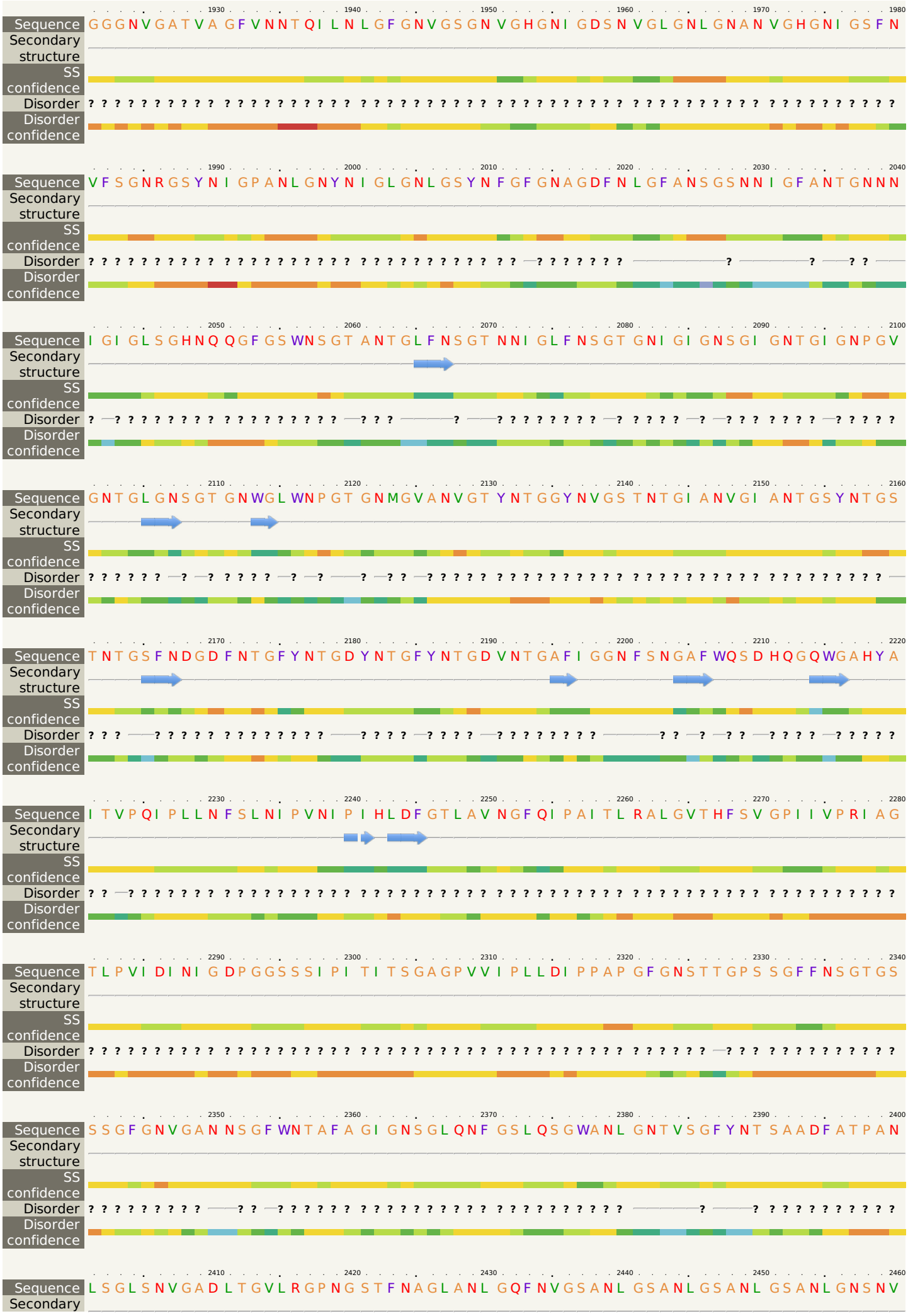
Email	mdejesus@rockefeller.edu
Description	RVBD0355c_(PPE8)_424778_434680
Date	Tue Jul 23 14:50:42 BST 2019
Unique Job ID	d4d863a0037eef76

