

CSpritz - Accurate detection of protein disorder

Version 1.2

Title: PF3D7_1117200.fasta emailaddress: mubasher.mohammed@su.se pid: 1976228859

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
						LKKDIFEDSYLKLLI
						СССИННИНИННИН
DDDDDDD	מסססססססס	וססססססססססס	ומממממממממ	וסססססססססס	וססססססססססס	מססססססססססססססס
71	80	90	100	110	120	130
						/ETKKKKKINKSEE1
						ССССССССССНИ
DDDDDDD	DDDDDDOOO	00000000000	OOODDDDDDDI	וססססססססססס	וססססססססססס	
141	150	160	170	180	190	200
						HFITSHYLAYNKMQN
						HCCCHHHHHCHHCC
211	220	230	240	250	260	270 SCKKKKYIFKYHNKI
						ССССССИНННСССЕ
						מסססססססססססססס
281	290	300	310	320	330	340
	RNNSNKKMK					KIARKKKKKKKKKK
						нининсссссения
DDDDDDD	מסססססססס	ומממממממממ	ומממממממממ	וסססססססססס	וססססססססססס	
351	360	370	380	390	400	410
						NSMLIFKEIINLCHE
нининин	инининни	нининнссс	cccccccc	cccccccc	ССССИННССО	ссинининининссо
DDDDDDD	מסססססססס	וססססססססססס	וסססססססססס	וסססססססססס	וססססססססססס	DDDD000000D000
421	430	440	450	460	470	480
						KQKYIKTQRNLSTRS
						ccccccccccccc
וטטטטטטנ	טטטטטטטטט	וטטטטטטטטטט	וטטטטטטטטטו	וטטטטטטטטטט	ועטעטעטעטעט	ממממממממממממממ
491	500	510	520	530	540	550
						EYEKKKRTKKQNEFI
						HHCCCCCCCCCEE DDDDDDDDDDDDDDDDDDD
561	570	580 HCTUDMBNETI	590	600	610	620 KEKQNIYKENQNIY
						НИННИННИНССССС
						מססססססססססססססס
631	640	650	660	670	680	690
						ONILKMQILKGLNQI
						снинининнесссо
DDDDDDD	מסססססססס	ומממממממממ	וםםםםםםםםםם	וסססססססססס	וססססססססססס	מססססססססססססססס
701	710	720	730	740	750	760
						QTYKNELKSIVQKM
						CCCCCHHHHHCCCC
771	780	790	800	810	820	830
						ZELCLKYISYINDDN НИННИНИННОСССО
						00000000000000000000000000000000000000
841	850	860	870	880	890	900
						900 AQIDNIIKDENKEYN
						CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
						וממממממממממממ

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

911	920	930	940	950	960	970
						ENTLIKYVQLHYD
						DD000000000000000000000000000000000000
981	990	1000	1010	1020	1030	1040
						LLYGNNKAKNOND CCCCCCCCCCCCC
						DDDDDDDDDDDD
1051 VNTNNNT	1060 PEMNDNUFET	1070	1080	1090	1100 *************	1110 KGKNLYINMNNVL
						CCCCEEECCCEE
						DDDDDD0000000
1121	1130	1140	1150	1160	1170	1180
						NNILNNNEFHYNY
EEECCCC	CCCCCCCC	CCCCCEEEC	СССССНИНС	CCCHEEEECC	CCCCCECCC	СССССССНННН
ODDDDDD	DDDDDDDDDD	DDDDDDDDDDI	מממממממממ	D000000DD	מממממממממ	סססססססססססס
1191	1200	1210	1220	1230	1240	1250
	PQGACNHFCH					DYETRGNNNKRNI
						cccccccccc
OOODDDD	DDDDDDDDDD	וססססססססססס	מממממממממ	DDDDDDDDDD	סססססססססס	DDDDDDDDDDDDD
1261	1270	1280	1290	1300	1310	1320
						HIYNNNKHIYNNN
						cccccccccc
טטטטטטט	טטטטטטטטטט	וטטטטטטטטטטט	טטטטטטטטטט	טטטטטטטטטט	טטטטטטטטטט	DDDDDDDDDDDD
1331	1340	1350	1360	1370	1380	1390
						KQYENDEAILLYI
						DDDOOOOOOOOO
טטטטטטט	טטטטטטטטטטט	D 000000000	300000000	000000000	טעעעססססססס	00000000000
1401	1410	1420	1430	1440	1450	1460
						GIIHFLNNNFNKA
						НИННИННССИНИН 000000000000
1471	1480	1490	1500	1510	1520	1530
						IYSSVVLGIYQRY EEHHHHHHHHHHH
						0000000000000
1541	1550	1560	1570	1580	1590	1600
						ITVCVEKIHFLRD CHHHHHHHHHHHH
						DDD0000000000
1611	1620	1630	1640	1650	1660	1670 ILYNMSIYYSIYQ
						нининининин
						000000000000
1681	1690 KVIIIIIEKN	1700 Dentkalhut.	1710 THIERTKKNK	1720 NWIDLEDVSI	1730 VIEUVIISID	1740 NGILFYDTRKMIN
						CCCEECCHHHHHH
						ODDDDDDDDDDDD
1751	1760	1770	1700	1700	1000	1010
1751 KORRNTY	1760 LFYNFFNOLE	1770 KTKHGSSLYF	1780 TYYSKIKRVR	1790 KFDTFLKKYI	1800 OERKHOEYGF	1810 EVAGGGFLCSEQT
						EECCCCCCCCCC
DD00000	00000DDDD	DDD00000000	OOOODDDDDD	DDD00000DD	DDDDDDDDDD	DDDDDDDDDDDDD
1821						
1821 K						
C						

Disordered segment motifs: (help) 97 ELM motif(s) in total found in disordered residues

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)

```
LIG_CYCLIN_1 = KLLI
residues (72,75) LIG_PDZ_3 =
```

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

Linear motif(s):

```
residues (109,114) LIG_14-3-3_3
                     = HSISHI
  residues (114,121)
                   LIG PP1 =
                    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 =
                        IDKI.
            residues (202,205)
      LIG_SH2_STAT5 = YLAY
```

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

strand, coil)

TXT

= ANTISEO

= GYTTSEE

EESV

TXT

= OOTNNII residues (393,396) $LIG_SH2_STAT5 = YTYQ$ residues (400,403) LIG_PDZ_3 =

Linear motif(s):

```
residues (249,255) LIG_FHA_2
            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
            residues (318,321)
      LIG_SH2_STAT5 = YTTS
            residues (320,323)
         LIG_TRAF2_1 = TSEE
residues (322,325) LIG_PDZ_3 =
            residues (330,333)
       LIG_CYCLIN_1 = KFLP
 residues (377,383) LIG_FHA_1
```

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

Linear motif(s): residues (440,446) LIG_SH3_3 =

strand, coil)

```
NHRVLHP
           residues (442,446)
    LIG_CYCLIN_1 = RVLHP
residues (451,457) LIG FHA 2
                = HSTDKDO
           residues (458,461)
```

SS Motif for disorder segment 2:

(start,end): (99,209)

128 138 118 148 ILFHNKNKQVHSISHIERDINFFNYENVETKKKKKINKSEEIIQNNIRRNNKNLIYIKGDEEKYINKKYI beta : 2221100123222111111112211112221111111000122100011001124442000112211122 coil: 2234677754554444443333455665455666557654322467666777643236876655577655 178 188 198 208 169 NDVNDQNNLYNLNELYKVDKLYNIDKLHFITSHYLAYNKMQ alpha: 22222333455666655544432334333333455544444 beta: 110000000000111100011101123221112111000 coil: 5666665433332222344456554433345322234444

SS Motif for disorder segment 3:

(start,end): (219,409)

