

	10	20	30	40	50	60
AQSV	VGV	SQIKAPALH	SGYTG	SNV	VVAIDSGID	SSHPDLKVAGGASMPSETNPFQD
P	P	PP	P P	P P	P	P
C		SS	C C	S S S		SS
E		EE	E E	E E		E
	70	80	90	100	110	120
NNSHGTHVAGTVAALNNSIGVLGVAPSASLYAVKVLGADGSGQYSWIINGIEWAIANNMD						
P	P P	P	P	PPP PP P	P	P P
CC C		C C	C	C C CCCC	C C C	CCC C
SS S	S S		S S	S S	S S	
T T			T	TTTTTT	T	
EE E	E	E	E	EE EEEE	E E E	E E
	130	140	150	160	170	180
VINMSLGGPSGSAALKAADVAVASGVVVVAAAG	NE	GTSGSS	TVG	YF	GKYP	SVIAVGAV
PPPPP PP P P	P	P	P P	PP		
CCCC C	CCCC	CC CCCC	C C	CCC	CC	C
SS			S SS		SS	
TTTTT	T		T TTT		T	
EEEE E	EEE	E	E	E EE	EE	
	190	200	210	220	230	240
DSSNQRA	SF	SSVGP	ELDV	M	APG	VSIQSTLPGNKYGA
P	PP	P		P	PPPPP	P
CCCC	CC	C	C C	CCC	CCCCCCC	C
S S	S			S	S	
	TT			T	TT	
E E	EE	E		E	EEEEEE	E
	250	260	270			
W	INTQVRS	SLENT	TKLGDS	FY	YKGLIN	VQAAAQ
P	P P	PP P P	P	P		
C C		CC C C				
S SS	S	SS S				
E EE		EE E	EE E			

- Rows :
1. Phylogeny (P)
 2. COC (C)
 3. SVM (S)
 4. Threading (T)
 5. Consensus (E)

Protein: 2SIC_E