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:	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
MNRMNDLDIEEYNRNIIQELNEAAEEGEYPLSMFLHDLIEIDMESNFSYKYMIINRLVEICINSINKKMF
CCCCCCCCHHHHHHHHHHHHHHHCCCCCHHHHHHHHHHHHHCCCCCHHHHHHHHHHHHHHHHHHHHHHHH
DDDDDDDDDOOOOOOOODDDDDDDDDDDDOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOO

71       80        90        100       110       120       130
FLADECMYFMRYCIDKCINLKDEIIKNSSFFNNINIIIDICSKEKVYNNDNLYIFEKTFFFFILDLNNNM
HHHHHHHHHHHHHHHHHHHHHHHHHHHHCCCCCCEEEEEECCCCCEECCCCCEEHHHHHHHHHHHHCCCC
OOOOOOOOOOOOOOOOOOOOOOOODDDDDDOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOO

141      150       160       170       180       190       200
DDFINLWKIYKNELIHFYTTLIYIISITISEFYVILNNIKGEDNVDIDYIHIGCELIKLIEICLDLSLVI
HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHCCCCCCCCHHHHHHHHHHHHHHHHHHHHHHHHH
OOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOODDDDDOOOOOOOOOOOOOOOOOOOOOOOOOOOO

211      220       230       240       250       260       270
FNNIDEIENIDILENHINVMIKNFHDIPDIEIKRKIMLMMKAILKKKNICDKEWNEEINNFNIKYNLLNN
HHCCCCHCHHHHHHHCEEEEECCCCCCCHHHHHHHHHHHHHHHHCCCCCHHHHHHHHHHHHHHHHHHHCC
OOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOODDDDDDDDDDDDOOOOOOODDDD

281      290       300       310       320       330       340
VSNKQKYKNKKNKKKNKNNDYYNYLNITKDKKHININYLKTNSYIYINNCYLFLNTYNENLNDITMNTSP
CCCCCCCCCCCCCCHCCCCCEEEEEEECCCCCCCCCCECCCCCEEEEECCEEEEEEECCCCCCCCCCCCC
DDDDDDDDDDDDDDDDDDDDOOOODOOOOODDDDDDDOOOOOOOOOOOOOOOOOOOOOODDDDDDDDDDDD

351      360       370       380       390       400       410
SRWNKIKLSSWGYKGSLLINFFYSYFYNTKHKLLVVISYDNMKIRSDPNYKSVFFYFKKEEISGVLSNKL
CCCCEEEECCCCCCCHHHHHHHHHHHHCCCCCEEEEEEECCEEEECCCCCCEEEEEECHHHHHHHHHHHH
DDDDDOOOODOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOODDDDOOOOOOOOOOOOOODDDDDDDDDD

421      430       440       450       460       470       480
RNTFKDKFLDNLEICIKLNSKDICNNVHELMMCRINKEKLSVDEKHKKKELYYIDEEHNLPEDTFNNTME
HHHHHHHHHHCCEEEEECCCHHHHHHHHHHHHHHCCCEEEECCCCCCCCEEEECCCCCCCCCCCCCCCCC
DDDDDDDOOOOOOOOOOOODDDDDOOOOOOOOOOOOODDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD

491      500       510       520       530       540       550
NVDNMDNDQICENDVKDNMEEIFQNKQNKQNNHIYFNNLGRNHISLINTNNLKNEEKLERRKVSFASTKE
CCCCCCCCHHHHHHHHHHHHHHHHCCCCCCCCCCCCCCCCCCEEEECCCCHHHHHHHHHHCCCEECCCCE
DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDOOO

561      570       580       590       600       610       620
LCLLNDDISVETKTMLLEESILKHVHSKYNNKCMNSNIIYDKHQSIHYDNNKKSLRENSGSMRNENLLFI
EEECCCCCECCCCECCHHHHHHHHCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCEEE
OOOOOOOODDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD

631      640       650       660       670       680       690
HDNHKKEKVEPIKISYATTRDLIGKKECLKGKLEVENNDVKDDEKGDNNNVKDDKKGDNNNVKDDKKGDN
ECCCCCCCCCCEEEEECCCCHHHCCHHHCCCCEEEECCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD

701      710       720       730       740       750       760
NNVKDDEKGDNNNDVKDEEKRDNNNNVKDDENDNMDNVKRVYNNDIKETTLNYKNLLVNHVIAKGKQINN
CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCEECCCCCCCCCCHHHHHHHHHHCCCCCCCCC
DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD

771      780       790       800       810       820       830
DKNRNEDYYTYKDNTEKKNEKEHMLNNYIHDKEKMKIIDNEDNTNNKEDTPINIYKKKNDNIYISKECIT
CCCCCCCCCCCCCCCCCCHHHHHHHHHHCCCCCCCEECCCCCCCCCCCCCCHHHCCCCCCEECCHHHH
DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD

841      850       860       870       880       890       900
NNNNNNNNNNNDNNENNENNENNENNENNSYYNNEGEKNTYNQNISNHLQNKDKKKYTNSIENEALIKNN
CCCCCCCCCCCCCCCCCCCCCCCCCCCCCEEECCCCCCCCCCCHHHHHHCCCCCCCCCHHHHHHHHHC
DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD
```

Total amino acids:		1467
Total % disorder:		69.66
Total no. of disordered regions > 30 amino acids:		4
Total no. of disordered regions > 50 amino acids:		3
Number of disordered segments:		21
Length distribution of segments (N to C terminal order):		9 11 6 5 12 23 1 7 16 1 4 17 5 100 583 146 11 1 8 19 37

```
911       920        930        940        950        960        970
IKNDEKYINYQNYKERKILHHKNNMINKNDIESTPQLQMSYILNNSQNNYSINKDNIIKSPIEIVRKLLN
CCCCCHHHHHHHHHHHHHHCCCCCCCCCCCCCCCCHHHHHHHHCCCCCCCCCCCCCCCCCHHHHHHHHHC
DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD

981       990       1000       1010       1020       1030       1040
FDEKQKNIEECIENINNNNNNINDKYPKEKNKLKEDQIKHLKYDDMNSMPNDNDNVHHNLNNLCMISKEE
CCHHHHHHHHHHHHHHHHHHCCCCCCCCCCCCCCHCCCHHHHHHCCCCCCCCCCCCCCCCCCCCCHCCCCCCC
DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD

1051      1060       1070       1080       1090       1100       1110
NIITKKNTTEKYCNIFKNINNKINCNNNEDNYLINRRNEKKEKSKINKNKNNYNKEYNDEEKKDKDHINH
HHCCCCCCCHHHHHHHCCCCCCCCCCCCCCHHHHHHCCCHHHHEECCCCCCCEEECCCCCCCCCCCCCC
DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD

1121      1130       1140       1150       1160       1170       1180
NISDDNFIMKNNNIKNVEGNQNRQDVVVDVGNIISINNKDEIHEHDTPRKKKQKKKFKNINLDNTSNEYS
CCCCCCHHHHCCCCCCCCCCCCCCCCEEEEECCCEEEECCCCCCCCCCCCCCCHHHCCCCCCCCCCCCCCCCCCE
DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDOOODDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD

1191      1200       1210       1220       1230       1240       1250
QIVNISGYDDEPSNELIFKLESNVVSPCNIDKSCLSSKSKKRISTTMINNTTPNNNNNNNNNNININNNN
EEEEECCCCCCCCCCHHHHHHHCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCECCCCCCCCCCCCCCCCEEEECCCC
DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD

1261      1270       1280       1290       1300       1310       1320
NIYKDNCNYYNNTYCKETNDTYSKNPIDSPYPIKKVKYNYYYDSKLFELLKKEDNLEKLSAKYLIRAYTL
CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCEEECCCCCHHHHHHHHHCCCHHHHHHHHHHHHHHH
DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDOOOOOOODDDDDDDDDDDDOOODOOOOOOOOO

1331      1340       1350       1360       1370       1380       1390
IQYNKRYVHIQIIDYFRYIKKEILLSYDNINIKYNKLLNHIQSQHDNKLQNILIKYYKHLKEHTNQKKNL
HHHHHHHHHHHHHHHHHHHHHHCHHHHHHHHHHHHHHHHHHHCHHHHHHHHHHHHHHHHHHHHCCCCCC
OOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOODDDDDDDDOOOOOOOOOOOOOODDDDDDDDDDDD

1401      1410       1420       1430       1440       1450       1460
NLNKNIPKSINRNIIKIKIKSLYDTLNIVQRTMKDKILNSTIMLNYKQSDIYTPSFSLGTIISKYSI
CCCCCCCCCCCHHHHHHHHHHHHHHHHHHHHHHHHHHHHCCHHHHCCCCCCCCCCCCCCCCCCCCCCCC
DDDDDDDOOOOOOOOOOOOOOOOOOOOOODDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD
```

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

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

