



Structures of the stator complex that drives rotation of the bacterial flagellum

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The bacterial flagellum is the prototypical protein nanomachine and comprises a rotating helical propeller attached to a membrane-embedded motor complex. The motor consists of a central rotor surrounded by stator units that couple ion flow across the cytoplasmic membrane to generate torque. Here, we present the structures of the stator complexes from *Clostridium sporogenes*, *Bacillus subtilis* and *Vibrio mimicus*, allowing interpretation of the extensive body of data on stator mechanism. The structures reveal an unexpected asymmetric A₅B₂ subunit assembly where the five A subunits enclose the two B subunits. Comparison to structures of other ion-driven motors indicates that this A₅B₂ architecture is fundamental to bacterial systems that couple energy from ion flow to generate mechanical work at a distance and suggests that such events involve rotation in the motor structures.

A motor is a machine that supplies motive power for a device with moving parts. Biological systems use both linear and rotary motors to generate a variety of outputs. One of the most fascinating and complex biological rotary motors is the flagellar apparatus used by bacteria to propel themselves through fluid environments¹. Although bacterial swimming was first observed in the seventeenth century², a mechanistic understanding of how the bacterial flagellum generates rotation is still lacking. The core of the flagellum is a highly conserved motor (Fig. 1a) consisting of a cytoplasmic membrane-embedded rotor complex surrounded by varying numbers of stator complexes that generate torque³. While high-resolution information has been available for monomeric components of the cytoplasmic portion of the rotor⁴ and has recently been obtained for the intact membrane-tethered rotor complex⁵, structural detail of the stators has thus far been limited to modelling studies⁶.

Stators collect energy from either H⁺ or Na⁺ ion flow across the cytoplasmic membrane, generating torque in the cytoplasmic portion (C-ring) of the rotor complex^{7–10}. Chimeras between H⁺- and Na⁺-dependent stators are functional, implying that the mechanism converting ion flow into work is the same for the two coupling ions¹¹. Stator complexes are built from two cytoplasmic membrane proteins, which for simplicity are generically referred to as MotA and MotB in this study. MotA is predicted to contain four transmembrane helices (TMHs) with a large cytoplasmic insertion between TMH2 and TMH3. MotB is predicted to contain a short cytoplasmic sequence, a single TMH and a C-terminal peptidoglycan-binding (PGB) domain. Early biochemical work defined the stator complex stoichiometry as MotA₅B₂ (ref. ¹²) and this subunit composition has informed attempts to derive the mechanism for conversion of ion flow into rotation (reviewed in Nirody et al.¹³). Extensive experimental studies have led to a model of stator complex function where docking of the MotA cytoplasmic loop to the rotor C-ring simul-

taneously induces ion permeation through the stator complex and release of the MotB-PGB domain to bind to the peptidoglycan surrounding the flagellar basal body^{14,15}. Ion flow is proposed to lead to conformational changes in the cytoplasmic domain of MotA that generate torque in the rotor^{16–18}. In the absence of a stator complex structure, various mechanistic hypotheses have been proposed to explain the coupling of ion flow to conformational change, most of which explicitly use the predicted twofold symmetry of an MotA₅B₂ complex^{19–20}.

Results

Flagellar stator complexes are MotA₅B₂ complexes. We used cryogenic microscopy (cryo-EM) to study stator complexes from a range of bacterial species with different ion specificities (Extended Data Fig. 1). Two-dimensional (2D) class averages of the complexes from three species (*Vibrio mimicus*, *Clostridium sporogenes* and *Bacillus subtilis*) clearly showed a distorted pentagonal structure (Fig. 1b). Three-dimensional (3D) reconstructions of these complexes yielded volumes that could only be interpreted as MotA₅B₂ assemblies (Fig. 1c, Extended Data Fig. 2 and Table 1), with five copies of MotA fully enclosing the TMHs of two copies of MotB (Fig. 2a). Although we did not observe the PGB domains of MotB in the resolved structures, these domains must be present in the imaged complexes because the stator complexes were purified using an affinity tag located after the PGB domain. Thus, the PGB domain of MotB has no fixed location with respect to the core complex in the context of the isolated protein. The stator complex structures are compatible with sequence conservation data, with inter- and intramolecular coevolution data, and with published cysteine cross-linking^{21,22} and tryptophan-scanning mutagenesis^{23,24} (Extended Data Fig. 3).

The four TMHs of MotA are arranged in two layers. TMH3 and TMH4 line the central pore, while TMH1 and TMH2 form a surrounding outer layer of helices (Fig. 2a,b). TMH1 and TMH2 are

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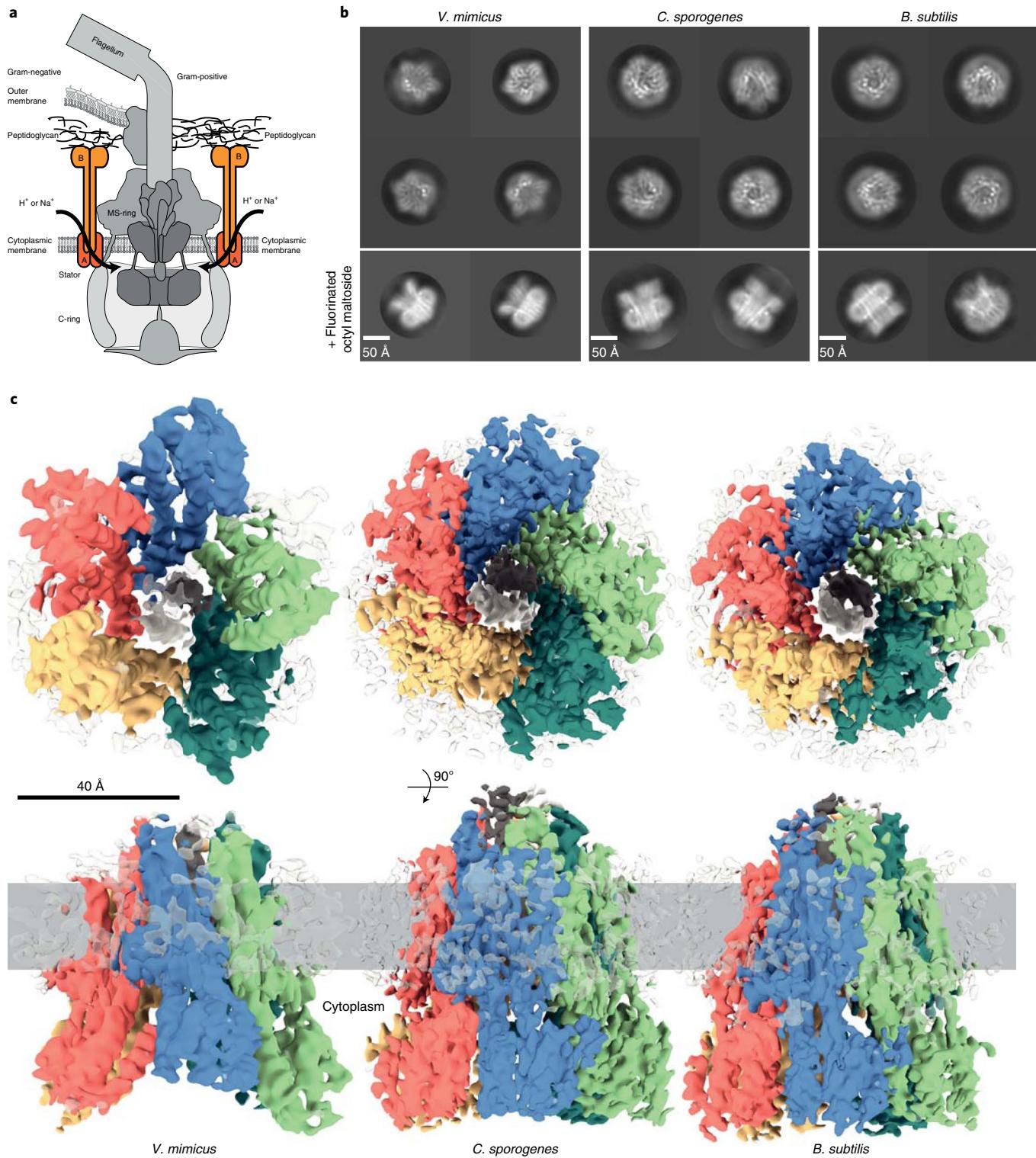


Fig. 1 | Stator complexes from multiple organisms have a MotA₅MotB₂ stoichiometry. **a**, Composite cartoon showing the general organization of bacterial flagellar complexes in Gram-negative (left) and Gram-positive (right) bacteria with the major components labelled. Stator complexes are shown in orange and the rotor components MS-ring and C-ring are shown in grey. **b**, 2D class averages of cryo-EM particles of stator complexes from the bacterial species indicated. The upper panels are representative 'top' views of the 5:2 complexes. The lower panels are 'side' views from data collected in the presence of fluorinated octyl maltoside. **c**, Cryo-EM volumes of stator complexes from the three bacterial species. The MotA subunits are coloured pink, blue, green, teal and yellow; the centrally located MotB subunits are coloured white and dark grey. Bound detergent is shown as transparent density at the periphery. The upper panels show views from the cytoplasm; the lower panels show side views with the likely membrane location (assigned from the position of the detergent micelle and from simulations; Extended Data Fig. 7) indicated by the grey bar.

Table 1 | Cryo-EM data collection, refinement and validation statistics

	<i>C. sporogenes</i> MotAB (EMDB-10895, PDB 6YSF)	<i>B. subtilis</i> MotAB (EMDB-10899, PDB ID 6YSL)	<i>V. mimicus</i> PomAB (EMDB-10901)	<i>E. coli</i> ExbBD (EMDB-10902)	<i>P. savastanoi</i> ExbBD (EMDB-10897)
Data collection and processing					
Magnification	165,000	165,000	165,000	165,000	165,000
Voltage (kV)	300	300	300	300	300
Electron exposure (e-/Å ²)	48	48	48	48	48
Defocus range (μm)	1.0–3.0	1.0–3.0	1.0–3.0	1.0–2.5	1.0–3.0
Pixel size (Å)	0.822	0.822	0.822	0.822	0.822
Symmetry imposed	C1	C1	C1	C1	C1
Initial particle images (no.)	1,998,900	1,532,430	2,383,022	2,045,350	1,342,937
Final particle images (no.)	314,230	122,615	244,654	227,700	65,617
Map resolution (Å)	3.4	3.5	4.2	4.6	3.8
FSC threshold	0.143	0.143	0.143	0.143	0.143
Map resolution range (Å)	3.2–5.2	3.3–6.0	3.9–6.5	4.0–6.5	3.6–6.1
Refinement					
Initial model used (PDB code)	None	None	–	–	–
Model resolution (Å)	3.4	3.5	–	–	–
FSC threshold	0.143	0.143	–	–	–
Model resolution range (Å)	3.2–5.2	3.3–6.0	–	–	–
Map sharpening B factor (Å ²)	–117	–104	–	–	–
Model composition					
Non-hydrogen atoms	10,220	10,128	–	–	–
Protein residues	1,327	1,324	–	–	–
Ligands	0	0	–	–	–
B factors (Å ²)					
Protein	53	99	–	–	–
Ligand	NA	NA	–	–	–
Root-mean-square deviations					
Bond lengths (Å)	0.004	0.007	–	–	–
Bond angles (°)	0.757	1.425	–	–	–
Validation					
MolProbity score	2.15	1.85	–	–	–
Clashscore	13.66	5.93	–	–	–
Poor rotamers (%)	0.90	0.47	–	–	–
Ramachandran plot					
Favoured (%)	91.47	90.92	–	–	–
Allowed (%)	8.53	9.01	–	–	–
Disallowed (%)	0.00	0.08	–	–	–
Model-versus-map FSC at FSC = 0.5	3.5	3.8	–	–	–
EMRinger score	2.12	1.19	–	–	–

not in contact with each other within a single subunit but instead interact between adjacent subunits, thereby stabilizing the MotA assembly. Immediately following TMH2 there is an amphipathic helix (AMPH) running perpendicular to the TMHs at the cytoplasmic membrane surface, with the five copies of this helix forming a belt around the outside of the structure. TMH3 and TMH4 extend 30 Å outside the membrane to form the core of the MotA cytoplasmic domain, with the rest of the domain built from helices inserted in the loop between the AMPH and TMH3. Both within and outside the membrane domain, the pentameric arrangement of MotA

is distorted (Fig. 2c). Charged residues shown to be essential for the interaction of the stator complex with the rotor C-ring²⁵ are located towards the base of this domain, forming a ring that decorates the surface of the pentamer (Extended Data Fig. 4).

The TMHs of the two copies of MotB are located in the central pore of the distorted MotA pentamer, with their hydrophobic side chains completely buried within the MotA ring. From the N-terminal ends of the MotB, TMHs clear densities extend down to contact the inner surfaces of TMH3 and TMH4 in the cytoplasmic domains of MotA (Fig. 3a,b and Extended Data Fig. 5a,b).

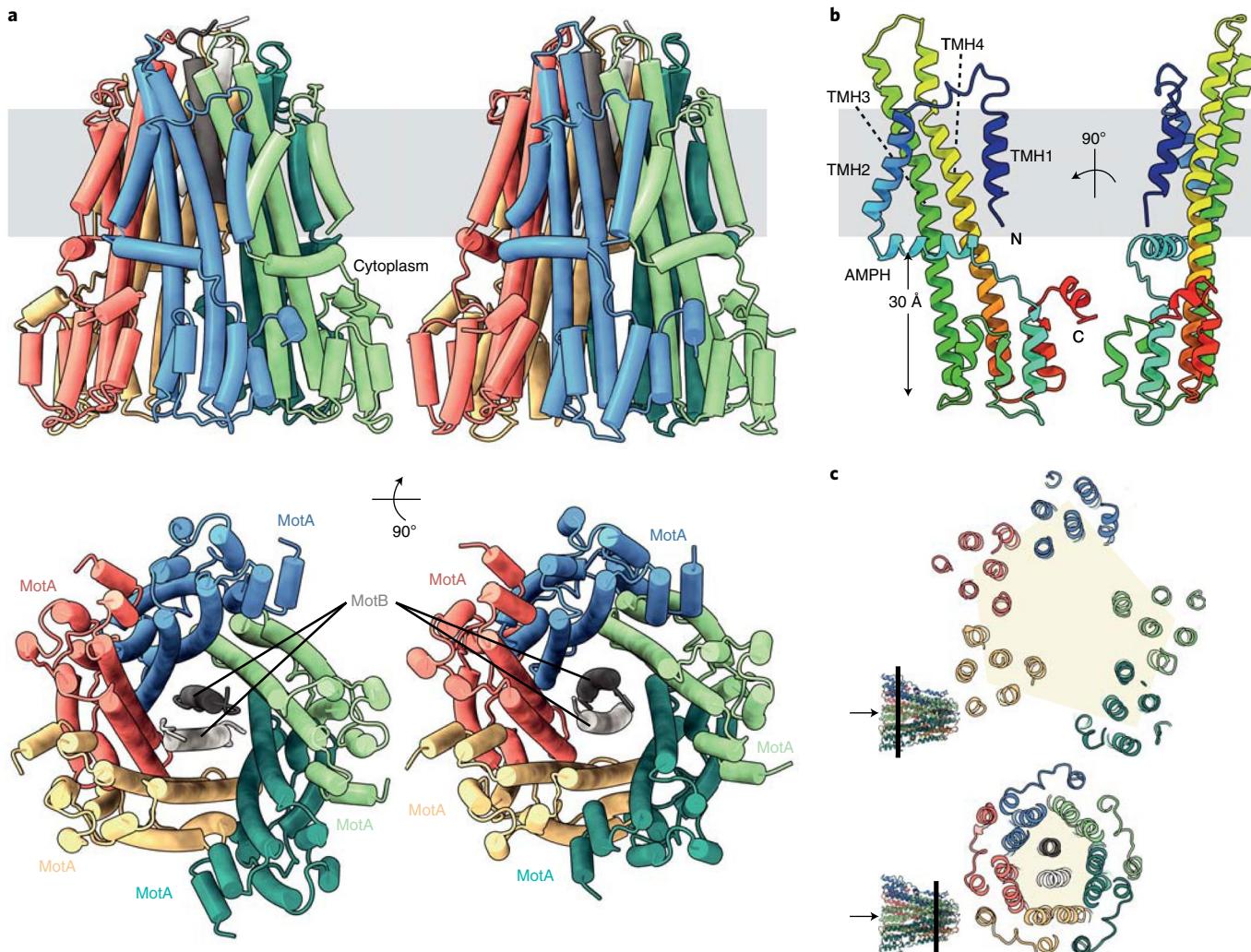


Fig. 2 | Structures of stator complexes from *C. sporogenes* and *B. subtilis*. **a**, The *C. sporogenes* (left) and *B. subtilis* (right) stator complexes are shown as cartoon representations and coloured as in Fig. 1c. Upper panel: side view with membrane indicated in grey. Lower panel: view from the cytoplasm. **b**, Two views of a single MotA subunit (*C. sporogenes*) coloured from blue at the N terminus to red at the C terminus. **c**, Slabs (viewed from the cytoplasm) through the *C. sporogenes* complex at the indicated positions on the inset structure (the arrow indicates the cytoplasmic side of the complex). Distortion of the MotA subunits from a regular pentagon arrangement is more extreme in the cytoplasmic regions.

Although the densities are too weak for the sequence to be traced, they are of sufficient length to account for most of the MotB N terminus, including a cluster of positive charges essential for motor function²⁶. At the non-cytoplasmic face of the complex, the MotB TMHs emerge vertically from the MotA pentamer and are followed by another short helical section that packs down between the TMH3-TMH4 loops of the MotA chains (Fig. 3a,b and Extended Data Fig. 5a,b). The connectivity of these densities defines them as the plug helices previously implicated by mutagenesis as critical to sealing the complexes in an off state²⁷.

Prior mutagenesis studies have established that a series of conserved residues in the TMHs of MotA and MotB are important for flagellar motion and/or ion flow through the stator (reviewed in Nakamura and Minamino³). Invariant MotB_{D32} (using the *Escherichia coli* numbering system) is the key protonatable residue and both copies lie within a ring formed by the five copies of another invariant polar residue, MotA_{T209} (Fig. 3c and Extended Data Fig. 6). A second threonine residue (at a position corresponding to residue A180 in the *E. coli* MotA) that is conserved in the Na⁺-dependent stators also contributes to this ring and forms part of a track of Na⁺/H⁺ specificity determining residues that line the

inner surface of the MotA pore (Extended Data Fig. 1). Two conserved proline residues in MotA are important for torque generation²⁸. One of these, MotA_{P222} can now be seen to be required for contacts between neighbouring MotA monomers. The other, MotA_{P173}, forms a second ring of conserved residues with MotA_{Y217}, two helical turns down from the threonine ring. This hydrophobic ring contacts MotB at the completely conserved MotB_{W26}. An MotB_{W26A} substitution completely abolished motility confirming the importance of this contact (Fig. 3d).

Asymmetry and the implications for activation of ion flow. The 5:2 stoichiometry of the stator complex leads to multiple levels of asymmetry in the structure (Fig. 2c and Extended Data Fig. 5c). The pentagon formed by the MotA subunits within the membrane is distorted to accommodate and seal around the two MotB TMHs. The asymmetry of this part of the complex is also driven by the two MotB plug helices sitting between the MotA loops, which divide the MotA chains into two groups separated in the extracytoplasmic region. Removal of the MotB plug has been shown to lead to uncontrolled ion flow through the MotAB channel²⁷. However, our structures show that the plug helices are not the sole block to

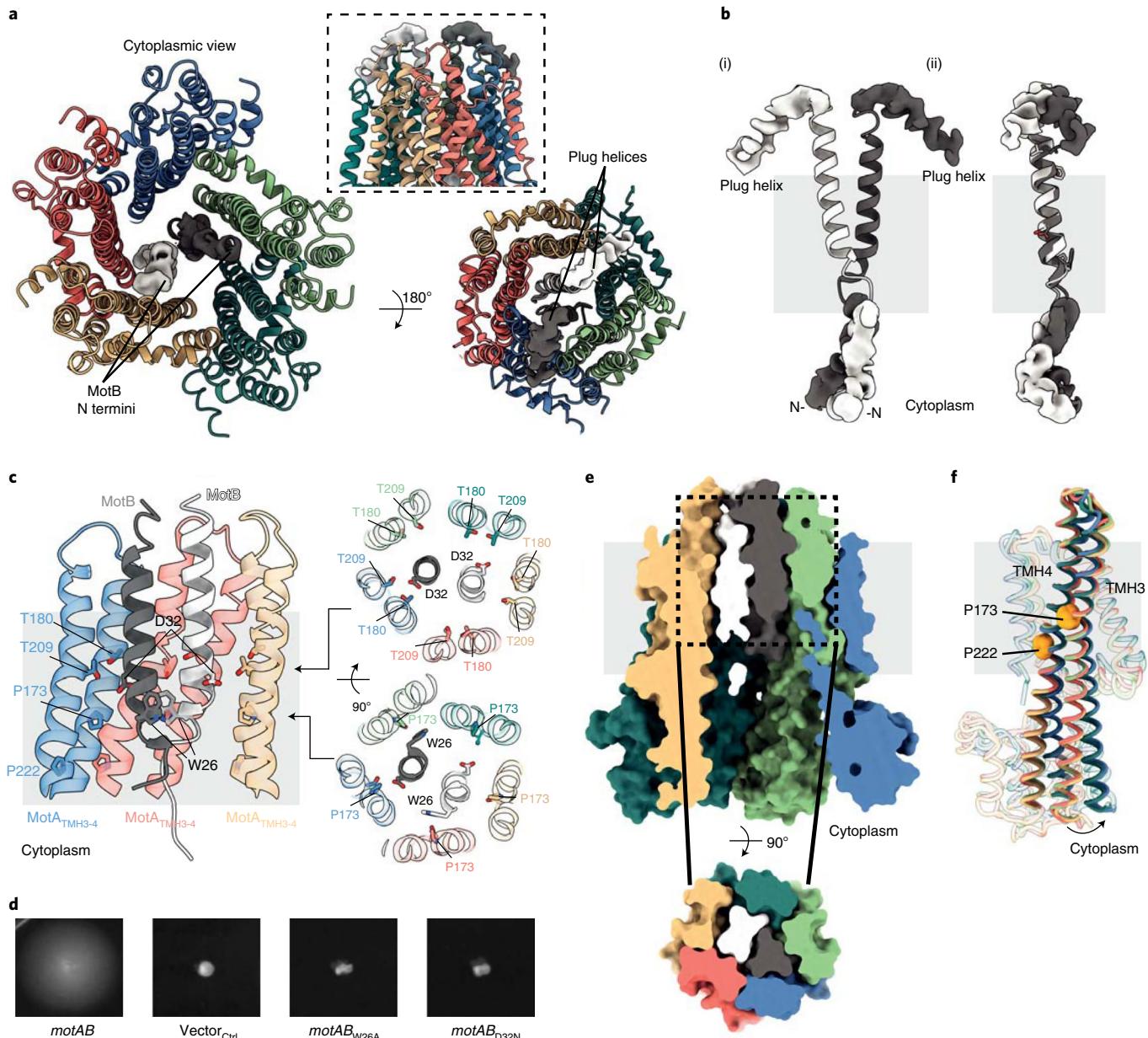


Fig. 3 | Functionally critical regions of the stator complex. **a**, Structure of the *C. sporogenes* stator complex shown as cartoon representations coloured as in Figs. 1 and 2, with the unmodelled density for the MotB N-terminal extensions (left) and plug helices (right) shown. The inset shows plug densities in the context of the top of the complex. **b**, (i) Isolated MotB dimer extracted from the *C. sporogenes* stator complex; (ii) superposition of the TMHs of the two MotB chains showing the relative rotation of the N-terminal extensions and plug helices. The location of the membrane is indicated in grey. **c**, The environment around MotB_{D32} within the membrane. Left: only the core MotA helices within the transmembrane region are shown and the two copies of MotA at the front of the view are removed. Right: slabs through the stator complex core at the indicated heights. Residue numbering is that of the *E. coli* MotAB stator complex but displayed on the *C. sporogenes* stator complex structure. Residues from MotA are coloured to denote the subunit. MotB residues are labelled in black. **d**, Motility in soft agar of *E. coli* RP6894 (Δ *motAB*) complemented with plasmids expressing *motAB* with the indicated mutations or the vector control (Vector_{Ctrl}). **e**, Surface representation of the model shows close packing. Top: side view with the front of the complex removed. Bottom: The top-down view of the slab is indicated by the dashed lines. **f**, Overlay of the five copies of the *C. sporogenes* MotA chain reveals that they fall into two conformational classes that differ in the degree of flexing at the highlighted prolines.

ion permeation since there are no detectable channels across the cytoplasmic membrane compartment (Fig. 3e and Extended Data Fig. 5d). Embedding plug-free structures in full lipid bilayer models and running extended simulations demonstrated that the observed structures are stable, low-energy states (Extended Data Fig. 7). No ion permeation across the bilayer was seen in any simulation, supporting the idea that the complexes currently seen will require rearrangement for activity.

Activation of ion flow is proposed to be triggered by docking of the inactive stator complex onto the flagellar C-ring via the MotA cytoplasmic domains, resulting in signal propagation from the cytoplasm to the plug region and plug release^{14,15}. Our structures reveal two potential routes for such a signal. The first involves the cytoplasmic N termini of the MotB subunits containing functionally essential residues²⁶ that interact with the inside of the MotA pentamer through highly evolutionarily coupled contacts (Extended Data Fig. 3d).

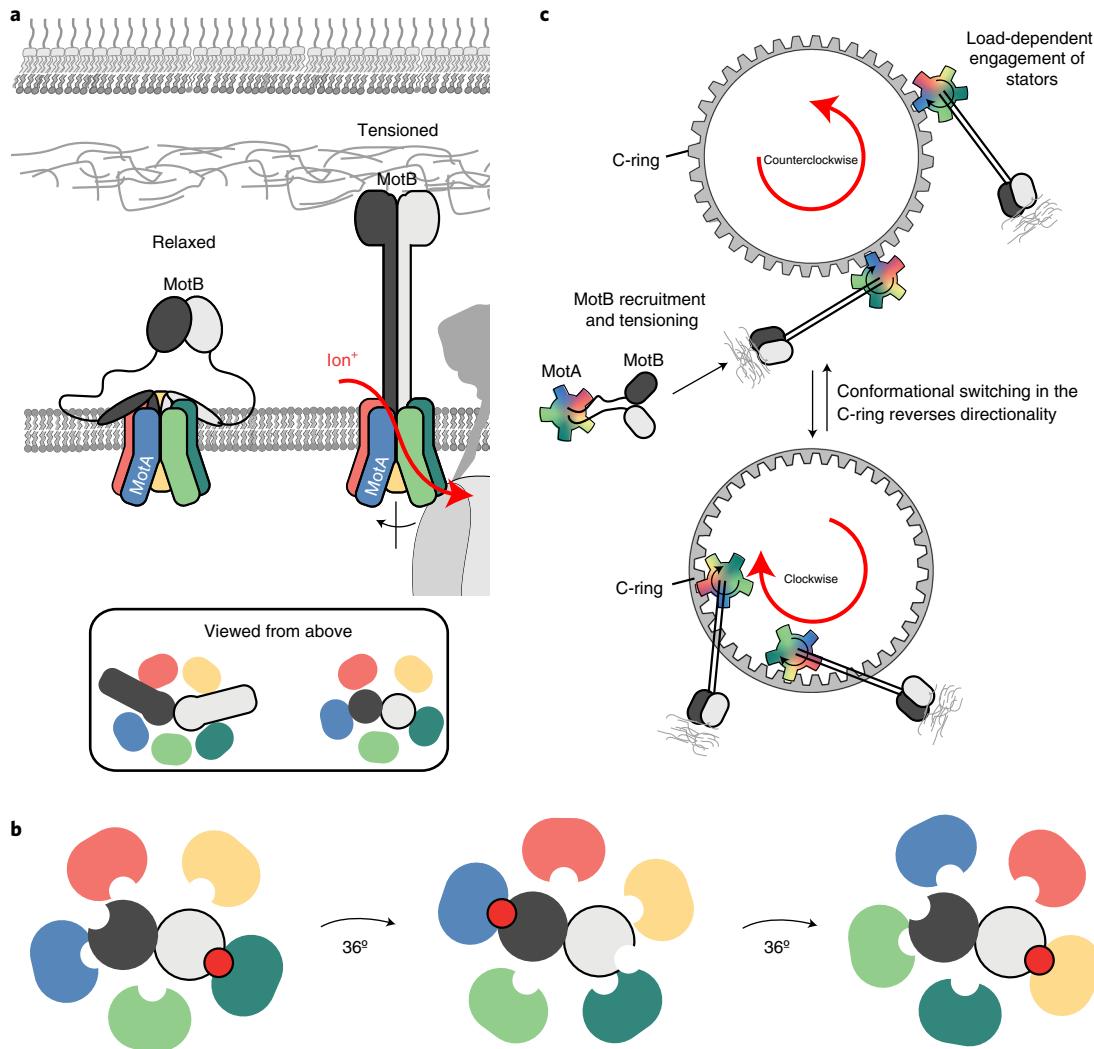


Fig. 4 | Mechanistic model for the generation of bidirectional flagellar torque. **a**, Activation of the stator complex from the structurally resolved state (termed ‘relaxed’) to form a ‘tensioned’ state permissive to ion flow. This conformational change is probably driven by interactions between the C-terminal peptidoglycan-binding domains (the black and white ovals) of MotB and the peptidoglycan layer, as well as interactions between the stator and C-ring complexes. **b**, Cartoon showing the top views of the intramembrane core of the stator complex, viewed from above (extracytoplasmic side), with five MotA chains surrounding two MotB subunits. Bound ions are shown as red spheres. Ion flow leads to rotation of the MotA ring through alternating formation of MotB-ion-MotA interactions by the two MotB chains that process around the surrounding MotA subunits. **c**, View from above of a model describing how a stator complex that rotates in one direction can drive either clockwise or counterclockwise rotation of the flagellum depending on the conformational state of the C-ring.

C-ring-induced movement of MotA would be communicated to MotB at this site leading to alterations at the opposite end of the MotB TMHs. The second possible route of signal propagation is directly through the MotA subunits, whereby hinging of the long TMH3 and TMH4 helices could alter the conformation of the plug helix binding loops to allow plug release. Our structures provide insight into how such a conformational change could occur since we observed differing degrees of hinging of the MotA cytoplasmic domains relative to the membrane-embedded helices (Fig. 3f and Extended Data Fig. 5e). Our structures also reveal that the two MotA residues known to be essential for interaction with the C-ring protein FliG²⁵ are located on opposite sides of the MotA cytoplasmic domain, with MotA_{R90} from one copy facing MotA_{E98} from the neighbouring copy (Extended Data Fig. 4). Therefore, docking of the C-terminal domain of FliG between two MotA subunits could trigger conformational change in the stator complex, which is consistent with earlier observations based on proteolytic sensitivity of MotA¹⁷.

Coupling of ion flow to flagellar rotation. The most striking feature of the asymmetry of the 5:2 subunit stoichiometry is that it places the TMHs of the two copies of MotB, including the critical MotB_{D32} residue, in different environments within the distorted MotA pentagon (Extended Data Fig. 6). Therefore, the system appears primed for differential binding of H⁺ or Na⁺ at the critical MotB_{D32} residue to induce changes in the relative positioning of the MotB and MotA helices. As MotB becomes tethered to the peptidoglycan on stator complex activation¹⁴ (Fig. 4a), this model predicts that the MotA ring moves around the MotB dimer. The 5:2 subunit stoichiometry is consistent with a model where the two MotB_{D32} residues alternate in terms of counter-ion occupancy and MotA binding mode. The coordination of ion binding to one MotB_{D32} residue with the simultaneous release from the other allows for a processive model of stepping, whereby opening of one channel triggers rotation of the MotA ring by approximately 36° (Fig. 4b). This motion would bring the second MotB chain into the same position relative to the surrounding

MotA subunits as the starting arrangement of the first MotB chain, thereby closing the first channel and opening the second. This model has the appeal that each subsequent ion binding event would be identical at a molecular level and trigger a further ratchet motion of 36°, with each turn of the MotA cytoplasmic domains providing a ‘power stroke’ to the rotor. This model would impart unidirectional rotation to the MotA pentamer and ten ion binding events would be required for a full 360° rotation. An alternative model, whereby ions binding sequentially to each MotB trigger first a 36° rotation and then a reset to the original position, would also be compatible with the structure. Such a model would act as a ratchet, only providing a ‘power stroke’ for every other binding event, and hence require twice as many ions as the unidirectional model for an equivalent movement of MotA. Although the stator complex would not undergo full rotation in this alternate model, it would still be capable of driving full rotation of the rotor component, acting like an energized escapement mechanism. Whether the ‘power stroke’ mechanism in either model also involves conformational change centred on MotA_{P173}, as has been proposed previously based on modelling studies, remains to be tested¹⁸. We note that the different conformations of MotA observed in our complexes hinge around the location of MotA_{P173} and the rotation mechanisms proposed would lead to each MotA altering conformation as it rotates around the MotBs. However, we also note that although MotA_{P173} is completely conserved, it can be substituted with non-proline residues without destroying function²⁸.

Any mechanism for coupling ion flow to flagellar rotation must also explain how the direction of rotation of the flagellum can reverse in response to chemotactic stimuli. All experimental evidence (reviewed in Minamino et al.²⁹) shows that the chemotaxis machinery leads to changes in the FliG subunit of the C-ring rather than the stator complex. A unidirectional rotation model for the stator complex mechanism can account for flagellar reversal if the chemotaxis-linked conformational changes induced in the C-ring lead to an alteration in the side of the stator complex that is driving the rotation (Fig. 4c). Consistent with this proposal, large conformational changes in the stator-interacting FliG component of the C-ring have been observed in crystal structures of FliG fragments³⁰ and in recent cryo-EM maps³¹. This model also predicts that any reversal of the ion flow through the stator complex would have the potential to reverse the direction of flagellar rotation even in the absence of switching by the chemotaxis machinery; this phenomenon has been observed in *Streptococcus* species assayed under high pH conditions^{32,33}. Alternatively, the oscillating ratchet mechanism would be able to operate in reverse by remodelling the C-ring to change the direction of the cogwheel teeth.

Common architecture across multiple bacterial ion-driven machines. The MotAB system is related at the sequence level to the ExbBD complex found in Gram-negative bacteria that uses ion flow across the cytoplasmic membrane to power transport processes at the outer membrane via the trans-periplasmic TonB protein³⁴. We determined the cryo-EM structures of ExbBD complexes from *E. coli* and *Pseudomonas savastanoi* (Extended Data Fig. 8 and Table 1). Both displayed a 5:2 ExbB:ExbD stoichiometry that differs from the subunit composition of earlier structures^{35,36}

but agrees with the subunit stoichiometry of a structure of the *E. coli* ExbBD reported while this manuscript was in preparation³⁷. Comparison of these recent ExbB₅D₂ structures to the stator complexes reveals a high level of structural conservation, particularly within the membrane domain (Extended Data Fig. 9a,b). Both the flattened pentagon geometry and the alignment of mechanistically important residues, such as the conserved aspartate within a ring of threonine residues, suggest that the two systems use the same molecular mechanism. Therefore, we predict that the ExbB will rotate relative to the ExbD helices in response to proton flow. Outside the core TMH region, there are structural differences between the systems that presumably reflect their very different biologies. ExbB is very differently elaborated relative to MotA, with only one TMH packing across the pair of helices that form the core inner ring and no bracing helices strengthening packing between subunits (Extended Data Fig. 9c). The ExbB cytoplasmic domains are only superficially similar to the corresponding MotA domain and lack the short pair of C-terminal helices found in MotA (Extended Data Fig. 9d).

P. savastanoi ExbB and ExbD were purified as a complex with TonB when all three proteins were coexpressed (Extended Data Fig. 10a). However, no extra density, at a comparable level to the ExbBD components, was observed in the cryo-EM maps of this complex relative to the ExbBD complex alone, suggesting that TonB is located on the outside of the ExbBD complex and dissociates on sample freezing. A peripheral location for TonB is consistent with both coevolution analysis (Extended Data Fig. 10b) and mutagenesis/suppressor data³⁸, which suggest that the TonB binding site is on the outside of the ExbB transmembrane domain (Extended Data Fig. 10b). TonB consists of a single-pass TMH, followed by an extended periplasmic region that interacts with the periplasmic domain of ExbD³⁹ and terminates in a folded domain that links with outer membrane receptor proteins⁴⁰. We speculate that the TonB TMH packs against the exterior of the ExbBD complex so that the conformational change in TonB is driven by rotation of the ExbB component relative to ExbD. In further support of this hypothesis, we note that, at a low contour level, a single additional density that we assign as the TonB TMH is seen to traverse the micelle on the exterior of the ExbBD complex (Extended Data Fig. 10c), packing against ExbB in the location predicted by analysis of covariance (Extended Data Fig. 10b). By extension, the homologous TolQRA system will also share this architecture and be mechanistically related⁴¹.

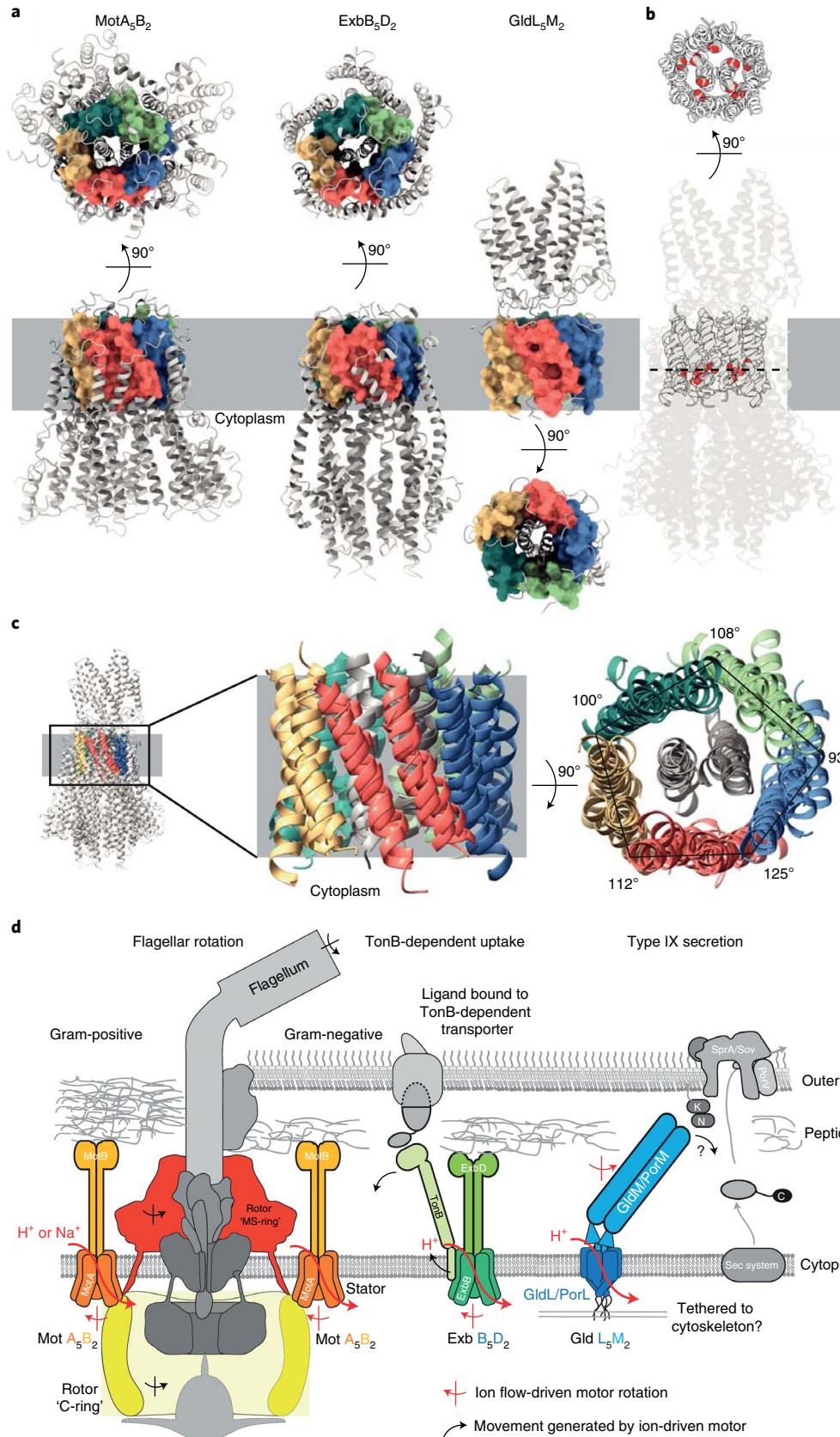
Discussion

The structures presented in this study demonstrate an asymmetric 5:2 stoichiometry for the MotA:MotB flagellar stator complex, in contrast to the previously proposed symmetric 4:2 models. This study also corroborates a recently observed 5:2 stoichiometry of the ExbB:ExbD motor component of the Ton transport system. A picture therefore emerges of the probable mechanistic importance of this shared stoichiometry for motor function. This link is further strengthened by another observation of this stoichiometry in an unrelated bacterial motor complex, the structure of which is described in a companion paper⁴². Bacteria from the Bacteroidetes phylum possess a two-component motor

