

Email	l.a.kelley@imperial.ac.uk
Description	Q46907
Date	Thu Jan 5 12:35:45 GMT 2012
Unique Job ID	861ebf6b11ce591d

	1	10	20	30	40	50	60	
Sequence	MNI	AI	VTI	NQENAAI	ASV	LAAQDFS	GCTLAHWQI	EPQPVVAAEQVLDALVEQVQRTPADVV
Secondary structure	[Blue arrow]			[Green alpha helix]			[Blue arrow]	[Green alpha helix]
SS confidence	[Color scale bar]							
Disorder	[Blue bar]							
Disorder confidence	[Color scale bar]							

	70	80	90	100	110	120	
Sequence	LFP	P	GT	F	GDE	L	STR
Secondary structure	[Blue arrow]	[Green alpha helix]			[Blue arrow]	[Blue arrow]	[Blue arrow]
SS confidence	[Color scale bar]						
Disorder	[Blue bar]						
Disorder confidence	[Color scale bar]						

	130	140	150	160	170	180	
Sequence	L	ARQAGAAK	NATL	P	SGM	QQL	NI
Secondary structure	[Blue arrow]	[Blue arrow]		[Blue arrow]	[Blue arrow]	[Blue arrow]	[Blue arrow]
SS confidence	[Color scale bar]						
Disorder	[Blue bar]						
Disorder confidence	[Color scale bar]						

	190	200	210	220	230	240	
Sequence	DNQE	I	AML	A	EKL	GAE	V
Secondary structure	[Green alpha helix]		[Blue arrow]	[Green alpha helix]	[Blue arrow]	[Blue arrow]	[Green alpha helix]
SS confidence	[Color scale bar]						
Disorder	[Blue bar]						
Disorder confidence	[Color scale bar]						

	250	260	270	280
Sequence	V	RNS	K	F
Secondary structure	[Green alpha helix]	[Blue arrow]	[Green alpha helix]	[Blue arrow]
SS confidence	[Color scale bar]			
Disorder	[Blue bar]			
Disorder confidence	[Color scale bar]			

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand