CSpritz - Accurate detection of protein disorder

Version 1.2

Title: PF3D7_1025400.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:	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
MDNNNIVYIEKKTKEKKKEEKEKNKEFDSFHMKNIFLLVIHFLFYIILVHIYYTYNNENLLQCFNNSFSY
CCCCCEEEEEEEEEEEEEEEEEEEEEEECCCCCHHHHHHHHHHHHHHHEEEEEEEEECCCCCHHHHHCCCCHE
DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDOOOOOOOOOOOOOOOOOODDDDDDDDDDDDDDDDDDD

71        80        90        100       110       120       130
ILKSPYLNIYDVEIIQNNLSNISQMCNHDKLNYSKYIDTDYFKYSFLFYNQHVNTYIDYVIIFHKLNQSE
EECCCCCCCHHHHHHHCCHHHHHHHCCCCCCCCCCCCCCCCCEEEEEHHCCCCCEEEEEEEEEECCCCHH
DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD

141       150       160       170       180       190       200
ILKKEIHISITKYFFWKEWVLYIFFNLMTCAIINIYWKKKERKENIFHVSVISLININIIYQQFIDSIEY
HHHHHHHCCCHHHHHHHHHHHHHHHHHHHHHHHHHCCCCCCEEEEEEEEEHHHHHHHHHHHHHCCCCC
DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDOOODDDDDDDDDDDDDDDDDDDDDDDDDD

211       220       230       240       250       260       270
GSTYEKFIALLIYIYYILLILNIFKELSKVSKIFRIPINIISNTLKHNKVLFISLSAFVVVPFVKYITSL
CCHHHHHHHHHHHHHHHHHHHHHHCCCEEECCHHHHHCCCCCCCCEEEEEECCEEEEEECCCEECCC
DDDDDDDDDDDDDOOOODDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDOOOOODDDDDDDDDDDDDDDDDD

281       290       300       310       320       330       340
QNYSDYIKSFDLFEKNNIYKNEYPYYFLFSLIYNFFFIPMIIVISTASTFLLVNKNDLLLNCKLRNMPLW
CCCCCCCCEECCCCCCCCCCCCCCHHHEEEEEEEEEEEEEEEEEEEEEEEEEEECCCCCCCCCCCCCCHHH
DDDDDDDDDDDDDDDDDDDDDDDDDOOOOOOOOOOOOOOOOOOOOOOOOOOODDDDDDDDDDDDDDDDDDD

351       360       370       380       390       400       410
LKIKEYLFFFQVNKKLNKQKMFISDEKNIKNMSILKFSNISCFGLFFIFLILKINFDQSSYDHINKKYNL
HHHHHHHHHHHHCCCCCCCCCCCCCHHHHHCHHHHHHHHHHEEEEEEEEEEEEECCCCCCHHHHHHHHH
DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDOOOOOOOOOOOOOODDDDDDDDDDDDDDDD

421       430       440       450       460       470       480
LLKEYFLTDTNMEKSYDTFTYSADYYNFLNSIVIKNIMRNKKDLQNKNLFDINLNLNDYNISIYDDFFNH
HCCCCCCCCCCCCCCCCCCCCHHHHHHHHHHHHHHHHHHCCCCCCCCCCCHHHHCCCCCCCEEEECCCCC
DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD

491       500       510       520       530       540       550
FPYDVFLKFSGNNQISDEITIANPLLAHESNTDSTKLENYKSIIEDNKGRIKYYDAYSILYNFEYSLSLL
CCCEEEEECCCCCCCCCEEECCCCCCCCCCCCCCHHHHHHHHHHCCCCCCCCCHHHHHHHHHHHCHEHH
DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD

561       570       580       590       600       610       620
IRTSFKVQHYGVFKKDKEIFVHEIYEDNYNNMYNYKYILLIIMFIITIIYLILTIFMVYYIRSKIYISFF
EHCCCCCCCCCCCCCCCCEEEEEEECCCCCCHHHHHHHHHEHHHHHHEEEEEEEEEEEEEEHCHHHHHHH
DDDDDDDDDDDDDDDDDDDDDDDDDOOOOOOOOOOOOOOOOOOOOOOOOOOOOODDDDDDDDDDO

631       640       650       660       670       680       690
SFFFLNFFFFFLFHFMSFTPVSYFYDYINDIKENQISEIFNNMNKQDNFRSLLFDLLKIKWYKFYANLFS
HHHHHEEEEEEEEEEECCCCHHHHHHHHHHHHCHHHHHHCHCHHCCHHHHHHHHHHHHHHHHHHHHH
OOOOOOOOOOOOOODDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDOO

701       710       720       730       740       750       760
YIIILTSLLNFFFLFFINHISFLIKHKKKKFLLVSIPIWISVFFMSLIGSYFPCNIQKNIFKWILLFYQIQ
HHHHHHHHHHHHHHHHHHHHHHHHHHCCCCCCCCHHHHHHHHHHHHHHHHC
OOOOOOOOOODDDDDDDDDDDDDDDDDDDDDOOOOODDDDDDDDDDDDDDDDDOOOOOODD

771       780       790       800       810       820       830
TNQNSFPYEVLNKFIFVFFLFYLTSIFLFIYVKKKPNIIKLKRRNYQNDKDPKQVPFNNTNICENYDILL
CCCCCCHHHHHHHHHHHHEEEHHHEEEEEECCCCCEEEEEECCCCCCCCCCCCCCCCCCCCCCCHHHHH
DDDDDDDDDDDOOOOOOOOOOOOOOOODOOODDDDDDDDDDDDDDDDDDDDDDDDDD

841       850       860       870       880       890       900
YFKALLYSLDKTFEKVQLLKEKNKFSQMLNLQINMYNMYEQQKMMLQYGNINAQGNYMNGQTNNVMNGQG
HHHHHHHCCCCCCCCCCCCCCCCCCCCCHHHHCCCCCCCCCCCCCCCCCCCCCCCC
DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD
```

Total amino acids:	1358
Total % disorder:	86.96
Total no. of disordered regions > 30 amino acids:	10
Total no. of disordered regions > 50 amino acids:	6
Number of disordered segments:	21
Length distribution of segments (N to C terminal order):	36 135 34 34 38 61 190 9 53 27 18 14 1 165 5 13 5 5 13 13 312

```
911       920        930        940        950        960        970
NNYMNGQTNNVMNGQGNNYMNGQKNNVMNGQGNNYTNSQMNNYMNIQTNNCMNGQENNYLNSQTNNYMNI
CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDOOODDDDDO

981       990       1000       1010       1020       1030       1040
QTNNCMSGQENNYLNSQTNNYMNIQTNNYMNIQTNNCMSGQENNYLNSQTNNYMNIQTNNYMNIQTNNYM
CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
OODDDDDDDDDDDDDDOOODDDDDOOODDDDDOOODDDDDDDDDDDDDDOOODDDDDDDDDDDDDDOOODDDDD

1051      1060       1070       1080       1090       1100       1110
NGQENNYMNGQTNNFMNDQTNNYMNSQVHTEIPYRPNENAQTSSQIMNGKHNYDHTMVGNIQDGKGINTH
CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD

1121      1130       1140       1150       1160       1170       1180
AKHKLYEIKKNDDHDIIDEDTSNNEDLERQNKNKDDEVDMIEKIENMSLFFTNILNEKYDFNFLKDENIK
CCCCCCCCCCCCCCCCCHHHHHCCCHHHHHCCCCCCEEEEEEEHHHHHHHHHHHHHHCCCCHHHCCHCCCC
DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD

1191      1200       1210       1220       1230       1240       1250
NNKKKTLVQWIISGLYDKDNYKRNEEDKEKRQKNTKQLKRMIENLNEDLYYIDKIKISFTYLLFLKIKKY
CCCCCHHHHHHCCCCCCCCCCCCHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH
DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD

1261      1270       1280       1290       1300       1310       1320
ILIQKFNNLKEKKGELKTTYQNKILYKSHLSKLQQNLTKQMYQLEKNVLITNNLRDGLIHIIEDEAFYKK
HHHHHHHHCCCCCCCCCHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHCCCCCCCEEEECCCCCCC
DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD

1331      1340       1350
DEQNSSEEKKEQIINEEAQSNKGRIFEK
CCCCCCHHHHHHHHHHHHCCCCCCCCCC
DDDDDDDDDDDDDDDDDDDDDDDDDDDD
```

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

SS Motif for disorder segment 1:
(start,end): (1,36)

```
      1        10        20        30
seq  : MDNNNIVYIEKKTKEKKKEEKEKNKEFDSFHMKNIF
S.S. : CCCCCEEEEEEEEEEEEEEEEEEEEEECCCCCHHHH
alpha: 00011222222222221111110000000023456666
beta : 00001466665554555667776665410000000122
coil : 99886210011222222211111233357754432210
```

SS Motif for disorder segment 2:
(start,end): (53,187)

```
      53        62        72        82        92        102       112
seq  : YTYNNENLLQCFNNSFSYILKSPYLNIYDVEIIQNNLSNISQMCNHDKLNYSKYIDTDYFKYSFLFYNQH
S.S. : EECCCCCHHHHHCCCCHEEECCCCCCCHHHHHHHCHHHHHHHHHCCCCCCCCCCCCCCCCCCEEEEEEHCC
alpha: 221123467665433333321001104455665544556777642112222220111111123344433
beta : 542000000000001233443102221012222100000000110012222233210024555443101
coil : 23577553222346543212588666443111134543322246776554444567876421111122355
      123       132       142       152       162       172       182
seq  : VNTYIDYVIIFHKLNQSEILKKEIHISITKYFFWKEWVLYIFFNLMTCAIINIYWKKKERKENIF
S.S. : CCCEEEEEEEEECCCCHHHHHHHHHCCCHHHHHHHHHHHHHHHHHHHHHHHHHHHCCCCCCEE
alpha: 22222222222233244565554433333444567777777776566666666655443332222
beta : 11345567665321000011111223322122211112222211111233322211000011245
coil : 554212000013456543233333333343332110000000122211000011234555555521
```

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

Linear motif(s):

residues (8,11)   LIG_SH2_STAT5 = YIEK

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

Linear motif(s):

residues (53,56)
LIG_SH2_STAT5 = YTYN
residues (55,58)
LIG_SH2_GRB2 = YNNE
residues (57,60)   LIG_PDZ_3 = NENL
residues (70,73)
LIG_SH2_STAT5 = YILK
residues (71,76)   LIG_WW_4 = ILKSPY
residues (76,79)
LIG_SH2_STAT5 = YLNI
residues (82,85)   LIG_PDZ_3 = VEII
residues (98,101)   LIG_PDZ_3 = HDKL
residues (106,109)
LIG_SH2_STAT5 = YIDT
residues (111,114)
LIG_SH2_STAT5 = YFKY
residues (114,118)
LIG_BRCT_BRCA1_1 = YSFLF
residues (122,127)   LIG_14-3-3_3 = HVNTYI
residues (123,129)   LIG_FHA_2 = VNTYIDY
residues (126,129)
LIG_SH2_STAT5 = YIDY
residues (127,130)   LIG_PDZ_3 = IDYV
residues (129,132)
LIG_SH2_SRC = YVII
residues (139,142)   LIG_PDZ_3 =

<div align="right">

SEIL
residues (143,150)
LIG_MAPK_1 = KKEIHISI
residues (153,156)
LIG_SH2_STAT5 = YFFW
residues (157,160)   **LIG_PDZ_3 =**
KEWV
residues (162,165)
LIG_SH2_STAT5 = YIFF
residues (167,173)   **LIG_FHA_1**
= LMTCAII
residues (182,186)
LIG_APCC_KENbox_2 = RKENI
residues (183,186)   **LIG_PDZ_3 =**
KENI

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

Linear motif(s):

residues (205,208)   **LIG_PDZ_3 =**
IDSI

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

Linear motif(s):

residues (239,248)
LIG_MAPK_1 = KVSKIFRIPI
residues (240,244)
LIG_BRCT_BRCA1_1 = VSKIF

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

Linear motif(s):

residues (276,279)
LIG_SH2_STAT5 = YITS
residues (284,287)   **LIG_PDZ_3 =**
SDYI
residues (286,289)
LIG_SH2_STAT5 = YIKS
residues (299,302)
LIG_SH2_GRB2 = YKNE

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

Linear motif(s):

residues (336,339)   **LIG_PDZ_3 =**
NDLL
residues (343,351)
LIG_MAPK_1 = KLRNMPLWL
residues (352,359)
LIG_MAPK_1 = KIKEYLFF
residues (354,357)   **LIG_PDZ_3 =**
KEYL
residues (354,372)   **LIG_IQ =**
KEYLFFFQVNKKLNKQKMF
residues (356,359)
LIG_SH2_STAT5 = YLFF
residues (364,373)
LIG_MAPK_1 = KKLNKQKMFI
residues (377,387)
LIG_MAPK_1 = KNIKNMSILKF

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

Linear motif(s):

</div>

SS Motif for disorder segment 3:
(start,end): (191,224)