Fig. 5 | Conservation of core architecture between diverse families of ion-driven motors. **a**, Representatives of three ion-driven motor families that share a common structural core. Complexes are shown as grey cartoons with helices equivalent to those in the MotA inner ring displayed in coloured surface representation. **b**, Overlay of the three complexes (common core in grey cartoons; other structure shown as semi-transparent cartoons). Mechanistically essential charged residues within the common core (space-filling side chains; C, grey; O, red) occur at the same height with respect to the membrane irrespective of whether they occur on the MotA or MotB equivalent chain. **c**, Overlay of the common core of the three complexes. The distortion from pentamer symmetry within the membrane is shared between all three families. **d**, Cartoon summarizing the updated view of how the three families of ion-driven motor complexes are coupled to their different biological effects. Note that ion movement is proposed to drive rotation of the central subunits in GldM but of the peripheral subunits in MotAB/ExbBD. The identity of the tether for GldL is unknown but is hypothesized to be a cytoskeletal component⁴².

complex in the cytoplasmic membrane that collects energy from ion flow to drive protein secretion and power bacterial motility via a non-flagellar mechanism termed gliding motility⁴³. Although the

constituent GldL and GldM subunits of this motor complex have no sequence similarity to the subunits of the MotAB or ExbBD complexes, the Bacteroidetes motor complex exhibits the same 5:2



subunit stoichiometry as these complexes (Fig. 5a). All three complexes have an intramembrane core consisting of a central subunit TMH dimer surrounded by a 10-TMH ring. Structural comparisons demonstrate the similarity between the three motor complexes in the arrangement of this intramembrane core and of the height within the membrane at which charged residues critical to function are located (Fig. 5b,c).

Such shared underlying architecture between otherwise highly dissimilar motor complexes (Fig. 5d) implies an unexpected commonality in their mechanism. Analysis of the structural asymmetry at the heart of the complexes strongly implies that this common mechanism involves processive rotation of the dimeric component relative to the pentameric component in response to the sequential binding of ions to the complex. The relatively simple core machinery in the membrane provides a template onto which elaborations can be built to provide specific biological function. This allows for a remarkable degree of adaptation and introduces means by which either component could be tethered to a cellular structure to drive rotation of the other component, for example, tethering of the dimer to the peptidoglycan in the case of the flagellar stator complexes or the proposed tethering of the pentamer in the Bacteroidetes motor. This work paves the way for future studies analysing the ubiquity of these mechanisms across the systems discussed in this manuscript and potentially related motors with different biological roles in other bacterial species.

Methods

Bacterial strains and plasmids. The bacterial strains and plasmids used in this study are listed in Supplementary Table 1. The pT12 backbone used for all protein expression was derived from Kuhlen et al.⁴⁴. Plasmids were generated by Gibson assembly of PCR fragments using the NEBuilder HiFi Master Mix (New England Biolabs). Fragments were created by PCR with the relevant primers (listed in Supplementary Table 2) using Q5 High-Fidelity DNA Polymerase (New England Biolabs) and genomic DNA templates obtained from the Liebniz Institute: *V. mimicus* (DSM 19130); *B. subtilis* 168 (DSM 402); *C. sporogenes* 388 (DSM 795); *E. coli* W (DSM 1116); and *P. savastanoi*, pv. phaseolicola 1448A (DSM 21482). Gibson assembly and PCR were carried out according to the manufacturer's recommendations. *E. coli* RP6894 (Δ motAB) for the motility assays was generated by J. S. Parkinson and gifted by D. F. Blair.

Purification of the MotAB/PomAB and ExbBD complexes. *V. mimicus* PomAB, its derivative PomAB $_{\Delta 61-120}$ lacking the unstructured periplasmic residues of PomB, *B. subtilis* MotAB, *C. sporogenes* MotAB, *E. coli* ExbBD and *P. savastanoi* TonB-ExbBD complexes were expressed in *E. coli* MT56 as a single operon from a pT12 vector encoding a C-terminal Twin-Strep tag. The purification steps were similar across all constructs and carried out at 4°C. Briefly, cells were grown at 37°C for 16 h in terrific broth medium containing kanamycin (50 µg ml⁻¹) and L-rhamnose monohydrate (0.1% w/v) then collected by centrifugation at 4,000g. Cell pellets were resuspended in Tris-buffered saline (TBS) (100 mM of Tris, 150 mM of NaCl, 1 mM of EDTA pH 8.0) plus 30 µg ml⁻¹ of DNase I and 400 µg ml⁻¹ of lysozyme for 30 min before passage through an EmulsiFlex-C5 homogenizer (Avestin) at 15,000 pound-force per square inch. Unbroken cells were removed by centrifugation at 24,000g for 20 min. The supernatant was recovered and total membranes were collected by centrifugation at 200,000g for 1.5 h. Membranes were resuspended in TBS and solubilized by incubation with 1% (w/v) lauryl maltose neopentyl glycol (LMNG; Anatrace) for 2 h. Insoluble material was removed by centrifugation at 100,000g for 30 min. Solubilized membranes were then applied to a Strep-Tactin XT column (IBA). The resin was washed with 10 column volumes of TBS containing 0.02% (w/v) LMNG and proteins were eluted in 5 column volumes of TBS supplemented with 0.01% (w/v) LMNG and 50 mM of D-biotin (IBA). Eluates were concentrated using a 100-kDa molecular weight cut-off (MWCO) Vivaspin 6 (GE Healthcare) centrifugal filter unit and injected onto a Superose 6 Increase 10/300 GL size-exclusion column (GE Healthcare) pre-equilibrated in TBS plus 0.01% (w/v) LMNG. Peak fractions were collected and concentrated using a 100-kDa MWCO Vivaspin 500 (GE Healthcare) centrifugal filter unit (Supplementary Fig. 1 and Extended Data Fig. 10).

For the *P. savastanoi* TonB-ExbBD and ExbBD complexes, size-exclusion chromatography–multiangle light-scattering analysis was carried out by injecting 100 µl (absorbance $A_{280\text{nm}} = 1.0$) of either sample onto a Superose 6 increase 10/300 GL size-exclusion column (GE Healthcare) equilibrated in TBS containing 0.02% (w/v) LMNG. Light scattering and refractive index changes were measured using a Wyatt DAWN Heleos-II light-scattering detector (Wyatt Technology) and an Optilab-TrEX refractive index monitor (Wyatt Technology). Analysis was carried out using the ASTRA v.6.1.1.17 software using a theoretical extinction coefficient

of 1.02 ($\text{Abs}_{0.1\%}$) and a protein dn/dc (specific refractive index increment) value of 0.186 ml g⁻¹ and a detergent dn/dc value of 0.143 ml g⁻¹ (Extended Data Fig. 10).

Cryo-EM sample preparation and imaging. Purified complexes (4 µl each) of *V. mimicus* PomAB ($A_{280\text{nm}} = 0.5$), PomAB $_{\Delta 61-120}$ ($A_{280\text{nm}} = 0.55$), *B. subtilis* MotAB ($A_{280\text{nm}} = 1.0$), *C. sporogenes* MotAB ($A_{280\text{nm}} = 0.8$), *E. coli* ExbBD ($A_{280\text{nm}} = 3.2$) or *P. savastanoi* TonB-ExbBD ($A_{280\text{nm}} = 2.0$) were adsorbed to glow-discharged holey carbon-coated grids (Quantifoil 300 mesh, Au R1.2/1.3) for 10 s. Grids were then blotted for 2 s at 100% humidity at 8°C and frozen in liquid ethane using a Vitrobot Mark IV (Thermo Fisher Scientific). Alternatively, specimens were prepared by supplementing *V. mimicus* PomAB ($A_{280\text{nm}} = 2.3$), PomAB $_{\Delta 61-120}$ ($A_{280\text{nm}} = 3.7$), *B. subtilis* MotAB ($A_{280\text{nm}} = 7.2$), *C. sporogenes* MotAB ($A_{280\text{nm}} = 8.6$), *E. coli* ExbBD ($A_{280\text{nm}} = 4.2$) with 0.7 mM of fluorinated octyl maltoside (Anatrace) before grid preparation.

Data were collected in counting mode on a Titan Krios G3 (Thermo Fisher Scientific) operating at 300 kV with a Gatan Imaging Filter (GIF) energy filter (Gatan) and K2 Summit detector (Gatan) using a pixel size of 0.822 Å, a dose rate of 4.05 e⁻ (pixel s)⁻¹ and an exposure of 8 s, corresponding to a total dose of 48 e⁻/Å². Videos were collected across 20 (*V. mimicus* PomAB and PomAB $_{\Delta 61-120}$ datasets) or 32 fractions (*B. subtilis* MotAB, *C. sporogenes* MotAB, *E. coli* ExbBD, and *P. savastanoi* ExbBD datasets). Except for *P. savastanoi* TonB-ExbBD, all datasets included videos from grids prepared with and without the presence of fluorinated octyl maltoside to improve distribution of particle orientations. Example micrographs are shown in Supplementary Fig. 2.

Cryo-EM data processing. Motion correction and dose weighting were performed using MotionCorr-2 implemented in Relion v3.0 (ref. ⁴⁵). Contrast transfer function parameters were estimated using CTFFIND4 (ref. ⁴⁶). Particles were picked in SIMPLE3.0 (ref. ⁴⁷) and subsequent processing was all carried out in Relion v3.0 (ref. ⁴⁵). Gold-standard Fourier shell correlations (FSCs) using the 0.143 criterion and local resolution estimations were calculated within Relion⁴⁵ (Extended Data Fig. 2).

V. mimicus PomAB particles (1,172,445) underwent 1 round of reference-free 2D classification, from which 253,681 particles were selected and used to generate an ab initio initial model. This model was low-pass-filtered to 30 Å and used as reference for 3D classification, generating a class that refined to 6.8 Å from 155,280 particles.

For the deletion construct PomAB $_{\Delta 61-120}$ that improved particle orientations and data quality, particles (2,383,062) were extracted from 13,980 videos. After 1 round of reference-free 2D classification, 800,844 particles were classified in 3D (4 classes) against a 40-Å low-pass-filtered map of PomAB. A class containing 244,654 particles was further subjected to masked refinement yielding a 4.8-Å map. Refinement after Bayesian particle polishing and per-particle defocus with beam tilt estimation further improved map quality to 4.2 Å (Supplementary Fig. 3).

B. subtilis MotAB particles (1,532,430) were extracted over 11,588 videos. After 2D classification, selected particles (397,584) underwent two rounds of 3D classification (3 classes each) using a 40-Å low-pass-filtered map generated from a subset of particles refined against a 60-Å low-pass-filtered map of PomAB $_{\Delta 61-120}$. A class made up of 122,615 particles was refined to 3.9 Å. Bayesian particle polishing further improved map resolution by 0.2 Å and subsequent CTF refinement using per-particle defocus with beam tilt estimation generated a 3.5-Å map (Supplementary Fig. 4). To improve MotB N-terminal and plug densities, a subset of fluorinated particles (43,375) was selected and refined against the 3.5-Å reconstruction, generating a 5.0-Å map that was used to depict these regions in Extended Data Fig. 5.

C. sporogenes MotAB particles (1,998,900) were extracted from 9,148 videos and subjected to a round of reference-free 2D classification. Initial 3D classification performed against a 60-Å low-pass-filtered map of *B. subtilis* MotAB revealed two prominent classes that represented a monomeric MotAB complex and a non-physiological end-to-end dimer of MotAB. These classes were used as references in a supervised multi-reference 3D classification against the full 1,137,357 particle set to exclude dimeric particles. Unsupervised 3D classification (4 classes) performed against 865,446 monomeric particles and further refinement yielded 3.8 Å from 314,230 particles. Bayesian particle polishing followed by per-particle defocus with beam tilt estimation further improved map quality to 3.4 Å (Supplementary Fig. 5).

Videos (6,902) were collected for *E. coli* ExbBD, resulting in the extraction of 2,045,350 particles. After 1 round of reference-free 2D classification, an initial model of ExbBD was generated by 3D classification and refinement of a particle subset against a 40-Å low-pass-filtered 5.1 ExbBD complex³⁶ (EMD-6928). The resulting map was used as the initial model for multiple rounds of 3D classification against the full 2D-classified particle set (755,677). After refinement of 227,700 particles, this protocol generated a 5.8-Å map, improving to 4.6 Å following Bayesian particle polishing and per-particle defocus plus beam tilt estimation (Supplementary Fig. 6).

