

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
MNKTANLE	KDETEKA	[VHFIVYLIG]	VLILCVYYN	ZIILKYYFYSI	LFWAFIISIP	LHHVKVKLKEFFKK
						ССССИННИНИННИН
וסססססססו	וססססססססו	0000000000	0000000000	0000000000	DOOOODDDDD	DDDDDDDDDDDDDD
71	80	90	100	110	120	130
						KDGHTNIIKKKKDS
						ccccccccccc
וסססססססו	וססססססססו	וסססססססססססס	וססססססססססססס	ומממממממממ	ומממממממממ	םססססססססססססססס
141	150	160	170	180	190	200
						RKELDIYLYIFFLI
						ннинининнин
ומממממממ	וססססססססו	וממממממממממ	ומממממממממ	ODDDDDDDOOO	0000000000	0000000000000
211	220	230	240	250	260	270
						ISSCIFFLYVFYKI
						ннининининнин 00000000000
281	290	300	310	320	330	340
						FFFIFNIYGESVYI
						HHHHHHEECCEEHH OOOOOOOOODDDD
30000000	ומטטטטטטו	סטטטטטטטטטט	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	ועעעטטטטטטטו	יסססססממממממ	מעשעסססססססססססס
351	360	370	380	390	400	410
						YSHLKRAIDIYENI
						нининининини
						DDD000000000
421	430	440	450		470	480
			450	460	470	
LYNFTKNI	KNVSLKACO	CLSLLVKRFVI	IKNNNLYNV	KKFVLALNEQI	KKHILEKNHD	FKNKKCMDKDENQK
LYNFTKNI НННННССО	KNVSLKACO CCCEHHHH	CLSLLVKRFVI НИНИНИНИНИ	IKNNNLYNVI IHCCCCHHHHI	ККFVLALNEQI НИНИНИНИН	CCCCCCCCC	FKNKKCMDKDENQK CCHHHHCCCCCCCC
LYNFTKNI НННННССО	KNVSLKACO CCCEHHHH	CLSLLVKRFVI НИНИНИНИНИ	IKNNNLYNVI IHCCCCHHHHI	ККFVLALNEQI НИНИНИНИН	CCCCCCCCC	FKNKKCMDKDENQK
LYNFTKNI НННННССО	KNVSLKACO CCCEHHHH	CLSLLVKRFVI НИНИНИНИНИ	IKNNNLYNVI IHCCCCHHHHI	ККFVLALNEQI НИНИНИНИН	CCCCCCCCC	FKNKKCMDKDENQK CCHHHHCCCCCCCC
LYNFTKNI HHHHHCCO OOOOODI 491	KNVSLKACO CCCEHHHHI DDDDDDDDDOO 500	CLSLLVKRFVI НИНИНИНИН DOOOOOOOOOOOOOOOOOOOOOOOO	IKNNNLYNVE HCCCCHHHH DOOOOOOOOOOOOOOOOOOOOOOOOOOOO	KKFVLALNEQI HHHHHHHHHH DOODDDDDDDD 530	KKHILEKNHDI CCCCCCCCCC DDDDDDDDDDDDDDDDDDDDDDDDD	FKNKKCMDKDENQK CCHHHHCCCCCCCC DDDDDDDDDDDDDDD
LYNFTKNI HHHHHCCO OOOOODI 491 VFFSLKKI	KNVSLKACO CCCEHHHHE DDDDDDDDOO 500 IIQYLSKNE	CLSLLVKRFVI HHHHHHHHHH DOOOOOOOOOOOOOOOOOOOOOOOOOO	TIKNNNLYNVI HCCCCHHHH DOOOOOOOOO 520 EVEDSSSSNN	KKFVLALNEQI HHHHHHHHHH DOO <mark>DDDDDDDI</mark> 530 NNNNNNDKTI	KKHILEKNHDI CCCCCCCCCC DDDDDDDDDDD 540 NQNNENKNNS	FKNKKCMDKDENQK CCHHHHCCCCCCCC DDDDDDDDDDDDDDDD 550
LYNFTKNI HHHHHCCO OOOOOODI 491 VFFSLKKI CHHHHHHI	KNVSLKACO CCCEHHHHE DDDDDDDDOO 500 I IQYLSKNI	CLSLLVKRFVI HHHHHHHHHH DOOOOOOOOO 510 KFFSSNKSKDI HHCCCCCCCC	TKNNNLYNVE HCCCCHHHH HOOOOOOOOO 520 EVEDSSSNNN CEEECCCCCC	KKFVLALNEQI HHHHHHHHHH DOODDDDDDDD 530 NNNNNNNDKTI CCCCCCCCC	SAO NONNENKNIS CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	FKNKKCMDKDENQK CCHHHHCCCCCCCC DDDDDDDDDDDDDDD 550 VSQNIFKTVFENLV
LYNFTKNI HHHHHCCC 000000DI 491 VFFSLKKI CHHHHHHI DDDDDDDI	KNVSLKACO CCCEHHHHH DDDDDDDDOO 500 IIQYLSKNI HHHHHHHHH	CLSLLVKRFVI HHHHHHHHHH DOOOOOOOOO 510 KFFSSNKSKDI HHCCCCCCCC	EIKNNNLYNVE HCCCCHHHHE DOOOOOOOOO 520 EVEDSSSSNN CEEECCCCCC DDDDDDDDDDD	KKFVLALNEQI HHHHHHHHHHH 530 NNNNNNNDKTI CCCCCCCCCC	SAO SOURCE CONTROL OF THE SAO C	FKNKKCMDKDENQK CCHHHHCCCCCCC DDDDDDDDDDDDDD 550 VSQNIFKTVFENLV CCCCHHHHHHHHHC DDDDDDDDDDDDDDDDD
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LYNFTKNI HHHHHCCC 000000DI 491 VFFSLKKI CHHHHHH DDDDDDDI 561 QYGNVEQI	KNVSLKACC CCCEHHHH DDDDDDDOOC 500 IIQYLSKNH HHHHHHHH DDDDDDDDDI 570 KQNGKSPER	CLSLLVKRFVI HHHHHHHHHH DOOOOOOOOO 510 KFFSSNKSKDI HHCCCCCCCCC DDDDDDDDDDD 580 RASHESEEEE	TIKNNNLYNVE HCCCCHHHHI DOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOO	KKFVLALNEQI HHHHHHHHHH 530 NNNNNNNDKTI CCCCCCCCCC DDDDDDDDDDD 600 KDDLASSEKDI	SKHILEKNHDI CCCCCCCCCC DDDDDDDDDDD 540 NQNNENKNNS CCCCCCCCCC DDDDDDDDDDDDDDDDDDDDDDDDD	FKNKKCMDKDENQK CCHHHHCCCCCCC DDDDDDDDDDDDDD 550 VSQNIFKTVFENLV CCCCHHHHHHHHHC DDDDDDDDDDDDDDDDD
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LYNFTKNE HHHHHCCC 000000DI 491 VFFSLKX: CHHHHHHH DDDDDDDDD 561 QYGNVEQE CCCCHHH DDDDDDDI 631 EKKDLQGI CCCCHHHC DDDDDDDDI 701 LKIMIFF\	KINVSLKACC CCCEHHHH DDDDDDDO 500 IIQYLSKNI HHHHHHHHH 570 GQNGKSPEI GCCCCCCC DDDDDDDDI 640 LKNMSKEKT CCCCCCCCC DDDDDDDDD 710 //LIFFNFFN	CLSLLVKRFVI HHHHHHHHHH DOOOOOOOOO 510 KFFSSMSKSD HHCCCCCCCCCC DDDDDDDDDDD 580 RASHESEEEE CCHHHHHHHH DDDDDDDDD 650 FSNNFMLNIYI CCCCCCCCCCC DDDDDDDDDDDD 720 4FTFDAIVQAV	IKNNNLYNVI HCCCCHHHH DOOOOOOOO 520 VEDSSSNNI EEECCCCCC DDDDDDDDDD 590 KKKKNINKQI KCCCCCCCCI DDDDDDDDDD 660 DPAKERNFKII CCCCCCCHH DDDDDDDDDDD 730 VIFFTALYYLI	KKFVLALNEQI HHHHHHHHHH 530 NININININDKTI CCCCCCCCCCC CODDDDDDDDD 600 KDLASSEKDI HHHHHHHHH DDDDDDDDDDDDD 670 KEFMSYVINILI HHHHHHHHHH DO000000000 740 ISSKKSVLNYI	KKHILEKNHDI CCCCCCCCC DDDDDDDDDD 540 NQNNENKNNS CCCCCCCCC DDDDDDDDDDD 610 KETNKKKDGII HCCCCCCCCCC DDDDDDDDDDDDDDDDDDDDDDDDD	FKNKKCMDKDENQK CCHHHHCCCCCCC DDDDDDDDDDDDD 550 VSQNIFKTVFENLV CCCHHHHHHHHHHC DDDDDDDDDDDDDDDD 620 DKKIYSDNKNKDND CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
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LYNFTKNE HHHHHCCC OOOOOODI 491 VFFSLKX: CHHHHHHH DDDDDDDDD 561 QYGNVEQE CCCCHHE DDDDDDDI 631 EKKDLQGI CCCCHHC DDDDDDDDI 701 LKIMIFFY HHHHHHHH OOOOOOOOC	KINVSLKACC CCCEHHHH DDDDDDDOO 500 IIQYLSKNI HHHHHHHHH 570 570 KQNGKSPEI GCCCCCCC DDDDDDDDI 640 LKNMSKEK* CCCCCCCCC DDDDDDDDD 710 //LIFFNFFN HHHHHHHHH DOOOOOOOO 780	CLSLLVKRFVI HHHHHHHHHH DOOOOOOOOO 510 KFFSSNKSKDI SFSSNKSKDI SFSS	EIKNNNLYNVE HCCCCHHHHI DOOOOOOOOO 520 VEDSSSSNNN EEECCCCCC DDDDDDDDDDD 590 KKKKNINKQI CCCCCCCCCC DDDDDDDDDDD 660 DPAKERNFKII CCCCCCCCHH DDDDDDDDDDDD 730 VIFFTALYYLI HHHHHHHHHHI DOOOOOOOOOOOOOOOOOOOOOOOOO	KKFVLALNEQI HHHHHHHHHH DOODDDDDDDD 530 NNNNNNNDKTI CCCCCCCCCCC DDDDDDDDDDD 600 KDLASSEKDI HHHHCHHHH DDDDDDDDDDD 670 KEFMSYVNNLI HHHHHHHHHH DOOOOOOOOO 740 ISSKKSVLNYI HCHHHHHHHHH DOOOOODDDOOO 810	SAU	FKNKKCMDKDENQK CCHHHHCCCCCCC DDDDDDDDDDDDD 550 VSQNIFKTVFENLV CCCHHHHHHHHC DDDDDDDDDDDDDDD 620 DKKIYSDNKNKDND CCCCCCCCCCCCC DDDDDDDDDDDDDD 690 GKLTKFLIFNNSYG HHHHHHHHCCHH DDOOOOOOOOOOO 760 SSIFFYNITNNLKA CCHHHHHHHHCHH