```
        191       200       210       220
seq  : VISLININIIYQQFIDSIEYGSTYEKFIALLIYI
S.S. : EEEHHHHHHHHHHHHCCCCCCCHHHHHHHHHHHH
alpha: 3334556778877753332111799999999999
beta : 6554321111010010122100000000000000
coil : 0000122110011235544677200000000000
```

SS Motif for disorder segment 4:
(start,end): (229,262)

```
        229       238       248       258
seq  : LILNIFKELSKVSKIFRIPINIISNTLKHNKVLF
S.S. : HHHHHHHHHHCCCCEEECCHHHHHCCCCCCCCHH
alpha: 8888887764432221100445433333322222
beta : 0111000000012344442223432110013566
coil : 0000011234555433456221124555564100
```

SS Motif for disorder segment 5:
(start,end): (268,305)

```
        268       277       287       297
seq  : FVVVPFVKYITSLQNYSDYIKSFDLFEKNNIYKNEYPY
S.S. : EEEEECCCEECCCCCCCCCCCCEECCCCCCCCCCCCCHH
alpha: 11111233333343332222223333322333222344
beta : 45654333332210000013343321100011111123
coil : 33233333323445556654333344566655666432
```

SS Motif for disorder segment 6:
(start,end): (331,391)

```
        331       340       350       360       370       380       390
seq  : LLVNKNDLLLNCKLRNMPLWLKIKEYLFFFQVNKKLNKQKMFISDEKNIKNMSILKFSNIS
S.S. : EEECCCCCCCCCCCCCCHHHHHHHHHHHHHHHHCCCCCCCCCCCCCHHHHHCHHHHHHHHHH
alpha: 221111223322222225788877788877654332211100124555544455554334
beta : 665410000000000000000001111111110011000124421000000122222233
coil : 012478766666666764211111000000123455567776545433444442111233 22
```

SS Motif for disorder segment 7:
(start,end): (405,594)

```
        405       414       424       434       444       454       464
seq  : NFDQSSYDHINKKYNLLLKEYFLTDTNMEKSYDTFTYSADYYNFLNSIVIKNIMRNKKDLQNKNLFDINL
S.S. : ECCCCCCHHHHHHHHHHCCCCCCCCCCCCCCCCCCCCHHHHHHHHHHHHHHHHHHCCCCCCCCCCHHHHC
alpha: 0001123567788876642111101111000111111689999988888887765333333223344433
```

