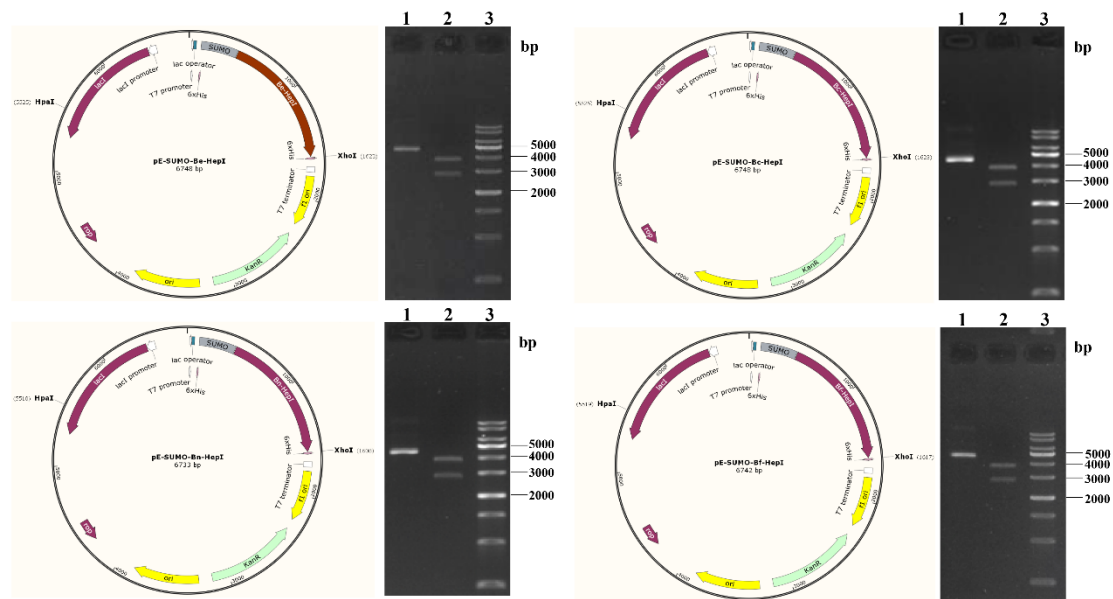


## Supplementary data

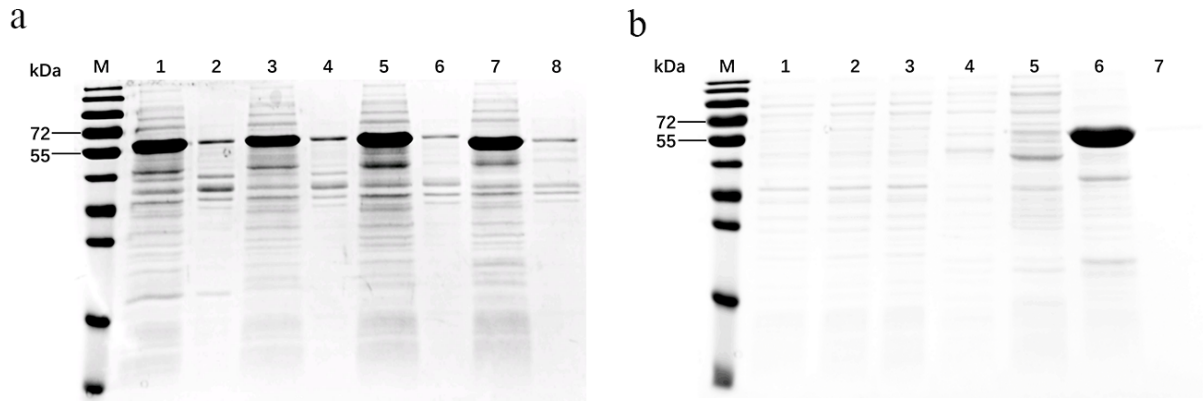
**Table S1.** Analysis of the CAZy database PL13 family and the Centrum bacteriophage library.

