Phyre2

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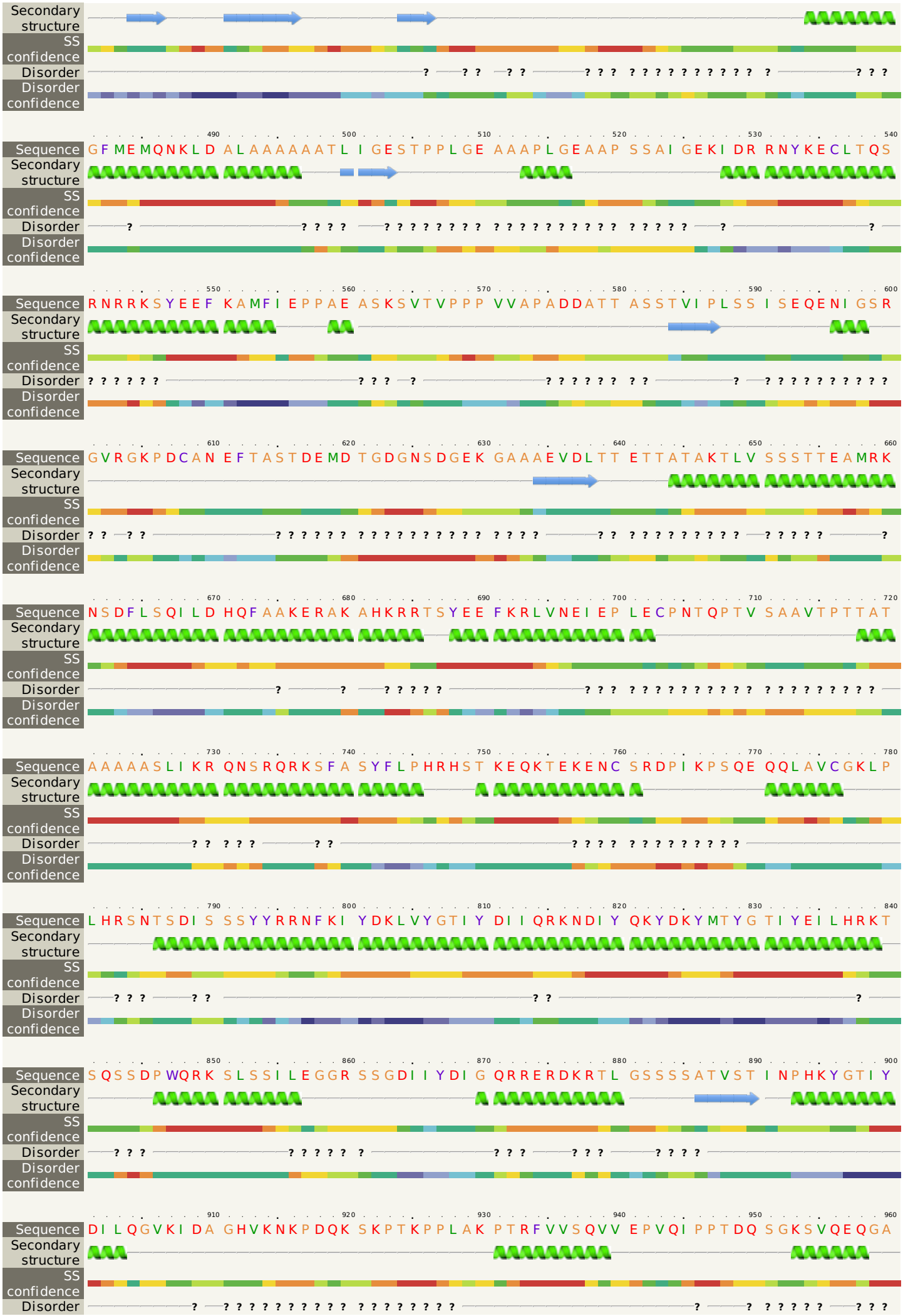
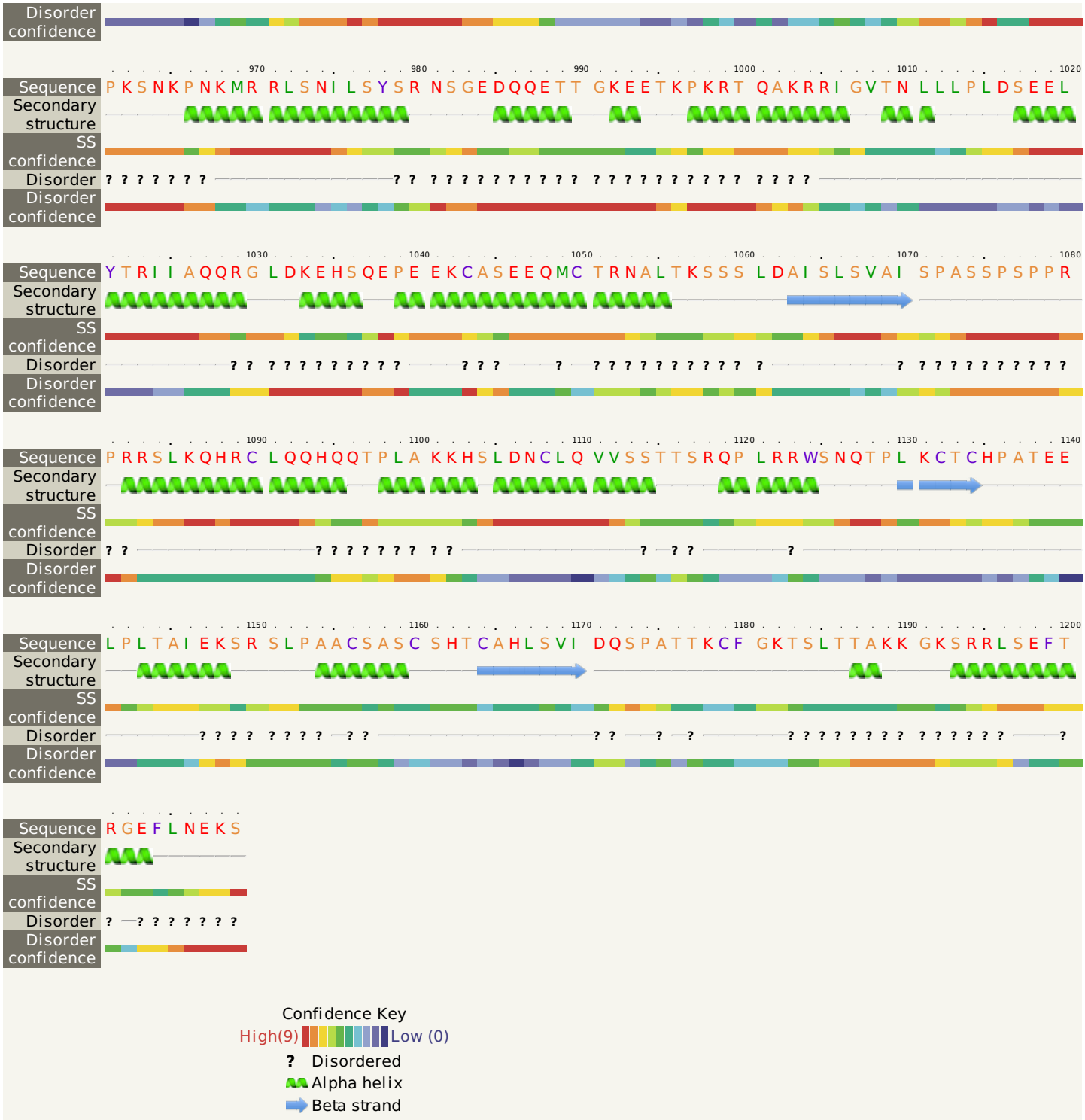
Description	A1Z6I9
Date	Tue Jan 22 12:00:06 GMT 2013
Unique Job ID	e856bc3d2f8076dd

Secondary structure and disorder prediction


Secondary structure
SS confidence
Disorder
Disorder confidence
Sequence
490 500 510 520 530 540
GFMEMQNKLD ALAAAAAATL IGESTPPLGE AAAPLGEAAP SSAIGEKIDR RNYKECLTQS
550 560 570 580 590 600
RNRRKSYEEF KAMFIEPPAE ASKSVTVPPP VVAPADDATT ASSTVIPLSS ISEQENIGSR
610 620 630 640 650 660
GVRGKPDCAN EFTASTDEMD TGDGNSDGEK GAAAEVDLTT ETTATAKTLV SSSTTEAMRK
670 680 690 700 710 720
NSDFLSQILD HQFAAKERAK AHKRRTSYEE FKRLVNEIEP LECPNTQPTV SAAVTPTTAT
730 740 750 760 770 780
AAAAASLIKR QNSRQRKSFA SYFLPHRHST KEQKTEKENC SRDPIKPSQE QQLAVCGKLP
790 800 810 820 830 840
LHRSNTSDIS SSYYRRNFKI YDKLVYGTIY DIIQRKNDIY QKYDKYMTYG TIYEILHRKT
850 860 870 880 890 900
SQSSDPWQRK SLSSILEGGR SSGDIIYDIG QRRERDKRTL GSSSSATVST INPHKYGTIY
910 920 930 940 950 960
DILQGVKIDA GHVKNKPDQK SKPTKPPLAK PTRFVVSQVV EPVQIPPTDQ SGKSVQEQGA


Disorder confidence
Sequence
Secondary structure
SS confidence
Disorder
Disorder confidence
970 980 990 1000 1010 1020
P K S N K P N K M R R L S N I L S Y S R N S G E D Q Q E T T G K E E T K P K R T Q A K R R I G V T N L L L P L D S E E L
1030 1040 1050 1060 1070 1080
Y T R I I A Q Q R G L D K E H S Q E P E E K C A S E E Q M C T R N A L T K S S S L D A I S L S V A I S P A S S P S P P R
1090 1100 1110 1120 1130 1140
P R R S L K Q H R C L Q Q H Q Q T P L A K K H S L D N C L Q V V S S T T S R Q P L R R W S N Q T P L K C T C H P A T E E
1150 1160 1170 1180 1190 1200
L P L T A I E K S R S L P A A C S A S C S H T C A H L S V I D Q S P A T T K C F G K T S L T T A K K G K S R R L S E F T
R G E F L N E K S
Confidence Key
High(9) Low (0)
? Disordered
Alpha helix
Beta strand