Secondary structure and disorder prediction

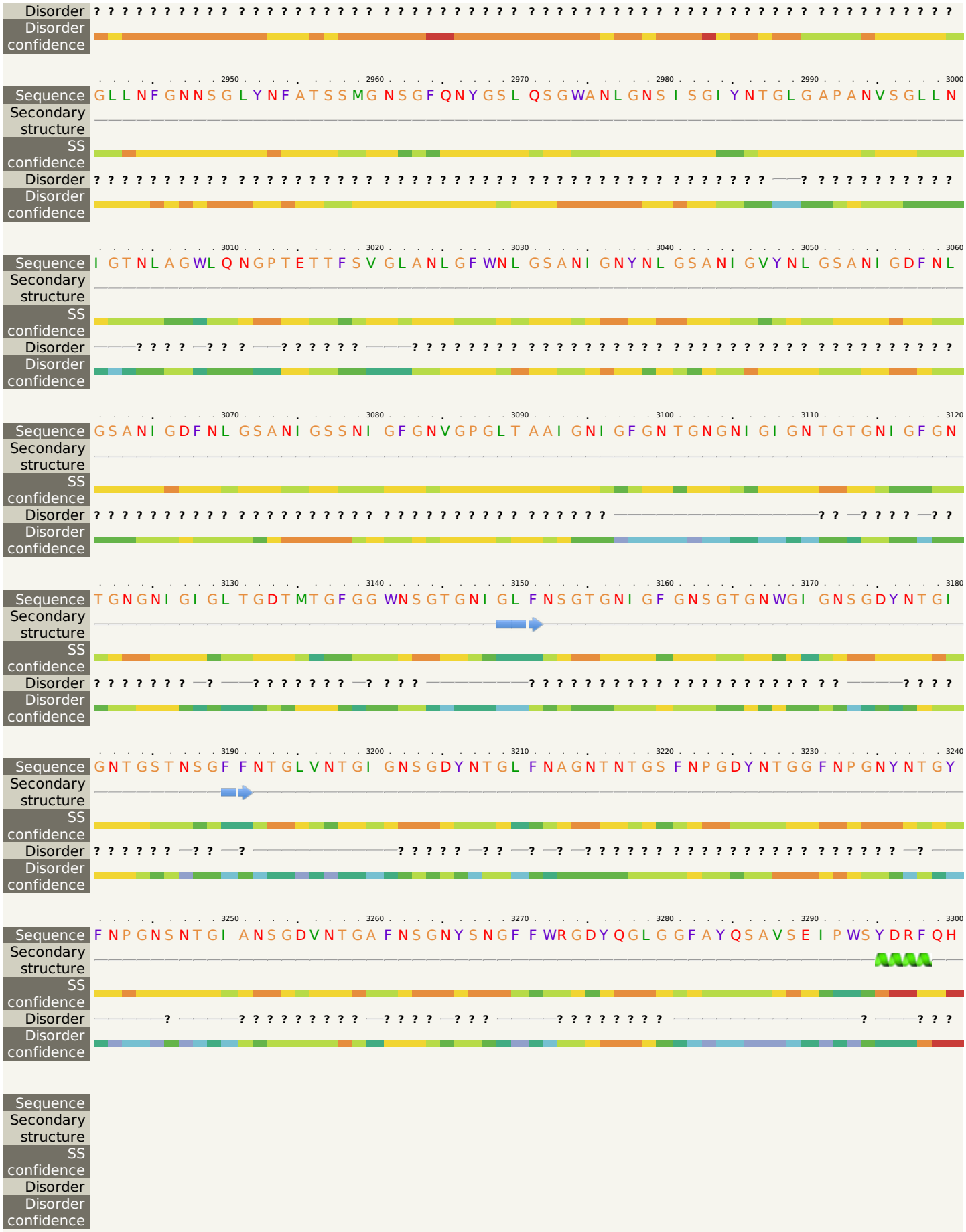
Sequence
Secondary structure
SS confidence
Disorder
Disorder confidence
RGDHQGLI FGSPGFFNSTSA PSSGFFNSGA GSASGFLNSGANNSGFFNSS SGAI GNSGLA
490 500 510 520 530 540
NAGVLVSGVI NSGNTVSGLF NMSLVAI TTP ALI SGFFNTGSNMSGFFGGP PVFNLGLANR
550 560 570 580 590 600
GVVNI LGNANI GNYNI LGSGNVGDFNI LGS GNLGSQNI LGSGNVGSFNI GSGNI GVFNVG
610 620 630 640 650 660
SGSLGNYNI GSGNLGI YNI GFGNVGDYNVGFGNAGDFNQGFANTGNNNI GFANTGNNNI G
670 680 690 700 710 720
I GLSGDNQQGFNI ASGWNSGTGNSGLFNSGTNNVGI FNAGTGNVGI ANSGTGNWGI GNPG
730 740 750 760 770 780
TDNTGI LNAGSYNTGI LNAGDFNTGFYNTGSYNTGGFNVGNTNTGNFNVGDTNTGSYNPG
790 800 810 820 830 840
DTNTGFFNPGNVNTGAFDTGDFNNGFLVAGDNQGQI AI DL SVTTPFI PI NEQMVI DVHNV
850 860 870 880 890 900
MTFGGNMI TVTEASTVFPQT FYLSGLFFFGPVNLSASTLTVPTI TLTI GGPTVTVPI SI V
910 920 930 940 950 960
GALESRTI TFLKI DPAPGI GNSTTNPSSGF FNSGTGGTSGFQNVGGGSSGVWNSGLSSAI

SS confidence
Disorder
Disorder confidence
Sequence
Secondary structure
970 980 990 1000 1010 1020
GNSGFQNLGS LQSGWANLGN SVSGFFNTST VNLSTPANVS GLNNI GTNLS GVFRGPTGTI
1030 1040 1050 1060 1070 1080
FNAGLANLGQ LNI GSANLGDFNL GSGNVGS FNVFSGNQGS YNI GPANLGNYNI GFANLGN
1090 1100 1110 1120 1130 1140
YNI GFGNAGD FNQGFANTGN NNI GFANTGN NNI GI GLSGD NQQGFNFAGG WNSGTANI GL
1150 1160 1170 1180 1190 1200
FNSGTNNVGI GNSGTGNWGI GNSGSGNTGI GNTGSTNTGF FNTGI VNTGV ANAGSYNTGW
1210 1220 1230 1240 1250 1260
YNTGDTNTGI ANLGDFNTGF YNTGNFSTGF ANQGDI ATGA FI TGDMGNGA FWRGDQQGLF
1270 1280 1290 1300 1310 1320
SAGYRVHVPE I PAHVTVEVP VNI PI TASFT NTVYSGI TLE QI NFGFTI DI AGI PLLAGAI
1330 1340 1350 1360 1370 1380
SKAVLPPI TGTGPAI TVNI GDPGGSTAI RI PATASVGPFDVTFVNI AATT GFFNATTDPS
1390 1400 1410 1420 1430 1440
SGFFNGGPGT VSGI ANI GANI SGFQNVANS ATSGFNNYGS LQSGLANLGD TVSGVFNTGI

Disorder confidence
1450 1460 1470 1480 1490 1500
Sequence GAPANVSGMF NI GSNLAGFF HDQATGMSMF NLGLGNI GQF NVGFSNVGDS NAGLANI GSF
Secondary structure
SS confidence
Disorder
Disorder confidence
1510 1520 1530 1540 1550 1560
Sequence NLGSGNLGSF NVFGGNQGSY NI GPANLGNY NI GLGNLGSY NFGFGNAGDF NLGFANTGNN
Secondary structure
SS confidence
Disorder
Disorder confidence
1570 1580 1590 1600 1610 1620
Sequence NI GFANTGNN NI GI GLSGDN QQGFNFAGGWNSGSGNSGLF NSGTNNI GLF NSGTGNI GI G
Secondary structure
SS confidence
Disorder
Disorder confidence
1630 1640 1650 1660 1670 1680
Sequence NSGTGNWGI A NTGDTNTGI F NTGDVNTGLL NAGNVNTGI F NTGHYNTGSF NAGSFNTAGF
Secondary structure
SS confidence
Disorder
Disorder confidence
1690 1700 1710 1720 1730 1740
Sequence NPGSYNTGYL NTGSYNTGLA NSGDVNTGGF I TGNYSNGF WWRGDYQGLAGI SQTI TVPDT
Secondary structure
SS confidence
Disorder
Disorder confidence
1750 1760 1770 1780 1790 1800
Sequence AVPVKLHVPI FLDI PVTGTL GTFTVHGFRF PEI TGDI FLI GI PFNAATLDAFSFPNI SI V
Secondary structure
SS confidence
Disorder
Disorder confidence
1810 1820 1830 1840 1850 1860
Sequence LPNI GI NLGS GPDPLI DI AGTGGLLPI KI P LI DI PAAPGF GNSTTTPSSGFFNAGTGTVS
Secondary structure
SS confidence
Disorder
Disorder confidence
1870 1880 1890 1900 1910 1920
Sequence GVGNVGSNSS GFFNLTSGSS GI SGVQNFGE LI SGGFNFGN TVSGLVNAST LGLSMPANLS
Secondary structure
SS confidence
Disorder
Disorder confidence