LYNFTKNEHHHHHCCOOOOOODI 491 491 VFFSLKKI CHHHHHHI DDDDDDDI 561 QYGNVEQE CCCCHHH DDDDDDDDI 631 EKKDLQGI CCCCCHHG DDDDDDDI 701 KKIMIFFV HHHHHHHHH 0000000C	KINVSLKACC CCEHHHH DDDDDDDD 500 IQYLSKNI HHHHHHHH DDDDDDDD 570 QNGKSPEI GCCCCCCC DDDDDDDDD 640 LKNMSKEK: CCCCCCCCC DDDDDDDDD 710 VLIFFNFFN HHHHHHHHH DDDDDDDDDDDDDDDDDDDDDDD	CLSLLVKRFVI HHHHHHHHH DOOOOOOOOO S10 KFFSNKSKDI HHCCCCCCCCC DDDDDDDDDD S80 RASHESEEEEE CCHHHHHHHH DDDDDDDDDDD 650 SNNFMLNIVI CCCCCCCCCCC DDDDDDDDDDDD 720 MFTFDAIVQAV HHHHHHHHHH DOOOOOOOOOOO 790 VLIFSFFGFPI	IKNNNLYNVI HCCCCCHHHHI OOOOOOOO 520 VEDESSSNNI SEEECCCCCC DDDDDDDDD 60 OKKKKNINKOI GCCCCCCCCC DDDDDDDDDD 60 OPAKENFKII CCCCCCCCHH DDDDDDDDDD 730 71FFTALYYLI HHHHHHHHHH 00000000000	KKFVLALNEQI HHHHHHHHHH OOODDDDDDD S30 NNNNNNDKTI CCCCCCCCC CDDDDDDDDDD 600 KDDLASSEKDI HHHHCHHHHI DDDDDDDDDDDD 670 KEFMSYNNLI HHHHHHHHHHH DOOOOOOOOO 740 ISSKKSVLNYI HKCHHHHHHHHH DOOOOODDDOOC 810 KLSLIPVISPI	KKHILEKNHDI CCCCCCCCC DDDDDDDDDD 540 NQNNENKNNS CCCCCCCCCC DDDDDDDDDD 610 KETNKKBGII HCCCCCCCCC DDDDDDDDDD 680 FLSLKKIEDL HHHHHHHHHHHH DDDDDDDDDDD 750 LKDVLLVVDP HHHHHEECCC DOOOOOOOOO	FKNKKCMDKDENQK CCHHHCCCCCCC DDDDDDDDDDDDD 550 VSQNIFKTVFENLV CCCHHHHHHHHHC DDDDDDDDDDDDDD 620 DKIYSDNKNKDND CCCCCCCCCCCC DDDDDDDDDDDDDD 690 GKLTKFLIFNNSYG HHHHHHHHCCCHH DD0000000000000 760 SSIFFYNITNNLKA CCHHHHHHHCHHH
LYNFTKNEHHHHHCCC OOOOOODI 491 VFFSLKX CCHHHHHH DDDDDDDD 5561 QYGNVEQE CCCCHHH DDDDDDDDD 631 EKKDLQGI CCCCHHK DDDDDDDD 701 LKIMIFFV HHHHHHHH HHHHHHHHHHHHHHHHHHHHHHHHHH	KINVSLKACC CCEHHHH DDDDDDDD 500 IQYLSKNI HHHHHHH DDDDDDDD 570 KQNGKSPEI GCCCCCCC DDDDDDDDD 640 LKNMSKEKT CCCCCCCCC DDDDDDDDD 710 711FNFFF HHHHHHHHH HHHHHHHHHHHHHHHHHHHHHH	CLSLLVKRFVI HHHHHHHHHH DOOOOOOOOO 510 KFFSSKKSKDI KFFSSKKSKDI KFFSSKKSKDI KFFSSKKSKDI KFFSSKKSKDI 580 RASHESEEEE CCHHHHHHHH DDDDDDDDDDDDD 650 FSNNFMLNIYI CCCCCCCCCC CDDDDDDDDDD 720 KFFFDAIVQAV HHHHHHHHHH HOOOOOOOO 790 KLIFSFFQFPI HEEEEECCCE	IKNNNLYNVI HCCCCCHHHHI OOOOOOOO 520 VEDSSSSNNN SEEECCCCCC DDDDDDDDDD CKKKKNINKOI CCCCCCCCCI DDDDDDDDDDD 660 DPAKERNFKII CCCCCCCHHI DDDDDDDDDD 730 VIFFTALYYLI HHHHHHHHHH HOOOOOOOO	KKFVLALNEQI HHHHHHHHHH DOODDDDDDD 530 NNNNNNDKTI 600 KDDLASSEKDI HHHHCHHHH DDDDDDDDDDD 670 KEFMSYVNNLI HHHHHHHHHHH DOOOOOOOO 1 SSKKSVLNYI HOOHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH	KKHILEKNHDI CCCCCCCCC DDDDDDDDDD 540 NQNNENKNNS CCCCCCCCCC DDDDDDDDDD 610 KETNKKKDGII HCCCCCCCCC DDDDDDDDDDD 680 FLSLKKIEDL HHHHHHHHHH DDDDDDDDD 750 LKDVLLVVDP: HHHHHECCC HOOOOOOOOO 820 EILILVIILH HHHHHHHHHHHHHHHHHHHHHHHHHHHHHH	FKNKKCMDKDENQK CCHHHHCCCCCCC DDDDDDDDDDDDD 550 VSQNIFKTVFENLV CCCHHHHHHHHHHC DDDDDDDDDDDDDDDD 620 DKKIYSDNKNKDND CCCCCCCCCCCCCC DDDDDDDDDDDDDDD 690 GKLTKFLIFNNSYG HHHHHHHHHCCHH DDOOOOOOOOOOOO 760 SSIFFYNITNNLKA CCHHHHHHHCHH
LYNFTKNEHHHHHCCC OOOOOODI 491 VFFSLKX CCHHHHHH DDDDDDDD 5561 QYGNVEQE CCCCHHH DDDDDDDDD 631 EKKDLQGI CCCCHHK DDDDDDDD 701 LKIMIFFV HHHHHHHH HHHHHHHHHHHHHHHHHHHHHHHHHH	KINVSLKACC CCEHHHH DDDDDDDD 500 IQYLSKNI HHHHHHH DDDDDDDD 570 KQNGKSPEI GCCCCCCC DDDDDDDDD 640 LKNMSKEKT CCCCCCCCC DDDDDDDDD 710 711FNFFF HHHHHHHHH HHHHHHHHHHHHHHHHHHHHHH	CLSLLVKRFVI HHHHHHHHH DOOOOOOOOO 510 KFFSSNKSKDI HHCCCCCCCCC DDDDDDDDDD 580 RASHESEEEEE CCHHHHHHHH DDDDDDDDDD 650 TSNNFMLNIYI 720 FFFDALVQAN HHHHHHHHH DOOOOOOOOOO 790 WLIFSFFQFPI HEEEEECCCE	IKNNNLYNVI HCCCCHHHHI OOOOOOOO 520 VEEECCCCCC ODDDDDDDDD 590 KKKKNINKOI GCCCCCCCCI ODDDDDDDDD 660 OPAKENFKII CCCCCCCCHH ODDDDDDDDD 730 VIFFTALYYLI HHHHHHHHH OOOOOOOOOO 800 CIYVPTLLCI EEEEEEEEEE	KKFVLALNEQI HHHHHHHHHH OOODDDDDDD 530 NNNNNNNCTT CCCCCCCCCC ODDDDDDDDDD 600 KDDLASSEKDI HHHHCHHHH OOOOOOOOO 740 ISSKSVLNYI HHCHHHHHHH OOOOOOOOOOO 810 ILSLIPVISPI EEEEEECCHI OOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOO	KKHILEKNHDI CCCCCCCCC CODDDDDDDD 540 NQNNENKNNS CCCCCCCCC CDDDDDDDDDD 610 KETNKKBGII HCCCCCCCCC CDDDDDDDDDD 750 LKDVLLVVDP; HHHHEECCC COOOOOOOOO 820 EILILVIILH HHHHHHHHHH	FKNKKCMDKDENQK CCHHHCCCCCCC DDDDDDDDDDDDDD 550 VSQNIFKTVFENLV CCCHHHHHHHHHH 620 DDDDDDDDDDDDDDD 620 DKIYSDNKNKDND CCCCCCCCCCCC DDDDDDDDDDDDDD 690 GKLTKFLIFNNSYG HHHHHHHHCCCHH DD000000000000 760 SSIFFYNITNNLKA CCHHHHHHHHCHHH 00000000000000000000000
LYNFTKNEHHHHHCCOOOOOODI 491 VFFSLKKI CHNHHHHB DDDDDDDI 561 QYGNVEQE CCCCHHH DDDDDDDI 631 EKKDLQGI CCCCHHH DDDDDDDI 701 HHHHHHHH 0000000C	KINVSLKACC CCEHHHH DDDDDDDD 500 LIQYLSKNI HHHHHHHH DDDDDDDD 570 QNGKSPEI GCCCCCCC DDDDDDDDD 640 LKNMSKEKT CCCCCCCCC DDDDDDDDD 710 711 FNFFF HHHHHHHH DD00000000 780 LYFYTLYIV HHHHHHHHH D000000000	CLSLLVKRFVI HHHHHHHHHH DOOOOOOOOO 510 KFFSSKKSKDI HHCCCCCCCCCCC DDDDDDDDDDD 650 FSNNFMLNIYI CCCCCCCCCCC DDDDDDDDDDDD 720 MFFFDAIVQA\ HHHHHHHHHH DOOOOOOOOOO 790 KLIFSFFQFPI HEEEEECCCE	IKNNNLYNVI HCCCCCHHHHI OOOOOOOO 520 VVEDSSSNNN EEEECCCCCC DDDDDDDDDD 660 PAKERNFKII CCCCCCCHHI DDDDDDDDDD 730 VIFFTALYYLI HHHHHHHHHH 0000000000 800 IVVPTLLCII EEEEEEEEEEE	KKFVLALNEQI HHHHHHHHHH OOODDDDDDD 530 NNNNNNDKTI CCCCCCCC CDDDDDDDDDD 600 KDDLASSEKDI HHHHCHHHH ODDDDDDDDDDD 670 KEFMSYVNNLI HHHHHHHHHH OOOOOOOOO 740 ISSKKSVLNYI HCHHHHHHHH OOOOODDDOO 810 ILSLIPVISPI EEEEEECCCHI OOOOOOOOOOO	KKHILEKNHDI CCCCCCCCCC DDDDDDDDDD 540 NQNNENKNNS CCCCCCCCCC DDDDDDDDDD 610 KETNKKDGII HCCCCCCCCC DDDDDDDDDD 680 FLSLKKIEDL HHHHHHHHH DDDDDDDDD 750 LKDVLLVVDP HHHHHEECCC DOOOOOOOOO 820 EILILVIILH HHHHHHHHHH	FKNKKCMDKDENQK CCHHHHCCCCCCC DDDDDDDDDDDDD 550 VSQNIFKTVFENLV CCCHHHHHHHHHHC DDDDDDDDDDDDDDD 620 DKKIYSDNKNKDND CCCCCCCCCCCC DDDDDDDDDDDDDD 690 GKLTKFLIFNNSYG HHHHHHHHHHCCCHH DDOOOOOOOOOOOOOOOOOOOOO

Total amino acids:	1096
Total % disorder:	62.13
Total no. of disordered regions > 30 amino acids:	4
Total no. of disordered regions > 50 amino acids:	4
Number of disordered segments:	12
Length distribution of	16 132 23 9 8
segments (N to C terminal	64 8 208 11 2 2
order):	198

KKKEKGKKKLSKNDOLMKKYTHKOLOKKFNOFHNIIKYSEOKYKKFKKKRNEKALLWKNKLDNLYKLIEI 981 990 1000 1010 1020 1030 1040 NRSNIHMYQMDDKKNNSNNKTDQILKRKISPFQQILYDDFMHKEDHKLALYIYRRNKEINNGKKTNHNLI 1051 1060 1070 1080 1090 SKKIHKTTKAPKHKFOYNKRTKSLIYLYDKFOONLDFLFSCITSNN нсссссссссссссснинниннинниннинниннин

Disordered segment motifs: (help)

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

SS Motif for disorder segment 1:

(start,end): (1,16)

1 10
seq : MNKTANLFKDETEKAI
S.S.: CCCCCCCCCCCHHHH
alpha: 001222222345555
beta: 000000100000123
coil : 9987666677654321

SS Motif for disorder segment 2:

(start,end): (51,182)

SS Motif for disorder segment 3:

(start,end): (211,233)

| 211 220 230 | Seq : KPIYKKEEKKNNFNNSFDSYENG | S.S. : HHHHHHCCCCCCCCCHHHHHC | alpha : 677654321122222224555421 | beta : 00000000000000000000 | coil : 32223467787767764444468

SS Motif for disorder segment 4:

(start,end): (295,303)

seq : YYEKYSFLF S.S.: HHHHHHHHC alpha: 999887664 beta: 00000000 coil: 000112234

SS Motif for disorder segment 5:

(start,end): (323,330)

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

Linear motif(s):

residues (2,8) LIG_FHA_1 = NKTANLF

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

Linear motif(s):

residues (86,89) LIG_SH2_SRC = YOYI residues (88,91) LIG_SH2_STAT5 = **YIPN** LIG TRAF6 = residues (88.96) **YIPNEKHET** residues (100,103) LIG_SH2_GRB2 = YKNE residues (102,105) $LIG_PDZ_3 =$ **NEKL** residues (116.119) $LIG_PDZ_3 =$ DEHL. residues (128,134) LIG FHA 1= **GHTNIIK** residues (149,153) LIG_APCC_KENbox_2 = TKENK residues (164,167) LIG_SH2_STAT5 = YTNN residues (166,172) LIG FHA 2= **NNTOHED** residues (171,174) $LIG_PDZ_3 =$

Graph of Probability(helix, strand, coil) PDF

Amino SS Probability(helix, strand, coil) TXT

Linear motif(s):

 $\begin{array}{c} Graph \ of \ Probability(helix, strand, coil) \\ PDF \end{array}$

Amino SS Probability(helix, strand, coil) TXT

Linear motif(s):

residues (299,303) LIG_BRCT_BRCA1_1 = YSFLF

Graph of Probability(helix, strand, coil)
PDF

14/01/2022, 09:51 CSpritz PID: 986020641

sea : IIILAIII s.s. : нининин alpha: 6666665 beta : 33333333 coil : 00000000

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

Linear motif(s):

coil)

TXT

Linear motif(s):

residues (348,351) LIG_SH2_STAT5 residues (356,359) LIG SH2 STAT5 = YLSV residues (357,361) LIG_BRCT_BRCA1_1 = LSVNF residues (379,382) LIG_PDZ_3 = KEDI residues (386,389) LIG_PDZ_3 =

Graph of Probability(helix, strand, coil)

Amino SS Probability(helix, strand, coil) TXT

Linear motif(s):

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

Linear motif(s):

residues (487,494) LIG PP1 = NOKSVFFS residues (489,493) $LIG_BRCT_BRCA1_1 = KSVFF$ residues (501,504) LIG_SH2_STAT5 = YLSK residues (514,517) LIG_PDZ_3 = residues (551,557) LIG FHA 2= FKTVFEN residues (555.558) $LIG_PDZ_3 =$ residues (562,565) LIG SH2 GRB2 = YGNV residues (570,575) LIG_WW_4 = NGKSPE residues (581,584) LIG_TRAF2_1 = SEEE residues (596,599) LIG_PDZ_3 = residues (612,615) LIG_PDZ_3 = **KDGI** residues (646,650) $LIG_BRCT_BRCA1_1 = TSNNF$ residues (655,658) LIG_SH2_SRC =

Graph of Probability(helix, strand, coil)

Amino SS Probability(helix, strand, coil) TXT

Linear motif(s):

residues (682,685) LIG PDZ 3 = IEDL

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

coil)

Linear motif(s):

SS Motif for disorder segment 6: (start,end): (346,409)

365 385 SVYIINSLNNYLSVNFKNAAIIKNFKRFYKKGGKEDIENLYELVDLSKVPFLSNTMISSIYSHI alpha: 3444555554544434558899988888641002357788888754211111124577777889 coil: 21001233443334544310000111112479976411110002456788677653111111110

SS Motif for disorder segment 7:

(start.end): (427.434)

: NKNVSLKA S.S. : CCCCEHHH alpha: 10012456 beta : 00024210 coil: 78853233

SS Motif for disorder segment 8:

(start,end): (459,666)

459 478 488 498 508 518 seq : VLALNEQKKHILEKNHDFKNKKCMDKDENQKSVFFSLKKIIQYLSKNKFFSSNKSKDIVEDSSSSNNNNN alpha: 99988764332221112124665444432111344588999876555443211110011111111111111 beta: 000000001111000000000000001343200000000011210000112455321000100 538 548 558 568 578 588 : NNNNDKTNQNNENKNNSVSQNIFKTVFENLVGQYGNVEQKQNGKSPERASHESEEEEKKKKKNINKQKDD сссссссссссссссниннинниннесссссниннинниннесссссснинниннинн alpha: 2223333221111111123444555555443222124555420002334455577875433443212455 coil : 6655555678877888655432111112334456864223478886655444421123555555676444 599 608 618 628 638 648 658 : LASSEKDKETNKKKDGIDKKIYSDNKNKDNDDEKKDLOGLKNMSKEKTSNNFMLNIYDPAKERNFKIK ннснининссессессессессессеснинссессессессессенин alpha: 544555444321111111122222233222123333355543221112233344332113344333489 coil: 4444444457777877765455666677776556644456777787655555557776555665400

SS Motif for disorder segment 9:

(start.end): (677.687)

677 : LSLKKIEDLGK : нинининини alpha: 88877776656 beta : 00000000000 coil: 11111122343

SS Motif for disorder segment 10:

(start,end): (899,1096)

299 918 928 938 948 958 : AIHKNKSVOSKKKKKEKGKKKLSKNDOLMKKYTHKOLOKKFNOFHNIIKYSEOKYKKFKKKRNEKALLWK 654211243333333211111122466665447899988876654655446665543233335667666 TXT

YDPA

```
residues (923,926) LIG PDZ 3 =
                           NDOL
residues (930,933)
                 LIG SH2 STAT5
                         = YTHK
residues (948,951)
                  LIG_SH2_STAT3
                          = YSEQ
residues (963.966)
                 LIG_CYCLIN_1 =
                           KALL
   residues (971,974)
                    LIG_PDZ_3 =
                           LDNL
  residues (999,1005)
                    LIG FHA 1 =
                       NKTDOIL
 residues (1001,1004)
                     LIG_PDZ_3 =
                            TDQI
 residues (1007,1012)
                    LIG WW 4=
                         RKISPF
  residues (1013,1022)
                    LIG_PCNA =
                   QQILYDDFMH
              residues (1031,1034)
          LIG_SH2_STAT5 = YIYR
 residues (1069,1075)
                    LIG_FHA_1 =
                        KRTKSLI
 residues (1069,1077)
                    LIG MAPK 1
                   = KRTKSLIYL
residues (1070,1075) LIG_14-3-3_3 =
                         RTKSLI
              residues (1072,1076)
          LIG_CYCLIN_1 = KSLIY
              residues (1076,1079)
          LIG_SH2_STAT5 = YLYD
 residues (1085,1088) LIG_PDZ_3 =
                           LDFL
```

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