

Email	l.a.kelley@imperial.ac.uk
Description	P16683
Date	Thu Jan 5 11:35:28 GMT 2012
Unique Job ID	b31cae06aa5efc9d

	1	10	20	30	40	50	60																																																					
Sequence	M	Q	T	I	T	I	A	P	P	K	R	S	W	F	S	L	L	S	W	A	V	V	L	A	V	L	V	V	S	W	Q	G	A	E	M	A	P	L	T	L	I	K	D	G	G	N	M	A	T	F	A	A	D	F	F	P	P	D	F	S
Secondary structure											[Alpha Helix]										[Alpha Helix]					[Alpha Helix]										[Alpha Helix]																								
SS confidence											[High]										[High]					[High]										[High]																								
Disorder	[Disordered]										[Ordered]										[Ordered]					[Ordered]										[Ordered]																								
Disorder confidence	[Low]										[High]										[High]					[High]										[High]																								

	70	80	90	100	110	120																																																						
Sequence	Q	W	Q	D	Y	L	T	E	M	A	V	T	L	Q	I	A	V	W	G	T	A	L	A	V	V	L	S	I	P	F	G	L	M	S	A	E	N	L	V	P	W	W	V	Y	Q	P	V	R	R	L	M	D	A	C	R	A	I	N	E	M
Secondary structure	[Alpha Helix]															[Alpha Helix]										[Alpha Helix]																																		
SS confidence	[High]															[High]										[High]																																		
Disorder	[Ordered]															[Ordered]										[Ordered]																																		
Disorder confidence	[High]															[High]										[High]																																		

	130	140	150	160	170	180																																																						
Sequence	V	F	A	M	L	F	V	V	A	V	G	L	G	P	F	A	G	V	L	A	L	F	I	H	T	T	G	V	L	S	K	L	L	S	E	A	V	E	A	I	E	P	G	P	V	E	G	I	R	A	T	G	A	N	K	L	E	E	I	L
Secondary structure	[Alpha Helix]										[Alpha Helix]										[Alpha Helix]										[Alpha Helix]																													
SS confidence	[High]										[High]										[High]										[High]																													
Disorder	[Ordered]										[Ordered]										[Ordered]										[Ordered]																													
Disorder confidence	[High]										[High]										[High]										[High]																													


  

	190	200	210	220	230	240																																																						
Sequence	Y	G	V	L	P	Q	V	M	P	L	L	I	S	Y	S	L	Y	R	F	E	S	N	V	R	S	A	T	V	V	G	M	V	G	A	G	G	I	G	V	T	L	W	E	A	I	R	G	F	Q	F	Q	Q	T	C	A	L	M	V	L	I
Secondary structure	[Alpha Helix]															[Alpha Helix]										[Alpha Helix]																																		
SS confidence	[High]															[High]										[High]																																		
Disorder	[Ordered]															[Ordered]										[Ordered]																																		
Disorder confidence	[High]															[High]										[High]																																		


  


	250																		
Sequence	I	V	T	V	S	L	L	D	F	L	S	Q	R	L	R	K	H	F	I
Secondary structure	[Alpha Helix]																		
SS confidence	[High]																		
Disorder	[Ordered]																		
Disorder confidence	[High]																		

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand