Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3806c_(-)_4269103_4270011
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Secondary structure and disorder prediction

Position	Sequence
1–60	M S E D V V T Q P P A N L V A G V V K A I R P R Q W V K N V L V L A A P L A A L G G G V R Y D Y V E V L S K V S M A F V
61–120	V F S L A A S A V Y L V N D V R D V E A D R E H P T K R F R P I A A G V V P E W L A Y T V A V V L G V T S L A G A W M L
121–180	T P N L A L V M V V Y L A M Q L A Y C F G L K H Q A V V E I C V V S S A Y L I R A I A G G V A T K I P L S K W F L L I M
181–240	A F G S L F M V A G K R Y A E L H L A E R T G A A I R K S L E S Y T S T Y L R F V W T L S A T A V V L C Y G L W A F E R
241–300	D G Y S G S W F A V S M I P F T I A I L R Y A V D V D G G L A G E P E D I A L R D R V L Q L L A L A W I A T V G A A V A
301–302	F G

Rows per block: Sequence, Secondary structure, SS confidence, Disorder, Disorder confidence

Confidence Key

High(9) … Low (0)

? Disordered (11%)

Alpha helix (75%)

Beta strand (0%)

TM helix (57%)