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Biogenesis and structure of a type VI secretion baseplate

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ABSTRACT

To support their growth in a competitive environment and cause pathogenesis, bacteria have evolved a broad repertoire of macromolecular machineries to deliver specific effectors and toxins. Among these multiprotein complexes, the type VI secretion system (T6SS) is a contractile nanomachine that targets both prokaryotic and eukaryotic cells. The T6SS comprises two functional sub-complexes: a bacteriophage-related tail structure anchored to the cell envelope by a membrane complex. As in other contractile injection systems, the tail is composed of an inner tube wrapped by a sheath and built on the baseplate. In the T6SS, the baseplate is not only the tail assembly platform, but also docks the tail to the membrane complex and hence serves as an evolutionary adaptor. Here we define the biogenesis pathway and report the cryo-EM structure the wedge protein complex of the T6SS from Enteroaggregative *Escherichia coli* (EAEC). Using an integrative approach, we unveil the molecular architecture of the whole T6SS baseplate and its interaction with the tail sheath, offering detailed insights into its biogenesis and function. We discuss architectural and mechanistic similarities but also revealed key differences with the T4 phage and Mu phage baseplates.

INTRODUCTION

The bacterial Type VI secretion system (T6SS) is one of the key players for microbial competition, and an important virulence factor during bacterial infections. This versatile nanomachine delivers a wide arsenal of effector proteins directly into prokaryotic and eukaryotic target cells¹⁻⁴. T6SS anti-bacterial activities promote privileged access to the niche, to nutrients or to DNA. In most cases, T6SS causes damage within competitor bacterial cells and therefore participates in the reshaping of bacterial communities such as the

49 microbiota^{5,6}. In addition, some T6SS confer anti-host capabilities, *e.g.* phagocytosis
50 inhibition, by remodelling the host cell cytoskeleton⁷⁻¹⁰.

51 The T6SS belongs to the broad family of contractile injection systems (CIS), that includes
52 bacteriophages, high-molecular-weight tailocins such as R-pyocins, and specific *apparati*
53 necessary for the establishment of symbiosis or for the induction of morphological changes¹¹⁻
54¹⁶. All these structures comprise a common core: the tail. CIS tails are composed of an inner
55 tube wrapped by a sheath built under an extended, metastable conformation on an assembly
56 platform, the baseplate. The T6SS tail tube/sheath is a hundred-nanometer-long cytoplasmic
57 structure. It is made of TssB/C subunits that polymerize to form the contractile sheath^{17,18},
58 which surrounds the attacking arrow composed of an inner tube of stacked Hcp hexameric
59 rings^{19,20} tipped by the trimeric VgrG puncturing spike²¹. Various signals, such as contact
60 with the target cell, chemical signals released by competitor or kin cells, response to attacking
61 cells or conjugative transfer, induce structural rearrangements of the sheath leading to its
62 contraction and to the propulsion of the Hcp-VgrG arrow into the target cell²²⁻²⁵. Assembly
63 of the tail tube/sheath is initiated on the baseplate. In addition to controlling sheath extension,
64 the baseplate also serves to trigger sheath contraction. During T6SS biogenesis, the baseplate
65 docks to a trans-envelope complex^{17,26-28} composed of TssJ, TssL and TssM^{29,30}. By
66 connecting the tail to the membrane complex and initiating tail tube/sheath polymerization,
67 the baseplate is a central piece of the T6SS machinery. In addition, by binding cargo effectors
68 through VgrG, the T6SS baseplate also serves as an effector-sorting platform^{2,3,31}.

69 CIS baseplates comprise a minimal core of five proteins that share homology with the
70 prototypical T4 phage gp6, gp7, gp25, gp53, and gp27 proteins¹¹. Gp6, gp7, gp25 and gp53
71 assemble into a unit called wedge³². Biogenesis of the baseplate occurs by the polymerization
72 of six wedges around the central gp27 hub^{32,33}. The T6SS baseplate is composed of five
73 essential subunits: TssE, TssF, TssG, TssK and VgrG²⁷. TssE is a structural homologue of
74 gp25³⁴ and has been recently identified as the sheath initiator³⁵; TssF shares a homology
75 with the N-terminal region of gp6, whereas TssG has been proposed to fulfill the role of gp7
76 or gp53^{27,36}. VgrG is a chimeric protein in which the gp27 hub is fused to the OB-fold/ β -
77 helix needle of gp5^{7,21}. TssF and TssG interact tightly and stabilize each other²⁷. TssK
78 interacts with the TssFG complex^{27,37}. Taylor *et al.* recently reported the purification of the
79 TssKFG complex bound to TssE³⁶. Hence, it is proposed that TssFG, TssKFG and TssKFGE
80 are assembly intermediates of the T6SS baseplate and have structural and functional
81 homologies to the bacteriophage wedges. In agreement with this hypothesis, contacts between
82 the TssFG complex and VgrG have been identified²⁷, suggesting that as in the T4 phage
83 biogenesis pathway, TssKFGE wedges could polymerize around the VgrG hub to form a
84 hexagonal baseplate. The baseplate is docked to the membrane complex mainly by
85 interactions between TssK and both the cytoplasmic domains of TssL and TssM^{26,27,38,39}. The
86 crystal structure of TssK recently revealed that it shares a similar structural architecture with
87 Siphoviridae phage receptor binding proteins and uses the membrane complex as a receptor to
88 anchor the tail²⁸.

89 Besides the critical role of the T6SS baseplate complex, we still lack crucial
90 information on its biogenesis and architecture. Recently, the 8.5-Å-resolution structure of an
91 assembled T6SS baseplate revealed its overall shape³⁵, but did not provide detailed
92 information on the molecular organization of the subunits. Here we used a hybrid approach
93 combining cryo-electron microscopy (cryo-EM), biochemical analysis, native mass
94 spectrometry, evolutionary covariance, and molecular modelling to unveil the assembly
95 pathway of the T6SS baseplate and report the detailed structure of the TssKFGE baseplate
96 wedge complex from the model organism Enteroaggregative *Escherichia coli* (EAEC). The
97 structure highlights unanticipated structural and functional conservation with orthologous
98 bacteriophage proteins. Finally, we fit the atomic model of the T6SS wedge complex into the

99 recent reconstruction of the fully assembled baseplate³⁵ to provide an unprecedented
100 structural and functional understanding of the T6SS baseplate.

101

102 RESULTS

103

104 *Biogenesis of the T6SS baseplate.*

105 Previous fluorescence microscopy studies have monitored T6SS baseplate dynamics using a
106 chromosomally-encoded and functional fusion protein between TssK and the super-folder
107 GFP (TssK_{sf}GFP) in EAEC²⁷. TssK_{sf}GFP assembles fluorescent foci that form independently of
108 the tail sheath and that are recruited to the membrane complex²⁷. To gain further insights into
109 the genetic requirements for TssK_{sf}GFP foci formation, we observed TssK_{sf}GFP in T6SS non-polar
110 gene deletion mutants corresponding to T6SS wedge potential components (see Strains
111 construction in Methods). Fluorescence microscopy recordings demonstrate that TssK_{sf}GFP foci
112 formation depends on TssF and TssG but is independent of TssE (**Fig. 1a & Supplementary**
113 **Fig. 1**). When monitored into additional baseplate mutants, we observed that these foci form
114 independently of TssA but require VgrG (**Fig. 1a**). Therefore, these foci likely represent
115 TssK_{sf}GFPFG complexes bound to VgrG.

116 To provide further information on the composition of the T6SS wedge, we investigated the
117 formation of stable TssK_{sf}GFP-containing subcomplexes in EAEC cells by native PAGE.
118 Native PAGE profiles immunodetected with anti-GFP antibodies revealed the presence of a
119 high-molecular weight complex (HMWC) with a size of ~ 800 kDa (**Fig. 1b**). This complex
120 does not contain TssE, TssA, VgrG and TssM and likely corresponds to TssK_{sf}GFPFG since (1)
121 it disappears in the absence of *tssF* or *tssG*, (2) a HMWC of a comparable size is observable
122 upon pull-down of TssK_{sf}GFP co-produced with TssF and TssG in the heterologous host *E. coli*
123 BL21(DE3), and (3) analysis of this HMWC on denaturing SDS-PAGE reveals the presence
124 of TssK_{sf}GFP, TssF and TssG (**Fig. 1b**).

125 Taken together, the fluorescence microscopy and native-PAGE results, and the previous
126 reports of TssKFG and TssKFGE complex purifications in *Serratia marcescens* and *E. coli*
127^{36,37}, suggest that the TssKFG complex represents a stable intermediate during T6SS baseplate
128 biogenesis. We therefore propose that T6SS baseplate biogenesis starts with the formation of
129 the TssKFG complex and then proceeds with the polymerization of TssKFG building units
130 around the VgrG hub. The observation that TssE is not required for TssKFG-VgrG complex
131 formation, further suggests that TssE binds to the TssKFG either prior to or after its
132 polymerization. This assembly pathway is comparable to that of the minimal phage baseplate,
133 in which gp25 attaches to the baseplate either after completion of the gp10-7-8-6-53 complex
134⁴⁰ or at a later stage, triggering the polymerization of the contractile sheath⁴¹.

135

136 *Interaction network within the T6SS baseplate*

137 To gain further insight into the connectivity network between the T6SS baseplate
138 components, we performed a systematic biochemical pull-down assay (**Supplementary Fig.**
139 **2a-e**). This approach confirmed or revealed a number of contacts including interactions
140 between TssG and TssF, TssE, and TssK (**Fig. 1c**). We then tested whether intermediate sub-
141 complexes, suggested by the assembly pathway defined above, could be purified. In
142 agreement with the proposed assembly pathway, we succeeded to pull-down biogenesis
143 intermediate complexes consisting of TssFG, TssKFG and TssKFGE (**Supplementary Fig.**
144 **2a-b**). Based on these data, we propose that the TssKFGE sub-complex represents the T6SS
145 equivalent of the bacteriophage wedge unit (TssFGE), bound to the TssK membrane complex
146 adaptor.

147

148 *Purification, stoichiometry and cryo-EM structure of a T6SS wedge complex*

149 To biochemically and structurally characterize T6SS baseplate building units, purification
150 tags were positioned on the *EAE*C TssK, TssF, TssG and TssE proteins, at locations that do
151 not interfere with their function. Upon overproduction in BL21(DE3), the TssKFG and
152 TssKFGE complexes were isolated by affinity chromatography followed by gel filtration
153 (**Fig. 1d & Supplementary Fig. 3a**). To gain further insight into the architecture of the T6SS
154 baseplate wedge assembly, the isolated TssKFGE complex was visualized by cryo-electron
155 microscopy (cryo-EM). The 4.6-Å resolution, three-dimensional reconstruction (**Fig. 2a**)
156 shows that the TssKFGE complex displays an intricate architecture with no apparent
157 symmetry. It can be, however, divided into distinct parts: (1) two wing-like structures
158 wrapping a central backbone and (2) a root-like structure with two identical entities
159 displaying apparent C3 symmetry linked to the first part by a thin stalk (**Fig. 2b**).

160 In order to properly interpret the density map, we first sought to determine the stoichiometry
161 and stability of the TssKFGE complex using native mass spectrometry (see **Supplementary**
162 **data for more details**) (**Supplementary Fig. 3b, 3c and 3d**). We determined that the
163 TssKFGE complex comprises 6 TssK, 2 TssF, 1 TssG and 1 TssE subunits (TssK₆F₂G₁E₁;
164 theoretical mass: 498,905 Da).

165 Based on this stoichiometry, we identified densities that could accommodate the two TssK
166 trimers, for which the crystal structure has been recently determined²⁸. The two trimers of
167 TssK readily fit in the density map corresponding to the root-like structure (**Fig. 2c**). The
168 remaining densities corresponding to the stalk and wing-like domains would contain TssF,
169 TssG and TssE. Careful inspection and segmentation of the map lead us to determine that the
170 wing-like domains are formed by two similar densities (**Fig. 2d-f**) that would correspond to
171 TssF. The remaining density, bridging TssK and TssF, would be attributed to TssG (**Fig. 2d**
172 **and Fig. 2g**), while TssE would be located at the tip of the complex (**Fig. 2h**)
173 (**Supplementary data**).

174

175 ***Structural analysis of the T6SS wedge complex***

176 *Biochemical and evolutionary covariance analyses establish TssG as a central structural*
177 *component of the T6SS wedge complex* – Data described above unveil TssG as the central
178 component of the baseplate. Unfortunately, no structural information is available for TssG.
179 We therefore used residue contact predictions based on evolutionary covariance⁴² to
180 determine the TssG domain organization. This analysis identified two putative independent
181 domains in TssG, TssG-D1 (amino-acids 15-140) and TssG-D2 (amino-acids 180-300)
182 (**Supplementary Fig. 4a**). Pull-down assays with these two domains demonstrated that TssG-
183 D1 interacts with TssE, whereas TssG-D2 interacts with TssK and TssF (**Fig. 1c &**
184 **Supplementary Fig. 4b-c**).

185 To further characterize the relative importance of these two domains *in vivo*, we performed a
186 dominant-negative approach by “small domain interference” (SDI)^{43,44} (**Supplementary**
187 **data**) (**Supplementary Fig. 5a-e and Supplementary Fig. 6a-b**) and confirmed that TssG-
188 D2 has a central role for T6SS wedge assembly. We then used the EVcomplex program⁴⁵ to
189 predict inter-molecular contacts between TssG and TssK using evolutionary covariance
190 analysis (see Methods section) (**Supplementary Fig. 6a**). Two TssG-D2 residues, Pro-240
191 and Leu-255, corresponding to predicted TssK-TssG-D2 interfacial residue pairs with the
192 highest scores, were substituted, to alanines (P240A and L255A and P240A-L255A) and
193 assayed by SDI in interbacterial competition experiments (**Supplementary Fig. 6b**)

194

195 *Structure of the TssK trimers* – The resolution of the density map corresponding to the two
196 TssK trimers was between 3.8 and 33 Å (**Fig. 2a**). This level of detail allowed us to obtain a
197 full atomic model of TssK (**Fig. 3a**) (**Supplementary Fig. 7a-b**) (see Methods for details).
198 As described previously, TssK can be divided into four parts from its N- to C-terminus: an N-

199 terminal α -helix, a β -sandwich domain (also named shoulder domain), a 4 α -helix bundle
200 domain (also named neck domain) and a C-terminal α/β domain (also named head domain)
201 (**Fig. 3a**). When compared with the published TssK crystal structure, with the exception of the
202 relative position of the C-terminal domain, the overall structure of the TssK protomer is
203 conserved in the T6SS wedge. The cryo-EM and crystal structures could be superimposed
204 with an RMSD of 1.14 Å (**Supplementary Fig. 7a-b**).

205 In the wedge complex, the two TssK trimers are in contact with each other and interact with
206 TssG. The TssK inter-protomer contacts define a large interacting surface of 2,700-2,800 Å²
207 stabilized by hydrogen bonds and salt bridges⁴⁶. The newly built loops 1-18 and 130-143
208 participate to this interface by forming contacts with the neighbouring protomer. Remarkably
209 the three loops located between residues 105 to 145 define a triangle that encompasses the
210 loop 1-18 and α 1 helix bundle at the centre of the trimer (**Supplementary Fig. 7c**), forming a
211 flat triangular surface at the top of each TssK trimer, which contacts the rest of the wedge
212 complex. This triangular surface is delineated by a polar scaffold made of the strands 105-143
213 and loops around a hydrophobic patch made of part of the loop 1-18 (residues 12-14).

214
215 *Structure of TssG and TssF* –The resolution of the densities corresponding to TssG and TssF
216 varied between 4.3 and 8 Å. Since there was no homologous structure of TssG and TssF
217 available, we built the structure of these proteins de novo helped by a priori knowledge on
218 their topology, secondary structure, and intra-molecular contacts predicted from evolutionary
219 covariance. We devised an iterative pipeline to integrate all this data (prior data and pipeline
220 are described in Methods sections "Evolutionary Covariance Analysis", "TssKFGE model
221 fitting and de novo tracing", as well as **Supplementary Fig. 12**). Eventually, we were able to
222 obtain an atomistic model of this part of the complex, in which most of the sequence of the
223 proteins could be assigned to the cryo-EM density and secondary structure elements could be
224 identified (**Fig. 3c-d**).

225 TssG is made of two globular domains, head and body/feet, separated by a neck domain (**Fig.**
226 **3c**). The N-terminal neck domain, corresponding to TssG-D1, is made of two short helices
227 and loops, whereas the C-terminal body domain, corresponding to TssG-D2, folds as an α/β
228 domain comprising a four-strand β -sheet and three helices (**Fig. 3c**). On each side of the β -
229 sheet, two loops extend to form the two-foot domains (foot1 and foot2). The last strand of the
230 sheet extends into a C-terminal extension of 17 residues.

231 TssF is a globular protein with an N-terminal elongated extension called antenna (**Fig. 3d**).
232 The antenna is made of 2 helices while the C-terminal globular domain can be divided into 5
233 sub-domains: domain 1 (TssF-D1) is a β -sandwich flanked by loops containing short helices;
234 domain 2 (TssF-D2) is a β -sandwich; domain 3 (TssF-D3) is an α -helical domain and
235 comprises 3 short helices; domain 4 (TssF-D4) is an α/β domain composed of one helix and a
236 4-strand β -sheet. The last domain, named branching domain (TssF-BD), is a β -sandwich that
237 is formed by strands that link the antenna with TssF-D1 (three strands of the fold), TssF-D1
238 with TssF-D2 (one strand of the fold) and TssF-D2 with TssF-D3 (two strands of the fold). As
239 previously noted from the two wing densities, the structures of the two TssF proteins (TssFa
240 and TssFb) are superimposable with the exception of the two antennas, which are in two
241 distinct orientations (**Supplementary Fig. 7d**).

