CSpritz - Accurate detection of protein disorder

Version 1.2

Title: PF3D7_0904300.fasta
emailaddress: mubasher.mohammed@su.se
pid: 1932353729

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
MSCINKLPLFIILIIYETLNKNWGAKNYYSQLNKGIYPRLLNVKCRAGESLTYDYKCDKCKEGFFNFSRD
CCCCCCCHHHHHHHHHHCCCCCCHHHHHHHCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCECCCCC
DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOO

71       80        90        100       110       120       130
NKKCSPCPIGTFSSYVGSIICENCPYGSTTKSIGSKSISDCVCNKGFKLSSYLNGGNKCVPCNSQEYCKS
CCCCCCCCCCCCCCCCCEEEEECCCCCCCCCCCCCCCCHHHHHCCCCCCCCCCCCCCCCCCCCCCHCCCC
OOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOO

141      150       160       170       180       190       200
NENTWCFRNMCLKDKNKENIKLCKKVKKKSIYNYEILCFKKGVCLNVKEKNSCLEGNKMIQCKICDENYR
CCCEEEHHHHHCCCCCCCEEEHHCCCCCEEEEEECCCCCCCEECCCCCCCCCCCCCEEEEECCCCCCC
OOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOO

211      220       230       240       250       260       270
YNFLAPLQQPCVLCNMSTYFIIFFFAIFIFVISIFIAMCINNEKEKSIIQLFFTYIQFVSLLRYVNSNYD
HHCCCCCCCHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHCCCCC
OOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOODDDDDDDDDDDOOOOOOOOOOOODDDDDDDDDD

281      290       300       310       320       330       340
HYLVKFLYFFTFGIPINEFLDCVFKRGSNLERIQKKITFLLYLPLLILICSLLCTFVITLFYKNVKRRED
CHEEEEEEEEECCCCHHHHHHHHCCCCCCHHHHHHHHHHHHHHHHHHHHHHHHHHHHEEEECCCCCCCC
OOOOOOOOOOOOODDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDOOOOOOOOOODDDDDDDD

351      360       370       380       390       400       410
VTICPFDKNYKQRSKKKHINKVDNSNVNNNNISEYKKKKDCSKRNEINIIDMNDRKEMNFCDSNNLFINE
CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCHHHHHCCCCCCCCCCCCCCCCCCCCCCCCCCCHHHC
DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD

421      430       440       450       460       470       480
ISQPKKFHHNIYSDDNITRCNLFSAENYVRSFLFFFIFYHDLIYIEIIKLCVLFCLCNYDEHREESFIII
CCCCCCCCCCCCCCCCCCCCCCCCHHHHHHHHHHHHHHCCHHHHHHHHHHHHHHCCCCCCCCCCCEEEE
DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDOOOOOOOOOOOOOOOOOOOOOODDDDDDDDDDDDDDDDDD

491      500       510       520       530       540       550
DDSINCEDMKSSYYKIMIIIIYNTFMKFFYLYFFQLLRKYVKRYQAVIDEYIILQQKAKIINKKDTLFLI
CCCCCCCHHCCHHHHEEEEEEHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHCCHHHHHHH
DDDDDDDDDDDDOOOOOOOOOOOOOODDOOOOOODDDDDDDDDDDDDDOOOOODDDDDDDDDDDOOOODOOO

561      570       580       590       600       610       620
IFIILFHKKFWITINPSLYYNYKNGLYNNNIHIFQFMIIIISFSIYVLIIHICVYERKDPHRFFFDIHTI
HHHHHHHHHHHHCCCCHHHCCCCCCCCCCEEEEEEEEEEEEEEEEEEEEEEEEECCCCCCCCCCCCCCH
OOOOODDDDDDDDDDDDDDDDDDDDDDDDDOOOOOOOOOOOOOOOOOOOOOODDDDDDDDDDDDDDDD

631      640       650       660       670       680       690
EKGKKKKKNVSNTRDCFDNDEGNKMCHMKLYSSCRIRNNKSNICHSVEKNNIKEYDKKEKEITNKRNNMW
HHCCCCCCCCCCCCCCCCCCCCCHCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCHH
DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD

701      710       720       730       740       750       760
YHFFIILFQNVKKKDTFLYSFSCLIYTTILLFYYTFLCYVHIKNFIKIITIISILCNITIYFVFILFFLI
HHHHHHHHHHCCCCCHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH
OOOOOODDDDDDDDDDDDDOOOOOOOOOOOOOOOOODDDDDDOOOOODDDDDDOOOOOOOOOOO

771      780       790       800       810       820       830
NHTIKKYNFSKKIIYIISFVKKRKRKWLGIYRKFKTLIWGNRKKMEDTYSRVKNKKGIENEQKKEQKLKS
HHCCCCCHHHHHHHHHHHHHHHHHHHHHCCCCCEECCCCCCCCCCCCCCCCCCCHHHHHHHHHH
DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD

841      850       860       870       880       890       900
LLLMSNVLNYYTDDEESILNTKNNNVKKKNNNIFMVKKWNVNNIKRHKLLNISEIWIHYLYNIISLSNEP
HHHHHHHHCCCCCCCHHCCCCCCCCCCCCCCCEEECCCCCCCCHHHHHHHHHHHHHHHHHCCCCCH
DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDOOOOOOOOOOODDOOOOO
```

Total amino acids:	**2487**
Total % disorder:	**68.63**
Total no. of disordered regions > 30 amino acids:	**14**
Total no. of disordered regions > 50 amino acids:	**10**
Number of disordered segments:	**50**
Length distribution of segments (N to C terminal order):	**27 11 11 38 109 30 2 13 10 1 26 85 14 7 6 122 2 9 12 21 31 173 1 164 41 75 28 3 8 108 10 68 3 4 16 91 24 3 6 10 5 6 22 26 30 13 16 110 41 15**

```
911       920       930       940       950       960       970
QKCLSILIKLTLEKKYPLISLKTCIHVLRKNHFFETDNFLIILKNFLKFTKKFVKVLRRKKYEQSYEYLI
HHHHHHHHHHHHHHCCCCCCHHHHHHHHHHCCCCCCHHHHHHHHHHHHHHHHHHHHHHCCCCCCHHHHH
OOOOOOOOOOOODDDDDDDDOOOOOOOOODDDDDDDDDDDDOOOODDDDDDDDDDDDDDDDDDDDDDDOOOO

981       990       1000      1010      1020      1030      1040
IYAWGMSILNYGNLRDINYNISHILFHVYSILNKCRFYKNIVEHFFNIYPYVNNNAMKGNMSLINMYNNM
HHHCCCCECCCCCHHHHHCCCCHHHHHHHHHHHHHHHHHHHHHHHHHHCCCCCCCCCCCCCCHHHHHCCCC
OOODDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDOOOOOOOOOOOOOOODDDDDDDDDDDDDDDDDDDDD

1051      1060      1070      1080      1090      1100      1110
CNFSFDKNNLYEEEKQSQKIKNNILIEQNFLDDNVNMDIKDDPCDEIEDMNNMLQMYGNSFCQSFMPLYNH
CCCCCCCCCHHHHHHCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCEEEEECCCCCCCCCCCCCC
DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD

1121      1130      1140      1150      1160      1170      1180
NFNRKNDQSIHMEETYMCDRERFNCLDKYMCSNTYINKRNSETFVNAHKGEYKYDISSDMNLIDYKKQST
CCCCCCCHHHHHHHCCCCCCCCCCCCCCCCCCCCCCCCCCCCCEEEECCCCCCCCCCCCCCCCCCCCCCCC
DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD

1191      1200      1210      1220      1230      1240      1250
RTKNFKGQRIFYHIHSLYIIELARIFIHCLLLDVSEFFFKIYHTHICEKYICNNLINLWGCYRNQNIYMK
CCCCCCCCEEEEEHHHHHHHHHHHHHHHHHHHHHHHHCCCCCCHHHHHHHHCHHHHHCCCCCCCHHHH
DDDDDDDDDDDOOOOOODOOOOOOOOOOOOOODDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD

1261      1270      1280      1290      1300      1310      1320
RFFEYIKKGEYKNQQNIIRYNICSIINEKRDDNNNNIDNTDNIDNILSITDFINKKVLDIDFYNEYEKLS
HHHHHHHHHCCCCCCHHEEECCCCCCCCCCCCCCCCCCCCCCCCCCEEEHHHHHCCCCEEEHHHHHHHHCC
DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD

1331      1340      1350      1360      1370      1380      1390
KNSKHYFINISEEKDYLNINELINFSKASDNIEELKRLQNNLIEKRNKKKLKIFSLIFCSAMPVHIIDDY
CCHHHHHHHHHHHCCCCCCHHHHHHHCCCCCCHHHHHHHHHHHHHHHHHHHHHHHHHHHCCCCEEEECCC
DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDOOOOODDDDDDDDD

1401      1410      1420      1430      1440      1450      1460
EMYLDEDDIKLIKERKRNFNILLENMSEQIMDQYVKENYNDKKYYFEMCNYGSSLNIRGEFLEAYSKKIV
HHHCCHHHHHHHHHHHCCHHHHHHHCHHHHHHHHHHHHHHCCCCEEEEECCCCCEEECCHHHHHHCCCCE
DDDDDDDDDDDDDDDDDDDDDDDDDDDDDOOOOOOOOOOOOOOOOOOOODDDDDDDDDDDDDDDDDDDD

1471      1480      1490      1500      1510      1520      1530
SEKNKNNIKELKTNIIDIKHIYNKGDDEDTDNLLNIKYIDILNKNKNDYMNYQYIKEYNSLLLIHNNYKG
HHCCCCCCHHCCCCCCCCCEECCCCCCCCCCHHHHHHHHHHCCCCCCCEEEECCCCCEEEEECCCCC
DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDOOOODDDDDDDDD

1541      1550      1560      1570      1580      1590      1600
CVGITGDLKGMNFYHSNASIIINPCIPLPTECTIELWLCCNPKKKYRNISGKKFAFCDKKGNSLFVLSLN
CCEECCCCCCCEECCCCEEEEECCCCCCCCCCEEEEEEEECCCCCCCCCCCCEEEEEECCCCCEEEEECC
DDDDDDDDDDDDDDDDOOOOOOOOODDDOOOOOOOOOOOODDDDDDDOOOOOOOOOOOOOODDDDDDD

1611      1620      1630      1640      1650      1660      1670
EDGLEDIEIYITNVELLSDYYKKMNYIQDIKTATHYHRLKDISKVLNYNNGIYIKSNMITKKCKKYKKYK
CCCEEEEEEEECCEHHCCHHHHHHHHHHHCCCCCCCCCCCCCCEEEECCCCCEEEEECCCCCCCHHHHHH
DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD

1681      1690      1700      1710      1720      1730      1740
IYKIYKIGKNYNMRNNIIKKKKWNLINITKSSQGLVYYINGKYISFISHEILNMQKTFEICLFGNSCFGN
HHHHHHHHHCHHHHHHCHEECCCCCEEEEECCCCCEEEEECCCCCCCCCHHHHHHCCCEEEEEECCCCCCC
DDDDDDDDDDDDDDDDDDDDDDDDDDDDOOOOOOOOOOOOODDDDDDDDDOOOOOOODDDDDDDDDD

1751      1760      1770      1780      1790      1800      1810
NNIGICSSFKIFNFLNKEEIKCRYKIIKNIKCKEMLGDNIKIQDDNNNNNNNNYNYYNYNNFVIEGIDVR
CCCCECCCHHHHHHHCHHHHHHHHHHHHHCCCCCCCCCCCEEEECCCCCCCCCEEEEEECCEEEEEEEEC
DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDOOOOODDDOOOD

1821      1830      1840      1850      1860      1870      1880
ETKPAEIIFLINFIQSSKYTNRVIPFINDSNYMLKIYQLKFFDIYKNNINLSNMNYYEDICDKYNDFSEG
CCCCCHEEHHHHHHCCCCCCCEEEEEECCCCCEEEEEEEEEEEEECCCCCCCCCCCCCCCCCCHHHHHCC
DDDOOOOOOOOOOOODDDDDDDDDDDDDDDDOOOOOOOOOOOOOODDDDDDDDDDDDDDDDDDDDDDDDD

1891      1900      1910      1920      1930      1940      1950
TKKHIIHHNSNQNISCWQEEKSKNVDMVKKKNIYINYNNDDNIINNYSSIDCRIIHIKNKDHYGYNVYVK
CCCEEEEECCCCCCCCCCCCCCCCCCCCCCCCCCCEEEECCCCCCCCCCCCCCCCCCEEEEECCCCCCCEEEEEE
DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDOOOOOOO

1961      1970      1980      1990      2000      2010      2020
KIIGRQDVPKIYGINIFSHNFGLACDLSKFYNLIISPSLSIYNELQKTLGYSICAWIFLPIEKSISYSSL
EECCCCCCCEEEEEEEECCCCEEECCHHHHHHEEECCCCHHHHHHCCCCCCEEEEEEEEECCCCCCEHHHE
OOODDDDDDDDDDDDDDDDDDDDDDDDDOOODDDOOOOOOODDDDDDOOOOOOOOOOOOOOOODDDDDDDD

2031      2040      2050      2060      2070      2080      2090
IAGKKDIHVCIFSDDMLLGSIQNYTSKGNLLFYHSSGYSIKNMKRGWYYLNVIGTLQGQYYFLNGKFKGY
ECCCCCEEEEEEECCCCEEEEEEEECCCCCEEEEECCCCEEEEECCCEEEEEEEEECCCEEEEEECEEECC
DDOOOOOOOOOOOOOOOOOODDDDDOOOOOOOOOOOODDDDDOOOOOOOOOOOOOOOOOOOOOOOODDD

2101      2110      2120      2130      2140      2150      2160
HTFCSFDNIKYICNSSLFINPFPYICFLKILNKPLSMNEVLYEFYTFSKLFNETSYESYNLHYIIHFLFP
CCCCCCCCEEEEECCCCCCCCCCEEEEEEEECCCCCCEEEEEEEECCCCCCCCCCCCCCEEEEEEEECC
DDDDDDDDDDDDDDDDOOOOOOOOOOOOOODDDDDDDDDDDDDDDDDDDDDDDOOOOOOOOOODD

2171      2180      2190      2200      2210      2220      2230
YFESKNKNNISYSSNDTSLCNSYDHNCSEGKYLHFYITENYDVHIYPIEQVKNYYYSVSLISIKNRKLYY
CCCCCCCCCCCEECCCCCEECCCCCCCCCCEEEEEEEEECCEEEEEEEEECCEEEEEEEEEECCCEEEE
DDDDDDDDDDDDDDDDDDDDDDDDDDOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOD

2241      2250      2260      2270      2280      2290      2300
FNSINEQSNNLNIHLKNYIILPEHHWTILAVINLTHINKLGYHCLVGGTNGNSHICINGFDLSIGVLINL
ECCCCCHCCCCEEEEEEEECCCCCEEEEEEEECCCCCCCCCEEEECCCCCCCEEEECCCCCEEEHHHHC
DDDDDDDDDDDOOOOOOOOOOOOOOOOOOOOOODDDDDDDDDDDDDDDDOOOOOOODDDDDDDD

2311      2320      2330      2340      2350      2360      2370
QNEYIYEEQLSLEDSFTSISDTLNGFSLLNEYMKVDSITKEKNNNNNDDDDDDLLCNSYDKKINKYNNNV
CCCEEEEECCCCCCCCCCCCCCCCCCCCCCCHHHHHCCCCCCCCCCCCCCCCCCEECCCCCCCCCCCCCCC
```

```
DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD

  2381      2390      2400      2410      2420      2430      2440
SDFDNVHIRNANKSYSTFCGCGYNLQNELNKNILITTTCRNYEQTFFINSTKVGITQACLDPITCIGNCA
CCCCCCHHHHHHHHHHHECCCCCCCCCCCCCCCEEEEEEECCCCEEEEEECCCEEEEEECCCCCEEEECCCC
DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDOOOOOOOODDDDDDDDDDDDDDDDDDDDDDDDDD

  2451      2460      2470      2480
SINNEFLSPFGSYKFLRIIFDYVSDEQIRQFYYSLKL
CCCCCCCCCCCCEEEEEEEEECCCCHHHHHHHHHCCCC
DDDDDDDDDDDOOOOOOOOOOOODDDDDDDDDDDDDDD
```

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

SS Motif for disorder segment 1:
(start,end): (1,27)

```
          1        10        20
seq  : MSCINKLPLFIILIIYETLNKNWGAKN
S.S. : CCCCCCCHHHHHHHHHHHCCCCCCHHH
alpha: 00122234555555455443223466
beta : 00010000133444321110000000
coil : 9876765420000012234566655322
```

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

Linear motif(s):

residues (16,19)   LIG_PDZ_3 = YETL

SS Motif for disorder segment 2:
(start,end): (249,259)

```
         249       258
seq  : CINNEKEKSII
S.S. : EECCHHHHHHH
alpha: 32237788889
beta : 54200000000
coil : 12562211100
```

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

Linear motif(s):

SS Motif for disorder segment 3:
(start,end): (270,280)

```
         270       279
seq  : SLLRYVNSNYD
S.S. : HHHHHHCCCCC
alpha: 77776531112
beta : 11111110000
coil : 00111357777
```

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

Linear motif(s):

residues (274,277)
LIG_SH2_STAT5 = YVNS

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): (294,331)

```
         294       303       313       323
seq  : IPINEFLDCVFKRGSNLERIQKKITFLLYLPLLILICS
S.S. : CCHHHHHHHCCCCCCHHHHHHHHHHHHHHHHHHHHHHHH
alpha: 00566665442100027899887766666789999999
beta : 21000011122100000000000112211000000000
coil : 77322223334789872100001111112110000000
```

residues (297,300)   LIG_PDZ_3 = NEFL
residues (310,313)   LIG_PDZ_3 = LERI
residues (313,320)   LIG_PP1 = IQKKITFL
residues (315,323)
LIG_MAPK_1 = KKITFLLYL
residues (316,322)   LIG_FHA_1 = KITFLLY
residues (322,325)
LIG_SH2_STAT5 = YLPL

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

Linear motif(s):

SS Motif for disorder segment 5:
(start,end): (342,450)

```
         342       351       361       371       381       391       401
seq  : YKNVKRREDVTICPFDKNYKQRSKKKHINKVDNSNVNNNNISEYKKKKDCSKRNEINIIDMNDRKEMNFC
S.S. : ECCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCHHHHHCCCCCCCCCCCCCCCCCCCCCCCCCC
alpha: 32111111100000111123223223333222122222225677653211221111122122233322
beta : 43111000013432100000111000111121000000000000000000001111111100000011111
coil : 24677777775466778866556666555655567776777632122456777677676566666544566
         412       421       431       441
seq  : DSNNLFINEISQPKKFHHNIYSDDNITRCNLFSAENYVR
S.S. : CCCCCHHHCCCCCCCCCCCCCCCCCCCCCCCCHHHHH
alpha: 22224554421022322111123322233321167655
beta : 00000000010000111233210111000011000001
coil : 67775334457876556665544566655666622334
```

Linear motif(s):

residues (342,345)
LIG_SH2_GRB2 = YKNV
residues (343,353)
LIG_MAPK_1 = KNVKRREDVTI
residues (348,351)   LIG_PDZ_3 = REDV
residues (348,354)
LIG_14-3-3_2 = REDVTIC
residues (393,399)
LIG_MAPK_1 = KRNEINI
residues (434,437)   LIG_PDZ_3 = DDNI

SS Motif for disorder segment 6:
(start,end): (473,502)

```
           473        482        492
 seq  : LFCLCNYDEHREESFIIIDDSINCEDMKSS
 S.S. : HHCCCCCCCCCCEEEEECCCCCCHHHCCH
 alpha: 54332111111111000001114665344
 beta : 22211110000235788741011000000
 coil : 12445677777653110147877434654
```

SS Motif for disorder segment 7:
(start,end): (525,537)

```
           525        534
 seq  : QLLRKYVKRYQAV
 S.S. : HHHHHHHHHHHHH
 alpha: 9999877677788
 beta : 0000000000000
 coil : 0000122322110
```

SS Motif for disorder segment 8:
(start,end): (543,552)

```
 seq  : ILQQKAKIIN
 S.S. : HHHHHHHHHC
 alpha: 9999988753
 beta : 0000000000
 coil : 0000011246
```

SS Motif for disorder segment 9:
(start,end): (566,591)

```
           566        575        585
 seq  : FHKKFWITINPSLYYNYKNGLYNNNI
 S.S. : HHHHHHHCCCCCHHHCCCCCCCCCCCE
 alpha: 87777653102343332222232223
 beta : 00000000100123322100111013
 coil : 01122235787532234676556653
```

SS Motif for disorder segment 10:
(start,end): (616,700)

```
           616      625      635      645      655      665      675
 seq  : ERKDPHRFFFDIHTIEKGKKKKKNVSNTRDCFDNDEGNKMCHMKLYSSCRIRNNKSNICHSVEKNNIKEY
 S.S. : ECCCCCCCCCCCCCCHHHCCCCCCCCCCCCCCCCCCCCCCCCCCHCCCCCCCCCCCCCCCCCCCCCCCCCC
 alpha: 10000111122333555421111111111222211111112333332233332211111222222213333
 beta : 64100001221121100000011211100111100001233211222111211000011112222101221
 coil : 24798876555444334577776667776556777787543354444455456788766665446754 45
           686      695
 seq  : DKKEKEITNKRNNMW
 S.S. : CCCCCCCCCCCCCHH
 alpha: 111122222443358
 beta : 000000000000000
 coil : 778776676555541
```

SS Motif for disorder segment 11:
(start,end): (709,722)

```
           709        718
 seq  : QNVKKKDTFLYSFS
 S.S. : HHCCCCCCHHHHHH
 alpha: 43322333444456
 beta : 22221112333322
 coil : 23455554211111
```

SS Motif for disorder segment 12:
(start,end): (741,747)

```
 seq  : HIKNFIK
 S.S. : HHHHHHH
 alpha: 8988888
 beta : 0000000
 coil : 0001111
```

SS Motif for disorder segment 13:
(start,end): (753,758)

```
 seq  : SILCNI
```

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

Linear motif(s):

residues (479,482)
LIG_SH2_SRC = YDEH
residues (491,494)   **LIG_PDZ_3 = DDSI**
residues (494,498)   **LIG_RB = INCED**

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

Linear motif(s):

residues (530,533)
LIG_SH2_STAT5 = YVKR

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 (568,574)
LIG_MAPK_1 = KKFWITI
residues (579,582)
LIG_SH2_GRB2 = YYNY
residues (587,590)
LIG_SH2_GRB2 = YNNN

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):

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

```
S.S. : HHHHHH
alpha: 666667
beta : 332211
coil : 000111
```

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): (771,892)

```
      771     780     790     800     810     820     830
seq : NHTIKKYNFSKKIIYIISFVKKRKRKWLGIYRKFKTLIWGNRKKMEDTYSRVKNKKGIENEQKKEQKLKS
S.S. : HHCCCCCCHHHHHHHHHHHHHHHHHHHHHHHHCCCCCEECCCCCCCCCCCCCCCCCCCCHHHHHHHHHHHH
alpha: 5542232356778887778888777665544332233332222221223333222467888876655
beta : 2110000000000011111100000012222212233321111000001122100000000000000
coil : 1246666643211000010001122212223444432246656677775433566775211011233344
      841     850     860     870     880     890
seq : LLLMSNVLNYYTDDEESILNTKNNNVKKKNNNIFMVKKWNVNNIKRHKLLNI
S.S. : HHHHHHHHCCCCCCCHHHCCCCCCCCCCCCCCCEECCCCCCCCHHHHHHHHH
alpha: 66665554321001244543321111111111122223333333345566655
beta : 000000122221000111110001221000135542100001222211110
coil : 33233332456888643333456776667788742224656665321111233
```

residues (781,789)
LIG_MAPK_1 = KKIIYIISF
residues (785,788)
LIG_SH2_STAT5 = YIIS
residues (791,798)
LIG_ULM_U2AF65_1 = KKRKRKWL
residues (791,800)
LIG_MAPK_1 = KKRKRKWLGI
residues (796,800)
LIG_CYCLIN_1 = KWLGI
residues (802,808)   **LIG_14-3-3_2 = RKFKTLI**
residues (805,808)
LIG_CYCLIN_1 = KTLI
residues (833,843)
LIG_MAPK_1 = KKEQKLKSLLL
residues (837,843)   **LIG_NRBOX = KLKSLLL**
residues (839,843)
LIG_CYCLIN_1 = KSLLL
residues (850,856)   **LIG_FHA_2 = YYTDDEE**
residues (851,854)
LIG_SH2_STAT5 = YTDD
residues (855,858)   **LIG_PDZ_3 = EESI**
residues (885,892)
LIG_MAPK_1 = KRHKLLNI
residues (888,892)
LIG_CYCLIN_1 = KLLNI

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

Linear motif(s):

SS Motif for disorder segment 15:
(start,end): (923,931)

```
seq : EKKYPLISL
S.S. : HHCCCCCCH
alpha: 653111007
beta : 000000100
coil : 245788882
```

residues (924,931)
LIG_MAPK_1 = KKYPLISL

SS Motif for disorder segment 16:
(start,end): (940,951)

```
      940     949
seq : KNHFFETDNFLI
S.S. : HCCCCCCCHHHH
alpha: 631111234899
beta : 000111100000
coil : 367766654100
```

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): (956,976)

```
      956     965     975
seq : FLKFTKKFVKVLRRKKYEQSY
S.S. : HHHHHHHHHHHHHHHCCCCCCH
alpha: 999887777776654322224
beta : 000000001222111000001
coil : 000012110000234567764
```

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

Linear motif(s):

residues (958,966)
LIG_MAPK_1 = KFTKKFVKV

SS Motif for disorder segment 18:
(start,end): (984,1014)

```
      984     993     1003    1013
seq : WGMSILNYGNLRDINYNISHILFHVYSILNK
S.S. : CCCCECCCCCHHHHHCCCCHHHHHHHHHHHH
alpha: 3223332111556543234667777889999
beta : 2112322100000011100012221100000
coil : 4664335677332334565521000000000
```

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

Linear motif(s):

residues (991,994)
LIG_SH2_GRB2 = YGNL
residues (998,1006)   **LIG_EH1_1 = NYNISHILF**

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

Linear motif(s):

residues (1031,1034)
LIG_SH2_STAT5 = YVNN
residues (1047,1050)
LIG_SH2_GRB2 = YNNM
residues (1069,1076)
LIG_MAPK_1 = KIKNNILI
residues (1082,1085)
LIG_PDZ_3 = DDNV
residues (1094,1097)
LIG_PDZ_3 = CDEI
residues (1106,1109)
LIG_SH2_GRB2 = YGNS
residues (1155,1158)
LIG_SH2_STAT5 = YINK
residues (1160,1164)
LIG_BRCT_BRCA1_1 = NSETF
residues (1174,1177)
LIG_SH2_SRC = YDIS
residues (1185,1188)
LIG_SH2_STAT3 = YKKQ

SS Motif for disorder segment 19:
(start,end): (1029,1201)

```
          1029      1038      1048      1058      1068      1078      1088
seq   : YPYVNNNAMKGNMSLINMYNNMCNFSFDKNNLYEEEKQSQKIKNNILIEQNFLDDNVNMDIKDDPCDEIE
S.S.  : CCCCCCCCCCCCCHHHHHCCCCCCCCCCCCCHHHHHCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
alpha : 3332112332123455554322111113346666543210112222221111111110001000012333
beta  : 1112100000001111111001111111000111111211111111222100110012233210000011
coil  : 5545777666676543333466666777554212223346777765444677777776665678887654
          1099      1108      1118      1128      1138      1148      1158
seq   : DMNMLQMYGNSFCQSFMPLYNHNFNRKNDQSIHMEETYMCDRERFNCLDKYMCSNTYINKRNSETFVNAH
S.S.  : CCCCEEEEECCCCCCCCCCCCCCCCCCCHHHHHHCCCCCCCCCCCCCCCCCCCCCCCCCCCCEEEECC
alpha : 33210000000001111333212223334455555543221121111101232110000000000111111
beta  : 1013688851011100100000111000001111101211012334321122102332210002466532
coil  : 4665200147877777765577665556543223334455676555456654678755678886422356
          1169      1178      1188      1198
seq   : KGEYKYDISSDMNLIDYKKQSTRTKNFKGQRIF
S.S.  : CCCCCCCCCCCCCCCCCCCCCCCCCCCCEEE
alpha : 10111111211123432110011111111011111
beta  : 11112332221011111111111011012113467
coil  : 77654455567764446777777776775320
```

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

Linear motif(s):

residues (1224,1228)
LIG_BRCT_BRCA1_1 = VSEFF
residues (1224,1230)
LIG_BRCT_BRCA1_2 = VSEFFFK
residues (1240,1243)
LIG_SH2_STAT5 = YICN
residues (1252,1255)
LIG_SH2_STAT3 = YRNQ
residues (1263,1266)
LIG_PDZ_3 = FEYI
residues (1265,1268)
LIG_SH2_STAT5 = YIKK
residues (1271,1274)
LIG_SH2_STAT3 = YKNQ
residues (1279,1287)
LIG_EH1_1 = RYNICSIIN
residues (1298,1304)
LIG_FHA_1 = DNTDNID
residues (1300,1303)
LIG_PDZ_3 = TDNI
residues (1308,1314)
LIG_FHA_1 = SITDFIN
residues (1310,1313)
LIG_PDZ_3 = TDFI
residues (1315,1322)
LIG_MAPK_1 = KKVLDIDF
residues (1316,1320)
LIG_CYCLIN_1 = KVLDI
residues (1326,1329)
LIG_PDZ_3 = YEKL
residues (1331,1340)
LIG_MAPK_1 = KNSKHYFINI
residues (1336,1339)
LIG_SH2_STAT5 = YFIN
residues (1344,1347)
LIG_PDZ_3 = KDYL
residues (1346,1349)
LIG_SH2_STAT5 = YLNI
residues (1350,1353)
LIG_PDZ_3 = NELI
residues (1359,1362)
LIG_PDZ_3 = SDNI
residues (1375,1383)
LIG_MAPK_1 = KRNKKKLKI
residues (1379,1383)
LIG_CYCLIN_1 = KKLKI

SS Motif for disorder segment 20:
(start,end): (1223,1386)

