CSpritz - Accurate detection of protein disorder

Version 1.2

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Status: finished

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

Available files: (help)

Your input parameters:	HTML
Fasta sequences (amino, secondary structure, disorder, confidence):	TXT
Disorder plot:	PDF
Graph of PDB homologue(s) found::	PDF
Disorder Prediction (with disorder probability):	TXT
Protein statistics :	TXT

Disordered residues and stats: (help)

```
1         10        20        30        40        50        60
MVDIKNIVVRRMINYYKNVKRNTSPFCMNLMFYNFHEDFILILIKTYMNILKKYESYNKTIHLLEEYYML
CCCHHHHHHHHHHHHHHHHCCCCCHHHHHHHHHCCCHHHHHHHHHHHHHHHHHHHHHHHCCCCCCHHHHHHH
DDDDDDDDDDOOOOOOOOODOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOODDDDDDDDDDDDOOOOOOOOOO


71        80        90        100       110       120       130
FNYVILSYIPLYVYELDINNLYLFDMLLHKFNEKRKRENNMKKNVIDNNIYKKYRILNRINKNGHVEANK
HHHHHHHHCCHHHHHHCCCCHHHHHHHHHHCCCCHHHHHHHHHHHCCCCCCHHHHHHHHHHHHCCCCCEECCC
OOOOOOOOOOOOOODOOOOOOOOOOOOOODDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD


141       150       160       170       180       190       200
LHCVHHKNVEYMNINKLNKHMNICFNDNKCDSIYSLKKQTSEDIQKNEKQNDKLILPSFQGSLKKNIYMK
EECCCCCCCHHHHHHHHHHHCCCCCCCCCCCCHHHHCCCCCHHHHHHHCCCCHCCCCCCCCCCCCCCCCC
DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD


211       220       230       240       250       260       270
NNTNRRICETNLFYKNNNNDHLKLKKNRSPIYLCEDNLKKRKDIIKNMIKEMDNLYAHVYYWKYLTELNI
CCCCCEEEECCCCCCCCCCCHHHCCCCCCCCCHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH
DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDOOOOOOOOOOOOOOOOOOOOOO


281       290       300       310       320       330       340
KCNNNNNNDKNNNLEVNYAINKGQDIYLNIYKNIYNLYKYMNKKHKQNLEKMNMKKEQLSITHNNEMENI
HHCCCCCCCCCCCCCHHHHHCCCCHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHCCCCCCCHHHHH
ODDDDDDDDDDDDDDDDDDDDOOOOOOOOOOOOOOOOOOOOOOOODOOODDDDDDDDDDDDDDDDDDDDDDD


351       360       370       380       390       400       410
INEKKIHKKNEEYHKNVNDMVFKHIAEKNALCRHIEHEMNIIQQINMKEYKENIFYIFSIISKNKQNLSL
HHCCCCCCCCCHHCCCHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHCCCCCCC
DDDDDDDDDDDDDDDOOOOOOOODDDDDDDDDDOOOOOOODOOODDOOOOOOOOOOOOOOOOOOOODDDDD


421       430       440       450       460       470       480
PPLPVEEERDIQKEVRPYHNEEKKKKHNNNNNNYNNICNNNNNNNVSNINNSGCNNFNMCENMNDLSKH
CCCCCHHHHHHCCCCCCCCCCCCCCCCCCCCCCCHHHHCCCCCCCCCCCCCCCCCCCCCCCCHCCCCCCCC
DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD


491       500       510       520       530       540       550
KCKDIKENYIYNDKNNITMEDKIKTYYHIEECYYHYKYIIKCFHFKYLYELIKSKIMIYNYLHFHIKKSL
CCCCCCCCCCECCCCCCCCCHHHHHEEEEHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH
DDDDDDDDDDDDDDDDDDDDDDDDDDDDOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOO


561       570       580       590       600       610       620
YNIMNVSIIFSLGEIYHIFEYDKKKNIQFQDNFFTTLRKMQIYNYNKYYQYMNMNEKGPDKYFNSFQIYE
HHCCCEEEEEECHHHHHHHHHCCCCCHHHHHHHHHHHHHHHCCCHHHHCCCCCCCCCCCCCCCCHHHHH
OOOOOOOOOOOOOOOOOOOODDDDDDDDDDOOOOOOOOOOOOODDOOOODDDDDDDDDDDDDDDDDDDDDD


631       640       650       660       670       680       690
EKKKKVTNVLEIQKDEDILKKDVNTNEWANPTGLKKKILHLLKGGTQINKDNEHMNKFVPIYNNSLLVNN
HCCCCCCCEEECCCCCHHHCCCCCCCCCCCCCCCHHHHHHHHCCCCCCCCCCCCCCCCCCCCCCCCHHHHH
DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD


701       710       720       730       740       750       760
ILSGYNAHDIKEQKGDDSLKCEESFYFDENGYFKYKKKRKGAKEFFNHNYSSTYNYINNNNTLYFMNNKM
HCCCCCCCCHHHCCCCCCCCCCCCCCCCCCCCCCCCCCCCCHHHHCCCCCCCCCCCCCCCCEHHHCCCC
DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDOOOOOOOOOOOODDDDD


771       780       790       800       810       820       830
DENIYNNNNNNNNNDIKINKLTIKDKKLNCLILFINEDISNYTKENVYNNIFNISLTKMDFIFPTIKEQL
CCHHHECCCCCCCCCCEECCCCCCCCCCCCEEEEECCCCCCCCCHHHHHHHHEEEECCCCCCCCCCCHHHHH
DDDDDDDDDDDDDDDDDDDDOOOOOOOOOODDDOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOO


841       850       860       870       880       890       900
HVVKEMYKGKKKEKLFSDDLYKKSIKNICNDISEKNESLSYGTIIITRHKNLKIAMQGKNNFKENHQTGDN
HHHHHHHHCCCEEECCCCCCCCCCCCCCCCCCCCCCCCCCCCCCEEECCCCCCCCCCCCCCCCCCCC
DDOOOODDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDOOODDDOOOODDDDDDDDDDDDDDDDDDDDDD
```

