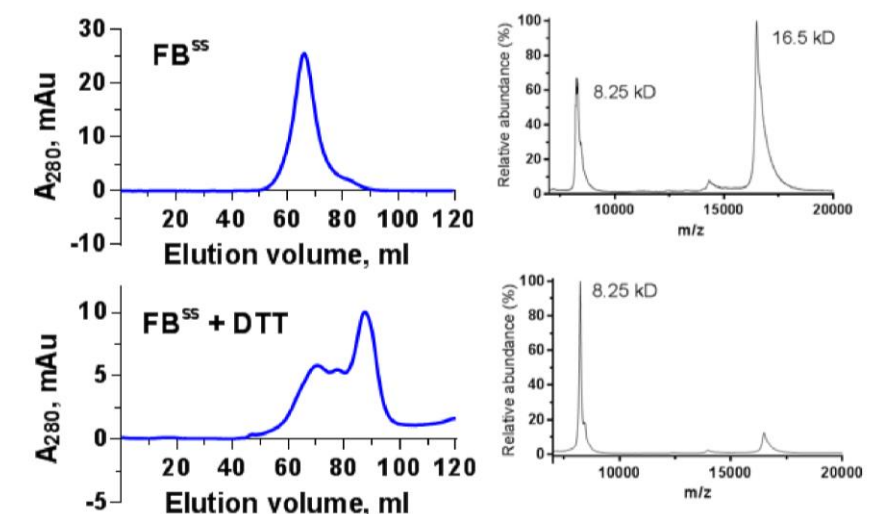
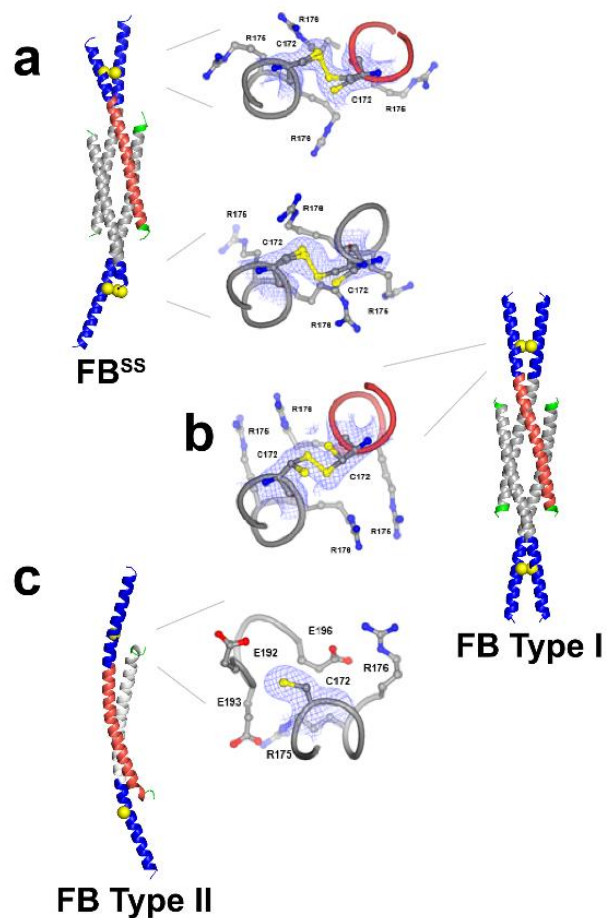


