Supplementary Materials

Tables

Table S1 Modified formulas for protein quantitation

Groups	Modified formula	Ranges of N/Ps
BSA–CTA	$C_{mg/mL} = 1.412A_{280} - 0.625A_{260}$	0–1.3280
BSA–dsDNA	$C_{mg/mL} = 1.272A_{280} - 0.579A_{260}$	0–1.4056
Lysozyme–CTA	$C_{mg/mL} = 1.435A_{280} - 0.605A_{260}$	0–1.5770
Lysozyme–dsDNA	$C_{mg/mL} = 1.852A_{280} - 0.942A_{260}$	0–1.5209
*Bsu*DnaG–CTA	$C_{mg/mL} = 1.216A_{280} - 0.513A_{260}$	0–1.4955
DBD–dsDNA	$C_{mg/mL} = 1.343A_{280} - 0.678A_{260}$	0–1.5190

Table S2 Quantitation of *Mtu*P49–CTG by Bradford assay and modified formulas

	Protein		Ranges
	Curves	mg/mL	
Bradford assay	$Y = 0.5176X + 0.2051$, $R^2 = 0.9927$	0.222 ± 0.008	0.076–1.22 mg/mL
Formula method	$C_{mg/mL} = 1.340A_{280} - 0.636A_{260}$	0.227 ± 0.010	0/1 to 3/1 of N/Ps

Figures

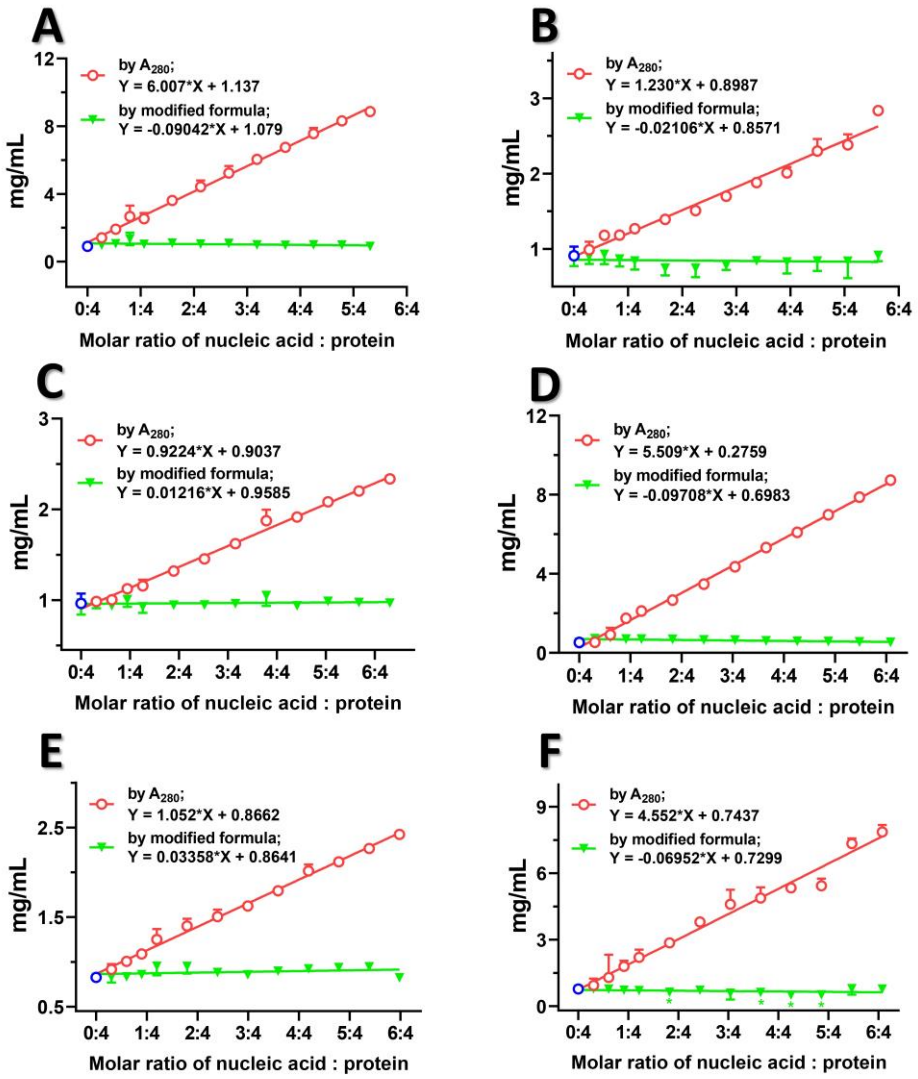

Fig. S1 Protein quantitation by modified formulas**. A** BSA–CTA mixture. **B** BSA–dsDNA mixture. **C** lysozyme–CTA mixture. **D** lysozyme–dsDNA mixture. **E** *Bsu*DnaG–CTA complex/mixture. **F** Fkh1–DBD–dsDNA complex/mixture. The protein concentrations among the groups were first measured by Nanodrop and marked as red circles, where the blue circles points represent the actual concentrations with no nucleic acid added. The green triangles points represent the quantified protein concentrations among the above groups, as calculated by the modified formulas in Supplementary Data-Table S1, based on A_{280} and A_{260}

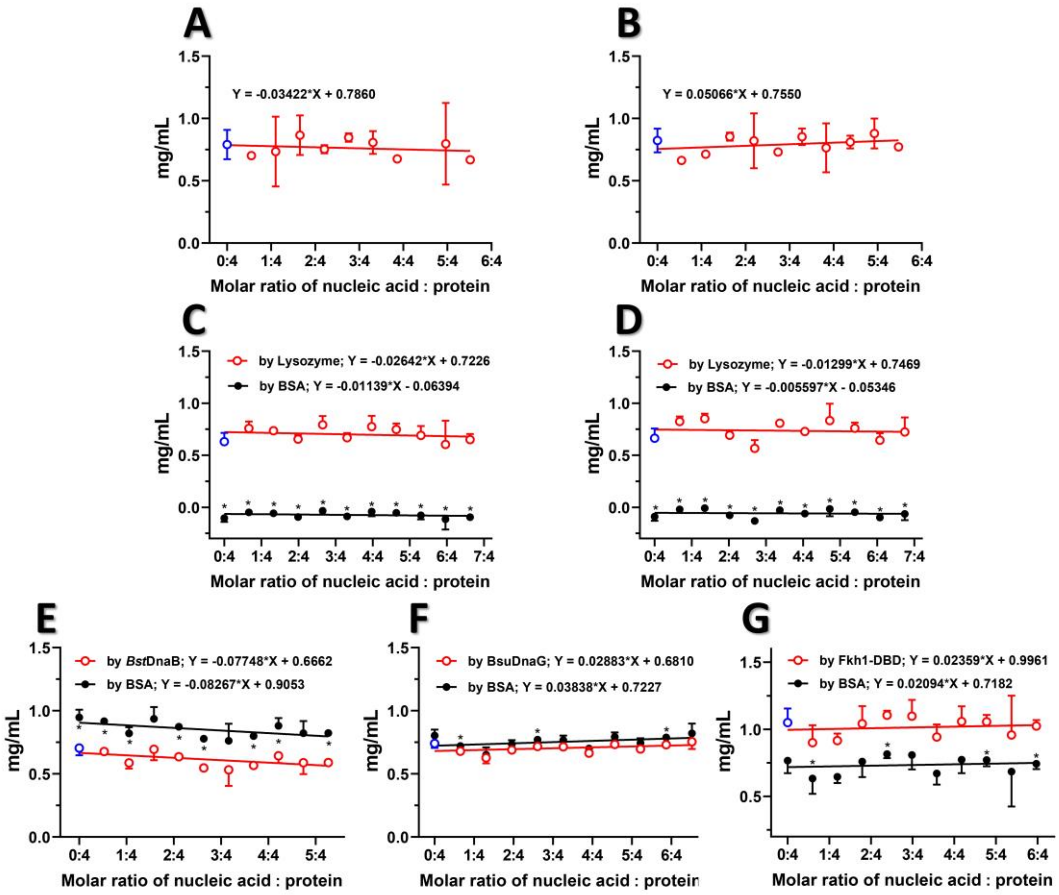

Fig. S2 Protein quantitation by Bradford assay. **A** BSA–CTA mixture. **B** BSA–dsDNA mixture. **C** lysozyme–CTA mixture. **D** Lysozyme–dsDNA mixture. **E** *Bst*DnaB–dT16 complex/mixture. **F** *Bsu*DnaG–CTA complex/mixture. **G** Fkh1–DBD–dsDNA complex/mixture. In panels **A** and **B**, the concentration was calculated based on a standard curve using BSA. In panels **C**–**G**, the concentration was calculated based on a standard curve using BSA (marked as black dots) and the target proteins themselves (marked as red circles). The blue circles represent the actual concentrations of the proteins. Unpaired *t*-test by the Holm-Sidak method was used to analyze statistical difference, with * for $p < 0.05$

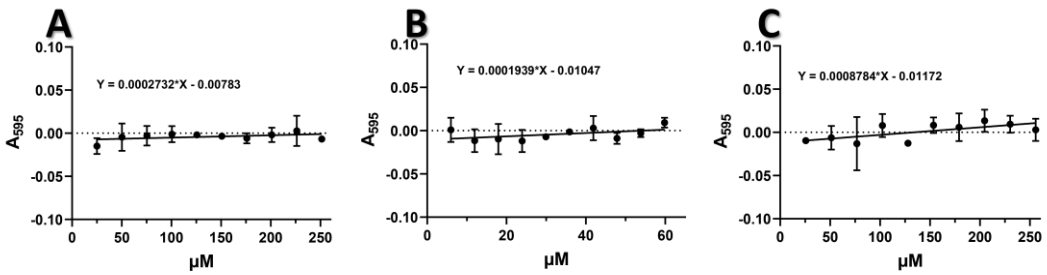

Fig. S3 Coomassie brilliant blue coloring with DNA. **A** CTA. **B** dT16. **C** dsDNA. The results showed that these nucleic acids hardly react with Coomassie brilliant blue G250 within a certain range