



CSpritz - Accurate detection of protein disorder

Version 1.2

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Status: finished

NB: The data will be kept for **two weeks**, after which it will be **deleted** without further notice.

Available files: [\(help\)](#)

- Your input parameters:

Fasta sequences (amino, secondary structure, disorder, confidence):

Disorder plot:

Graph of PDB homologue(s) found::

Disorder Prediction (with disorder probability):

Protein statistics :
- HTML

TXT

PDF

PDF

TXT

TXT

Disordered residues and stats: [\(help\)](#)

1102030405060

MFLSIQFIILFFALIHINKNIIALKLEIFKGRFGSPNSTSSMFKNDNKIKRRKEVPLLFVSSNKCLKDLY

CC

DD

718090100110120130

LLKHSGVSPFEKGSFIYILKRGERNRKDKNYPFTLFIEYGTSKSANILEKDSNKYEKGQKYNVIMEGC

HHCC

DD

141150160170180190200

KDIIDCTKSEGLQNLNQKVVENNKMDENIKMDENKKMDENIKMDENIKMDKNIKMDKNIKMDE

CCHHHCCCCCHHHHCCCEEECC

DD

211220230240250260270

NIKMDENIKMDKNIKMDKNIKMDKNIKMDKNIKMDKNIKMDKNIKMDKNIKMDKNIMMRENNKV

CCCCCHHHCC

DD

281290300310320330340

EGKSRKGNINRNKSLVLKRIKGRVYNNKRRKITSRVVDIQNTNVRDYLPLSPQGRSLKLLNIIYNSWKE

CC

DD

351360370380390400410

KNFDFNFVLSDDFDHTCIEWLKHSISLSKKYLKIKIGDHILVRNYYEKENKTLKEYKITYSIIN

HCCCCCEEECCCCCCCCCHHHHHHHHHHHCCCCCCCCCCCCCCCCCCCCCCCCCHHHHCCCHHHH

DD

421430440450460470480

KCLKILININIKFCSYEITSILWASIIILIKSFKNSTYIGNNINVDNVKHNEMIINVIETFINFLSLIIN

HHHHHHHHHHCCCCCHHH

DD

491500510520530540550

NLNKVKYVLSIDESLWAVWSICKLLYFNISFDNYIYIKLKRISILNKDNKNELRASNELLNNVEDSLVM

HHHHHHCCCCCHHH

DD

561570580590600610620

YKNNNENYDKVRNIMIDKEFMLKDNKKDEENICYDNIYNNSSYTNQIYSYMMKFKLSDDIVNILDVF

HCCCCCCCCCHHHCCCCCHHH

DD

631640650660670680690

NLYLKKLYKNISYLKEYIYIPFIIFESQTLMLNNSIILLNKILYLILKNDVLLSLFDFDIKIKETILPP

HH

DD

701710720730740750760

VTKKVEDYEEKLLHYNKSDFRIKTLKSIYKLIKISKIFPLKQNIYNIHLNHNKYKLNSSILIKFV

CCCCCCCCCHHHHHCCCCCEEEHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH

DD

771780790800810820830

QACNDVLIKYIDYFVYIYGYKRIKSKDYSSKCNTRYNEKDTSKNSMHHNNNNNNNNNNCEVVIQKDDTKRN

HH

DD

841850860870880890900

VKGASININENVMKDNRSNDFHNNMNDVITYNKTYDEINNMNINHNIRFKNEIIFYNCLKSSLVSLI

CC

DD

Total amino acids:	2021
Total % disorder:	91.93
Total no. of disordered regions > 30 amino acids:	12
Total no. of disordered regions > 50 amino acids:	9
Number of disordered segments:	29
Length distribution of segments (N to C terminal order):	172 3 1 1 1 1 1 3 3 3 3 3 3 130 48 32 24 113 9 125 392 36 12 61 14 22 132 79 431

[illegible]

Disordered segment motifs: [\(help\)](#)

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

SS Motif for disorder segment 1:
(start,end): (1,172)

```

1      10      20      30      40      50      60
seq : MFLSIQIILFFALIHIIKNIITALKLEIFKGRFGSPNSTSMFNKDNKIKCRKEVPLFLVSSNCKLKDLY
S.S. : CCCCCHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCHHHHHH
alpha: 024577788888887776666655554210000000112221111111100001110011334565
beta : 00001111111111110011122222211111000001110001232112223341000110011
coil : 96531100000000011221112222367778888877666777855567777754457776543322
      71      80      90      100      110      120      130
seq : LLKHSVGSFPEEKGFSYILKRGERNRKNKYPTFLIEYGTGSKSANLEKDSNKYEENQKRYNTVMIEGC
S.S. : HHCCCCCCCCCCCCCEEECCCCCCCCCCCCCCCCCEEECCCCCCCCCHCCCCCCCCCCCCCCCCCECCCCC
alpha: 5432100011110011111011111011110000000110012324443222332101111222212
beta : 111100111111102566542011100000113467763111000011100011100012333453211
coil : 2346888766678322346877778888864311257877654344566655568875444324576
      141      150      160      170

```

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

Linear motif(s):

residues (3,7)
LIG_BRCT_BRCA1_1 = LSIQF
 residues (31,36) **LIG_WW_4 =**
RFGSPN
 residues (38,42)
LIG BRCT BRCA1 1 = TSSMF

seq : KDIIDCTKSEGLQNL MNQKVVENNKMDENIKM
S.S. : CCHHHCCCCCHHHHCCCEEECCCCCCCCCCC
alpha: 234433334445555431111111121111
beta : 12222211000011111245542233211343
coil : 54323455555433345543345655566544

SS Motif for disorder segment 2:
(start,end): (176,178)

seq : KKM
S.S. : CCC
alpha: 211
beta : 233
coil : 555

SS Motif for disorder segment 3:
(start,end): (224,226)

seq : IKM
S.S. : CCC
alpha: 322
beta : 111
coil : 556

SS Motif for disorder segment 4:
(start,end): (230,232)

seq : IKM
S.S. : CCC
alpha: 322
beta : 111
coil : 556

SS Motif for disorder segment 5:
(start,end): (236,238)

seq : IKM
S.S. : CCC
alpha: 322
beta : 111
coil : 556

SS Motif for disorder segment 6:
(start,end): (242,244)

seq : IKM
S.S. : CCC
alpha: 333
beta : 111
coil : 445

SS Motif for disorder segment 7:
(start,end): (248,250)

seq : IKM
S.S. : CCC
alpha: 222

residues (38,44)
LIG_BRCT_BRCA1_2 =
TSSMFNK
residues (49,59) LIG_MAPK_1
= KCRRKVEPLL
residues (67,71)
LIG_CYCLIN_1 = KDLYL
residues (70,73)
LIG_SH2_STAT5 = YLLK
residues (75,80) LIG_WW_4 =
SGVSPF
residues (79,82) LIG_TRAF2_1
= PFEE
residues (88,91)
LIG_SH2_STAT5 = YLKR
residues (102,108) LIG_FHA_1
= PFTLFIE
residues (125,128)
LIG_SH2_SRC = YEEG
residues (131,137) LIG_FHA_1
= KYTNVIM
residues (132,135)
LIG_SH2_STAT5 = YTNV
residues (141,144) LIG_PDZ_3 =
KDII
residues (145,151) LIG_FHA_2
= DCTKSEG
residues (149,152) LIG_PDZ_3 =
SEGL
residues (167,170) LIG_PDZ_3 =
DENI

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

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):

```
beta : 111
coil : 556
```

SS Motif for disorder segment 8:
(start,end): (254,256)

```
seq  : IKM
S.S. : CCC
alpha: 222
beta  : 111
coil  : 555
```

SS Motif for disorder segment 9:
(start,end): (260,389)

	260	269	279	289	299	309	319
seq	IKMDKNIKMDDNIMMREKNKVEGSKRGKNINRKSILVLRIGNRKVYNKKRKSITSRVVDIQNTNVRDYL						
S.S.	CCCCCCCCCCCCHHHCCCCCCCCCCCCCCCCCCCCCEEEEECCCCCECCCCCCCCCEEEEECCCCCHHC						
alpha	222222222234544432111000011111111111222110000000000000110001111123443						
beta	111000111000111100133321110001221234544431124553222211012565432222222						
coil	56666656665333456654577777876667643223458874335676777875323456543333						
	330	339	349	359	369	379	
seq	FLPSQGRSLKLLNIYNSWKEKNFDNFFDLVNSDDFDHTCCTIENWLHKFSISLSKKYLKIK						
S.S.	CCCCCGGSCCHHHHHHHHHHHHHHCCCCCEEECCCCCHHHHHHHHHHHHHCCCCCCCCEEEE						
alpha	20112124789998765665433333332111124567777665432222211000						
beta	21000001000000000000000012333320000011110000012333210124777						
coil	587778641000000100000003334555332335788774211112223334566654211						

SS Motif for disorder segment 10:
(start,end): (394,441)

```

394      403      413      423      433
seq : HILVRNEYEYKENKTLKEYKITYTISIINKCLKLININIDKFCSEYETIS
S.S. : EEEEECCCCCCCCCHHHHECHSHHHHHHHHHHHHHHHHHHCHSCCHHHHHH
alpha: 000001222223222344332277888999999876544433457889
beta : 58986211100001222333200000000000000000000000000000
coil : 410135555666666322343521111000000023454455431100

```

SS Motif for disorder segment 11:
(start,end): (452,483)

```

      452      461      471      481
seq  : SFKNSTYIGNNINVNVKHNEMIINVIVETPNI
S.S. : HHHCCCCCCCCCCCCCHHHHHHHHHHHHHHH
alpha: 6421111101000112334578999999999
beta : 11100011012332101100000000000000
coil : 23678877877665665543100000000000

```

SS Motif for disorder segment 12:
(start,end): (487,510)

```

      487      496      506
seq  : LIINNLNKVKNLSIDESLWAVWS
S.S. : HHHHHHHHHHCCCCCHHHHHHHH
alpha: 999877665532113467888888
beta : 000000000101110000000000
coil : 000012323356775532100000

```

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 (269,272)   LIG_PDZ_3 =
                      DDNI
                      residues (293,297)
                      LIG_CYCLIN_1 = KSLVL
residues (311,316)   LIG_14-3-3_3
                      = KSITSR
                      residues (312,318)   LIG_FHA_1
                      = SITSRVV
residues (326,329)   LIG_PDZ_3 =
                      RDYL
                      residues (328,331)
                      LIG_SH2_STAT5 = YLFI
                      residues (336,340)
                      LIG_CYCLIN_1 = RSLKL
residues (357,360)   LIG_PDZ_3 =
                      FDLV
                      residues (361,365)
                      LIG_BRCT_BRCA1_1 = NSSDF
residues (366,372)   LIG_FHA_2
                      = DHTCEN
                      residues (384,388)
                      LIG_CYCLIN_1 = KYLKI
                      residues (385,388)
                      LIG_SH2_STAT5 = YLKI

```

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

Linear motif(s):

residues (403,407)
LIG_APCC_KENbox_2 = EKENK
 residues (406,412) **LIG_FHA_2**
= NKTKEY
 residues (413,419) **LIG_FHA_1**
= KITYSII
 residues (421,425)
LIG_CYCLIN_1 = KCLKI

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

Linear motif(s):

residues (458,461) **LIG_SH2_STAT5 = YIGN**
residues (465,468) **LIG_PDZ_3 = VDNV**
residues (471,474) **LIG_PDZ_3 = NEMI**

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

Linear motif(s):

```

residues (494,501)
LIG_MAPK_1 = KVKNLSI
residues (502,505) LIG_PDZ_3 =
DES

```

SS Motif for disorder segment 13:
(start,end): (514,626)

```

      514      523      533      543      553      563      573
seq  : LLYFNISFDNYIYIKLKKRISSILNKDNKNELRASNELLNNVEDSLVMYKNNNNENYDKVRNIKIDKEFML
S.S.  : HHHHHCCHHHHHHHHCCCCCHHHHCCCCCCHCCHHHHCCCCCCHHHHCCCCCCHHCCCCCHHHHH
alpha: 776643256777754334455432113344322456542333455554211223344433322267765
beta  : 111111100011000001111110000011210000000000011111000000012211111000000
coil  : 111234533321113455432235677654346643335655533224677776643344556732233
      584      593      603      613      623
seq  : KDNKKDEENICVDNIYNNSSYTNYQISYMMKKFKLSSDDIVNI
S.S.  : HCCCCCCCCCCCCCCCCCHHHHHHHHHHCCCCCHHHHHHH
alpha: 432222344332222111112688888886531005567789
beta  : 000000000111001100000000000000001000000000
coil  : 4567665544456766788777210000012457894431110
```

SS Motif for disorder segment 14:
(start,end): (636,644)

```

seq  : KLYKNISYL
S.S.  : HHHHHHHHH
alpha: 999888887
beta  : 000000000
coil  : 000111112
```

SS Motif for disorder segment 15:
(start,end): (653,777)

```

      653      662      672      682      692      702      712
seq  : PFIIFESQTLMLNNSILLNKILYLKNDVLLSLFSFDKIKETILPPVTKKVEDYEEKLLHYNKSKDIF
S.S.  : CEEEECCCHHHHHCCCHHHHHHHHHHHHHHHHHHCCCHHHHCCCCCCCCCCCCCHHHHHCHCCCCCEE
alpha: 12111235555445778888888875444555432454444320012233344566554432111123
beta  : 3566421111100001100000000000001222111000111110000001110000000110000134
coil  : 421234433223453100010000001355322234644444446898766544433344456787632
      723      732      742      752      762      772
seq  : RIKTLSKIYKLIKISKIFYPLKNQNIYNIHLHNNYKYLNSSILIKFVQACNDVL
S.S.  : EHHHHHHHHHHHHHHHHHHHCCCCCCCCCCCCCCCCCCCCCHHHHHHHHHHHHHHHHH
alpha: 334478888888766554312211223333332234333688899988878888
beta  : 442100000000001011211000001222111000011000000000000001
coil  : 1123210000001223334667777644344456654456210000000011100
```

SS Motif for disorder segment 16:
(start,end): (789,1180)

