

**Supporting information for:**

**Mechanisms of Nanonewton Mechanostability in  
a Protein Complex Revealed by Molecular  
Dynamics Simulations and Single-Molecule Force  
Spectroscopy**

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## Protein Sequences

### **pET28a-ybbR-HRV3C-6xHIS-CBM(C63S)-CttA-XDoc**

MGTDLSLEFIASKLALAVLFLFQGPLQHSHHHHPWTSASMANPVSGLNKVEFYNSNPS  
DTTNSINPQFKVTNTGSSAIDLKSLTLRYYYTVDGQKDQTFWSDHAAIIGSNNGSYNG  
ITSNVKGTFFVKMSSSTNNADTYLEISFTGGTLEPGAHVQIQGRFAKNDWSNYTQSN  
DYSFKSASQFVEWDQVTAYLNGVLVWGKEPGGSSVVPSTQPVTTPPATTKPPATTI  
PPSDDPNAVVPNTVTSVKTQYVEIESVDGFYFNTEDKFDTAQIKKAVLHTVYNEG  
YTGDDGVAVVLREYESEPDITAELTFGDATPANTYKAVENKFDYEIPVYNNATL  
KDAEGNDATVTVYIGLKGDTDLNIVDGRDATATLTYAATSTDGKDATTVALSP  
STLVGGNPESVYDDFSAFLSDVKVDAGKELTRFAKKAERLIDGRDASSILTFYTKSS  
VDQYKDMAANEPNKLWDIVTGDAEEE\*

### **pET28a-ybbR-HRV3C-6xHIS-CBM(C63S)-ScaB-XDoc**

MGTDLSLEFIASKLALAVLFLFQGPLQHSHHHHPWTSASMANPVSGLNKVEFYNSNPS  
DTTNSINPQFKVTNTGSSAIDLKSLTLRYYYTVDGQKDQTFWSDHAAIIGSNNGSYNG  
ITSNVKGTFFVKMSSSTNNADTYLEISFTGGTLEPGAHVQIQGRFAKNDWSNYTQSN  
DYSFKSASQFVEWDQVTAYLNGVLVWGKEPGGSSVVPSTQPVTTPPATTKPPATTI  
PPSDDPNAVVPATNSGDVSVYYTIVAGYFVSHDTGVRGNGEAGGFVKNQVVK  
ITKYTKDKNGNIIANDLDLANVNYNGYTPNKAYIDRFVGDPAQNPTDQTLANFADN  
FAYDIPVYYGGDQLVDENGQPLTVKAYIGVKGDTNLDVDFVDFGRDATATLTYARVS  
TDNYTEADTPISPAPFITGADDPLDDLAFLSDVDTNEWKDNWKLAREDRILDGR  
DATNILTYARASAGDGEYAGLDAQELWNTVVPNRFG\*

### **pET28a-CohE-CBM(C63S)-HIS-ybbR**

MGTALTDTRGMTYDLDPKDGSSAATKPVLEVTKKVFDTAADAAGQTVTVEFKVSG  
AEGKYATTGYHIYWDERLEVVAATKTGAYAKKGALEDSSLAKAENNGNGVFFVAS  
GADDDFGADGVMWTVELKVPADAKAGDVYPIDVAYQWDPSKGLFTDNKDSAQ  
GKLMQAYFFTQGIKSSSNPSTDEYLVKANATYADGYIAIKAGEPGSSVVPSTQPVTTP  
PATTKPPATTIPPSDDPNAMANTPVSGLNKVEFYNSNPSDTTNSINPQFKVTNTGSS

AIDLSKLTLRYYYYTVDGQKDQTFWSDHAAIIGSNGSYNGITSNVKGTFVKMSSSTNN  
ADTYLEISFTGGTLEPGAHVQIQGRFAKNDWSNYTQSNDYSFKSASQFVEWDQVTA  
YLNGVLVWGKEPGELKLPRSRHHHHHHGSLEVLFGPDSLEFIASKLA\*