```
          1223      1232      1242      1252      1262      1272      1282
seq   : DVSEFFFKIYHTHICEKYICNNLINLWGCYRNQNIYMKRFFEYIKKGEYKNQQNIIRYNICSIINEKRDD
S.S.  : HHHHHHCCCCCCHHHHHHHCHHHHHCCCCCCCHHHHHHHHHHHHHCCCCCHHEEECCCCCCCCCCCCC
alpha : 6888876432333456666654455443223334678999999886544434343332223322001111
beta  : 0000010012222211111000122211110001000000000000000112345421111110000000
coil  : 2110013554443321111245322235555665210000000012455554432112455556887778
          1293      1302      1312      1322      1332      1342      1352
seq   : NNNNIDNTDNIDNILSITDFINKKVLDIDFYNEYEKLSKNSKHYFINISEEKDYLNINELINFSKASDNI
S.S.  : CCCCCCCCCCCCEEEHHHHHCCCCEEEHHHHHHHCCCCHHHHHHHHHHCCCCCCHHHHHHHCCCCCCH
alpha : 110000000133321145665533332223566676531335889998752111134666544332238
beta  : 012331000000145421111001334421100000000000000000000232111111100000000
coil  : 876567888865424222235653333322322235866310000012468855533222344567761
          1363      1372      1382
seq   : EELKRLQNNLIEKRNKKKLKIFSL
S.S.  : HHHHHHHHHHHHHHHHHHHHHHHH
alpha : 999999877776654555555555
beta  : 000000000111111111122333
coil  : 000000012111123322221111
```

SS Motif for disorder segment 21:
(start,end): (1392,1432)

Graph of Probability(helix, strand, coil) PDF

```
          1392      1401      1411      1421      1431
seq : MPVHIIDDYEMYLDEDDIKLIKERKRNFNILLENMSEQIMD
S.S. : CCEEEECCCHHHCCHHHHHHHHHHHHCCHHHHHHHCHHHHHH
alpha: 11122233355521778999998764344444554579999
beta : 12455410011110000000000000002344310000000
coil : 76322356532257221000001234532111245410000
```

SS Motif for disorder segment 22:
(start,end): (1452,1526)

```
          1452      1461      1471      1481      1491      1501      1511
seq : GSSLNIRGEFLEAYSKKIVSEKNKNNIKELKTNIIDIKHIYNKGDDEDTDNLLNIKYIDILNKNKNDYMN
S.S. : CCEEEECCHHHHHHHCCCCEHHCCCCCCCCHHCCCCCCCCCEECCCCCCCCCCCHHHHHHHHHHHHCCCCCCC
alpha: 01111115788875222233332111233433221111222100112233455677777664211112111
beta : 12565410000000002333210000112222222222344420000000000011111100011233
coil : 76323463100124665332346788643334555555433468877665333111112467776544
```

```
seq : YQYIK
S.S. : EEEEC
alpha: 33332
beta : 34442
coil : 21124
```

SS Motif for disorder segment 23:
(start,end): (1531,1558)

```
          1531      1540      1550
seq : LLLIHNNYKGCVGITGDLKGMNFYHSNA
S.S. : EEEEECCCCCCCEECCCCCCCCEECCCCE
alpha: 0000000000000000011000000000
beta : 7888631222344543222345431015
coil : 2001367667654446666554457874
```

SS Motif for disorder segment 24:
(start,end): (1568,1570)

```
seq : LPT
S.S. : CCC
alpha: 001
beta : 100
coil : 787
```

SS Motif for disorder segment 25:
(start,end): (1583,1590)

```
seq : KKKYRNIS
S.S. : CCCCCCCC
alpha: 11111110
beta : 00011001
coil : 77776787
```

SS Motif for disorder segment 26:
(start,end): (1604,1711)

```
          1604      1613      1623      1633      1643      1653      1663
seq : LFVLSLNEDGLEDIEIYITNVELLSDYYKKMNYIQDIKTATHYHRLKDISKVLNYNNGIYIKSNMITKKC
S.S. : EEEEECCCCCEEEEEEEECCEHHCCHHHHHHHHHHHCCCCCCCCCCCCCEEEECCCCCEEEEECCCCCCC
alpha: 00000000000000000012333345677778875332110000111000000000000000011111233
beta : 68997410024567888633332100000000001100000011210136665321138997421100000
coil : 300025899743321012443344322111111135667887767775223456886100246777665
          1674      1683      1693      1703
seq : KKYKKYKIYKIYKIYKIGKNYNMRNNIIKKKKWNLINITKS
S.S. : CHHHHHHHHHHHHHHHCHHHHHCHEECCCCCEEEEECC
alpha: 3445566667776654455554433221122211111
beta : 1111222111111000100001344322334555432
coil : 4443111111111244433334432235554322346
```

LIG_SH2_STAT5 = YIQD
residues (1654,1658)
LIG_CYCLIN_1 = KVLNY
residues (1658,1661)
LIG_SH2_GRB2 = YNNG
residues (1663,1666)
LIG_SH2_STAT5 = YIKS
residues (1699,1704)
LIG_ULM_U2AF65_1 =
KKKKWN
residues (1699,1708)
LIG_MAPK_1 = KKKKWNLINI

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

Linear motif(s):

residues (1729,1732)
LIG_PDZ_3 = HEIL

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

Linear motif(s):

residues (1767,1770)
LIG_PDZ_3 = KEEI
residues (1780,1784) LIG_RB = IKCKE
residues (1783,1786)
LIG_PDZ_3 = KEML
residues (1787,1790)
LIG_PDZ_3 = GDNI

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 (1838,1844)
LIG_FHA_1 = KYTNRVI
residues (1839,1842)
LIG_SH2_STAT5 = YTNR

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

Linear motif(s):

residues (1865,1868)
LIG_SH2_GRB2 = YKNN
residues (1877,1880)
LIG_SH2_SRC = YEDI
residues (1915,1918)
LIG_PDZ_3 = VDMV
residues (1919,1925)
LIG_MAPK_1 = KKKNIYI

SS Motif for disorder segment 27:
(start,end): (1724,1733)

```
seq  : ISFISHEILN
S.S. : CCCCCHHHHH
alpha: 3322245554
beta : 3222223333
coil : 3444421012
```

SS Motif for disorder segment 28:
(start,end): (1741,1808)

```
        1741      1750      1760      1770      1780      1790      1800
seq  : CLFGNSCFGNNNIGICSSFKIFNFLNKEEIKCRYKIIKNIKCKEMLGDNIKIQDDNNNNNNNNYNYYN
S.S. : EEECCCCCCCCCCCCCECCCHHHHHHHCHHHHHHHHHHHHHHCCCCCCCCCCCCEEEECCCCCCCCCCEEEE
alpha: 111011110000001123567787646788776666654322222111111112222111111111110
beta : 7641111110013444211111000000000011222222111333112455542100111234556676
coil : 12477666788875434542100113532111121111234665444666432235677666665643212
```

SS Motif for disorder segment 29:
(start,end): (1814,1816)

```
seq  : IEG
S.S. : EEE
alpha: 000
beta : 887
coil : 112
```

SS Motif for disorder segment 30:
(start,end): (1820,1823)

```
seq  : RETK
S.S. : CCCC
alpha: 1100
beta : 3100
coil : 5788
```

SS Motif for disorder segment 31:
(start,end): (1835,1850)

```
        1835      1844
seq  : QSSKYTNRVIPFINDS
S.S. : CCCCCCCEEEEEECCC
alpha: 2111000000000002
beta : 2100013688875200
coil : 4678876311124797
```

SS Motif for disorder segment 32:
(start,end): (1864,1954)

```
        1864      1873      1883      1893      1903      1913      1923
seq  : IYKNNINLSNMNYYEDICDKYNDFSEGTKKHIIHHNSNQNISCWQEEKSKNVDMVKKKNIYINYNNDDNI
S.S. : EECCCCCCCCCCCCCCCCCHHHHCCCCCEEEECCCCCCCCCCCCCCCCCCCCCCCCCCCEEEECCCCCCC
alpha: 21100001110001221003555543211111111111000001112222234432222222211001223
beta : 5531011000001000100000000000002455420012221100001111111223335554210002
coil : 2357878788888777788643334577763224677766677777765664444444422246788764
        1934      1943      1953
seq  : INNYSSIDCRIIHIKNKDHYG
S.S. : CCCCCCCCCEEEEECCCCCCC
alpha: 321111100000000023210
beta : 221111223688873000122
coil : 34666666520002586566
```

residues (1924,1927)
LIG_SH2_STAT5 = YINY
residues (1930,1933)
LIG_PDZ_3 = DDNI

SS Motif for disorder segment 33:
(start,end): (1964,1987)

```
        1964      1973      1983
 seq  : GRQDVPKIYGINIFSHNFGLACDL
 S.S. : CCCCCCEEEEEEECCCCEEECCH
 alpha: 00000111111122333333334
 beta : 22221145666542113333321
 coil : 66677742222234543322344
```

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

Linear motif(s):

residues (1977,1981)
LIG_BRCT_BRCA1_1 = FSHNF

SS Motif for disorder segment 34:
(start,end): (1991,1993)

```
 seq  : YNL
 S.S. : HHE
 alpha: 433
 beta : 235
 coil : 221
```

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

Linear motif(s):

SS Motif for disorder segment 35:
(start,end): (2001,2006)

```
 seq  : IYNELQ
 S.S. : HHHHHC
 alpha: 566653
 beta : 221111
 coil : 212235
```

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

Linear motif(s):

SS Motif for disorder segment 36:
(start,end): (2023,2032)

```
 seq  : KSISYSSLIA
 S.S. : CCCEHHHEEC
 alpha: 1111344320
 beta : 1344333443
 coil : 6544221125
```

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

Linear motif(s):

residues (2023,2028) LIG_14-3-3_3 = KSISYS

SS Motif for disorder segment 37:
(start,end): (2051,2055)

```
 seq  : IQNYT
 S.S. : EEEEC
 alpha: 00000
 beta : 77653
 coil : 11235
```

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

Linear motif(s):

SS Motif for disorder segment 38:
(start,end): (2068,2073)

```
 seq  : YSIKNM
 S.S. : CEEEEC
 alpha: 001111
 beta : 365543
 coil : 532235
```

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

Linear motif(s):

SS Motif for disorder segment 39:
(start,end): (2098,2119)

