

10	20	30	40	50									
MMQDLR	LILI	IVGAI	AIAL	LVHGF	WTSRK	ERSSM	FRDRP	LKR	MKSKR	DD			
60	70	80	90	100	110	120	130	140	150	160			
DSYDED	VEDD	EGVGE	VRVHR	VNHAP	ANAQE	HEAAR	PSPQH	QYQPP	YASAQ				
160	170	180	190	200	210	220	230	240	250	260			
PRQPV	QQPPE	AQVPP	QHAPH	PAQPV	QQPAY	QPQPE	QPLQQ	PVSPQ	VAPAP				
260	270	280	290	300	310	320							
QPVHS	SAPQA	QQA	FQPA	EAEPV	AAQPE	PEPVAE	PAPVM	DKPKR	KEA	VI	IMNVA		
AHHG	SELNGE	LLLNS	IQQAG	FIFGD	MNI	YH	RHLSP	DGSGP	ALFSL	AN	MVK		
PGTFD	PEMKD	FTTPG	V	T	I	F	M	QVPSY	GDELQ	N	FKLMLQSAQ	HIAD	EVGGVV
LDDQ	R	MMTP	QKL	REY	QDII	REV	KDANA						

Highlighted are positions of M44V, L211T, Y229C, N281S (*zipA1* mutations). Note that Y229 is adjacent to a strong FtsZ contacting residue (I228)

Highlighted are residues in contact with FtsZ

Highlighted are residues that form strong crosslinking species containing FtsZ

TM is in orange