## Supplementary Figures

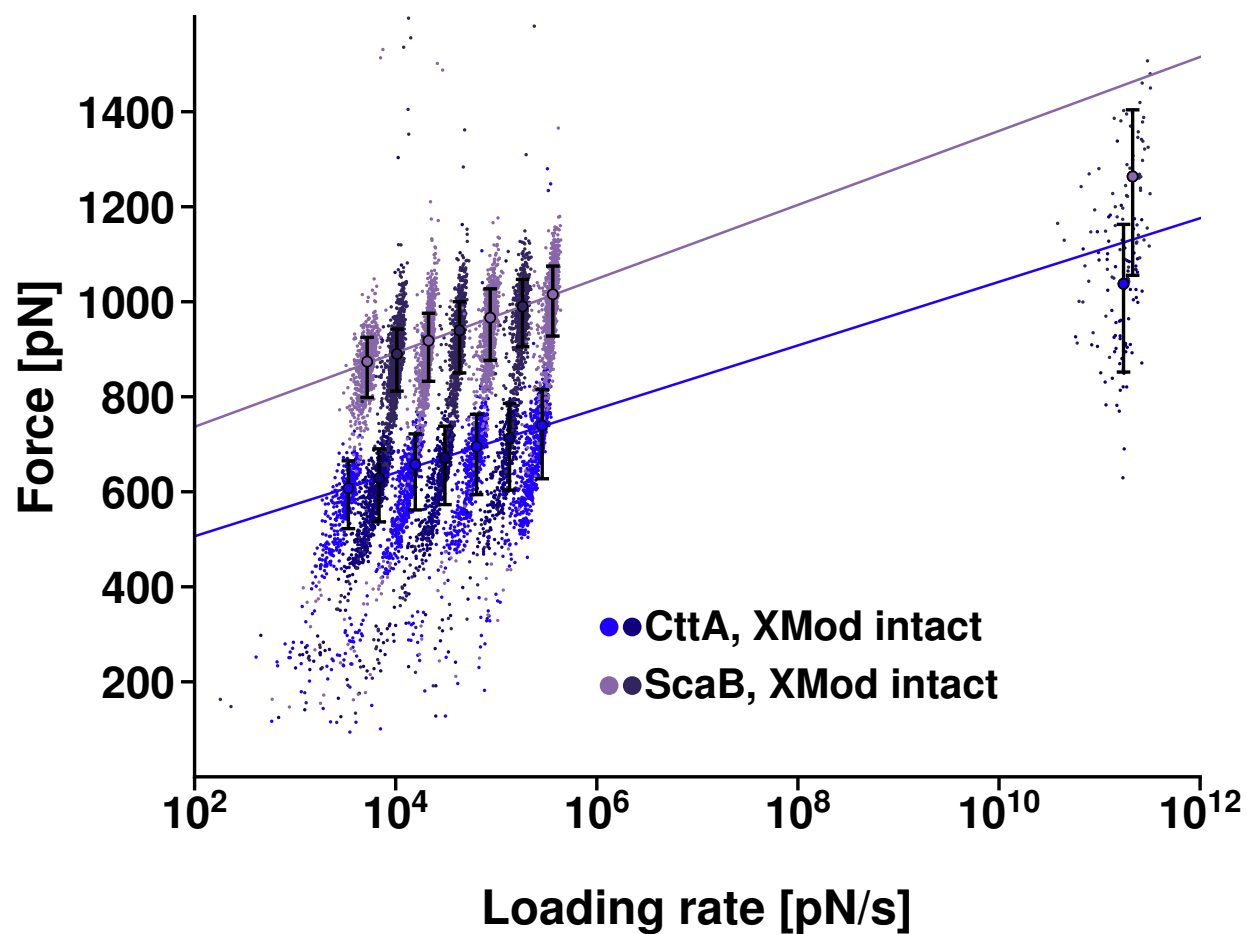


Figure S1: Dynamic force spectrum of curves with no apparent X-module unfolding fitted with a Bell Evans model. Extrapolating this fit to the simulated data reveals that the simulated rupture forces are approximately 8% lower than expected for the CttA-XDoc:CohE complex and 14% lower than expected for the ScaB-XDoc:CohE complex.