Videos (4,232) were collected for *P. savastanoi* TonB-ExbBD and 1,342,900 particles were extracted. Particles were subjected to two rounds of 2D classification with centred re-extraction between classifications. The cleaned 499,697 particles were subjected to C5-symmetric 3D classification against a low-pass-filtered map

previously generated from 3D classification and refinement (C1) of an earlier subset of particles against a 40-Å low-pass-filtered map of our 5:2 *E. coli* ExbBD structure. The resultant 202,356 particles were refined with C5 symmetry to generate a 3.5-Å map that lacked density for the TMHs of ExbD. Particles were polished and subjected to an additional round of 2D classification followed by 3D classification with C1 symmetry, resulting in a 3.9-Å map from 110,164 particles after refinement in C1. An additional round of Bayesian polishing and per-particle defocus and beam tilt estimation followed by refinement (C1) yielded a 3.8-Å map. Alignment-free 3D classification and subsequent local refinement (C1) yielded a 3.8-Å map with improved density for the TMHs of ExbD from 65,617 particles (Supplementary Fig. 7).

Directional FSC and orientation distribution plots are provided in the Supplementary Information (Supplementary Figs. 8 and 9, respectively).

Model building and refinement. Atomic models were built using Coot v.0.8.9.2 (ref. ⁴⁸). Models were built only in the two volumes that allowed unambiguous docking of sequence into side chain density in the central pair of helices (MotAB *C. sporogenes* and *B. subtilis*). Multiple rounds of rebuilding (in both the globally sharpened and local resolution-filtered maps) and real-space refinement in PHENIX dev-3126-000 (ref. ⁴⁹) using secondary structure, rotamer and Ramachandran restraints yielded the final models described in Table 1. All models were validated using MolProbity within PHENIX dev-3126-000 (ref. ⁵⁰). Conservation analysis was carried out using the Consurf server⁵¹. A homology model of *E. coli* MotAB was generated by sequence threading against the *Clostridium* model using Phyre2 (ref. ⁵²). Figures were prepared using UCSF ChimeraX v.1.0 (ref. ⁵³) and PyMOL v.2.4.0 (The PyMOL Molecular Graphics System, v.2.0; Schrödinger). All models depicted in the figures are based on the highest-resolution *Clostridium* model, unless otherwise specified. Residue numbering adopts the reference *E. coli* sequence and model; a residue conversion table is provided (Supplementary Table 3). Close-ups of density for the side chains shown in Fig. 3 are shown in Supplementary Fig. 10.

Evolutionary covariance analysis. Coevolutionary contacts for *E. coli* W MotA were determined by the Gremlin web server⁶. Searches used the JackHMMER algorithm for multiple sequence alignment, an E-value threshold of 10^{-10} and a minimum coverage of 75%. Intra- and intermolecular contacts were mapped to the *E. coli* MotA structure using Gremlin beta⁶. Intermolecular contacts between MotA and MotB (residues 1–120) were determined using an E-value threshold of 10^{-20} and 10^{-2} , respectively. Intermolecular contacts between TonB and ExbB were determined using an E-value threshold of 10^{-20} . Contacts with a probability score greater than 0.9 were regarded as significant and listed in Supplementary Table 4.

Simulation set-up. All simulations were run using GROMACS 2018 (ref. ⁵⁴). The systems were initially set up using the Martini 2.2 coarse-grain force field and solvated with water and 0.15 M of NaCl to neutralize the system⁵⁵. The membranes were constructed using INSANE with a 4:1 ratio of POPE:POPG lipids⁵⁶. An elastic network of $1,000 \text{ kJ mol}^{-1} \text{ nm}^{-2}$ was applied between all backbone beads between 0.5 and 1 nm. Electrostatics were described using the reaction field method, with a cut-off of 1.1 nm using the potential shift modifier and the van der Waals interactions were shifted between 0.9 and 1.1 nm. The systems were first energy-minimized by steepest descent algorithm to $1,000 \text{ kJ mol}^{-1} \text{ nm}^{-2}$ and then simulated for a total of 1 us. The temperature and pressure were kept constant throughout the simulation at 310 K and 1 bar, respectively, with protein, lipids and water/ions coupled individually to a temperature bath by the V-rescale method⁵⁷ and a semi-isotropic Parrinello–Rahman barostat⁵⁸. The final snapshots from the coarse-grain simulations were then converted back to an atomistic description using CG2AT⁵⁹.

Atomistic simulations. The charged N and C termini of the converted protein were capped using acetyl and methyl moieties, respectively. All ionizable groups were simulated with default protonation states, unless otherwise mentioned. The virtual site model for hydrogen atoms⁶⁰, adapted for the CHARMM36 force field⁶¹ was employed, allowing the use of a 4-fs timestep during the simulations. Electrostatics were described using the particle mesh Ewald method, with a cut-off of 1.2 nm; the van der Waals interactions were shifted between 1 and 1.2 nm. The TIP3P water model was used and the water bond angles and distances were constrained by SETTLE⁶². All other bonds were constrained using the LINCS algorithm⁶³. The systems were then equilibrated for a further 1 ns using a 4-fs timestep with positional restraints of $1,000 \text{ kJ mol}^{-1} \text{ nm}^{-2}$ on the heavy atoms, in an NPT ensemble with temperature V-rescale coupling at 310 K (ref. ⁵⁷) and semi-isotropic Parrinello–Rahman barostat at 1 bar with protein, lipids and water/ions coupled individually⁵⁸. The Production simulations were performed without position restraints for a total of 200 ns and were run in triplicate.

Motility assay. *E. coli* RP6894 (Δ motAB) was transformed with pT12-derived plasmids encoding C-terminal Twin-Strep-tagged MotAB containing point mutations or appropriate controls. Saturated overnight cultures (2 μ l) were injected into soft agar plates (0.3% w/v agar in tryptone broth) containing kanamycin (30 μ g ml⁻¹) plus rhamnose monohydrate (0.5% w/v) and incubated in a humidified chamber for 23 h at 25 °C.

Pulldowns. *E. coli* RP6894 (Δ motAB) or MT56 were transformed with pT12-derived plasmids encoding C-terminal Twin-Strep-tagged MotAB containing the specified point mutations. Cultures were grown at 37 °C for 16 h in terrific broth containing kanamycin (50 μ g ml⁻¹) and rhamnose monohydrate (0.1% w/v). Normalized cell counts were lysed by resuspension in 200 mM of Tris pH 8.0, 300 mM of NaCl, 2 mM of EDTA plus 30 μ g ml⁻¹ DNase I and 400 μ g ml⁻¹ lysozyme for 30 min then solubilized in 1.5% w/v LMNG for 1 h. Insoluble material was removed by centrifugation at 18,000 g for 30 min. LMNG-solubilized lysates were added to TBS-prewashed MagStrep XT magnetic beads (IBA) for 1 h with mild shaking. Beads were isolated and washed twice with TBS plus 0.025% w/v LMNG followed by elution with TBS plus 0.025% w/v LMNG and 50 mM of D-biotin. Eluates were diluted in SDS-polyacrylamide gel electrophoresis sample buffer and run on a 4–20% polyacrylamide gel (NuSep), followed by staining with InstantBlue (Expedeon). Assays were performed in duplicate. Results are shown in Supplementary Fig. 11.

Reporting Summary. Further information on research design is available in the Nature Research Reporting Summary linked to this article.

Data availability

The data that support the findings of this study are available from the corresponding author upon reasonable request. Cryo-EM volumes and atomic models have been deposited with the Electron Microscopy Data Bank (accession nos. EMD-10895, EMD-10899, EMD-10901, EMD-10902, EMD-10897) and Protein Data Bank (accession nos. 6YSF and 6YSL), respectively. Source data are provided with this paper.

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Author contributions

J.C.D. carried out all biochemical work except as credited otherwise, prepared the cryo-EM grids, collected and processed the EM data and determined the structures. J.C.D., S.J. and S.M.L. designed the project, interpreted the data, built the models and wrote the first draft of the paper. S.J. performed the MALS experiments. O.V. and P.J.S. performed the molecular dynamics simulations. A.A., H.M. and T.G. carried out the biochemical work on *Pseudomonas* TonB-ExbB-ExbD. R.H.J. and B.C.B. contributed to the GldLM structure. J.W.C. initiated and provided materials for the ExbBD project. All authors commented on drafts of the manuscript.

Competing interests

The authors declare no competing interests.