258 * NFNMNKTSKFDKHTKGINKTYHHSTHYNIGANTTSEOSHVLOVDHAPSCKKKKYTFKYHNKTYSKKMKRN alpha: 22233444444454322222222333321212223333322111122222233444333444443322 coil: 7665543444443356666656543334677665555543334678776666542233454344445567 308 318 328 338 alpha: 1222333333332222233455421121000013444333332246677765444334445566666665 388 378 398 alpha: 556666555555544333322223321111100001111113454432356 beta : 001111111111111122222112221000000122221000111100011 coil: 332222333333344444445553357877788866566775433456531

SS Motif for disorder segment 4:

(start,end): (421,704)

```
440
                          450
                                  460
     NKIFTFKNKIKHKQNDTKKNHRVLHPERFIHSTDKDQYIKIGEKHNVDNKESFDNKQKYIKTQRNLSTRS
alpha: 2222222333222211111111100234322111223222101110011221122233332222211233
beta : 012332111111110000000123210012221000013443111111100011100011222211111011
coil : 7644445555556678877765467654345778664323577667777666667654434555677654
                   510
                          520
                                  530
                                         540
     491
     {\tt YMNTYYKDDINNSENCLLKRNKVQNELEKDHIYTSQGLHKKRSFSSCSDYVNKQDEYEKKKRTKKQNEFIL
alpha: 4332222232345555555555555544333222212211112233444334455543222222233
coil: 4554445666676433333443333344554456676666666554455544344666666666422
           570
                   580
                          590
                                  600
   : INKNIIIKGKEDIISHSIVDMRNKIKKRNYEGGVKNELKNESKDIYDECKENQNIYKEKQNIYKENQNIY
```

CSpritz PID: 1976228859 LIG SH2 STAT5 = YIKI alpha: 3222211112233332355556655444322123445543224577777655334556555666532223 residues (479,482) LIG SH2 STAT5 = YIKT residues (491,494) : KENQNIYKENQNIYKEKQNIYKEKQNIYKEKQNDILTKKKKNIHFLNFMNIKKKKDDNILKMQILKGLNQT $LIG_SH2_GRB2 = YMNT$: нинининининининининининининин SS residues (497,500) LIG_PDZ_3 = alpha: 5655567776778888877777655455555444555555567787776544323346788888643221 **KDDI** residues (519,522) LIG PDZ 3 = coil: 333432222321100112222233442222345533333321111122345676542200001345667 **KDHI** seq : HYDP residues (523,526) S.S. : CCCH $LIG_SH2_STAT5 = YTSQ$ alpha: 1005 residues (538,541) LIG_PDZ_3 = beta : 1100 SDVV coil: 7794 residues (540,543) LIG_SH2_STAT5 = YVNK residues (557,560) LIG PDZ 3 = NEFT residues (570,573) LIG_PDZ_3 = 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 = residues (698,704) LIG_FHA_2 = NQTHYDP Graph of Probability(helix, strand, SS Motif for disorder segment 5: coil) PDF Amino SS Probability(helix, (start,end): (709,780) strand, coil) TXT 709 728 738 748 758 : KIVNCKSGGIIYNHOTKTKEDEEKKKKKKKKKKNLYKDEONCMEMTNIOTYKNELKSIVOKMNKHFVFKNM Linear motif(s): residues (720,723) beta: 000111001343222112211111222332222211000012222221100000112110012233321 LIG_SH2_STAT3 = YNHQ coil: 0124667875334567776654445555666555445445543223455666444433456764322345 residues (724,730) LIG_FHA_2 seq : SV S.S. : HH = TKTKEDE residues (740,743) alpha: 35 LIG_CYCLIN_1 = KNLY beta : 22 residues (758,761) coil: 32 LIG SH2 GRB2 = YKNE SS Motif for disorder segment 6: Graph of Probability(helix, strand, (start,end): (839,859) coil) PDF Amino SS Probability(helix, 839 848 858 strand, coil) DNIDGNNINGNNINGNNINGD s.s. : ccccccccccccccccccc alpha: 1111111110110011111122 **Linear motif(s):** beta: 000001233333432222100 coil: 777776545555456656776 Graph of Probability(helix, strand, SS Motif for disorder segment 7: (start,end): (879,887) Amino SS Probability(helix, strand, coil) TXT : KLNKLKLSI Linear motif(s): S.S. : нининссси alpha: 998764224 beta : 000000111 residues (879,887)

alpha: 33222223333333221111122223333322221121112221102 beta: 221111000001000000000001111112222111112333100 coil : 34565665566556677787776665554554555666665444786

