

**Figure S1**. *Thecate morphology and flow*. (A) Computational thecate choanoflagellate with five attached bacteria on its collar. Streamlines in the plane of flagellar beat. Colors depict velocity magnitude. (B) Thecate model with no attached bacteria. Streamlines in the plane of flagellar beat. (C) The zoomed-in region about a captured bacterium in (A). (D) Thecate model with five attached bacteria. Streamlines in the plane of flagellar beat. (E) Thecate model with no attached bacteria. Streamlines in the plane normal to flagellar beat. (E) Thecate model with no attached bacteria. Streamlines in the plane normal to flagellar beat. The last column (A - B) and (D - E) show the flow differences around the thecate choanoflagellates with and without bacteria captured outside their collar in the flagellar plane and in the normal plane.



**Figure S2**. Details of bacterial arrangement effect on inward flux, work, and efficiency. Examination of the effects of bacterial arrangement and relative position to the cell body and flagellum on the inward flux to the capture zone, the work done by the flagellum, and the efficiency defined as the inward flux divided by the work. (A) - (M): Simulations with different arrangements of two bacteria on the collar in the order of increasing inward flux. (N) The choanoflagellate model with no attached bacteria is shown with a capture zone (0.67  $\mu m$  away from the collar). (A), (D), (H), (M) were selected to present in Figure 3 in the manuscript.



**Figure S3**. Linear least-squares regression of average translational velocities (or swimming speeds) for choanoflagellate models with different numbers and sizes of bacteria attached to the collar. Model with long-wide bacteria (length =  $2 \mu m$ , radius =  $0.67 \mu m$ ) in pink; Model with long-slender bacteria (length =  $2 \mu m$ , radius =  $0.335 \mu m$ ) in blue; Model with short-slender bacteria (length =  $1 \mu m$ , radius =  $0.335 \mu m$ ) in gray. For each number and size of attached bacteria, there are 5 simulations generated from the model with the flagellar frequency of 24.3 *Hz*. Left: linear regression analysis on dimensional quantities; Right: linear regression analysis on normalized quantities (i.e., dimensional data normalized by the case without bacteria).

Bacterial type	Dimensional speed (Fig. S3, left)	Normalized speed (Fig. S3, right)
Long-wide	y = -0.18x + 6.77; R <sup>2</sup> = 0.94	y = -0.025x + 0.94; R <sup>2</sup> = 0.94
Long-slender	y = -0.12x + 7.09; R <sup>2</sup> = 0.97	y = -0.017x + 0.98; R <sup>2</sup> = 0.97
Short-slender	y = -0.11x + 7.17; R <sup>2</sup> = 0.97	y = -0.015x + 0.99; R <sup>2</sup> = 0.97

**Table S1**. *Linear least-squares regression of average translational velocities (or swimming speeds) for choanoflagellate models with different bacterial attachment.* 



**Figure S4**. *Linear least-squares regression of inward flux for choanoflagellate models with different numbers and sizes of bacteria attached to the collar.* Solid curves show inward flux computed using the full model, where attached bacteria affect the flow. Dashed curves show inward flux computed using the "void" model, where the attached bacteria do not affect the flow, but the region that they occupy on the capture zone is omitted from the flux calculations. The capture zone is 0.67  $\mu$ m away from the collar for the simulations with long-wide bacteria and is 0.335  $\mu$ m for those with long-slender or short-slender bacteria. Top: linear regression analysis on dimensional inward flux quantities of the full models; Bottom right: linear regression analysis on normalized quantities of the full models (i.e., dimensional data normalized by the case without bacteria).

Bacterial type	Dimensional inward flux (Fig. S4, bottom left)	Normalized inward flux (Fig. S4, bottom right)		
Long-wide	y = -0.81x + 21.83; R <sup>2</sup> = 0.98	y = -0.036x + 0.96; R <sup>2</sup> = 0.98		
Long-slender	y = -0.49x +18.56; R <sup>2</sup> = 0.99	y = -0.026x + 0.99; R <sup>2</sup> = 0.99		
Short-slender	y = -0.37x + 18.69; R <sup>2</sup> = 0.98	y = -0.020x + 0.99; R <sup>2</sup> = 0.98		

**Table S2**. Linear least-squares regression of inward flux for choanoflagellate models with different bacterial attachment.



**Figure S5**. *Linear least-squares regression of total work for choanoflagellate models with different numbers and sizes of bacteria attached to the collar.* Left: linear regression analysis on dimensional quantities; Right: linear regression analysis on normalized quantities (i.e., dimensional data normalized by the case without bacteria).

Bacterial type	Dimensional work (Fig. S5, left)	Normalized work (Fig. S5, right)		
Long-wide	y = 0.00057x + 0.18; R <sup>2</sup> = 0.91	y = 0.0031x + 1.003; R <sup>2</sup> = 0.91		
Long-slender	y = 0.00036x + 0.18; R <sup>2</sup> = 0.88	y = 0.0020x + 1.002; R <sup>2</sup> = 0.88		
Short-slender	y = 0.00028x + 0.18; R <sup>2</sup> = 0.87	y = 0.0015x + 1.001; R <sup>2</sup> = 0.87		

**Table S3**. *Linear least-squares regression of total work for choanoflagellate models with different bacterial attachment.* 



**Figure S6**. *Linear least-squares regression of feeding efficiency for choanoflagellate models with different numbers and sizes of bacteria attached to the collar*. The feeding efficiency is defined as the inward flux divided by the work. Left: linear regression analysis on dimensional quantities; Right: linear regression analysis on normalized quantities (i.e., dimensional data normalized by the case without bacteria).

**Table S4**. Linear least-squares regression of feeding efficiency for choanoflagellate models with different bacterial attachment.

Bacterial type	Dimensional efficiency (Fig. S6, left)	Normalized efficiency (Fig. S6, right)
Long-wide	y = -4.51x + 118.14; R <sup>2</sup> = 0.97	y = -0.036x + 0.95; R <sup>2</sup> = 0.97
Long-slender	y = -2.73x + 100.85; R <sup>2</sup> = 0.98	y = -0.027x + 0.98; R <sup>2</sup> = 0.98
Short-slender	y = -2.10x + 101.76; R <sup>2</sup> = 0.98	y = -0.021x + 0.99; R <sup>2</sup> = 0.98

Link to the spreadsheet that contains all the simulated data for swimming speed, inward flux, and work. For the choanoflagellate models with 5 long-wide bacteria on the collar, we included data to analyze the effects of the captured bacteria on performance of thecate choanoflagellates attached to surfaces compared with swimming choanoflagellates.

## Movies with fluid particles initially placed on the plane normal to the flagellar plane and close to the cell body

*Case 1*: No bacteria attached to collar (top planar view: <u>link</u>, tilted 3D view: <u>link</u>) *Case 2*: Seven bacteria attached to collar (tilted 3D view: link)