

Table S3: Primers for the *Ec* 1ALigN (multiple) mutants and degree of reversibility upon thermal unfolding.

Name ⁽¹⁾	Mutated residues ⁽²⁾	Template	Forward primer	Analyzed ⁽³⁾	Rev. / % ⁽⁴⁾
Ex1D	41	<i>WT</i>	5'- ACGCTTCGCCATCATGATTATCTTTATCATGTGAT -3'	Yes	100
Ex2D	24,27	<i>WT</i>	5'-GCAGGCTTCATGGATTCAATCGATCAACAACACTGACAGAACT-3'	Yes	100
Ex3D	63,66,68	<i>WT</i>	5'-TGATGCGCGATCTGCGCGATCTGGATACCAAACATCC-3'	Yes	100
Ex4D	41,63,66,68	<i>Ex1D</i>	5'- TGATGCGCGATCTGCGCGATCTGGATACCAAACATCC -3'	Yes	100
Ex5D	24,27,63,66,68	<i>Ex2D</i>	5'- TGATGCGCGATCTGCGCGATCTGGATACCAAACATCC -3'	Yes	100
Dx2E	54,58	<i>WT</i>	5'- AAATTCCCGAAGCTGAATACGAAAGGCTGATGCGCGAACT -3'	Yes	100
Dx3E	54,58,78	<i>Dx2E</i>	5'- AGAACTGATTACGCCTGAATCGCCTACCCAACGTGTA -3'	Yes	100
Dx4E	48,54,58,78	<i>Dx3E</i>	5'- CTTTATCATGTGATGGAAGCGCCGAAATCCCGA -3'	Yes	100
Ex2Q	24,27	<i>WT</i>	5'- GCAGGCTTCATGCAATCAATCCAACAACAACACTGACAGAACT -3'	Yes	100
Qx2E	28,29	<i>WT</i>	5'- ATGGAATCAATCGAAGAAGAAGACTGACAGAAGCTGCGAACGA -3'	Yes	100

(1) XY_nWZ involves *n* substitutions from X or Y to W or Z respectively. The quotation mark indicates that an alternative cumulative pathway has been used. (2) From the sequence: MSYYHHHHHHLESTSLYKKAGFMESIEQQLTELRTTLRHHEYLYHVMDAPEIPDAEYDRLMRELRELETKHPELITPDSPTQRVGAAPLAAF (3) Yes = Protein expressed, purified and tested over KCl. No = DNA used as an intermediate for cloning. (4) Reversibility upon unfolding. The value corresponds to the lower value found for all the salt concentrations. Values in red indicate that a change in the T_m is observed after varying the scanning rate in the experiment and these values have not been used in the study.