Structural Insights on PHA Binding Protein PhaP from *Aeromonas hydrophila*

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Fig.S1. Gel filtration profiles and SDS-PAGE gels of purified whole length PhaP$_{Ah}$ and N-terminal truncation PhaP$_{Ah}$. The coordinate graph on the top right of each figure is a plot of log molecular weight against elution volume of the column. Gel filtration standards (Bio-Rad) used in the experiment were vitamin B12 (1.3 kD), horse myoglobin (17 kD),chicken ovalbumin (44 kD), bovine gamma-globulin (158 kD), and bovine thyroglobulin (670 kD). Calculated molecular weight from gel filtration of whole length PhaP$_{Ah}$ and N-terminal truncation PhaP$_{Ah}$ is 34.980 and 10.814 kD. However, the plots which Lg values were below 4 couldn't fit the line well. Static Light Scattering (SLS) have been done to measure the exact molecular weight of whole length PhaP$_{Ah}$ and N-terminal truncation PhaP$_{Ah}$ (Fig. S3).

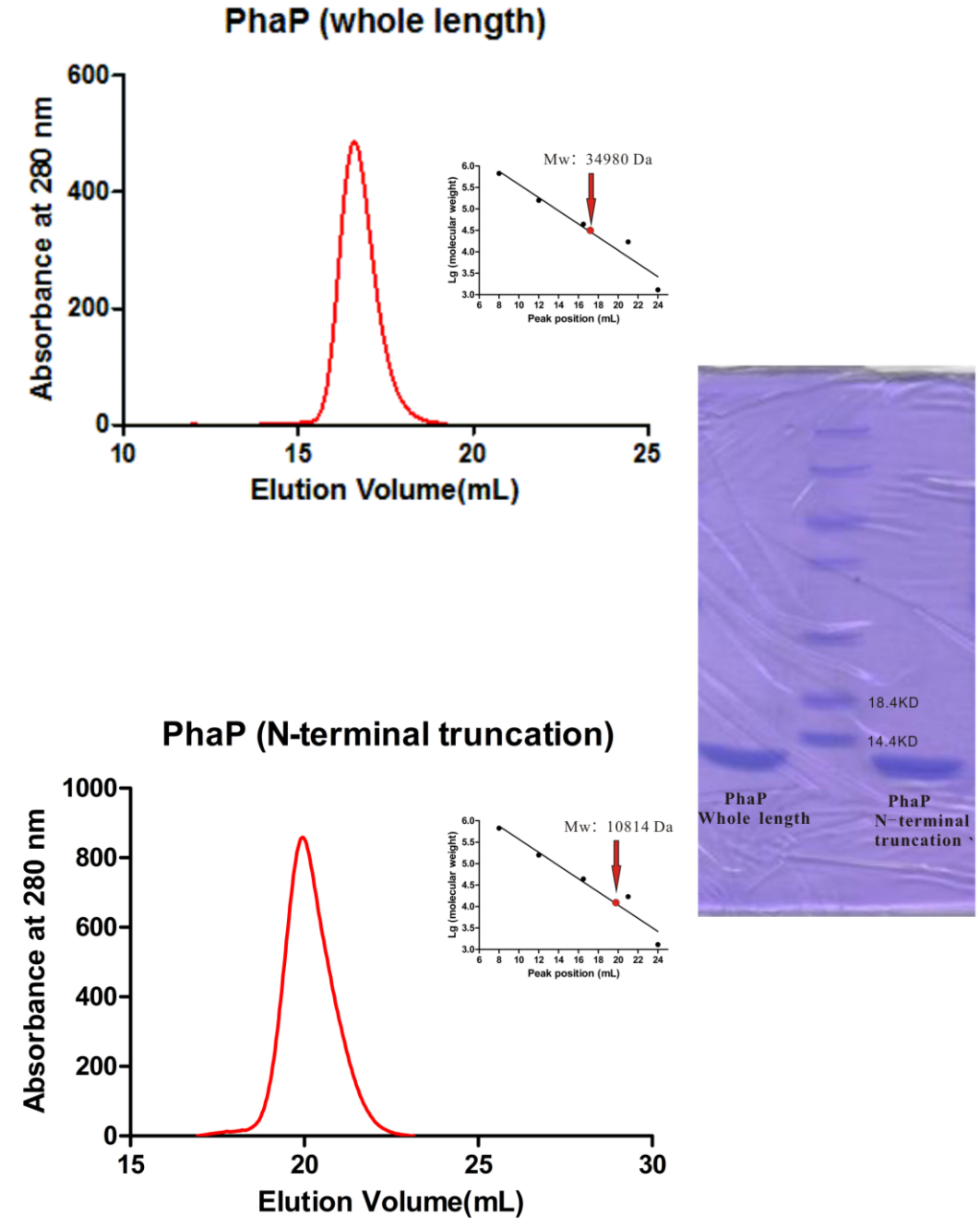
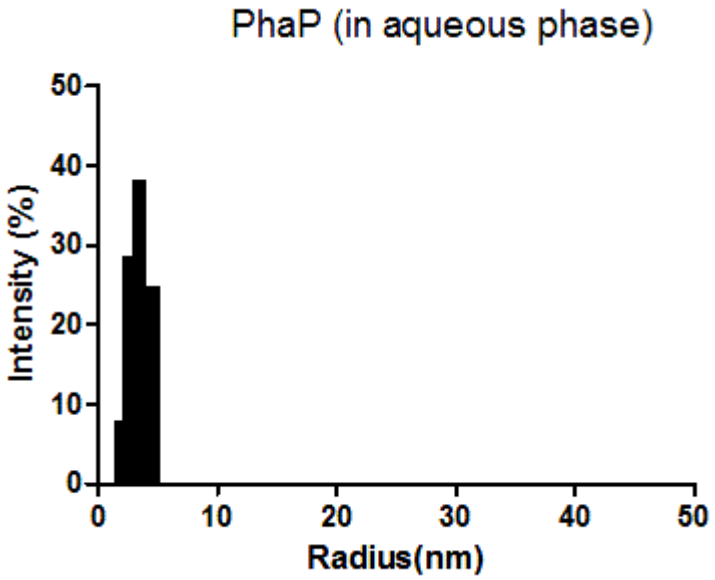


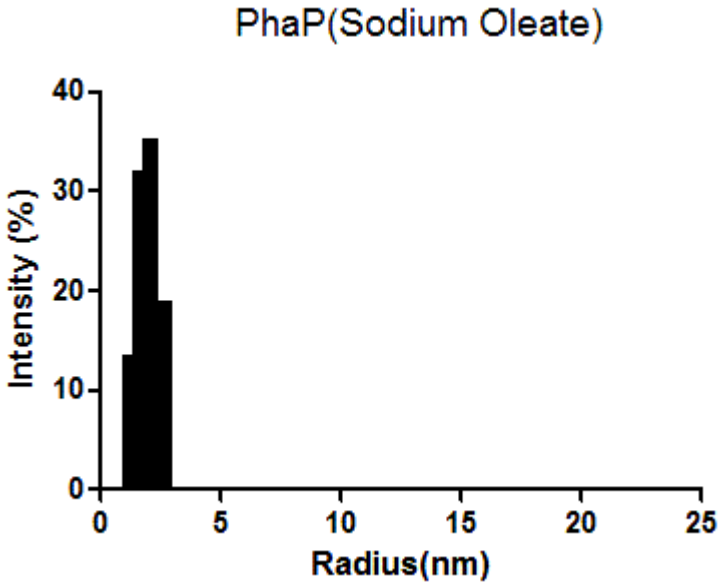
Fig. S2. DLS measurements of 0.5 mg/ml PhaP$_{Ah}$ sample in aqueous phase (A) and sodium oleate phase(B).

A



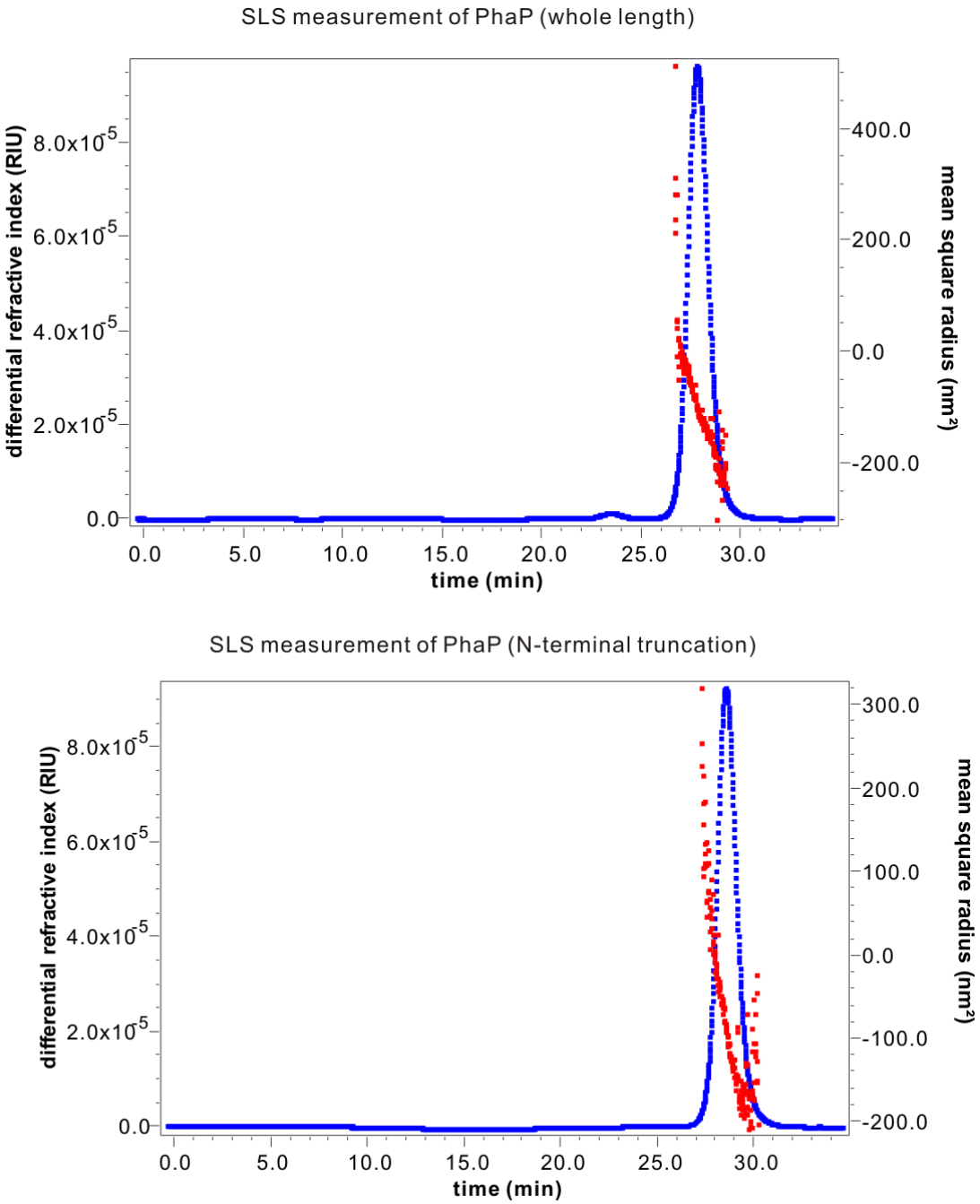
Buffer	Radius(nm)	Pd(%)	Mw-R(kDa)
50mM Tris Buffer	3.4	22.5	69

B



Buffer	Radius(nm)	Pd(%)	Mw-R(kDa)
10mM sodium oleate,50mM Tris Buffer	1.93	24.0	16

Fig. S3. SLS measurements of purified whole length PhaP$_{Ah}$ and N-terminal truncation PhaP$_{Ah}$



	PhaP（whole length）	PhaP（N-terminal truncation）
Calculated Mass (μg)	320.71	301.86
Mn（Da）	4.370×10^4	3.805×10^4
Mp（Da）	4.561×10^4	3.984×10^4
Mw（Da）	4.388×10^4	3.826×10^4

Fig. S4. Packing of in the space and interaction between each tetramer

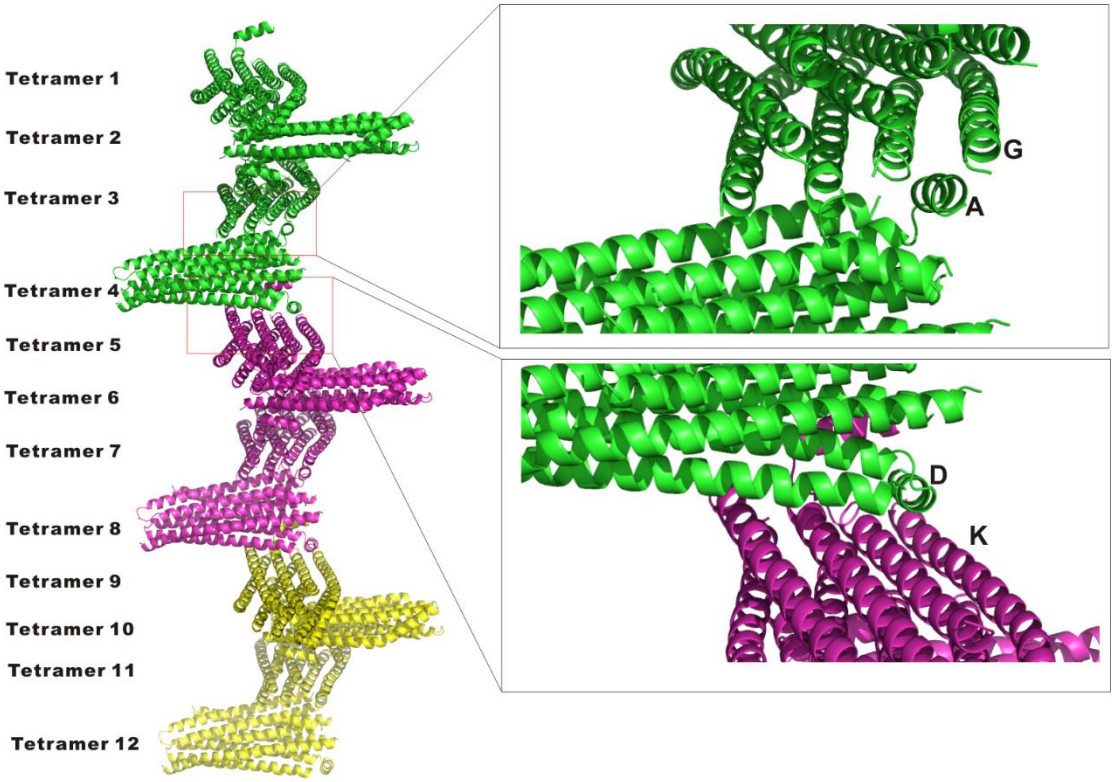


Fig. S5. N-terminal tail and the positive groove of the tetramer

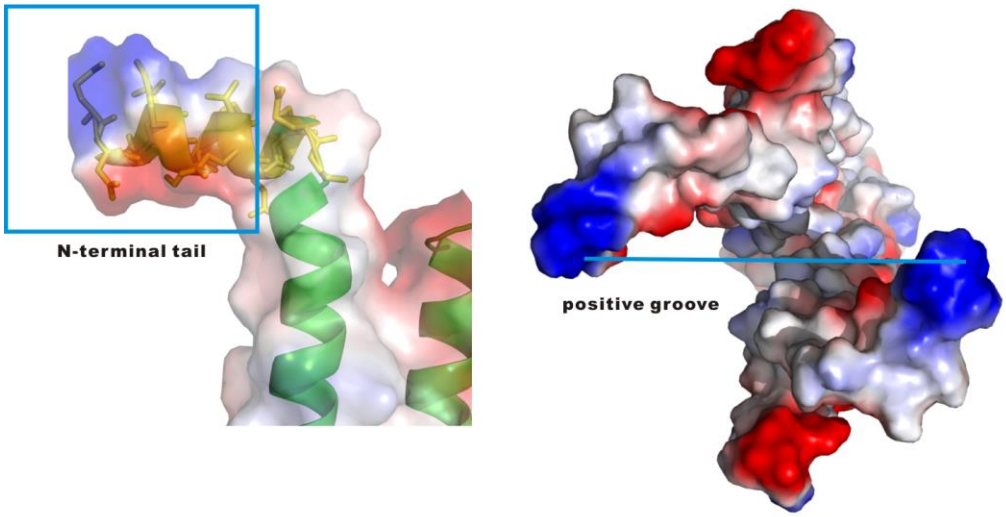


Fig. S6. Tyr residues has been labelled in the structure. All these Tyr residues are in the hydrophobic core which are inside the tetramer.

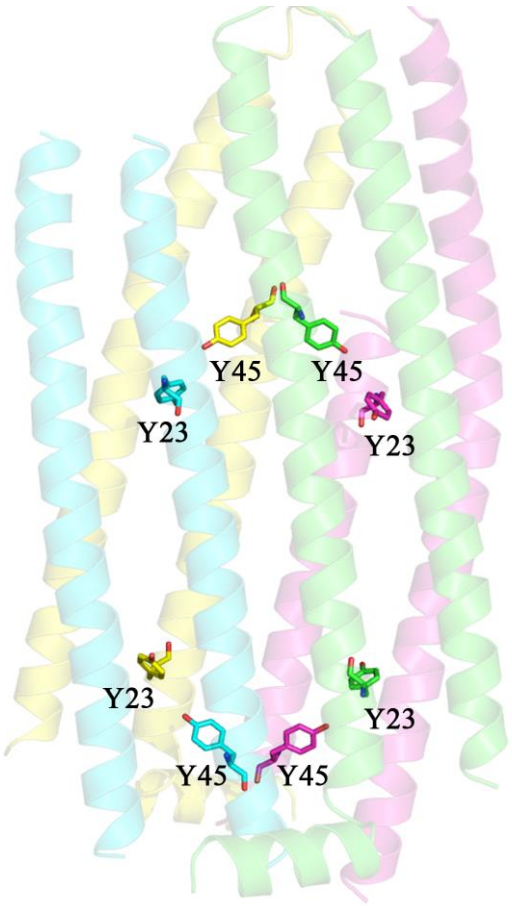


Fig. S7. Circular dichroism measurements of PhaP$_{Ah}$ and the buffer control (50 mM Tris and 500 mM NaCl)