# CSpritz - Accurate detection of protein disorder

## Version 1.2

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## Status: finished

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**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
MRKKKKTCLVLLILSFLCFFYSSLSYDEDYDEEYNYEDKNSDYECNNLIPLFLNNLEYSNISQEISLSKT
CCCCCCHHHHHHHHHHHHHCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCEECCCCCCCCCCCCCEEECCCC
DDDDDDDDOOOOOOOOOOOODDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDOOOOODDDDDDDDDDDDDDDDDDO

71       80        90        100       110       120       130
FSLKYPVHYMYFKYSSDQSIFVNYNIYNSLSFGYVKKIELYEYEIIKNESVLLLQAEKDSDKNIKILYTI
CEECCCEEEEEEEECCCCCEEEEEEEECCCCCCCEEEEEEEEEEEECCCEEEEECCCCCCCCCEEEEEEEE
OOOOOOOOOOOOOOOOOOOOOOOOOOOOOODDDDDDOOOOOOOOOOOOOOOOOOOODOOOOOOOOO

141      150       160       170       180       190       200
TKIDNRKNYEGEKDQRLFYFIIYTTIENDNDIIKSCINVNMSIHIRIIKDDTQTNNHNNNNIINNNNNY
EEECCCCCCCCCCCEEEEEEEECCCCCCCHHCEEEEEEEEEEEEEECCCCCCCCCCCCEEEEECCCCE
OOOODDDDDDDDDOOOOOOOOOOOOODDDDDOOOOOOOOOOOOOODDDDDDDDDDDDDDDDDDDOOOO

211      220       230       240       250       260       270
YYNYVHNNYGMRGIMPNHLYNHLLPLHNKSYIIIKDNYYYCTNEDYYYNMNNIEDYYYDEKSGDKVVVIY
EEEEEEECCCCCCCCCCCCCCCCCCCCCCEECCCCCCCCCCEEEECCCCCEEECCCCCCCCCCCCCCCCCEEEEE
OOOOOOODDDDDDDDDDDDDOOOOOOOOOOOOOOOOOOOOOOOODDDDDDDOOOOOOOOOD

281      290       300       310       320       330       340
SVLLFIEFKKEANIKFTSFLKHDINKYNNFVIHIKKIDIHNNYLNNMDMEHILKVGNNEEYINGNKKKS
EEEEEEEHCCCCCCEEHHHHCCCCCCCCCEEEEEEEECCCCCCCCCCCHHHHHHCCCHHHHCCCCCCCC
DDOOOOOOOOOODDDOOOODDDDDDOOOOOOOOOOOODDDDOOOOOOOOOOOODDDDDDDDDDDDDD

351      360       370       380       390       400       410
MECEEDCVESYITSQGIYIDTILNNNHLYRLDILYKMGKNEINNKTTEIIKKENNNNNNNNNNNNNNNN
CCCCCCCCEEECCCCEEEEHHHCCCCEEEEEEEHHCCCCCCCCCCEEEEEECCCCCCCCCCCCCCCCCC
DDDDDDDDDDDDOOOOOOOOOOOOOOOOOOODDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD

421      430       440       450       460       470       480
NNNKNNNNNNNNNNKNNNNNNYYDYDNDKMGDIKNMKDNGKDPFLSSLLFFNFELSIYNITDNYIPMNY
CCCCCCCCCCCCCCCCCCCCCCCECCCCCCCCCCCCCCCCCCCCCCCCCHHHHECEEEEEEECCCCCCHHHH
DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDOOOOOOOOOOOOOOOOOOOO

491      500       510       520       530       540       550
INKRLYTECSNNSHAPNKIVQTKEENMLNIFYTNECSKNIEKCSLYDVNEYIIYNNKVIDIHDNFLLNFD
HHHHHHHHHCCCCCCCCCCEEEECCCCCCCCCCCCCCHCCCCCCCCCCCCCCCCEEEEECCEEEEECCCEEECCC
OOOOODDDDDDDDOOODDDDDDDDDDDDDDDDDDDDDDDDDDDDDOOOOOOOOOOOOOOOOOOOO

561      570       580       590       600       610       620
IINSFKNEQIIDIYINEDSIFNFSMLIKSDHIFVNLLKNNSSEKICNTYYMNNINDYNIYDYKKNNKSDF
HHHHCCCCEEEEEEEECCCCEEEEEEEECCCCEEEEEEECCCCCCEECEEEECCCCCCCEECCCCCCCCC
OOOOOOOOOOOOOOOOOOOOOOOOOOOOOOODDDDDOOOOOOOOOOOOOOOOODDDDDDDDD

631      640       650       660       670       680       690
FHKHYNDSFLYNQNMNYNNTFEYQNYYQHDHHLKNFPLQNIIYINCILKKGYYDLKIILNGYNNICESND
CCCCCCCHHHHCCCCCCCCCEECCCCCCCCCCCCCCCCCCEEEEEEECCCCCEEEEEEEECCCCCCCCCC
DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDOOOOOOOOOOOOOOOOOOOOOOOOOOODDDOOOO

701      710       720       730       740       750       760
FNLLIYPMSLYKNQHQCDDKMNQVTNLFNNILKRKYQHNISHVPNQIQTFDQIYQNKWILNNHIFEYFDF
CEEEEEEECCHCCCCCCCCHHHHHHHHHHHHHHCCCCCCCCCCHHHHHHHHHHHHCCCHHHHCCCC
OOOOOOOOODDDDDDDOOOOOOOOOOOOODDDDDDDDDDDDOOOOOOOOOOOOOOOOOOOOOO

771      780       790       800       810       820       830
VIIYEKELLPQQYKEIMVTINNSPGLDLFFILVENVQGQKYYHIYKDTRKKNKYILKDKHPCTLYVLVST
EEEEECCCCCCCCCEEEEECCCCCCEEEEEEEECCCCEEEEEEEECCCCCEEEEEECCCCEEEEEEC
OOOOOOOODOOOOOOOOOOOOOOOOOOOOOOOOOOODDDOOOOOOOOOOOOOOOOO

841      850       860       870       880       890       900
LLYTTQDVCGFFFVDIEYVDNMKLLNQNDHPNDIMNGTYQHNMIQKINYIPTIIIGYDSYSYSHFCYVPY
CCCCCEEEEEEEEHHHHHHHHHCCCCCCCCCCCCCCCHHHCCCCCEEEEECCCCCCCCEEEC
OOODDDOOOODOOOOOOODDDDDDDDDDDDOOOOOOOOOOOOOOOOOOOOOOO
```

| | |
|---|---|
| Total amino acids: | 2472 |
| Total % disorder: | 46.48 |
| Total no. of disordered regions > 30 amino acids: | 10 |
| Total no. of disordered regions > 50 amino acids: | 3 |
| Number of disordered segments: | 63 |
| Length distribution of segments (N to C terminal order): | 8 29 15 6 1 9 5 19 17 8 3 3 6 4 26 81 8 30 5 44 3 12 13 1 3 3 1 24 17 2 1 43 16 2 15 101 13 30 26 40 35 20 38 8 6 34 30 42 2 23 1 15 1 3 1 1 7 19 4 109 29 6 22 |

```
911       920       930       940       950       960       970
YKKHKLTILLKPKTIVKINCFTHNYIYIYLLDKSNNNNNNKNNNDNNKKKLYEGYNHLYIESFVEGEYEI
CCCEEEEEEECCCCEEEEEEECCCEEEEEEECCCCCCCCCCCCCCCCCCCCCCEEEEEEEECCCEEEEE
OOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOODDDDDDDDDDDDDDDOOOOOOOOOOOOOOOOOOOO

981       990       1000      1010      1020      1030      1040
IFEFNTQNDKNMNSFFYLQIYIYNLNTLDKCLFFNNNMNYIKESSINKFINTNNYDTFDLSKYEYNDIII
EEEEECCCCCCCCCEEEEEEEEEECCCCCHHHCCCCCCCCCCCCCCCCCCCCCCCCCCCEECCCCCCCCCCCCCCC
OOOOOOOODDOOOOOOOOOOOOOOOOOOOOOODOOODDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD

1051      1060      1070      1080      1090      1100      1110
NKNVPRVIKKENNMFFIYQTINFYYLYKSFFLYILPTQHKDGNITNEQDKNRIKKKIILPKINYLSNQNF
CCCCCEEEEECCCCEEEEECCCHEEEEEEEEEEEECCCCCCCCCCCCCCCCCEEEEECCCCCCCCCCCCE
DDDDDDDDDDOOOOOOOOOOOOOOOOOOOOOOOOOOOODDDDDDDDDDDDDDDOOOOOOOODDOOOOO

1121      1130      1140      1150      1160      1170      1180
ILKIELSFHKNIFPYKMYIDENYDDIIMISTNTYRNKNIMLLKILNNNTNYINIYIDTYEDINDEIRKNY
EEEEEEEECCCCCCEEEEEECCCCCEEEEEEECCCCCCCHHHHHHCCCCCEEEEEEECHHHHHHHHHCC
OOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOO

1191      1200      1210      1220      1230      1240      1250
CSYAYFNITYTNQTEEETVDRQQINLYNKITLPLLLNNILSKDYVPMINKNIVENKNDQTYKADHLYYED
CCCEEEEEEEECCCCHHCCCCHHHHHHCCCCCHHHHHHHHHHCCCCCCCCCCEEEECCCCCCCCCEEEECC
OOOOOOOOOOOODDDDDDDDDDDDDDDDOOOOOOODDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD

1261      1270      1280      1290      1300      1310      1320
DNIGVINSVSNNYFSGENKNMGDIKNKMNNEYGSVHTEQMVHFQNNDNLNNNNNIIFGNVYPYLENHLRG
CCCEEEECCCCCCCCCCCCCHHHHHHHCCCCCCCCCCHHHHHCCCCCCCCCCCEEECCCCHHHHHCCCC
DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDOOOD

1331      1340      1350      1360      1370      1380      1390
IISLKNSNSLILNQSVNYNFEVVNNNYTLLIIPNDAFLNMYIRNNDDDDDDDNDKNNNNNNNNSNNNNSN
EEEECCCCCCEECCCCCCCEEEECCCEEEECCCCCHHHHEEECCCCCCCCCCCCCCCCCCCCCCCCCCC
DDDDDDDDDDDOOOOOOOOOOOOOOOOOOOOOOOOOOOOOODDDDDDDDDDDDDDDDDDDDDDDDDDDD

1401      1410      1420      1430      1440      1450      1460
SSKKNITLNVYRILDVPKLTNEGISFNEVKKQILSLSHPFLTFTDKYINVYRYLERGLYIFKFDDDSNKE
CCCCCEEEEEEEEECCCCCCCCCCHHHHHHHHHCCCCCCCCCCCHHHHHHHHCCCCEEEEEECCCCCCC
DDDDDOOOOOOOOOOOODDDDDDDDDDDDDDDDDDDDDDDDDDDDOOOOOOOOOOOOOOOOOOOODDDDD

1471      1480      1490      1500      1510      1520      1530
NSSYTFRNSSNIYKNNINNYNYHSSDSIKPLSFFMHFNIMPIYTNDIEYKDNIKNNNYNDKTFNYQGHDK
CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCHCCCCCCCCEECCCCCHHCCCCCCCCCCCCCCCCCCCCC
DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDOOOOODDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD

1541      1550      1560      1570      1580      1590      1600
NMYPSVIHNYIFKNELLYYFNKEYSCDKENMLFFEHKKIDDVSNFLEHTWNNIPFEIYINDKLDITLNRD
CCCCHHHHHHHHHHHHHHHCCCCCCCCCCCEECCCCCCCHHHHHHHHHHHCCCEEEEECCCCEEEEECC
DDDDDOOOOOOOOOOODDDDDDDDDDDDDDDDDDDDDDDOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOO

1611      1620      1630      1640      1650      1660      1670
NYNTLILKRFFICFEKEKNVNNNDNINNSNNSYVNNTDNINESQDDSYINFNDTIKKEYLLFNIVLNVK
CCCEEEEEEEEEECCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCEEEEEEEEEEE
OOOOOOOOOOOOOOOODDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDOOOOOOOOOOOO

1681      1690      1700      1710      1720      1730      1740
GNIYIEIQPHYHYFIYPFILTIKSKNNPTQLNKSHDKLFLTTDLGVGEYEIYITFLSNNHYKNVKMKKVM
CEEEEEEECCCEEEEEEEEEEEEEECCCCCCCCCCCCCCEEEEEEECCCCEEEEEEEECCCCCCCHHHHHHHH
OOOOOOOOOOOOOOOOOOOOOOOOOOOODDDDDDDDOOOOOOOOOOOOOOOOOOOOOOODDDDDDOOOOO

1751      1760      1770      1780      1790      1800      1810
FDLFIFIDILKNKNIQLGKNNLYLPYGNHLDDTIDFKIYDNTCKTDNYKRLFHEVKLLENNNSSNVHMNE
EEEEEEEHHCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCHHHHHHHHHHCCCCCCCCCCC
OOOOOOOOOOOODDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDOOOOOOODDDDDDDDDDDDDDDDD

1821      1830      1840      1850      1860      1870      1880
SYIKNKNNIISTNMNTNYFHIYDTYYMKVREHEISFEIPKEAYILKIFCIHIDEQNYDEDITSGDFYNNT
CCCEECCCEECCCCCCCEEEEECEEEEEECEEEEEEEECCCCCEEEEEEEECCCCCCCCCCCCCCCCCCC
DDDDDDDDDDDDDOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOODDDDDDDDDDDDDDDD

1891      1900      1910      1920      1930      1940      1950
NAYNNNNNYGNNNNYYKIEQTDNLSHFSFNYLNTYFDIQNLFHINVITNEDSKFFSDEHTNDQDLYVKPF
CHHHCCCCCCCCCCEECCCCCCCCCCCCCCCEEEEEEEEEEEEEECCCCCCCCCCCCCCCCCCCCCCCC
DDDDDDDDDDDDDDDDDDDDDDOOOOOOOOOOOOOOOODDOOOOOOOODDDDDDDDDDDDDDDDDDDD

1961      1970      1980      1990      2000      2010      2020
FSNEENEHILNWYKIDKNFKLVIKKNNYDCTYFKLIISLYPMDYFNSIDYLKYNNYLNKYFTNIFDTLSL
CCCCCCCEEEEEEEECCCCEEEEEECCCCCCEEEEEEEECCCCCCCCCCHHHHHHHHHHHHHHHECEEEE
DDDDOOOOOOOOOOOOOOODOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOO

2031      2040      2050      2060      2070      2080      2090
KVNQYQDISFEQIKNKNYLYDYLKTNVIFLKSLNSRDLFSYPLTIKMPSYVKINFGYNFTLTSFEIKLLK
EECCCCCCEEEEEECCCCCEEEEEEEEEEEEEECCCCCCCCCCCEEEEECCEEEEEEECCCCCEEEEEEEEC
ODDDDDDDDDDDDDDOOOOOOOOODOOOOOOOODDDOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOO

2101      2110      2120      2130      2140      2150      2160
NNMIIATSNKVQANINNNNINIFENVSIYLEKGNYVVQIYSYDLIEKSSNIINKLSFPFYAEIEIVQFVN
CCCEEECCCCEEEEEECCCCCCEEEEEEEEECCCEEEEEEEECHHHHHHHHHCCCCCEEEEEEEEEEC
OOOODOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOODOOOOOOOOOOOOOOOO

2171      2180      2190      2200      2210      2220      2230
DQIDEPILLDVFPHNSVIVNRNYPFFVDLIFWGRANENISVLDTKENNIKLNNTKLIKYGNVEIHKYVLS
CCCCCEEEEECCCCCEEECCCCCCEEEEEEECCCCCCEEECCCCCCCCCCCCEEEEECCEEEEEEECC
OOOOOOOOOOOOODDDDDDDOOOOOOOOOOOOOOOODDDDDDDDDDDDDDDDDDOOOOOOOOOOOOOO

2241      2250      2260      2270      2280      2290      2300
SEQMRSLENNFTLKLQSNVHISAWMEKRMNFSFTNEGWNYDGQTEHGKLMKNGIKTNNIVDESSKISKGE
HHHHHHHCCCEEEEECCCEEHHHHHHCCCCEECCCCCCCCCCHHHHHCCCCCCCCCCCCCCCCCCCCCCC
OODDDDOOOOOOOOOOOOOOODDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD

2311      2320      2330      2340      2350      2360      2370
KLNETVLLEYGKREIKNESEGESKSENKIEGNSNNESDGESEKRSFLQNGVIEKSNLFDLNEVIKNFRYN
CCCHHHHHHCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCHHCCCCCCCCCCCCCCHHHHHHHHHH
```

<span style="color:red">DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD</span>OOOO<span style="color:red">DDDDDDD</span>

```
2381      2390      2400      2410      2420      2430      2440
KKKKKEEEDFLLNGSYMNSNDKCFSLSIFSFEIYCFEKFYFFIFIFILTVLWISCAFIFLIIKIYKNWKG
CCCCCCCCCCHCCCCCCCCCCCCCCEECEEEEEEEEHHHHHHHHEEEEEEHHHHHHHHHHEEEEEEECCCC
```
<span style="color:red">DDDDDDDDDDDDDDDDDDDDDDDDD</span>OOOOOOOOOOOOOOOOOOOOOOOOOOO<span style="color:red">DDDDDD</span>OOOOOOOOOOOOOOOOOOO

```
2451     2460      2470
YRNYDIVGEMDEVIGLFHGDDL
CCCCCCCCCCCCCEECCCCCCCC
```
<span style="color:red">DDDDDDDDDDDDDDDDDDDDDD</span>

---

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

## SS Motif for disorder segment 1:
**(start,end): (1,8)**

```
seq  : MRKKKKTC
S.S. : CCCCCCHH
alpha: 00122355
beta : 00000011
coil : 98876532
```

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): (21,49)**

```
        21      30      40
seq  : YSSLSYDEDYDEEYNYEDKNSDYECNNLI
S.S. : CCCCCCCCCCCCCCCCCCCCCCCCCCCCC
alpha: 32211111122333222211112332222
beta : 21111210000011111100001111112
coil : 45666677766544556678876545654
```

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): (55,69)**

```
        55        64
seq  : NLEYSNISQEISLSK
S.S. : CCCCCCCCCEEECCC
alpha: 122221222110010
beta : 111221112455432
coil : 765556654333457
```

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

Linear motif(s):

residues (58,61)
**LIG_SH2_GRB2 = YSNI**

---

## SS Motif for disorder segment 4:
**(start,end): (101,106)**

```
seq  : SFGYVK
S.S. : CCCCEE
alpha: 110000
beta : 111355
coil : 677533
```

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): (145,153)**

```
seq  : NRKNYEGEK
S.S. : CCCCCCCCC
alpha: 001000011
beta : 111111011
coil : 877778877
```

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

Linear motif(s):

---

## SS Motif for disorder segment 6:
**(start,end): (168,172)**

```
seq  : NDNDI
S.S. : CCCCH
alpha: 01233
beta : 00002
coil : 87753
```

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

Linear motif(s):

---

## SS Motif for disorder segment 7:
**(start,end): (187,205)**

```
        187      196
seq  : IIKDDTQTNNHNNNNIIIN
S.S. : EEECCCCCCCCCCCCEEEEE
alpha: 0000001112222222222
beta : 8863101222222246665
coil : 1135887665444431011
```

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

Linear motif(s):

---

## SS Motif for disorder segment 8:
**(start,end): (220,236)**

```
        220      229
seq  : GMRGIMPNHLYNHLLPL
```

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

```
S.S. : CCCCCCCCCCCCCCCCC
alpha: 11111123443322122
beta : 12222100001001110
coil : 66666776544566766
```

**SS Motif for disorder segment 9:**
**(start,end): (264,271)**

```
seq  : EDYYYDEK
S.S. : CCCCCCCC
alpha: 22222221
beta : 11222210
coil : 55544567
```

**SS Motif for disorder segment 10:**
**(start,end): (280,282)**

```
seq  : YSV
S.S. : EEE
alpha: 012
beta : 876
coil : 000
```

**SS Motif for disorder segment 11:**
**(start,end): (292,294)**

```
seq  : ANI
S.S. : CCC
alpha: 222
beta : 013
coil : 664
```

**SS Motif for disorder segment 12:**
**(start,end): (299,304)**

