

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)

ccccc	10					
ccccc	10	20	30	40	50	60
	KFPNEMNLFI	LINSIYTLTLL	MFLEIFFFL	LDGINTFEVI:	TLKERISQII	WCFFFCLHLALLKI
DDDDDDD	ССССИНННИ	инининнин	нннннннн	HCCCCCEEEE	снининини	ннинининнинн
ועעעעעע	DDD0000000	0000000000	000000000	0000000000	000000000	0000000000000000
71	80	90	100	110	120	130
	TSGKPTTST	IVI.FTI.VTTTI	PLSSSLLET			IHIRKLLLICNITL
						нинининининин
						000000000000000
יששטטטט		,0000000000	000000000000000000000000000000000000000		300000000	000000000000000000000000000000000000000
	150	1.00	150	100	100	200
141	150	160	170	180	190	200
						DNIEPYFHELEKKA:
						нссининининин
000000	000000000	0000000000	000000000	0000000000	000000 <mark>DD</mark> 0	000000000000000
211	220	230	240	250	260	270
LIRNNL	IYYQQNKISV	/DILGNYLFEN	EVKYGINKI	KTINKSKINL	EDYYDETTNV	QYDTPMDISDINYY
нинини	ННННССССЕ	ЕЕССССИННИ	HHHCCCCEE	EEECCCCEEC	CCCCCCCE	EECCCCCCCCCCC
000000	000000000	0000000000	000000000	ומממממממממ	000000000	000000000000D0
281	290	300	310	320	330	340
			0-0			DNRNLCNENYTYSK
						CCCCCCCCCCCCCC
ועעטטטט	וטטטטטטטטטט	טטטטטטטטטטט	וטטטטטטטטטט	וטטטטטטטטטט	עעעעעעעעעע	וטטטטטטטטטטטטטטט
351	360	370	380	390	400	410
						YISQNNSSSSHKDN
						HHCCCCCCCCCCCC
DDDDDDD	DDDDDDDDDI	ממממממממממ	וסססססססססס	וססססססססססס	מסססססססססס	ומממממממממממממ
421	430	440	450	460	470	480
TLYSHS	NFKRFNNKIV	/NKKLDALNNE	DYGETYKKK:	IVOKHFSLLR	SGPGKCNRKR	NILLSEELKNKINY
CCCCCH	нниниссни	ннининссс	СССИННИНИ	нининнинн	сссссснин	нининининиссе
						000000000000000
491	500	510	520	530	540	550
491 YEDKNG	500 KVKOSKTTPI	510 .vvi.erhni.nd	520 J.STYLKNDT	530	540 FTTFNNNSNI.	550 TTDGVSYGKGVINM
YFDKNG	KVKQSKIIPI	LYVLERHNLND	LSTYLKNDT	CIKINSYYNFI	FTIFNNNSNL	TTDGVSYGKGVINM
YFDKNG: EECCCC	KVKQSKIIPI CCCCCEEEI	LYVLERHNLND EEEHHHCCCCH	LSTYLKNDTO HHHHHHCCC	CIKINSYYNFI CCCCCCHHHHI	FTIFNNNSNL HHHHCCCCCC	TTDGVSYGKGVINM CCCCCCCCCEECC
YFDKNG: EECCCC	KVKQSKIIPI CCCCCEEEI	LYVLERHNLND EEEHHHCCCCH	LSTYLKNDTO HHHHHHCCC	CIKINSYYNFI CCCCCCHHHHI	FTIFNNNSNL HHHHCCCCCC	TTDGVSYGKGVINM
YFDKNG EECCCC 000000	KVKQSKIIPI CCCCCCEEE DDDDOOOOO	LYVLERHNLND EEEHHHCCCCH	LSTYLKNDT(HHHHHHCCC)	CIKINSYYNFI CCCCCCHHHHI DDOOOOOOO	FTIFNNNSNL HHHHCCCCCC DOOOOOODD	TTDGVSYGKGVINM CCCCCCCCCEECC DDDDDDDDDDDDDDDDD
YFDKNG EECCCC 000000	KVKQSKIIPI CCCCCCEEEE DDDDOOOOOO	LYVLERHNLND EEEHHHCCCCH OOOOOOOOOOOOOO	LSTYLKNDT HHHHHHCCC OOOOOODDD 590	CIKINSYYNFI CCCCCCHHHHI DDOOOOOOOO	FTIFNNNSNL HHHHCCCCCC DOOOOOODD 610	TTDGVSYGKGVINM CCCCCCCCCEECC DDDDDDDDDDDDDDDDDDDDDDDD
YFDKNG EECCCC 0000000 561 SIKSTL	KVKQSKIIPI CCCCCCEEEE DDDDDOOOOOO 570 KTNNTSIYD	LYVLERHNLND EEEHHHCCCCH OOOOOOOOOO 580 FKSRSKNEDTK	LSTYLKNDT(IHHHHHHCCC) OOOOODDDI 590 LNCFHLKTS	CIKINSYYNFI CCCCCCHHHHI DDOOOOOOOO 600 ILRNCPILKKI	FTIFNNNSNL HHHHCCCCCC DOOOOOODD 610 KYFYKYNYNN	TTDGVSYGKGVINM CCCCCCCCCEECC DDDDDDDDDDDDDDD 620 SSSGSSIKYFMNHE
YFDKNG EECCCC 0000000 561 SIKSTLI CCCEEC	KVKQSKIIPI CCCCCCEEE DDDDOOOOOO 570 KTNNTSIYDT CCCCCEEEC	LYVLERHNLND EEEHHHCCCCH 00000000000 580 FKSRSKNEDTK CCCCCCCCCCC	DESTYLKNDT(HHHHHHHCCC) OOOOOODDDD 590 CLNCFHLKTS: CCCCCEEEE	CIKINSYYNFI CCCCCCHHHHI DDOOOOOOOO 600 ILRNCPILKKI	FTIFNNNSNL HHHHCCCCCC DOOOOOODD 610 KYFYKYNYNN CCCCCCCCCC	TTDGVSYGKGVINM CCCCCCCCCEECC DDDDDDDDDDDDDDD 620 SSSGSSIKYFMNHE CCCCCCCHHHHCCC
YFDKNG EECCCC 0000000 561 SIKSTLI CCCEEC	KVKQSKIIPI CCCCCCEEE DDDDOOOOOO 570 KTNNTSIYDT CCCCCEEEC	LYVLERHNLND EEEHHHCCCCH 00000000000 580 FKSRSKNEDTK CCCCCCCCCCC	DESTYLKNDT(HHHHHHHCCC) OOOOOODDDD 590 CLNCFHLKTS: CCCCCEEEE	CIKINSYYNFI CCCCCCHHHHI DDOOOOOOOO 600 ILRNCPILKKI	FTIFNNNSNL HHHHCCCCCC DOOOOOODD 610 KYFYKYNYNN CCCCCCCCCC	TTDGVSYGKGVINM CCCCCCCCCEECC DDDDDDDDDDDDDDD 620 SSSGSSIKYFMNHE
YFDKNG EECCCC 0000000 561 SIKSTLI CCCEEC	KVKQSKIIPI CCCCCCEEE DDDDOOOOOO 570 KTNNTSIYDT CCCCCEEEC	LYVLERHNLND EEEHHHCCCCH 00000000000 580 FKSRSKNEDTK CCCCCCCCCCC	DESTYLKNDT(HHHHHHHCCC) OOOOOODDDD 590 CLNCFHLKTS: CCCCCEEEE	CIKINSYYNFI CCCCCCHHHHI DDOOOOOOOO 600 ILRNCPILKKI EECCCCCCCCC	FTIFNNNSNL HHHHCCCCCC DOOOOOODD 610 KYFYKYNYNN CCCCCCCCCC	TTDGVSYGKGVINM CCCCCCCCCEECC DDDDDDDDDDDDDDD 620 SSSGSSIKYFMNHE CCCCCCCHHHHCCC
YFDKNG EECCCC 0000000 561 SIKSTLI CCCEEC	KVKQSKIIPI CCCCCCEEE DDDDOOOOOO 570 KTNNTSIYDT CCCCCEEEC	LYVLERHNLND EEEHHHCCCCH 00000000000 580 FKSRSKNEDTK CCCCCCCCCCC	DESTYLKNDT(HHHHHHHCCC) OOOOOODDDD 590 CLNCFHLKTS: CCCCCEEEE	CIKINSYYNFI CCCCCCHHHHI DDOOOOOOOO 600 ILRNCPILKKI	FTIFNNNSNL HHHHCCCCCC DOOOOOODD 610 KYFYKYNYNN CCCCCCCCCC	TTDGVSYGKGVINM CCCCCCCCCEECC DDDDDDDDDDDDDDD 620 SSSGSSIKYFMNHE CCCCCCCHHHHCCC
YFDKNG EECCCC OOOOOO 561 SIKSTLI CCCEEC DDDDDDD	KVKQSKIIPI CCCCCCEEE DDDDOOOOOO 570 KTNNTSIYD CCCCCEEEC DDDDDDDDDI	LYVLERHNLND EEEHHHCCCH DOOOOOOOOO 580 PKSRSKNEDTK CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	DESTYLKNDTO HHHHHHHCCO HOOOOOODDDI 590 LINCFHLKTS CCCCCEEEE DDDDDDDDDDI 660	CIKINSYYNFI CCCCCCHHHHI DD00000000 600 ILRNCPILKKI EECCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	FTIFNNSNL HHHHCCCCC DOOOOOODD 610 KYFYKYNYNN CCCCCCCCC	TTDGVSYGKGVINM. CCCCCCCCCEECC DDDDDDDDDDDDDDD 620 SSSGSSIKYFMNHE. CCCCCCCHHHHHCCC
YFDKNG EECCCC OOOOOO 561 SIKSTLI CCCEEC DDDDDDD	KVKQSKIIPI CCCCCCEEEE DDDDOOOOOO 570 KTNNTSIYDI CCCCCEEECC DDDDDDDDDDI 640 TFDVRNSKFI	LYVLERHNLND EEEHHHCCCH OOOOOOOOOO 580 FKSRSKNEDTK CCCCCCCCCC DDDDDDDDDDD 650	LSTYLKNDTO HHHHHHCCO OOOOOODDD 590 LNCFHLKTS CCCCCEEE DDDDDDDDD 660 SKFYSINEN	CIKINSYYNFI CCCCCCHHHHI DDOOOOOOOO 600 ILRNCPILKKI EECCCCCCCC DDDDDDDDDDD 670 SHYDALILKC	FTIFNNNSNL HHHHCCCCCC DOOOOOODD 610 KYFYKYNYNN CCCCCCCCCC DDDDDDDDDDD 680 GNDKRVFYSI	TTDGVSYGKGVINM CCCCCCCCCECC DDDDDDDDDDDDDD 620 SSSGSSIKYFMNHE CCCCCCHHHHHCCC DDDDDDDDDDDDDDDD
YFDKNG EECCCC OOOOOO 561 SIKSTLI CCCEEC DDDDDDD 631 KISQDK CCCCCC	KVKQSKIIPI CCCCCCEEEE DDDDOOOOOO 570 KTNNTSIYDT CCCCCEEEC DDDDDDDDDDDDDDDDDDDDDDDDDDD	LYVLERHNLND EEEHHHCCCCH DOOOOOOOOO 580 EKSRSKNEDTK CCCCCCCCCCC DDDDDDDDDDD 650 ENATEKRRICT	LSTYLKNDTG HHHHHHCCG OOOOODDD 590 LINCFHLKTS: CCCCCEEEE DDDDDDDDDD 660 SKFYSINEN:	CIKINSYYNFI CCCCCHHHHI DDOOOOOOOO 600 ILRNCPILKKI EECCCCCCCCC DDDDDDDDDDD 670 SHYDALILKCC	FTIFNNNSNL HHHHCCCCC DOOOOOODD 610 KYFYKYNYNN CCCCCCCCC DDDDDDDDD 680 GNDKRVFYSI CCCCCEEEEEE	TTDGVSYGKGVINM: CCCCCCCCCEECC DDDDDDDDDDDDDDD 620 SSGSSIKYFMNHE: CCCCCCCHHHHHCCC DDDDDDDDDDDDDDDD 690 YSDNMENSESQSEN: CCCCCCCCCHHHHH
YFDKNG EECCCC OOOOOO 561 SIKSTLI CCCEEC DDDDDDD 631 KISQDK CCCCCC	KVKQSKIIPI CCCCCCEEEE DDDDOOOOOO 570 KTNNTSIYDT CCCCCEEEC DDDDDDDDDDDDDDDDDDDDDDDDDDD	LYVLERHNLND EEEHHHCCCCH DOOOOOOOOO 580 EKSRSKNEDTK CCCCCCCCCCC DDDDDDDDDDD 650 ENATEKRRICT	LSTYLKNDTG HHHHHHCCG OOOOODDD 590 LINCFHLKTS: CCCCCEEEE DDDDDDDDDD 660 SKFYSINEN:	CIKINSYYNFI CCCCCHHHHI DDOOOOOOOO 600 ILRNCPILKKI EECCCCCCCCC DDDDDDDDDDD 670 SHYDALILKCC	FTIFNNNSNL HHHHCCCCC DOOOOOODD 610 KYFYKYNYNN CCCCCCCCC DDDDDDDDD 680 GNDKRVFYSI CCCCCEEEEEE	TTDGVSYGKGVINM CCCCCCCCCEECC DDDDDDDDDDDDDD 620 SSSGSSIKYFMNHE CCCCCCHHHHHCCC DDDDDDDDDDDDDDDD 690 YSDNMENSESQSENI
YFDKNG EECCCC 0000000 561 SIKSTL CCCEEC DDDDDDD 631 KISQDK CCCCCC	KVKQSKIIPI CCCCCCEEE DDDDOOOOOO 570 KTNNTSIYD CCCCCEEEC DDDDDDDDD 640 TTPDVRNSKFI EEEEECCHHE DOOODDDDDD	LYVLERHNLND EEEHHHCCCCH DOOOOOOOO 580 EKSRSKNEDTK CCCCCCCCCCC DDDDDDDDDDD 650 INATERRICT HHHHHHCCC DDDDDDDDDDDDDDDDDDDDDDDDDDD	LSTYLKNDTG HHHHHHCCC HOOOOODDDD 590 LNCFHLKTS: CCCCCEEEE DDDDDDDDDD 660 SKFYSINEN: CCCCEEECCC	CIKINSYYNFI CCCCCHHHHI DDOOOOOOO 600 ILRNCPILKKI EECCCCCCC DDDDDDDDDD 670 SHYDALILKCC CCCHEEECCC	FTIFNNNSNL HHHHCCCCC DOOOOOODD 610 KYFYKYNNN CCCCCCCCC DDDDDDDDDD 680 GNDKRVFYSI CCCCEEEEEE	TTDGVSYGKGVINM CCCCCCCCCECC DDDDDDDDDDDDDD 620 SSSGSSIKYFMNHE CCCCCCHHHHHCCC DDDDDDDDDDDDDD 690 YSDMMENSESQSEN: CCCCCCCCHHHHH DDDDDDDDDDDDDDDDDDDDDDDD
YFDKNG EECCCC 0000000 561 SIKSTLI CCCEEC DDDDDDD 631 KISQDK CCCCCC DDDDDDD	KVKQSKIIPI CCCCCEEEE DDDDDOOOOOC 570 KTNNTSIYDT CCCCCEEECC DDDDDDDDDD 640 TFPVRNSKFI EEEEECCHH DOOODDDDDD 710	LYVLERHNLND EEHHHCCCCH 000000000 580 EKSRSKNEDTK CCCCCCCCCCCCC DDDDDDDDDD 650 ENATEKRICT HHHHHHHCCC DDDDDDDDDDD 720	DESTYLKNDT(HHHHHHCCC OOOOOODDD 590 LINCFHLKTS: CCCCCEEEI DDDDDDDDDD 660 CSKFYSINEN: CCCCEEECCC DDDDDDDDDDD 730	CIKINSYYNFI CCCCCHHHHI DDOOOOOOO 600 ILRNCPILKKI EECCCCCCC DDDDDDDDDD 670 SHYDALILKC CCCHEEEECC DDDDDDDDDDD 740	FTIFNNNSNL HHHHCCCCC DODOOOODD 610 XYFYKYNYNN CCCCCCCCC DDDDDDDDDD 680 GNDKRVFYSI CCCCEEEEEE DDDDDDDDDDD 750	TTDGVSYGKGVINM CCCCCCCCCCEECC DDDDDDDDDDDDDD 620 SSGSSIKYFMNHE CCCCCCHHHHHCCC DDDDDDDDDDDDDDD 690 YSDNMENSESQSEN CCCCCCCCCHHHHH DDDDDDDDDDDDDDDDDD
YFDKNG EECCCC 0000000 561 SIKSTLI CCCEEC DDDDDDD 631 KISQDK CCCCCC DDDDDDD 701 YASGNEI	KVKQSKIIPI CCCCCCEEE DDDDOOOOOO 570 KTNNTSIYD CCCCCEEEC DDDDDDDDDD 640 TFDVRNSKFI EEEEECCHH DOOODDDDDD 710 NENENESESS	LYVLERHNLND EEEHHHCCCCH 0000000000 580 FKSRSKNEDTK CCCCCCCCCCC DDDDDDDDDD 650 INATEKRICT HHHHHHHCCC DDDDDDDDDDD 720 ENGHSDVNIKR	LSTYLKNDTG HHHHHHCCC OOOOOODDDD 590 LINCFHLKTS: CCCCCEEEI DDDDDDDDDD 660 SKFYSINEN: CCCEEECCC DDDDDDDDDDD 730 ERTSYIQHFH:	CIKINSYYNFI CCCCCHHHHI DDOOOOOOO 600 ILRNCPILKKI EECCCCCCCC DDDDDDDDDDD 670 SHYDALILKCC CCCHEEECCC DDDDDDDDDDD 740 SNVQEPDDVII	FTIFNNNSNL HHHHCCCCCC DOOOOOODD 610 KYFYKYNNNN CCCCCCCCCC DDDDDDDDDD 680 GNDKRVFYSI CCCCEEEEEE DDDDDDDDDDDD 750 HRKISKFQIN	TTDGVSYGKGVINM CCCCCCCCCEECC DDDDDDDDDDDDDD 620 SSSGSSIKYFMNHE CCCCCCCHHHHHCCC DDDDDDDDDDDDDDDD 690 YSDNMENSESQSENI CCCCCCCCHHHHH DDDDDDDDDDDDDDDDD 760 KSVKTQNTLFSEES
YFDKNG EECCCC 0000000 561 SIKSTL CCCEEC DDDDDDD 631 KISQDK CCCCCC DDDDDDD 701 YASGNE HHCCCC	KVKQSKIIPI CCCCCCEEEE DDDDOOOOOO 570 KTNNTSIYDD CCCCCEEECC DDDDDDDDDDD 640 1640 1640 1640 1710 NEBENESESI CCEEEEECCHIE CCCCCEEEECCC	LYVLERHNLND EEEHHHCCCCH DOOOOOOOOO 580 PKSRSKNEDTK CCCCCCCCCCC DDDDDDDDDDD 650 ENATEKRICT HHHHHHHCCC DDDDDDDDDD 720 ENGHSDVNIKR CCCCCCCHHC	LSTYLKNDTG HHHHHHCCC OOOOOODDD 590 LNCFHLKTS: CCCCCEEEE DDDDDDDDDD 660 SKFYSINEN: CCCEEECCC DDDDDDDDDD 730 RTSYIQHFH: CCHHHHHHHHH	CIKINSYYNFI CCCCCHHHHI DDOOOOOOOO 600 ILRNCPILKKI EECCCCCCCCC DDDDDDDDDDD 670 SHYDALILKC CCCHEEECCC DDDDDDDDDDD 740 SNVQEPDDVII HHCCCCCCEE	FTIFNNNSNL HHHHCCCCC DOOOOOODD 610 KYFYKYNNN CCCCCCCCCC DDDDDDDDDD 680 GNDKYFYSI CCCCEEEEE DDDDDDDDDDD 750 HRKISKFQIN EEECCEEEEE	TTDGVSYGKGVINM CCCCCCCCCEECC DDDDDDDDDDDDDD 620 SSSGSSIKYFMNHE CCCCCCCHHHHCCC DDDDDDDDDDDDDDD 690 YSDMENSESQSENI CCCCCCCCHHHH DDDDDDDDDDDDDDD 760 KSVKTQNTLFSEESI CCCCCCCEEEECCC
YFDKNG EECCCC 0000000 561 SIKSTL CCCEEC DDDDDDD 631 KISQDK CCCCCC DDDDDDD 701 YASGNE HHCCCC	KVKQSKIIPI CCCCCCEEEE DDDDOOOOOO 570 KTNNTSIYDD CCCCCEEECC DDDDDDDDDDD 640 1640 1640 1640 1710 NEBENESESI CCEEEEECCHIE CCCCCEEEECCC	LYVLERHNLND EEEHHHCCCCH DOOOOOOOOO 580 PKSRSKNEDTK CCCCCCCCCCC DDDDDDDDDDD 650 ENATEKRICT HHHHHHHCCC DDDDDDDDDD 720 ENGHSDVNIKR CCCCCCCHHC	LSTYLKNDTG HHHHHHCCC OOOOOODDD 590 LNCFHLKTS: CCCCCEEEE DDDDDDDDDD 660 SKFYSINEN: CCCEEECCC DDDDDDDDDD 730 RTSYIQHFH: CCHHHHHHHHH	CIKINSYYNFI CCCCCHHHHI DDOOOOOOOO 600 ILRNCPILKKI EECCCCCCCCC DDDDDDDDDDD 670 SHYDALILKC CCCHEEECCC DDDDDDDDDDD 740 SNVQEPDDVII HHCCCCCCEE	FTIFNNNSNL HHHHCCCCC DOOOOOODD 610 KYFYKYNNN CCCCCCCCCC DDDDDDDDDD 680 GNDKYFYSI CCCCEEEEE DDDDDDDDDDD 750 HRKISKFQIN EEECCEEEEE	TTDGVSYGKGVINM CCCCCCCCCEECC DDDDDDDDDDDDDD 620 SSSGSSIKYFMNHE CCCCCCCHHHHHCCC DDDDDDDDDDDDDDDD 690 YSDNMENSESQSENI CCCCCCCCHHHHH DDDDDDDDDDDDDDDDD 760 KSVKTQNTLFSEES
YFDKNG EECCCC 000000 561 SIKSTLI CCCEEC DDDDDDD 631 KISQDK CCCCCC DDDDDDD 701 YASGNEI HHCCCC DDDDDDD	KVKQSKIIPI CCCCCCEEEE DDDDDOOOOOO 570 KTNNTSIYDT CCCCCEEECC DDDDDDDDDDD 640 TFDVRNSKFI EEEEECCHHE DOOODDDDDD 710 NENENESESE CCEEEEEECC DDDDDDDDDDDDDDDDDDDDDDD	LYVLERHNLND EEHHHCCCCH DOOOOOOOO 580 EKSRSKNEDTK CCCCCCCCCC DDDDDDDDDDD 650 INATERRICT HHHHHHHCCC DDDDDDDDDDD 720 ENGHSDVNIRR CCCCCCCHHCC DDDDDDDDDDDDDDDDDDDDDDDDD	LSTYLKNDT(HHHHHHCCC OOOOOODDDD 590 LNCFHLKTS: CCCCCEEEE DDDDDDDDD 660 CSKFYSINEN: CCCEEECCC DDDDDDDDDD 730 RTSYIQHFH: CCHHHHHHHHHI DDDDDDDDDDDD	CIKINSYNFICCCCCCHHHHIDDOOOOOOOOOOOOOOOOOOOOOOOOOO	FTIFNNNSNL HHHHCCCCC DOOOOOODD 610 KYFYKYNYNN CCCCCCCCC DDDDDDDDD 680 GNDKRVFYSI CCCCEEEEEE DDDDDDDDDD 750 HRKISKFQIN EEECCEEEEE	TTDGVSYGKGVINM: CCCCCCCCCCEECC DDDDDDDDDDDDDDD 620 SSGSSIKYFMNHE: CCCCCCHHHHHCCC DDDDDDDDDDDDDDDDD 690 YSDNMENSESQSEN: CCCCCCCCCHHHHH DDDDDDDDDDDDDDDDDD 760 KSVKTQNTLFSEES: CCCCCCCEEEECCC
YFDKNG EECCCC 000000 561 SIKSTLI CCCECC DDDDDDD 631 KISQDK CCCCCC DDDDDDD 701 YASGNE HHCCCC DDDDDDD 771	KVKQSKIIPI CCCCCCEEE DDDDOOOOOO 570 KTNNTSIYD CCCCCEEEC DDDDDDDDD 640 TFDVRNSKFI EEEEECCHH DOOODDDDD 710 NENENESESI CCEEEEEEC DDDDDDDDDDD 780	LYVLERHNLND EEEHHHCCCCH DOOOOOOOOO 580 FKSRSKNEDTK CCCCCCCCCCC DDDDDDDDDD 650 INATEKRICT HHHHHHHCCC DDDDDDDDDDD 720 ENGHSDVNIKR CCCCCCCHHCC DDDDDDDDDDDD 790	DESTYLKNDTG HHHHHHCCC OOOOOODDD 590 LINCFHLKTS: CCCCCEEEE DDDDDDDDDD 660 SKFYSINEN: CCCEEECCC DDDDDDDDDD 730 RTSYIQHFH: CHHHHHHHHI DDDDDDDDDD	CIKINSYNFICCCCCHHHHIDDOOOOOOOOOOOOOOOOOOOOOOOOOOO	FTIFNNNSNL HHHHCCCCC COOOOOODD 610 KYFYKYNNNN CCCCCCCCC CDDDDDDDDD 680 GNDKRVFYSI CCCCEEEEEE DDDDDDDDDDD 750 HRKISKFQIN EEECCEEEEE	TTDGVSYGKGVINM CCCCCCCCCEECC DDDDDDDDDDDDD 620 SSGGSSIKYFMNHE CCCCCCHHHHHCCC DDDDDDDDDDDDDDD 690 YSDNMENSESQSENI CCCCCCCCCHHHH DDDDDDDDDDDDDDD 760 KSVKTQNTLFSEES CCCCCCCCEEEECCC 00DDDDDDDDDDDDD
YFDKNG EECCCC 0000000 561 SIKSTL CCCEEC DDDDDDD 631 KISQDK CCCCCC DDDDDDD 701 YASGNE HHCCCC DDDDDDD 771 ENMLFSI	KVKQSKIIPI CCCCCCEEE DDDDOOOOO 570 KTNNTSIYDI CCCCCEEEC DDDDDDDDDD 640 710 NEMENESESI CCEEEEEC DDDDDDDDDDD 780 NNAFYVDDGI	LYVLERHNLND EEEHHHCCCCH DOOOOOOOOO 580 ***CCCCCCCCCCCC DDDDDDDDDDD 650 ***INATEKRRICT HHHHHHCCC DDDDDDDDDD 720 ENGHSDVNIKR CCCCCCCHHC DDDDDDDDDDD 790 LDKSVNTDNIQ	LSTYLKNDTG (HHHHHHCCC) (OOOOOODDD) 590 (LNCFHLKTS: (CCCCCEEE) (DDDDDDDDD) 660 (SKFYSINEN: (CCCEEECCC) (DDDDDDDDDD) 730 (RTSYIQHFH: (CHHHHHHHH) (DDDDDDDDDD) 800 (DNEIESNKY)	CIKINSYYNFI CCCCCHHHHI CCCCCCHHHHI DDOOOOOOO 600 ILRNCPILKKI EECCCCCCCC CDDDDDDDDDDD 670 SHOALILKCC CCCHEEECC CDDDDDDDDDDD 740 SNVQEPDDVII HHCCCCCEEI DDDDOOOOOO 810 NTSSCSSFSI	FTIFNNNSNL HHHHCCCCC DOOOOOODD 610 KYFYKYNNN CCCCCCCC DDDDDDDDDD 680 GNDKYFYSI CCCCEEEEE DDDDDDDDDD 750 HRKISKFQIN EEECCEEEEE DOOOOOOOOO	TTDGVSYGKGVINM CCCCCCCCCEECC DDDDDDDDDDDDDD 620 SSSGSSIKYFMNHE CCCCCCCHHHHCCC DDDDDDDDDDDDDDD 690 YSDMENSESQSENI CCCCCCCCHHHH DDDDDDDDDDDDD 760 KSVKTQNTLFSESS CCCCCCCEEEECCC 00DDDDDDDDDDDDDD 830 KNIICMYDNIVLPK
YFDKNG EECCCC OOOOOOO 561 SIKSTLI CCCCECC DDDDDDD 631 KISQDK CCCCCCC DDDDDDD 701 YASGNE HHCCCC DDDDDDD 771 EMMLFSI CCCCCCC	KVKQSKIIPI CCCCCCEEEE DDDDOOOOOO 570 KTNNTSIYDT CCCCCEEECC DDDDDDDDDD 640 TFPVRNSKFI EEEEECCHH DOOODDDDD 710 NENENESESSI CCEEEEEECC DDDDDDDDDDDDDDDDDDDDDDDDDDD	LYVLERHNLND EEEHHHCCCCH 0000000000 580 EKSRSKNEDTK CCCCCCCCCCCC DDDDDDDDDD 650 ENATEKRICT HHHHHHHCC DDDDDDDDDD 720 ENGHSDVNIKR CCCCCCCHHC DDDDDDDDDDD 790 LOKSVNTDNIQ	LSTYLKNDT(HHHHHHCCC OOOOOODDD 590 LINCFHLKTS: CCCCCEEEI DDDDDDDDD 660 SKFYSINEN: CCCEEECCC DDDDDDDDDD 730 RTSYIQHFH: CCHHHHHHHHH DDDDDDDDDD 800 DDEIESNKYI CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	CIKINSYNFICCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	FTIFNNSNL HHHHCCCCC DOOOOOODD 610 KYFYKYNYNN CCCCCCCCCC DDDDDDDDD 680 GNDKRVFYSI CCCCEEEEE DDDDDDDDDD 750 HRKISKFQIN EEECCEEEEE DOOOOOOOOO	TTDGVSYGKGVINM: CCCCCCCCCCEECC DDDDDDDDDDDDDDD 620 SSGSSIKYFMNHE: CCCCCCHHHHHCCC DDDDDDDDDDDDDDD 690 YSDNMENSESQSEN: CCCCCCCCCHHHHH DDDDDDDDDDDDDDD 760 KSVKTQNTLFSEES: CCCCCCCCEEECCCC 00DDDDDDDDDDDDDDDD 830 KNIICMYDNIVLPK: CEEEEECCCCCCCC
YFDKNG EECCCC OOOOOOO 561 SIKSTLI CCCCECC DDDDDDD 631 KISQDK CCCCCCC DDDDDDD 701 YASGNE HHCCCC DDDDDDD 771 EMMLFSI CCCCCCC	KVKQSKIIPI CCCCCCEEEE DDDDOOOOOO 570 KTNNTSIYDT CCCCCEEECC DDDDDDDDDD 640 TFPVRNSKFI EEEEECCHH DOOODDDDD 710 NENENESESSI CCEEEEEECC DDDDDDDDDDDDDDDDDDDDDDDDDDD	LYVLERHNLND EEEHHHCCCCH 0000000000 580 EKSRSKNEDTK CCCCCCCCCCCC DDDDDDDDDD 650 ENATEKRICT HHHHHHHCC DDDDDDDDDD 720 ENGHSDVNIKR CCCCCCCHHC DDDDDDDDDDD 790 LOKSVNTDNIQ	LSTYLKNDT(HHHHHHCCC OOOOOODDD 590 LINCFHLKTS: CCCCCEEEI DDDDDDDDD 660 SKFYSINEN: CCCEEECCC DDDDDDDDDD 730 RTSYIQHFH: CCHHHHHHHHH DDDDDDDDDD 800 DDEIESNKYI CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	CIKINSYNFICCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	FTIFNNSNL HHHHCCCCC DOOOOOODD 610 KYFYKYNYNN CCCCCCCCCC DDDDDDDDD 680 GNDKRVFYSI CCCCEEEEE DDDDDDDDDD 750 HRKISKFQIN EEECCEEEEE DOOOOOOOOO	TTDGVSYGKGVINM CCCCCCCCCEECC DDDDDDDDDDDDDD 620 SSSGSSIKYFMNHE CCCCCCCHHHHCCC DDDDDDDDDDDDDDD 690 YSDMENSESQSENI CCCCCCCCHHHH DDDDDDDDDDDDD 760 KSVKTQNTLFSESS CCCCCCCEEEECCC 00DDDDDDDDDDDDDD 830 KNIICMYDNIVLPK
YFDKNG EECCCC 000000 561 SIKSTLI CCCCCC DDDDDDD 631 KISQDK CCCCCC DDDDDDD 701 YASGNE HHCCCC DDDDDDD 771 EMMLFSI CCCCCC DDDDDOO	KVKQSKIIPI CCCCCCEEE DDDDOOOOOO 570 KTNNTSIYD CCCCCEEEC DDDDDDDDD 640 TFDVRNSKFI EEEEECCHH DOOODDDDD 710 NENENESESI CCEEEEEEC DDDDDDDDDD 780 NNAFYVDDGI CCCEEEECC OOOOOOOOOO	LYVLERHNLND EEEHHHCCCCH DOOOOOOOOO 580 FKSRSKNEDTK CCCCCCCCCCC DDDDDDDDDD 650 INATEKRICT HHHHHHHCCC DDDDDDDDDDD 720 ENGHSDVNIKR CCCCCCHHCC DDDDDDDDDDD 790 LDKSVMTDNIQ CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	DESTYLKNDTO HHHHHHHCCC OOOOOODDD 590 LINCFHLKTS: CCCCCEEEE DDDDDDDDDD 660 SKFYSINEN: CCCEEECCC DDDDDDDDDDD 730 RTSYIQHFH: CCHHHHHHHH DDDDDDDDD 800 DDEESNKYI CCCCCCCCCCC DDDDDDDDDDDD	CIKINSYNFICCCCCCHHHHIDDOOOOOOOOOOOOOOOOOOOOOOOOOO	FTIFNNNSNL HHHHCCCCC DOOOOOODD 610 KYFYKYNNNN CCCCCCCCC DDDDDDDDDD 680 GNDKRVFYSI CCCCEEEEE DDDDDDDDDDD 750 HRKISKFQIN EEECCEEEEE DOOOOOOOOO 820 SDAKNKKNNK CCCCCCCCC	TTDGVSYGKGVINM CCCCCCCCCCECC DDDDDDDDDDDDD 620 SSGGSSIKYFMNHE CCCCCCHHHHHCCC DDDDDDDDDDDDDDD 690 YSDNMENSESQSENI CCCCCCCCHHHHH DDDDDDDDDDDDDD 760 KSVKTQNTLFSEESI CCCCCCCEEEECCC 00DDDDDDDDDDDDD 830 KNIICMYDNIVLPK CEEEEECCCCCCCC
YFDKNG EECCCC OOOOOOO 561 SIKSTLI CCCCECC DDDDDDD 631 KISQDK CCCCCCC DDDDDDD 701 YASGNE HHCCCC DDDDDDD 771 EMMLFSI CCCCCCC	KVKQSKIIPI CCCCCCEEEE DDDDOOOOOO 570 KTNNTSIYDT CCCCCEEECC DDDDDDDDDD 640 TFPVRNSKFI EEEEECCHH DOOODDDDD 710 NENENESESSI CCEEEEEECC DDDDDDDDDDDDDDDDDDDDDDDDDDD	LYVLERHNLND EEEHHHCCCCH 0000000000 580 EKSRSKNEDTK CCCCCCCCCCCC DDDDDDDDDD 650 ENATEKRICT HHHHHHHCC DDDDDDDDDD 720 ENGHSDVNIKR CCCCCCCHHC DDDDDDDDDDD 790 LOKSVNTDNIQ	LSTYLKNDT(HHHHHHCCC OOOOOODDD 590 LINCFHLKTS: CCCCCEEEI DDDDDDDDD 660 SKFYSINEN: CCCEEECCC DDDDDDDDDD 730 RTSYIQHFH: CCHHHHHHHHH DDDDDDDDDD 800 DDEIESNKYI CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	CIKINSYNFICCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	FTIFNNSNL HHHHCCCCC DOOOOOODD 610 KYFYKYNYNN CCCCCCCCCC DDDDDDDDD 680 GNDKRVFYSI CCCCEEEEE DDDDDDDDDD 750 HRKISKFQIN EEECCEEEEE DOOOOOOOOO	TTDGVSYGKGVINM: CCCCCCCCCCEECC DDDDDDDDDDDDDDD 620 SSGSSIKYFMNHE: CCCCCCHHHHHCCC DDDDDDDDDDDDDDD 690 YSDNMENSESQSEN: CCCCCCCCCHHHHH DDDDDDDDDDDDDDD 760 KSVKTQNTLFSEES: CCCCCCCCEEECCCC 00DDDDDDDDDDDDDDDD 830 KNIICMYDNIVLPK: CEEEEECCCCCCCC
YFDKNG EECCCC OOOOOO 561 SIKSTLI CCCEEC DDDDDDDD 631 KISQDK CCCCCCC DDDDDDDD 701 YASGNEI HHCCCC DDDDDDD 771 ENMLFSI CCCCCCC DDDDDOOO 841	KVKQSKIIPI CCCCCCEEE DDDDOOOOO 570 KTNNTSIYDI CCCCCCEECC DDDDDDDDDD 640 710 NEMENESESI CCEEEEECC DDDDDDDDDDD 780 NNAFYVDDGI CCCEEECCC 0000000000	LYVLERHNLND EEEHHHCCCCH DOOOOOOOOO 580 TKSRSKNEDTK CCCCCCCCCCC DDDDDDDDDDD 650 INATEKRRICT HHHHHHHCCC DDDDDDDDDD 720 ENGHSDVNIKR CCCCCCCHHC DDDDDDDDDDD 790 LDKSVNTDNIG CCCCCCCCCCCCCC DDDDDDDDDDDD 860	DESTYLKNDTO CHHHHHHHCCC COOOOOODDD 590 CLNCFHLKTS: CCCCCEEEC CDDDDDDDDDD 660 CKFYSINEN: CCCEEECCC CDDDDDDDDDD 730 CRTSYIQHFH: CCHHHHHHHHI CDDDDDDDDDD 800 CDNEIESNKYI CCCCCCCCCCC CDDDDDDDDDDD 870	CIKINSYNFI CCCCCHHHHI CCCCCCHHHHI CDOOOOOOO 600 ILRNCPILKK EECCCCCCCCC CODDDDDDDDDD 670 SHYDALILKC CCCHEEECC CDDDDDDDDDD 740 SNYQEPDDVII HHCCCCCEEI CDDDDOOOOOO 810 NTSSCSSFSI CCCCCCCCCCCCC CDDDDDDDDDDD	FTIFNNNSNL HHHHCCCCC DOOOOOODD 610 KYFYKYNNN CCCCCCCCCC DDDDDDDDDD 680 GNDKYFYSI CCCCEEEEE DDDDDDDDDD 750 HRKISKFQIN EEECCEEEEE DOOOOOOOO 820 SDAKNKKMNK CCCCCCCCC	TTDGVSYGKGVINM CCCCCCCCCCECC DDDDDDDDDDDDD 620 SSGGSSIKYFMNHE CCCCCCHHHHHCCC DDDDDDDDDDDDDDD 690 YSDNMENSESQSENI CCCCCCCCHHHHH DDDDDDDDDDDDDD 760 KSVKTQNTLFSEESI CCCCCCCEEEECCC 00DDDDDDDDDDDDD 830 KNIICMYDNIVLPK CEEEEECCCCCCCC
YFDKNG EECCCC 000000 561 SIKSTLI CCCECC DDDDDDD 631 KISQDK CCCCCC DDDDDDD 701 YASGNE HHCCCC DDDDDDD 771 ENMLFSI CCCCCC DDDDD000 841 ESFIKL	KVKQSKIIPI CCCCCCEEEE DDDDOOOOOO 570 KTNNTSIYDT CCCCCEEECC DDDDDDDDDD 640 TFPVRNSKFI EEEEECCHH DOOODDDDDD 710 NENENESESI CCCEEEEEECC DDDDDDDDDDDD 780 NNAFYVDDGI CCCCEEECCC 0000000000	LYVLERHNLND EEHHHCCCCH DOOOOOOOO 580 EKSRSKNEDTK CCCCCCCCCCCCC DDDDDDDDDDD 720 ENGHSDVNIER CCCCCCCCHHC CDDDDDDDDDDD 790 LDKSVNTDNIQ CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	DESTYLKNDTG HHHHHHCCG OOOOOODDD 590 LINCPHLKTS: CCCCCEEEI DDDDDDDDD 660 CSKFYSINEN: CCCEEECCG DDDDDDDDDD 730 CRTSYIQHFH: CCHHHHHHHHHI DDDDDDDDDDD 800 DDNEIESNKYI CCCCCCCCG DDDDDDDDDDD 870 SFLNGSYEGSI	CIKINSYYNFICCCCCCHHHHIDOOOOOOOOOOOOOOOOOOOOOOOOOOO	FTIFNNNSNL HHHHCCCCC DOOOOOODD 610 KYFYKYNYNN CCCCCCCCCC DDDDDDDDDD 680 SINDKRVFYSI CCCCEEEEE DDDDDDDDDD 750 HRKISKFQIN EEECCEEEEE DOOOOOOOOO 820 SDAKNKKMNK CCCCCCCCCC DDDDDDDDDD 890 AENYGIQVGI	TTDGVSYGKGVINM CCCCCCCCCEECC DDDDDDDDDDDDDD 620 SSSGSSIKYFMNHE CCCCCCCHHHHCCC DDDDDDDDDDDDDDD 690 YSDNMENSESQSENI CCCCCCCCHHHH DDDDDDDDDDDDDD 760 KSVKTQNTLFSESS CCCCCCCEEEECCC 00DDDDDDDDDDDDDD 830 KNIICMYDNIVLPK CEEEEECCCCCCCC D00000000DDDDD
YFDKNG EECCCC 000000 561 SIKSTLI CCCCCCC DDDDDDD 631 KISQDK CCCCCC DDDDDDD 701 YASGNEI HHCCCC DDDDDDD 771 EMNLFSI CCCCCCC DDDDDD0 841 ESFIKL' HHHHHH	KVKQSKIIPI CCCCCCEEEE DDDDOOOOOO 570 KTNNTSIYD CCCCCEEECC DDDDDDDDD 640 TFDVRNSKFI EEEEECCHH DOOODDDDDD 710 NENENESESE CCEEEEECC DDDDDDDDDD 780 NNAFYVDDGI COCCCCCEEECCC 000000000 850 TNNSRNKNKK HHHHCCCCCC	LYVLERHNLND EEEHHHCCCCH DOOOOOOOO 580 TKSRSKNEDTK CCCCCCCCCCCC DDDDDDDDDDD 720 ENGHSDVNIKE CCCCCCCHHC DDDDDDDDDD 790 LDKSVNTDNIQ CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	LSTYLKNDTG HHHHHHCCCG HHHHHHHCCCG HOOOOODDDD 590 LINCFHLKTS: CCCCCEEEI CDDDDDDDDDD 660 SKFYSINEN: CCCEEECCG DDDDDDDDDDD 730 RTSYIQHFH: CCHHHHHHHHHI DDDDDDDDDDD 800 DNEIESNKYI GCCCCCCCGG DDDDDDDDDDD 870 FLNGSYEGSI CCCCCCCCGG	CIKINSYYNFICCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	FTIFNNNSNL HHHHCCCCC DOOOOOODD 610 KYFYKYNNNN CCCCCCCCCC DDDDDDDDDD 680 SMDKRVFYSI CCCCEEEEE DDDDDDDDDD 750 HRKISKFQIN EEECCEEEEE DOOOOOOOO 820 SDAKNKKMNK CCCCCCCCCC DDDDDDDDDDD 890 AENYGIQVGI	TTDGVSYGKGVINM: CCCCCCCCCCEECC DDDDDDDDDDDDDDD 620 SSGSSIKYFMNHE: CCCCCCCHHHHHCCC DDDDDDDDDDDDDDD 690 YSDNMENSESQSEN: CCCCCCCCCHHHHH DDDDDDDDDDDDDDDD 760 KSVKTQNTLFSES: CCCCCCCEEECCC OODDDDDDDDDDDDDD 830 KNIICMYDNIVLPK: CEEEEECCCCCCCC DOOOOOOODDDDDD

Total amino acids:	1378
Total % disorder:	46.87
Total no. of disordered regions > 30 amino acids:	5
Total no. of disordered regions > 50 amino acids:	4
Number of disordered segments:	26
Length distribution of segments (N to C terminal order):	9 2 2 2 11 1 146 1 1 4 2 4 5 94 99 17 40 149 13 5 1 4 1 1 9 23

IOGGIPTFDHNNREOKRIKENIONKKFNSRDTCEGEKKERTEDSIGNHHFSLCKKCTSKKHFDGII.SKKK 981 990 1000 1010 1020 1030 1040 GTCKYISNLSLNKRKSKESHLSIYKKYFFEFYDCIPINYKKKPHNIEKHKFSYNIKNAFLCIKLFNIIWI 1070 1080 1090 1100 1051 1060 KIKTWYKKIDKKEKYWKRYNDILYTSOWKNNIODNELEYILKYKNFMKWYNYWVKTVLFNYYKSTWALNL 1140 1150 1160 LLYILNVLLIYLQMHMFYFLFEINSDQPKYSNVLKKEENSKTKFPLNHFMDKNKYIPFTYIRISLQLIIN 1191 1200 1210 1220 1230 1240 1250 IIFCLPSMIIKNFKRIKMLHIFSILNCLVNIFFGMIDIVYSLNDRIFNINDLYVLLNHYNIFDVFLIGKL ITSIFLIPFFTNFNESKTCALIYFSCICYISTFYYSYNPLSFSIKLMYLTIFVILIAVTLTTSYYAKLIM **ННЕЕЕЕССЕЕССССССЕЕЕЕЕЕЕЕЕЕЕЕЕЕЕСССССНИННИННИННИННИННИННИННИННИНН** 1340 1350 1360 1370 KSRKMLFVKYVLPYFIYLTFLNTDPHIQMKIKEKKRKKKKKKQRNIGK DDDDDDD0000000000000DDDD

Disordered segment motifs: (help)

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

SS Motif for disorder segment 1: (start,end): (1,9)

seq : MKKYHKKFP s.s. : CCCCCCCCC alpha: 011210003 beta: 000000000 coil: 987778886

SS Motif for disorder segment 2:

(start,end): (246,256)

246 255 : KTINKSKINLE S.S. : EEECCCCEECC alpha: 22111000000 coil: 22345554446

SS Motif for disorder segment 3:

(start,end): (285,430)

285 304 314 324 : KVNVENDSEDIEMCSLKKMNAEENKINDNYSRNIIRCDNEENLNVESNIEIDNRNLCNENYTYSKNKKKK seq alpha: 0000112456666556775445543210000110000011110001100000123333211000111123 beta: 666542000000000000000011221011124776212333333213553100121001232100011 3233466433323342223544344467888764213676555555676345665444677656677765 355 374 384 394 404 seq : EKLKKNKTNISLKDNSSAYIDNNNNNNNNEINNHVTSYDKYLSPQNNDYISQNNSSSSHKDNNTLYS alpha: 3332211110022111112232210111222112112222332200334455542101344333222223 coil: 5555677776767787642223578877777755544445556688654433356788645556777654 sea : HSNFKR : СНННН alpha: 444566 beta : 110000

SS Motif for disorder segment 4:

(start,end): (460,463)

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

Linear motif(s):

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Graph of Probability(helix, strand, coil)
                                     PDE
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 (292,295) LIG_PDZ_3 = SEDI

```
residues (324,327) LIG_PDZ_3 = EENL
  residues (345,348) LIG_SH2_STAT5 =
residues (354,357) LIG_PDZ_3 = KEKL
    residues (356,366)
                     LIG_MAPK_1 =
                    KLKKNKTNISL
  residues (373,376) LIG_SH2_STAT5 =
                              YIDN
     residues (391,396) LIG_14-3-3_3 =
                           HVTSYD
      residues (391,397) LIG_FHA_2 =
                         HVTSYDK
  residues (397,401) LIG_CYCLIN_1 =
                            KYLSP
      residues (397,402) LIG_WW_4 =
                           KYLSPO
  residues (398,401) LIG_SH2_STAT5 =
```