Total amino acids:	**1162**
Total % disorder:	**65.74**
Total no. of disordered regions > 30 amino acids:	**7**
Total no. of disordered regions > 50 amino acids:	**4**
Number of disordered segments:	**28**
Length distribution of segments (N to C terminal order):	**10 1 11 1 163 20 1 37 10 1 2 102 11 2 149 30 3 2 32 3 74 25 6 1 7 2 47 11**

```
911       920       930       940       950       960       970
NNDNNNNKNNKNDNNNNNNNNKDIKNKEENNIYYNNHNLDNLNYIPFDNFFFSLLNMPEQVMRTSHFSIN
CCCCCCCCCCCCCCCCCCCCCCCCCCHHHHCHHCCCCCCCCCCCCCCCCCCCCHCCCCHHHHHHCCCCECC
DDDDDDDDDDDDDDDDDDDDDDDDDDDDHHDDDDDDDDDDDDDDDDDDDDDDDDOOOOODDDDDDDDDDDD
```

```
981       990       1000      1010      1020      1030      1040
EKMFPKKKKKKIYIDIIFHVLIPKKINRKSFKIILFSLFKILDLCKLYNIYCINCSFPYVHDIVYKNKRP
CCCCCCCCCCCEEEEEEEEECCCCCCCCCCHHHHHHHHHHHHHHHHHCCCEEECCCCCCEEEEEECCCCH
DDDDDDDDDDDOOOOOOOOOOOODDDDDOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOODOOOOOOO
```

```
1051      1060      1070      1080      1090      1100      1110
IIYSFIYSFIMTIMKYIKKGQPEDHNNTVRIFHFIFPPLQFYEKLTTEQMENKNDGKNQFKENINKNYDN
HHHHHHHHHHHHHHHHCCCCCCCCCCEEEEEEECCCHHHHCCCCHHHHHCCCCCCCCCCCCCCCCCCCC
OOOOOOOOOOOOOOOODDDDDDDOOOODDOOOOOOOOOODDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD
```

```
1121      1130      1140      1150      1160
KENNINYDYIHNVDKTKISNITYFIDKLIHDLKEKYMLIESI
CCCCCCCCCCCCCCHHHHHHHHHHHHHHHHHHHHHHHHHHCCC
DDDDDDDDDDDDDDDDDDDDDOOOOOOOOOOODDDDDDDDDDDO
```

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

SS Motif for disorder segment 1:
(start,end): (1,10)

```
seq  : MVDIKNIVVR
S.S. : CCCHHHHHHH
alpha: 0247899999
beta : 0000000000
coil : 9752100000
```

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): (52,62)

```
       52        61
seq  : KKYESYNKTIH
S.S. : HHHHHCCCCCC
alpha: 98776431122
beta : 00000000011
coil : 01123568765
```

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 (151,154)　LIG_SH2_GRB2 = YMNI
residues (156,165)　LIG_MAPK_1 = KLNKHMNICF
residues (170,173)　LIG_PDZ_3 = CDSI
residues (178,184)　LIG_FHA_2 = KQTSEDI
residues (181,184)　LIG_PDZ_3 = SEDI
residues (186,196)　LIG_MAPK_1 = KNEKQNDKLIL
residues (191,194)　LIG_PDZ_3 = NDKL
residues (193,212)　LIG_IQ = KLILPSFQGSLKKNIYMKNN
residues (224,227)　LIG_SH2_GRB2 = YKNN
residues (229,232)　LIG_PDZ_3 = NDHL
residues (233,243)　LIG_MAPK_1 = KLKKNRSPIYL
residues (236,241)　LIG_WW_4 = KNRSPI
residues (242,245)　LIG_SH2_STAT5 = YLCE
residues (245,248)　LIG_PDZ_3 = EDNL
residues (252,255)　LIG_PDZ_3 = KDII

SS Motif for disorder segment 3:
(start,end): (99,261)

```
       99        108       118       128       138       148       158
seq  : HKFNEKRKRENNMKKNVIDNNIYKKYRILNRINKNGHVEANKLHCVHHKNVEYMNINKLNKHMNICFNDN
S.S. : HCCCCHHHHHHHHHCCCCCHHHHHHHHHHCCCCCEECCCEECCCCCCHHHHHHHHHHHHCCCCCCCC
alpha: 5432466777765553333347887777765421000112111111111123444455554443332111
beta : 00000000000000000000001111110000354224443200012222110000001121100
coil : 34665332122334455555521111101224678853355444567776432333334444455445788
       169       178       188       198       208       218       228
seq  : KCDSIYSLKKQTSEDIQKNEKQNDKLILPSFQGSLKKNIYMKNNTNRRICETNLFYKNNNNDHLKLKKNR
S.S. : CCCCHHHHCCCCHHHHHHCCCCHCCCCCCCCCCCCCCCCCCCCCEEEECCCCCCCCCCCCCHHHCCC
alpha: 1123565543214567665544334442222112222222111000000011232111123445543 21
beta : 00000001111000000000000000010000000000012332100135554322221000001 00000
coil : 777633334566532223444455544466667776665445678886433455544678876543 34678
       239       248       258
seq  : SPIYLCEDNLKKRKDIIKNMIKE
S.S. : CCCCCHHHHHHHHHHHHHHHHHH
alpha: 0111257778888899999999
beta : 0012100000000000000000
coil : 8866542221111000000000
```

SS Motif for disorder segment 4:
(start,end): (282,301)

```
       282       291
seq  : CNNNNNNDKNNNLEVNYAIN
S.S. : HCCCCCCCCCCCCHHHHHHC
alpha: 44321112221224566654
beta : 10000000000123211100
coil : 44677777777642121235
```

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): (330,366)

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

```
          330       339       349       359
seq  : EKMNMKKEQLSITHNNEMENIINEKKIHKKNEEYHKN
S.S. : HHHHHHHHHCCCCCCCCHHHHHHHCCCCCCCCCCCHHCCC
alpha: 99998767654322234678887543221111455322
beta : 00000000000100000000000000001110000001
coil : 00012223456666653211124556677775544665
```

Linear motif(s):

residues (335,341)   **LIG_MAPK_1 = KKEQLSI**
residues (336,339)   **LIG_PDZ_3 = KEQL**
residues (347,350)   **LIG_PDZ_3 = MENI**

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

SS Motif for disorder segment 6:
(start,end): (375,384)

```
seq  : IAEKNALCRH
S.S. : HHHHHHHHHH
alpha: 9998888888
beta : 0000000000
coil : 0001111111
```

Linear motif(s):

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

SS Motif for disorder segment 7:
(start,end): (416,517)

```
          416       425       435       445       455       465       475
seq  : QNLSLPPLPVEEERDIQKEVRPYHNEEKKKKHNNNNNNYNNICNNNNNNNVSNINNSGCNNFNNMCENMN
S.S. : CCCCCCCCCCHHHHHHHCCCCCCCCCCCCCCCCCCCCCCCCHHHHHCCCCCCCCCCCCCCCCCCCCCCHCCC
alpha: 10000000045677765432100111212222111123444443221111122211111122234444432
beta : 01110000000000000011110000000000000001112221111124332100000000000000000
coil : 87789999943322234456778777777666788875443223567765444567888776665544566
          486       495       505       515
seq  : DLSKHKCKDIKENYIYNDKNNITMEDKIKTYY
S.S. : CCCCCCCCCCCCCCCECCCCCCCCCHHHHHEEEE
alpha: 3333332223333333221111111566533333
beta : 0000001000011233210002200012330443
coil : 6655666655554434577776633332223
```

Linear motif(s):

residues (418,424)   **LIG_SH3_3 = LSLPPLP**
residues (421,424)   **LIG_WW_2 = PPLP**
residues (424,427)   **LIG_TRAF2_1 = PVEE**
residues (438,441)   **LIG_SH2_GRB2 = YHNE**
residues (454,457)   **LIG_SH2_GRB2 = YNNI**
residues (495,499)
LIG_APCC_KENbox_2 = IKENY
residues (499,502)   **LIG_SH2_STAT5 = YIYN**
residues (506,512)   **LIG_FHA_2 = NITMEDK**
residues (510,513)   **LIG_PDZ_3 = EDKI**

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

SS Motif for disorder segment 8:
(start,end): (579,589)

```
          579       588
seq  : FEYDKKKNIQF
S.S. : HHHCCCCCHHH
alpha: 65433332456
beta : 21100000111
coil : 12366666432
```

Linear motif(s):

residues (583,589)   **LIG_MAPK_1 = KKKNIQF**

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

SS Motif for disorder segment 9:
(start,end): (608,756)

```
          608       617       627       637       647       657       667
seq  : YYQYNMNNEKGPDKYFNSFQIYEEKKKKVTNVLEIQKDEDILKKDVNTNEWANPTGLKKKILHLLKGGTQ
S.S. : HHHHCCCCCCCCCCCCCCCHHHHHHCCCCCCEEECCCCHHHCCCCCCCCCCCCCCCHHHHHHHHHCCCCC
alpha: 44443322110001222234445554211111333322245654432222332012346677777521011
beta : 22222100000000111123322100123223433100000000000000000000000001000000012
coil : 32234677889987655653221234676555222356643344556776657877643211111368875
          678       687       697       707       717       727       737
seq  : INKDNEHMNKFVPIYNNSLLVNNILSGYNAHDIKEQKGDDSLKCEESFYFDENGYFKYKKKRKGAKEFFN
S.S. : CCCCCCCCCCCCCCCCCCHHHHHCCCCCCHHHHCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCHHHHC
alpha: 11112343321112222456665543111445555421111222333222211222322222345542
beta : 21000000122232101111111111100000000000012222222100012332211100111111
coil : 56776545665654466422123345776544334568887654444456777543445566532236

seq  : HNYSSTYNY
S.S. : CCCCCCCCC
alpha: 111122233
beta : 111111222
coil : 776665543
```

Linear motif(s):

residues (622,625)   **LIG_SH2_STAT5 = YFNS**
residues (632,642)   **LIG_MAPK_1 = KKKKVTNVLEI**
residues (635,641)   **LIG_FHA_1 = KVTNVLE**
residues (645,648)   **LIG_PDZ_3 = DEDI**
residues (665,671)   **LIG_MAPK_1 = KKKILHL**
residues (667,671)   **LIG_CYCLIN_1 = KILHL**
residues (692,695)   **LIG_SH2_GRB2 = YNNS**
residues (716,719)   **LIG_PDZ_3 = DDSL**
residues (719,723)   **LIG_RB = LKCEE**
residues (723,727)
LIG_BRCT_BRCA1_1 = ESFYF
residues (726,729)   **LIG_SH2_STAT5 = YFDE**
residues (732,735)   **LIG_SH2_STAT5 = YFKY**

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

SS Motif for disorder segment 10:
(start,end): (767,796)

```
       767        776        786
seq  : NNKMDENIYNNNNNNNNNNDIKINKLTIKDK
S.S. : CCCCCCHHHECCCCCCCCCCEECCCCCCCCC
alpha: 322333433332221111111111111111
beta : 100001233321111111244433343210
coil : 576655322245666677643344544677
```

Linear motif(s):

residues (771,774)   LIG_PDZ_3 = DENI
residues (775,778)   LIG_SH2_GRB2 =
YNNN
residues (790,796)   LIG_FHA_2 =
KLTIKDK

SS Motif for disorder segment 11:
(start,end): (810,812)

```
seq  : SNY
S.S. : CCC
alpha: 333
beta : 001
coil : 555
```

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

Linear motif(s):

SS Motif for disorder segment 12:
(start,end): (847,878)

```
       847        856        866        876
seq  : YKGKKEKLFSDDLYKKSIKNICNDISEKNESL
S.S. : HCCCCCEEECCCCCCCCCCCCCCCCCCCCCCCC
alpha: 52000000001122222222221011211110
beta : 00001355421001111222221100000122
coil : 36887533467766666554456877678766
```

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

Linear motif(s):

residues (851,854)   LIG_PDZ_3 = KEKL
residues (853,858)   LIG_14-3-3_3 =
KLFSDD
residues (856,859)   LIG_PDZ_3 = SDDL
residues (875,878)   LIG_PDZ_3 = NESL

SS Motif for disorder segment 13:
(start,end): (882,884)

```
seq  : TII
S.S. : CEE
alpha: 000
beta : 488
coil : 510
```

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): (889,962)

```
       889        898        908        918        928        938        948
seq  : KNLKIAMQGKNNFKENHQTGDNNNDNNNNKNNKNDNNNNNNNNNKDIKNKEENNIYYNNHNLDNLNYIPFD
S.S. : CCCEEECCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCHHHHCHHCCCCCCCCCCCCCCCC
alpha: 111121100001123321100011222211111111111112233443355543443222333322002 2
beta : 113554321000111111100001111112222111111111100111100001121100000012211 00
coil : 664223467888655566788887666666666667666766655444443345434566666666556 766
```

```
seq  : NFFF
S.S. : CCCC
alpha: 2224
beta : 0111
coil : 6654
```

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

Linear motif(s):

residues (889,893)   LIG_CYCLIN_1 =
KNLKI
residues (901,905)
LIG_APCC_KENbox_2 = FKENH
residues (943,946)   LIG_SH2_GRB2 =
YNNN
residues (949,952)   LIG_PDZ_3 = LDNL
residues (954,957)   LIG_SH2_STAT5 =
YIPF

SS Motif for disorder segment 15:
(start,end): (968,992)

```
       968        977        987
seq  : PEQVMRTSHFSINEKMFPKKKKKKI
S.S. : HHHHHHCCCCECCCCCCCCCCCCCCE
alpha: 6787642122223332111112110
beta : 0000000023332100000011135
coil : 3111246754334456877766653
```

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

Linear motif(s):

residues (968,971)   LIG_PDZ_3 = PEQV

SS Motif for disorder segment 16:
(start,end): (1004,1009)

```
seq  : KKINRK
S.S. : CCCCCC
alpha: 333244
beta : 000000
coil : 656655
```

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): (1070,1076)

```
seq  : GQPEDHN
S.S. : CCCCCCC
alpha: 0001110
beta : 0000000
coil : 8987778
```

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 (1110,1114)
LIG_APCC_KENbox_2 = FKENI
residues (1111,1114)   **LIG_PDZ_3 =**
KENI
residues (1118,1121)   **LIG_SH2_GRB2 =**
YDNK
residues (1120,1124)
LIG_APCC_KENbox_2 = NKENN
residues (1127,1130)   **LIG_SH2_SRC =**
YDYI
residues (1129,1132)   **LIG_SH2_STAT5 =**
YIHN

SS Motif for disorder segment 18:
(start,end): (1093,1139)

```
        1093      1102      1112      1122      1132
seq  : EKLTTEQMENKNDGKNQFKENINKNYDNKENNINYDYIHNVDKTKIS
S.S. : CCCCHHHHHCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCHHHHH
alpha: 42124454431111222333210000111111113344310055666
beta : 11011122221000012221110000000000110001000000000
coil : 46763323346888654444678888887788775544588843333
```

SS Motif for disorder segment 19:
(start,end): (1151,1161)

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

Linear motif(s):

```
        1151      1160
seq  : DLKEKYMLIES
S.S. : HHHHHHHHHCC
alpha: 87665444421
beta : 00000123331
coil : 12333432236
```

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