242
243 *Structure of the TssFG complex* – TssG and the two copies of TssF (TssFa and TssFb) are
244 assembled to form the pyramidal cap of the T6SS wedge complex (**Fig. 3e**). TssG-D1 forms
245 an heterotrimeric helical bundle with the two TssF antennas (**Fig. 3e-f**). Interestingly, the fold
246 of the TssG body is similar to the TssF-D1 domain (**Supplementary Fig. 7e**), and these three
247 domains define a triangular assembly at the base of the T6SS wedge complex (**Fig. 3f**).
248 Together with the heterotrimeric helical bundle, this structure forms the heterotrimeric

249 scaffold of the TssFG complex (**Fig. 3g**). The D2, D3, D4 and BD domains from TssFa and
250 TssFb form the wing-like domains on both sides of the trimeric scaffold (**Fig. 3G**). TssG is
251 the central backbone of the wedge complex: it interacts with both TssFa and TssFb all along
252 its structure, whereas TssFa and TssFb have very few points of contact between each other.
253

254 *The TssK-TssFG interface* – The interaction of the two TssK trimers with the TssFG complex
255 is mainly mediated through the two TssG-D2 foot domains (**Fig. 3h-i**). The TssG foot1
256 domain (residues 227-242) interacts with residues 10-15 of the three TssK protomers of the
257 TssK1 trimer (**Fig. 3i, upper panel; Supplementary Fig. 7f**). The situation is more complex
258 for the TssK2 trimer: residues 10-15 of the three TssK2 protomers and 138-143 of one
259 monomer (green) make contacts with the TssG foot2 domain (residues 303-322), and the
260 TssG C-terminal extension (residues 345-347) makes contact with residues 116-117 of one
261 TssK monomer (green in **Fig. 3i, lower panel; Supplementary Fig. 7g**), whereas the TssG
262 foot1 domain (residues 221-224) also contributes to the stabilization of the edifice by
263 interacting with the loop 116-120 in TssK2.
264

265 ***Molecular model of the T6SS baseplate***

266 Recently, an 8-Å-resolution cryo-EM structure of the *V. cholerae* T6SS baseplate associated
267 to a non-contractile sheath was reported³⁵. Although no density could be attributed to specific
268 baseplate components, densities corresponding to the Hcp tube and VgrG spike are clearly
269 visible³⁵. We used the deposited map (EMD-3879) to build a molecular model of the entire
270 T6SS baseplate from EAEC (See Methods for more details) (**Fig. 4a**) (**Supplementary Fig.**
271 **8a-b**).

272 The fully assembled T6SS baseplate is 337 Å in diameter and 180 Å in height (**Fig. 4a**).
273 These dimensions are compatible with the densities attributed to the baseplate complex in the
274 cryotomogram of the *Myxococcus xanthus* T6SS⁴⁷. The rings formed by TssFG (wedge ring)
275 and TssK (connector ring) are 100 Å and 110 Å in height respectively (**Fig. 4a**). Within the
276 wedge ring, the individual wedge complexes are organized side by side. Their main axis,
277 along the helical bundle, makes a 30° angle with the symmetry axis of the ring (**Fig. 4b**). The
278 lateral contacts are mediated by interactions between TssFa and TssFb from two adjacent
279 wedge complexes (**Fig. 4b**). Overall, the two protomers are perpendicular to each other,
280 TssFa wrapping the adjacent TssFb (**Fig. 4c**). In detail, the TssFa D1 and BD domains interact
281 with the antenna of the adjacent TssFb whereas TssFa D3 and D4 domains interact with the
282 adjacent TssFb D3 and BD domains (**Fig. 4c**). To a lesser extent, contacts also exist between
283 two adjacent TssFb, two adjacent TssFa, and TssG and TssFb (**Fig. 4b**). In the TssK ring, one
284 TssK protomer, belonging to the TssK1 trimer (grey density), interacts with two TssK
285 protomers belonging to the TssK2 trimer in the adjacent wedge complex (green and brown
286 densities) (**Fig. 4b**). Finally, there are contacts between TssFa and two TssK protomers from
287 the TssK2 trimer from the adjacent wedge complex (**Fig. 4b**).

288 The D1, D2 and BD domains of the TssFa proteins delineate the inner surface of the wedge
289 ring, defining a chamber named TssF chamber (**Fig. 4a**). Together with the wedge ring, the
290 connector ring defines another chamber, named the TssK chamber. Both chambers are
291 separated by a central constriction of ~ 40 Å in diameter due to TssFa D2 and BD domains
292 (**Fig. 4a**). Fitting of the VgrG crystal structure in the assembled baseplate reveals that the
293 TssFa chamber accommodates perfectly the gp27-like hub domain of VgrG while the VgrG
294 gp5-like spike crosses the TssFa constriction and extends into the TssK chamber
295 (**Supplementary Fig. 8b**). In agreement with previous bacterial two-hybrid data²⁷, this
296 reconstruction suggests that the interactions between VgrG and the baseplate are exclusively
297 mediated by TssFa-VgrG interactions (**Fig. 4c; Supplementary Fig. 8b**).

298 Surprisingly, there is no density in the cryo-EM map of the *V. cholerae* baseplate that could
299 accommodate TssE. All the densities seen in the baseplate region of this map could be
300 attributed to TssK, TssG or TssF. The rest of the map corresponds to the VipAB sheath, the
301 Hcp tube, and the VgrG spike. The fact that TssE is invisible in this map could be explained
302 by some degree of flexibility of the protein within the structure after sheath assembly.
303 However, based on the location of TssE in the cryo-EM of the EAEC TssKFGE complex,
304 TssE elegantly fits in a space between the wedge helical bundle and TssB in the model of the
305 assembled baseplate (**Fig. 4d**).

306

307

308 **DISCUSSION**

309

310 ***The T6SS baseplate - sheath connection***

311 The TssFGE wedge ring interacts directly with the sheath structure. A homology model of the
312 EAEC extended sheath was fitted into the molecular model of the baseplate attached to the
313 sheath. Our model suggests that the main contacts are established between the TssFb D2
314 domain and the TssBC N-terminal antenna. In addition, the TssG head domain and TssE
315 likely stabilize the interaction between the sheath and the baseplate (**Fig. 4c-d**) by interacting
316 with the C-terminal domain of TssB as recently proposed⁴⁸.

317

318 ***The T6SS baseplate - membrane complex connection***

319 A number of contacts have been identified between the baseplate components and the
320 cytoplasmic domains of the TssL and TssM inner membrane proteins^{26-28,38,39}. The main
321 contacts involve binding of TssK to both TssL and TssM^{26,28,39} but additional contacts,
322 notably between TssL and TssE, and between TssM and TssG have been reported^{27,39}. While
323 these contacts could not be explained by the current structure, it is known that structural
324 rearrangements occur in the bacteriophage T4 upon sheath contraction⁴⁹⁻⁵¹. If such
325 conformational changes occur in the T6SS baseplate, different contacts may stabilize the
326 interaction of the baseplate with the membrane complex after sheath contraction.

327 However, the position of the TssK connector ring confirms that TssK is the major determinant
328 for mediating baseplate docking to the membrane complex. We have recently shown that the
329 TssK_S domain shares homology with siphophage receptor-binding proteins, whereas it has
330 evolved a specific C-terminal head domain, TssK_H, to use the membrane complex as a
331 receptor²⁸. In agreement with these results, the orientation of the TssK trimers in the
332 baseplate places the TssK_S domains in contact with the TssFG cap complex (**Fig. 2c**), whereas
333 the TssK_H domains extend in the opposite direction compared to the sheath, at the predicted
334 location of the membrane complex (**Fig. 4a**).

335

336 ***Comparison between T6SS and bacteriophage baseplates.***

337 ***(A detailed version of this section is provided in supplementary information)***

338

339 While our data confirms a strong analogy between the T6SS baseplate and the “simple
340 contractile baseplate” from the Mu phage, it is also clear that T6SS and T4 phage wedge
341 components are structurally related to each other. Indeed, the structures of TssF and TssG
342 revealed that they are gp6 and gp7 counterparts in the T4 phage baseplate (**Fig. 5a-b**)
343 (**Supplementary Fig. 9a-b**). Interestingly, a detailed analysis of both baseplate architectures
344 revealed that, while inter-wedge contacts are different in the T4 and the T6SS baseplates (**Fig.**
345 **4b & Fig. 5c**), interactions with the central spike and the contractile sheath are quite well
346 conserved (**Fig. 5c-d, Supplementary Fig. 9c-e**). Finally, this comparison revealed how the

347 apical part of the each baseplate is structurally specialized to interact with different targets
348 (Fig. 5c-e).

349

350 *Assembly mechanism and stability of of the T4 and T6SS baseplates*

351 *(A detailed version of this section is provided in supplementary information)*

352

353 While the T4 bacteriophage wedge complex appears to be transient, the T6SS wedge complex
354 is stable, as shown by the isolation of TssKFG or TssKFGE complexes in EAEC, *S.*
355 *marcescens* and uropathogenic *E. coli* (this work; ^{36,37}). By contrast, the fully assembled T4
356 phage baseplate is much more stable than the T6SS baseplate, since we did not succeed to
357 purify the T6SS hexagonal baseplate. This higher stability of a preformed T6SS baseplate
358 intermediate may reflect an adaptation to the secretion process. Delayed polymerization of the
359 wedge around the VgrG hub and fast recycling of the wedge complexes might be necessary
360 during each secretion cycle

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364 **Concluding remarks**

365

366 In this work, we provide an unprecedented functional and structural study of the T6SS
367 baseplate building block, the wedge complex. Due to the conservation of T6SS wedge
368 complexes among pathogenic bacteria, the atomic model of the TssKFGE complex will
369 facilitate the design of anti-T6SS compounds targeting hot spots of the baseplate assembly,
370 paving the way towards new therapeutic avenues to replace or help classical antibiotherapies.

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503
504

505 **Figures legends.**

506
507 **Figure 1. Composition of the T6SS wedges complex.** a. Fluorescence microscopy
508 recordings showing TssK_{s/GFP} localisation in the absence of the TssF, TssG, TssE, VgrG and
509 TssA proteins. The positions of foci corresponding to fully-assembled baseplates are indicated
510 by arrowheads. Microscopy analyses were performed independently three times, each in
511 technical triplicate, and a representative experiment is shown. Scale bars, 1 μm. b. Native 4-
512 16% gel analysed by Coomassie staining (upper left panel) or immunoblotting using anti-GFP
513 antibodies (right panel) or anti-GFP, anti-Streptag and anti-FLAG antibodies (lower left
514 panels). The TssK_{s/GFP}-6 × His and TssK_{s/GFP}-6 × His-FG produced and purified from
515 BL21(DE3) cells show the positions of two high-molecular weight complexes (HMWC,
516 indicated by * and **). Formation of the higher HMWC is monitored in different *tss* mutant
517 backgrounds, revealing that the * and ** complexes correspond to a TssK_{s/GFP} trimer and
518 TssK_{s/GFP}-TssF-TssG complex, respectively. Native gel experiment was performed
519 independently three times and a representative experiment is shown. c. Summary of protein-
520 protein interactions within the TssKFGE complex, as defined by pair-wise pull-down
521 experiments (see Supplementary Fig. 2 and 4). Arrows indicate interactions between the two
522 proteins or domains. d. Purification and biochemical characterization of the TssKFGE wedge
523 complex. Analytical size-exclusion chromatography analysis of the purified TssKFGE
524 complex (continuous line) on a Superose 6 column, calibrated with 43-, 75-, 158-, 440- and
525 660-kDa molecular mass markers (dotted lines). The molecular mass of each marker (in
526 kilodaltons) is indicated on the top of the corresponding peak. An arrow indicates the position
527 of the peak fraction corresponding to the TssKFGE complex. Inset: Purified TssKFGE
528 complex subjected to sodium dodecyl sulfate 12.5%-acrylamide PAGE and Coomassie
529 staining. The different proteins are indicated on the right, whereas molecular weight markers
530 are indicated on the left. TssKFGE complex purification and analytical size-exclusion
531 chromatography analysis experiments were performed at least three times and a representative
532 result is shown.
533

534 **Figure 2. Cryo-EM density map of the TssKFGE wedge complex.** a. Surface
535 representation of the composite cryo-EM density map of the TssKFGE complex. The maps
536 corresponding to the root and stalk/wings regions were refined separately (see material and
537 methods section). Dimensions and labelling of the various densities of the complex are
538 shown. b. Schematic representation of the different densities of the TssKFGE map. c. Two
539 copies of the TssK trimer crystal structure (PDB:5M30; ²⁸) can be fitted in the density
540 corresponding to the “roots”. d. Segmentation of the stalk and wing regions of the density
541 map (shown in the same orientation than B). Two regions forming the wings (in cyan and
542 blue) interact with a central backbone (in yellow). e-f. Densities corresponding to the two
543 wing sub-regions, positioned in the same orientation (e) and superimposed (f). Each of these
544 densities corresponds to one TssF subunit. g. The density corresponding to the central
545 backbone is displayed alone. It corresponds to one TssG subunit. h. At lower density
546 threshold, a density appears at the tip of the TssFG density. A TssE homology model could be

547 fitted into this new density with a correlation of 0.870. The scale bars correspond to 25 Å for
548 each panel.

549

550 **Figure 3. Structure of the TssKFGE complex.** **a.** Ribbon diagram of one TssK protomer.
551 The structure can be divided into 4 parts, from N- to C-terminus: N-terminal helix (residues 1-
552 42, blue), shoulder domain (residues 43-185, cyan), neck domain (residues 186-312, green)
553 and head domain (residues 313-444, red). **b.** Ribbon diagram and surface representation
554 (transparent) of one TssK trimer viewed from the side (top panel) and from the bottom
555 (Bottom panel). Each TssK protomer is colored in beige, dark green and brown. **c.** Ribbon
556 diagram of the TssG protomer. The structure can be divided into 6 parts, from N- to C-
557 terminus: N-terminal head domain (residues 8-144, blue), neck domain (residues 145-192,
558 green), body domain (residues 146-215, 252-300 and 331-342, red) and C-terminal extension
559 (residues 342-356, purple, foot1 (residues 216-252) and foot2 (residues 300-330), in yellow.
560 **c.** Ribbon diagram of the TssF protomer. The structure can be divided into 6 parts, from N- to
561 C-terminus: N-terminal antenna (residues 4-82, blue), domain 1 (residues 140-295, green),
562 domain 2 (residues 304-416, red), domain 3 (residues 453-502, magenta) and domain 4
563 (residues 503-587, purple). A branching domain connects domains 1, 2 and 3 (residues 83-
564 139, 296- 303 and 417-452, yellow). **e.** Ribbon diagram of the TssFG complex. It contains
565 one copy of TssG (yellow) and two copies of TssF, named TssFa (cyan) and TssFb (blue). **f.**
566 Ribbon diagram of the TssG-TssFa-TssFb trimer scaffold. TssG, TssFa and TssFb are
567 represented in yellow, cyan and blue respectively. The triangular organization is highlighted
568 by the red dotted-line triangle. **g.** The TssG-TssFa-TssFb trimer scaffold is decorated by TssF
569 wing and TssG N-terminal head domains. The trimer scaffold is represented as ribbons
570 (magenta). The decorations are represented as ribbons and transparent surfaces. The colour
571 code is the same as in panel e. **h.** Ribbon diagram of the whole TssKFGE wedge complex.
572 The complex made of TssG (yellow), TssFa (cyan) and TssFb (blue) interacts with two TssK
573 trimers (TssK1 and TssK2), same color code as in B. **i.** Interaction between TssG foot
574 domains and TssK trimers. The same color code is used as in B. and E. TssK1 and TssK2 are
575 depicted in surface rendition and ribbon diagram respectively. TssG antenna and body are
576 represented as ribbons while the feet are represented as surfaces.

577

578 **Figure 4. Structural model of the EAEC T6SS baseplate.**

579 **a.** Overall view of the interaction between the T6SS baseplate and the TssB/C sheath. The
580 color code used to identify the various subunits is shown on the left of the panel. Left panel:
581 surface representation of the model of the EAEC T6SS baseplate in interaction with a model
582 EAEC sheath. While TssB/C protomers are colored in grey, the TssB/C protomers interacting
583 with the baseplate are colored in orange. The different parts of the tail (connector ring, wedge
584 ring, extended sheath) are indicated, as well as the putative location of the membrane
585 complex. Middle panel: central slice of the complex seen in the left panel. The different parts
586 of the tail, as well as the two chambers delimited by the TssFa and TssK subunits (TssF and
587 TssK chamber, respectively) are indicated. Right panel: surface representation of the
588 baseplate viewed from the membrane complex (top view) and from the sheath (bottom view).
589 **b.** Interaction surface between two wedge complexes as they are assembled in the baseplate.
590 The color code used to identify the various subunits is shown on the left of the panel. The
591 predicted interacting residues between two wedge complexes are colored in red. Left panel:
592 the two bound wedge complexes as they are assembled in the baseplate. The red dotted lines
593 represent the baseplate symmetry axis (vertical line) and the wedge complex main axis (tilted
594 line). Right panel: the same two wedge complexes are split open to reveal the interaction
595 surfaces between them. The main interfaces are identified. **c.** Ribbon diagram and transparent
596 surface representation of TssFa-TssFb belonging to two adjacent wedge complexes (main

597 interface between wedge complexes within the T6SS baseplate). TssFa and TssFb are
598 represented in cyan and blue respectively. Within each subunit, the regions interacting with
599 VgrG and TssBC are colored in magenta and orange respectively. **d.** Ribbon diagram and
600 surface representation of the wedge-TssB/C interaction. The color code used to identify the
601 various subunits is shown on the left of the panel. Top panel: surface representation views
602 (rotated 180° along the axis) of TssBC bound to the TssFa-TssFb-TssG-TssE complex. The
603 ribbon diagram of the same complex is shown on bottom.

604

605 **Figure 5. Comparison between the T4 bacteriophage and T6SS baseplates.**

606 In all panels, T6SS and T4 bacteriophage representations are shown on left and right,
607 respectively. For panels **c-e**, the color code used to identify the various subunits or domains is
608 shown on the left of each panel. **a.** T6SS and T4 bacteriophage trimer scaffolds share the
609 same structural organization. In the T4 baseplate, the backbone of the wedge domain is made
610 of a heterotrimeric helical bundle and a trifurcation unit (in purple), which are made of the
611 gp6/gp7 antennas and of the gp6/gp7 α/β domains, respectively. As seen in Fig. 3F, this
612 organization is conserved in the T6SS baseplate (purple). In gp6, two consecutive β -sandwich
613 domains following the N-terminal antenna are called the wing domains (green). These
614 domains resemble the TssF D2, and BD (green). **b.** Same assembly as in **a.**, seen from the
615 bottom. Both T6SS and T4 bacteriophage wedge complexes contain a trifurcation unit made
616 of the α/β domains in TssFa-TssFb-TssG and gp6a-gp6b-gp7 respectively. A red triangle
617 delineates this trifurcation unit. **c.** Top views of the T6SS and T4 bacteriophage baseplates.
618 For the T4 bacteriophage baseplate, the inner and intermediate baseplate are separated by a
619 red dotted line. The inter-wedge gp6a/gp6b main interface is indicated. **d.** Bottom views of
620 the T6SS and T4 bacteriophage baseplates. The domains interacting with the sheath are
621 indicated and colored in orange. **e.** Side views of the T6SS and T4 bacteriophage baseplates.

622

623 **Figure 6. Schematic representation of the T6SS assembly pathway.**

624 Upper panel: schematic representation of the T6SS assembly pathway, starting with the initial
625 positioning of the membrane complex (MC, blue) (stage 1), the assembly of the wedge
626 complexes (grey), their polymerization around the VgrG spike (pink), the recruitment of
627 effectors (light orange skull), and the recruitment of the baseplate (BP) to the MC (stage 2);
628 and the polymerization of the tail tube/sheath complex (TTC, salmon). A surface
629 representation of the modeled T6SS baseplate with the extended sheath bound to the
630 membrane complex is shown on right. OM, outer membrane; PG, peptidoglycan; IM, inner
631 membrane. Lower panel: from left to right, the TssKFGE wedge structure (same color code as
632 in Fig. 3); the structure of the assembled T6SS BP (same color code as in Fig. 4) and a
633 schematic representation of the protein-protein contacts and topology of the fully-assembled
634 baseplate.

635

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637

638 **SUPPLEMENTARY INFORMATION**

639

640 Supplementary Information includes 19 figures and 3 tables.

641

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643

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662
663

664 **AUTHORS CONTRIBUTION**

665

666 E.D., R.F. and E.C. designed research, assembled results, and wrote the paper with input from
667 all authors. E.D. and Y.C. performed biochemical experiments and initial negative stain EM
668 observations. C.R. performed sample preparation for cryo-EM, *de novo* reconstruction, and
669 structure refinement. C.R. and R.F. analyzed the cryo-EM data and the final structure. C.M.
670 and M.R. performed MS experiments. Y.C. performed all *in vivo* experiments. R.P. and G.B.
671 performed method development, and structural modeling; B.B. and F.A. performed structural
672 modeling. J.C.R. performed design and analysis of MS experiments.

673

674 **DECLARATION OF INTERESTS**

675

676 The authors declare no competing interests.

677

678 **Methods**

679

680 A key resource table (supplementary table 1) provides details about the reagents, strains, and
681 software used in this study.

682

683 **Strains, media and chemicals**

684 The strains, plasmids and oligonucleotides used in this study are listed in Supplementary Table 1. The
685 *E. coli* K-12 DH5 α strain was used for cloning procedures; *E. coli* K-12 BL21(DE3) strain was used
686 for protein expression and purification; *E. coli* K-12 W3110 bearing the pUA66-*rrnB* vector (Kan^R
687 and GFP⁺, ¹) was used as recipient for antibacterial competition assays. Strains were routinely grown
688 in lysogeny broth (LB) rich medium or in Sci-1-inducing medium (SIM; M9 minimal medium,
689 glycerol 0.2%, vitamin B1 1 $\mu\text{g.mL}^{-1}$, casaminoacids 100 mg.mL^{-1} , LB 10%, supplemented or not with
690 bactoagar 1.5%) ² with shaking at 37°C. Plasmids were maintained by the addition of streptomycin
691 (100 $\mu\text{g.mL}^{-1}$), kanamycin (50 $\mu\text{g.mL}^{-1}$), chloramphenicol (30 $\mu\text{g.mL}^{-1}$) or ampicillin (100 $\mu\text{g.mL}^{-1}$).
692 Expression of genes from pCDF, pRSF and pETDuet vectors was induced with 1 mM of isopropyl- β -
693 D-thio-galactopyrannoside (IPTG, Eurobio) for 16h at 16 °C.

694

695 **Strains construction**

696 Gene deletion into the enteroaggregative *E. coli* 17-2 *tssK_{sfgfp}* strain ³ was achieved by using a
697 modified one-step inactivation procedure ⁴ as previously described ⁵ using plasmid pKOBEG ⁶.

698 Briefly, a kanamycin cassette was amplified from plasmid pKD4 using oligonucleotide pairs carrying
699 5' 50-nucleotide extensions homologous to regions adjacent to the gene to be deleted. After
700 electroporation of 600 ng of column-purified PCR product, kanamycin-resistant clones were selected
701 and verified by colony-PCR. The kanamycin cassette, inserted at the gene locus on the bacterial
702 chromosome, was then excised using plasmid pCP20, leaving an FRT scar⁴. Gene deletions were
703 confirmed by colony-PCR and sequencing. All the mutations have been previously trans-
704 complemented for the T6SS-dependent bacterial competition or Hcp secretion phenotype by plasmid
705 expressing the WT version of the T6SS genes TssFG⁷ and TssK⁸.
706

707 708 **Plasmid construction**

709 PCRs were performed using the Phusion DNA polymerase (Thermo Scientific). Restriction enzymes
710 were purchased from New England Biolabs and used according to the manufacturer's instructions.
711 Custom oligonucleotides were synthesized by Sigma Aldrich and are listed in Supplementary Table 1.
712 Enteroaggregative *E. coli* 17-2 chromosomal DNA was used as a template for all PCRs. Construction
713 of pCDF-TssK^H-S^F-G^F has been previously described⁹. Plasmids pCDF-TssK^H-S^F-G^{Flag}-E^{HA} and
714 pETDuet-VgrG^{HA} were engineered by restriction cloning. Briefly, the sequences encoding the full-
715 length *tssE* and *vgrG* were PCR-amplified using primers 5-pRSF-E^{HA}
716 (ATAAAGCTTAAGGAGATATACATATGCCGCGTCCTTCCCTTTATGAAATTCTCTATGGC)
717 and 3-pRSF-E^{HA}
718 (ATAGCGGCCGCTCAAGCGTAATCTGGAACATCGTATGGGTACGTCTGCACGTAGCGCTGCT
719 GTTTCAGATGGC), and 5-pETDuet-VgrG^{HA}
720 (ATAGGATCCAAGGAGATATACATATGAATCTCACTGACTCCCTGCAAATGTTTTATCCG
721 G) and 3-pETDuet-VgrG^{HA}
722 (TATAAGCTTTCAAGCGTAATCTGGAACATCGTATGGGTATTCTGTTTCTCCATGAATTTTAC
723 CTCCCAAATC), respectively. Primers introduced a C-terminal HA epitope tag extension
724 (italicized in the primer sequences), and HindIII/NotI and BamHI/HindIII restriction sites (underlined
725 in the primer sequences) respectively. All other plasmids were constructed by restriction-free cloning
726¹⁰. Briefly, the gene of interest was amplified with oligonucleotides carrying 5' extensions annealing to
727 the target vector. The product of the first PCR was then used as oligonucleotide for a second PCR
728 using the target vector as template. All constructs have been verified by DNA sequencing (Eurofins
729 Genomics).
730

731 **Interbacterial competition assay**

732 The antibacterial growth competition assay was performed as previously described¹¹. Wild-type *E.*
733 *coli* K-12 strain W3110 bearing the pUA66-*rrnB* plasmid (conferring kanamycin resistance and
734 constitutive GFP fluorescence (*gfp* gene under the control of the ribosomal *rrnB* promoter,¹² was used
735 as recipient. Attacker and recipient cells were grown for 16 h in LB medium, diluted in SIM to allow
736 maximal expression of the *sci-1* gene cluster². Once the culture reached $A_{600nm} \sim 0.8$, cells were
737 harvested and normalized to $A_{600nm} = 0.5$ in SIM. Attacker and recipient cells were mixed to a 4:1 ratio
738 and 15- μ l drops of the mixture were spotted in triplicate onto a pre-warmed dry SIM agar plate
739 supplemented or not with arabinose 0.5 mg.mL⁻¹. After incubation for 4 h at 37°C, the bacterial spots
740 were resuspended in LB and bacterial suspensions were normalized to $A_{600nm} = 0.5$. For the
741 enumeration of viable prey cells, bacterial suspensions were serially diluted and spotted onto
742 kanamycin LB plates. The assays were performed from at least three independent cultures, with
743 technical triplicates and a representative technical triplicate is shown.
744

745 **TssKFGE complex production and purification**

746 The tags were rationally positioned at specific locations in the TssKFGE complex: Introduction of the
747 tags (i) still permits protein-protein interaction as assayed by bacterial two hybrid (BTH) and (ii)
748 allows trans-complementation of the T6SS-dependent "interbacterial competition" phenotype in a
749 mutant deleted for a specific gene with a plasmid encoding a tagged version of this same gene. The
750 pCDF-TssK^H-S^F-G^F-E^{HA} plasmid was transformed into the *E. coli* BL21(DE3) expression strain. Cells
751 were grown at 37°C in lysogeny broth (LB) to $A_{600nm} \sim 0.6$ and the expression of the *tssKFGE* genes

752 was induced with 1.0 mM IPTG for 16 h at 16 °C. Cell pellets were resuspended in ice-cold 50 mM
753 Tris-HCl pH 8.0, 150 mM NaCl, 1 mM EDTA supplemented with DNase I (100 mg.mL⁻¹), lysozyme
754 (100 mg.mL⁻¹), MgCl₂ (10mM) and EDTA-free protease inhibitor (Roche) to an *A*_{600nm} of 125. Cells
755 were broken using an Emulsiflex-C5 (Avestin) and clarified by ultracentrifugation at 20,000×g for 30
756 min. The supernatant was loaded onto a 5-mL HisTrap HP (GE Healthcare) column equilibrated in
757 affinity buffer (50 mM Tris-HCl pH 8.0, 150 mM NaCl) supplemented with 20 mM imidazole. The
758 column was then washed using the affinity buffer supplemented with 50 mM imidazole and the
759 TssKFG complex was eluted in the same buffer supplemented with 250 mM imidazole. Peak
760 fractions were pooled and loaded onto a Superose 6 10/300 column (GE Healthcare) equilibrated in 50
761 mM HEPES pH 7.5, 150 mM NaCl. The complex eluted as a single monodisperse peak and the
762 sample was used for EM sample preparation.

763

764 **Protein production and purification for interaction studies**

765 Plasmids expressing the genes combination of interest were co-transformed into *E. coli* BL21(DE3)
766 and cells were treated as described before. For His-tag affinity, the supernatant was loaded, washed
767 and eluted as above. For strep-tag affinity, the supernatant was loaded onto a 5-mL StrepTrap HP
768 column (GE Healthcare), washed with affinity buffer and eluted in affinity buffer supplemented with
769 2.5 mM desthiobiotin (IBA Technologies). The lysate, flow through, wash and elution fractions were
770 collected, resuspended in Laemmli loading buffer supplemented with 300 mM 2-Mercaptoethanol,
771 heated for 10 min at 96°C prior to analyses by SDS-PAGE and immunoblotting.

772

773 **SDS-PAGE, protein transfer, immunostaining and antibodies**

774 SDS-PAGE was performed on Bio-Rad Mini-PROTEAN[®] systems using standard protocols. For
775 immunostaining, proteins were transferred onto 0.2-µm nitrocellulose membranes (Amersham
776 Protran). Immunoblots were probed with primary antibodies and goat secondary antibodies coupled to
777 alkaline phosphatase, and developed in alkaline buffer in presence of 5-bromo-4-chloro-3-
778 indolyphosphate and nitro-blue tetrazolium. The anti-HA (HA-7 clone, Sigma Aldrich), anti-Flag
779 (M2 clone, Sigma Aldrich), anti-StrepII (Sigma Aldrich), anti VSV-G (Sigma Aldrich) and anti-5His
780 (Sigma Aldrich) monoclonal antibodies, and mouse secondary antibodies (Millipore) were purchased
781 as indicated.

782

783 **Native polyacrylamide gel electrophoresis**

784 After overnight cultures in LB, the enteroaggregative *E. coli* EAEC strain 17-2-*tssK_{sfgfp}* and its mutant
785 variants were diluted 1/100 in 500 mL of SIM and grown at 37°C to an *A*_{600nm} ~ 1,2. Cells were
786 harvested, resuspended in ice-cold 50 mM Tris-HCl pH 8.0, 150 mM NaCl, 1 mM EDTA to an *A*_{600nm}
787 = 120 and broken using an Emulsiflex-C5 (Avestin). After clarification by ultracentrifugation at
788 20,000×g for 30 min, lysates were loaded on a native 4-16% gel (Mini-PROTEAN[®] TGX, Bio-Rad).
789 After migration, proteins and protein complexes were transferred onto a nitrocellulose membrane and
790 immunoblotted as described above.

791

792 **Mass spectrometry**

793 Purified TssKFG and TssKFG complex were first buffer exchanged with 500 mM
794 ammonium acetate by size exclusion chromatography on Superdex 200 increase (3.2 / 300) using a
795 ÄKTAmicro System (GE healthcare) at isocratic flow of 50 µL.min⁻¹. Samples were then nano-
796 electrosprayed using a TriVersa NanoMate (Advion Biosciences, Ithaca, USA) coupled to a Synapt
797 G2-Si mass spectrometer (Waters Corporation, Manchester, UK). The instrument was calibrated from
798 1,000 m/z to 12,000 m/z with CsI (50 mg/mL⁻¹) with an accuracy of 6 ppm. Native mass
799 measurements were recorded between 2,000 and 20,000 m/z with sensitivity mode activated. The
800 following settings were chosen: sampling cone 150 V, source offset 45 V, source temperature 40°C,
801 trap gas flow 5 mL.min⁻¹, helium cell gas flow 180 mL.min⁻¹. Sub-complexes were obtained with the
802 same parameters and additional collisional activation up to 60 NCE (Normalized Collisional Energy).
803 Data were accumulated several minutes, averaged and smoothed with the Mass Lynx smoothing
804 Algorithm (30 cycles, 30 amu large channel). Theoretical masses were calculated with the algorithm
805 embedded within MassLynx using the protein sequence of the constructs. Measured masses were

806 obtained averaging the mass calculated for the most intense charge states of the complex with a
807 minimum of 3 charge states.

808

809 **Fluorescence microscopy, image treatment and analyses**

810 Fluorescence microscopy experiments were performed as described^{8,13}. Briefly, cells were grown
811 overnight in LB medium and diluted to $A_{600nm} \sim 0.04$ in SIM. Exponentially growing cells ($A_{600nm} \sim$
812 $0.8-1$) were harvested, washed in phosphate-buffered saline buffer (PBS), resuspended in PBS to
813 $A_{600nm} \sim 50$, spotted on a 1.5% agarose pad and covered with a cover slip. For domain interference, the
814 *E. coli* 17-2 *tssK-sfgfp* or *tssB-mCherry* strains expressing TssK or TssG domains were cultured as
815 described above, except that 0.05% (w/v) arabinose was added in the culture once reached $A_{600nm} \sim 0,6$
816 for 30 min. Fluorescence and phase contrast micrographs were captured using AxioImager M2
817 microscope (Zeiss) equipped with an OrcaR2 digital camera (Hamamatsu). Fluorescence images were
818 acquired with a minimal exposure time to reduce bleaching and phototoxicity effects, typically 500 ms
819 for TssK-sfGFP and 200 ms for TssB-mCherry. Noise and background were reduced using the
820 ‘Subtract Background’ (20 pixels Rolling Ball) and Band plugins of imageJ (Image J, National
821 Institutes of Health). The sfGFP foci were automatically detected using the microbeJ plugin
822 (<http://www.microbej.com/index.html>). Box plots representing the number of detected foci for each
823 strain were made using microbeJ. The number of sheath per cells was measured manually. Microscopy
824 analyses were performed at least three times, each in technical triplicate, and a representative
825 experiment is shown.

826

827 **Cryo-EM grids preparation and data acquisition**

828 For cryo-EM analyses, the buffer of the purified TssKFGE complex was exchanged for 50 mM
829 HEPES pH 7.5, 150 mM NaCl to a final protein concentration of $0.2 \text{ mg}\cdot\text{mL}^{-1}$. $3.5 \mu\text{L}$ of the protein
830 solution was deposited on Lacey grids and vitrified using a Vitrobot (Thermo Fisher, Waltham, MA,
831 USA) (parameters: blotting 4 s, temperature 4°C , humidity 100 %). Micrographs (Supplementary Fig.
832 11a) were recorded at a specimen temperature of 85 K in a Titan Krios electron microscope (Thermo
833 Fisher, Waltham, MA, USA) at 300 kV and a nominal magnification of 130,000 on a K2 summit
834 direct electron detector mounted on a Bioquantum LS/967 energy filter (Gatan, Pleasanton, California)
835 in counting mode with a pixel size of 1.1 \AA , at an electron flux of about $12.35 \text{ e-}/\text{px}\cdot\text{s}$. Dose-
836 fractionated movie frames (30 in total) were acquired for 4 s with 0.13 s exposure time per frame. The
837 total electron dose was $\sim 45 \text{ e-}/\text{\AA}^2$ ($1.5 \text{ e-}/\text{\AA}^2/\text{frame}$). The defocus range chosen for the automatic
838 collect was 0.7 to $2 \mu\text{m}$, which resulted in an actual range between 0.4 to $3 \mu\text{m}$.

839

840 **Cryo-EM image processing**

841 750 micrographs were processed (Supplementary Fig. 10a). Subframes were divided into 5×5 patches
842 and corrected with MotionCor2, with dose weighting ($1.5 \text{ e-}/\text{\AA}^2/\text{frame}$) to dampen the high-resolution
843 signal in later frames¹⁴. CTF parameters were estimated by gCTF¹⁵. Particles on micrographs were
844 picked manually in box size of 450 pixels and classified into 2D class averages. Selected classes were
845 used as references for autopicking in RELION 2.1¹⁶. The total number of initial extracted particles
846 (167,825) was reduced to 52,069 by subsequent rounds of 2D classifications (Supplementary Fig. 10b)
847 and an initial model (Supplementary Fig. 10c) of what appears to be 2 TssKFGE full complexes
848 ($12 \times \text{TssK}$, $4 \times \text{TssF}$, $2 \times \text{TssG}$, $2 \times \text{TssE}$) was generated on cryoSPARC 0.6¹⁷. The selected particles
849 from the 2D classifications were converted back to RELION 2.1 using the script *csparc2star.py*¹⁸ and
850 then subjected to an additional round of 2D and 3D classification (Supplementary Fig. 10c), with the
851 initial model low-pass filtered to 60 \AA . A final cleaner dataset of 32,504 particles was selected for
852 further processing. The 40 \AA low-pass filtered 3D class was then used as an initial model for 3D
853 refinement with a solvent mask corresponding to most well defined half of the larger TssKFGE
854 complex ($6 \times \text{TssK}$, $2 \times \text{TssF}$, $1 \times \text{TssG}$, $1 \times \text{TssE}$). No symmetry was applied during any of the 3D
855 classifications and refinements. To obtain the density map of the single repeating unit of the assembly
856 of the two complexes (hereafter called TssKFGE), the complex with the least defined wing was
857 subtracted, and a soft mask was applied to the remaining region for 3D auto-refinement. The final
858 resolution was 4.6 \AA , calculated with masked post-process by refining two half-maps independently,

859 according to the “gold standard” FSC 0.143 criterion. The B factor applied of -136 gave a local
860 resolution range between 3.9 and 18 Å (Supplementary Fig. 11a-c).

861 To obtain the best density map for the root-like domains that correspond to TssK, the regions
862 corresponding to the wings were subtracted and a soft mask was applied to the TssK trimers during
863 autorefinement, producing a map with a 4.3-Å overall resolution. The calculated B factor was -111
864 and it gave a local map resolution of 3.8-33 Å (Supplementary Fig. 11d-f, j-k).

865 Masking was not sufficient to improve the density map of the flexible regions. A re-centering of the
866 particles in the wings region was thus performed using the REP algorithm¹⁹ and the box size was
867 reduced to 200 pixels. A masked 3D auto-refinement to exclude the root-like domains was performed
868 to obtain a resolution of 4.7 Å (4.3-8 Å local with B factor of -202; Supplementary Fig. 11g-i).

869 All of the densities obtained were subjected to Autosharpen²⁰ in the Phenix software package. All the
870 models were built on autosharpened densities. Subsequent molecular graphics and analyses were
871 performed using UCSF Chimera²¹.

872

873 **Evolutionary Covariance Analysis.**

874 Residue–residue contacts can be predicted based on sequence information alone through the
875 evolutionary covariance analysis²² Essentially, the prediction of residue–residue contacts is linked to
876 strong evolutionary constraints, such as the presence of functionally important structures, and is
877 measured by the covariance of contacting residues. Evolutionary constraints can be detected at a
878 sequence level by aligning thousands of homologous protein sequences. Statistical probability models
879 can separate direct from indirect residue–residue couplings, increasing the signal-to-noise ratio in the
880 predicted contact map. Therefore, contacts with the strongest signal, indicated by the highest global
881 statistical scores, are most likely to represent the true residue interactions in a protein. In this work we
882 use two software packages that uses distinct statistical probability models: EVcomplex²³ and RaptorX
883²⁴ for inter-molecular and intra-molecular contact prediction, respectively. EVcomplex computes co-
884 evolution between proteins, pairing up protein sequences and assuming proximity of the two
885 interacting partners on the genome, with the goal of reducing incorrect pairings. The paired sequences
886 are concatenated and statistical co-evolution analysis is performed using EVcoupling²⁵. The RaptorX
887 algorithm predicts intra-molecular contacts by integrating evolutionary coupling, pairwise potentials,
888 and sequence conservation information through an ultra-deep neural network.

889

890

891 **TssKFGE model fitting and de novo tracing**

892 Two copies of the trimeric TssK unit (PDB: 5M30;⁹ were docked into the EM density map of the
893 TssKFGE complex and fit as rigid bodies in Chimera²¹. Missing regions were manually built using
894 Coot²⁶. The final model was refined by multiple rounds of manual refinement in Coot²⁶, Rosetta
895 refine²⁷ and the real-space refine function of Phenix²⁸.

896 Owing to the lack of structural information for TssF and TssG and the limited resolution of the density
897 map in that region, we devised an iterative semi-automatic protocol that employed several sources of
898 information and pieces of software (Supplementary Fig. 12). The sources of information included the
899 EM density map, the stoichiometry and the symmetry of the TssFG subcomplex, the position of bulky
900 residues in the sequence, a homology model of TssF based on the T4 bacteriophage gp6 (generated
901 using i-TASSER, consensus secondary structure obtained using PSIPRED²⁹, Rosetta²⁷, Phyre2³⁰,
902 DeepCNF²⁵, and i-TASSER³¹, and intra-molecular contact predictions for TssF and TssG using the
903 RaptorX contact prediction tool³¹ (Supplementary Fig. 12b). Contact maps are binary two-
904 dimensional matrices that represent the proximity between all residue pairs for a given protein²⁷. The
905 RaptorX algorithm predicts contacts by integrating evolutionary coupling, pairwise potentials, and
906 sequence conservation information through an ultra-deep neural network. Predicted contact maps were
907 obtained by filtering RaptorX contacts with a score higher than 0.4. Model contact maps, which are
908 compared with the predicted ones, were obtained from a structure calculating the pairwise distances
909 between C α atoms and considering as a contact any distance below 12 Å. We tested the quality the
910 predicted contact maps by calculating the accuracy on a known structure. Using the enteroaggregative
911 *E. coli* TssK structure as model⁹; PDB: 5M30) (Supplementary Fig. 12c), the ratio between predicted
912 contacts consistent with the structure and the total contacts within the structure gave an accuracy of
913 0.97 (Supplementary Table S3).

914 The protocol described below iterates between structural refinement and sequence-structure
915 registration based on contact prediction. It is organized into four steps (Supplementary Fig. 12a):
916 *Step 1. Initial segmentation and manual tracing.* The TssFG map was segmented using Segger v1.9.4
917 in UCSF Chimera ²¹ and the density of one half of the wing superimposed with the other half to
918 identify repeating patterns due to the presence of two TssF monomers in the complex. The segmented
919 map identified densities corresponding to TssG and the two TssF subunits. An initial C α tracing of the
920 TssFG complex was based on the three density segments. The sequence registering was guided by
921 sequence position of bulky amino-acids and consensus prediction of secondary structures. The model
922 building was aided by the use of the Coot-trimmings script ³² and sharpening of the map was
923 modulated by varying the resolution limit.

924 *Step 2. Sequence Registration using predicted contact maps.* The model was validated and registered
925 using residue contact prediction ³³. The contact map of the obtained model was computed and aligned
926 to the predicted contact-map using the MapAlign software ³⁴. Using the resulting contact-map
927 alignment we identified regions of the model that agree and disagree with the predicted contact-map.
928 The boundaries of these regions were used to divide the structure into several fragments. The
929 connectivity and the sense (N- to C-terminus orientation) of the fragments were globally optimized
930 using dynamic programming and the MapAlign scoring function.

931 *Step 3. De novo modeling of inconsistent regions.* The model generated in the previous step was again
932 validated comparing its contact-map with the predicted contact-map. Regions in disagreement (TssG-
933 D1, residues 1-144; TssG-D2 body, residues 180-300; and TssF-D1, residues 495-585) were modeled
934 de novo using ARIA with predicted contacts as distance restraints ³⁵. Inter-residue contacts for the
935 TssG-D1, TssG-D2 and TssF-D1 domains were predicted from co-evolution analysis using RaptorX ³¹
936 and the top scoring contacts were converted to distance restraints. Secondary structure predictions
937 from DeepCNF ^{25,36} were converted to canonical dihedral angle restraints for residues predicted to be
938 in α -helical and β -strand conformation. Additionally, hydrogen bond restraints were generated
939 between residues i and $i+4$ in regions predicted as α -helical (same face of the helix). Atomic models
940 were calculated by successive rounds of restrained molecular dynamics simulated annealing with CNS
941 ³⁷ using the iterative ARIA approach ^{35,38}. At each iteration, 100 conformations were produced using
942 inter-residue distance, dihedral angle and hydrogen bond restraints and clustered from the coordinates
943 of C α atoms. The 15 best conformations of the lowest-energy cluster were then used to refine the list
944 of predicted contacts on the basis of their structural consistency. A conformational database potential
945 term was also used in the energy function during simulated annealing ³⁹.

946 *Step 4. Refinement.* All the models of different domains independently generated in step 2 and 3 were
947 merged together in a single chain. The coordinates of the obtained single-chain model were modified
948 manually using Coot ²⁶ and refined with repeated rounds of Coot, Rosetta refine ⁴⁰ and the Phenix real-
949 space refine function ²⁸. Steps 2-4 were repeated until a model maximally consistent with the EM map
950 (Supplementary Fig 12e) and the predicted contact-maps was obtained.