916

: QIDNIIKDENKEYNKHDSDDNNKNYKNKYNNICNYNYNYNYQCFLDP

coil: 001235663

(start.end): (897.943)

SS Motif for disorder segment 8:

906

residues (898,901) LIG_PDZ_3 = residues (921,924) $LIG_SH2_GRB2 = YKNK$

Linear motif(s):

LIG_MAPK_1 = KLNKLKLSI

Graph of Probability(helix, strand,

Amino SS Probability(helix,

strand, coil)

residues (925,928)

coil) PDF

TXT

LIG_SH2_GRB2 = YNNI residues (935,938) LIG_SH2_STAT3 = YNYQ

SS Motif for disorder segment 9:

(start,end): (959,969)

959 968
seq : GTHQLKIHEEN
S.S. : CCCCCCCCHC
alpha: 1222223344
beta : 21222322111
coil : 55544444444

SS Motif for disorder segment 10:

(start,end): (994,1007)

994 1003
seq : TMDNIQKYDIKEYM
S.S. : CCCCCCCCHHHHH
alpha: 12233332367765
beta : 10001121000001
coil : 77665445522123

SS Motif for disorder segment 11:

(start,end): (1013,1113)

1032 1042 1052 1062 seq : ITFEFVKDPRSRKNNIYSIQINDKNLLYGNNKAKNQNDYNINNNIRKMNRNVEKTQNCYYNRKSELRDGC alpha: 0001110011211111100001113344322233332233455556666543332222222345543210 5422246887777774322236765444666555667654344422224555556665455544445688 1092 1102 1112 : YDPKRLMYHFPFFDEKKNKNKKKKKKKGKNLY sea CCCCHHHHCCCCCCCCCCCCCCCCEE alpha: 0034444431123333332211100000000 beta: 1000112111111001111112333223466 coil: 7854333356755555456665555666432

SS Motif for disorder segment 12:

(start,end): (1122,1158)

SS Motif for disorder segment 13:

(start,end): (1166,1190)

SS Motif for disorder segment 14:

(start.end): (1194.1349)

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 (995,998) LIG_PDZ_3 = MDNI

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 (1122,1125)
LIG_SH2_STAT5 = YINN
residues (1136,1139)
LIG_CYCLIN_1 = KYLY
residues (1137,1140)
LIG_SH2_STAT5 = YLYS
residues (1144,1147)
LIG_SH2_STAT5 = YFVD
residues (1152,1155)
LIG_TRAF2_1 = SDEE
residues (1153,1156)
LIG_PDZ_3 = DEEI

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

Linear motif(s):

residues (1173,1176) LIG_SH2_STAT5 = YTVN

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

Linear motif(s):

