

Supplementary figures and figure legends

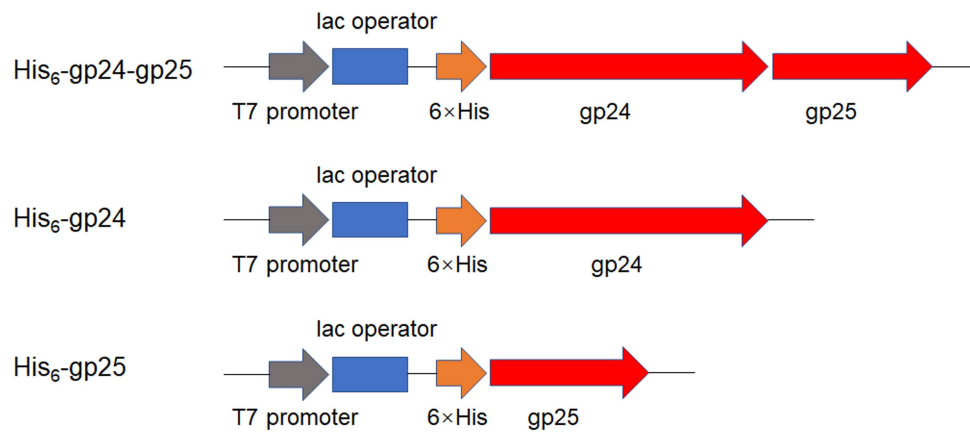


Figure S1. The vectors' architecture of *His₆-gp24-gp25*, *His₆-gp24* and *His₆-gp25*.

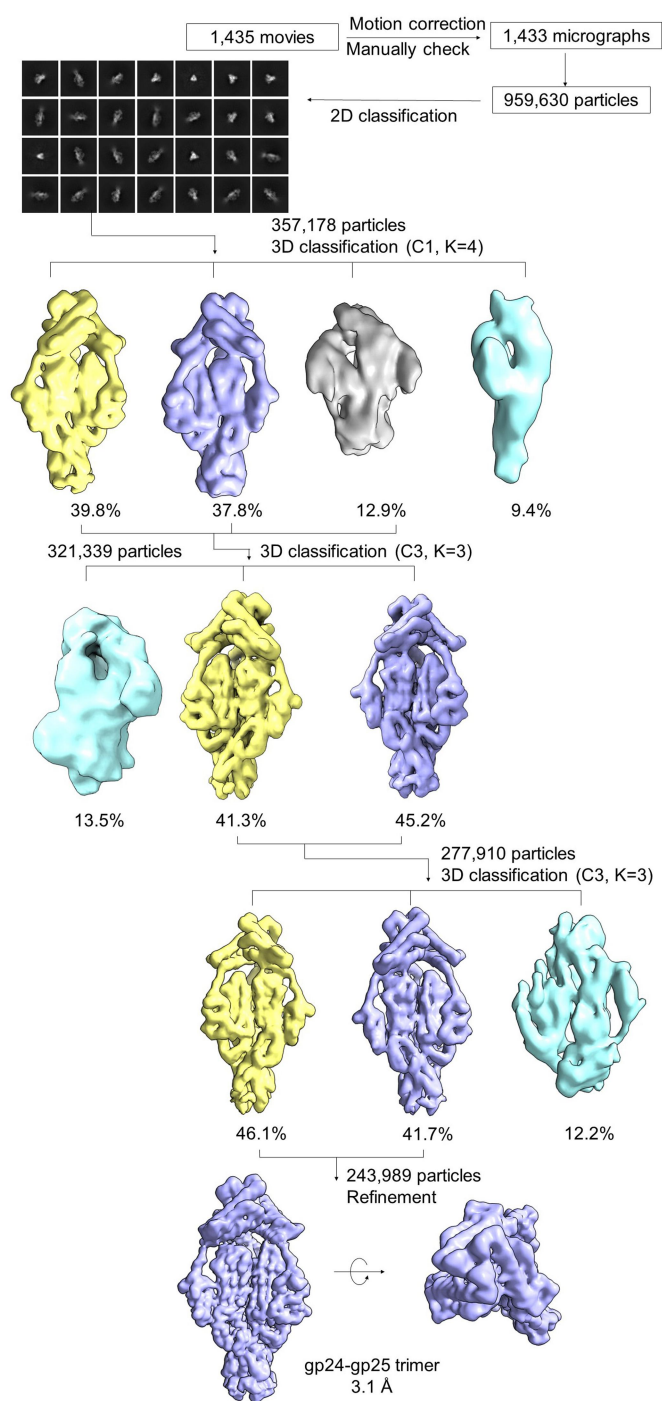


Figure S2. A flowchart of cryo-EM data processing of the gp24-gp25 complex.

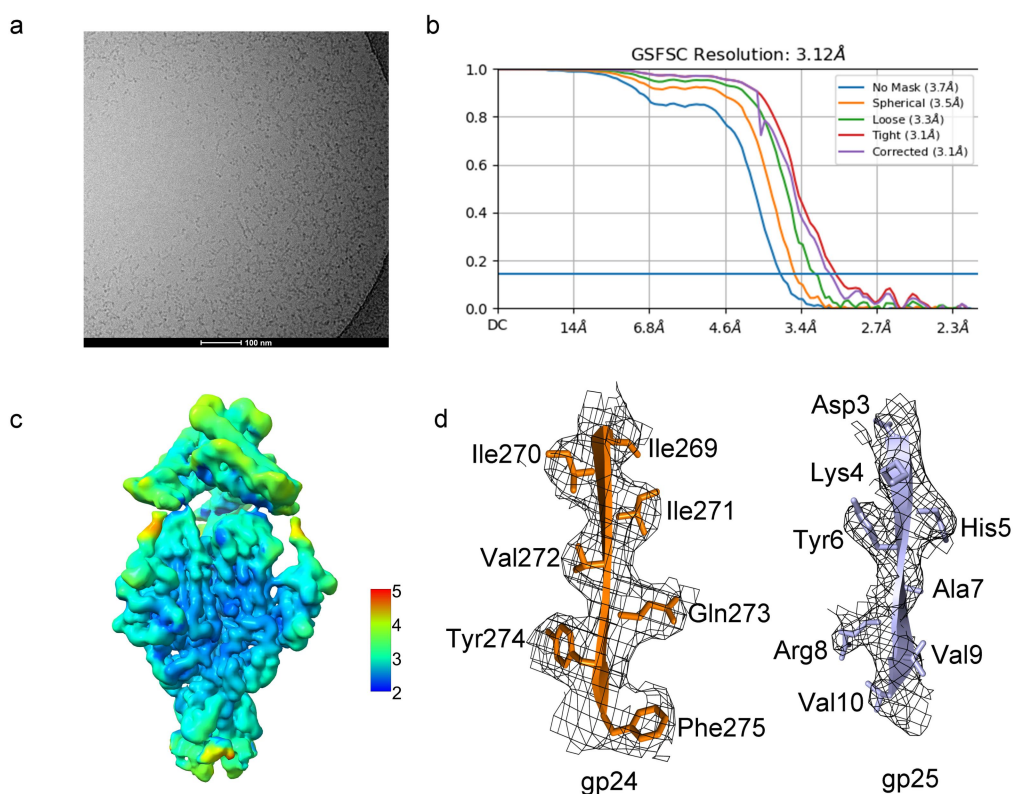


Figure S3. The cryo-EM data analysis of gp24-gp25 complex. (a) A representative raw micrograph of the gp24-gp25 complex. (b) The resolution curve of the cryo-EM maps estimated using the gold-standard Fourier shell correlation at 0.143 criterion. (c) The local resolution map of the gp24-gp25 complex estimated by cryoSPARC 3.1. (d) The models and the corresponding maps for the representative segments of gp24 and gp25.

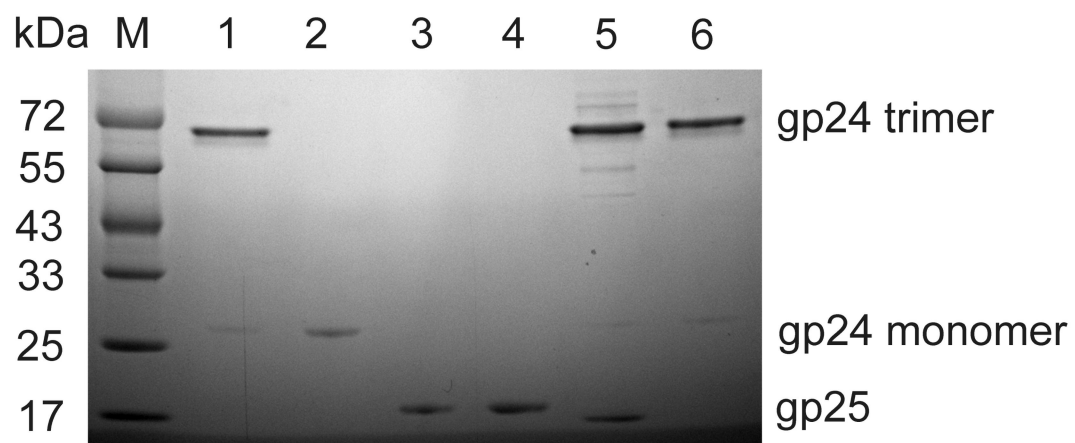


Figure S4. The SDS-PAGE analysis of the purified gp24, gp25 and gp24-gp25 complex. The protein samples were treated with β -Mercaptoethanol without boiling. The lane M represents the standard protein marker, whereas the samples 1~6 are the same as in Figure 1b.

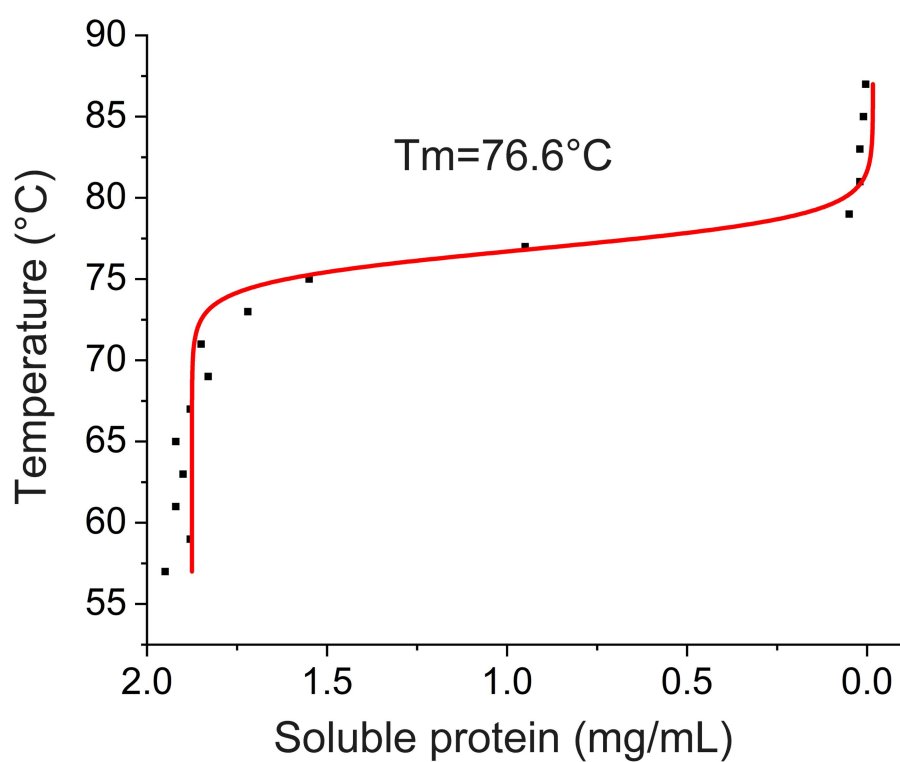


Figure S5. The protein denaturation curve of the gp24 trimer. The calculated T_m value of 76.6°C is labeled.

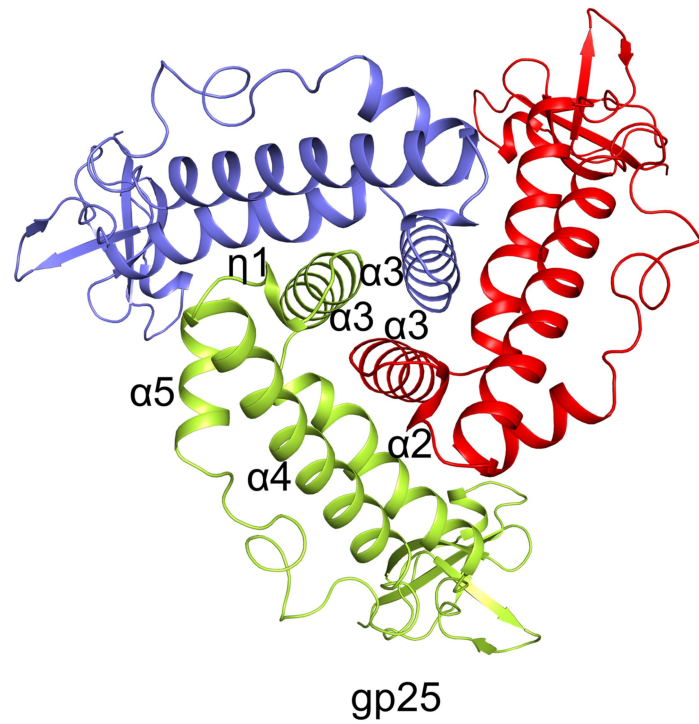


Figure S6. Cartoon representation of gp25 trimer, shown in top view. Three subunits are colored in blue, red and green, respectively.

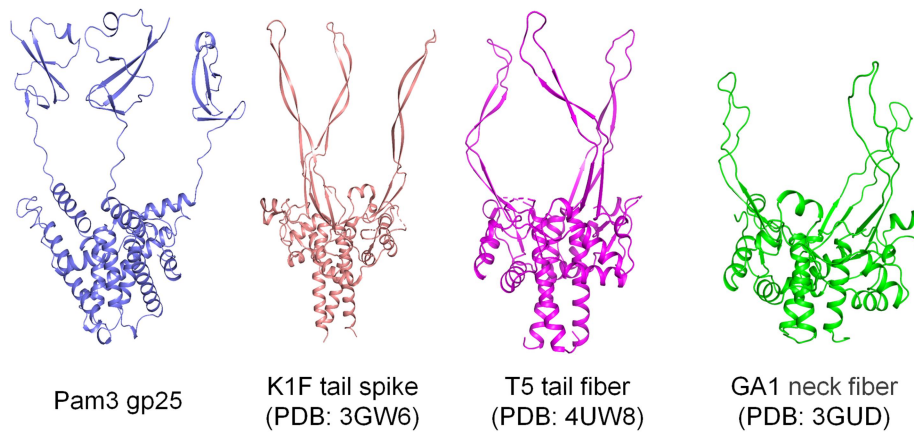


Figure S7. Structures of gp25 and the intermolecular chaperone domains from different phages. The structures are shown in cartoon and colored differently.

Table S1. The mass spectrometry analysis of the intact Pam3 virions.

Gene product	Mw (kDa)	Length (AA)	Coverage	PSMs	Unique Peptides	Predicted protein
gp6	17.2	166	98	1017	18	Cement
gp7	34.1	310	67	949	33	Major capsid
gp3	69.7	621	72	505	37	Portal
gp16	62.3	588	66	325	31	Tape measure protein
gp14	15.3	142	80	144	8	Tube
gp13	41.8	384	65	138	25	Sheath
gp18	11.7	106	69	116	7	Plug
gp22	32.6	299	63	99	10	Baseplate wedge
gp23	26.2	238	50	85	9	Baseplate wedge
gp4	29.8	268	55	83	12	Phage minor capsid protein
gp21	13.9	125	70	77	7	Sheath initiator
gp20	23.5	221	72	70	12	Spike
gp9	13.9	131	50	68	6	Adaptor
gp24	27.3	280	33	66	5	Tail fiber
gp10	16.6	152	45	55	6	Hypothetical protein
gp17	19.8	191	57	51	11	Tube initiator
gp12	17.7	156	62	49	11	Terminator
gp5	377	40.7	32	44	10	Prohead protease
gp11	12	110	60	41	6	Connector
gp19	25.1	229	62	34	9	Hub
gp27	25.6	233	11	2	2	Hypothetical protein
gp57	14.8	138	11	1	1	Deoxycytidylate deaminase