Additional information

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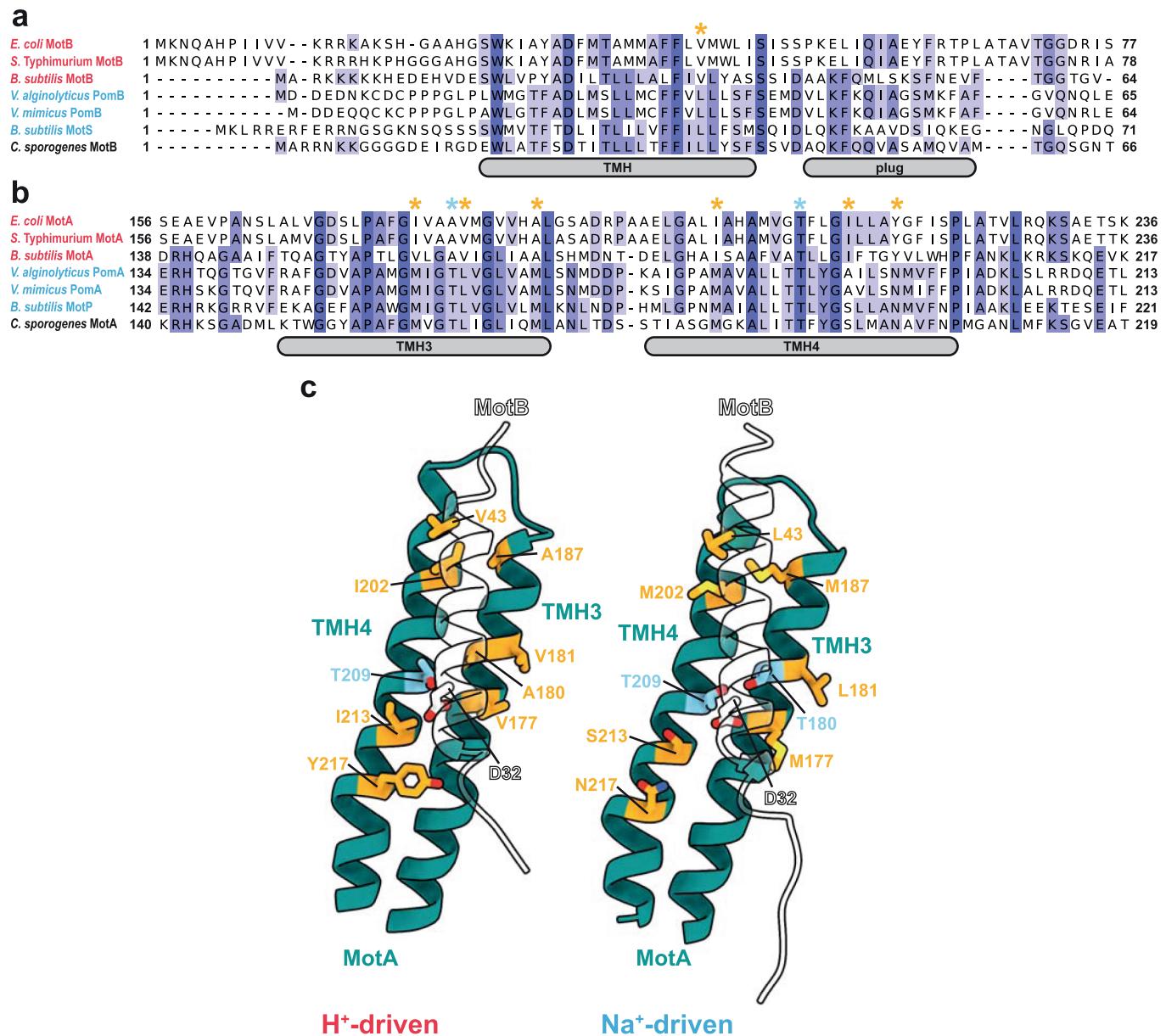
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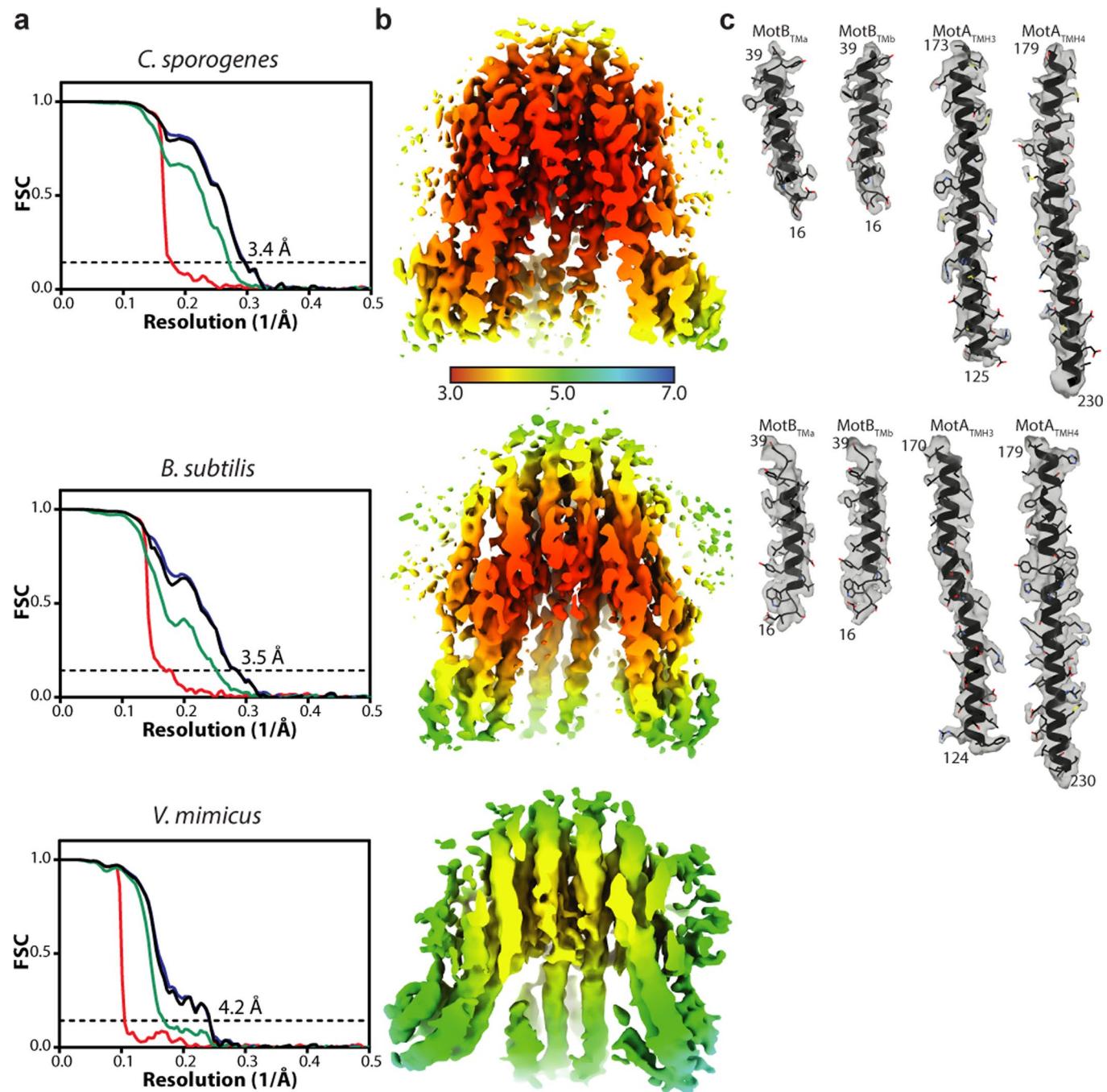
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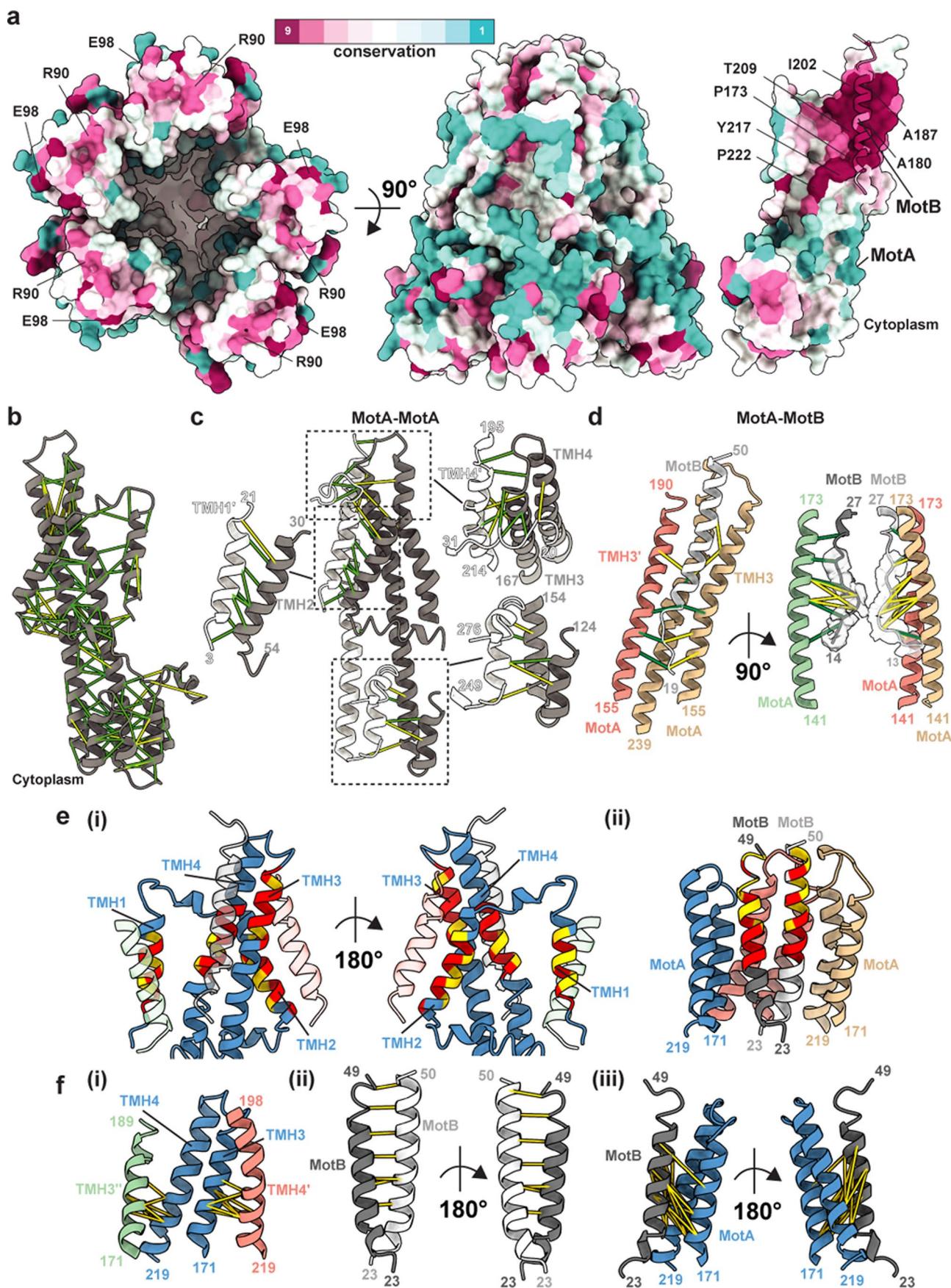
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Extended Data Fig. 1 | Ion specificity of stator complexes. Sequence alignment of the **(a)** transmembrane and plug helices of MotB and **(b)** transmembrane helices (TMHs) 3 and 4 of MotA from *E. coli* and other relevant bacterial species. Species are classified based on ion specificity (red, H⁺-driven; blue, Na⁺-driven). Residues that are conserved just within either the H⁺ or Na⁺-driven classes of stator and map to the MotA-MotB interface **(c)** are indicated with orange asterisks in the alignment and same residue colouring across H⁺-driven (Left) and Na⁺-driven (Right) models (using *E. coli* MotAB numbering equivalents). The threonine ring is highlighted with light blue asterisks **(a, b)** or residues **(c)**. Pairwise identity tables of MotB and MotA species used in alignments are found in Supplementary Tables 5 and 6, respectively. The ion used by *C. sporogenes* is ambiguous in that it is annotated as a proton-driven system, but the sequence alignment has more commonality with the sodium driven stators. We therefore do not colour it as definitively belonging to either class.

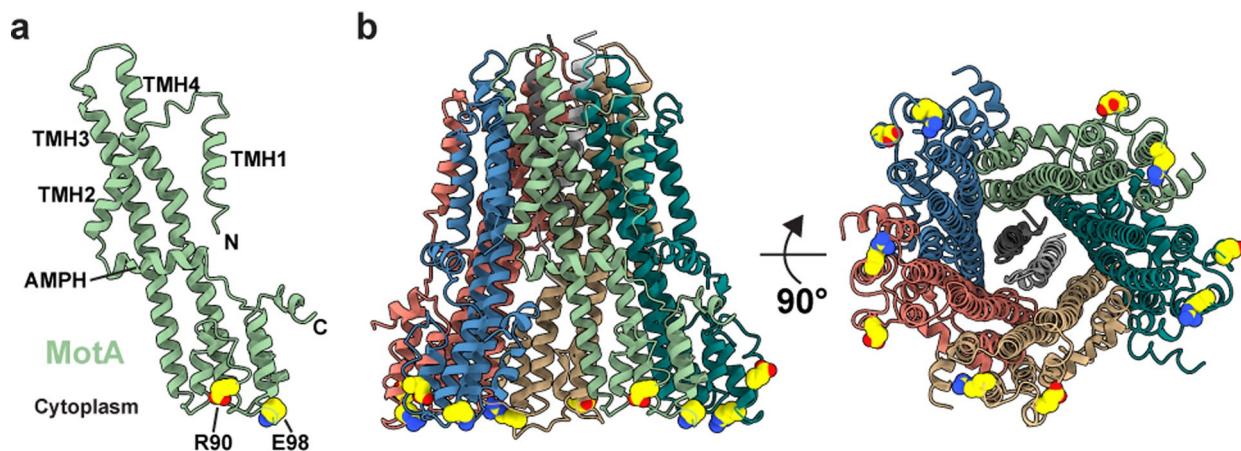


Extended Data Fig. 2 | Cryo-EM map quality and resolution estimates of stator complexes. **a**, Gold-standard Fourier shell correlation (FSC) curves of RELION-postprocessed stator complex volumes. Resolution at the gold-standard cutoff ($\text{FSC} = 0.143$) is indicated. Curves: red, phase-randomized; green, unmasked; blue, masked; black, corrected. **b**, Local resolution estimates (in Å) of the sharpened volumes. **c**, Representative modelled densities.

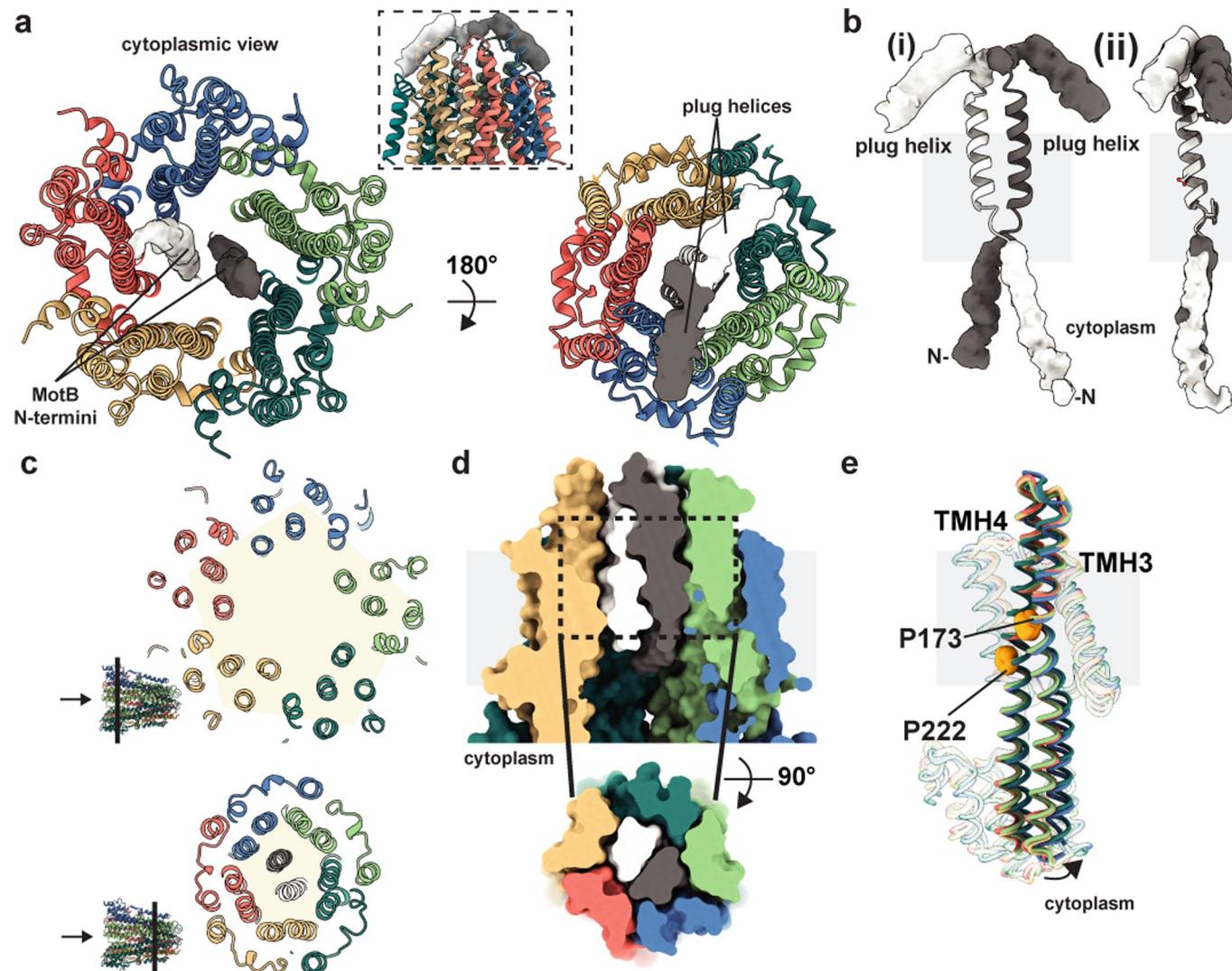


Extended Data Fig. 3 | See next page for caption.

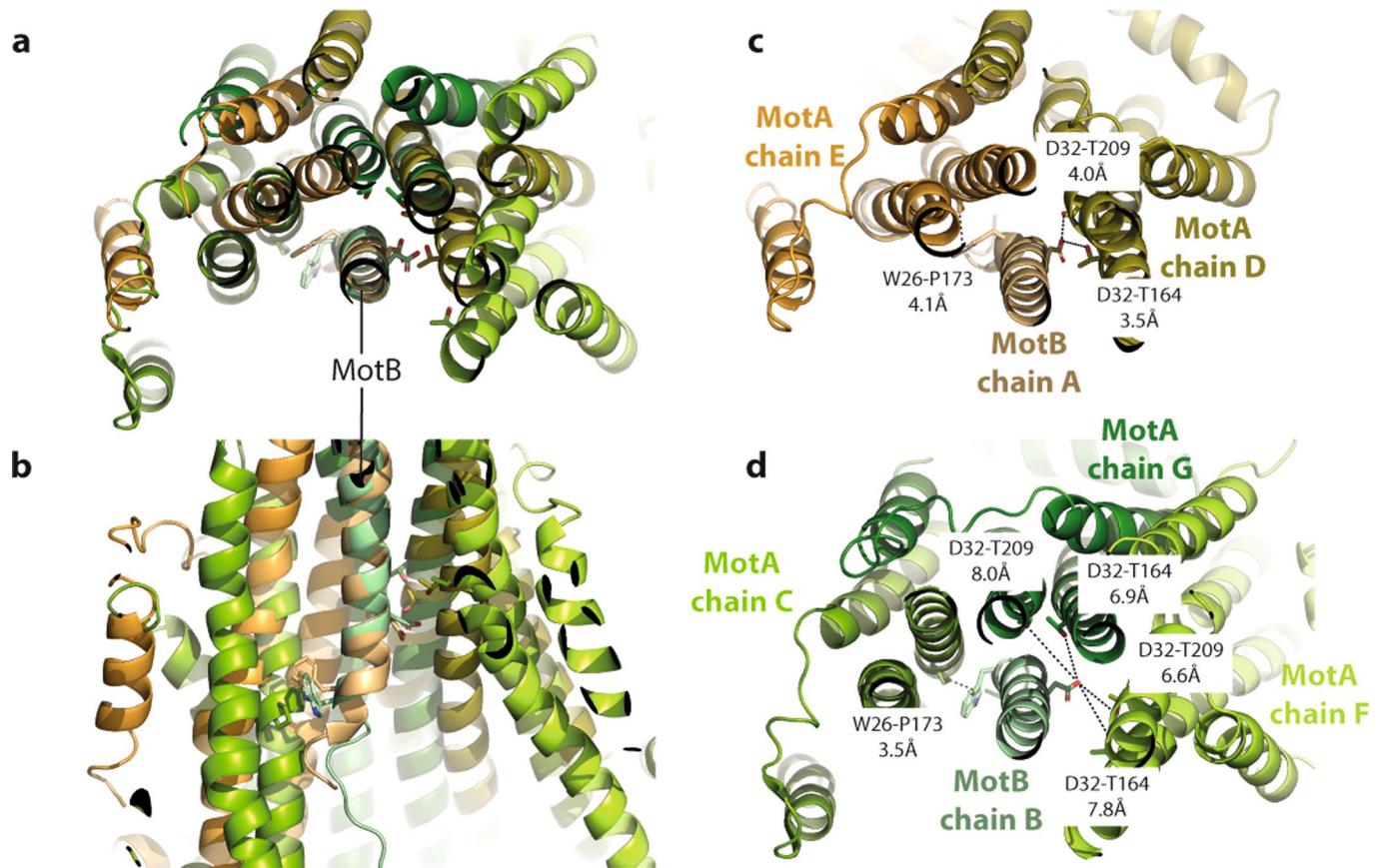
Extended Data Fig. 3 | Conservation, covariance, and prior mutagenesis data mapped onto the stator complex structure. **a**, Surface conservation as determined by Consurf⁵¹ (maroon high conservation, cyan low conservation). (Left) View from the cytoplasm showing conservation at the cytoplasmic MotA domains, including residues previously identified to be important for torque generation²⁵ (R90 and E98). (Centre) Side view showing poor conservation within membrane-interfacing residues of MotA. (Right) Cutaway displaying high level of conservation at the MotA-MotB interface; MotA shown as surface representation, MotB as ribbon. **b-d**, Evolutionary co-variation of residues (**b**) within MotA, (**c**) between MotA subunits, with boxes highlighting regions of strong covariance that are illustrated in more detail in the adjacent fragments, or (**d**) between MotA and MotB with the left hand side showing contacts for modelled MotB regions and the right hand side showing contacts in the unmodelled N-terminal MotB density represented here as a poly-alanine backbone. Predictions were carried out in Gremlin⁶ and contacts with a probability score of > 0.9 are shown. Contacts are coloured by $\text{C}\alpha\text{-C}\alpha$ distance ($\leq 10 \text{ \AA}$ in green, $\leq 15 \text{ \AA}$ in yellow). **e**, Mapping previous tryptophan scanning mutagenesis performed on MotA TMHs²³ (i) or MotB²⁴ (ii) to the stator complex structure. MotA and MotB are coloured as in Figs. 2 and 3 with targeted residues coloured according to toleration to mutagenesis; yellow corresponds to tolerated mutants (relative swarm rates > 0.5), red are poorly tolerated mutants (relative swarm rates of ≤ 0.5). In (i), TMH4 (green) and TMH2 (red) of neighbouring MotA subunits and MotB (white) are shown as transparent silhouettes. Poorly tolerated mutants cluster at subunit interfaces. In (ii) only TMH3-TMH4 of three MotA subunits are shown for clarity. **f**, Mapping previously determined cysteine crosslinks between (i) MotA-MotA²¹, (ii) MotB-MotB²², or (iii) MotA-MotB²¹ to our structure. For displaying crosslinks, a yield of $\geq 30\%$ disulfide-linked adduct under iodine oxidizing conditions was used as threshold, except for MotA_{TMH4}-MotB crosslinks which used a $\geq 10\%$ threshold. All analyses in this figure were performed using an *E. coli* MotAB structure generated by homology threading onto *C. sporogenes* MotAB.



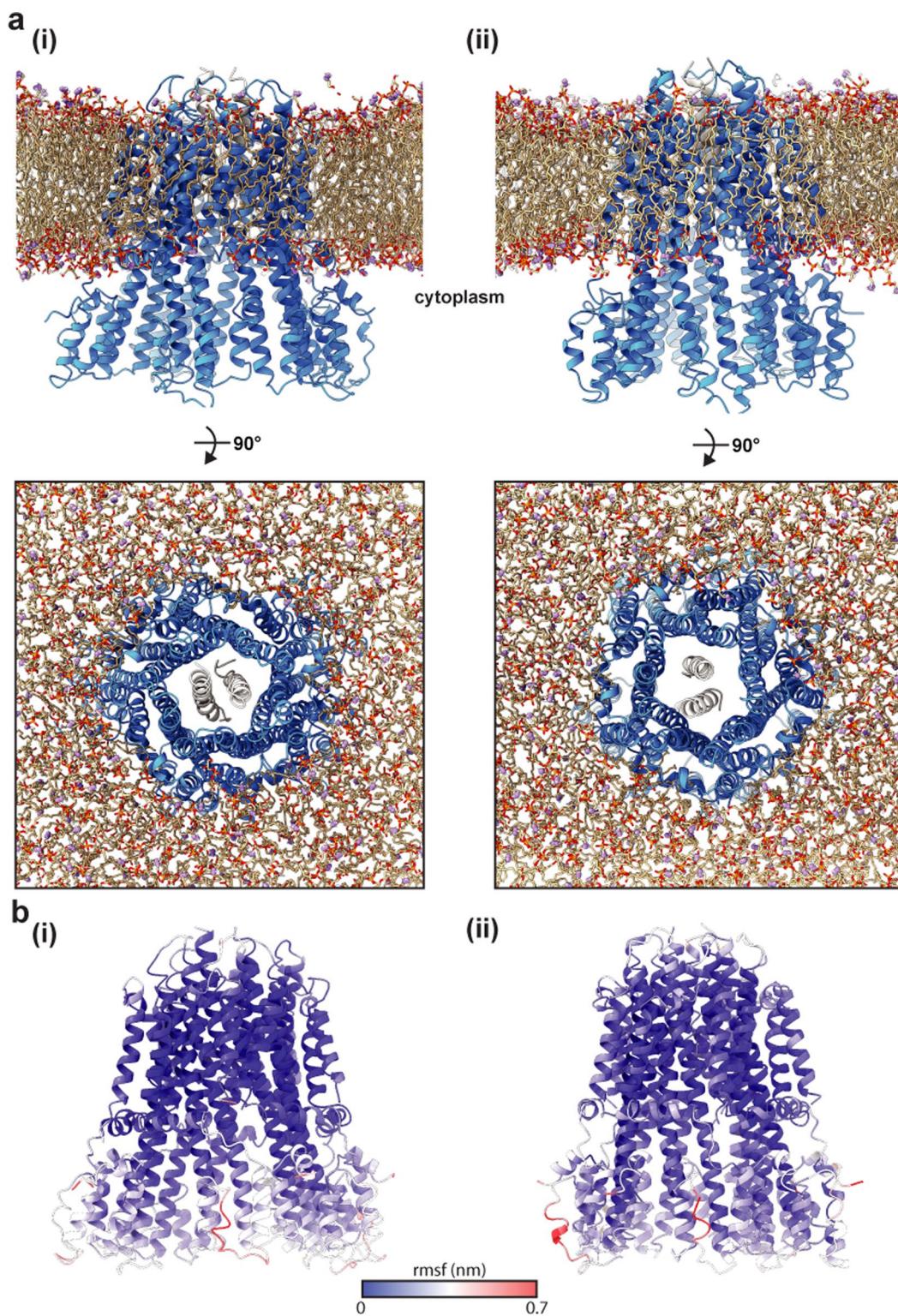
Extended Data Fig. 4 | Residues that interact with the flagellar C-ring form a charged ring on the cytoplasmic face of MotA. **a**, An isolated MotA subunit with the essential torque-generating charged residues R90 and E98²⁵ displayed in yellow spheres representation. **b**, The full *C. sporogenes* stator complex viewed from the side (Left) or from the cytoplasm (Right), coloured as in Figs. 2 and 3, and with the torque-generating charged residues represented as in (a) using *E. coli* MotAB numbering scheme.



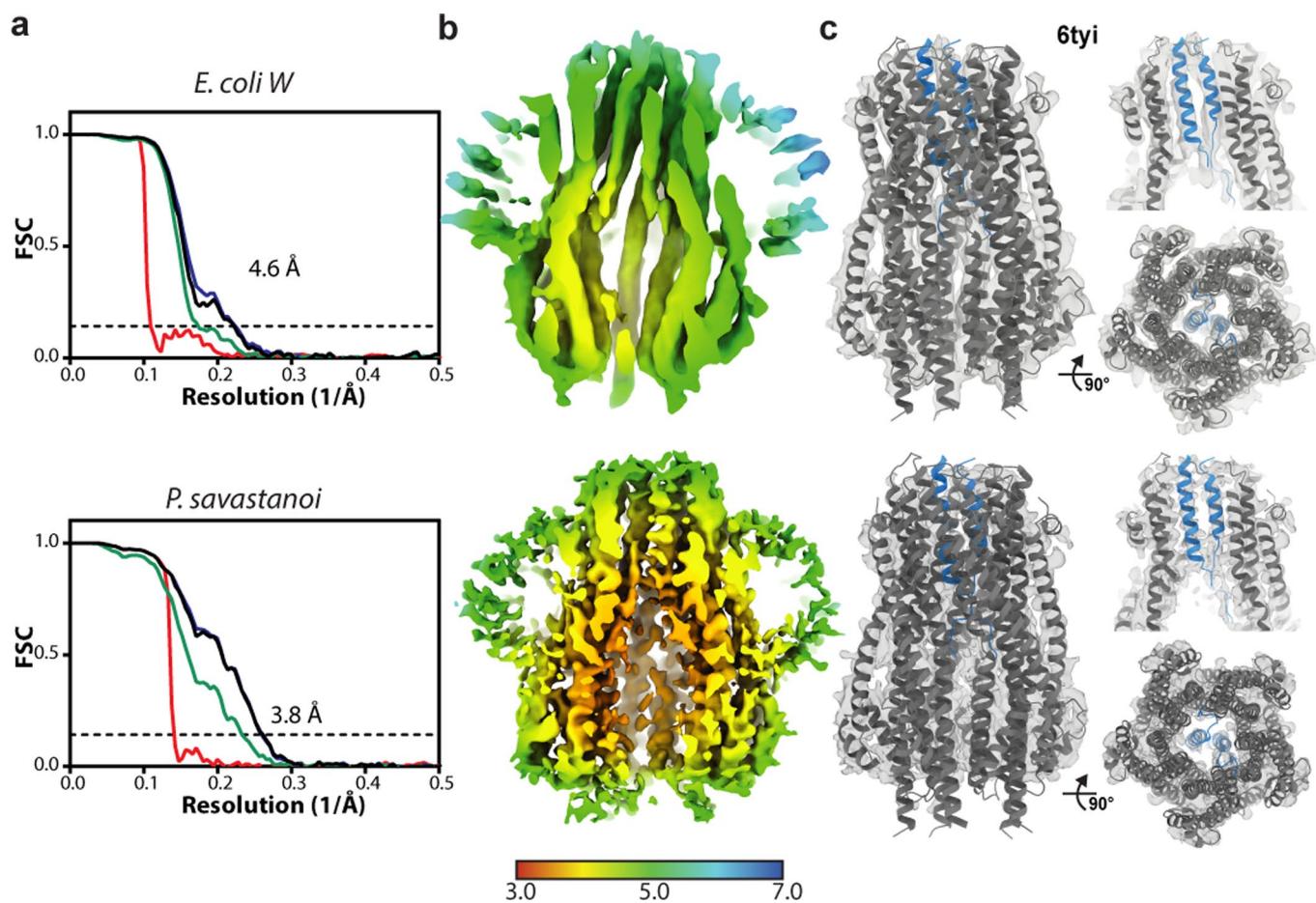
Extended Data Fig. 5 | Structural elements of the *B. subtilis* stator complex. **a**, Structure of the *B. subtilis* stator complex depicting unmodeled density for the MotB N-terminal extensions (Left) and plug helices (Right). Inset shows plug densities in context of top of complex. **b**, (i) Isolated *B. subtilis* MotB dimer represented as in (a), and (ii) superposition of the TMHs of the two MotB chains showing the relative rotation of the plug helices. The location of the membrane is indicated in grey. **c**, Slabs at the heights indicated through *B. subtilis* MotAB show distortion from a regular pentagon (arrow indicates the cytoplasmic side of the complex) as viewed from the cytoplasm. **d**, Surface representation of *B. subtilis* MotAB showing tight packing. (Top) Side view with the front of the complex removed. (Bottom) Top-down view of the slab indicated by dashed lines. **e**, Structural alignment of the five *B. subtilis* MotA chains reveal they fall into two conformational classes which differ in the degree of flexing at the highlighted prolines.



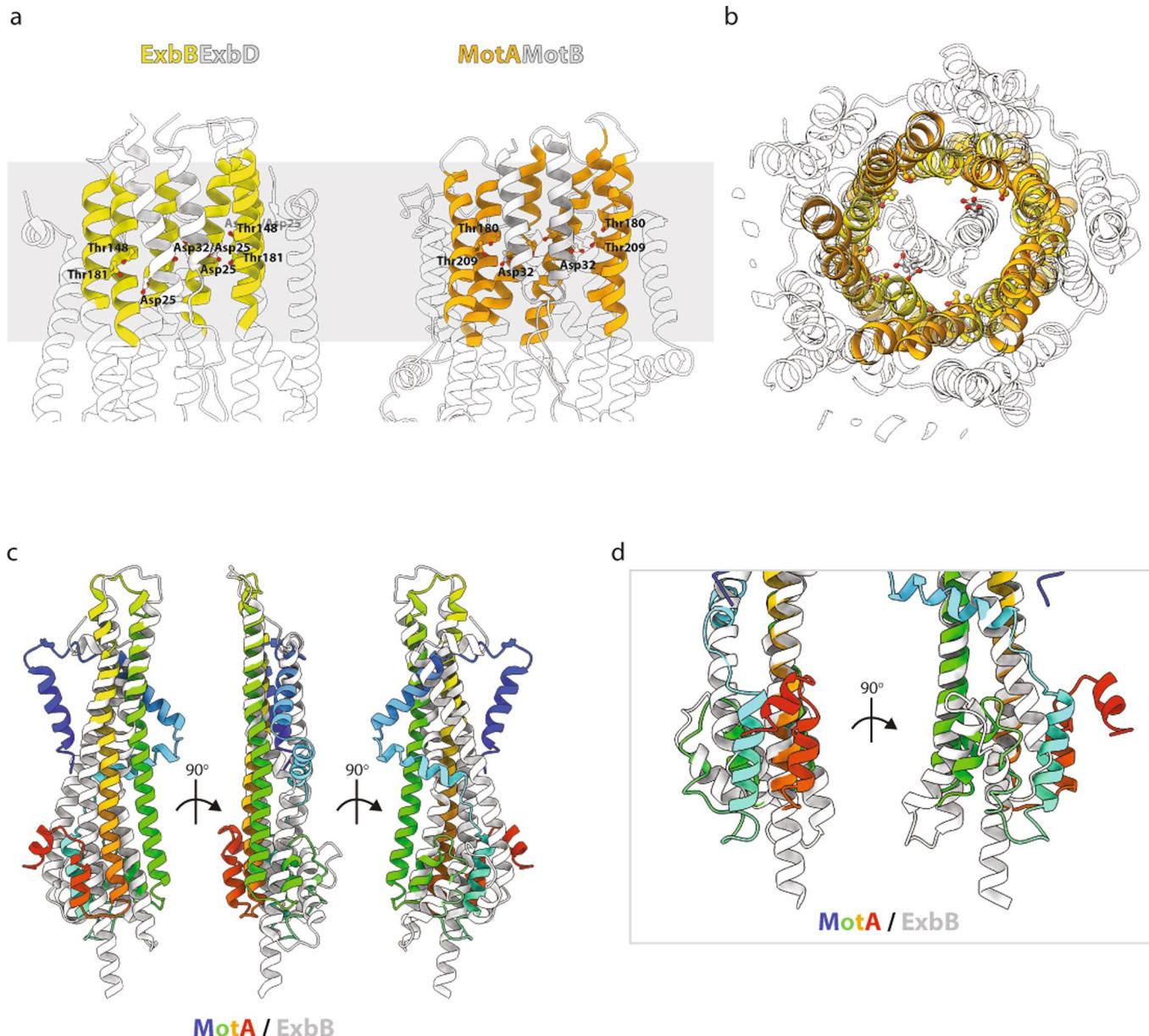
Extended Data Fig. 6 | Overview of differences in MotB environment caused by asymmetry of stator complex. **a**, Each chain of MotB is shown with its respective surrounding MotA subunits, superposed by overlay of MotB₃₀₋₃₄ (that is a turn of helix centered on the critical D32). MotB-chain A and its two neighbouring MotA subunits (chains E and D) shown in orange tones, MotB-chain C and its three neighbouring MotA subunits (chains C, F & G) shown in green **b**, same representation as **a** but rotated 90 degrees **c** & **d** show each MotB and neighbouring MotA chains, coloured as in **a** & **b** but with closest approaches between critical residue pairs shown to highlight the very different arrangement of the MotA subunits w.r.t. MotB D32. All panels drawn using PyMol (The PyMOL Molecular Graphics System, Version 2.0 Schrödinger, LLC).



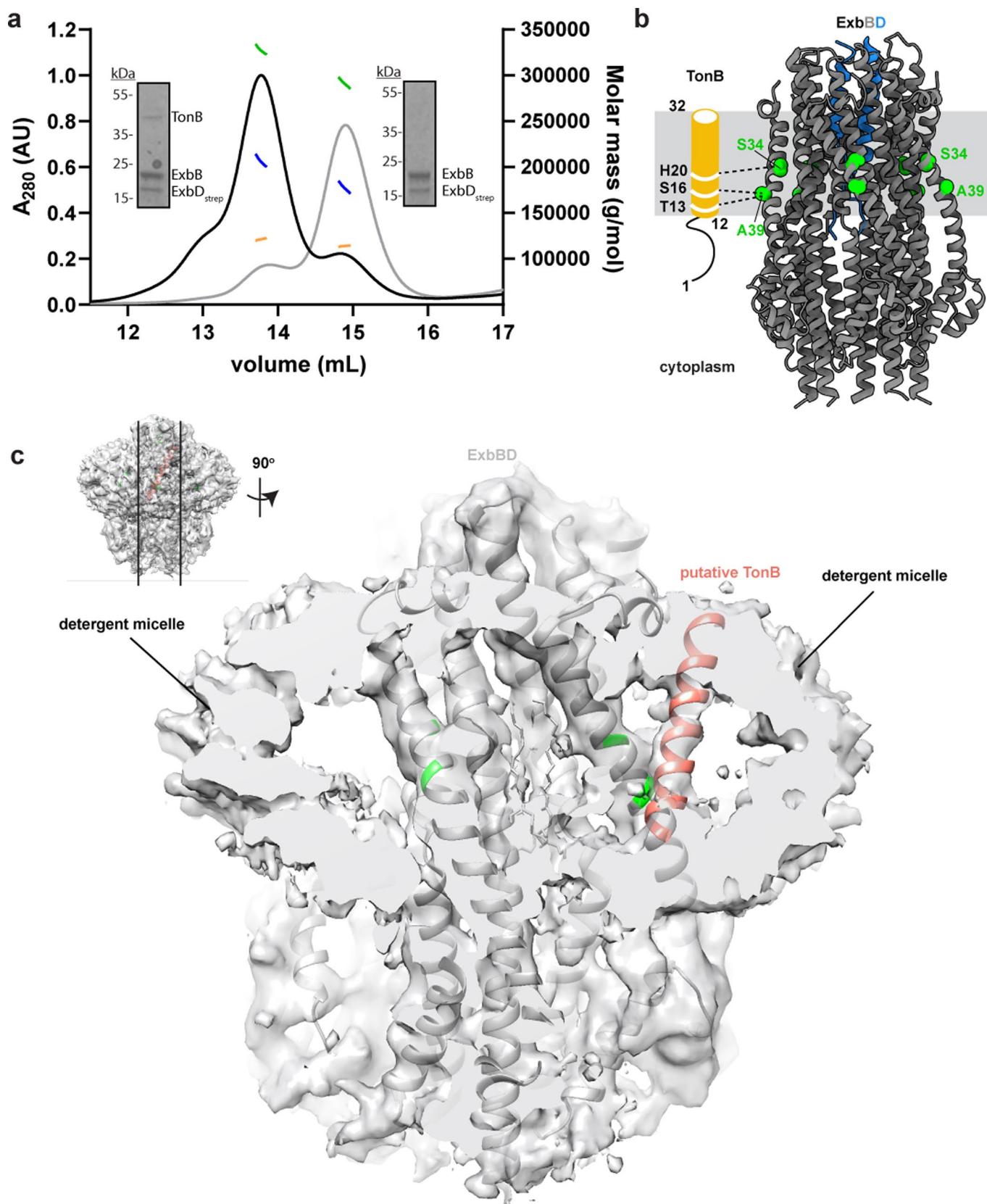
Extended Data Fig. 7 | Molecular dynamics simulations of stator complex structures in lipid bilayers. **a**, Side (top) and top-down (bottom) views of (i) *C. sporogenes* and (ii) *B. subtilis* MotAB inserted within a lipid bilayer after extended simulations (coarsegrain for 1 μ s then atomistic for a further 200 ns). **b**, Cartoon representation of (i) *C. sporogenes* MotAB and (ii) *B. subtilis* MotAB coloured (blue to red) by the average rmsf of the 3 replica simulations performed.



Extended Data Fig. 8 | Cryo-EM map quality and resolution estimates of ExbBD complexes. **a**, Gold-standard Fourier shell correlation (FSC) curves of RELION-postprocessed ExbBD maps. Resolution at the gold-standard cutoff ($\text{FSC} = 0.143$) is indicated. Curves: red, phase-randomized; green, unmasked; blue, masked; black, corrected. **b**, Local resolution estimates (in Å) of the sharpened maps. **c**, Structure of the 5:2 ExbBD complex from *E. coli*³⁷ (PDB 6tyi) fit into the *E. coli* W (top) and *P. savastanoi* ExbBD (bottom) maps. ExbB is coloured dark grey and ExbD is coloured blue. Top right panels have three ExbB subunits removed to demonstrate density for the two TMHs of ExbD. Bottom right panels reveal the 5:2 ExbB:ExbD arrangement as viewed from the cytoplasm.



Extended Data Fig. 9 | Structural alignment of MotAB and ExbBD. **a**, side views of the cores of the *C. sporogenes* MotAB (orange) and *E. coli* ExbBD³⁷ (yellow) complexes with two front MotA/ExbB subunits removed showing the conserved Asp residues lying at the same height with respect to a ring of Thr on the MotA/ExbD components **b**, Overlaying the cores of *C. sporogenes* MotAB (orange) and *E. coli* ExbBD (yellow) by alignment of the MotA/ExbD helices demonstrates alignment of the critical polar residues between the two systems. Regions outside the core shown as transparent grey; MotB/ExbD shown in grey. **c**, Aligning a single subunit of MotA (rainbow colouring) with ExbB (white) via the pore lining helices reveals the different elaborations of this core unit in each protein. **d**, Aligning a single subunit of MotA with ExbB via the cytoplasmic extensions of the two core helices reveals the different folding of the rest of the cytoplasmic regions. Proteins coloured as in **(c)**.



Extended Data Fig. 10 | See next page for caption.

Extended Data Fig. 10 | TonB recruitment to the ExbBD complex. **a**, SEC-MALS profile of purified *Pseudomonas* TonB-ExbBD (black curve; absorbance at 280 nm (A_{280})) and ExbBD (grey curve; absorbance at 280 nm (A_{280})) with SDS-PAGE analysis of each sample inlayed. Total protein-detergent complex molar mass (green) and deconvoluted protein (blue) and detergent (orange) molar masses are shown. A ~30 kDa difference in molar mass is observed between the complexes consistent with the TonB-ExbBD complex containing one TonB subunit. Similar data were obtained from three independent purifications. **b**, Evolutionary co-variation of residues between TonB and ExbB displayed on the *E. coli* ExbBD coordinates³⁷ (PDB 6tyi). For clarity, a topological model of the TMH of TonB is shown in orange with TonB-ExbB contacts indicated as dashed lines. ExbB residues that coevolve with TonB decorate the external surface of ExbB and are displayed in green. ExbB (grey) and ExbD (blue) are displayed as ribbon cartoons. Contacts shown were generated by Gremlin⁶ and have a probability score of > 0.9. **c**, inspection of the cryo-em volume derived from the ExbBDTonB sample, prior to post-processing, at a low contour level reveals a single, tube of density, consistent with the predicted location of the TonB transmembrane helix running across the exterior of a single copy of ExbB. Although likely at a low occupancy c.f. the other components, we tentatively assign this as TonB.

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