Graph of Probability(helix, strand, coil) PDF

residues (404,407) LIG_PDZ_3 = NDYI residues (406,409) LIG_SH2_STAT5 =

YLSP

CSpritz PID: 986020641 Amino SS Probability(helix, strand, coil) sea : HFSL S.S. : HHHH alpha: 6666 Linear motif(s): beta : 0111 coil : 2211 SS Motif for disorder segment 5: Graph of Probability(helix, strand, coil) (start,end): (497,500) Amino SS Probability(helix, strand, coil) seq : KVKQ s.s. : cccc alpha: 0001 Linear motif(s): beta : 2433 coil: 7555 SS Motif for disorder segment 6: Graph of Probability(helix, strand, coil) (start,end): (523,527) Amino SS Probability(helix, strand, coil) seq : NDTCI s.s. : ccccc alpha: 32123 Linear motif(s): beta : 00001 coil : 57765 Graph of Probability(helix, strand, coil) Amino SS Probability(helix, strand, coil) SS Motif for disorder segment 7: (start.end): (544.637) Linear motif(s): 544 553 563 573 583 593 603 residues (545,551) LIG_FHA_1 = : NLTTDGVSYGKGVINMSSIKSTLKTNNTSIYDTKSRSKNEDTKLNCFHLKTSILRNCPILKKKYFYKYNY sea LTTDGVS residues (547,550) LIG PDZ 3 = TDGVbeta: 0111001111235542223454332123454421000011112233334444432111112222223332 residues (591,596) LIG_14-3-3_3 = 8878988777754455665434455776444467877776665444443332234565444344433345 coil : HLKTSI 614 623 633 residues (592,598) LIG_FHA_1 = : NNSSSGSSIKYFMNHEKKISODKT seq : CCCCCCCHHHHHCCCCCCCCCE LKTSILR alpha: 110111234555433211000000 residues (607,610) LIG_SH2_STAT5 = beta: 110000022222111111100148 coil: 778888742212345677888851 residues (613,616) LIG_SH2_GRB2 = residues (624.627) LIG SH2 STAT5 = Graph of Probability(helix, strand, coil) SS Motif for disorder segment 8: (start,end): (641,739) Amino SS Probability(helix, strand, coil) : RNSKFINATEKRRICTSKFYSINENSHYDALILKCGNDKRVFYSIYSDNMENSESOSENEYASGNENENE Linear motif(s): s.s. alpha: 004677777665432221111000011344443200000000011111221135667776421012223 beta: 5200000000111111234543100123444431000147886532000000000000000122334 residues (668,671) LIG_PDZ_3 = YDAL coil: 4753211122233455654334678873210124789874101235677777754332223468765332 residues (680,686) LIG_14-3-3_2 = RVFYSIY : NESESENGHSDVNIKRRTSYIQHFHSNVQ residues (726,732) LIG FHA 1= : EEEECCCCCCCHHHCCHHHHHHHHHCC S.S. alpha: 33332210013445434578887665532 **RRTSYIO** 44443210000001000000000111111 residues (730,733) LIG_SH2_STAT5 = coil: 21224578876443454321111222356 SS Motif for disorder segment 9: Graph of Probability(helix, strand, coil) (start,end): (758,774) Amino SS Probability(helix, strand, coil) : VKTQNTLFSEESNENML : CCCCCEEECCCCCCC S.S. alpha: 0000000011223333 Linear motif(s): 43223666532100112 coil: 55665322456665544 Graph of Probability(helix, strand, coil) SS Motif for disorder segment 10: (start,end): (787,826) Amino SS Probability(helix, strand, coil) 806 DKSVNTDNIQDNEIESNKYNTSSCSSFSISDAKNKKMNKK seq: Linear motif(s): alpha: 1111133322222322111000122210114432211000

old.protein.bio.unipd.it/cspritz/work/pid_986020641/batch/PF3D7_0926600.fasta_cspritz.html

beta: 1112111122100000012221100111100001122112

coil: 6766655555666667776677766677775556556787

SS Motif for disorder segment 11:

(start.end): (835,983)

PDF

TXT

PDE

TXT

TXT

VFVK

YNNS

YFMN

TXT

PDF

TXT

PDF

TXT

VNTDNIO

residues (790,796) LIG_FHA_1 =

residues (792,795) LIG_PDZ_3 = TDNI

Graph of Probability(helix, strand, coil)

Amino SS Probability(helix, strand, coil)

14/01/2022, 09:49

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CSpritz PID: 986020641
                                                                                                                         TXT
       835
               844
                        854
                                 864
                                          874
                                                   884
                                                             894
      IVLPKKESFIKLTNNSRNKNKHSLGSISSMNDFLNGSYEGSLKNEKKKKTNAENYGIQVGINDMSNDKLY
sea
      Linear motif(s):
alpha: 1101145678877655421111100122222222111211222222221223443111101111123322
residues (839,846) LIG_MAPK_1 =
      6678754210112234567877677655566667777666555554556664445544455556655433
                                                                                                                    KKESFIKL
       905
              914
                       924
                                934
                                          944
                                                   954
                                                            964
                                                                                            residues (865,868) LIG_PDZ_3 = NDFL
      {\tt NRDTTSIQGGIPTFDHNNREQKRIKENIQNKKFNSRDTCEGEKKERTEDSIGNHHFSLCKKCTSKKHFDG}
      residues (882,888)
                                                                                                                 LIG FHA 2=
alpha: 11001111000000011234443455555433322222211122112211223344332210222100
                                                                                                                    KKTNAEN
residues (889,892) LIG_SH2_STAT3 =
coil : 567765568876556776544454333345557765445676665567777754434455567777787
                                                                                                                         YGIO
                                                                                           residues (900,903) LIG PDZ 3 = NDKL
    : ILSKKKGTC
                                                                                                 residues (906,912) LIG_FHA_1 =
alpha: 000110000
                                                                                                                     RDTTSIQ
beta: 443110025
                                                                                                              residues (928,932)
coil: 445678863
                                                                                                  LIG APCC KENbox 2 = IKENI
                                                                                            residues (929,932) LIG_PDZ_3 = KENI
                                                                                                 residues (950,956) LIG_14-3-3_2 =
                                                                                            residues (952.955)
                                                                                                             LIG PDZ 3 = EDSI
                                                                                            residues (972,975)
                                                                                                             LIG_PDZ_3 = FDGI
SS Motif for disorder segment 12:
                                                                                            Graph of Probability(helix, strand, coil)
(start,end): (989,1001)
                                                                                                                          PDF
                                                                                            Amino SS Probability(helix, strand, coil)
       989
                                                                                                                         TXT
    : LSLNKRKSKESHL
    : ССССССССССН
alpha: 1211111112345
                                                                                                      Linear motif(s):
beta: 3321111000011
coil: 4456767776542
SS Motif for disorder segment 13:
                                                                                            Graph of Probability(helix, strand, coil)
(start,end): (1021,1025)
                                                                                            Amino SS Probability(helix, strand, coil)
                                                                                                                          TXT
seq : KKPHN
    : CCCCC
s.s.
                                                                                                      Linear motif(s):
beta : 00000
coil: 78877
SS Motif for disorder segment 14:
                                                                                            Graph of Probability(helix, strand, coil)
(start,end): (1079,1082)
                                                                                                                          PDF
                                                                                            Amino SS Probability(helix, strand, coil)
                                                                                                                         TXT
    : KNNI
S.S. : HHCC
alpha: 6544
                                                                                                      Linear motif(s):
beta : 0000
coil : 2355
SS Motif for disorder segment 15:
                                                                                            Graph of Probability(helix, strand, coil)
(start,end): (1329,1337)
                                                                                                                          PDF
                                                                                            Amino SS Probability(helix, strand, coil)
                                                                                                                          TXT
seq : IMKSRKMLF
s.s.
    : нинссссии
alpha: 654433334
                                                                                                      Linear motif(s):
beta : 111001233
coil: 224455321
SS Motif for disorder segment 16:
                                                                                            Graph of Probability(helix, strand, coil)
(start,end): (1356,1378)
                                                                                                                          PDF
                                                                                            Amino SS Probability(helix, strand, coil)
       1356
               1365
                        1375
                                                                                                                          TXT
seq : HIQMKIKEKKKKKKKKKKQRNIGK
alpha: 45555555443333333221100
                                                                                                      Linear motif(s):
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coil: 42222333455666666667899

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