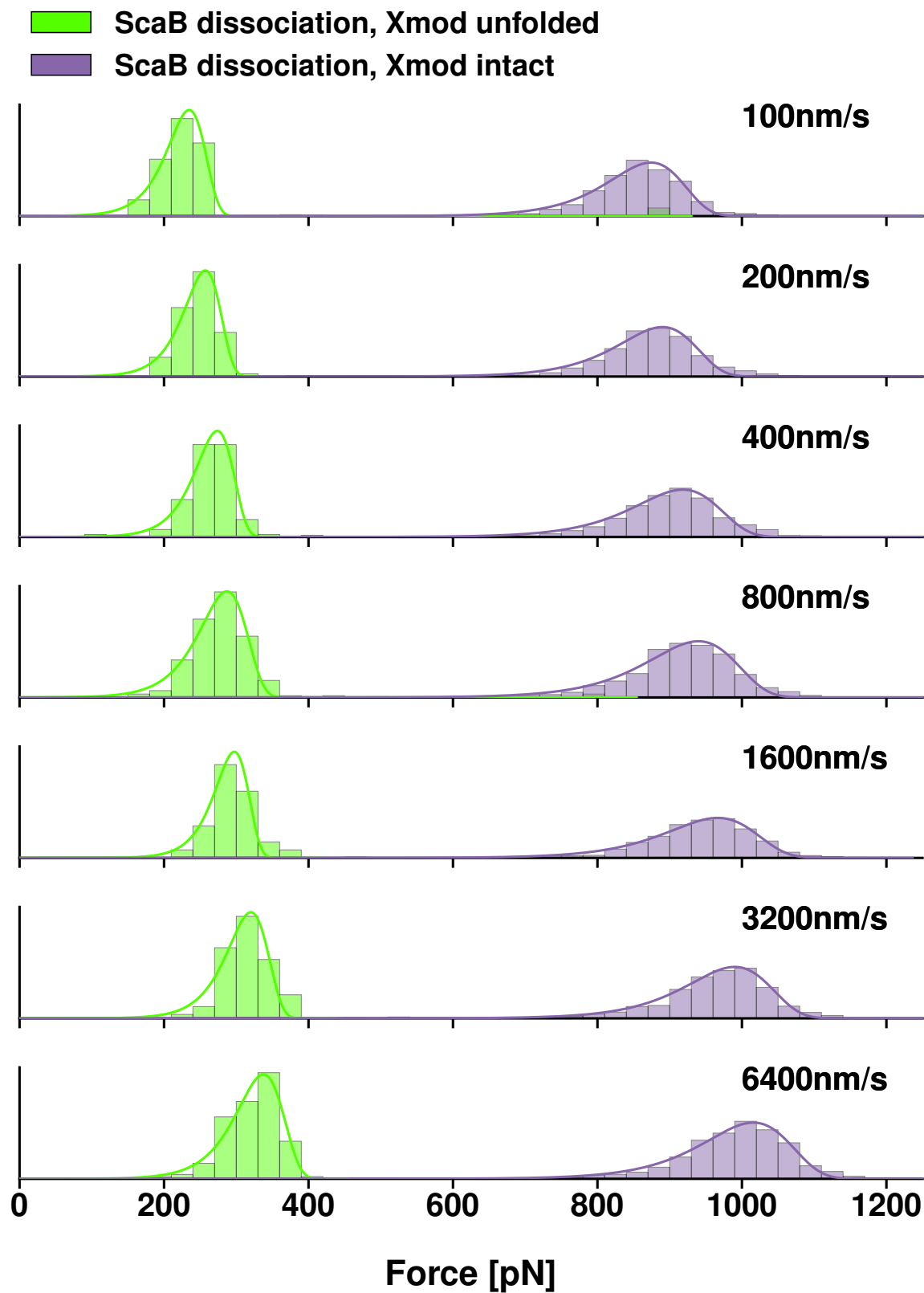


Figure S2: **Complex rupture forces of *Rf* ScaB-XDoc:CoHE.** Green bars shows the rupture force of the complex following Xmod unfolding. Purple bars show the rupture force of the complex with Xmod intact.

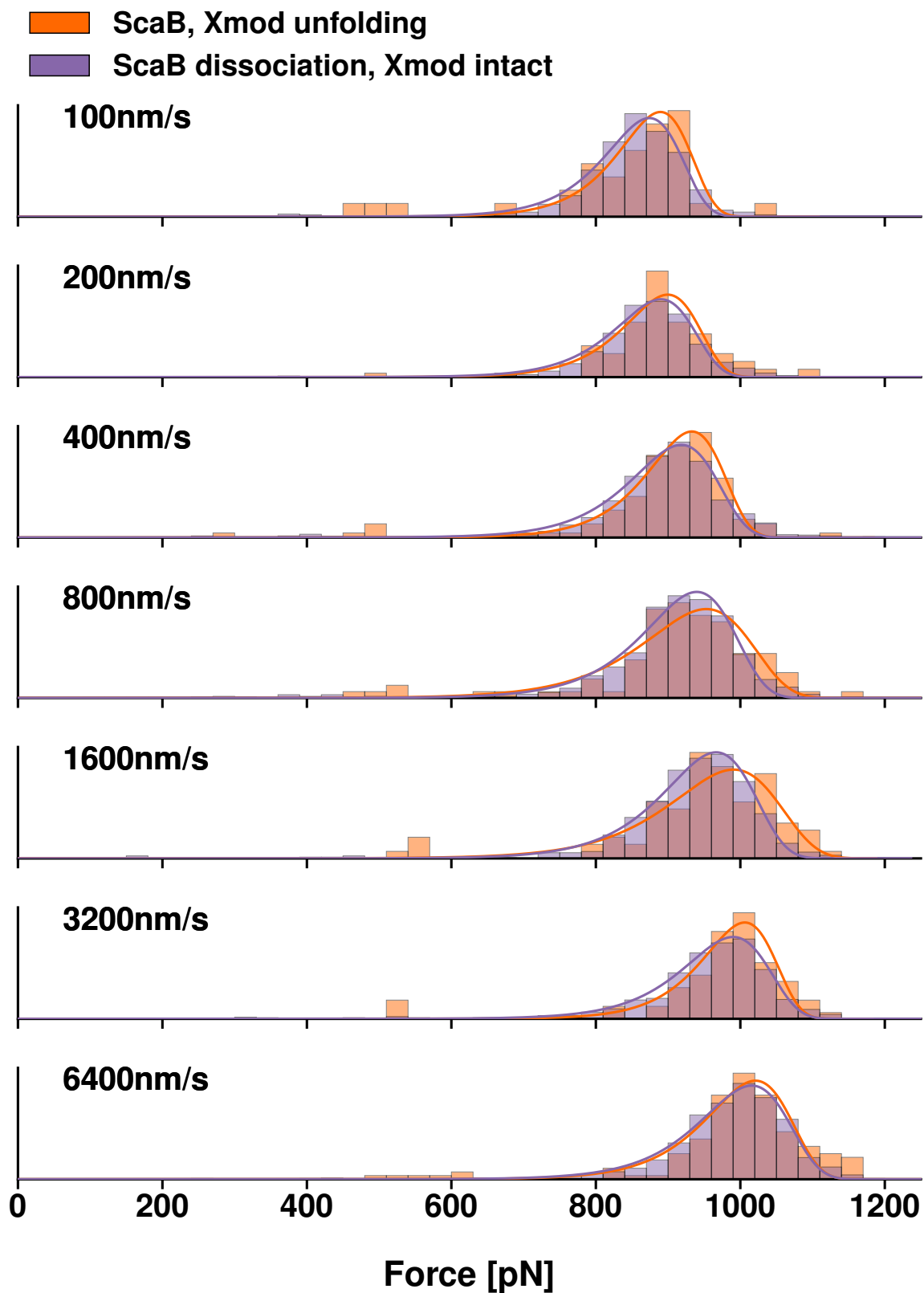


Figure S3: Complex rupture forces with XMod intact vs. X-module unfolding forces for *Rf* ScaB-XDoc:CohE. Orange bars show the unfolding force distribution of Xmod domains. Purple bars show the force distribution of complex rupture events with Xmod intact.

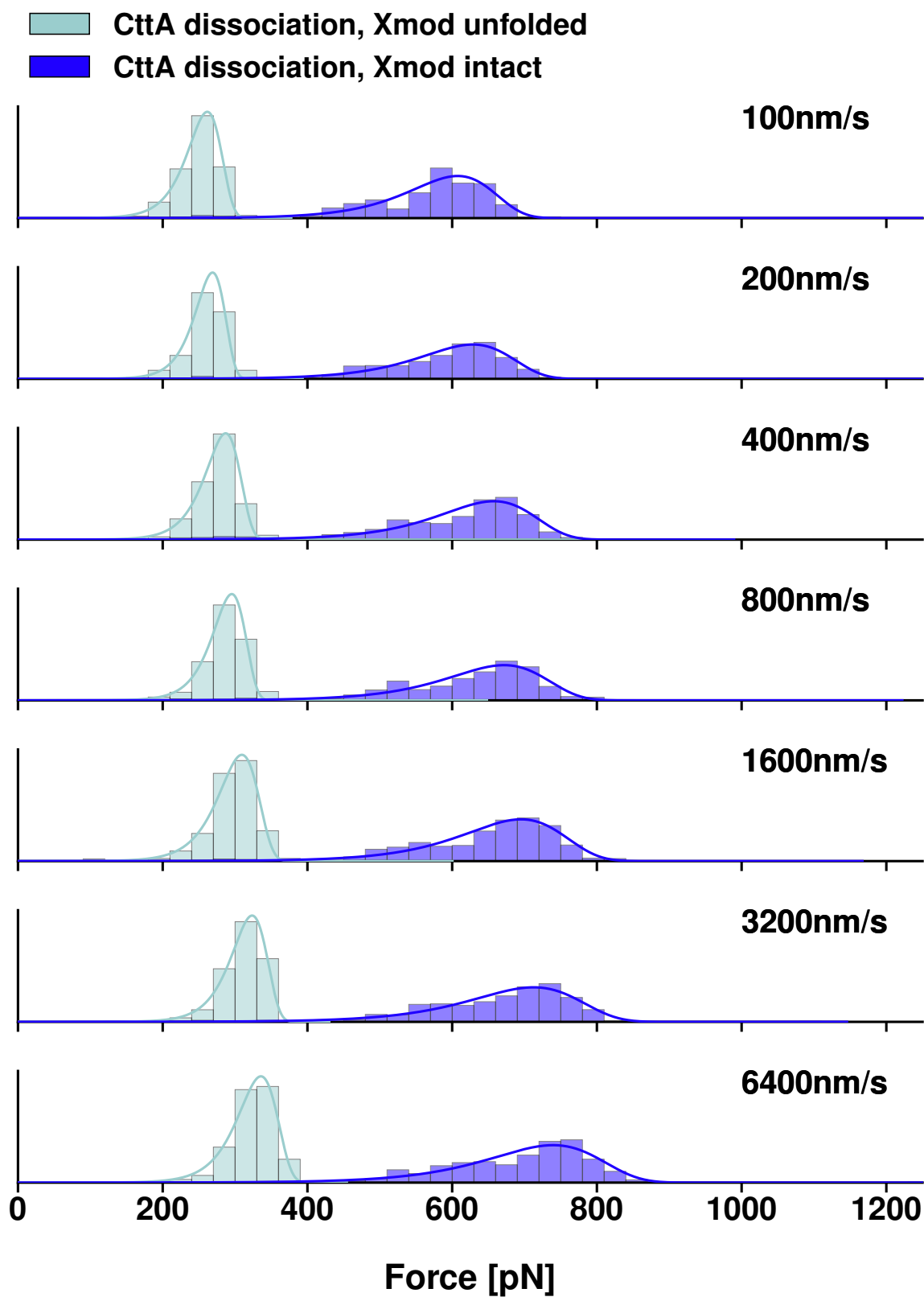


Figure S4: **Complex dissociation forces of *Rf* CttA-XDoc:CohE.** Teal bars shows the rupture forces of the complex following XMod unfolding. Blue bars show the rupture force distribution of the complex with XMod intact.