```
seq  : FLKHDI
S.S. : HHHCCC
alpha: 444433
beta : 211111
coil : 334455
```

**SS Motif for disorder segment 13:**
**(start,end): (320,323)**

```
seq  : HNNY
S.S. : CCCC
alpha: 1223
beta : 1001
coil : 6665
```

**SS Motif for disorder segment 14:**
**(start,end): (338,363)**

```
       338       347       357
seq  : NEEYINGNKKKKSMECEEDCVESYIT
S.S. : CHHHHCCCCCCCCCCCCCCCCCCEEEC
alpha: 35665311000000012233322211
beta : 00011000012233431001233442
coil : 64223578877655455655433336
```

**SS Motif for disorder segment 15:**
**(start,end): (388,468)**

```
       388       397       407       417       427       437       447
seq  : GKNEINNKTTEIIKKENNNNNNNNNNNNNNNNNNKNNNNNNNNNNKNNNNNNYYDYDNDKMGDIKNM
S.S. : CCCCCCCCCEEEEEEECCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCECCCCCCCCCCCCC
alpha: 11122212333333332222222222233222222222222221122111111111111121123321
beta : 00133211245555543221122222211111222211110000001111111123442100000011111
coil : 87644565421001123455555555545555444555556666666676666777644456776776556
       458       467
seq  : KDNGKDPFLSS
S.S. : CCCCCCCCCCH
alpha: 11000022334
beta : 10000000012
coil : 77899876543
```

**SS Motif for disorder segment 16:**
**(start,end): (496,503)**

---

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):**

---

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

**Linear motif(s):**

residues (339,342)   **LIG_PDZ_3 = EEYI**
residues (341,344)   **LIG_SH2_STAT5 = YING**
residues (355,358)   **LIG_PDZ_3 = EDCV**

---

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

**Linear motif(s):**

residues (394,400)   **LIG_FHA_1 = NKTTEII**
residues (397,400)   **LIG_PDZ_3 = TEII**
residues (401,405)   **LIG_APCC_KENbox_2 = KKENN**
residues (446,449)   **LIG_SH2_GRB2 = YDND**
residues (463,465)   **LIG_AP2alpha_2 = DPF**

---

**Graph of Probability(helix, strand, coil)**   **PDF**

```
seq  : YTECSNNS
S.S. : HHHHCCCC
alpha: 44444211
beta : 11111001
coil : 43334677
```

**Amino SS Probability(helix, strand, coil) TXT**

**Linear motif(s):**

residues (496,499)
**LIG_SH2_STAT5 = YTEC**

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

## SS Motif for disorder segment 17:
**(start,end): (507,536)**

```
       507       516       526
seq  : NKIVQTKEENMLNIFYTNECSKNIEKCSLY
S.S. : CCEEEECCCCCCCCCCCCHCCCCCCCCCC
alpha: 22110012223332212344433332221
beta : 02576521000112321011100112112
coil : 75212356666554445654445555445666
```

**Linear motif(s):**

residues (510,516) **LIG_FHA_2 = VQTKEEN**
residues (512,515)
**LIG_TRAF2_1 = TKEE**
residues (522,525)
**LIG_SH2_STAT5 = YTNE**

## SS Motif for disorder segment 18:
**(start,end): (600,604)**

```
seq  : NSSEK
S.S. : CCCCC
alpha: 01111
beta : 00113
coil : 88764
```

**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**

## SS Motif for disorder segment 19:
**(start,end): (622,665)**

```
       622       631       641       651       661
seq  : YKKNNKSDFFHKHYNDSFLYNQNMNYNNTFEYQNYYQHDHHLKN
S.S. : CCCCCCCCCCCCCCCCCHHHCCCCCCCCCCEECCCCCCCCCCCC
alpha: 33321111222322344543322221101222221122321
beta : 21000011111221112221111111244432221012222
coil : 44567776665545654223456666676443455566664445
```

**Linear motif(s):**

residues (627,631)
**LIG_BRCT_BRCA1_1 = KSDFF**
residues (627,633)
**LIG_BRCT_BRCA1_2 = KSDFFHK**
residues (647,650)
**LIG_SH2_GRB2 = YNNT**
residues (653,656)
**LIG_SH2_GRB2 = YQNY**

## SS Motif for disorder segment 20:
**(start,end): (694,696)**

```
seq  : NIC
S.S. : CCC
alpha: 122
beta : 133
coil : 644
```

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

**Linear motif(s):**

## SS Motif for disorder segment 21:
**(start,end): (712,723)**

```
       712       721
seq  : KNQHQCDDKMNQ
S.S. : CCCCCCCCHHHH
alpha: 332111124567
beta : 110111000000
coil : 456677764331
```

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

**Linear motif(s):**

## SS Motif for disorder segment 22:
**(start,end): (735,747)**

```
       735       744
seq  : KYQHNISHVPNQI
S.S. : HHHHCCCCCCCCC
alpha: 7665422101111
beta : 0000000000013
coil : 1234567788765
```

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

**Linear motif(s):**

## SS Motif for disorder segment 23:
**(start,end): (822,824)**

```
seq  : NKY
S.S. : EEE
alpha: 000
beta : 468
coil : 421
```

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

**Linear motif(s):**

### SS Motif for disorder segment 24:
(start,end): (844,846)

```
seq   : TTQ
S.S.  : CCC
alpha : 011
beta  : 101
coil  : 776
```

### SS Motif for disorder segment 25:
(start,end): (860,883)

```
        860       869       879
seq   : DNMKLLNQNDHPNDIMNGTYQHNM
S.S.  : HHHHHHCCCCCCCCCCCCCCCCCC
alpha : 545665532001123212344444
beta  : 100000000000000000110111
coil  : 343333457888765676544444
```

### SS Motif for disorder segment 26:
(start,end): (945,961)

```
        945       954
seq   : NNNNNNKNNNDNNKKKL
S.S.  : CCCCCCCCCCCCCCCCC
alpha : 11111111111222333
beta  : 11122333111222333
coil  : 77665545776554333
```

### SS Motif for disorder segment 27:
(start,end): (1018,1060)

```
        1018      1027      1037      1047      1057
seq   : MNYIKESSINKFINTNNYDTFDLSKYEYNDIIINKNVPRVIKK
S.S.  : CCCCCCCCCCCCCCCCCCEECCCCCCCCCCCCCCCCCCCEEEE
alpha : 222222222211000000110112221233332100000000
beta  : 013332111112210012345311122210111001257876
coil  : 654345666655578876543566555566444688732123
```

### SS Motif for disorder segment 28:
(start,end): (1090,1105)

```
        1090      1099
seq   : KDGNITNEQDKNRIKK
S.S.  : CCCCCCCCCCCCCCEE
alpha : 1001112333322111
beta  : 0001332211002456
coil  : 8887555455665432
```

### SS Motif for disorder segment 29:
(start,end): (1204,1218)

```
        1204      1213
seq   : TEEETVDRQQINLYN
S.S.  : CHHCCCCHHHHHHCC
alpha : 344422156654432
beta  : 111111000011111
coil  : 433456733233446
```

### SS Motif for disorder segment 30:
(start,end): (1226,1326)

```
        1226      1235      1245      1255      1265      1275      1285
seq   : LNNILSKDYVPMINKNIVENKNDQTYKADHLYYEDDNIGVINSVSNNYFSGENKNMGDIKNKMNNEYGSV
S.S.  : HHHHHHCCCCCCCCCCEEEECCCCCCCCCCCEEEECCCCCEEEECCCCCCCCCCCCCCHHHHHHHCCCCCCCC
alpha : 766654322223321000000000010100000010000000001111001111155666654322111
beta  : 100011000111222356652001222235565310146775432111211110000000000000001112
coil  : 12223456665445554223688876665433467885311355667677766774322334566765
        1296      1305      1315      1325
seq   : HTEQMVHFQNNDNLNNNNNIIFGNVYPYLEN
S.S.  : CCCHHHHCCCCCCCCCCCCEEECCCCHHHHH
alpha : 1233444332222332211111111112345665
beta  : 22233333211000100135652222111000
coil  : 543322224566655667532356544322233
```

## Right column (per segment)

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):

 residues (1020,1023)
 **LIG_SH2_STAT5 = YIKE**
 residues (1035,1041)
 **LIG_FHA_1 = YDTFDLS**
 residues (1046,1049)
 **LIG_PDZ_3 = NDII**

---

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 (1204,1207)
 **LIG_TRAF2_1 = TEEE**
 residues (1206,1209)
 **LIG_PDZ_3 = EETV**

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

Linear motif(s):

 residues (1232,1235)
 **LIG_PDZ_3 = KDYV**
 residues (1234,1237)
 **LIG_SH2_STAT5 = YVPM**
 residues (1253,1256)
 **LIG_PDZ_3 = ADHL**
 residues (1260,1263)
 **LIG_PDZ_3 = DDNI**
 residues (1273,1276)
 **LIG_SH2_STAT5 = YFSG**
 residues (1306,1309)
 **LIG_PDZ_3 = NDNL**
 residues (1323,1326)
 **LIG_SH2_STAT5 = YLEN**

---

**SS Motif for disorder segment 31:**
**(start,end): (1330,1342)**

```
          1330      1339
 seq  : GIISLKNSNSLIL
 S.S. : CEEEECCCCCCEE
 alpha: 2211111111222
 beta : 2455431002344
 coil : 4322357775323
```

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

Linear motif(s):

_____

**SS Motif for disorder segment 32:**
**(start,end): (1376,1405)**

```
          1376      1385      1395
 seq  : DDDDDDDNDKNNNNNNNNSNNNNSNSSKKN
 S.S. : CCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
 alpha: 11122333333332222221111111111000
 beta : 11000001112111000000000011111234
 coil : 77766555444456676777777777777665
```

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

Linear motif(s):

_____

**SS Motif for disorder segment 33:**
**(start,end): (1417,1442)**

```
          1417      1426      1436
 seq  : PKLTNEGISFNEVKKQILSLSHPFLT
 S.S. : CCCCCCCCCCHHHHHHHHHCCCCCCC
 alpha: 22221100144554444432100111
 beta : 01111012211112223221100223
 coil : 75567776644323222235788655
```

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

Linear motif(s):

residues (1421,1424)
**LIG_PDZ_3 = NEGI**
residues (1430,1436)
**LIG_MAPK_1 = KKQILSL**
residues (1436,1440)
**LIG_BRCT_BRCA1_1 = LSHPF**

_____

**SS Motif for disorder segment 34:**
**(start,end): (1466,1505)**

