

Table S2. Cryo-electron microscopy data collection and processing statistics

	Wild-type CgeA	CgeA (A42C/D97C)
Data collection and processing		
Magnification	92000	105000
Voltage (kV)	200	300
Frame exposure time (s)	14.62	5.45
Exposure fractionations (n)	50	51
Electron exposure (e ⁻ /Å ²)	49.97	63.6
Defocus range (μm)	-2.0 to -1.0	-1.7 to -0.8
Pixel size (Å)	1.1	0.828
Symmetry imposed	C6	C6
Box size (pixel)	150	200
Micrographs collected (n)	1952	10593
Segments extracted (n)	3559545	436793
Segments after Class 2D (n)	661869	88923
Map resolution (Å)	6.8	3.05
FSC threshold	0.143	0.143
Model building		
Initial model		AlphaFold 3 model
Model composition		
Chains		6
Non-hydrogen atoms		3294
Protein residues		438
R.M.S deviations		
Bond lengths (Å)		0.004
Bond angles (°)		0.666
Validation		
MolProbity score		1.87
Clash score		10.20
Rotamer outliers (%)		0
<i>Ramachandran plot</i>		
Outliers (%)		0
Allowed (%)		3.44
Favored (%)		96.56
PDB accession code		9L9D
EMDB accession code		EMD-62902