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
MEKIQEIIHEFVNIRSRLRRHKNKKKNEEDRVFIYSNEGNYYYEKRNLYNLYIIIKCYYYLLTHSIKHEK
CHHHHHHHHHHHHHHHHHHHCCCCCCCCCCCEEEEECCCCCCCHHHHHHHHHHHHHHHHHHHHCCCCCCCC
DDDDOOOOOOOOOODDDDDDDDDDDDDDDDDDDDDDDDOOOODOOOOOOOOOOOOOOOOOOOOOODDDDDD

71        80        90        100       110       120       130
WKIKYKEEKQQKCEKKKLVVEEEKEILLKKRIQKQYVHKIKNYIIMNRHIHAFKFLLEKYVYMNKYNDPI
CCHCHHHHHCCCCCCCCEHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHCCCCCCCC
DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOODDO

141       150       160       170       180       190       200
NEKKIEIKIKKRRQKQNKRKRNIRISIDKNVLFNKFISYIQQFIYDMLVTNDITYHMCSNNIFFSFFQKI
CCHHHHHHHHHHHHHCCCCCCCCEECCCHHHHHHHHHHHHHHHHHHHHHCCCCCCEECCCCHHHHHHHEE
OOOODDDDDDDDDDDDDDDDDDDDDOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOO

211       220       230       240       250       260       270
QMNKYELSNDGNNMKNSSQLTIITKNEKKTKRKKKKKRKKKEITNLLYKNNNHMFYNDLNSQYYYNSFML
CCCCCCCCCCCCCCCCCCCEEECCCCCCCHHCCCCCCCCCHHHHHHHCCCCCEEECCCCCCCCCCCEE
ODDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDOOOOOOOOOOOOOOOOOODOOOOOOOOO

281       290       300       310       320       330       340
KTIDPNLLYLIDNDFDLIKILFFFQVPHLFIMYVYIITCDKNKNNSNYYHNMYHKFYMSLLFKIINAFYS
EECCCCCEEEECCCHHHHHHHHHHCCCCCEEEEEEEEEECCCCCCCCCCHHHHHHHHHHHHHHHHHHHHHC
OOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOODDDDDOOOOOOOOOOOOOOOOOOOOOOOOO

351       360       370       380       390       400       410
SFILTYNKLVSNKDLIILFKIFSNILKKNHILLFKWLRCYEPIYKKLNERDKKNKKQNEPHNNNMHPIKS
CEEEECCCCCCHHHHHHHHHHHHHHHHHHHHHHHHHHHHCCHHHHHCCCCCCCCCCCCCCCCCCCCCCCC
OOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOODDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD

421       430       440       450       460       470       480
VDKKGSFSFHHLKGAYPSNVKKIKEHEKTKQEDVPKKYISQGTYLIDCEYEDRNRLNKVNTEKGDKYKIG
CCCCCCCCCCCCCCCCCCHHHHHCCCCCCCCCCCCCCCCCCCEEECCCCCCCCCCCCCCCCCCCCCCCCC
DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD

491       500       510       520       530       540       550
CSKELEGVNLLLHKKDGMNFAFLKDGSFLYRNLFNYFKGNEGGKKENEEKKKENEGKKKENDCTTCDDSN
CCCCCCCCCHHCCCCCCCCCCCHCCCCCHHHHHHHHHHCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD

561       570       580       590       600       610       620
ICNYESMCDKDNDSDGNNICDSNSNNSNSSDSYNNYNSNYNYNVGDFIFHQYVKGEDEIDCINFTINVIN
CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCEEEEEEECCCCCCEEEEEEEEEEEEC
DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDOOODOOOOOOOOOOOOOOOOOOOO

631       640       650       660       670       680       690
NQDDNIRFYKSYIKEHIDSMFLSKYNLKVAKKFGSTLNDESKKKKKRTKDQNNTENNNTSIFDNYKELVQ
CCCCCHHHHHHHHHHHHHHHHHHHHHHHHHHCCCCCCCCCCCCCCCCCCCCCCCCCCCCHHHHHHHHHH
ODOOOOOOOOOOOOOOODOOOODDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDOOOOOOOOOOD

701       710
NFFLVKKVFMNTNK
HHHHHHHHCCCCC
DDDDDDDDDDDDDD
```

Total amino acids:	**714**
Total % disorder:	**57.14**
Total no. of disordered regions > 30 amino acids:	**4**
Total no. of disordered regions > 50 amino acids:	**1**
Number of disordered segments:	**15**
Length distribution of segments (N to C terminal order):	**4 23 1 40 2 22 41 1 5 213 1 1 1 38 15**

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

SS Motif for disorder segment 1:　　　　　　　　　　　　**Graph of Probability(helix, strand, coil)**

(start,end): (1,4)

```
seq   : MEKI
S.S.  : CHHH
alpha: 0578
beta : 0000
coil : 9420
```

SS Motif for disorder segment 2:
(start,end): (14,36)

```
        14        23        33
seq   : IRSRLRRHKNKKKNEEDRVFIYS
S.S.  : HHHHHHCCCCCCCCCCCEEEEC
alpha: 7777665322111111111110
beta : 00000000000000001256653
coil : 11222345677778777532235
```

SS Motif for disorder segment 3:
(start,end): (65,104)

```
        65        74        84        94
seq   : SIKHEKWKIKYKEEKQQKCEKKKLVVEEEKEILLKKRIQK
S.S.  : CCCCCCCCHCHHHHHCCCCCCCCCEHHHHHHHHHHHHHHHH
alpha: 2222333333446654332211223567888888887766
beta : 01111122221100000000012333100000000000000
coil : 6665554333443335666666643332110001122222
```

SS Motif for disorder segment 4:
(start,end): (145,166)