```

      789      798      808      818      828      838      848
seq  : YGYKNIKSKDYSSKCNTYNEKDTSKNSMHHNNNNNNNNNCEV1IQKDDTKRNVKGASINENVFMKDNR
```

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

Linear motif(s):

residues (516,519)
[LIG_SH2_STAT5 = YFNI](#)
residues (525,528)
[LIG_SH2_STAT5 = YIKL](#)
residues (548,551) [LIG_PDZ_3 =](#)
[NELL](#)
residues (555,558) [LIG_PDZ_3 =](#)
[EDSL](#)
residues (561,564)
[LIG_SH2_GRB2 = YKNN](#)
residues (568,571) [LIG_PDZ_3 =](#)
[YDKV](#)
residues (590,593) [LIG_PDZ_3 =](#)
[EENI](#)
residues (595,598)
[LIG_SH2_SRC = YDNI](#)
residues (599,602)
[LIG_SH2_GRB2 = YNNS](#)
residues (604,607)
[LIG_SH2_STAT5 = YTNY](#)
residues (607,610)
[LIG_SH2_SRC = YQIS](#)
residues (617,622) [LIG_14-3-3_3](#)
[= KLSSDD](#)
residues (620,623) [LIG_PDZ_3 =](#)
[SDDI](#)

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

Linear motif(s):

residues (638,641)
[LIG_SH2_GRB2 = YKNI](#)

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

Linear motif(s):

residues (659,665) [LIG_FHA_1](#)
[= SQTMLN](#)
residues (673,677)
[LIG_CYCLIN_1 = KILYL](#)
residues (676,679)
[LIG_SH2_STAT5 = YLIL](#)
residues (681,684) [LIG_PDZ_3 =](#)
[NDVL](#)
residues (687,691)
[LIG_Clathr_ClathBox_1 = LFSFD](#)
residues (690,693) [LIG_PDZ_3 =](#)
[FDKI](#)
residues (694,697) [LIG_PDZ_3 =](#)
[KETI](#)
residues (700,706) [LIG_FHA_1](#)
[= PVTKKVE](#)
residues (709,712) [LIG_PDZ_3 =](#)
[EEKL](#)
residues (711,715)
[LIG_CYCLIN_1 = KLLHY](#)
residues (725,730) [LIG_14-3-3_3](#)
[= KTLSKI](#)
residues (737,741)
[LIG_BRCT_BRCA1_1 = ISKIF](#)
residues (760,763)
[LIG_SH2_STAT5 = YLNS](#)
residues (774,777) [LIG_PDZ_3 =](#)
[NDVL](#)

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

[illegible]strand, coil) **TXT**

Linear motif(s):

residues (791,794)
LIG_SH2_GRB2 = YKNI
residues (803,809) LIG_FHA_2
= CNTYNEK
residues (828,831) LIG_PDZ_3 =
CEVI
residues (848,851) LIG_PDZ_3 =
NENV
residues (857,861)
LIG_BRCT_BRCA1_1 = RSND
residues (866,869) LIG_PDZ_3 =
NDVI
residues (872,878) LIG_FHA_2
= NKTYDE
residues (875,878)
LIG_SH2_SRC = YDEI
residues (888,897)
LIG_MAPK_1 = RFKFKNEIIF
residues (893,896) LIG_PDZ_3 =
NEII
residues (909,913)
LIG_Clathr_ClatBox_1 = LIKLD
residues (918,921)
LIG_SH2_STAT5 = YIYE
residues (920,923) LIG_PDZ_3 =
YEWL
residues (930,933)
LIG_MAPK_2 = FQFP
residues (936,939)
LIG_SH2_STAT5 = YVDK
residues (945,948) LIG_PDZ_3 =
SEYI
residues (947,950)
LIG_SH2_STAT5 = YIQA
residues (958,961) LIG_PDZ_3 =
NEEI
residues (974,977)
LIG_SH2_STAT5 = YINV
residues (985,988)
LIG_SH2_GRB2 = YDNM
residues (991,994)
LIG_SH2_STAT5 = YVEE
residues (993,996) LIG_PDZ_3 =
EENV
residues (1024,1027)
LIG_PDZ_3 = KDDV
residues (1033,1036)
LIG_PDZ_3 = GDEL
residues (1037,1040)
LIG_SH2_STAT5 = YVDN
residues (1043,1046)
LIG_SH2_STAT3 = YNNQ
residues (1049,1053)
LIG_APCC_KENbox_2 = KKEE
residues (1052,1055)
LIG_PDZ_3 = NEIL
residues (1069,1072)
LIG_SH2_STAT5 = YINS
residues (1075,1078)
LIG_PDZ_3 = KDDI
residues (1080,1083)
LIG_PDZ_3 = LESL
residues (1088,1091)
LIG_PDZ_3 = KDTI
residues (1106,1109)
LIG_SH2_STAT5 = YIDN
residues (1131,1134)
LIG_PDZ_3 = LDVL
residues (1143,1146)
LIG_SH2_GRB2 = YSNE
residues (1149,1152)
LIG_CYCLIN_1 = KKLI
residues (1152,1155)
LIG_PDZ_3 = IDNV
residues (1157,1161)
LIG_CYCLIN_1 = KSLE

SS Motif for disorder segment 17:
(start,end): (1193,1228)

