



Email	l.a.kelley@imperial.ac.uk
Description	P33360
Date	Thu Jan 5 11:52:02 GMT 2012
Unique Job ID	4a4bbcc817e0b590


	1	10	20	30	40	50	60																																																					
Sequence	M	I	E	F	S	H	V	S	K	L	F	G	A	Q	K	A	V	N	D	L	N	L	N	F	Q	E	G	S	F	S	V	L	I	G	T	S	G	S	G	K	S	T	T	L	K	M	I	N	R	L	V	E	H	D	S	G	E	I	R	F
Secondary structure	[Diagram showing alpha helices and beta strands for residues 1-60]																																																											
SS confidence	[Confidence bars for residues 1-60]																																																											
Disorder	[Disorder prediction for residues 1-60]																																																											
Disorder confidence	[Disorder confidence for residues 1-60]																																																											
	70	80	90	100	110	120																																																						
Sequence	A	G	E	E	I	R	S	L	P	V	L	E	L	R	R	M	G	Y	A	I	Q	S	I	G	L	F	P	H	W	S	V	A	Q	N	I	A	T	V	P	Q	L	Q	K	W	S	R	A	R	I	D	D	R	I	D	E	L	M	A	L	
Secondary structure	[Diagram showing alpha helices and beta strands for residues 70-120]																																																											
SS confidence	[Confidence bars for residues 70-120]																																																											
Disorder	[Disorder prediction for residues 70-120]																																																											
Disorder confidence	[Disorder confidence for residues 70-120]																																																											
	130	140	150	160	170	180																																																						
Sequence	L	G	L	E	S	N	L	R	E	R	Y	P	H	Q	L	S	G	G	Q	Q	R	V	G	V	A	R	A	L	A	A	D	P	Q	V	L	L	M	D	E	P	F	G	A	L	D	P	V	T	R	G	A	L	Q	Q	E	M	T	R	I	
Secondary structure	[Diagram showing alpha helices and beta strands for residues 130-180]																																																											
SS confidence	[Confidence bars for residues 130-180]																																																											
Disorder	[Disorder prediction for residues 130-180]																																																											
Disorder confidence	[Disorder confidence for residues 130-180]																																																											
	190	200	210	220	230	240																																																						
Sequence	H	R	L	L	G	R	T	I	V	L	V	T	H	D	I	D	E	A	L	R	L	A	E	H	L	V	L	M	D	H	G	E	V	V	Q	Q	G	N	P	L	T	M	L	T	R	P	A	N	D	F	V	R	Q	F	F	G	R	S	E	L
Secondary structure	[Diagram showing alpha helices and beta strands for residues 190-240]																																																											
SS confidence	[Confidence bars for residues 190-240]																																																											
Disorder	[Disorder prediction for residues 190-240]																																																											
Disorder confidence	[Disorder confidence for residues 190-240]																																																											
	250	260	270	280	290	300																																																						
Sequence	G	V	R	L	L	S	L	R	S	V	A	D	Y	V	R	R	E	E	R	A	D	G	E	A	L	A	E	E	M	T	L	R	D	A	L	S	L	F	V	A	R	G	C	E	V	L	P	V	V	N	M	Q	G	Q	P	C	G	T	L	H
Secondary structure	[Diagram showing alpha helices and beta strands for residues 250-300]																																																											
SS confidence	[Confidence bars for residues 250-300]																																																											
Disorder	[Disorder prediction for residues 250-300]																																																											
Disorder confidence	[Disorder confidence for residues 250-300]																																																											
Sequence	F	Q	D	L	L	V	E	A																																																				
Secondary structure	[Diagram showing alpha helices and beta strands for residues 301-307]																																																											
SS confidence	[Confidence bars for residues 301-307]																																																											
Disorder	[Disorder prediction for residues 301-307]																																																											
Disorder confidence	[Disorder confidence for residues 301-307]																																																											

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand