

Email	l.a.kelley@imperial.ac.uk
Description	P36771
Date	Thu Jan 5 11:53:52 GMT 2012
Unique Job ID	ceb833048838d9b8

	1	10	20	30	40	50	60																																																					
Sequence	M	I	S	A	N	R	P	I	I	N	L	D	L	D	L	R	T	F	V	A	V	A	D	L	N	T	F	A	A	A	A	A	V	C	R	T	Q	S	A	V	S	Q	Q	M	Q	R	L	E	Q	L	V	G	K	E	L	F	A	R		
Secondary structure											[Alpha Helix]										[Alpha Helix]										[Alpha Helix]										[Coiled-coil]																			
SS confidence	[Confidence bars]																																																											
Disorder	[Disorder prediction]																																																											
Disorder confidence	[Disorder confidence bars]																																																											

	70	80	90	100	110	120																																																						
Sequence	H	G	R	N	K	L	L	T	E	H	G	I	Q	L	L	G	Y	A	R	K	I	L	R	F	N	D	E	A	C	S	S	L	M	F	S	N	L	Q	G	V	L	T	I	G	A	S	D	E	S	A	D	T	I	L	P	F	L	L	N	R
Secondary structure	[Loop]		[Loop]		[Alpha Helix]										[Loop]										[Alpha Helix]																																			
SS confidence	[Confidence bars]																																																											
Disorder	[Disorder prediction]																																																											
Disorder confidence	[Disorder confidence bars]																																																											

	130	140	150	160	170	180																																																						
Sequence	V	S	S	V	P	K	L	A	L	D	V	R	V	K	R	N	A	Y	M	A	E	M	L	E	S	Q	E	V	D	L	M	V	T	T	H	R	P	S	A	F	K	A	L	N	L	R	T	S	P	T	H	W	Y	C	A	A	E	Y	I	
Secondary structure	[Alpha Helix]		[Loop]										[Alpha Helix]										[Loop]										[Alpha Helix]										[Loop]																	
SS confidence	[Confidence bars]																																																											
Disorder	[Disorder prediction]																																																											
Disorder confidence	[Disorder confidence bars]																																																											

	190	200	210	220	230	240																																																						
Sequence	L	Q	K	G	E	P	I	P	L	V	L	L	D	D	P	S	P	F	R	D	M	V	L	A	T	L	N	K	A	D	I	P	W	R	L	A	Y	V	A	S	T	L	P	A	V	R	A	A	V	K	A	G	L	G	V	T	A	R	P	V
Secondary structure	[Alpha Helix]		[Loop]										[Alpha Helix]										[Loop]										[Alpha Helix]										[Loop]																	
SS confidence	[Confidence bars]																																																											
Disorder	[Disorder prediction]																																																											
Disorder confidence	[Disorder confidence bars]																																																											

	250	260	270	280	290	300																																																						
Sequence	E	M	M	S	P	D	L	R	V	L	S	G	V	D	G	L	P	P	L	P	D	T	E	Y	L	L	C	Y	D	P	S	S	N	N	E	L	A	Q	V	I	Y	Q	A	M	E	S	Y	H	N	P	W	Q	Y	S	P	M	S	A	P	E
Secondary structure	[Alpha Helix]		[Loop]										[Alpha Helix]										[Alpha Helix]																																					
SS confidence	[Confidence bars]																																																											
Disorder	[Disorder prediction]																																																											
Disorder confidence	[Disorder confidence bars]																																																											

	310											
Sequence	G	D	D	S	L	L	I	E	R	D	I	E
Secondary structure	[Loop]											
SS confidence	[Confidence bars]											
Disorder	[Disorder prediction]											
Disorder confidence	[Disorder confidence bars]											

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand