCCCCCCCCCCCCCCC
OOOOOOOOOOOOOOOOOODDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD

491       500       510       520       530       540       550
DIQYTVPERINNNMNISSFHNLDDNKYAESQQNFEESTFNMNNIIKNKTDKKKENIETYYYYKKYQETLS
CCCCCCCHHHCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCHHHHHCCCCCCCCCCCHHHHHHHHHCCCC
DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD

561       570       580       590       600       610       620
NKQLKDMHINTYNTSEEYELIINNIIEIDDFSYDMIKSILIPHFTNNQDICNYIYKYIGGNIKLIKTICK
CCHHHCCCCCCCCCHHHHHHHHCCEEECCCCHHHHHHHCCCCCCCCHHHHHHHHHHHCCCHHHHHHHHH
DDDDDDDDDDDDDDDDOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOO

631       640       650       660       670       680       690
SLYELNQQFDECEIIKQIENARKENITYDMDEEEEDILNSPKKTIEQIITYKKNEKEKLFLKDLCEQVLH
HHHHHHHCCCHHHHHHHHHCCCHHHCCCCCCCCHHHHCCCCCCCHHHHHHHHHHHHHHHHHHHHHHHHHH
OOOOOOOOOOOOOOOOOODDDDDDDDDDDDDDDDDDDDDDOOOOOOOODDDDDDDDOOOOOOOOOOO

701       710       720       730       740       750       760
NFILNFEQKIIQFFSLPNIEKMKINQYDKEANDKYNNNNDDDDDKIKQTNDNKSNHEHHIQNNKPLNFIQ
HHHHHHHHHCCCCHHHHHHHHHHHHCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCHEE
OOOOOOOOOOOOOOODDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDOOOOOOO

771       780       790       800       810       820       830
FYFTIFETIRYFLKKQKVFCYNIINLNNPILLGLIDVNIIHYNYQDKYLELTNKFYHILLLNYIELKYKQ
EHHHHHHHHHHHHHCCCCEEEEECCCCCCCCCEEEEEECCCEEEECCCCCEEEECHHHHHHHHHHHHHHHHC
OOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOO

841       850       860       870
YPFKLRVQYNVNYMLNYKIIEHEYKLLECKN
CCCHHHEEHHHHHHHHHHHHHHHHHHHHCCCC
OOOOOOOOOOOOOOOOOOOOOOODDDDDDDDD
```

Total amino acids:	**871**
Total % disorder:	**50.17**
Total no. of disordered regions > 30 amino acids:	**4**
Total no. of disordered regions > 50 amino acids:	**2**
Number of disordered segments:	**16**
Length distribution of segments (N to C terminal order):	**132 47 3 7 1 1 10 3 11 4 1 137 21 8 42 9**

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

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

Linear motif(s):

residues (5,15)   LIG_MAPK_1 = KKGYRKLFIHF
residues (9,13)   LIG_CYCLIN_1 = RKLFI
residues (25,31)   LIG_FHA_1 = FSTLDIN
residues (44,47)   LIG_PDZ_3 = FEEV
residues (44,51)   LIG_MDM2 = FEEVWKNI
residues (53,63)   LIG_MAPK_1 = RKKYIKKIVDI
residues (56,59)   LIG_SH2_STAT5 = YIKK
residues (70,82)   LIG_MAPK_1 = KKKKKKKDYYVNV
residues (79,82)   LIG_SH2_STAT5 = YVNV
residues (101,104)   LIG_PDZ_3 = DENV
residues (121,127)   LIG_FHA_2 = EYTCDDN
residues (122,125)   LIG_SH2_STAT5 = YTCD

SS Motif for disorder segment 1:
(start,end): (1,132)

```
          1        10        20        30        40        50        60
seq  : MTFYKKGYRKLFIHFNNNVIIKHNFSTLDINRGSLKKKQTKEKFEEVWKNIIRKKYIKKIVDIFEIEEEK
S.S. : CCCCCCCCCCEEEECCCCCEEECCCCCCCCCCCCCCCCCCCCHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH
alpha: 000111111111111111112111111121111123333366788898888877766666566666654
beta : 012211012345543101455421112222100110000000000000000000001122112222221
coil : 986667765432234776432357665556677766556532211000111111222111211011123
         71       80        90       100       110       120       130
seq  : KKKKKKDYYVNVDLYDKHKKCNNHNKYRKIDENVKGIHLVDGSKKNIQNDEYTCDDNQIVDP
S.S. : CCCCCCCEEEECCCCCCCCCCCCCCCCCCCCCCCCCCCEEECCCCCCCCCCCCCCCCCCCCC
alpha: 321100110111234433233211122222222210000000011222221111111121000
beta : 221111145553210000011000011222211112455420011121101222100023210
coil : 456777643334555566556777655455666764334688665566765567755689
```

SS Motif for disorder segment 2:
(start,end): (139,185)

