

Email	l.a.kelley@imperial.ac.uk
Description	P36979
Date	Thu Jan 5 11:54:07 GMT 2012
Unique Job ID	26c3f3f3b50790fc

	1	10	20	30	40	50	60																																																				
Sequence	M	S	E	Q	L	V	T	P	E	N	V	T	T	K	D	G	K	I	N	L	L	D	L	N	R	Q	M	R	E	F	F	K	D	L	G	E	K	P	F	R	A	D	Q	V	M	K	W	M	Y	H	Y	C	C	D	N	F	D	E	M
Secondary structure																				AA		AAAAAA					AAAAAA					AAAAAA					AA																						
SS confidence																				0.80		0.90					0.90					0.90					0.80																						
Disorder	?																			?																																							
Disorder confidence	0.00																			0.00		0.00					0.00					0.00																											

	70	80	90	100	110	120																																																						
Sequence	T	D	I	N	K	V	L	R	G	K	L	K	E	V	A	E	I	R	A	P	E	V	V	E	E	Q	R	S	S	D	G	T	I	K	W	A	I	A	V	G	D	Q	R	V	E	T	V	Y	I	P	E	D	D	R	A	T	L	C	V	S
Secondary structure	AAAAAA															AAAAAA					AAAAAA					AAAAAA					AAAAAA																													
SS confidence	0.80															0.80					0.80					0.80					0.80																													
Disorder	?															?					?																																							
Disorder confidence	0.00															0.00					0.00					0.00																																		

	130	140	150	160	170	180																																																						
Sequence	S	Q	V	G	C	A	L	E	C	K	F	C	S	T	A	Q	Q	G	F	N	R	N	L	R	V	S	E	I	I	G	Q	V	W	R	A	A	K	I	V	G	A	A	K	V	T	G	Q	R	P	I	T	N	V	V	M	M	G	M	G	E
Secondary structure	AAAAAA							AAAAAA					AAAAAA					AAAAAA					AAAAAA																																					
SS confidence	0.80							0.80					0.80					0.80					0.80																																					
Disorder																					?																																							
Disorder confidence	0.00					0.00					0.00					0.00					0.00																																							

	190	200	210	220	230	240																																																						
Sequence	P	L	L	N	L	N	N	V	V	P	A	M	E	I	M	L	D	D	F	G	F	G	L	S	K	R	R	V	T	L	S	T	S	G	V	V	P	A	L	D	K	L	G	D	M	I	D	V	A	L	A	I	S	L	H	A	P	N	D	E
Secondary structure	AAAAAA					AAAAAA										AAAAAA					AAAAAA					AAAAAA																																		
SS confidence	0.80					0.80										0.80					0.80					0.80																																		
Disorder						?																																																						
Disorder confidence	0.00					0.00					0.00					0.00					0.00																																							

	250	260	270	280	290	300																																																						
Sequence	I	R	D	E	I	V	P	I	N	K	K	Y	N	I	E	T	F	L	A	A	V	R	R	Y	L	E	K	S	N	A	N	Q	G	R	V	T	I	E	Y	V	M	L	D	H	V	N	D	G	T	E	H	A	H	Q	L	A	E	L	L	K
Secondary structure	AAAAAA					AAAAAA										AAAAAA					AAAAAA																																							
SS confidence	0.80					0.80										0.80					0.80																																							
Disorder																					?																																							
Disorder confidence	0.00					0.00										0.00					0.00																																							

	310	320	330	340	350	360																																																					
Sequence	D	T	P	C	K	I	N	L	I	P	W	N	P	F	P	G	A	P	Y	G	R	S	S	N	S	R	I	D	R	F	S	K	V	L	M	S	Y	G	F	T	T	I	V	R	K	T	R	G	D	I	D	A	A	C	G	Q	L	A	G
Secondary structure	AAAAAA					AAAAAA										AAAAAA					AAAAAA																																						
SS confidence	0.80					0.80										0.80					0.80																																						
Disorder																					?																																						
Disorder																																																											

Confidence Key
High(9)  Low (0)
? Disordered
 Alpha helix
 Beta strand