```
          1466      1475      1485      1495
 seq  : DSNKENSSYTFRNSSNIYKNNINNYNYHSSDSIKPLSFFM
 S.S. : CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCHC
 alpha: 1111111122211122333322212122221110123332
 beta : 0000111123331001111111111112110011111233
 coil : 8777677654456776444555666655567877754333
```

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

Linear motif(s):

residues (1468,1472)
**LIG_APCC_KENbox_2 = NKENS**
residues (1472,1476)
**LIG_BRCT_BRCA1_1 = SSYTF**
residues (1474,1477)
**LIG_SH2_STAT5 = YTFR**
residues (1483,1486)
**LIG_SH2_GRB2 = YKNN**
residues (1495,1498)
**LIG_PDZ_3 = SDSI**
residues (1499,1503)
**LIG_CYCLIN_1 = KPLSF**

_____

**SS Motif for disorder segment 35:**
**(start,end): (1511,1545)**

```
          1511      1520      1530      1540
 seq  : PIYTNDIEYKDNIKNNNYNDKTFNYQGHDKNMYPS
 S.S. : CEECCCCHHCCCCCCCCCCCCCCCCCCCCCCCCCCC
 alpha: 01111134433333321111111111111111221134
 beta : 34431011110011000100122211000001001
 coil : 54457744345655677777755667777777753
```

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

Linear motif(s):

residues (1512,1518)
**LIG_FHA_1 = IYTNDIE**
residues (1513,1516)
**LIG_SH2_STAT5 = YTND**
residues (1520,1523)
**LIG_PDZ_3 = KDNI**

_____

**SS Motif for disorder segment 36:**
**(start,end): (1557,1576)**

```
          1557      1566
 seq  : LYYFNKEYSCDKENMLFFEH
 S.S. : HHHHCCCCCCCCCCEECCC
 alpha: 7764211000022222211111
 beta : 1112112331001134541 0
 coil : 11135655678665433467
```

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

Linear motif(s):

residues (1559,1562)
**LIG_SH2_STAT5 = YFNK**
residues (1567,1571)
**LIG_APCC_KENbox_2 = DKENM**

_____

**SS Motif for disorder segment 37:**
**(start,end): (1628,1665)**

```
          1628      1637      1647      1657
 seq  : KNVNNNDNINNSNNSYVNNTDNINESQDDSYINIFNDT
 S.S. : CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
```

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

```
alpha: 210012322211112221111222111122221111
beta : 222100001110001332111111111100012332112
coil : 556887665677776445777666677777754445676
```

## SS Motif for disorder segment 38:
**(start,end): (1708,1715)**

```
seq  : PTQLNKSH
S.S. : CCCCCCCC
alpha: 00100111
beta : 13442100
coil : 75456787
```

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): (1740,1745)**

```
seq  : HYKNVK
S.S. : CCHHHH
alpha: 234455
beta : 011121
coil : 654322
```

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

Linear motif(s):

residues (1741,1744)
LIG_SH2_GRB2 = YKNV

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

Linear motif(s):

## SS Motif for disorder segment 40:
**(start,end): (1762,1795)**

```
        1762      1771      1781      1791
seq  : NKNIQLGKNNLYLPYGNHLDDTIDFKIYDNTCKT
S.S. : CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
alpha: 222333111111111100001111111211111
beta : 000111111222210121000001121112322
coil : 776445777655667777788877766665556
```

residues (1773,1776)
LIG_SH2_STAT5 = YLPY
residues (1776,1779)
LIG_SH2_GRB2 = YGNH
residues (1781,1784)
LIG_PDZ_3 = DDTI
residues (1789,1792)
LIG_SH2_GRB2 = YDNT

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

Linear motif(s):

## SS Motif for disorder segment 41:
**(start,end): (1804,1833)**

```
        1804      1813      1823
seq  : EVKLLENNNSSNVHMNESYIKNKNNIISTN
S.S. : HHHHHHCCCCCCCCCCCCCCCEECCCEECCC
alpha: 655555321111100011212221100000
beta : 122111100000221100124432355421
coil : 112223578777667777653345533467
```

residues (1822,1825)
LIG_SH2_STAT5 = YIKN

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

Linear motif(s):

## SS Motif for disorder segment 42:
**(start,end): (1875,1916)**

```
        1875      1884      1894      1904      1914
seq  : QNYDEDITSGDFYNNTNAYNNNNNYGNNNNYYKIEQTDNLSH
S.S. : CCCCCCCCCCCCCCCCCHHHCCCCCCCCCCCCEECCCCCCCCCC
alpha: 2111111112333333344432111111111111000111110
beta : 111001110001111222211111222333444321101110
coil : 667777677654444433335676555555444567777778
```

residues (1878,1881)
LIG_PDZ_3 = DEDI
residues (1880,1886)
LIG_FHA_2 = DITSGDF
residues (1882,1886)
LIG_BRCT_BRCA1_1 = TSGDF
residues (1887,1890)
LIG_SH2_GRB2 = YNNT
residues (1893,1896)
LIG_SH2_GRB2 = YNNN
residues (1899,1902)
LIG_SH2_GRB2 = YGNN
residues (1909,1915)
LIG_FHA_1 = EQTDNLS
residues (1911,1914)
LIG_PDZ_3 = TDNL

Graph of Probability(helix, strand, coil)   PDF

## SS Motif for disorder segment 43:
**(start,end): (1942,1964)**

