



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:

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]

Total amino acids:	1096
Total % disorder:	62.13
Total no. of disordered regions > 30 amino acids:	4
Total no. of disordered regions > 50 amino acids:	4
Number of disordered segments:	12
Length distribution of segments (N to C terminal order):	16 132 23 9 8 64 8 208 11 2 2 198

[illegible]

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

(start,end): (1,16)

```

      1      10
seq  : MNKTANLFKDETEKAI
S.S. : CCCCCCCCCCHHHH
alpha: 001222222345555
beta : 0000000100000123
coil : 9987666677654321

```

(start,end): (51,182)

	51	60	70	80	90	100	110
seq	:IISIPLHHVKLKEFFKKKIIKKKNKAKSVNGKTYQYIPNEKHETCNKYKNEKLIKNGPGEIEDEHLL						
S.S.	:ECCCCCCHNNHHNNHHNNHHNNHCCCCCCCCCCCCCECCCCCCCCCCCCCHNNHCCCCCCCCCHNNH						
alpha	:32100222334466765545543221222100001000011222222223445432000011234455						
beta	:5442111122221000000111110001111024442100011110000001111000122110001						
coil	:1346766543222234433345667765688754446887766666666543356899865555443						
	121	130	140	150	160	170	180
seq	:HCLNYKDGHTNIIKKKKDSYKTKTNNCTCNKNKNEDKYQIFQKYTNNTQHEDDLILKNKASY						
S.S.	:NHCCCCCCTCCCCCCCCCCCCCCCCCHNNHHNNHHNNHCCCCCHNNHHNNHHNNHNNH						
alpha	:5543211011232211112110000011111112245566543111122566776534578						
beta	:111110000123221100011111100110000000011111100001000000000000						
coil	:33456788765334577767778887777776643223578876633222455321						

(start,end): (211,233)

```

      211      220      230
seq  : KPIYKKEEKDKNFNNFSFDSYENG
S.S. : HHHHHHCCCCCCCCCHHHHHCC
alpha: 6776543211222224555421
beta : 000000000000000000000000
coil : 32223467787767764444468

```

(start,end): (295,303)

```
seq  : YYEKYSFLF
S.S. : HHHHHHHHC
alpha: 999887664
beta  : 000000000
coil  : 000112234
```

(start,end): (323,330)

Amino SS Probability(helix, strand, coil) TXT

Linear motif(s):

residues (2,8) **LIG_FHA_1 =**
NKTANLF

Amino SS Probability(helix, strand, coil) TXT

Linear motif(s):

residues (86,89) LIG_SH2_SRC = YQYI
residues (88,91) LIG_SH2_STAT5 = YIPN
residues (88,96) LIG_TRAF6 = YIPNEKHET
residues (100,103) LIG_SH2_GRB2 = YKNE
residues (102,105) LIG_PDZ_3 = NEKL
residues (116,119) LIG_PDZ_3 = DEHL
residues (128,134) LIG_FHA_1 = GHTNIIK
residues (149,153) LIG_APCC_KENbox_2 = TKEN
residues (164,167) LIG_SH2_STAT5 = YTNN
residues (166,172) LIG_FHA_2 = NNTQHEH
residues (171,174) LIG_PDZ_3 = EDDL

Amino SS Probability(helix, strand, coil) TXT

Linear motif(s):

```

residues (211,218)  LIG_SH3_4 =
                    KPIYKKEE
residues (230,233)  LIG_SH2_SRC =
                    YENG

```

Amino SS Probability(helix, strand, coil) TXT

Linear motif(s):

residues (299,303)
LIG_BRCT_BRCA1_1 = YSFLF

Amino SS Probability(helix, strand,

coil) TXT

```
seq      : IIIILAIII
S.S.     : HHHHHHHHH
alpha    : 66666665
beta     : 33333333
coil     : 00000000
```

Linear motif(s):

SS Motif for disorder segment 6:

(start,end): (346,409)

[illegible]

Graph of Probability(helix, strand, coil)