```
        139      148       158       168       178
seq  : VVGSEGVGKKFIIEKAKEIFVNSPHNVQYGDCHNSEMKKNKKKKKNI
S.S. : EECCCCCCCHHHHHHCHHEEECCCCCCCCCCCCCCCHHHCCCCCCCCCE
alpha: 000001113444444343332000111110122345542100000000
beta : 873110111334432123344200001210000000000000112347
coil : 126777764210112432223688876678766543357887766642
```

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

Linear motif(s):

residues (142,145)   LIG_PDZ_3 = SEGV
residues (156,162)   LIG_SH3_3 = EIFVNSP
residues (158,163)   LIG_WW_4 = FVNSPH

SS Motif for disorder segment 3:
(start,end): (194,196)

```
seq  : MND
S.S. : CCC
alpha: 433
beta : 001
coil : 455
```

SS Motif for disorder segment 4:
(start,end): (216,222)

```
seq  : LKELNDD
S.S. : HHHHHHH
alpha: 9987666
beta : 0000000
coil : 0012332
```

SS Motif for disorder segment 5:
(start,end): (241,250)

```
seq  : DNINKSYNML
S.S. : CCCCCCCCHH
alpha: 2111224467
beta : 0000000000
coil : 7777775521
```

SS Motif for disorder segment 6:
(start,end): (267,269)

```
seq  : YDY
S.S. : HHH
alpha: 565
beta : 000
coil : 333
```

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): (328,338)

```
          328       337
seq  : LGDYEEYDYYK
S.S. : HHHHHHHHHHH
alpha: 76566666654
beta : 00000000000
coil : 23332222334
```

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): (343,346)

```
seq  : NILI
S.S. : CEEE
alpha: 1100
beta : 1466
coil : 7322
```

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

Linear motif(s):

SS Motif for disorder segment 9:
(start,end): (439,575)

```
          439       448       458       468       478       488       498
seq  : RDKHVVNQTKSKHIEKAQHNDLYLKKIQCNPNIKNINNKNKNNSNNNMCFSKDIQYTVPERINNNMNISS
S.S. : CCCCCCCCCCCCHHHHCCCCCHHCCCCCCCCCCCCHCCCCCCCCCCCCCCCCCCCCCCCHHHCCCCCCCC
alpha: 2111111012244555433223443332100013343333222111111111112221112456543211333
beta : 2101221100001110000011111111100001122222221101233101233210011000001111
coil : 567666777764333334566644455677988865433444556677654466654555432346776554
          509       518       528       538       548       558       568
seq  : FHNLDDNKYAESQQNFEESTFNMNNIIKNKTDKKKENIETYYYYKKYQETLSNKQLKDMHINTYNTS
S.S. : CCCCCCCCCCCCCCCCCCCCCCHHHHCCCCCCCCCCCHHHHHHHHCCCCCCHHHHCCCCCCCCCC
alpha: 33211223344333333343333445554311122222334444555444322345555443321113
beta : 1110000010000001111111000111100000011223333211110000000000012222100
coil : 556777654445555544455554323457777666543222223334456664444444456776
```

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

Linear motif(s):

residues (461,464)	LIG_SH2_STAT5 = YLKK
residues (493,499)	LIG_FHA_2 = QYTVPER
residues (494,497)	LIG_SH2_STAT5 = YTVP
residues (497,500)	LIG_PDZ_3 = PERI
residues (517,520)	LIG_SH2_SRC = YAES
residues (528,536)	LIG_EH1_1 = TFNMNNIIK
residues (542,546)	
LIG_APCC_KENbox_2 = KKENI	
residues (543,546)	LIG_PDZ_3 = KENI
residues (556,559)	LIG_PDZ_3 = QETL

SS Motif for disorder segment 10:
(start,end): (649,669)

```
          649       658       668
seq  : ENARKENITYDMDEEEEDILN
S.S. : HCCCHHHCCCCCCCCHHHCC
alpha: 64445443310103466530
beta : 00000012210000000000
coil : 35554444578865333468
```

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

Linear motif(s):

residues (652,656)	
LIG_APCC_KENbox_2 = RKENI	
residues (653,656)	LIG_PDZ_3 = KENI
residues (664,667)	LIG_PDZ_3 = EEDI

SS Motif for disorder segment 11:
(start,end): (681,688)

```
seq  : YKKNEKEK
S.S. : HHHHHHHH
alpha: 88999999
beta : 00000000
coil : 11000000
```

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

Linear motif(s):

SS Motif for disorder segment 12:
(start,end): (722,763)

```
          722       731       741       751       761
seq  : MKINQYDKEANDKYNNNNDDDDDKIKQTNDNKSNHEHHIQNN
S.S. : HHHHCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
alpha: 88754333321111110112233332110011223322111
beta : 00000000100011111000000011210000000100000
coil : 11245665567876677887766555567887776556666888
```

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

Linear motif(s):

| residues (735,738) | LIG_SH2_GRB2 = YNNN |
| residues (743,746) | LIG_PDZ_3 = DDKI |

SS Motif for disorder segment 13:
(start,end): (863,871)

```
seq  : EYKLLECKN
S.S. : HHHHHCCCC
alpha: 665543210
beta : 011111100
coil : 223334579
```

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

Linear motif(s):