```
        2098      2107      2117
 seq  : KGYHTFCSFDNIKYICNSSLFI
 S.S. : ECCCCCCCCCCEEEEECCCCCC
 alpha: 0000000011110000011211
 beta : 5444344421146775212232
 coil : 4555655567642124665555
```

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

Linear motif(s):

residues (2106,2109)
LIG_PDZ_3 = FDNI
residues (2111,2114)
LIG_SH2_STAT5 = YICN
residues (2114,2118)
LIG_BRCT_BRCA1_1 = NSSLF

SS Motif for disorder segment 40:
(start,end): (2134,2159)

```
        2134      2143      2153
 seq  : PLSMNEVLYEFYTFSKLFNETSYESY
 S.S. : CCCCEEEEEEEEECCCCCCCCCCCCC
 alpha: 00022322222222112222210011
 beta : 33323466655433110111234211
 coil : 66643110111234666665545677
```

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

Linear motif(s):

residues (2138,2141)
LIG_PDZ_3 = NEVL

residues (2145,2148)
LIG_SH2_STAT5 = YTFS
residues (2147,2151)
LIG_BRCT_BRCA1_1 = FSKLF
residues (2152,2158)
LIG_FHA_2 = NETSYES

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

Linear motif(s):

residues (2171,2174)
LIG_SH2_STAT5 = YFES

SS Motif for disorder segment 41:
(start,end): (2169,2198)

```
        2169      2178      2188
 seq  : FPYFESKNKNNISYSSNDTSLCNSYDHNCS
 S.S. : CCCCCCCCCCCEECCCCCCEECCCCCCCCC
 alpha: 001100011000000100000001111000
 beta : 211101000113554211234431100000
 coil : 677787888875434677754457778888
```

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

Linear motif(s):

residues (2240,2243)
LIG_SH2_STAT5 = YFNS

SS Motif for disorder segment 42:
(start,end): (2240,2252)

```
        2240      2249
 seq  : YFNSINEQSNNLN
 S.S. : EECCCCCHCCCCE
 alpha: 0112334433211
 beta : 7641101121124
 coil : 1245554445554
```

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

Linear motif(s):

SS Motif for disorder segment 43:
(start,end): (2279,2294)

```
        2279      2288
 seq  : KLGYHCLVGGTNGNSH
 S.S. : CCCCEEEECCCCCCCE
 alpha: 1100000000000000
 beta : 2113778743210148
 coil : 6775211256788851
```

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

Linear motif(s):

residues (2312,2315)
LIG_PDZ_3 = NEYI
residues (2314,2317)
LIG_SH2_STAT5 = YIYE
residues (2316,2319)
LIG_SH2_STAT3 = YEEQ
residues (2317,2320)
LIG_PDZ_3 = EEQL
residues (2330,2333)
LIG_PDZ_3 = SDTL
residues (2345,2348)
LIG_PDZ_3 = VDSI
residues (2361,2364)
LIG_PDZ_3 = DDDL
residues (2376,2379)
LIG_SH2_GRB2 = YNNN
residues (2383,2386)
LIG_PDZ_3 = FDNV
residues (2391,2395)
LIG_USP7_1 = ANKSY
residues (2393,2398) **LIG_14-3-3_3 = KSYSTF**
residues (2403,2406)
LIG_SH2_STAT3 = YNLQ

SS Motif for disorder segment 44:
(start,end): (2303,2412)

```
        2303      2312      2322      2332      2342      2352      2362
 seq  : SIGVLINLQNEYIYEEQLSLEDSFTSISDTLNGFSLLNEYMKVDSITKEKNNNNNDDDDDDLLCNSYDKK
 S.S. : EEEHHHHCCCCEEEECCCCCCCCCCCCCCCCCCCCCCCCCCCCHHHHCCCCCCCCCCCCCCCCEECCCCCC
 alpha: 2344443322221111111222110011122111233444444432222221111122221111111101
 beta : 5444443100145543222111100111122111210001122111122332222111113443211001
 coil : 2110013576632235556666778766655677655554332334654444566666654334667887
        2373      2382      2392      2402
 seq  : INKYNNNVSDFDNVHIRNANKSYSTFCGCGYNLQNELNKN
 S.S. : CCCCCCCCCCCCCCHHHHHHHHHHHECCCCCCCCCCCCCCC
 alpha: 1121100111112346676654443211111122233233
 beta : 2222111111100111110000112332223432110012
 coil : 5555788777764311122344333456654445556654
```

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

Linear motif(s):

residues (2423,2429)
LIG_FHA_1 = EQTFFIN
residues (2440,2443)
LIG_PDZ_3 = LDPI
residues (2454,2457)
LIG_PDZ_3 = NEFL
residues (2455,2460)
LIG_WW_4 = EFLSPF

SS Motif for disorder segment 45:
(start,end): (2421,2461)

```
        2421      2430      2440      2450      2460
 seq  : NYEQTFFINSTKVGITQACLDPITCIGNCASINNEFLSPFG
 S.S. : CCCEEEEEECCCEEEEECCCCCEEEECCCCCCCCCCCCCCCC
 alpha: 000000000000000001110001000112211112111110
 beta : 21358998511346664321014554222222102332111
 coil : 77641001477643234456874334665556775446777
```

SS Motif for disorder segment 46:
(start,end): (2473,2487)

```
        2473      2482
 seq  : VSDEQIRQFYYSLKL
 S.S. : CCHHHHHHHHHCCCC
 alpha: 006776666654100
 beta : 200012222111000
 coil : 683211001124899
```

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

Linear motif(s):

residues (2475,2478)
LIG_PDZ_3 = DEQI

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SS Motif for disorder segment 46:
(start,end): (2473,2487)

```
        2473      2482
 seq  : VSDEQIRQFYYSLKL
 S.S. : CCHHHHHHHHHCCCC
 alpha: 006776666654100
 beta : 200012222111000
 coil : 683211001124899
```

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

Linear motif(s):

residues (2475,2478)
LIG_PDZ_3 = DEQI