Sequence
Secondary structure
SS confidence
Disorder
Disorder confidence
1930 1940 1950 1960 1970 1980
GGGNVGATVA GFVNNTQI LNLGFGNVGS GNVGHGNI GDSNVGLGNL GNANVGHGNI GSFN
1990 2000 2010 2020 2030 2040
VFSGNRGSYN IGPANLGNYN IGLGNLGSYN FGFGNAGDFN LGFANSGSNN IGFANTGNNN
2050 2060 2070 2080 2090 2100
IGIGLSGHNQ QGFGSWNSGT ANTGLFNSGT NNIGLFNSGT GNIGIGNSGI GNTGIGNPGV
2110 2120 2130 2140 2150 2160
GNTGLGNSGT GNWGLWNPGT GNMGVANVGT YNTGGYNVGS TNTGIANVGI ANTGSYNTGS
2170 2180 2190 2200 2210 2220
TNTGSFNDGD FNTGFYNTGD YNTGFYNTGD VNTGAFIGGN FSNGAFWQSD HQGQWGAHYA
2230 2240 2250 2260 2270 2280
ITVPQIPLLN FSLNIPVNIP IHLDFGTLAV NGFQIPAITL RALGVTHFSV GPIIVPRIAG
2290 2300 2310 2320 2330 2340
TLPVIDINIG DPGGSSSIPI TITSGAGPVV IPLLDIPPAP GFGNSTTGPS SGFFNSGTGS
2350 2360 2370 2380 2390 2400
SSGFGNVGAN NSGFWNTAFA GIGNSGLQNF GSLQSGWANL GNTVSGFYNT SAADFATPAN
2410 2420 2430 2440 2450 2460
LSGLSNVGAD LTGVLRGPNG STFNAGLANL GQFNVGSANL GSANLGSANL GSANLGNSNV

structure
SS confidence
Disorder
Disorder confidence
Sequence
Secondary structure
2470 2480 2490 2500 2510 2520
GFGNI GNANI GGANI GDFNV GI ANTGPGLT AAVNNI GI GNTGNYNI GVGNTGNYNI GFGN
2530 2540 2550 2560 2570 2580
TGNNNI GI GL SGDNQI GFGP LNAGI ANMGL FNLGDNNFGMANAGNFNQGI ANTGNNNI GL
2590 2600 2610 2620 2630 2640
FNTGNNNVGI GLTGDGLSGF SSLNSGAGNT GFFNSGTANT GLFNSGTGNT GLFNSGTGNV
2650 2660 2670 2680 2690 2700
GI GNMGTGGF GVGLSGDSQV GI GGTNSGSF NI GLFNSGTGNVGI GNSGTGNVGI GNTGTG
2710 2720 2730 2740 2750 2760
NTGI GNSGNY NTGLLNAGLV NTGI ANPGNH NTGLFNI GTF NTGI ANPGHY NTGSYNTGSY
2770 2780 2790 2800 2810 2820
NTGMANAGDY GTGAFI TGSMNNGLLWRADR QGLLAANYTI TI ERPAAFLNVDI PVNI PIT
2830 2840 2850 2860 2870 2880
GDI TNVSI PAI TFPRI DASGSVDI GI LSGT VLAPVGPI TL HGGDASAPLDTPI EI DFGPS
2890 2900 2910 2920 2930 2940
PAI NLNI GKP DGSTVI NI VGGAGAGPI SI PIIDLRPAPGF FNATTGPSSGFLNWGAGSAS


Disorder
Disorder confidence
Sequence
Secondary structure
SS confidence
2950 2960 2970 2980 2990 3000
GLLNFGNNSGLYNFATSSMGNSGFQNYGSLQSGWANLGNSISGIYNTGLGAPANVSGLLN
3010 3020 3030 3040 3050 3060
IGTNLAGWLQNGPTETTFSVGLANLGFWNLGSANIGNYNLGSANIGVYNLGSANIGDFNL
3070 3080 3090 3100 3110 3120
GSANIGDFNLGSANIGSSNIGFGNVGPGLTAAIGNIGFGNTGNGNIGIGNTGTGNIGFGN
3130 3140 3150 3160 3170 3180
TGNGNIGIGLTGDTMTGFGGWNSGTGNIGLFNSGTGNIGFGNSGTGNWGIGNSGDYNTGI
3190 3200 3210 3220 3230 3240
GNTGSTNSGFFNTGLVNTGIGNSGDYNTGLFNAGNTNTGSFNPGDYNTGGFNPGNYNTGY
3250 3260 3270 3280 3290 3300
FNPGNSNTGIANSGDVNTGAFNSGNYSNGFFWRGDYQGLGGFAYQSAVSEIPWSYDRFQH
Confidence Key
High(9) Low (0)
? Disordered (85%)
Alpha helix (4%)
Beta strand (3%)
TM helix (0%)