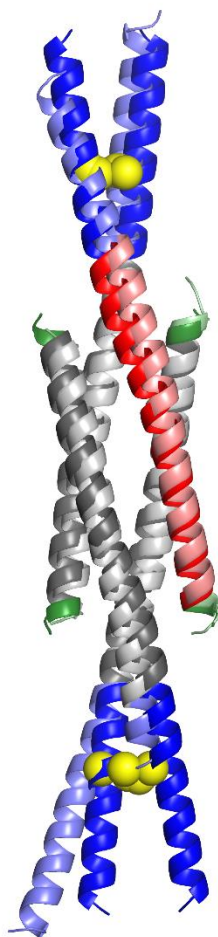
## SUPPLEMENTARY MATERIAL



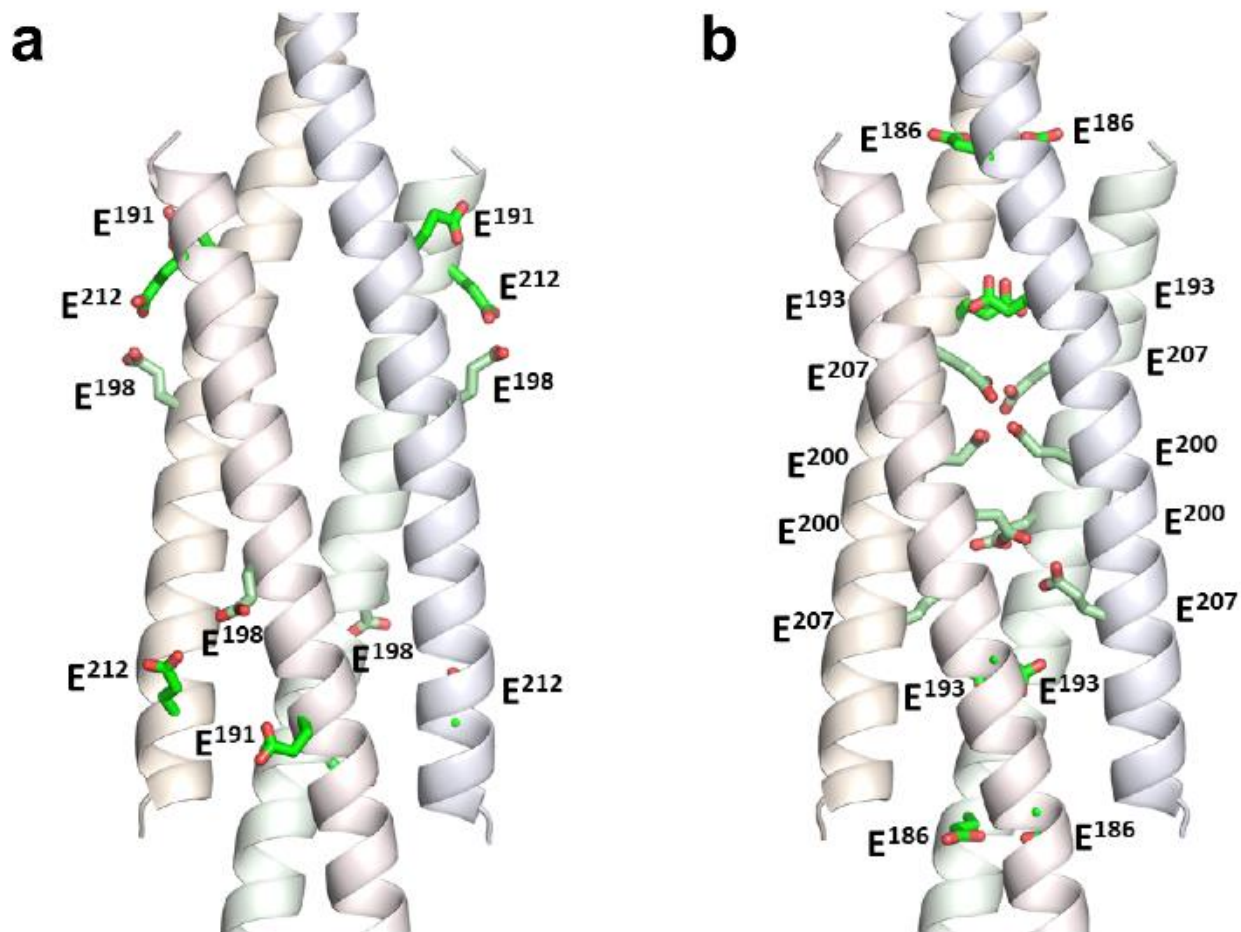
**Figure S1. FB purified under non-reducing and reducing conditions.** FB was dialyzed overnight in 20 mM Tris pH 8, 0.2 M NaCl at room temperature resulting in an oxidized form, FB<sup>SS</sup>. Size-exclusion chromatogram of FB<sup>SS</sup> in 20 mM Tris pH 8, 0.2 M NaCl without reducing-agent (top) or with 2 mM DTT (bottom). MALDI-TOF mass spectra of oxidized and reduced FB are also shown, indicating the molecular ion peaks. Peak heights are normalized to the observed maximum. The theoretical molecular weight ( $M_w$ ) of dimeric FB is 16.5 kDa and of monomeric FB 8.25 kDa.



**Figure S2. FB assemblies containing or lacking an inter-molecular disulfide bond.** a) FB<sup>SS</sup> crystal structure. Zoomed-in views show that C<sup>172</sup> forms a disulfide bond (model refined to permit partial occupancy); b) FB Type I crystal structure. Zoomed-in view shows that C<sup>172</sup> forms a disulfide bond with its crystallographic symmetry mates that constitute the tetramer (model refined to permit partial occupancy); c) FB Type II crystal structure. Zoomed-in views show the free-thiol group of C<sup>172</sup>. The 2F<sub>o</sub>-F<sub>c</sub> electron density map is contoured at 1  $\sigma$ .



**Figure S3. Superposition of the FB Type I and FB<sup>SS</sup> tetrameric assemblies.** FB Type I is shown in darker and FB<sup>SS</sup> in lighter colors. For each crystal structure, the leucine zipper region of one representative chain is shown in red and for all other chains in grey. The basic regions are shown in blue. Residues C-terminally to the leucine zippers are shown in green. Cys<sup>172</sup> is represented as a yellow ball. The r.m.s.d. between 211 structurally equivalent residues from FB Type I (out of 240) and FB<sup>SS</sup> (out of 230) is 1.91Å for C $\alpha$  atoms.



**Figure S4. Distribution of glutamate residues in FB Type I.** a) glutamate residues at the e-position; b) glutamate residues at the g-position. Ordered side chains are shown in green; disordered side chains are modeled to show their approximate location and shown in pale green.