```
seq   : MNRMNDLDI
S.S.  : CCCCCCCCH
alpha : 001112228
beta  : 000000000
coil  : 988877761
```

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

Linear motif(s):

SS Motif for disorder segment 2:
(start,end): (19,29)

```
        19        28
seq   : ELNEAAEEGEY
S.S.  : HHHHHHCCCC
alpha : 99999874111
beta  : 00000000001
coil  : 00000125887
```

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

Linear motif(s):

residues (23,26)   LIG_TRAF2_1 = AAEE

SS Motif for disorder segment 3:
(start,end): (93,98)

```
seq   : EIIKNS
S.S.  : HHHHHC
alpha : 887643
beta  : 000000
coil  : 011246
```

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

Linear motif(s):

SS Motif for disorder segment 4:
(start,end): (182,186)

```
seq   : EDNVD
S.S.  : CCCCC
alpha : 11100
beta  : 00011
coil  : 87877
```

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

Linear motif(s):

residues (182,185)   LIG_PDZ_3 = EDNV

SS Motif for disorder segment 5:
(start,end): (258,269)

```
        258       267
seq   : NICDKEWNEEIN
S.S.  : CCCCHHHHHHH
alpha : 100478889998
```

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

Linear motif(s):

```
beta : 000000000000
coil : 888511110001
```

SS Motif for disorder segment 6:
(start,end): (277,299)

```
        277      286      296
seq  : LLNNVSNKQKYKNKKNKKKNKNN
S.S. : HHCCCCCCCCCCCCCCCCHCCCC
alpha: 6431111222221123344321
beta : 0000000133321001111111
coil : 3467787754345 6775444566
```

SS Motif for disorder segment 7:
(start,end): (310,316)

```
seq  : DKKHINI
S.S. : CCCCCCC
alpha: 1111002
beta : 1001443
coil : 7776543
```

SS Motif for disorder segment 8:
(start,end): (340,355)

```
        340      349
seq  : NLNDITMNTSPSRWNK
S.S. : CCCCCCCCCCCCCCCE
alpha: 2212110000001100
beta : 1001332110000125
coil : 6676556789887774
```

SS Motif for disorder segment 9:
(start,end): (395,398)

```
seq  : RSDP
S.S. : ECCC
alpha: 0000
beta : 6410
coil : 3589
```

SS Motif for disorder segment 10:
(start,end): (411,427)

```
        411      420
seq  : EISGVLSNKLRNTFKDK
S.S. : HHHHHHHHHHHHHHHHH
alpha: 77666667888777776
beta : 00000000000000000
coil : 22232222111122222
```

SS Motif for disorder segment 11:
(start,end): (440,444)

```
seq  : SKDIC
S.S. : CHHHH
alpha: 24566
beta : 00000
coil : 64432
```

SS Motif for disorder segment 12:
(start,end): (458,557)

```
        458      467      477      487      497      507      517
seq  : EKLSVDEKHKKKELYYIDEEHNLPEDTFNNTMENVDNMDNDQICENDVKDNMEEIFQNKQNKQNNHIYFN
S.S. : CEEEECCCCCCCCEEEECCCCCCCCCCCCCCCCCCCCCCCCCCCHHHHHHHHHHHHHHHHHHCCCCCCCCCCCC
alpha: 2100001110111111112321001111112332111233445655666689999865433221222221
beta : 3456531000113455421000000011000000000000011100000000000000000000023331
coil : 4333467888765433456568887777776556788876543333433331000012455666754346
        528      537      547
seq  : NLGRNHISLINTNNLKNEEKLERRKVSFAS
S.S. : CCCCCCEEEECCCCHHHHHHHHHHCCCEECC
alpha: 110100000000234556666 6543211211
beta : 0000146776410000000000112234432
coil : 7888753222566543322222334544345
```

residues (265,268)　LIG_PDZ_3 = NEEI

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

Linear motif(s):

residues (287,290) LIG_SH2_GRB2 = YKNK

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 (346,351)　LIG_WW_4 = MNTSPS

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 (421,427)　LIG_FHA_2 = RNTFKDK

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 (469,473) LIG_CYCLIN_1 = KELYY
residues (473,476) LIG_SH2_STAT5 = YIDE
residues (489,492)　LIG_PDZ_3 = MENV
residues (497,500)　LIG_PDZ_3 = NDQI
residues (509,512)　LIG_PDZ_3 = MEEI
residues (516,526) LIG_MAPK_1 = KQNKQNNHIYF
residues (525,528) LIG_SH2_STAT5 = YFNN
residues (531,537)　LIG_14-3-3_2

SS Motif for disorder segment 13:
(start,end): (569,1151)

