



## CSpritz - Accurate detection of protein disorder

## Version 1.2

**Title:** PF3D7\_1136200.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>679</b>
<b>Total % disorder:</b>	<b>81.2%</b>
<b>Total no. of disordered regions &gt; 30 amino acids:</b>	<b>5</b>
<b>Total no. of disordered regions &gt; 50 amino acids:</b>	<b>4</b>
<b>Number of disordered segments:</b>	<b>12</b>
<b>Length distribution of segments (N to C terminal order):</b>	<b>264 59 54 15 3 17 4 34 6 11 81 4</b>

### Disordered segment motifs: [\(help\)](#)

**37 ELM motif(s) in total found in disordered residues**

**SS Motif for disorder segment 1:**  
(start,end): (1,264)

### Graph of Probability(helix, strand, coil)

PDF

**Amino SS Probability(helix, strand, coil)**

**TXT**

**Linear motif(s):**

alpha: 00123445555544221222211111112221000111122111110111111000001122233  
beta : 0000011211122211012343112223321100133211111111100013321100000000000  
coil : 9987543222222235765334676665544567876566666666778886445788998777665  
71 80 90 100 110 120 130  
seq : LSFQELLRKRSSDDDDDDNDDDEGDNDDDDDNDNNNNNNNNNNNNRPFYNMASIQPAAFNNISQNGNQSF  
S.S. : CCHHHHHHCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCHHCHHCCCCCHHHCCCCCCCCCHH  
alpha: 4467877542111111111111111222222111122233444444424555444322112345  
beta : 00100  
coil : 542211235788888888777888888877777777777777777776654444445565443455567876543  
141 150 160 170 180 190 200  
seq : ARMKQNL SKYNPFKKSGSNNNGKVNNTNENVDEDNNDNVDDNNTKKKRRHIKHKSQGTLSNDGSGNNMNN  
S.S. : HHHHHHHCC  
alpha: 6666654433111111111101111222112222111111111222322111111111222222  
beta : 0000000000000000000000001210000110000000000000001111110000111000000000  
coil : 3223344556887778888888767777766767777777777777877766556677787677887776667  
211 220 230 240 250 260  
seq : NVNNNNVNNNVNNNVNNNVNNNVNNNVNNNMNNNNNNNNNNNNNNNNNNNNNNNNNNNN  
S.S. : CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCHHCCCCCCCCCCCCCCCCCCCCCCCC  
alpha: 22  
beta : 011000110001100011000110001000010000000000000000000000000000001  
coil : 66

SS Motif for disorder segment 2:  
(start,end): (279,337)

279 288 298 308 318 328  
seq : NMNNNNVNASILLGASALTGAAISGQNGNGINNNQNVVNNNTNNGTIQNSIMLNNSS  
S.S. : CCCCCCCCCCHHHHHCHHHCHCCCHCCCCCCCCCCCCCHHCCCCCCCCCHHHHHCCCC  
alpha: 3222212244555445554334322221111111121110000123344442124  
beta : 0000000110011110010000122111101110012444210001232112211000  
coil : 66667766443223443345433566667766776533467888753332345775

SS Motif for disorder segment 3:  
(start,end): (349,402)

349 358 368 378 388 398  
seq : KFNTEMICSSINCTINSQNDKIPLTDCSNVLYCGNCPFSSSPKQDCASIKT  
S.S. : CCCCCEEEECCCCCCCCCCCCCCCCCCCCCEEECCCCCCCCCHHHHHHHHHH  
alpha: 100111111111000000122100001111100000000000003567766664  
beta : 122235665323333210000023321112367742111110000000000000  
coil : 7676432124555566677778876666665322478877888543222334

SS Motif for disorder segment 4:  
(start,end): (416,430)

416 425  
seq : DSLQLLNKNNLVNIP  
S.S. : HHHHHHHCCCCCCC  
alpha: 467776532110000  
beta : 200000000123344  
coil : 331112467755555

SS Motif for disorder segment 5:  
(start,end): (439,441)

seq : DFS  
S.S. : CCC  
alpha: 133  
beta : 411  
coil : 454

SS Motif for disorder segment 6:  
(start,end): (449,465)

449 458  
seq : KFKLATKDLFPNKDKNEV  
S.S. : HHHHHHCCCCCHHHH  
alpha: 88887642012327899  
beta : 00000000000000000  
coil : 00011257987672100

SS Motif for disorder segment 7:  
(start,end): (484,487)

seq : EDNN  
S.S. : HCCC

residues (9,16) LIG\_PP1 = LLKHIFK  
residues (16,22) LIG\_FHA\_1 = KNTLYIF  
residues (20,23) LIG\_SH2\_STAT5 = YIFD  
residues (22,25) LIG\_PDZ\_3 = FDNV  
residues (39,42) LIG\_PDZ\_3 = SDTI  
residues (51,54) LIG\_SH2\_SRC = YDNS  
residues (57,60) LIG\_PDZ\_3 = LDKV  
residues (58,64) LIG\_SH3\_3 = DKVPDTP  
residues (60,65) LIG\_WW\_4 = VPDTPL  
residues (61,67) LIG\_FHA\_2 = PTDPLDN  
residues (72,75) LIG\_TRAF2\_1 = SFQE  
residues (74,77) LIG\_PDZ\_3 = QELL  
residues (150,154) LIG\_EH\_1 = YNPFK  
residues (168,171) LIG\_PDZ\_3 = NENV  
residues (176,179) LIG\_PDZ\_3 = NDNV

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 (353,356) LIG\_PDZ\_3 = SEMI  
residues (370,373) LIG\_PDZ\_3 = NDKI  
residues (383,386) LIG\_SH2\_STAT5 = YCGN  
residues (388,392) LIG\_USP7\_1 = PFSSS  
residues (389,394) LIG\_WW\_4 = FSSSPK

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

Linear motif(s):

residues (424,430) LIG\_SH3\_3 =>NNLVNIP

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 (451,456) LIG\_14-3-3\_3 = KLATKD  
residues (452,458) LIG\_FHA\_1 = LATKDLP  
residues (455,458) LIG\_CYCLIN\_1 = KDLP

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

<div>alpha: 3211</div> <div>beta : 3200</div> <div>coil : 3578</div>		<div>Linear motif(s):</div> <div></div>
		<div>Graph of Probability(helix, strand, coil)</div> <div>PDF</div> <div>Amino SS Probability(helix, strand, coil)</div> <div>TXT</div>
<div>SS Motif for disorder segment 8:</div> <div>(start,end): (502,535)</div>		<div>Linear motif(s):</div> <div>residues (502,505) LIG_PDZ_3 = IDSL</div> <div>residues (506,512) LIG_FHA_1 = KPTEQLA</div> <div>residues (506,513) LIG_SH3_4 = KPTEQLAN</div> <div>residues (508,511) LIG_PDZ_3 = TEQL</div> <div>residues (528,534) LIG_FHA_1 = IKTYNIH</div>
<div>SS Motif for disorder segment 9:</div> <div>(start,end): (550,555)</div>		<div>Graph of Probability(helix, strand, coil)</div> <div>PDF</div> <div>Amino SS Probability(helix, strand, coil)</div> <div>TXT</div>
<div>seq : IYNALN</div> <div>S.S. : CHHHCC</div> <div>alpha: 444321</div> <div>beta : 111222</div> <div>coil : 444346</div>		<div>Linear motif(s):</div> <div></div>
<div>SS Motif for disorder segment 10:</div> <div>(start,end): (559,569)</div>		<div>Graph of Probability(helix, strand, coil)</div> <div>PDF</div> <div>Amino SS Probability(helix, strand, coil)</div> <div>TXT</div>
<div>seq : IMINITSDPGY</div> <div>S.S. : EEEEECCCCC</div> <div>alpha: 0000000000</div> <div>beta : 57887420013</div> <div>coil : 42112479986</div>		<div>Linear motif(s):</div> <div></div>
<div>SS Motif for disorder segment 11:</div> <div>(start,end): (585,665)</div>		<div>Graph of Probability(helix, strand, coil)</div> <div>PDF</div> <div>Amino SS Probability(helix, strand, coil)</div> <div>TXT</div>
<div>seq : TNDIIEENIYPTATLPQTNQQTQQLTQQTIPTPIENNPQQNETKNGTPPKNDTSVQLLKNTSSKDSR</div> <div>S.S. : CCHHHHHHECCCCCCCCCEHHHCC</div> <div>alpha: 115555443111100112223333321100000122112333221000000000111001100011111</div> <div>beta : 000122233321110011233433211232100001110000011000000000244321100000011</div> <div>coil : 8742112234567887665432223455567888766686655667898899998644567788887776</div> <div>seq : RGYSYRNSSHS</div> <div>S.S. : CCCCCCCCCCH</div> <div>alpha: 10001000133</div> <div>beta : 11222210012</div> <div>coil : 77766788753</div>		<div>Linear motif(s):</div> <div>residues (586,589) LIG_PDZ_3 = NDII</div> <div>residues (594,600) LIG_FHA_1 = YPTATLP</div> <div>residues (605,611) LIG_FHA_1 = QTTQQLT</div> <div>residues (613,619) LIG_SH3_3 = QTIPQTP</div> <div>residues (615,620) LIG_WW_4 = IPQTPI</div> <div>residues (616,622) LIG_FHA_2 = PQTPIEN</div> <div>residues (630,635) LIG_WW_4 = KNGTTP</div> <div>residues (659,662) LIG_SH2_GRB2 = YRNS</div>
<div>SS Motif for disorder segment 12:</div> <div>(start,end): (676,679)</div>		<div>Graph of Probability(helix, strand, coil)</div> <div>PDF</div> <div>Amino SS Probability(helix, strand, coil)</div> <div>TXT</div>
<div>seq : ILFL</div> <div>S.S. : EECC</div> <div>alpha: 2210</div> <div>beta : 5530</div> <div>coil : 1249</div>		<div>Linear motif(s):</div> <div></div>