

Email	l.a.kelley@imperial.ac.uk
Description	P16433
Date	Thu Jan 5 11:35:09 GMT 2012
Unique Job ID	846d9a7ae17a6117

	1	10	20	30	40	50	60																																																					
Sequence	M	S	N	L	L	G	P	R	D	A	N	G	I	P	V	P	M	T	V	D	E	S	I	A	S	M	K	A	S	L	L	K	K	I	K	R	S	A	Y	V	Y	R	V	D	C	G	G	C	N	G	C	E	I	E	I	F	A	T	L	S
Secondary structure											[Alpha Helix]										[Loop]		[Alpha Helix]																																					
SS confidence	[Confidence Scale]																																																											
Disorder	[Disorder Prediction]																																																											
Disorder confidence	[Disorder Confidence Scale]																																																											


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

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


	190	200	210	220	230	240																																																						
Sequence	E	I	L	H	G	D	M	V	Q	P	L	R	V	K	V	D	R	E	A	R	R	L	A	G	Y	R	Y	G	R	Q	I	A	D	D	Y	L	T	Q	L	G	Q	G	E	E	Q	V	A	R	V	L	E	A	E	N	D	P	R	L	N	E
Secondary structure	[Alpha Helix]		[Alpha Helix]		[Alpha Helix]		[Alpha Helix]		[Alpha Helix]		[Alpha Helix]		[Alpha Helix]		[Alpha Helix]		[Alpha Helix]																																											
SS confidence	[Confidence Scale]																																																											
Disorder	[Disorder Prediction]																																																											
Disorder confidence	[Disorder Confidence Scale]																																																											


	250														
Sequence	I	V	S	H	L	N	H	V	V	E	E	A	R	I	R
Secondary structure	[Alpha Helix]														
SS confidence	[Confidence Scale]														
Disorder	[Disorder Prediction]														
Disorder confidence	[Disorder Confidence Scale]														

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand