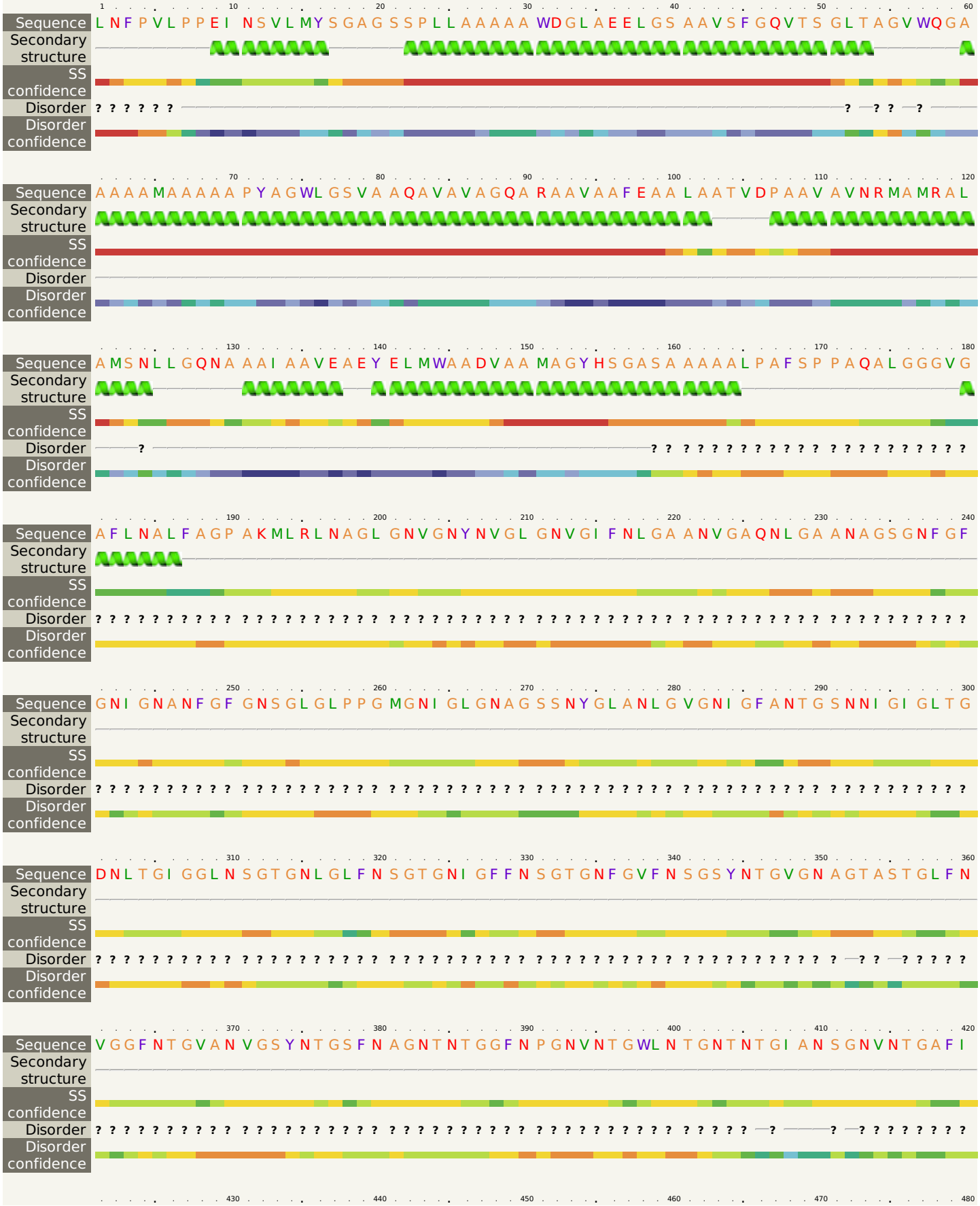
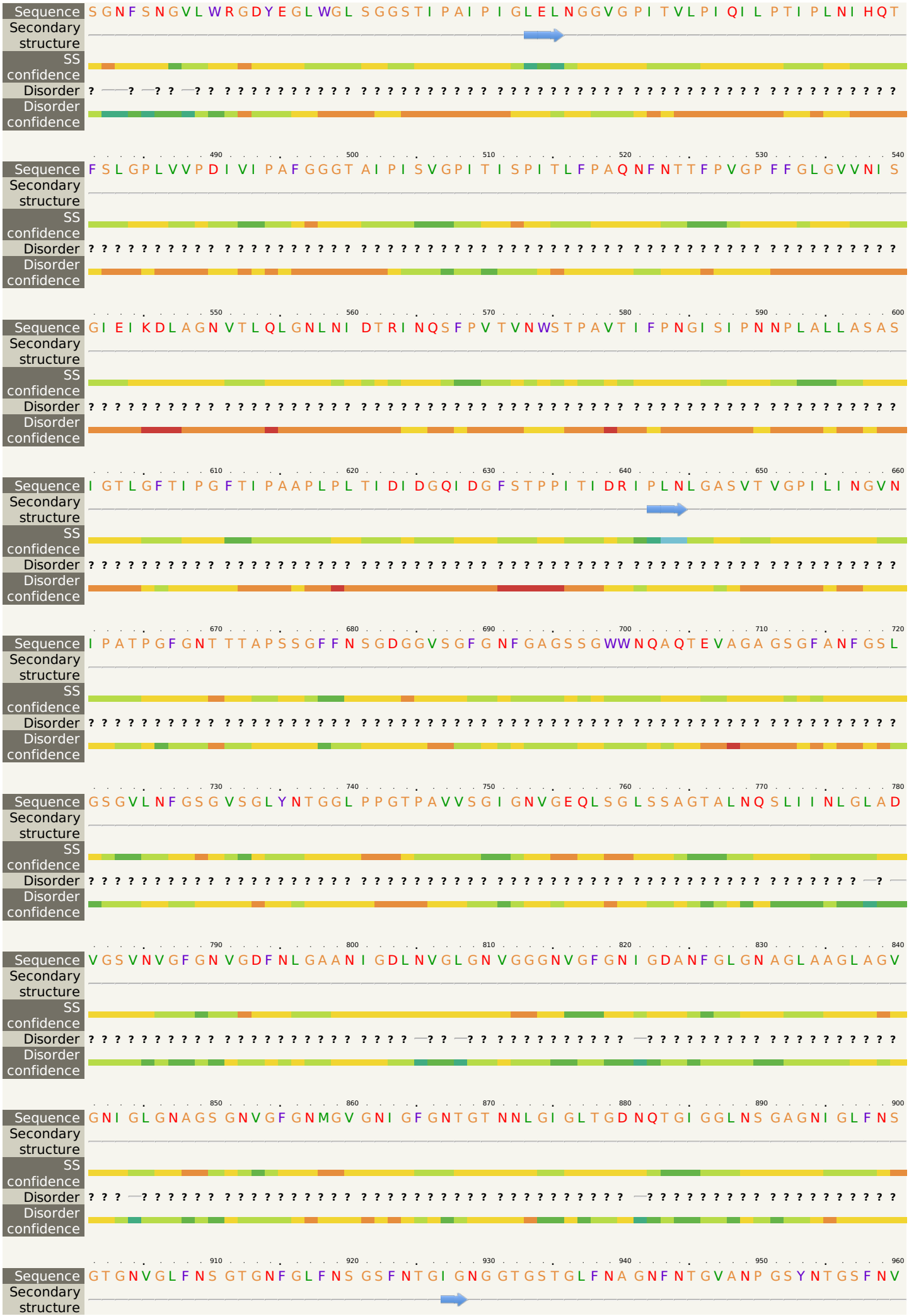
Email	mdejesus@rockefeller.edu
Description	RVBD3347c_(PPE55)_3743882_3753355
Date	Thu Aug 8 16:20:56 BST 2019
Unique Job ID	e86e9629ba82bcbf

Secondary structure and disorder prediction




Sequence
Secondary structure
SS confidence
Disorder
Disorder confidence
S G N F S N G V L W R G D Y E G L W G L S G G S T I P A I P I G L E L N G G V G P I T V L P I Q I L P T I P L N I H Q T
490 500 510 520 530 540
F S L G P L V V P D I V I P A F G G G T A I P I S V G P I T I S P I T L F P A Q N F N T T F P V G P F F G L G V V N I S
550 560 570 580 590 600
G I E I K D L A G N V T L Q L G N L N I D T R I N Q S F P V T V N W S T P A V T I F P N G I S I P N N P L A L L A S A S
610 620 630 640 650 660
I G T L G F T I P G F T I P A A P L P L T I D I D G Q I D G F S T P P I T I D R I P L N L G A S V T V G P I L I N G V N
670 680 690 700 710 720
I P A T P G F G N T T T A P S S G F F N S G D G G V S G F G N F G A G S S G W W N Q A Q T E V A G A G S G F A N F G S L
730 740 750 760 770 780
G S G V L N F G S G V S G L Y N T G G L P P G T P A V V S G I G N V G E Q L S G L S S A G T A L N Q S L I I N L G L A D
790 800 810 820 830 840
V G S V N V G F G N V G D F N L G A A N I G D L N V G L G N V G G G N V G F G N I G D A N F G L G N A G L A A G L A G V
850 860 870 880 890 900
G N I G L G N A G S G N V G F G N M G V G N I G F G N T G T N N L G I G L T G D N Q T G I G G L N S G A G N I G L F N S
910 920 930 940 950 960
G T G N V G L F N S G T G N F G L F N S G S F N T G I G N G G T G S T G L F N A G N F N T G V A N P G S Y N T G S F N V

SS confidence
Disorder
Disorder confidence
970 980 990 1000 1010 1020
Sequence GDTNTGGFNP GSI NTGWFNT GNANTGVANS GNVDTGALMS GNFSNGI LWR GNFEGLFGLN
Secondary structure
1030 1040 1050 1060 1070 1080
Sequence VGI TI PEFPI HWTSTGGI GP III PDTTI LP PI HLGLTGQA NYGFAVPDI P I PAI HI DFDG
1090 1100 1110 1120 1130 1140
Sequence AADAGFTAPA TTLLSALGI T GQFRFGPI TV SNVQLNPFNV NLKLQFLHDA FPNEFPDPTI
1150 1160 1170 1180 1190 1200
Sequence SVQI QVAI PL TSATLGGLAL PLQQTI DAI E LPAI SFSQSI PI DI PPI DI P ASTI NGI SMS
1210 1220 1230 1240 1250 1260
Sequence EVVPI DVSVDI PAVTI TGTRI DPI PLNFDV LSSAGPI NI S I I DI PALPGF GNSTELPSSG
1270 1280 1290 1300 1310 1320
Sequence FFNTGGGGGS GI ANFGAGVS GLLNQASSPM VGTLSGLGNA GSLASGVLNS GVDI SGMFNV
1330 1340 1350 1360 1370 1380
Sequence STLGSAPAVI SGFGNLGNHV SGVSI DGLLA MLTSGGSGGS GQPSI I DAAI AELRHLNPLN
1390 1400 1410 1420 1430 1440
Sequence I VNLGNVGSY NLGFANVGDV NLGAGNLGNL NLGGGNLGGQ NLGLGNLGDG NVGFGNLGHG

Disorder confidence
Sequence
Secondary structure
SS confidence
Disorder
Disorder confidence
1450 1460 1470 1480 1490 1500
NVGFGNSGLGALPGIGNIGLGNAGSNNVGFGNMGLGNIGFGNTGTNNLGIGLTGDNQTGF
1510 1520 1530 1540 1550 1560
GGLNSGAGNLGLFNSGTGNIGFFNTGTGNWGLFNSGSYNTGIGNSGTGSTGLFNAGSFNT
1570 1580 1590 1600 1610 1620
GLANAGSYNTGSLNAGNTNTGGFNPGNVNTGWFNAGHTNTGGFNTGNVNTGAFNSGSFNN
1630 1640 1650 1660 1670 1680
GALWTGDHHGLVGFSYSIEITGSTLVDINETLNLGPVHIDQIDIPGMSLFDIHELVNIGP
1690 1700 1710 1720 1730 1740
FRIEPIDVPAVVLDIHETMVIPPIVFLPSMTIGGQTYTIPLDTPPAPAPPPFRLPLLFVN
1750 1760 1770 1780 1790 1800
ALGDNWIVGASNSTGMSGGFVTAPTQGILIHTGPSSATTGSLALTLPTVTIPTITTSPIP
1810 1820 1830 1840 1850 1860
LKIDVSGGLPAFTLFPGGLNIPQNAIPLTIDASGVLDPITIFPGGFTIDPLPLSLALNIS
1870 1880 1890 1900 1910 1920
VPDSSVPIIIVPPTPGFGNATATPSSGFFNSGAGGVSGFGNFGAGSSGWWNQAHAALAGA

