Phyre²

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Description	Dangers_of_Intensive
Date	Sun Sep 7 17:29:03 BST 2014
Unique Job ID	093f1646326a5fe1

Secondary structure and disorder prediction

Confidence Key

High(9) 🟥🟧🟨🟩🟦🟪 Low (0)

CDD sites

High(9) 🟥🟧🟨🟨🟩🟩🟦🟦🟪🟪 Low (0)

• putative proteinase inhibition site

? Disordered (41%)

Alpha helix (33%)

➡ Beta strand (31%)

TM helix (6%)