



## CSpritz - Accurate detection of protein disorder

## Version 1.2

**Title:** PF3D7\_1117200.fasta  
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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:**

**Fasta sequences (amino, secondary structure, disorder, confidence):**

**Disorder plot:**

**Graph of PDB homologue(s) found::**

**Disorder Prediction (with disorder probability):**

### Protein statistics :

## HTML

**TXT**

PDF

PDF

**TXT**

**TXT**

Disordered residues and stats: [\(help\)](#)[illegible]

<b>Total amino acids:</b>	<b>1821</b>
<b>Total % disorder:</b>	<b>72.10</b>
<b>Total no. of disordered regions &gt; 30 amino acids:</b>	<b>10</b>
<b>Total no. of disordered regions &gt; 50 amino acids:</b>	<b>7</b>
<b>Number of disordered segments:</b>	<b>31</b>
<b>Length distribution of segments (N to C terminal order):</b>	<b>82 111 191 1 284 72 2 21</b> <b>9 47 11 14 101 37 25 156</b> <b>7 2 2 10 8 39 12 4 4 1 3</b> <b>14 8 9 26</b>

[illegible]

**Disordered segment motifs:** [\(help\)](#)  
97 ELM motif(s) in total found in disordered residues

**SS Motif for disorder segment 1:**  
(start,end): (1,82)

```

      1      10      20      30      40      50      60
seq : MSCYPSDEKSRKIRKNDSEYEIDTNKLEYISFLCEEDDINYFCSFNEDENVNFKLKLDIFEDSYLKLLI
S.S. : CCCCCCCCCCCCCCCCCCCCCCCCCCHHECCCCCCCCCCCCCCCCCCCCCCCCCHHHHHHHHHHH
alpha: 000000111222211112222223333221222333321112222223333445556688887
beta : 00000000000111000011221001233333221001123321000001101100000000000000
coil : 99888888777666788765446675432233455666554345677776665555544433311011
      71      80
seq : ENEKIEQDAPSC
S.S. : HHHHHCCCCCCC
alpha: 655554311224
beta : 000000000000
coil : 234444678764

```

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

**Linear motif(s):**

residues (22,28) **LIG\_FHA\_1 =**  
**IDTNKLE**  
residues (27,30) **LIG\_PDZ\_3 =**  
**LEYI**  
residues (29,32) **LIG\_SH2\_STAT5 =**  
**YISF**  
residues (36,39) **LIG\_PDZ\_3 =**  
**EDDI**  
residues (41,44) **LIG\_SH2\_STAT5 =**  
**YFCS**  
residues (48,51) **LIG\_PDZ\_3 =**  
**DENV**  
residues (65,68) **LIG\_SH2\_STAT5 =**  
**YLKL**  
residues (67,70)

SS Motif for disorder segment 2:  
(start,end): (99,209)

```

      99      108      118      128      138      148      158
seq  : ILFHNKNKQVHSISHIERDINFFNYENVETKKKKKINKSEEIIQNNIRRNKNLIYIKGDEEKYINKKYI
S.S.  : HHHCCCCCCCCCCCCCHHHHHCCCCCCCCCCCCCCCCCHHHCCCCCCCCCCCCCEEECCCCCCCCCCCC
alpha: 4443211111113344344443322222222222123455432222111122221112232211222
beta  : 22211001232221111111221111222111111000122100011001124442000112211122
coil  : 223467775455444443333455665455666557654322467666777643236876655577655
      169      178      188      198      208
seq  : NDVNDQNNLNLNELYKVDKLYNIDKLHFITSHYLAYNKMQ
S.S.  : CCCCCCCHHHHHHHHHHCHCCCCCHHCCCCCHHHHHCHHC
alpha: 222233345566665554443233433333455544444
beta  : 11000000000000111100011101123221112111000
coil  : 566666543332222344456554433345322234444
```

SS Motif for disorder segment 3:  
(start,end): (219,409)

```

      219      228      238      248      258      268      278
seq  : NFNMNKISKFDKHIKGLNKTYHHSIHYNLGANTISEQSHVLQVDHAPSCKKKKYIFKYHNKIYSKMKRN
S.S.  : CCCCCHHCCCCHHCCCCCCCCCHCCCCCCCCCCCCCCCCCCCCCHHHHCCCCCHCCCCCCCC
alpha: 22233444444454322222223332121222333332211112222233444333444443322
beta  : 000000110000111000112112222100011111112333100000000123221101111000000
coil  : 76655434444335666665654333467766555543334678776666542233454344445567
      289      298      308      318      328      338      348
seq  : NSNKKMKYKKKQIKSSSLNISKLLFPFFGYTTSEESVMSFSKFLPEHKIARKKKKKKKKRQKEQKEQKK
S.S.  : CCCCCCCCCCCCCCCCCCHHHHCCCCCCCCCHCCCCCCCCCHHHHHHHHCCCCCHHHHHHHHHHH
alpha: 1222333333322222334554211210000134443333224667776544433444556666665
beta  : 01233211111110000001232100122210000134431111100011100011222211111011
coil  : 777655445555666654334677667677544455456675332122344554444332222223
      359      368      378      388      398      408
seq  : QKEQKEQKKQKEQKKQKEQQTNNIINNDHHDKPITYQSKDKKEIKHNSML
S.S.  : HHHHHHHHHHHHHHCCCCCCCCCCCCCCCCCCCCCCCCCHHCCCCCHH
alpha: 5566665555554433322223321111100001111113454432356
beta  : 0011111111111112222112221000000122221000111100011
coil  : 3322233333334444444555357877788866566775433456531
```

SS Motif for disorder segment 4:  
(start,end): (421,704)

```

      421      430      440      450      460      470      480
seq  : NKIFTFNKIKHKQNDTKKNHRVLHPERFIHSTDQDYIKIGEKHNVDNKNESFDNKQYIKTQNLSTRS
S.S.  : CCCCCCCCCCCCCCCCCCCCCCHCCCCCCCCCEEECCCCCCCCCCCCCCCCCCCCCCCCCCCC
alpha: 2222223332221111111100234322112232221011100112211223333222211233
beta  : 01233211111100000001232100122210000134431111100011100011222211111011
coil  : 764444555555667887776546765434577866432357766777666667654434555677654
      491      500      510      520      530      540      550
seq  : YMNTYYKDDINNSENLKRNKVQNELEKDHITYTSQGLHKKRSFSSCSDYVVKQDEYEKKKRTKKQNEFI
S.S.  : CCCCCCCCCCCCCCHHHHHHHHHHHHCCCCCCCCCCCCCCCCCCCCCCCCCHHHCCCCCCCCCEEE
alpha: 4332222232234555555565544333222122211112233444334455543222222233
beta  : 1112221100000000000000000000012211000111111000011100000000011111233
coil  : 455444566667643333344333334455445667666666666554455443446666666422
      561      570      580      590      600      610      620
seq  : INKNI I IKGKEDIISHSIVDMRNKIKKRNYEGGVKNELKNESKDIYDECKENQNIYKEKQNIYKENQNIY
```

LIG\_CYCLIN\_1 = KLLI  
residues (72,75) LIG\_PDZ\_3 = NEKI

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

Linear motif(s):

residues (109,114) LIG\_14-3-3\_3 = HSISHI  
residues (114,121) LIG\_PPI = IERDINFF  
residues (123,126) LIG\_SH2\_SRC = YENV  
residues (137,140) LIG\_PDZ\_3 = SEEI  
residues (146,155) LIG\_MAPK\_1 = RRNNKNLIYI  
residues (150,154) LIG\_CYCLIN\_1 = KNLIY  
residues (154,157) LIG\_SH2\_STAT5 = YIKG  
residues (162,165) LIG\_SH2\_STAT5 = YINK  
residues (167,170) LIG\_SH2\_STAT5 = YIND  
residues (186,189) LIG\_PDZ\_3 = VDKL  
residues (192,195) LIG\_PDZ\_3 = IDKL  
residues (202,205) LIG\_SH2\_STAT5 = YLAY

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

Linear motif(s):

residues (249,255) LIG\_FHA\_2 = ANTISEQ  
residues (272,275) LIG\_SH2\_STAT5 = YIFK  
residues (276,279) LIG\_SH2\_GRB2 = YHNK  
residues (297,308) LIG\_MAPK\_1 = KKKQIKSSSLNI  
residues (310,314) LIG\_CYCLIN\_1 = KLLFP  
residues (317,323) LIG\_FHA\_2 = GYTTSEE  
residues (318,321) LIG\_SH2\_STAT5 = YTTS  
residues (320,323) LIG\_TRAF2\_1 = TSEE  
residues (322,325) LIG\_PDZ\_3 = EESV  
residues (330,333) LIG\_CYCLIN\_1 = KFLP  
residues (377,383) LIG\_FHA\_1 = QQTNNII  
residues (393,396) LIG\_SH2\_STAT5 = YTYQ  
residues (400,403) LIG\_PDZ\_3 = KEEI

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

Linear motif(s):

residues (440,446) LIG\_SH3\_3 = NHRVLHP  
residues (442,446) LIG\_CYCLIN\_1 = RVLHP  
residues (451,457) LIG\_FHA\_2 = HSTDQDQ  
residues (458,461)

LIG\_SH2\_STAT5 = YIKI  
residues (479,482)  
LIG\_SH2\_STAT5 = YIKT  
residues (491,494)  
LIG\_SH2\_GRB2 = YMNT  
residues (497,500) LIG\_PDZ\_3 =  
KDD  
residues (519,522) LIG\_PDZ\_3 =  
KDHI  
residues (523,526)  
LIG\_SH2\_STAT5 = YTSQ  
residues (538,541) LIG\_PDZ\_3 =  
SDYV  
residues (540,543)  
LIG\_SH2\_STAT5 = YVNK  
residues (557,560) LIG\_PDZ\_3 =  
NEFI  
residues (570,573) LIG\_PDZ\_3 =  
KEDI  
residues (609,613)  
LIG\_APCC\_KENbox\_2 = CKENQ  
residues (623,627)  
LIG\_APCC\_KENbox\_2 = YKENQ  
residues (630,634)  
LIG\_APCC\_KENbox\_2 = YKENQ  
residues (637,641)  
LIG\_APCC\_KENbox\_2 = YKENQ  
residues (663,666) LIG\_PDZ\_3 =  
NDIL  
residues (668,675) LIG\_PP1 =  
KKKNIHFL  
residues (668,677)  
LIG\_MAPK\_1 = KKKNIHFLNF  
residues (685,688) LIG\_PDZ\_3 =  
DDNI  
residues (698,704) LIG\_FHA\_2  
= NQTHYDP

**(start,end): (709,780)**

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

Linear motif(s):

residues (720,723)  
LIG\_SH2\_STAT3 = YNHQ  
residues (724,730) LIG\_FHA\_2  
= TTKTKEDE  
residues (740,743)  
LIG\_CYCLIN\_1 = KNLY  
residues (758,761)  
LIG\_SH2\_GRB2 = YKNE

**(start,end): (839,859)**

**Graph of Probability(helix, strand, coil) PDF**  
**Amino SS Probability(helix, strand, coil) TXT**  
**Linear motif(s):**

**(start,end): (879,887)**

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

**Linear motif(s):**

residues (879,887)  
**LIG MAPK 1 = KLNKLKLSI**

**(start,end): (897,943)**

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

Linear motif(s):

residues (898,901) LIG\_PDZ\_3 =  
IDNI  
residues (921,924)  
LIG\_SH2\_GRB2 = YKNK  
residues (925,928)



```

residues (1209,1212)
LIG_SH2_STAT5 = YTIK
residues (1222,1225)
LIG_SH2_STAT5 = YTNK
residues (1232,1236)
LIG_CYCLIN_1 = KKLGV
residues (1232,1240)
LIG_MAPK_1 = KKLGVLENI
residues (1261,1264)
LIG_SH2_GRB2 = YNNK
residues (1265,1268)
LIG_SH2_STAT5 = YIHD
residues (1271,1274)
LIG_SH2_STAT5 = YIHD
residues (1279,1282)
LIG_SH2_GRB2 = YDNN
residues (1284,1287)
LIG_SH2_STAT5 = YIHD
residues (1292,1295)
LIG_SH2_GRB2 = YNNN
residues (1306,1309)
LIG_SH2_GRB2 = YNNN
residues (1320,1323)
LIG_SH2_GRB2 = YNNN
residues (1327,1330)
LIG_SH2_GRB2 = YNNN

```

**(start,end): (1384,1390)**

```
seq   : TKERKQY
S.S.  : HHHHHHC
alpha: 7777643
beta  : 1100000
coil  : 1112346
```

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

**Linear motif(s):**

**(start,end): (1436,1445)**

```
seq  : KKYYYKEEKY
S.S. : CCEECCCCCE
alpha: 3211001000
beta : 1344422235
coil : 5334576653
```

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

**Linear motif(s):**

**(start,end): (1500,1507)**

```
seq   : TKNRKKNY
S.S.  : CCCCCCCC
alpha: 22222211
beta  : 00001112
coil  : 76666666
```

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

**Linear motif(s):**

**(start,end): (1541,1579)**

```

1541      1550      1560      1570
seq : KNGMNDNINKNKNVDDKINKNKINIDIRTDNGIDIDVDKKN
S.S. : HCCCCCCCCCCCCCCCCCHHHHHCCCCCCCCCCCCCCCCCCCC
alpha: 53122222211111145555543332211001100010
beta : 000000000000001000000001122110013433112
coil : 467766667778877443434455445678754557776

```

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

**Linear motif(s):**

residues (1545,1548)  
**LIG\_PDZ\_3 = NDNI**

**(start,end): (1589,1600)**

```

      1589      1598
seq   : YNNPSGKSNITV
S.S.  : ECCCCCCCCCHH
alpha: 100000111345
beta  : 530000001233
coil  : 258888876420

```

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

**Linear motif(s):**

residues (1589,1592)  
LIG\_SH2\_GRB2 = YNNP

**(start,end): (1611,1614)**

```
seq   : ILSK
S.S.  : HHHH
alpha: 9998
beta  : 0000
coil  : 0001
```

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

**Linear motif(s):**

**SS Motif for disorder segment 21:**

### Graph of Probability(helix, strand

13/01/2022, 09:09	CSpritz PID: 1976228859	
(start,end): (1636,1639)		coil) <a href="#">PDF</a> Amino SS Probability(helix, strand, coil) <a href="#">TXT</a>
seq : RKEY S.S. : HHHH alpha: 6665 beta : 0000 coil : 2223		Linear motif(s): <hr/>
<a href="#">SS Motif for disorder segment 22:</a> (start,end): (1683,1685)		Graph of Probability(helix, strand, coil) <a href="#">PDF</a> Amino SS Probability(helix, strand, coil) <a href="#">TXT</a>
seq : IYE S.S. : HHH alpha: 545 beta : 000 coil : 443		Linear motif(s): <hr/>
<a href="#">SS Motif for disorder segment 23:</a> (start,end): (1739,1752)		Graph of Probability(helix, strand, coil) <a href="#">PDF</a> Amino SS Probability(helix, strand, coil) <a href="#">TXT</a>
1739 1748 seq : GILFYDTRKMINKQ S.S. : CCEECCHHHHHHCC alpha: 11123356766444 beta : 13442100000000 coil : 74333442223445		Linear motif(s): <hr/>
<a href="#">SS Motif for disorder segment 24:</a> (start,end): (1763,1770)		Graph of Probability(helix, strand, coil) <a href="#">PDF</a> Amino SS Probability(helix, strand, coil) <a href="#">TXT</a>
seq : FNQLETK S.S. : HHHHHHCC alpha: 77665532 beta : 00001100 coil : 12223356		Linear motif(s): <hr/>
<a href="#">SS Motif for disorder segment 25:</a> (start,end): (1782,1790)		Graph of Probability(helix, strand, coil) <a href="#">PDF</a> Amino SS Probability(helix, strand, coil) <a href="#">TXT</a>
seq : KIKRVRKFD S.S. : HHHHHHCC alpha: 887666444 beta : 000000000 coil : 112223444		Linear motif(s): <hr/>
<a href="#">SS Motif for disorder segment 26:</a> (start,end): (1796,1821)		Graph of Probability(helix, strand, coil) <a href="#">PDF</a> Amino SS Probability(helix, strand, coil) <a href="#">TXT</a>
1796 1805 1815 seq : YIQERKHQEYGFVAGGGFLCSEQTK S.S. : HHHHHCCCCCCECCCCCCCCCCC alpha: 87765432221111000000111100 beta : 00110000111344200133210000 coil : 11123566566534688755667789		Linear motif(s):  residues (1796,1799) <a href="#">LIG_SH2_STAT5 = YIQE</a> <hr/>