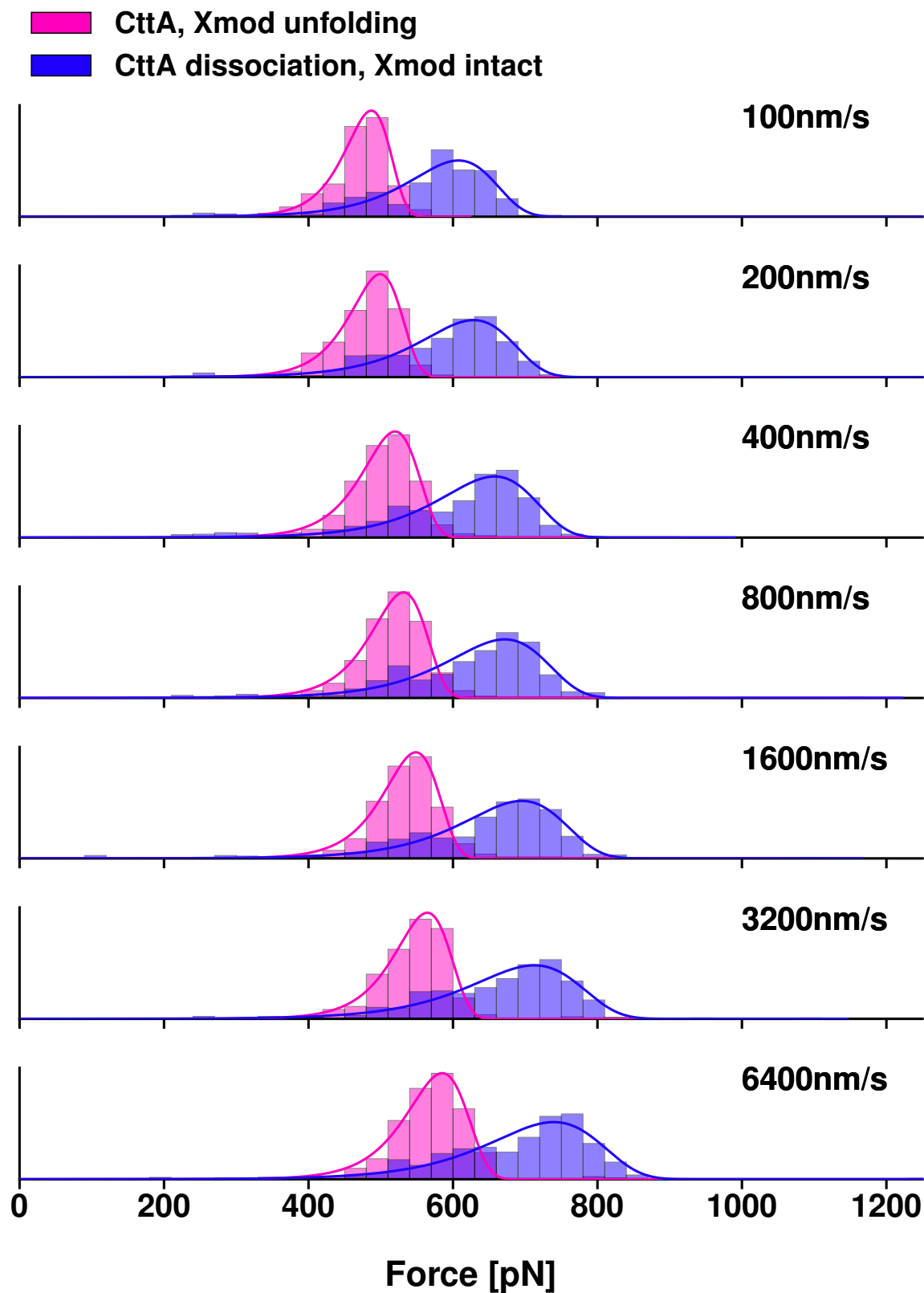
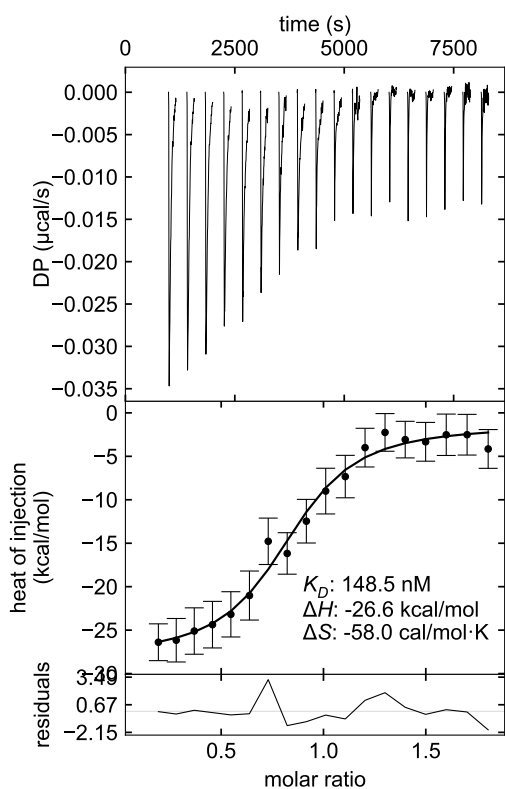


