Phyre²

Email	l.a.kelley@imperial.ac.uk
Description	P76558
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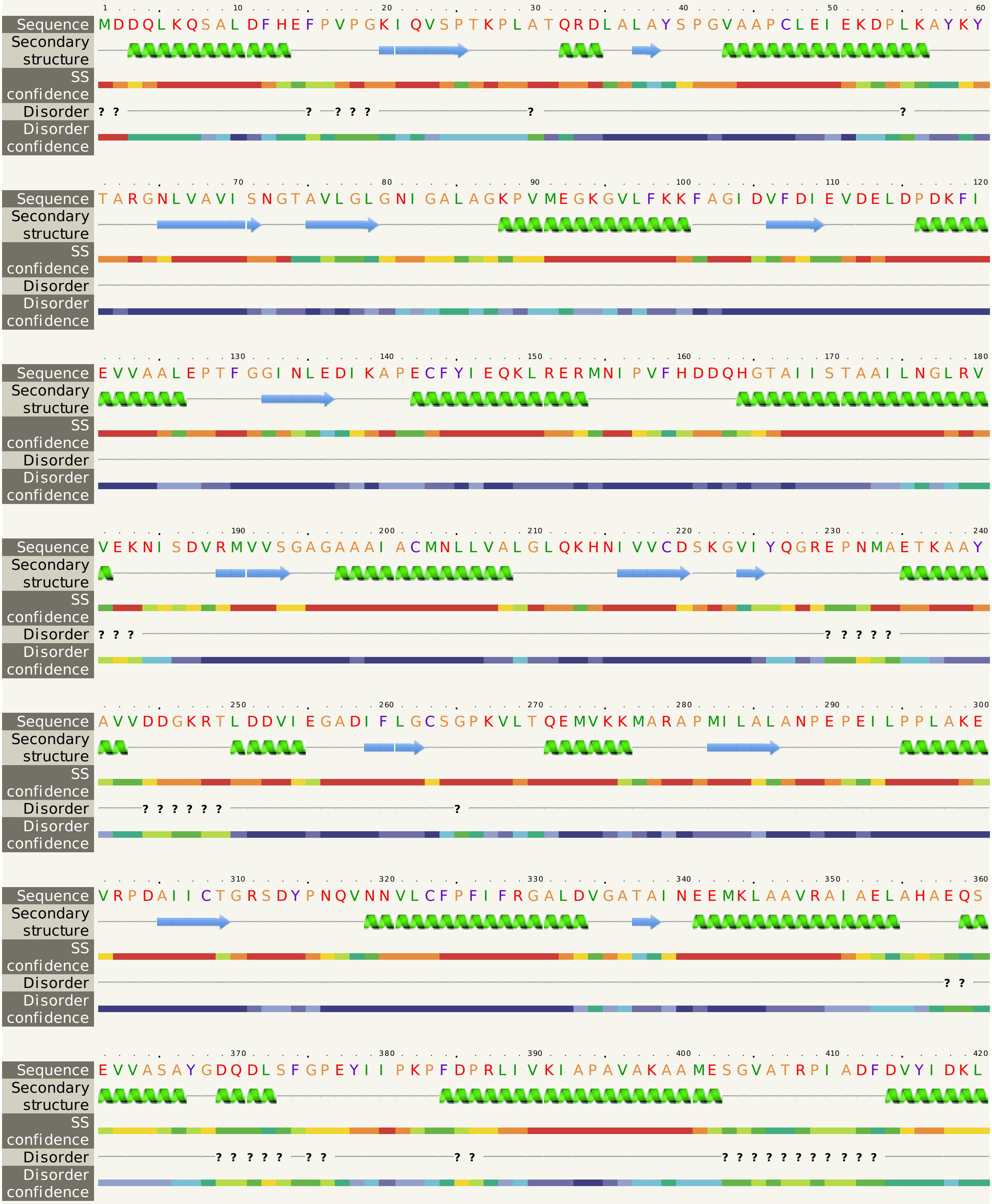
Unique Job ID	3e1b2ff60c958c08

Secondary structure and disorder prediction



Sequence 1–60: M D D Q L K Q S A L D F H E F P V P G K I Q V S P T K P L A T Q R D L A L A Y S P G V A A P C L E I E K D P L K A Y K Y

Sequence 61–120: T A R G N L V A V I S N G T A V L G L G N I G A L A G K P V M E G K G V L F K K F A G I D V F D I E V D E L D P D K F I

Sequence 121–180: E V V A A L E P T F G G I N L E D I K A P E C F Y I E Q K L R E R M N I P V F H D D Q H G T A I I S T A A I L N G L R V

Sequence 181–240: V E K N I S D V R M V V S G A G A A A I A C M N L L V A L G L Q K H N I V V C D S K G V I Y Q G R E P N M A E T K A A Y

Sequence 241–300: A V V D D G K R T L D D V I E G A D I F L G C S G P K V L T Q E M V K K M A R A P M I L A L A N P E P E I L P P L A K E

Sequence 301–360: V R P D A I I C T G R S D Y P N Q V N N V L C F P F I F R G A L D V G A T A I N E E M K L A A V R A I A E L A H A E Q S

Sequence 361–420: E V V A S A Y G D Q D L S F G P E Y I I P K P F D P R L I V K I A P A V K A A M E S G V A T R P I A D F D V Y I D K L


430 440 450 460 470 480
Sequence TEFVYKTNLFMKPIFSQARKAPKRVVLPEGEEARVLHATQELVTLGLAKPILIGRPNVIE
Secondary structure
SS confidence
Disorder ? ?
Disorder confidence
490 500 510 520 530 540
Sequence MRIQKLGLQIKAGVDFEIVNNESDPRFKEYWTEYFQIMKRRGVTQEQAQRALISNPTVIG
Secondary structure
SS confidence
Disorder ? ? ?
Disorder confidence
550 560 570 580 590 600
Sequence AIMVQRGEADAMICGTVGDYHEHFSVVKNVFGYRDGVHTAGAMNALLLPSGNTFIADTYV
Secondary structure
SS confidence
Disorder ? ?
Disorder confidence
610 620 630 640 650 660
Sequence NDEPDAEELAEITLMAAETVRRFGIEPRVALLSHSNFGSSDCPSSSKMRQALELVRERAP
Secondary structure
SS confidence
Disorder ? ? ? ? ? ? ? ? ?
Disorder confidence
670 680 690 700 710 720
Sequence ELMIDGEMHGDAALVEAIRNDRMPDSSLKGSANILVMPNMEAARISYNLLRVSSSEGVTV
Secondary structure
SS confidence
Disorder ? ?
Disorder confidence
730 740 750
Sequence GPVLMGVAKPVHVLTPIASVRRIVNMVALAVVEAQTQPL
Secondary structure
SS confidence
Disorder ? ? ? ? ? ?
Disorder confidence
Confidence Key
High(9)
Low (0)
? Disordered
Alpha helix
Beta strand