```
beta : 5420000000000000000001332100023332221100000000000100000000000000122222
coil : 3577775422211122356765567888765566677310000011000001234566666666432334
       475       484       494       504       514       524       534
seq  : NLNDYNISIYDDFFNHFPYDVFLKFSGNNQISDEITIANPLLAHESNTDSTKLENYKSIIEDNKGRIKYY
S.S. : CCCCCCEEEECCCCCCCCCCEEEEEECCCCCCCCCCEEECCCCCCCCCCCCCCCCHHHHHHHHHHHCCCCCCCCC
alpha: 2211000011222100001000000000001222111123432111134566666677643222232233
beta : 1100135775312111112478986200133213565310111100000000000011000001221
coil : 5678763112465677786410012799865664223576444578876543223322124676665544
       545       554       564       574       584
seq  : DAYSILYNFEYSLSLLIRTSFKVQHYGVFKKDKEIFVHEIYEDNYNNMYN
S.S. : HHHHHHHHHHHCHEHHEHCCCCCCCCCCCCCCCCEEEEEEEECCCCCCHHHH
alpha: 4566665555544444443221222100011111222233332235677
beta : 1112222211001244444222233211332112467665320000000000
coil : 3211011233443100013455445676567763100012366664321
```

SS Motif for disorder segment 8:
(start,end): (621,629)

```
seq  : IRSKIYISF
S.S. : EHCHHHHHH
alpha: 334555655
beta : 431123333
coil : 124321000
```

SS Motif for disorder segment 9:
(start,end): (646,698)

```
       646       655       665       675       685       695
seq  : MSFTPVSYFYDYINDIKENQISEIFNNMMNKQDNFRSLLFDLLKIKWYKFYANL
S.S. : EECCCCHHHHHHHHHHHHHCHHHHHHCHCHHCCHHHHHHHHHHHHHHHHHHHHHH
alpha: 1000134455678777764478887645455446889999877788899989
beta : 5532211110000000000000000000000000000000000000000000
coil : 3457644333221112234521111354544453100000112211000010
```

SS Motif for disorder segment 10:
(start,end): (713,739)

```
       713       722       732
seq  : FLFFINHISFLIKHKKKFLLVSIPIWI
S.S. : HHHHHHHHHHHHHHHHHHHHHHHHHHHH
alpha: 66666677888776655554445666
beta : 2233211101100001233332222
coil : 0000110000012232110112210
```

SS Motif for disorder segment 11:
(start,end): (745,762)

```
            745        754
seq  : SLIGSYFPCNIQKNIFKW
S.S. : HHCCCCCCCCHHHHHHHH
alpha: 543100022355667777
beta : 322110010000000111
coil : 124788866543331100
```

SS Motif for disorder segment 12:
(start,end): (769,782)

```
            769        778
seq  : IQTNQNSFPYEVLN
S.S. : HCCCCCCCHHHHHH
alpha: 43211011688887
beta : 32210000000000
coil : 23578887310012
```

SS Motif for disorder segment 13:
(start,end): (807,971)

```
            807        816        826        836        846        856        866
seq  : NIIKLKRRNYQNDKDPKQVPFNNTNICENYDILLYFKALLYSLDKTFEKVQLLKEKNKFSQMLNLQINMY
S.S. : CEEEEEECCCCCCCCCCCCCCCCCCCHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH
alpha: 00000001121100000000001223334678888888887665678888887765568899999999999
beta : 16888642110000012222100111000011111111000000000000000000000000000000
coil : 831013466678999887777777644553200000000012333210000123443110000000000
            877        886        896        906        916        926        936
seq  : NMYEQQKMMLQYGNINAQGNYMNGQTNNVMNGQGNNYMNGQTNNVMNGQGNNYMNGQKNNVMNGQGNNYT
S.S. : HHHHHHHHHHHCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
alpha: 999999988642122221222101112221000112211111221001222211111110000011
beta : 00000000000000011110111000111110000110011112210001110000113322221011
coil : 000000011257766667666787766557888766678777656788876567877764567668877
            947        956        966
seq  : NSQMNNYMNIQTNNCMNGQENNYLN
S.S. : CCCCCCCCCCCCCCCCCCCCCCCCC
alpha: 111111111111111111111111
beta : 101100111011101110110012
coil : 7776776677667766777677667
```

SS Motif for disorder segment 14:
(start,end): (975,979)