```
           569        578        588        598        608        618        628
seq  : SVETKTMLLEESILKHVHSKYNNKCMNSNIIYDKHQSIHYDNNKKSLRENSGSMRNENLLFIHDNHKKEK
S.S. : ECCCCECCHHHHHHHHCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCEEEECCCCCCC
alpha: 000011124566665532232111111222221110001112211233321112333321111111110
beta : 433334321000000111000002211012332222221100011111110001111246653100111
coil : 456544443322223356666776667665445666666666777655556777655554311357888777
           639        648        658        668        678        688        698
seq  : VEPIKISYATTRDLIGKKECLKGKLEVENNDVKDDEKGDNNNVKDDKKGDNNNVKDDKKGDNNNVKDDEK
S.S. : CCCEEEEECCCCHHHCCHHHCCCCEEEECCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
alpha: 000000011234433334443100000011111111111112221111111111111111111111111
beta : 234688864321122221111113677520011000000001110000000011100000000111000
coil : 765211124554333443345786322367767777787776667877887776678888777667777
           709        728        738        748        758        768
seq  : GDNNNDVKDEEKRDNNNNVKDDENDNMDNVKRVYNNDIKETTLNYKNLLVNHVIAKGKQINNDKNRNEDY
S.S. : CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCEECCCCCCCCCCHHHHHHHHHCCCCCCCCCCCCCCCCC
alpha: 111122333444322222212222222333223322222333333345555555543222221121212222
beta : 000000110000000000110000000002334310011111111111111122221012210000000012
coil : 888776555544567776667766776665332357765444454332222222457654677777764
           779        788        798        808        818        828        838
seq  : YTYKDNTEKKNEKEHMLNNYIHDKEKMKIIDNEDNTNNKEDTPINIYKKKNDNIYISKECITNNNNNNNN
S.S. : CCCCCCCCCCHHHHHHHHHHCCCCCCCEECCCCCCCCCCCCCCCCHHHCCCCCEEEECCHHHHCCCCCCCC
alpha: 222211233445677665554334442221112211111110233433211111112344333322222222
beta : 333210000000000000011000113443100000000001222322100145532233221111111
coil : 444567655553322234345654454335777778877886433345678632244322345655555
           849        858        868        878        888        898        908
seq  : NNNDNNENNENNENNENNENNSYYNNEGEKNTYNQNISNHLQNKDKKKYTNSIENEALIKNNIKNDEKYI
S.S. : CCCCCCCCCCCCCCCCCCCCEEECCCCCCCCCCCHHHHHHHCCCCCCCCCCCHHHHHHHHHCCCCCCHH
alpha: 222222233333222222222211122211111112344455554432222322235677887643323455
beta : 111111222222222222233444321011110001000000000011100000000000000000111
coil : 566665444444444455445323467776665544334345667665566532211013556664322
           919        928        938        948        958        968        978
seq  : NYQNYKERKILHHKNNMINKNDIESTPQLQMSYILNNSQNNYSINKDNIIKSPIEIVRKLLNFDEKQKNI
S.S. : HHHHHHHHHHCCCCCCCCCCCCCHHHHHHHCCCCCCCCCCCCCCCCCCHHHHHHHHHHCCHHHHHHHH
alpha: 455455555654433333332323211455456665422222122123333216888887753346665 58
beta : 100000001000000011000000000101111110000012110001110000000000000000000
coil : 334444333234556655556666785434321124676666566665556721000012465532 3341
           989        998       1008       1018       1028       1038       1048
seq  : EECIENINNNNNNNINDKYPKEKNKLKEDQIKHLKYDDMNSMPNDNDNVHHNLNNLCMISKEENIITKKNT
S.S. : HHHHHHHHHCCCCCCCCCCCHCCCHHHHHHCCCCCCCCCCCCCCCCCCCCCCCCHHCCCCCCHHCCCCCC
alpha: 998888764333332111234444456677654333332100011234443444433234444322112
beta : 000000000110000000001222111122333333222112334443222221001111112221100
coil : 000001124555556677876545554322233455666788887764445554433455444333 45677
           1059       1068       1078       1088       1098       1108       1118
seq  : TEKYCNIFKNINNKINCNNNEDNYLINRRNEKKEKSKINKNKNNYNKEYNDEEKKDKDHINHHNISDDNFI
S.S. : CHHHHHHHHHCCCCCCCCCCCCCHHHHHHCCCHHHHHEECCCCCCCCEEECCCCCCCCCCCCCCCCCCHH
alpha: 345666666554322221111334555544333333333332222111112122221122332211122344
beta : 0001101111100112110000012221111223333332211233444322222100111111100012
coil : 543222222345655567876653222344433332223455555433345544566654566677 7633
           1129       1138       1148
seq  : MKNNNNIKNVEGNQNRQDVVVDVG
S.S. : HHCCCCCCCCCCCCCCCEEEECC
alpha: 433212221111101000000000
beta : 221012222211111123677521
coil : 335665555567777766312467
```

Right column:

```
                              = RNHISLI
residues (537,543)    LIG_FHA_1
                      = INTNNLK
residues (545,548)    LIG_PDZ_3 =
                      EEKL
              residues (547,555)
LIG_MAPK_1 = KLERRKVSF
residues (549,556)    LIG_PP1 =
                      ERRKVSFA
```

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

Linear motif(s):

```
residues (572,578)    LIG_FHA_1
                      = TKTMLLE
residues (578,581)    LIG_PDZ_3 =
                      EESI
              residues (589,592)
LIG_SH2_GRB2 = YNNK
              residues (608,611)
LIG_SH2_GRB2 = YDNN
residues (624,627)    LIG_PDZ_3 =
                      NENL
              residues (635,644)
LIG_MAPK_1 = KKEKVEPIKI
residues (636,639)    LIG_PDZ_3 =
                      KEKV
residues (646,652)    LIG_FHA_2
                      = YATTRDL
residues (647,653)    LIG_FHA_1
                      = ATTRDLI
residues (650,653)    LIG_PDZ_3 =
                      RDLI
residues (656,659)    LIG_PDZ_3 =
                      KECL
residues (735,738)    LIG_PDZ_3 =
                      MDNV
              residues (742,745)
LIG_SH2_GRB2 = YNND
              residues (753,756)
LIG_SH2_GRB2 = YKNL
              residues (754,758)
LIG_CYCLIN_1 = KNLLV
residues (778,784)    LIG_FHA_2
                      = YYTYKDN
              residues (779,782)
LIG_SH2_STAT5 = YTYK
              residues (798,801)
LIG_SH2_STAT5 = YIHD
residues (817,822)    LIG_WW_4 =
                      KEDTPI
              residues (826,834)
LIG_MAPK_1 = KKKNDNIYI
residues (829,832)    LIG_PDZ_3 =
                      NDNI
              residues (833,836)
LIG_SH2_STAT5 = YISK
residues (836,839)    LIG_PDZ_3 =
                      KECI
              residues (871,874)
LIG_SH2_GRB2 = YYNN
residues (896,902)    LIG_FHA_1
                      = KYTNSIE
              residues (897,900)
LIG_SH2_STAT5 = YTNS
residues (903,906)    LIG_PDZ_3 =
                      NEAL
              residues (917,920)
LIG_SH2_STAT5 = YINY
residues (941,946)    LIG_WW_4 =
                      IESTPQ
residues (942,948)    LIG_FHA_1
                      = ESTPQLQ
              residues (951,954)
LIG_SH2_STAT5 = YILN
residues (964,967)    LIG_PDZ_3 =
                      KDNI
residues (967,972)    LIG_WW_4 =
                      IIKSPI
residues (972,975)    LIG_PDZ_3 =
                      IEIV
              residues (976,979)
```

LIG_CYCLIN_1 = RKLL
residues (978,982)
LIG_Clathr_ClatBox_1 = LLNFD
residues (989,992)   LIG_PDZ_3 =
EECI
residues (1015,1018)
LIG_PDZ_3 = EDQI
residues (1019,1023)
LIG_CYCLIN_1 = KHLKY
residues (1033,1036)
LIG_PDZ_3 = NDNV
residues (1047,1050)
LIG_TRAF2_1 = SKEE
residues (1049,1052)
LIG_PDZ_3 = EENI
residues (1062,1065)
LIG_SH2_STAT5 = YCNI
residues (1082,1085)
LIG_SH2_STAT5 = YLIN
residues (1115,1118)   LIG_PDZ_3
= KDHI
residues (1144,1147)
LIG_PDZ_3 = QDVV

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

Linear motif(s):

residues (1159,1162)
LIG_PDZ_3 = KDEI
residues (1164,1169)
LIG_WW_4 = EHDTPR
residues (1170,1182)
LIG_MAPK_1 =
KKKQKKKFKNINL
residues (1183,1189)
LIG_FHA_2 = DNTSNEY
residues (1204,1207)
LIG_PDZ_3 = NELI
residues (1211,1217)   LIG_SH3_3
= ESNVVSP
residues (1213,1218)
LIG_WW_4 = NVVSPC
residues (1232,1238)   LIG_14-3-
3_2 = RISTTMI
residues (1233,1239)
LIG_FHA_1 = ISTTMIN
residues (1239,1244)
LIG_WW_4 = NNTTPN
residues (1269,1272)
LIG_SH2_GRB2 = YYNN
residues (1274,1277)
LIG_SH2_STAT5 = YCKE
residues (1286,1291)
LIG_WW_4 = PIDSPY

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

Linear motif(s):

residues (1313,1316)
LIG_PDZ_3 = EDNL

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):

SS Motif for disorder segment 14:
(start,end): (1155,1300)

