Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1067c_(PE_PGRS19)_1188426_1190429
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Unique Job ID	98d236198b1377c6

Secondary structure and disorder prediction

430 440 450 460 470 480

Sequence LYGNGGAGGAGNSGGDGGTGLNAALGGNGGGGGVGGNAGAGGTGGSAGWLSGNGGAGGSG
Secondary structure
SS confidence
Disorder ??
Disorder confidence

490 500 510 520 530 540

Sequence GSAGAGGAGGKGGDTPNGLAINPGIGGNGGDTGNAGNGGNGGSAARLFGGGGAGGAGGTG
Secondary structure
SS confidence
Disorder ??
Disorder confidence

550 560 570 580 590 600

Sequence STAGSGGSGGTNPPTGLQAAGGNGGSGHAGGHGGNGGGAGLLGGGGTGGNGGGGGQGGLG
Secondary structure
SS confidence
Disorder ??
Disorder confidence

610 620 630 640 650 660

Sequence AAAGGVDGNGGNGGNGGKGGDAQLVGDGGNGGNGGKGGAGLIAGLDGAGGAGGTRGLIFG
Secondary structure
SS confidence
Disorder ??
Disorder confidence

Sequence NAGTPGQ
Secondary structure
SS confidence
Disorder ???????
Disorder confidence

Confidence Key

High(9) Low (0)

? Disordered (87%)

Alpha helix (15%)

Beta strand (1%)