



## CSpritz - Accurate detection of protein disorder

## Version 1.2

**Title:** PF3D7\_0926600.fasta  
**emailaddress:** mubasher.mohammed@su.se  
**pid:** 986020641

**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>1378</b>
<b>Total % disorder:</b>	<b>46.87</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>26</b>
<b>Length distribution of segments (N to C terminal order):</b>	<b>9 2 2 2 1 1 1 146 1 1 4 2 4 5 94 99 17 40 149 13 5 1 4 1 1 9 23</b>

911	920	930	940	950	960	970
IQGGIPTDHNREQKRRIKENIQNKKFNSRDTCEGEKKERTEDSIGNHHFSLCKKCTSKKHFDGILSKKK CCCCCCCCCCCCCHCCHHHHHHHCCCCCCCCCCCCCCCCCCCCCCCCCHCCCCCCCCCCCCCCCC DD						
981	990	1000	1010	1020	1030	1040
GTCKYISNLSLNKRKSKESHLSIYKKYFFEFYDCIPINYKKKPHNIEKHKFSYNIKNAFLCIKLPNIIWI CCEEEEECCCCCCCCCCCCCHHHHHHHHHHHHHCCCCCCCCCCCCCCCCCHHHHHHHHHHHHHHHHH DD						
1051	1060	1070	1080	1090	1100	1110
KIKTWYKIDIKKEKYWKRYNDILYTSQWKNNIQDNELEYILKYKNFMKWYNYWVKTVLVFNYYKSTWALNL HHHHHHHCCCCCEHHHHCHHHHHHHHHHCCCCCHHHHHHHHHHCHHHHHHHHHHHHHHHHHHHHHHHHH OOOOOOOOOOOODOOOOOOOOOOOOOOOOODODDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD						
1121	1130	1140	1150	1160	1170	1180
LLYILNVLLIYLQMHMFYFLFEINSDQPKYSNVLKKEENSKTKFPLNHFMKKNYIPFTYIRISLQLIIN HHHHHHHHHHHHHHHEEEEECCCCCCCCCCCCCCCCCECCCECCCCCCCCCHEEEEHHHHHHHHHH OOOOOOOOOOOOOOOOOOOOOOOOOOOODOOOOOOOOOOOOODOOOOOOOOOOOOOOOOOOOOOOOO						
1191	1200	1210	1220	1230	1240	1250
IIFCLPSMIKKNFKRIKMLHIFSILNCLVNIFFGMIDIVYSLNDRIFNINDLYVLLNHYNIFDVFLIGKL HHHHCHHHHHCCCCCHHHHHHHHHHHHHHHHCHEEEECHHCCHCHHHHHHHHHHCCCCEEEEEECHH OO						
1261	1270	1280	1290	1300	1310	1320
ITSIFLIPFFTFNFESKTCALIYFSCICYISTFYYSYNPLSFSIKMLYLTIFVILIAVTLTTSYYAKLIM HHEEEECCECCCCCCCCCEEEEEEEEEEEEEEECCCCCHHHHHHHHHHHHHHHHHHHHHHHHHHHHH OOOD						
1331	1340	1350	1360	1370		
KSRKMLFVKYVLPYFIYLTFLNTDPHIQMKIKEKKRKKKKKKQRNIGK HCCCCHHHECCCCEEEEEECCCCCHHHHHHHHHHCCCCCCCCCCCCC DD						

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

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

SS Motif for disorder segment 1:  
(start,end): (1,9)

seq : MKKYHKKFP  
S.S. : CCCCCCCCC  
alpha: 011210003  
beta : 000000000  
coil : 987778886

SS Motif for disorder segment 2:  
(start,end): (246,256)

246 255  
seq : KTINKSKINLE  
S.S. : EEECCCCECC  
alpha: 22111000000  
beta : 45433345542  
coil : 2234555446

SS Motif for disorder segment 3:  
(start,end): (285,430)

285 294 304 314 324 334 344  
seq : KVVNVDSEDIEMCSLKKMNAEENKINDNYSRNIIRCDNEENLVESNIEIDNRNLCNENYTYSKNKKK  
S.S. : EEECCCCCHHHHHHHHHHCCCCCCCCCEEECCCCCCCCCCCCCECCCCCCCCCCCCCCCCC  
alpha: 0000112456665677544554321000011000001110000110000012333211000111123  
beta : 666542000000000000000001122101112477621233333213553100121001232100011  
coil : 32334664332334222354434446788876421367655555676345665444677656677765  
355 364 374 384 394 404 414  
seq : EKLKKNKTNISLKDSSAYIDNNNNNNNNNNEINNHVTSYDKYLSPONNDYISQNNSSSSHKDNNLTYS  
S.S. : CCCCCCCCCCCCCCEEECCCCCCCCCCCCCCCCCCCCCCCCCHHCCCCCCCCCCCCCCCCC  
alpha: 3332211110022111122322101112221121122233220033445554210134433322223  
beta : 100111112110001235543210000000022233311001000000000000000000011  
coil : 55556777767677876422235788777775554444556688654433356788645556777654  
  
seq : HSNFKR  
S.S. : CHHHHH  
alpha: 444566  
beta : 110000  
coil : 444333

SS Motif for disorder segment 4:  
(start,end): (460,463)