```
        1155      1164      1174      1184      1194      1204      1214
seq  : SINNKDEIHEHDTPRKKKQKKKFKNINLDNTSNEYSQIVNISGYDDEPSNELIFKLESNVVSPCNIDKSC
S.S. : EECCCCCCCCCCCCCHHHCCCCCCCCCCCCCCCCCEEEEEECCCCCCCCCCHHHHHHHCCCCCCCCCCCCC
alpha: 00013343332113455543322111100001111100000000000124566655432000011100122
beta : 64200011111000000000011123321000123468876311000000112211101232111111111
coil : 24786544456785444445556654567888765320013577888875311123456667777777766
        1225      1234      1244      1254      1264      1274      1284
seq  : LSSKSKKRISTTMINNTTPNNNNNNNNNININNNNNNNIYKDNCNYYNNTYCKETNDTYSKNPIDSPYPIK
S.S. : CCCCCCCCCCCCCCECCCCCCCCCCCCCCCEEEECCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
alpha: 21122111111122210011211221111122222211122222222221111111122321000000011
beta : 11100112322333233211111111124443211123321111111123332100000000000001123
coil : 66776665555543456666666666666432345665445665555567644567776567988899875 4

seq  : KVKYNY
S.S. : EEECCC
alpha: 100111
beta : 455433
coil : 434455
```

SS Motif for disorder segment 15:
(start,end): (1308,1318)

```
        1308      1317
seq  : ELLKKEDNLEK
S.S. : HHHHHCCCHHH
alpha: 99865433777
beta : 00000000000
coil : 00134565222
```

SS Motif for disorder segment 16:
(start,end): (1369,1376)

```
seq  : NHIQSQHD
S.S. : HHHHHHHC
alpha: 99987654
beta : 00000000
coil : 00012345
```

SS Motif for disorder segment 17:
(start,end): (1390,1408)

```
        1390      1399
seq  : LKEHTNQKKNLNLNKNIPK
S.S. : HHHHHCCCCCCCCCCCCCCC
alpha: 8887544444433321001
```

```
beta : 0000000000000000000
coil : 0012455555555678998
```

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

Linear motif(s):

SS Motif for disorder segment 18:
(start,end): (1431,1467)

```
        1431     1440      1450      1460
seq  : RTMKDKILNSTIMLNYKQSDIYTPSFSLGTIISKYSI
S.S. : HHHHHHHCCHHHHCCCCCCCCCCCCCCCCCCCCCCCC
alpha: 776666543445554222210000112233332100
beta : 000000000012211111001210011001222110 0
coil : 223333345532234566667888776643446789
```

residues (1434,1437)
LIG_PDZ_3 = KDKI
residues (1439,1445)
LIG_FHA_1 = NSTIMLN
residues (1450,1455)
LIG_WW_4 = DIYTPS
residues (1451,1457)
LIG_SCF_FBW7_1 = IYTPSFS
residues (1452,1455)
LIG_SH2_STAT5 = YTPS