Phyre2

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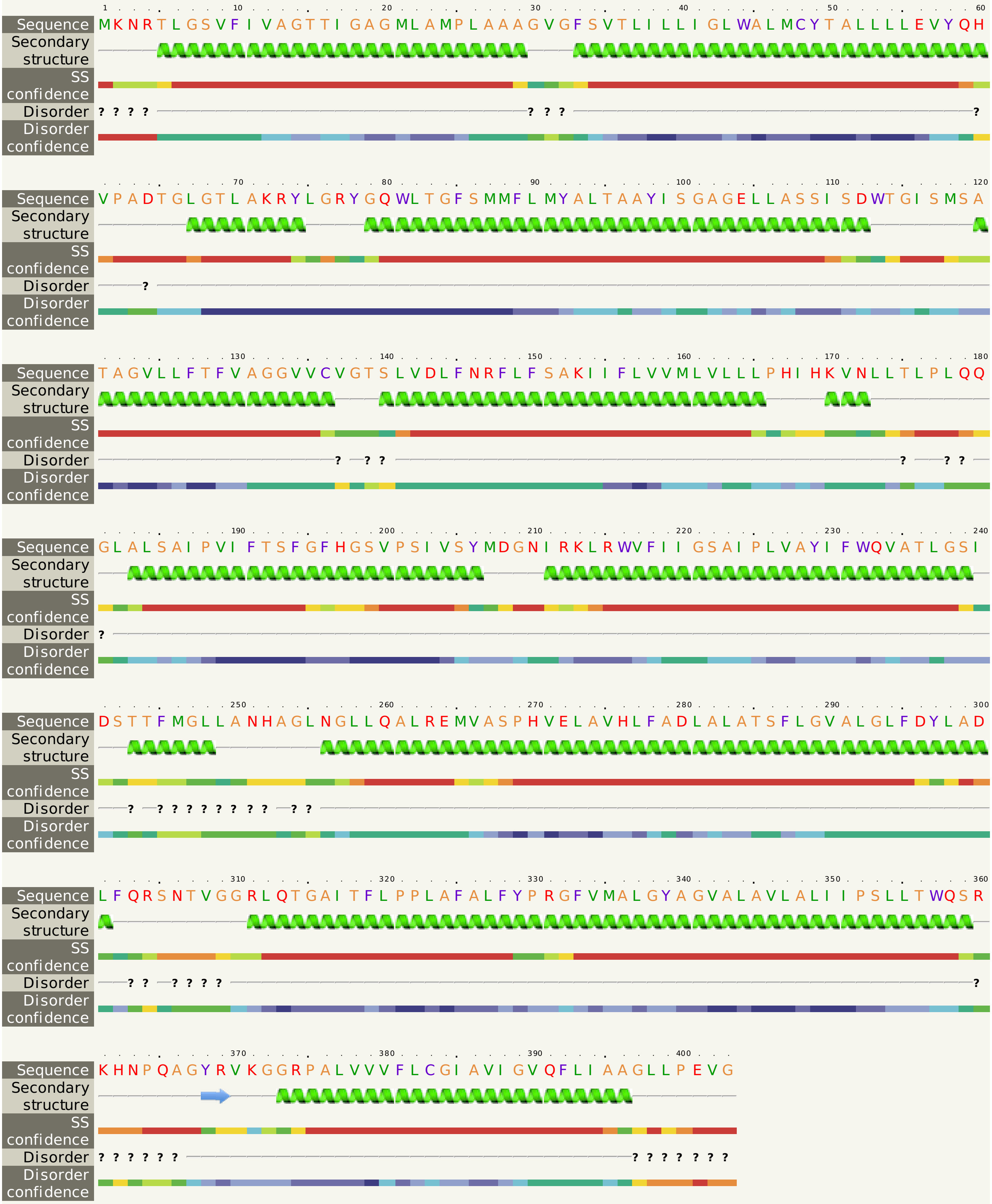
Description	P0AAD4
Date	Thu Jan 5 11:12:36 GMT 2012
Unique Job ID	7077d9a850922332

Secondary structure and disorder prediction



1-60
Sequence: MKNRTLGSVFIVAGTTIGAGMLAMPLAAAGVGFSVTLILLIGLWALMCYTALLLLEVYQH
Disorder: ? ? ? ? ? ? ? ?

61-120
Sequence: VPADTGLGTLAKRYLGRYGQWLTGFSMMFLMYALTAAYISGAGELLASSISDWTGISMSA
Disorder: ?

121-180
Sequence: TAGVLLFTFVAGGVVCVGTSLVDLFNRFLFSAKIIFLVVMLVLLLPHIHKVNLLTLPLQQ
Disorder: ? ? ? ? ? ?

181-240
Sequence: GLALSAIPVIFTSFGFHGSVPSIVSYMDGNIRKLRWVFIIGSAIPLVAYIFWQVATLGSI
Disorder: ?

241-300
Sequence: DSTTFMGLLANHAGLNGLLQALREMVASPHVELAVHLFADLALATSFLGVALGLFDYLAD
Disorder: ? ? ? ? ? ? ? ? ? ? ?

301-360
Sequence: LFQRSNTVGGRLQTGAITFLPPLAFALFYPRGFVMALGYAGVALAVLALIIPSLLTWQSR
Disorder: ? ? ? ? ? ? ?

361-403
Sequence: KHNPQAGYRVKGGRPALVVVFLCGIAVIGVQFLIAAGLLPEVG
Disorder: ? ? ? ? ? ? ? ? ? ? ? ? ?

Confidence Key
High(9) 🟥🟧🟨🟩🟩🟩🟦🟦🟪🟪 Low (0)
? Disordered
〰 Alpha helix
➡ Beta strand