```
        1942      1951      1961
seq : SKFFSDEHTNDQDLYVKPFFSNE
S.S. : CCCCCCCCCCCCCCCCCCCCCC
alpha: 1111111111111111111112
beta : 0011000000011121233210
coil : 8767888888877767544566
```

**Graph of Probability(helix, strand,
    coil)    PDF**

### SS Motif for disorder segment 44:
(start,end): (2032,2046)

```
        2032      2041
seq : VNQYQDISFEQIKNK
S.S. : ECCCCCCEEEEECCC
alpha: 112211001111101
beta : 433212466554210
coil : 344466422234588
```

**Amino SS Probability(helix,
    strand, coil)    TXT**

Linear motif(s):

    residues (2035,2038)
LIG_SH2_SRC = YQDI
    residues (2040,2043)
LIG_PDZ_3 = FEQI

### SS Motif for disorder segment 45:
(start,end): (2065,2067)

```
seq : SRD
S.S. : CCC
alpha: 333
beta : 101
coil : 555
```

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

Linear motif(s):

### SS Motif for disorder segment 46:
(start,end): (2185,2191)

```
seq : NSVIVNR
S.S. : CCEEECC
alpha: 0000000
beta : 1367641
coil : 8632357
```

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

Linear motif(s):

### SS Motif for disorder segment 47:
(start,end): (2208,2226)

```
        2208      2217
seq : NISVLDTKENNIKLNNTKL
S.S. : CCEEECCCCCCCCCCCCCEE
alpha: 0001111111000111111
beta : 2455520011244311256
coil : 6533367767654577631
```

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

Linear motif(s):

    residues (2214,2218)
LIG_APCC_KENbox_2 = TKENN

### SS Motif for disorder segment 48:
(start,end): (2243,2246)

```
seq : QMRS
S.S. : HHHH
alpha: 9887
beta : 0000
coil : 0112
```

**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 49:
(start,end): (2261,2369)

```
        2261      2270      2280      2290      2300      2310      2320
seq : ISAWMEKRMNFSFTNEGWNYDGQTEHGKLMKNGIKTNNIVDESSKISKGEKLNETVLLEYGKREIKNESE
S.S. : HHHHHHCCCCEECCCCCCCCCCCCHHHHHCCCCCCCCCCCCCCCCCCCCCCCCHHHHHHCCCCCCCCCCC
alpha: 45676544311000001112223344445431000001222221100001122556665422232211111
beta : 42100001123564210010001122221101343111111123310121112222210123321000
coil : 12122344555335677776765433322357865577655567656887556310012476433356777
        2331      2340      2350      2360
seq : GESKSENKIEGNSNNESDGESEKRSFLQNGVIEKSNLFD
S.S. : CCCCCCCCCCCCCCCCCCCCCCCCCHHCCCCCCCCCCCC
alpha: 1112233322111110001222233443100112222222
beta : 0011111121110000100001112222102331111232
coil : 877655555677778888876654322468655566444
```

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

Linear motif(s):

    residues (2280,2283)
LIG_SH2_STAT3 = YDGQ
    residues (2294,2300)
LIG_FHA_1 = IKTNNIV
    residues (2308,2318)
LIG_MAPK_1 =
    KGEKLNETVLL
    residues (2309,2312)
LIG_PDZ_3 = GEKL
    residues (2313,2316)
LIG_PDZ_3 = NETV
    residues (2313,2319)
LIG_FHA_1 = NETVLLE
    residues (2364,2368)
LIG_BRCT_BRCA1_1 = KSNLF

### SS Motif for disorder segment 50:
(start,end): (2374,2402)

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

```
        2374      2383       2393
seq   : IKNFRYNKKKKKEEEDFLLNGSYMNSNDK
S.S.  : HHHHHHHCCCCCCCCCHCCCCCCCCCCCC
alpha: 99877644332223344320001001111
beta : 00000000000111112221000000002
coil : 00112345567654443357888888876
```

**SS Motif for disorder segment 51:**
**(start,end): (2428,2433)**

```
seq   : LTVLWI
S.S.  : EHHHHH
alpha: 455555
beta : 444433
coil : 000000
```

**SS Motif for disorder segment 52:**
**(start,end): (2451,2472)**

```
        2451      2460       2470
seq   : YRNYDIVGEMDEVIGLFHGDDL
S.S.  : CCCCCCCCCCCCCEECCCCCCCC
alpha: 1111121112332211100100
beta : 3323333222224333210000
coil : 4555434555433345688889
```

**strand, coil) TXT**

**Linear motif(s):**

residues (2388,2391)
**LIG_PDZ_3 = EDFL**
residues (2396,2399)
**LIG_SH2_GRB2 = YMNS**

**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 (2451,2454)
**LIG_SH2_GRB2 = YRNY**
residues (2454,2457)
**LIG_SH2_SRC = YDIV**
residues (2460,2463)
**LIG_PDZ_3 = MDEV**