Figure S5: Complex rupture forces with Xmod intact vs. X-module unfolding forces for *Rf* CttA-XDoc:CohE. Pink bars show the unfolding force distribution of Xmod domains. Blue bars show the force distribution of complex rupture events with XMod intact.



## A - ScaB



## B - CttA

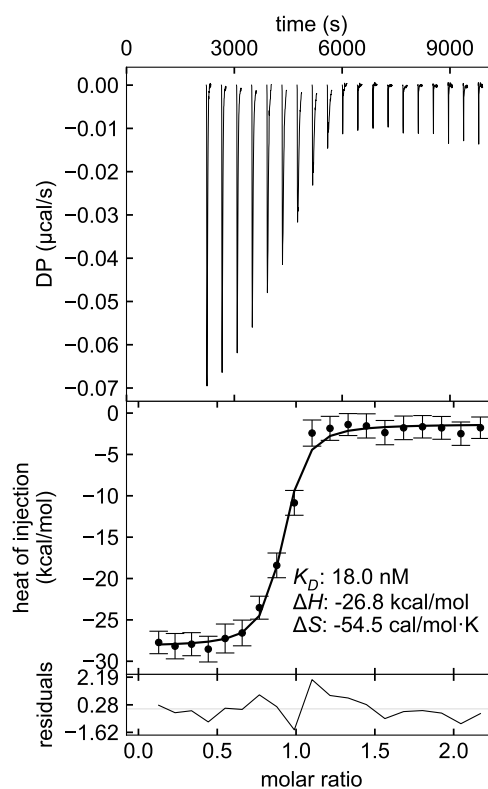


Figure S6: **Isothermal titration calorimetry.** **A:** The calorimeter's cell contained ybbR-CBM(C63S)-ScaB-XDoc at  $4.04 \mu\text{M}$ , the injection syringe  $35.0 \mu\text{M}$  CohE-NGL. **B:** The calorimeter's cell contained ybbR-CBM(C63S)-CttA-XDoc at  $4.04 \mu\text{M}$ , the injection syringe contained  $34.7 \mu\text{M}$  CohE-NGL.