Number	Organism	Database	Speciality
1	<i>Bacteroides caecimuris</i>	CAZy	
2	<i>Bacteroides cellulosilyticus</i>		
3	<i>Bacteroides helcogenes</i>		
4	<i>Bacteroides heparinolyticus</i>		
5	<i>Bacteroides intestinalis</i>		
6	<i>Bacteroides ovatus</i>		
7	<i>Bacteroides sp</i>		
8	<i>Bacteroides stercoris</i>		
9	<i>Bacteroides thetaiotaomicron</i>		
10	<i>Bacteroides xylanisolvens</i>		
11	<i>Bacteroides uniformis</i>	Our Center	Y
12	<i>Bacteroides fragilis</i>		Y
13	<i>Bacteroides thetaiotaomicron</i>		
14	<i>Bacteroides caccae</i>		Y
15	<i>Bacteroides eggerthii</i>		Y
16	<i>Bacteroides merdae</i>		Y
17	<i>Bacteroides cellulosilyticus</i>		
18	<i>Bacteroides ovatus</i>		
19	<i>Bacteroides clarus</i>		Y
20	<i>Parabacteroides distasonis</i>		Y
21	<i>Bacteroides vulgus</i>		Y
22	<i>Bacteroides stercoris</i>		
23	<i>Bacteroides nordii</i>		Y
24	<i>Bacteroides fingoldii</i>		Y
25	<i>Bacteroides cellulosilyticus</i>		
26	<i>Bacteroides xylanisolvens</i>		
27	<i>Bacteroides sp</i>		

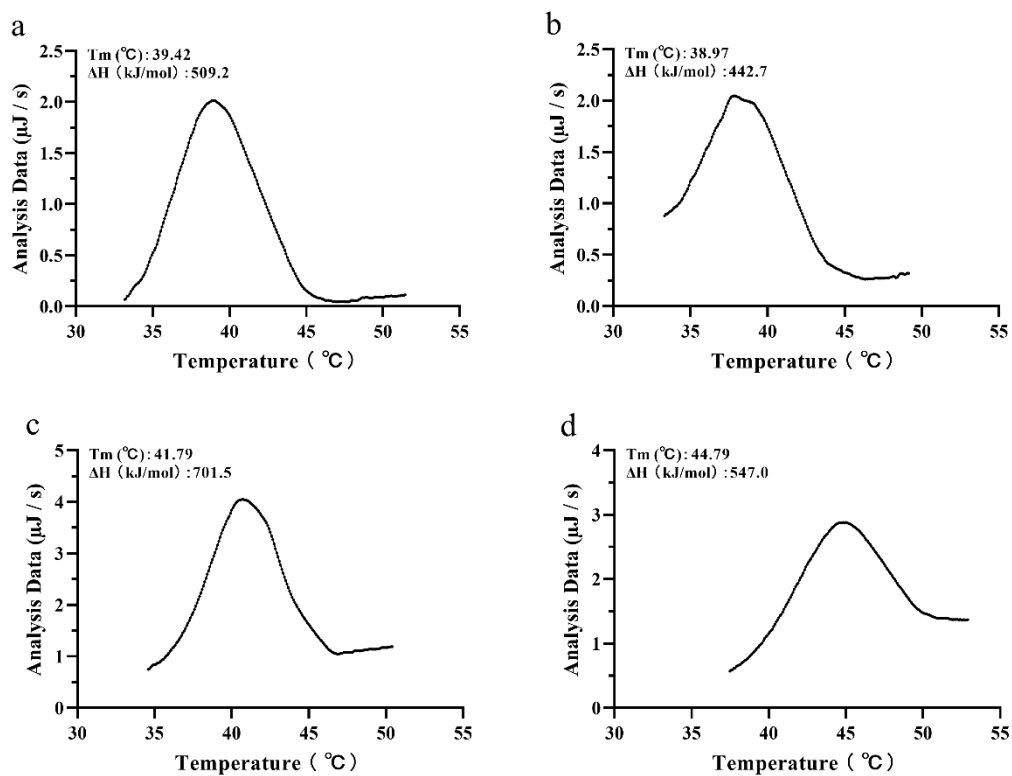
Y means only present in Our Center.



