

	Viable?	Telomere length	23°	36°
I73A I73S I73Y	Neatly inviable	Very long Extremely long Very long	+ +/- +	+/- — +/- to (+)
L75A L75S L75Y	inviable	Med long Very long n/a	+ (+) to +	(+) to + +/- to (+)
I79A I79S I79Y	inviable	Med long Very long n/a	++ + to ++	+ (+)
I93A I93S I93Y		Med long Very long Slightly long	++ + ++	+ +/- to (+) +
L97A L97S L97Y	inviable	Very long n/a Very long	(+) (+) to +	+/- +/-
L106A L106S L106Y		Wild type Wild type Wild type	++ ++ ++	++ ++ ++
L140A L140S L140Y		Wild type Wild type Wild type	++ ++ ++	++ ++ ++
V142A V142S V142Y	Neatly inviable inviable	Slightly long n.t. n/a	+ to ++ +/-	+ —
L153A L153S L153Y	inviable	Very long n/a Very long	(+) (+)	+/- +/-
V155A V155S V155Y	Neatly inviable inviable	Very long n.t. n/a	+ +/-	(+) —
L158A L158S L158Y		Very long Very long n.t.	+ + (+)	+ + +/-
G77A G77S G77Y	Neatly inviable	Very long n.t. n.t.	(+) to + (+) +/-	+/- to + +/- —
G137A G137S G137Y	+ + inviable	Very long Long n/a	+(+) ++	(+) +

Figure S5 Summary of viability and telomere length of a panel of *stn1*⁻ missense mutations introduced into 11 hydrophobic residues with side-chains located in the interior of the β -barrel of the essential N-terminal OB-fold domain of Stn1. Telomere length of selected mutant isolates is shown in Figure S4. The results for mutagenesis of two highly conserved glycine residues are also included.