

Electronic Supporting Information
for
**Controlling Macromolecular Topology with Genetically Encoded
SpyTag-SpyCatcher Chemistry**

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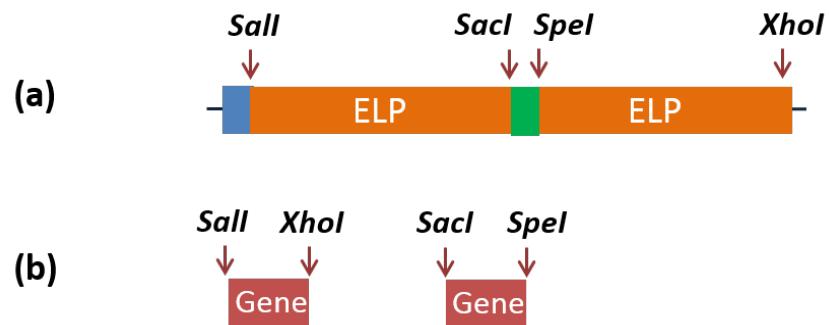


Figure S1. (a) Cartoon illustration of the original ELP construct. It contains four restriction sites: SalI (GTCGAC), SacI (GAGCTC), SpeI (ACTAGT), and XhoI (CTCGAG) as shown. (b) The gene inserts can be made in a way that is either flanked by SalI and XhoI for insertion into the N-terminus or C-terminus or by SacI and SpeI for insertion into the middle of the chain. The restriction sites SalI and XhoI share the same sticky ends. Therefore, the insert can be used to ligate the vector that is digested by SalI or XhoI. The inserts can be SpyTag or SpyCatcher.

1 MKGSSHHHHHVDAHIVMV D AYKPTKLDGHGVGVPGVGVP
41 GVGVPGEVPGVGVPGVGVPGVGVPGVGVPGVGPGEVPGVGVP
81 GVGVPGVGVPGVGVPGVGPGEVPGVGVPGVGELEYAVTGRGDSP
121 ASSAPIATSVPGVGVPGVGVPGVGPGEVPGVGVPGVGVPGVGV
161 PGVGVPGEVPGVGVPGVGVPGVGVPGVGVPGVGPGEVPGVG
201 PGVGVPGLLDIPTTENLYFQGAMVDTLSLSSEQQSGD
241 MTIEEDSATHIKFS K RDEDGKELAGATMELRDSSGKTIST
281 WISDGQVKDFYLYPGKYTFVETAAPDGYEVATAITFTVNE
321 QQQVTVNGKATKGDAHIDGPQGIWGQLEWKK

Figure S2. Full amino acid sequence of AB20D (351 a.a. MW = 34002). The reactive aspartic acid (20D) is shown in the box at the first line. It is changed to nonreactive alanine (20A) in AB20A. The reactive lysine (255K) is shown in the box at the 7th line. The segments highlighted in red, yellow, and purple are the SpyTag, TEV protease recognition sequence, and SpyCatcher, respectively.