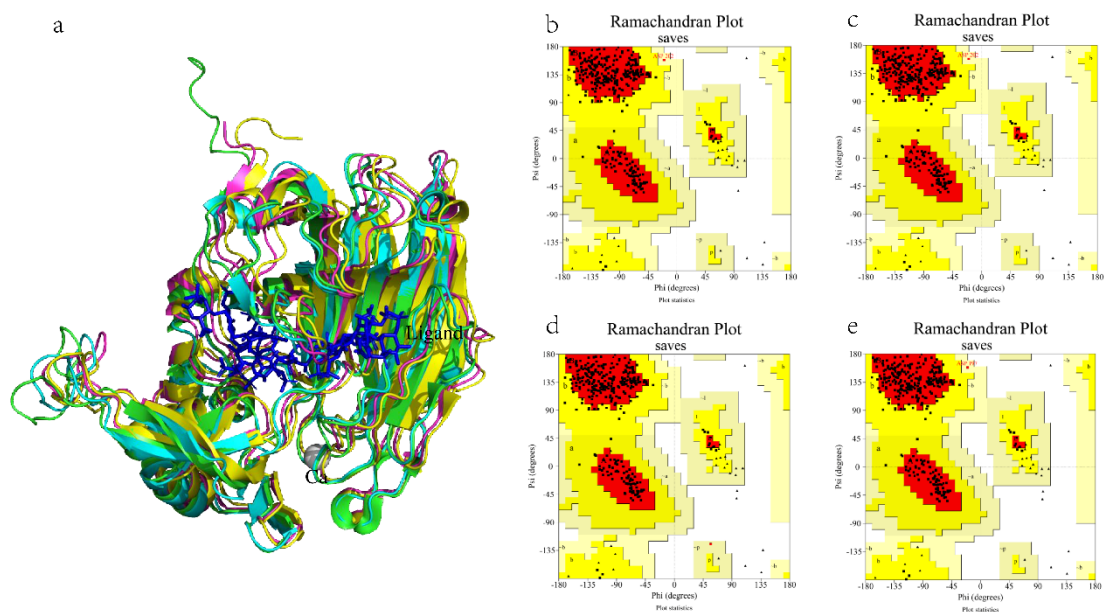
**Figure S1.** The heterologous expression vector was constructed with the fusion tag SUMO-Tag and verified using double digestion with HpaI and XhoI.



**Figure S2.** Protein expression purification analysis (a) Lane M- protein marker; Lanes 1, 3, 5, and 7- Bc-HepI, Be-HepI, Bf-HepI, and Bn-HepI recombinant strains of bacteriophage lysate supernatants; Lanes 2, 4, 6, and 8- bacterial lysis precipitate of Bc-HepI, Be-HepI, Bf-HepI, and Bn-HepI recombinant strains; (b) Lane M- protein marker; Lanes 1–7- protein eluate imidazole concentrations of 5, 10, 50, 100, 150, 300, 500. The short black line indicates that the molecular weights of the markers are 72 kDa and 55 kDa.



**Figure S3.** Determination of melting temperatures ( $T_m$ ) of Bc-HepI (a), Be-HepI (b), Bf-HepI (c), and Bn-HepI (d) using differential scanning calorimetry.



**Figure S4.** Protein three-dimensional (3D) structure simulation, overlap, and evaluation. (a) The 3D structures of Bc-HepI, Be-HepI, Bf-HepI, and Bn-HepI are shown overlapping. The blue rod-like structure is the substrate ligand. (b-e) Evaluation of the 3D simulated structures of Bc-HepI, Be-HepI, Bf-HepI, and Bn-HepI.