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):

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

Linear motif(s):

residues (292,295) [LIG\\_PDZ\\_3 = SEDI](#)  
residues (324,327) [LIG\\_PDZ\\_3 = EENL](#)  
residues (345,348) [LIG\\_SH2\\_STAT5 = YTYS](#)  
residues (354,357) [LIG\\_PDZ\\_3 = KEKL](#)  
residues (356,366) [LIG\\_MAPK\\_1 = KLKKNKTNISL](#)  
residues (373,376) [LIG\\_SH2\\_STAT5 = YIDN](#)  
residues (391,396) [LIG\\_14-3-3\\_3 = HVTSYD](#)  
residues (391,397) [LIG\\_FHA\\_2 = HVTSYDK](#)  
residues (397,401) [LIG\\_CYCLIN\\_1 = KYLSP](#)  
residues (397,402) [LIG\\_WW\\_4 = KYLSPQ](#)  
residues (398,401) [LIG\\_SH2\\_STAT5 = YLSP](#)  
residues (404,407) [LIG\\_PDZ\\_3 = NDYI](#)  
residues (406,409) [LIG\\_SH2\\_STAT5 = YISQ](#)

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



835844854864874884894

seq : IVLPKKESFIKLTNNSRNKNKHSLSGSISSMNDFLNGSYEGSLKNEKKKKKTNAENYGIQVGINDMSNDKLY

S.S. : CCCCCCHHHHHHHHHCC

alpha: 110114567887765542111110012222222111211222222212223443111101111123322

beta : 121000000000000000011112211100000001122112222111111234433222111234

coil : 66787542101122345678776776555666677776665555455666444554445556655433

905914924934944954964

seq : NRDTTSIQGGIPTFDHNNREQKRIKENIQNKKFNSRDTCEGEGKKERTEDSIGNHHFSLCKKCTSKKHFDG

S.S. : CCCCCCCCCCCCCCHHCHHHHHHCCCCCCCCCCCCCCCCCCCCCCCCCCCCCHHCCCCCCCCCCCC

alpha: 11001111000000011234443455554333222221112211221121223344332210222100

beta : 3211223200223321000011100001100110011222110112211000012111111221000001

coil : 56776556887655677654445443333455577654456766655677775443445556777787

seq : ILSKKKGTC

S.S. : CCCCCCCE

alpha: 000110000

beta : 443110025

coil : 445678863

Linear motif(s):

residues (839,846) LIG\_MAPK\_1 = KKESEFIK

residues (865,868) LIG\_PDZ\_3 = NDFL

residues (882,888) LIG\_FHA\_2 = KKTNAEN

residues (889,892) LIG\_SH2\_STAT3 = YGIQ

residues (900,903) LIG\_PDZ\_3 = NDKL

residues (906,912) LIG\_FHA\_1 = RDTTSIQ

residues (928,932) LIG\_APCC\_KENbox\_2 = IKENI

residues (929,932) LIG\_PDZ\_3 = KENI

residues (950,956) LIG\_14-3-3\_2 = RTEDSIG

residues (952,955) LIG\_PDZ\_3 = EDSI

residues (972,975) LIG\_PDZ\_3 = FDGI

SS Motif for disorder segment 12:

(start,end): (989,1001)

989998

seq : LSLNKRKSKESH

S.S. : CCCCCCCCCCHH

alpha: 1211111112345

beta : 3321111000011

coil : 445676776542

SS Motif for disorder segment 13:

(start,end): (1021,1025)

seq : KKPHN

S.S. : CCCCC

alpha: 10112

beta : 00000

coil : 78877

SS Motif for disorder segment 14:

(start,end): (1079,1082)

seq : KNNI

S.S. : HHCC

alpha: 6544

beta : 0000

coil : 2355

SS Motif for disorder segment 15:

(start,end): (1329,1337)

seq : IMKSRKMLF

S.S. : HHHCCCCCHH

alpha: 654433334

beta : 111001233

coil : 224455321

SS Motif for disorder segment 16:

(start,end): (1356,1378)

135613651375

seq : HIQMKIKEKKRKKKKKKQRNIGK

S.S. : HHHHHHHHHCCCCCCCCCCCC

alpha: 4555555544333333221100

beta : 0111111000000000000000

coil : 4222233345566666667899

Graph of Probability(helix, strand, coil)  
PDF

Amino SS Probability(helix, strand, coil)  
TXT

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Linear motif(s):

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old.protein.bio.unipd.it/cspritz/work/pid\_986020641/batch/PF3D7\_0926600.fasta\_cspritz.html

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