Phyre2

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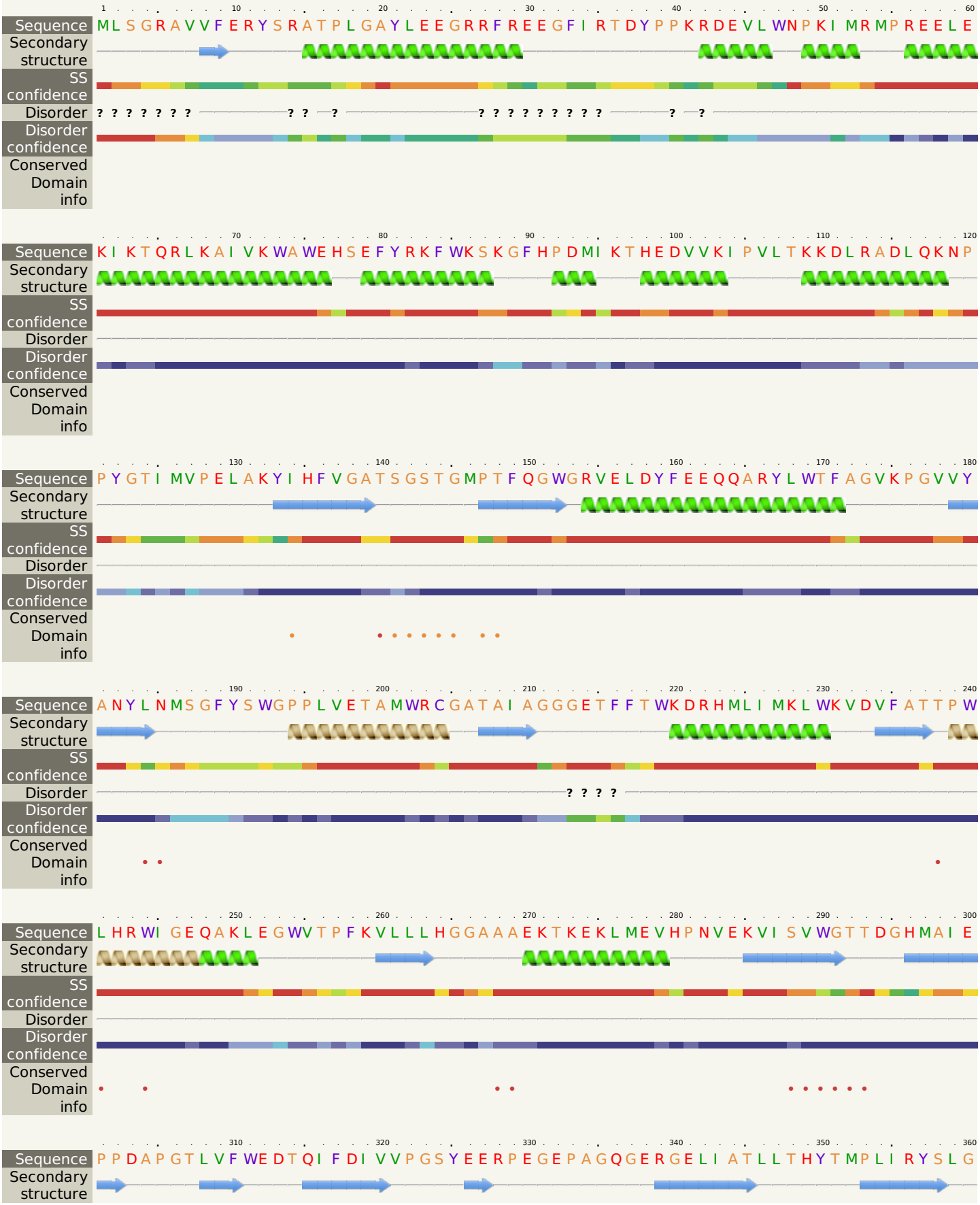
Description	Igni_0379
Date	Sat Jun 20 19:05:36 BST 2015
Unique Job ID	a7f612e2257f23f7

Secondary structure and disorder prediction



SS confidence
Disorder
Disorder confidence
Conserved Domain info
Sequence
Secondary structure
370 380 390 400 410 420
DYVKNEFI CDPTPELGI THCRFAELI PGRVEWMF KVKGKLLFPI VVENAVSQI PDTTGAY
430 440 450 460 470 480
NI VVYDDNMDKLKI KVETRKPI PPPPEYDKEAREI I AREL GLSPEDVEI EWI RPGESVWK
490
GYKLQVFLDERKK
Confidence Key
CDD sites
AMP binding site
active site
CoA binding site
acyl-activating enzyme (AAE) consensus motif
High(9)
Low (0)
Disordered (7%)
Alpha helix (33%)
Beta strand (25%)
TM helix (9%)