```

      1193      1202      1212      1222
seq  : YIVSLYDEETKTFYKKKNK NIEFRNIIMPKQLSIFIN

```

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

S.S. : CEEEECCCCCHHCCCCCEEECCCCCHHHHHHHH
alpha: 2222223333443210111222210356666666
beta : 35554310011222210113443331000012222
coil : 42112455554334678644334447532210001

SS Motif for disorder segment 18:
(start,end): (1233,1244)

1233 1242
seq : NIYLIDKNKLNK
S.S. : CEEEECCCHHH
alpha: 111001334555
beta : 256653000001
coil : 632235554442

SS Motif for disorder segment 19:
(start,end): (1253,1313)

1253 1262 1272 1282 1292 1302 1312
seq : INITKFNFTSNDIIHFQGLLNYSVQNDNKVVNIYNNKNDINDNSNNYTSNNKIINDYI
S.S. : HCCCCCCCCCHHHHHHHHHHHHHHHCCCCCEEECCCCCCCCCCCCCCCCCHHHHHHH
alpha: 432222211135789998776655432110000000111112222111111245789999
beta : 222222122100000000000001232210025655410001110000000000000000
coil : 2344555567542000001222323345788632334688766678888777753110000

SS Motif for disorder segment 20:
(start,end): (1323,1336)

1323 1332
seq : IAEDTFLKWKLANV
S.S. : HHHHHHHHHHHHH
alpha: 88876777776668
beta : 00000000000000
coil : 01123222223331

SS Motif for disorder segment 21:
(start,end): (1342,1363)

1342 1351 1361
seq : LLTKFKHIHKNIFNKFDEFLNT
S.S. : HHHHHHHHHHHHHHHHHHHHH
alpha: 998887787777778888765
beta : 00000000000000000001
coil : 0001121111111221111223

SS Motif for disorder segment 22:
(start,end): (1367,1498)

1367 1376 1386 1396 1406 1416 1426
seq : PQYVYQKEKSYIRNNSSTEINDHKEKNTYDTYDMNHTCEEMLSINQNNNNNNNNNNNNNNNNNDNN
S.S. : CHHHHHCCCCCCCCCCCCCCCCCCCCCHHHHHCCCCCCCCCCCCCCCCCCCCCCCCCCCC
alpha: 356654433221100122222332111111111135655433332222221111222223333211
beta : 0012221101221100011100000011111100000000000000000000000011100
coil : 53111234655567876556666677666677778543344555666666777787766666555677
1437 1446 1456 1466 1476 1486 1496
seq : DNNNSNIKTSYNNYTNEKNNVVHNKKNNIYINEFKYDNLGSLWALSSLNKNILKKKYILK
S.S. : CCCCCCECCCCCCCCCCCCCECCCCCEEECECCCHHHHHHHHHHHHHHHHHHHHHHHHH
alpha: 1122222110111111222112211110001122233355789999887666776666666
beta : 0001234432100111100013432111256543332000000000000000011112212
coil : 877653345777776777666434567763223333554321000011222111111111

Linear motif(s):

residues (1193,1196)
LIG_SH2_STAT5 = YIVS
residues (1207,1214)
LIG_MAPK_1 = KKNKNIEF
residues (1208,1215) LIG_PPI =
KNKNIEFR
residues (1221,1225)
LIG_CYCLIN_1 = KQLSI

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

Linear motif(s):

residues (1235,1238)
LIG_SH2_STAT5 = YLID

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