PDF

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

Linear motif(s):

residues (348,351) **LIG_SH2_STAT5**
= YIIN
residues (356,359) **LIG_SH2_STAT5**
= YLSV
residues (357,361)
LIG_BRCT_BRCA1_1 = LSVNF
residues (379,382) **LIG_PDZ_3** =
KEDI
residues (386,389) **LIG_PDZ_3** =
YELV

SS Motif for disorder segment 7:

(start,end): (427,434)

```
seq  : NKNVSLKA
S.S. : CCCCEHHH
alpha: 10012456
beta : 00024210
coil : 78853233
```

Linear motif(s):

Graph of Probability(helix, strand, coil)

PDF

Amino SS Probability(helix, strand, coil) TXT

Linear motif(s):

residues (487,494) **LIG_PP1 =**
NQKSVEFFS
residues (489,493)
LIG_BRCT_BRCA1_1 = KSVFF
residues (501,504) **LIG_SH2_STAT5**
= YLSK
residues (514,517) **LIG_PDZ_3 =**
KDIV
residues (551,557) **LIG_FHA_2 =**
FKTVFEN
residues (555,558) **LIG_PDZ_3 =**
FENL
residues (562,565) **LIG_SH2_GRB2 =**
YGNV
residues (570,575) **LIG_WW_4 =**
NGKSPE
residues (581,584) **LIG_TRAF2_1 =**
SEEE
residues (596,599) **LIG_PDZ_3 =**
KDDL
residues (612,615) **LIG_PDZ_3 =**
KDGI
residues (646,650)
LIG_BRCT_BRCA1_1 = TSNNF
residues (655,658) **LIG_SH2_SRC =**
YDPA

SS Motif for disorder segment 8:

(start,end): (459,666)

[illegible]

Graph of Probability(helix, strand, coil)

PDF

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

Linear motif(s):

residues (682,685) **LIG_PDZ_3 =**
IEDL

SS Motif for disorder segment 9:

(start,end): (677,687)

```

          677          686
seq   : LSLKKIEDLGK
S.S.  : HHHHHHHHHHHH
alpha: 88877776656
beta  : 00000000000
coil  : 11111122343

```

Linear motif(s):

SS Motif for disorder segment 10:

```
(start,end): (899,1096)
```

```

      899       908       918       928       938       948       958
seq : AIHKNSVQSKKKKKEGKKLKSNDQLMKYTHRQLQKFNFQHNI IKYSEQYKKFKKKRNEKALLWK
S.S. : NHHCCCCCCCCCCCCCCCCCCCHNNHNCCHNNNNNNNNNNNNNNNNNNNNHCCCCCCHNNNNNH
alpha: 654211243333333211111224666654478998887665465544666554323333567666
beta : 22100001000000000000100000000000000000000000000001222100000000000001110

```

Graph of Probability(helix, strand, coil)

PDF

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

residues (923,926) LIG_PDZ_3 =
NDQL
residues (930,933) LIG_SH2_STAT5
= YTHK
residues (948,951) LIG_SH2_STAT3
= YSEQ
residues (963,966) LIG_CYCLIN_1 =
KALL
residues (971,974) LIG_PDZ_3 =
LDNL
residues (999,1005) LIG_FHA_1 =
NKTDQIL
residues (1001,1004) LIG_PDZ_3 =
TDQI
residues (1007,1012) LIG_WW_4 =
RKISPF
residues (1013,1022) LIG_PCNA =
QQILYDDFMH
residues (1031,1034)
LIG_SH2_STAT5 = YIYR
residues (1069,1075) LIG_FHA_1 =
KRTKSLI
residues (1069,1077) LIG_MAPK_1
= KRTKSLIYL
residues (1070,1075) LIG_14-3-3_3 =
RTKSLI
residues (1072,1076)
LIG_CYCLIN_1 = KSLIY
residues (1076,1079)
LIG_SH2_STAT5 = YLYD
residues (1085,1088) LIG_PDZ_3 =
LDLF