residues (1195,1198) LIG_SH2_STAT5 = YIVP

residues (1209.1212) LIG SH2 STAT5 = YTIK beta: 1332101232101233200133200123320012221001232100122100012221001233100111 residues (1222,1225) coil: 5445676445776444677644677644457765567876434577755577764345776434677655 LIG SH2 STAT5 = YTNK seq : HNNYHHIDDDHHNNYL residues (1232,1236) S.S. : CCCCCCCCCCCCCC LIG_CYCLIN_1 = KKLGV alpha: 2222221112222222 residues (1232,1240) beta : 1001122100000134 LIG MAPK 1 = KKLGVELNI coil: 5666555677777643 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) $LIG_SH2_GRB2 = YNNN$ SS Motif for disorder segment 15: Graph of Probability(helix, strand, (start,end): (1384,1390) coil) PDF Amino SS Probability(helix, strand, coil) TXT seq : TKERKQY S.S. : HHHHHHC alpha: 7777643 **Linear motif(s):** beta : 1100000 coil: 1112346 SS Motif for disorder segment 16: Graph of Probability(helix, strand, (start.end): (1436.1445) coil) PDF Amino SS Probability(helix, strand, coil) TXT seq : KKYYYKEEKY S.S. : CCEECCCCCE alpha: 3211001000 **Linear motif(s):** beta : 1344422235 coil: 5334576653 SS Motif for disorder segment 17: Graph of Probability(helix, strand, (start,end): (1500,1507) coil) PDF Amino SS Probability(helix, strand, coil) seq : TKNRKKNY s.s. : ccccccc alpha: 22222211 **Linear motif(s):** beta : 00001112 coil: 76666666 Graph of Probability(helix, strand, SS Motif for disorder segment 18: coil) PDF (start,end): (1541,1579) Amino SS Probability(helix, strand, coil) TXT 1560 : KNGMNDNINKNKNVDKDKNINKNIDIRTDNGIDIDVDKN Linear motif(s): alpha: 531222222111111455555433332211001100010 beta: 0000000000001100000011221100134331112 residues (1545,1548) coil: 467766667778877443434455445678754557776 $LIG_PDZ_3 = NDNI$ Graph of Probability(helix, strand, SS Motif for disorder segment 19: coil) PDF (start,end): (1589,1600) Amino SS Probability(helix, strand, coil) TXT 1589 seq : YNNPSGKSNITV **Linear motif(s):** S.S. : ECCCCCCCCHH alpha: 100000111345 beta : 530000001233 residues (1589,1592) coil: 258888876420 $LIG_SH2_GRB2 = YNNP$ SS Motif for disorder segment 20: Graph of Probability(helix, strand, (start,end): (1611,1614) coil) PDF Amino SS Probability(helix, strand, coil) TXT seq : ILSK S.S. : HHHH alpha: 9998 **Linear motif(s):** beta : 0000 coil: 0001

SS Motif for disorder segment 21:

Graph of Probability(helix, strand,

13/01/2022, 09:09 CSpritz PID: 1976228859 (start,end): (1636,1639) coil) PDF Amino SS Probability(helix, strand, coil) TXT seq : RKEY S.S. : HHHH **Linear motif(s):** alpha: 6665 beta : 0000 coil: 2223 SS Motif for disorder segment 22: Graph of Probability(helix, strand, (start,end): (1683,1685) coil) PDF Amino SS Probability(helix, strand, coil) TXT seq : IYE S.S. : HHH alpha: 545 **Linear motif(s):** beta : 000 coil: 443 SS Motif for disorder segment 23: Graph of Probability(helix, strand, (start,end): (1739,1752) coil) PDF Amino SS Probability(helix, 1739 1748 strand, coil) TXT seq : GILFYDTRKMINKQ S.S. : CCEECCHHHHHHCC alpha: 11123356766444 **Linear motif(s):** beta: 13442100000000 coil: 74333442223445 SS Motif for disorder segment 24: Graph of Probability(helix, strand, (start,end): (1763,1770) coil) PDF Amino SS Probability(helix, strand, coil) TXT seq : FNQLEKTK S.S. : HHHHHHCC alpha: 77665532 beta: 00001100 **Linear motif(s):** coil: 12223356 SS Motif for disorder segment 25: Graph of Probability(helix, strand, (start,end): (1782,1790) coil) PDF Amino SS Probability(helix, strand, coil) TXT seq : KIKRVRKFD S.S. : HHHHHHHCC alpha: 887666444 **Linear motif(s):** beta : 000000000 coil : 112223444 Graph of Probability(helix, strand, SS Motif for disorder segment 26: coil) PDF (start,end): (1796,1821) Amino SS Probability(helix, strand, coil) TXT 1796 1805 1815

(c) Ian Walsh, Alberto J. Martin and Silvio Tosatto for Biocomputing UP, 11/2016

alpha: 87765432221111000000111100 beta: 00110000111344200133210000

coil: 11123566566534688755667789

Linear motif(s):

residues (1796,1799)

 $LIG_SH2_STAT5 = YIQE$