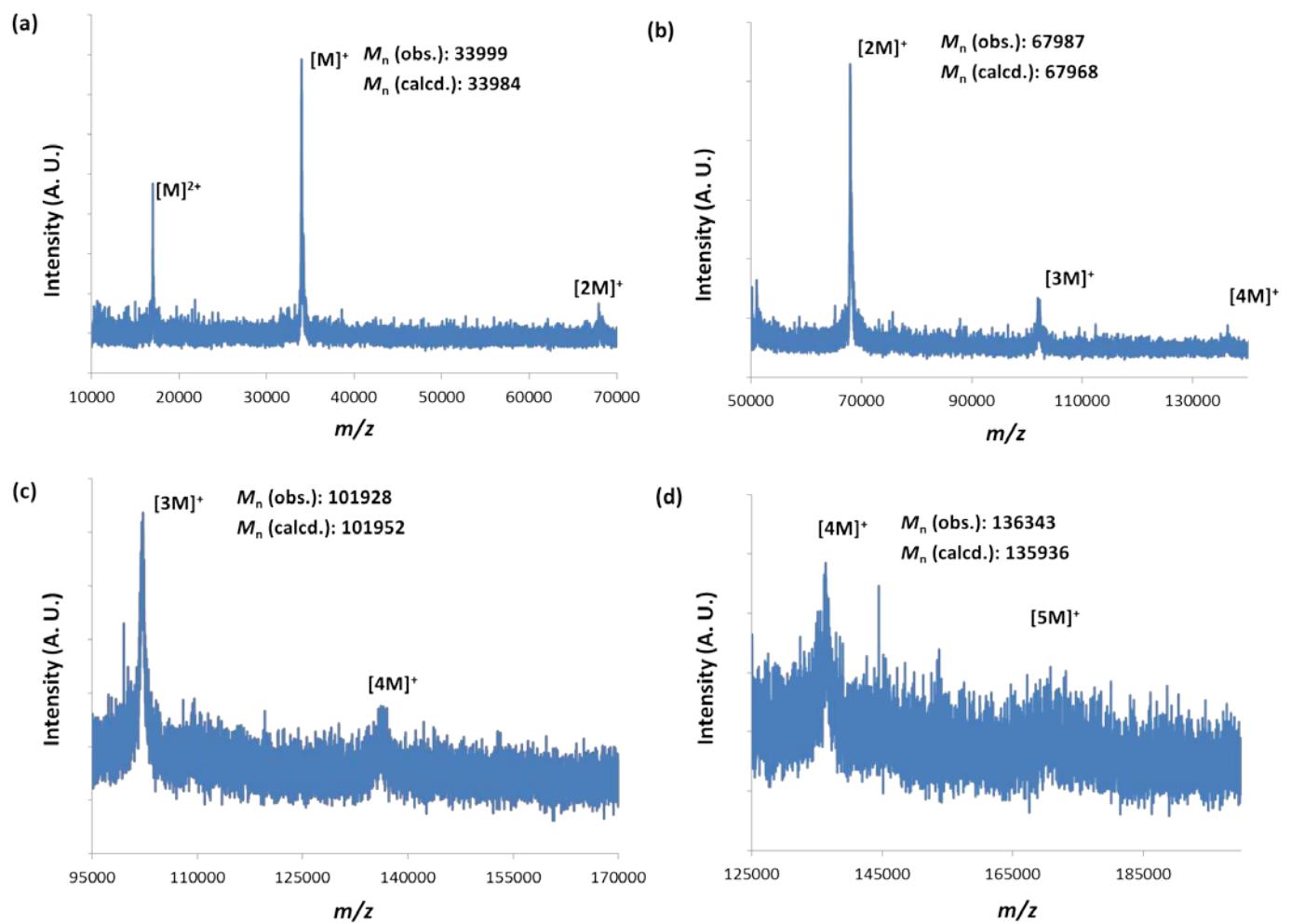


Figure S3. MALDI-TOF mass spectra of AB20D expressed at 37 °C with induction: (a) monomer; (b) dimer; (c) trimer; and (d) tetramer.

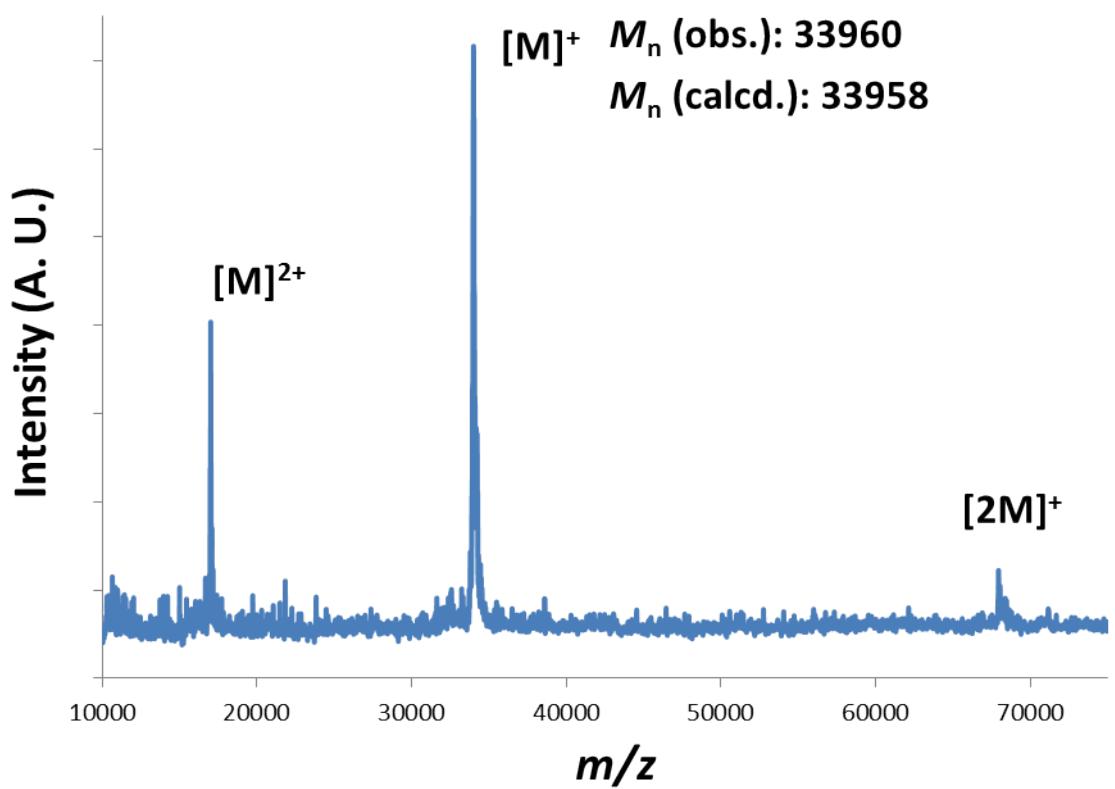


Figure S4. MALDI-TOF mass spectrum of AB20A.

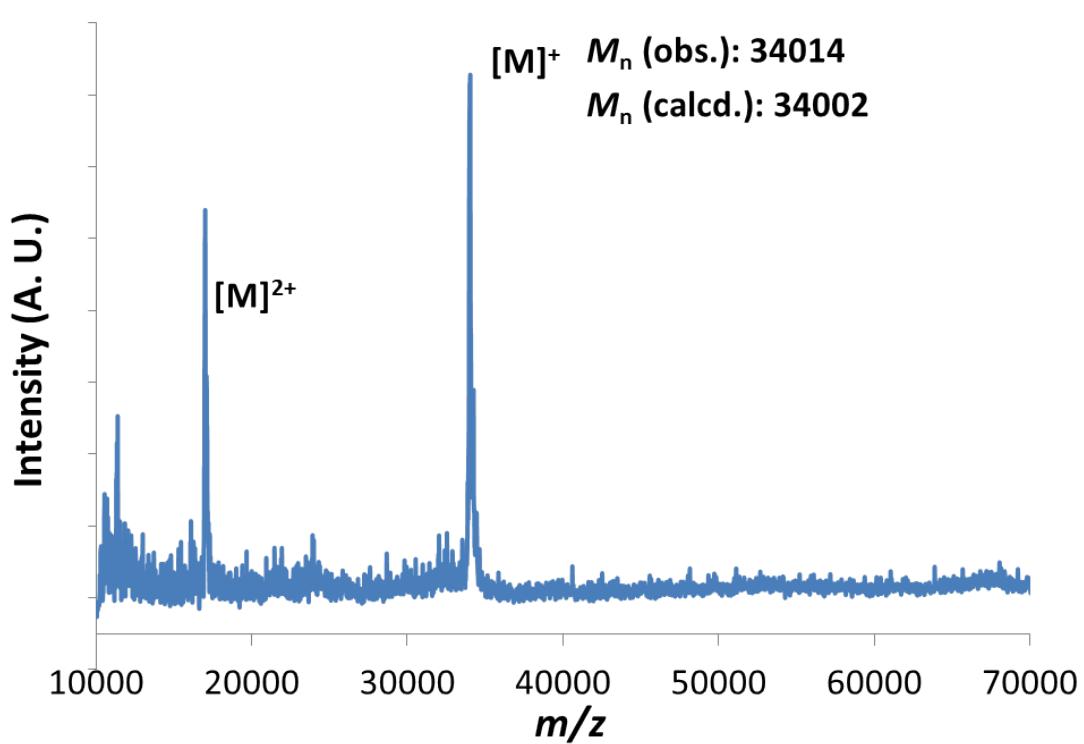


Figure S5. MALDI-TOF mass spectrum of relinearized AB20D.

1 MKGSSHHHHHVDGHGVGVPGVGVPGVGPGEVPGVGP
41 GVGVPGVGVPGVGVPGVPGEGVPGVGVPGVGVPGVGP
81 GEGVPGVGVPGVGE_{AHIVMV} **D** AYKPTKTSVPGVGVPGV
121 VPGEVPGVGVPGVGVPGVGVPGVGVPGVGVPGVGV
161 VPGVGVPGVGVPGVPGEGVPGVGVPGVGVPGVGVPGV
201 FQGAMVDTLSGLSSEQGQSGDMTIEEDSATHIKFS **K** RDED
241 GKELAGATMELRDSSGKTISTWISDGQVKDFYLYPGKYTF
281 VETAAPDGYEVATAITFTVNEQQQVTVNGKATKGDAHIDG
321 PQGIWGQLEWKK

Figure S6. Full amino acid sequence of EAEB (332 a.a. MW = 32172). The reactive aspartic acid (102D) and lysine (236K) are shown in the box at the 3th and 6th lines, respectively. The segments highlighted in red, yellow, and purple are the SpyTag, TEV protease recognition sequence, and SpyCatcher, respectively.

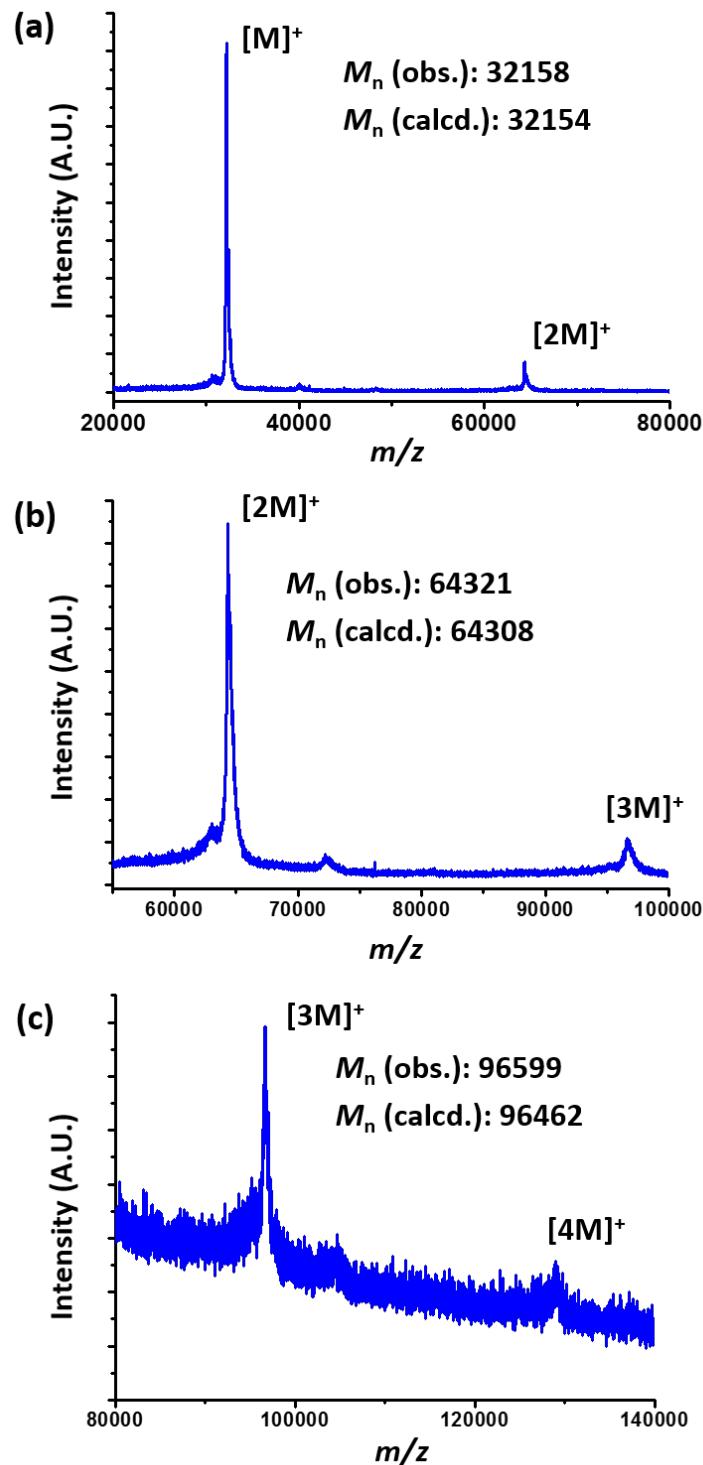


Figure S7. MALDI-TOF mass spectra of EAEB expressed at 37 °C with 1 mM IPTG induction: (a) monomer; (b) dimer; and (c) trimer.

(a) EA: 214 a.a. MW = 19242

1 MKGSSHHHHHV DGHGVGVPGVPGVGPVGVPGEVPGVGVP
41 GVGPGVGVPVGVPGEVPGVGVPVGVPVGVPVGVPVGVP
81 GEGVPGVGVPVGELYAVTGRGDSPASSAPIATS VPGVGV
121 PGVGVPGEVPGVGVPVGVPVGVPVGVPVGVPGEVPGVGV
161 PGVGVPGVGVPGVGVPGEVPGVGVPVGVPVGVL LD AHIV
201 MV [D] AYKPTKLEWKK

(b) EB: 336 a.a. MW = 32319

1 MKGSSHHHHHV DGHGVGVPGVPGVGPVGVPGEVPGVGVP
41 GVGPGVGVPVGVPGEVPGVGVPVGVPVGVPVGVPVGVP
81 GEGVPGVGVPVGELYAVTGRGDSPASSAPIATS VPGVGV
121 PGVGVPGEVPGVGVPVGVPVGVPVGVPVGVPGEVPGVGV
161 PGVGVPGVGVPGVGVPGEVPGVGVPVGVPVGVL DIPTT
201 ENLYFQG AMVDTLSGLSSEQGQSGDMTIEEDSATHIKFS [K]
241 RDEDGKELAGATMELRDSSGKTISTWISDGQVKDFYLYPG
281 KYTFVETAAPDGYEVATAITFTVNEQQQVTVNGKATKGDA
321 HID GPQGIWGQLEWKK

Figure S8. Full amino acid sequence of (a) EA and (b) EB. The reactive aspartic acid (203D) and lysine (240K) are shown in the box. The segments highlighted in red and purple are SpyTag and SpyCatcher, respectively.

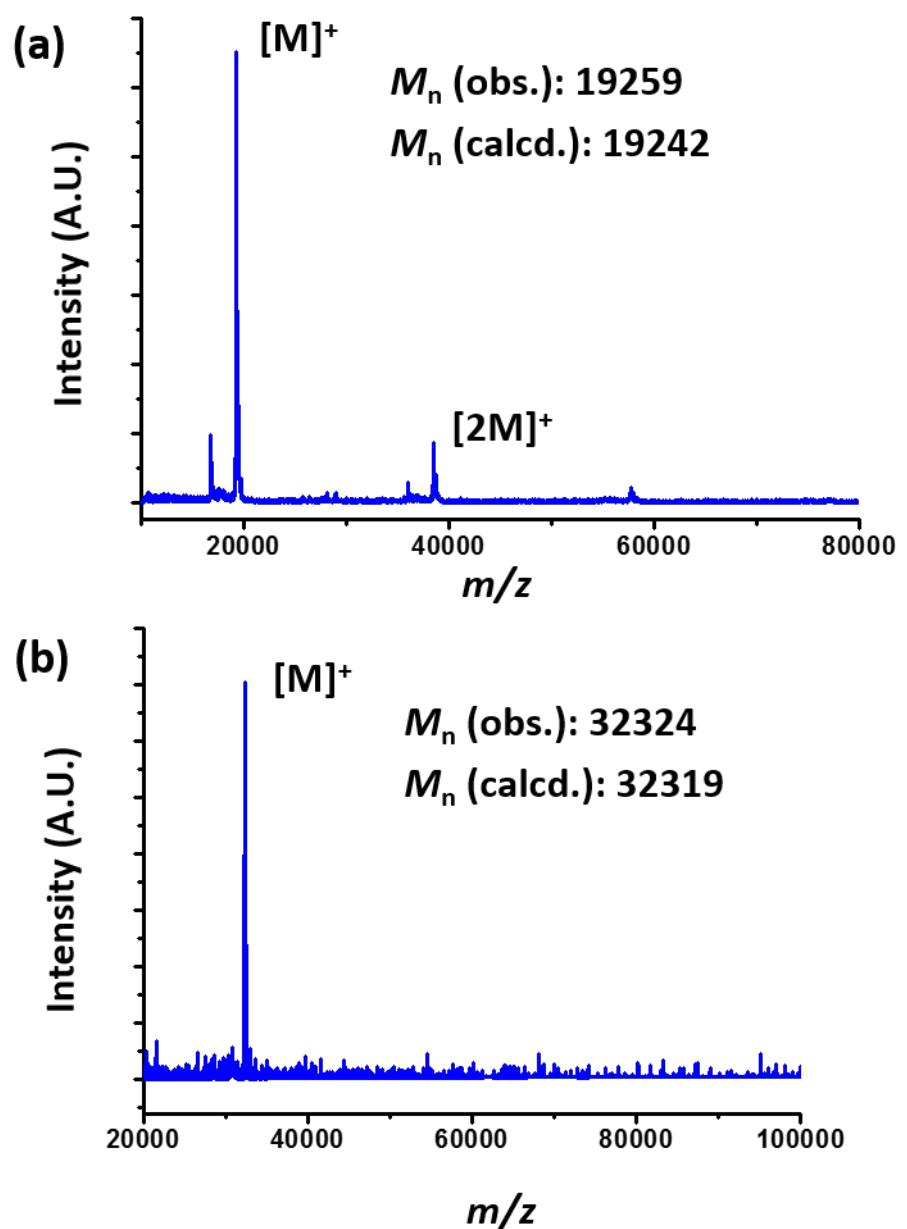


Figure S9. MALDI-TOF mass spectra of EA (a) and EB (b).

(a) EAE: 205 a.a. MW = 18409

1 MKGSSHHHHHVVDGHGVGVPGVGVPGVGPGEVPGVGP
41 GVGVPGVGVPGVGVPGVGPGEVPGVGVPGVGVPGVGP
81 GEGVPGVGVPGVGE[AHIVMV]D AYKPTKTSVPGVGVPGV
121 VPGEVPGVGVPGVGVPGVGVPGVGVPGVGPGEVPGVGVPGV
161 VPGVGVPGVGVPGVGPGEVPGVGVPGVGVPGVGVPGV
201 LEKKM

(b) EBE: 327 a.a. MW = 31486

1 MKGSSHHHHHVVDGHGVGVPGVGVPGVGPGEVPGVGP
41 GVGVPGVGVPGVGVPGVGPGEVPGVGVPGVGVPGVGP
81 GEGVPGVGVPGVGE[LIPTTENLYFQG]AMVDTLSGLSSEQG
121 QSGDMTIEEDSATHIKFS[K]RDEDGKELAGATMELRDSSGK
161 TISTWISDGQVKDFYLYPGKYTFVETAAPDGYEVATAITF
201 TVNEQQQVTVNGKATKGDAHIDGPQGIWGQTSVPGVGVPG
241 VGVPGEVPGVGVPGVGVPGVGVPGVGVPGVGPGEVPGVGVPG
281 VGVPGVGVPGVGVPGVGPGEVPGVGVPGVGVPGVGVPG
321 GQLEKKM

Figure S10. Full amino acid sequence of (a) EAE and (b) EBE. The reactive aspartic acid (102D) and lysine (139K) are shown in the box. The segments highlighted in red and purple are SpyTag and SpyCatcher, respectively.

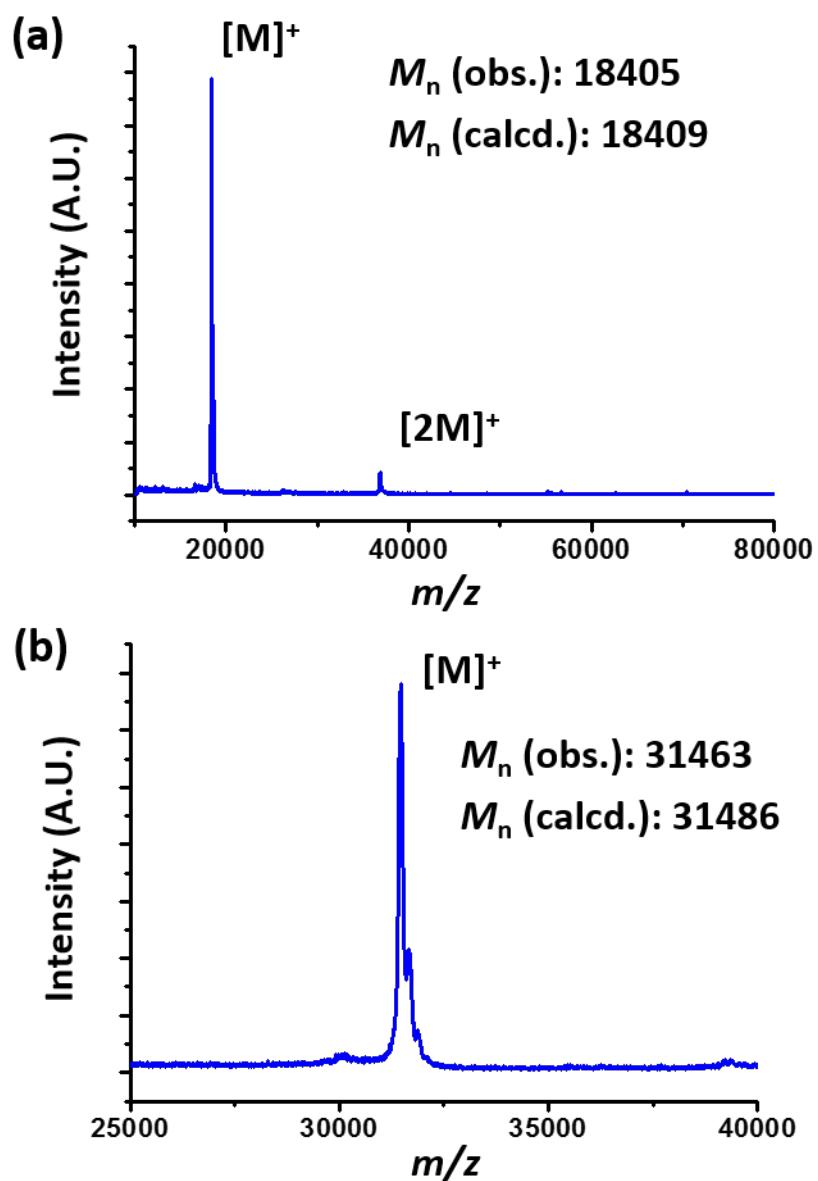


Figure S11. MALDI-TOF mass spectra of EAE (a) and EBE (b).

(a) AA: 229 a.a. MW = 20925

1 MKGSSHHHHHVDAHIVMV [D] AYKPTKLDGHGVGVPGVGVP
41 GVGVPGEVGPGVGPGVGPGVGPGVGPGVGPGVGEGVPGVGVP
81 GVGVPGVGVPGVGPGVGEGVPGVGPGVGELYAVTGRGDSP
121 ASSAPIATSVPGVGVPGVGVPGEVGPGVGPGVGPGVGVPGV
161 PGVGVPGEVGPGVGPGVGPGVGPGVGPGVGVPGEVGPGVG
201 PGVGVPGLLD[AHIVMV [D] AYKPTKLEWKK*

(b) BB: 473 a.a. MW = 47080

1 MKGSSHHHHHVDIPTTENLYFQG[AMVDTLSGLSSEQGQS
41 GDMTIEEDSATHIKFS [K] RDEDGKELAGATMELRDSSGKTI
81 STWISDGQVKDFYLYPGKYTFVETAAPDGYEVATAITFTV
121 NEQGQVTVNGKATKGDAHIDGPQGIWGQLDGHGVGVPGVG
161 VPGVGVPGEVGPGVGPGVGPGVGPGVGPGVGVPGEVGPGVG
201 VPGVGVPGVGVPGVGVPGEVGPGVGPGVGELYAVTGRGD
241 SPASSAPIATSVPGVGVPGVGVPGEVGPGVGPGVGVPGV
281 GPVGVPGEVGPGVGPGVGPGVGPGVGPGVGVPGEVGPGVG
321 GPVGVPGLLDIPTTENLYFQG[AMVDTLSGLSSEQGQS
361 GDMTIEEDSATHIKFS [K] RDEDGKELAGATMELRDSSGKTI
401 STWISDGQVKDFYLYPGKYTFVETAAPDGYEVATAITFTV
441 NEQGQVTVNGKATKGDAHIDGPQGIWGQLEWKK*

Figure S12. Full amino acid sequence of (a) AA and (b) BB. The reactive aspartic acid (20D and 218D) and lysine (57K and 377K) are shown in the box. The segments highlighted in red and purple are SpyTag and SpyCatcher, respectively.

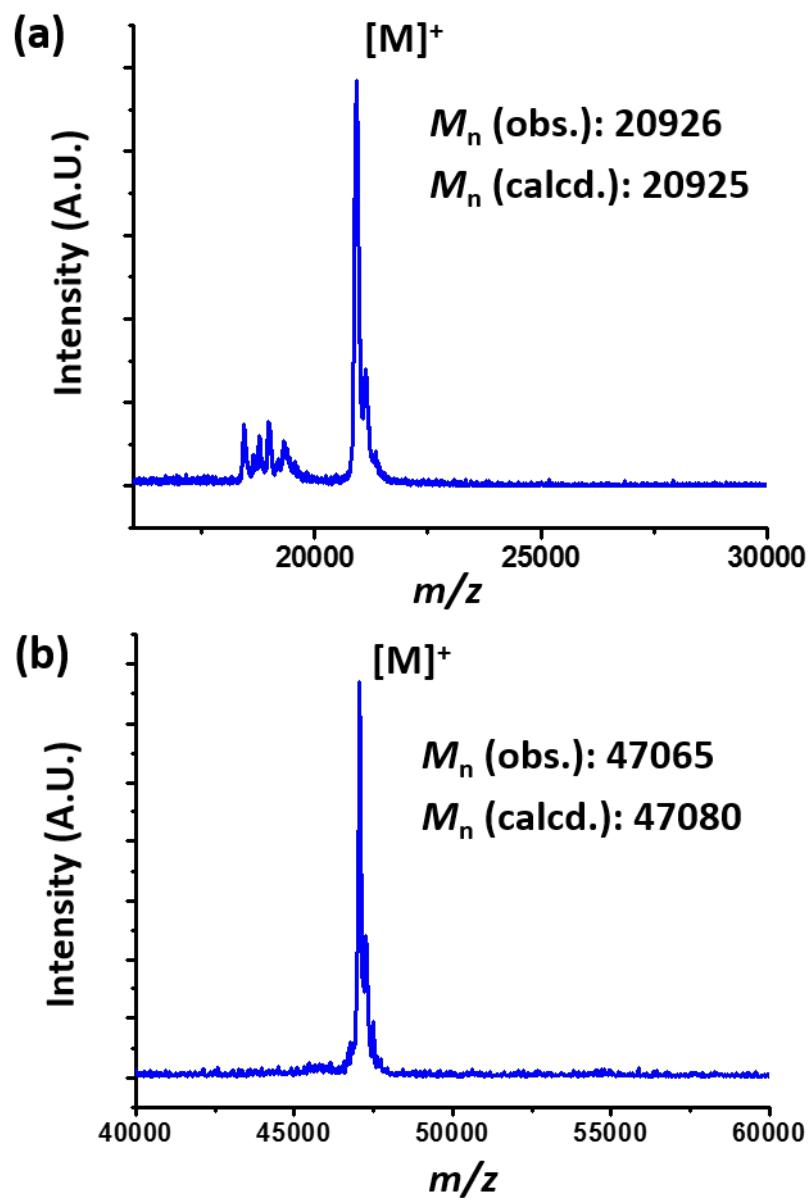


Figure S13. MALDI-TOF mass spectra of AA (a) and BB (b).

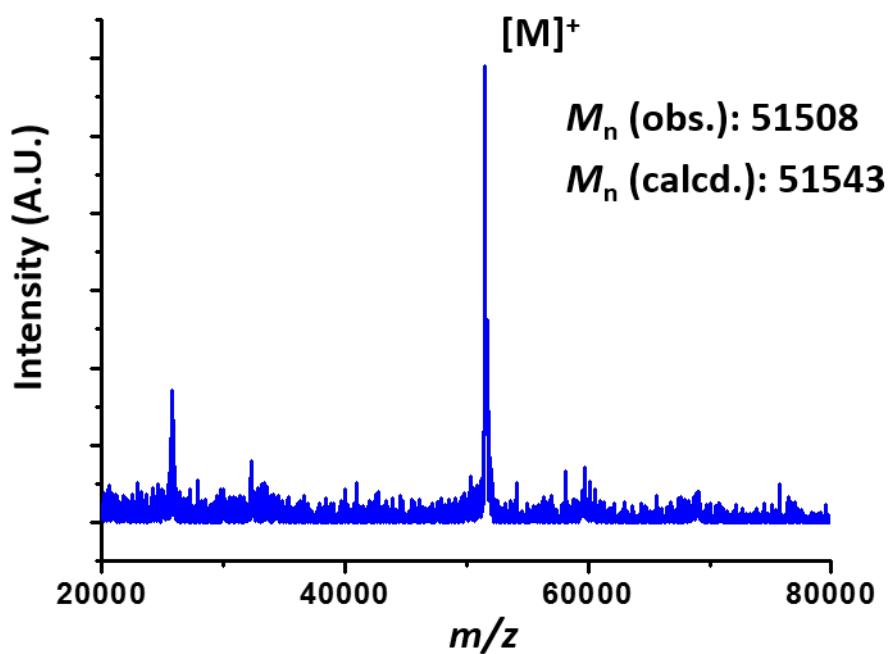


Figure S14. MALDI-TOF mass spectrum of the block protein (EA+EB).

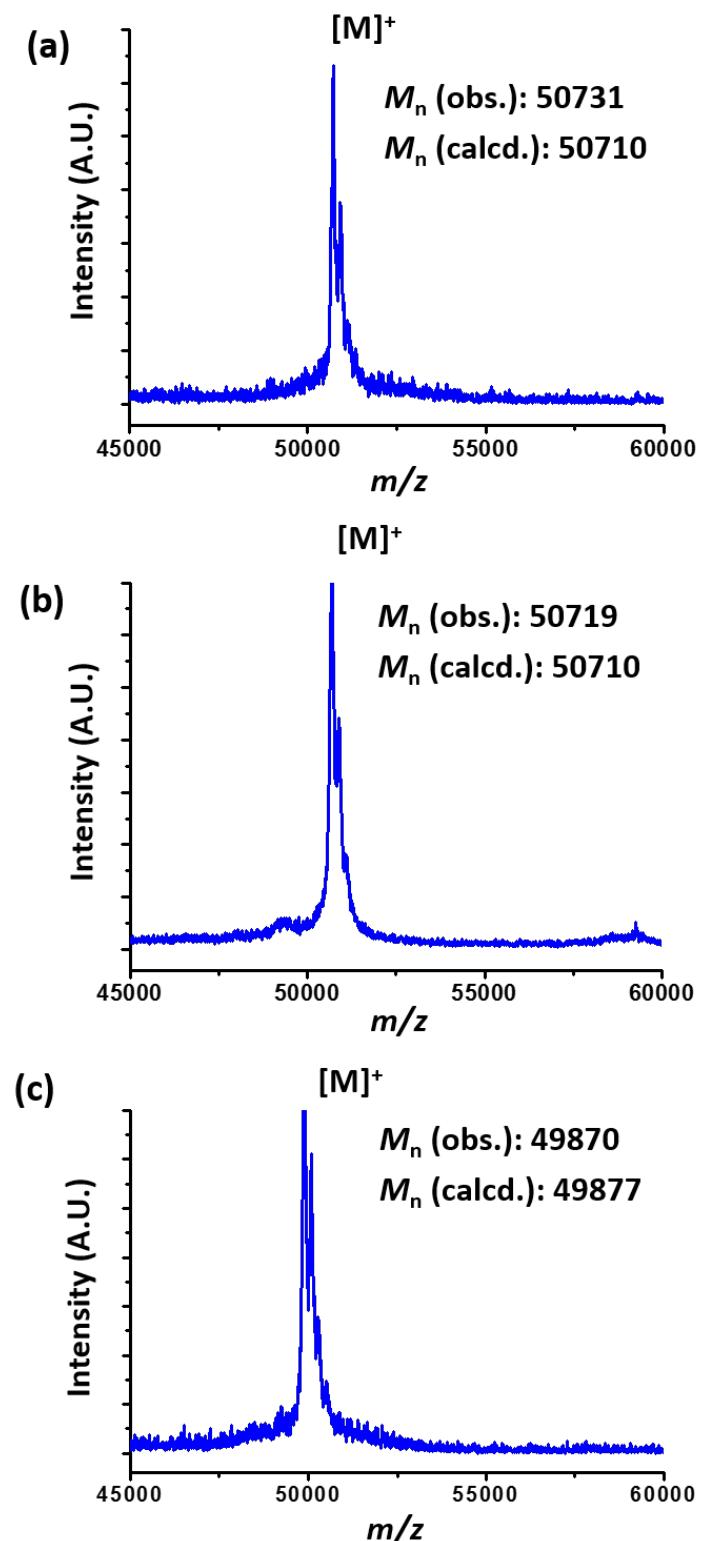


Figure S15. MALDI-TOF mass spectra of the 3-arm star proteins EA+EBC (a) and EAE+EB (b) and the 4-arm star protein EAE+EBC (c).

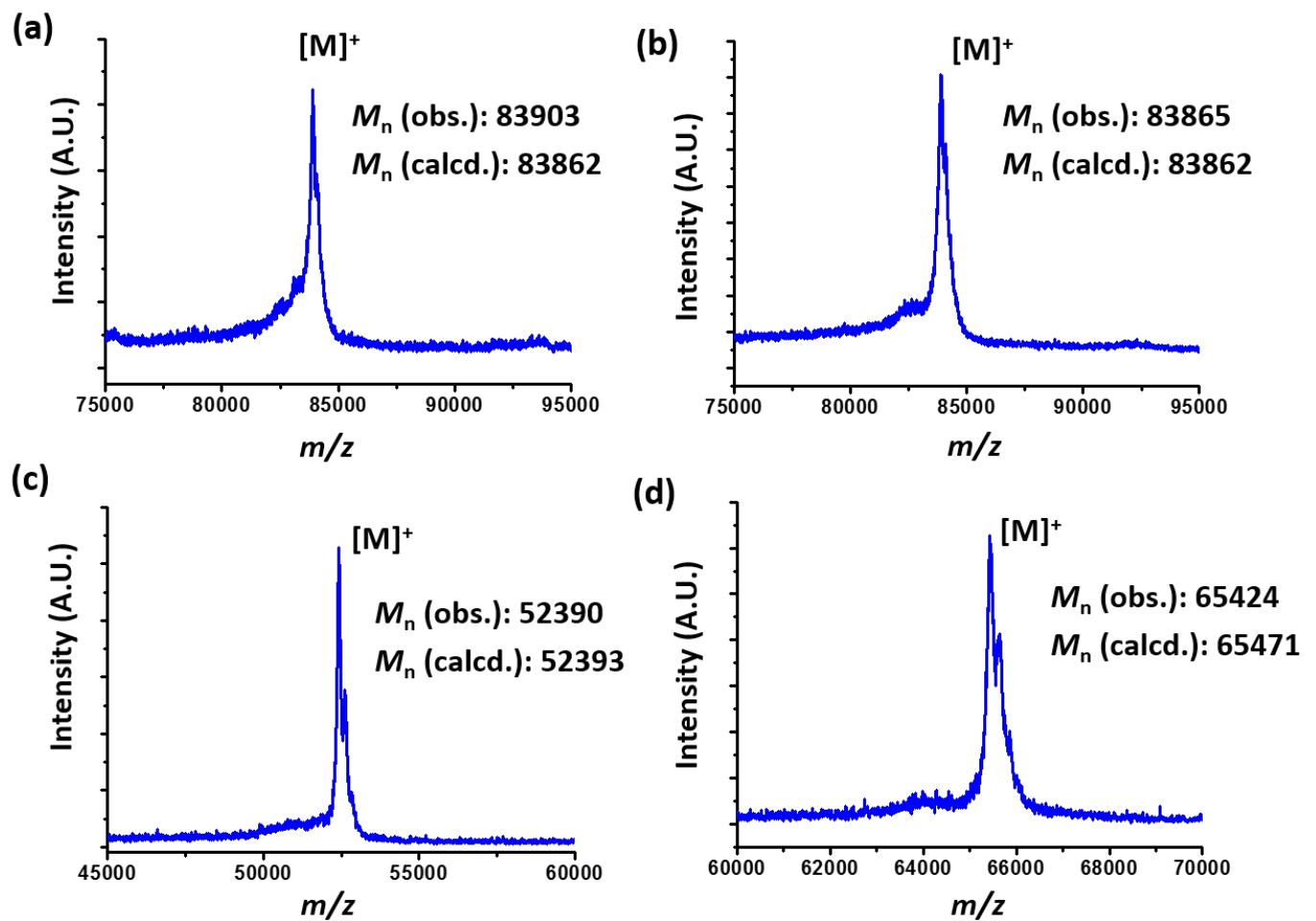


Figure S16. MALDI-TOF mass spectra of the H-shaped proteins AA+2EBE (a) and BB+2EAE (b) and the corresponding intermediate 3-arm proteins AA+EAE (c) and BB+EAE (d).

Table S1. Summary of bacterial strains and plasmids used in this study

Strains	Relevant Characteristics	Sources
<i>E. coli</i>		
DH5 α		Stratagene
BL21 star(DE3)		Invitrogen
Plasmids		
pQE-80L	T5 promoter-operator, N-terminal His tag, Amp ^r	Qiagen
pQE-ELP	The pQE-80L plasmid containing the gene encoding elastin	The starting vector for all the constructions of recombinant proteins in this study
pQE-AB20D	The plasmid for the expression of circular protein	This study
pQE-AB20A	The plasmid mutant for the expression of the control linear protein	This study
pQE-EAEB	The plasmid for the expression of tadpole protein	This study
pQE-EA	The plasmid for the expression of Elastin-SpyTag	This study
pQE-EB	The plasmid for the expression of Elastin-SpyCatcher	This study
pQE-EAE	The plasmid for the expression of Elastin-SpyTag-Elastin	This study
pQE-EBE	The plasmid for the expression of Elastin-SpyCatcher-Elastin	This study
pQE-AA	The plasmid for the expression of SpyTag-Elastin-SpyTag	This study
pQE-BB	The plasmid for the expression of SpyCatcher-Elastin-SpyCatcher	This study