1930 1940 1950 1960 1970 1980
Sequence GSGVLNVGTL NSGVLNVGSGI SGLYNTAI V GLGTPALVSGAGNVGQQLSG VLAAGTALTQ
Secondary structure
SS confidence
Disorder
Disorder confidence
1990 2000 2010 2020 2030 2040
Sequence SPI I NLGLAD VGNYNLGLGN VGDF NLGAANLGDLNLGLGNI GNANVGF GNI GHGNVGF GN
Secondary structure
SS confidence
Disorder
Disorder confidence
2050 2060 2070 2080 2090 2100
Sequence SGLGAALGI G NI GLGNAGST NVGLANMGVG NI GFANTGTN NLGI GLTGDN QTGI GGLNSG
Secondary structure
SS confidence
Disorder
Disorder confidence
2110 2120 2130 2140 2150 2160
Sequence AGNI GLFNSGTGNI GFFNSGTGNWGLFNSGSFNTGI GNSGTGSTGLFNAGGFTTGLANAG
Secondary structure
SS confidence
Disorder
Disorder confidence
2170 2180 2190 2200 2210 2220
Sequence SYNTGSFNVG DTNTGGFNPGSI NTGWFNTG NANTGI ANSGNVDTGALMSGNFSNGI LWRG
Secondary structure
SS confidence
Disorder
Disorder confidence
2230 2240 2250 2260 2270 2280
Sequence NYEGLFSYSY SLDVPRI TI L DAHFTGAFGP VVVPPI PVLAI NAHLTGNAA MGAFTI PQI D
Secondary structure
SS confidence
Disorder
Disorder confidence
2290 2300 2310 2320 2330 2340
Sequence I PALNPNVTGSVGFGPI AVP SVTI PALTAA RAVLDMAASV GATSEI EPFI VWTSSGAI GP
Secondary structure
SS confidence
Disorder
Disorder confidence
2350 2360 2370 2380 2390 2400
Sequence TWYSVGRI YN AGDLFVGGNI I SGI PTLSTT GPVHAVFNAA SQAFNTPALNI HQI PLGFQV
Secondary structure
SS confidence
Disorder
Disorder confidence
2410 2420 2430 2440 2450 2460
Sequence PGSI DAI TLF PGGLTFPANS LLNLDVFVGT PGATI PAI TF PEI PANADGE LYVI AGDI PL
Secondary

structure
SS confidence
Disorder
Disorder confidence
Sequence
Secondary structure
2470 2480 2490 2500 2510 2520
I NI PPTPGI GNTTTVPSSGF FNTGAGGGSG FGNFGANMSG WWNQAHTALA GAGSGI ANVG
2530 2540 2550 2560 2570 2580
TLHSGVLNLG SGLSGI YNTS TLPLGTPALV SGLGNVGDHL SGLLASNVGQ NPI TI VNI GL
2590 2600 2610 2620 2630 2640
ANVGNGNVGL GNI GNLNLGA ANI GDVNLGF GNI GDVNLGF GNI GGGNVGF GNI GDANFGF
2650 2660 2670 2680 2690 2700
GNSGLAAGLA GMGNI GLGNA GSGNVGWANM GLGNI GFGNT GTNNLGI GLT GDNQSGI GGL
2710 2720 2730 2740 2750 2760
NSGTGNI GLF NSGTGNI GFF NSGTANFGLF NSGSYNTGI GNSGVASTGLV NAGGFNTGVA
2770 2780 2790 2800 2810 2820
NAGSYNTGSF NAGDTNTGGF NPGSTNTGWF NTGNANTGVA NAGNVNTGAL I TGNFSNGI L
2830 2840 2850 2860 2870 2880
WRGNYEGLAG FSFGYPI PLF PAVGADVTGDI GPATI I PPI HI PSI PLGFA AI GHI GPI SI
2890 2900 2910 2920 2930 2940
PNI AI PSI HL GI DPTFDVGP I TVDPI TLTI PGLSLDAAVS EI RMTSGSSS GFKVRPSFSF

Disorder
Disorder confidence
Sequence
Secondary structure
SS confidence
Disorder
Disorder confidence
2950 2960 2970 2980 2990 3000
F A V G P D G M P G G E V S I L Q P F T V A P I N L N P T T L H F P G F T I P T G P I H I G L P L S L T I P G F T I P G
3010 3020 3030 3040 3050 3060
G T L I P Q L P L G L G L S G G T P P F D L P T V V I D R I P V E L H A S T T I G P V S L P I F G F G G A P G F G N D T
3070 3080 3090 3100 3110 3120
T A P S S G F F N T G G G G G S G F S N S G S G M S G V L N A I S D P L L G S A S G F A N F G T Q L S G I L N R G A G I
3130 3140 3150
S G V Y N T G T L G L V T S A F V S G F M N V G Q Q L S G L L F A G T G P
Confidence Key
High(9) Low (0)
? Disordered (89%)
Alpha helix (4%)
Beta strand (2%)