```
        145       154       164
seq   : IEIKIKKRRQKQNKRKRNIRIS
S.S.  : HHHHHHHHHHCCCCCCCCEEC
alpha: 5566666665543322221111
beta : 2222100000000000113454
coil : 2111122234456666664334
```

SS Motif for disorder segment 5:
(start,end): (212,252)

```
        212       221       231       241       251
seq   : MNKYELSNDGNNMKNSSQLTIITKNEKKTKRKKKKKRKKKE
S.S.  : CCCCCCCCCCCCCCCCCCEEECCCCCCCHHCCCCCCCCCCH
alpha: 112222111111111133333332333333333332333344
beta : 11123310000000000123432000012221100111112
coil : 67644467888777765432224665554334566544442
```

SS Motif for disorder segment 6:
(start,end): (323,327)

```
seq   : KNNSN
S.S.  : CCCCC
alpha: 11223
beta : 00000
coil : 77765
```

SS Motif for disorder segment 7:
(start,end): (393,605)

```
        393       402       412       422       432       442       452
seq   : IYKKLNERDKKNKKQNEPHNNNMHPIKSVDKKGSFSFHHLKGAYPSNVKKIKEHEKTKQEDVPKKYISQG
S.S.  : HHHHHCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCHHHHHCCCCCCCCCCCCCCCCCCCCC
alpha: 77775444333222210011110012211000000123322000133455555433222101222100
beta : 00000000000000000000001111222100012222111000001111100000110001223211
coil : 22223455566666788877888775556788876544456888765432334455666678865444578
        463       472       482       492       502       512       522
seq   : TYLIDCEYEDRNRLNKVNTEKGDKYKIGCSKELEGVNLLLHKKDGMNFAFLKDGSFLYRNLFNYFKGNEG
S.S.  : CEEECCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCHHCCCCCCCCCCHCCCCCHHHHHHHHHCCCC
alpha: 001111233333332211000111101233322233333211111123322112456666665421110
beta : 35554221100000112211100223321111112222211001233321001211111101110000
coil : 53234555555555556778886555676554543334467887533346776321122223467888
        533       542       552       562       572       582       592
seq   : GKKENEEKKKENEGKKKENDCTTCDDSNICNYESMCDKDNDSDGNNICDSNSNNSNSSDSYNNYNSNYNY
S.S.  : CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
alpha: 011222222221001111111100112222233221111111111111111111112233322221110
beta : 011110011111001121111111100022211111000000002333211111111112222222333
coil : 8766666666678776677777777765555545667777787644566677776654445555555
```

```
seq   : NVG
S.S.  : CCC
alpha: 011
beta : 321
coil : 666
```

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

Linear motif(s):

residues (1,4) **LIG_PDZ_3 = MEKI**

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

Linear motif(s):

residues (29,32) **LIG_PDZ_3 = EDRV**

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

Linear motif(s):

residues (82,90) **LIG_MAPK_1 =**
KCEKKKLVV
residues (86,90) **LIG_CYCLIN_1 =**
KKLVV
residues (94,97) **LIG_PDZ_3 = KEIL**

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

Linear motif(s):

residues (155,165) **LIG_MAPK_1 =**
KQNKRKRNIRI

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

Linear motif(s):

residues (232,238) **LIG_FHA_2 =**
IITKNEK

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):

residues (417,421) **LIG_USP7_1 =**
PIKSV
residues (425,429)
LIG_BRCT_BRCA1_1 = GSFSF
residues (435,439) **LIG_USP7_1 =**
AYPSN
residues (447,453) **LIG_FHA_2 =**
EKTKQED
residues (449,452) **LIG_TRAF2_1 =**
TKQE
residues (451,454) **LIG_PDZ_3 = QEDV**
residues (458,461) **LIG_SH2_STAT5 =**
YISQ
residues (461,467) **LIG_FHA_1 =**
QGTYLID
residues (464,467) **LIG_SH2_STAT5 =**
YLID
residues (472,480) **LIG_APCC_Dbox_1**

= DRNRLNKVN
residues (495,498)　LIG_PDZ_3 = LEGV
residues (504,510)　LIG_MAPK_1 =
KKDGMNF
residues (520,523)　LIG_SH2_GRB2 =
YRNL
residues (521,524)　LIG_CYCLIN_1 =
RNLF
residues (526,529)　LIG_SH2_STAT5 =
YFKG
residues (534,538)
LIG_APCC_KENbox_2 = KKENE
residues (541,545)
LIG_APCC_KENbox_2 = KKENE
residues (548,552)
LIG_APCC_KENbox_2 = KKEND
residues (552,558)　LIG_FHA_2 =
DCTTCDD
residues (593,596)　LIG_SH2_GRB2 =
YNNY

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

Linear motif(s):

residues (664,670)　LIG_FHA_2 =
GSTLNDE

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): (653,690)

```
        653       662       672       682
seq  : SKYNLKVAKKFGSTLNDESKKKKKRTKDQNNTENNNTS
S.S. : HHHHHHHHHCCCCCCCCCCCCCCCCCCCCCCCCCCCCH
alpha: 66545666542111112222111101111111110134
beta : 00000010000011110000012222100001100001
coil : 33343223346876677777776666777777788754
```

SS Motif for disorder segment 9:
(start,end): (700,714)

```
        700       709
seq  : QNFFLVKKVFMNTNK
S.S. : HHHHHHHHHHCCCCC
alpha: 877655444432100
beta : 000111222211000
coil : 112223322356899
```

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