```
seq  : NNYMN
S.S. : CCCCC
alpha: 11111
beta : 11121
coil : 77667
```

SS Motif for disorder segment 15:
(start,end): (983,995)

```
            983        992
seq  : NNCMSGQENNYLN
S.S. : CCCCCCCCCCCCC
alpha: 1111111111111
beta : 0011101111221
coil : 7766777677667
```

SS Motif for disorder segment 16:
(start,end): (999,1003)

```
seq  : NNYMN
S.S. : CCCCC
alpha: 11111
beta : 00221
coil : 77667
```

Amino SS Probability(helix, strand, coil)   TXT

Linear motif(s):

residues (750,753)
LIG_SH2_STAT5 = YFPC

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

Linear motif(s):

residues (778,781)   LIG_PDZ_3 = YEVL

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

Linear motif(s):

residues (816,819)
LIG_SH2_GRB2 = YQND
residues (836,839)   LIG_PDZ_3 = YDIL
residues (841,844)
LIG_SH2_STAT5 = YFKA
residues (843,847)
LIG_CYCLIN_1 = KALLY
residues (853,856)   LIG_PDZ_3 = FEKV
residues (862,871)
LIG_MAPK_1 = KNKFSQMLNL
residues (872,881)   LIG_PCNA = QINMYNMYEQ
residues (879,882)
LIG_SH2_STAT3 = YEQQ
residues (888,891)
LIG_SH2_GRB2 = YGNI
residues (897,900)
LIG_SH2_GRB2 = YMNG
residues (900,906)   LIG_FHA_1 = GQTNNVM
residues (913,916)
LIG_SH2_GRB2 = YMNG
residues (916,922)   LIG_FHA_1 = GQTNNVM
residues (929,932)
LIG_SH2_GRB2 = YMNG
residues (945,948)
LIG_SH2_STAT5 = YTNS
residues (953,956)
LIG_SH2_GRB2 = YMNI

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 (987,990)
LIG_TRAF2_1 = SGQE

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

Linear motif(s):

SS Motif for disorder segment 17:
(start,end): (1007,1011)

```
seq  : NNYMN
S.S. : CCCCC
alpha: 11111
beta : 11221
coil : 77667
```

SS Motif for disorder segment 18:
(start,end): (1015,1027)

```
       1015      1024
seq  : NNCMSGQENNYLN
S.S. : CCCCCCCCCCCCC
alpha: 1111111111111
beta : 1122101111221
coil : 7766776677667
```

SS Motif for disorder segment 19:
(start,end): (1031,1043)

```
       1031      1040
seq  : NNYMNIQTNNYMN
S.S. : CCCCCCCCCCCCC
alpha: 1111111111111
beta : 1122101111221
coil : 7766776677667
```

SS Motif for disorder segment 20:
(start,end): (1047,1358)