Linear motif(s):

residues (1260,1263)
LIG_SH2_STAT5 = YFTS
residues (1260,1266)
LIG_FHA_2 = YFTSNDI
residues (1264,1267)
LIG_PDZ_3 = NDII
residues (1269,1275)
LIG_NRBOX = FLQGLLN
residues (1277,1280)
LIG_SH2_STAT3 = YSVQ
residues (1289,1292)
LIG_SH2_GRB2 = YNNK
residues (1302,1305)
LIG_SH2_STAT5 = YTSN
residues (1310,1313)
LIG_PDZ_3 = NDYI

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 (1358,1361)
LIG_PDZ_3 = DEFL

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

Linear motif(s):

residues (1369,1372)
LIG_SH2_STAT5 = YVYQ
residues (1377,1380)
LIG_SH2_STAT5 = YIRN
residues (1400,1406)
LIG_FHA_2 = NHTCEEM
residues (1402,1405)
LIG_TRAF2_1 = TCEE
residues (1404,1407)
LIG_PDZ_3 = EEML
residues (1447,1450)
LIG_SH2_GRB2 = YSNN
residues (1451,1454)
LIG_SH2_STAT5 = YTNE

[illegible]

residues (1599,1603)
LIG_CYCLIN_1 = KESLY
 residues (1603,1606)
LIG_SH2_STAT5 = VVLY
 residues (1637,1640)
LIG_PDZ_3 = EEKL
 residues (1739,1742)
LIG_PDZ_3 = ADKI
 residues (1773,1776)
LIG_PDZ_3 = VDDL
 residues (1778,1781)
LIG_SH2_STAT5 = YLYN
 residues (1782,1785)
LIG_PDZ_3 = LDYI
 residues (1784,1787)
LIG_SH2_STAT5 = YIKD
 residues (1794,1800)
LIG_FHA_2 = IKTLNDI
 residues (1801,1804)
LIG_PDZ_3 = NETI
 residues (1807,1810)
LIG_PDZ_3 = HDDI
 residues (1817,1822) **LIG_14-3-**
3_3 = KSSSSF
 residues (1818,1822)
LIG_BRCT_BRCA1_1 = SSSSF
 residues (1825,1829)
LIG_USP7_1 = PKSSD
 residues (1828,1831)
LIG_PDZ_3 = SDIL
 residues (1836,1842)
LIG_FHA_2 = KKTNKEK
 residues (1836,1847)
LIG_MAPK_1 =
KKTNKEKKGIVI
 residues (1848,1855)
LIG_MAPK_1 = KKDKFLIF
 residues (1851,1855)
LIG_CYCLIN_1 = KFLIF
 residues (1857,1860)
LIG_PDZ_3 = NERI
 residues (1862,1866)
LIG_BRCT_BRCA1_1 = LSNEF
 residues (1864,1867)
LIG_PDZ_3 = NEFI

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residues (1866,1872)
LIG_NRBOX = FLNKLLT
residues (1869,1874) LIG_14-3-3 = KLLTKI
residues (1876,1882)
LIG_FHA_1 = EYTKLIL
residues (1877,1880)
LIG_SH2_STAT5 = YTKL
residues (1904,1913)
LIG_MAPK_1 = KKNRMEIDL
residues (1908,1911)
LIG_PDZ_3 = MEH
residues (1941,1944)
LIG_PDZ_3 = VEKL
residues (1961,1964)
LIG_SH2_STAT5 = YIYH
residues (1966,1972)
LIG_FHA_1 = IDTYSLI
residues (1976,1979)
LIG_SH2_STAT5 = YVLD
residues (1980,1986)
LIG_FHA_1 = DFTKNII
residues (1987,1990)
LIG_PDZ_3 = REFV
residues (1999,2002)
LIG_PDZ_3 = EEKI
residues (2001,2005)
LIG_CYCLIN_1 = KILDM
residues (2007,2014)
LIG_MAPK_1 = KKKITLSI
residues (2009,2015)
LIG_FHA_1 = KITLSIQ

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