```
       1047    1056    1066    1076    1086    1096    1106
seq  : NNYMNGQENNYMNGQTNNFMNDQTNNYMNSQVHTEIPYRPNENAQTSSQIMNGKHNYDHTMVGNIQDGKG
S.S. : CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
alpha: 111111111111111111111122111111111111111111111111111111112222211112211111
beta : 1122111111221111112201111221111011211110011111001110111101111001110111011
coil : 7766776677667766776677667766776677677776666677667776556666677667766767876
       1117    1126    1136    1146    1156    1166    1176
seq  : INTHAKHKLYEIKKNDDHDIIDEDTSNNEDLERQNKNKDDEVDMIEKIENMSLFFTNILNEKYDFNFLKD
S.S. : CCCCCCCCCCCCCCCCCCCCCCHHHHCCCHHHHHCCCCCCEEEEEEEHHHHHHHHHHHHHCCCCHHHCCH
alpha: 11111112333332112222345554444456654322333323333344455667777654332455444
beta : 21100011111110000011111100000001110000013555544321111111100000110000000
coil : 6677776654444677766654433345544322345666531000112233211111124555644344
       1187    1206    1206    1216    1226    1236    1246
seq  : ENIKNNKKKTLVQWIISGLYDKDNYKRNEEDKEKRQKNTKQLKRMIENLNEDLYYIDKIKISFTYLLFLK
S.S. : CCCCCCCCCHHHHHHHCCCCCCCCCCCCHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH
alpha: 443221234577776531111333332566777777777777777667777888766668889988
beta : 000000000101111110012100000000000000000011111122211100000000111100000000
coil : 555678765311001257766666666643222112211000000011111111011222100000000
       1257    1266    1276    1286    1296    1306    1316
seq  : IKKYILIQKFNNLKEKKGELKTTYQNKILYKSHLSKLQQNLTKQMYQLEKNVLITNNLRDGLIHIIEDEA
S.S. : HHHHHHHHHHHHCCCCCCCCCHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHCCCCCCCEEEECCCC
alpha: 877788877664433221234554445556778899999999999998765554333221111111233
beta : 00010000000000011111111101211000000000000000000000122100000256653100
coil : 111100011234555677544333443222121100000000000001222223566677631124655
       1327    1336    1346    1356
seq  : FYKKDEQNSSEEKKEQIINEEAQSNKGRIFEK
S.S. : CCCCCCCCCCHHHHHHHHHHHHCCCCCCCCCC
alpha: 43222221234557777767654321111000
beta : 11100000000000000000000023210
coil : 44566777764442211222235678865689
```

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 (1019,1022)
LIG_TRAF2_1 = SGQE

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

Linear motif(s):

residues (1033,1036)
LIG_SH2_GRB2 = YMNI

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

Linear motif(s):

residues (1049,1052)
LIG_SH2_GRB2 = YMNG
residues (1057,1060)
LIG_SH2_GRB2 = YMNG
residues (1073,1076)
LIG_SH2_GRB2 = YMNS
residues (1075,1085)
LIG_SxIP_EBH_1 = NSQVHTEIPYR
residues (1080,1086)   **LIG_SH3_3 = TEIPYRP**
residues (1090,1094)
LIG_USP7_1 = AQTSS
residues (1134,1137)
LIG_PDZ_3 = HDII
residues (1144,1147)
LIG_PDZ_3 = NEDL
residues (1155,1158)
LIG_PDZ_3 = DDEV
residues (1161,1164)
LIG_PDZ_3 = IEKI
residues (1167,1171)
LIG_BRCT_BRCA1_1 = MSLFF
residues (1170,1176)
LIG_FHA_1 = FFTNILN
residues (1186,1189)
LIG_PDZ_3 = DENI
residues (1195,1198)
LIG_CYCLIN_1 = KTLV
residues (1223,1229)
LIG_FHA_1 = KNTKQLK
residues (1232,1235)
LIG_PDZ_3 = IENL
residues (1236,1239)
LIG_PDZ_3 = NEDL
residues (1241,1244)
LIG_SH2_STAT5 = YIDK
residues (1242,1245)
LIG_PDZ_3 = IDKI
residues (1244,1250)   **LIG_PP1 = KIKISFT**
residues (1248,1254)
LIG_FHA_1 = SFTYLLF
residues (1251,1254)
LIG_SH2_STAT5 = YLLF
residues (1256,1263)
LIG_MAPK_1 = KIKKYILI
residues (1260,1263)

LIG_SH2_STAT5 = YILI
residues (1280,1283)
LIG_SH2_GRB2 = YQNK
residues (1283,1286)
LIG_CYCLIN_1 = KILY
residues (1309,1315)
LIG_FHA_1 = LITNNLR
residues (1314,1322)
LIG_APCC_Dbox_1 =
LRDGLIHII
residues (1315,1318)
LIG_PDZ_3 = RDGL
residues (1335,1338)
LIG_TRAF2_1 = SSEE
residues (1340,1343)
LIG_PDZ_3 = KEQI

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