951 For TssK and TssFGE the EMRinger ⁴¹ scores were 1.74 and 0.23 and the Molprobit ⁴² scores were
952 1.9 and 2.36 respectively. Final accuracies of the TssF and TssG contact maps generated from the
953 structures were 0.85 and 0.87, respectively (Supplementary Table 2). The models built in TssK and
954 TssFGE were then fit as rigid bodies in the TssKFGE structure with EMRinger and Molprobit scores
955 of 1.62 and 1.94 respectively (Supplementary Table 2).

956 FSC curves were calculated between the model and the map using Phenix after real space refinement.
957 To assess the presence of overfitting, as described before ⁴³, the FSC computed between the model and
958 the autosharpened map (FSC-sum) was compared to the FSC calculated between the "shaken" model
959 (applying a random perturbation of 0.5Å to the atomic coordinates, with the module pdbtools of
960 Phenix, Adams et al., 2010) refined against the first half map (FSC-work) and the resulting model
961 refined with the second half map (FSC-free, Supplementary Figure 11c,f,i). The overlapping between
962 the FSC-free and FSC-work curves demonstrates the absence of overfitting. Interaction surfaces were
963 analysed using the PISA software ⁴⁵. For illustration purposes, TssFGE secondary structures were
964 predicted using Cablam ⁴⁶.

965

966 **Data and software availability**

967 The cryo-EM structure of the full complex TssKFG , TssK and TssFGE have been deposited in the
968 EMDDB under ID codes EMD-0008, 0010, 0009. The TssKFG, TssK and TssFGE model have been
969 deposited in the PDB under ID codes PDB 6GIY, 6GJ3, 6GJ1. Raw cryo-EM data are available on
970 request.

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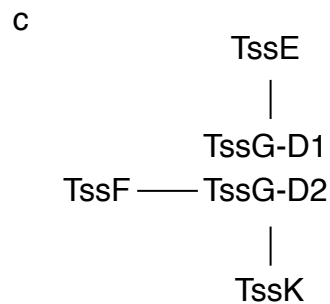
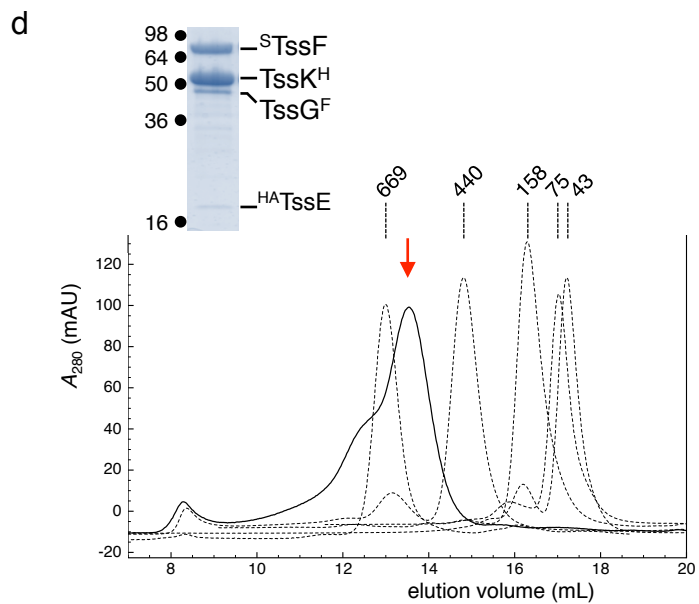
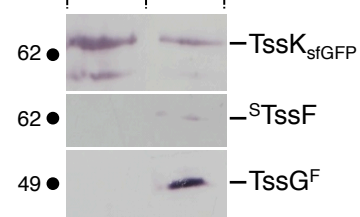
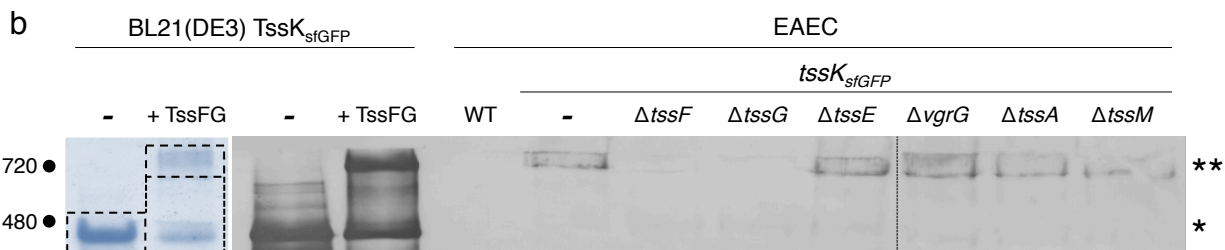
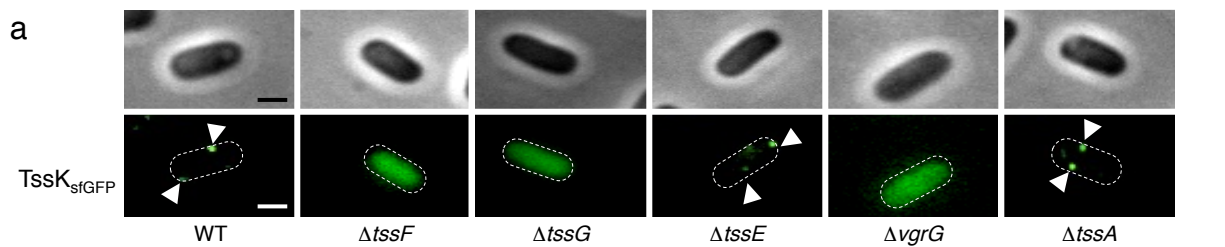


Figure 1

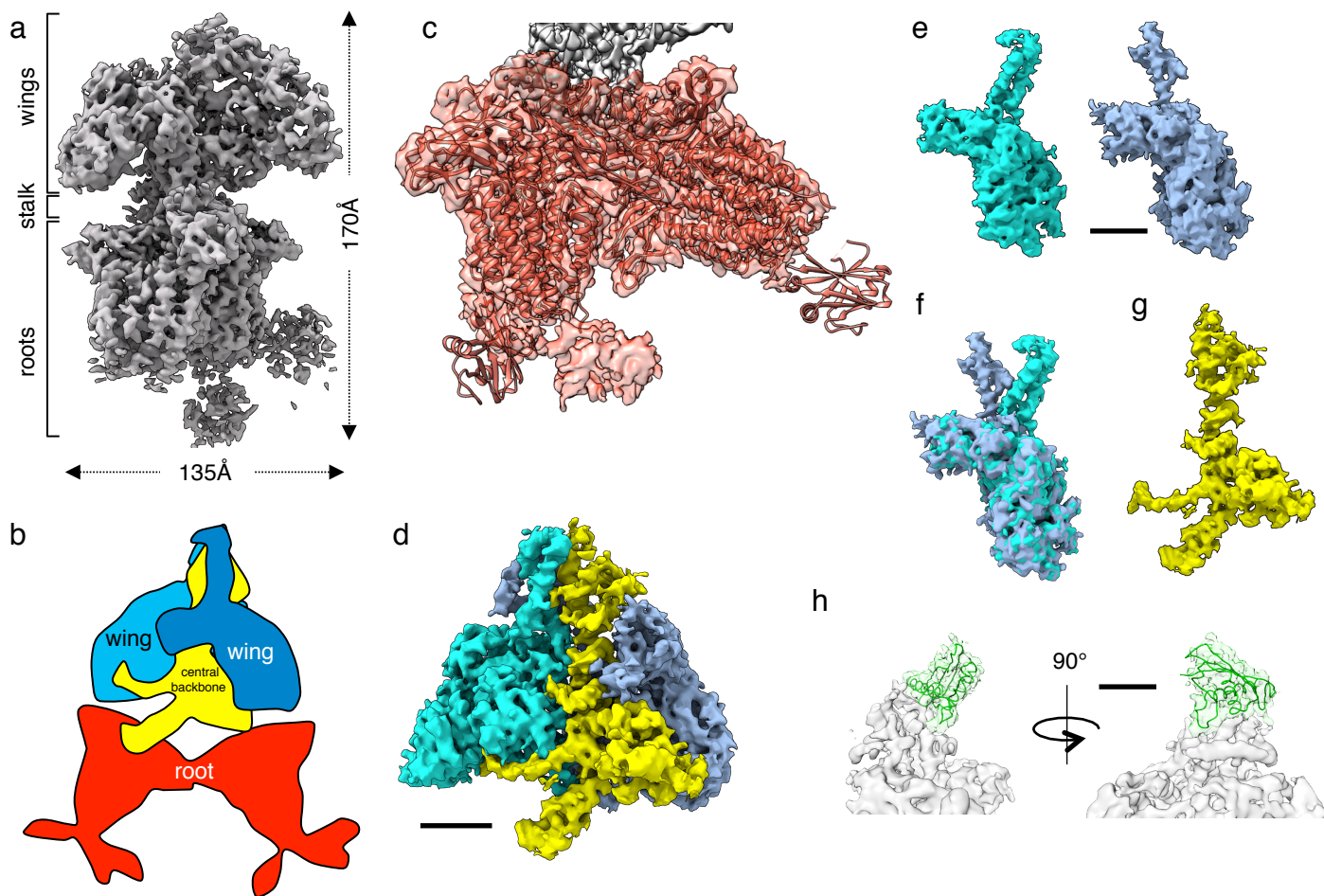


Figure 2

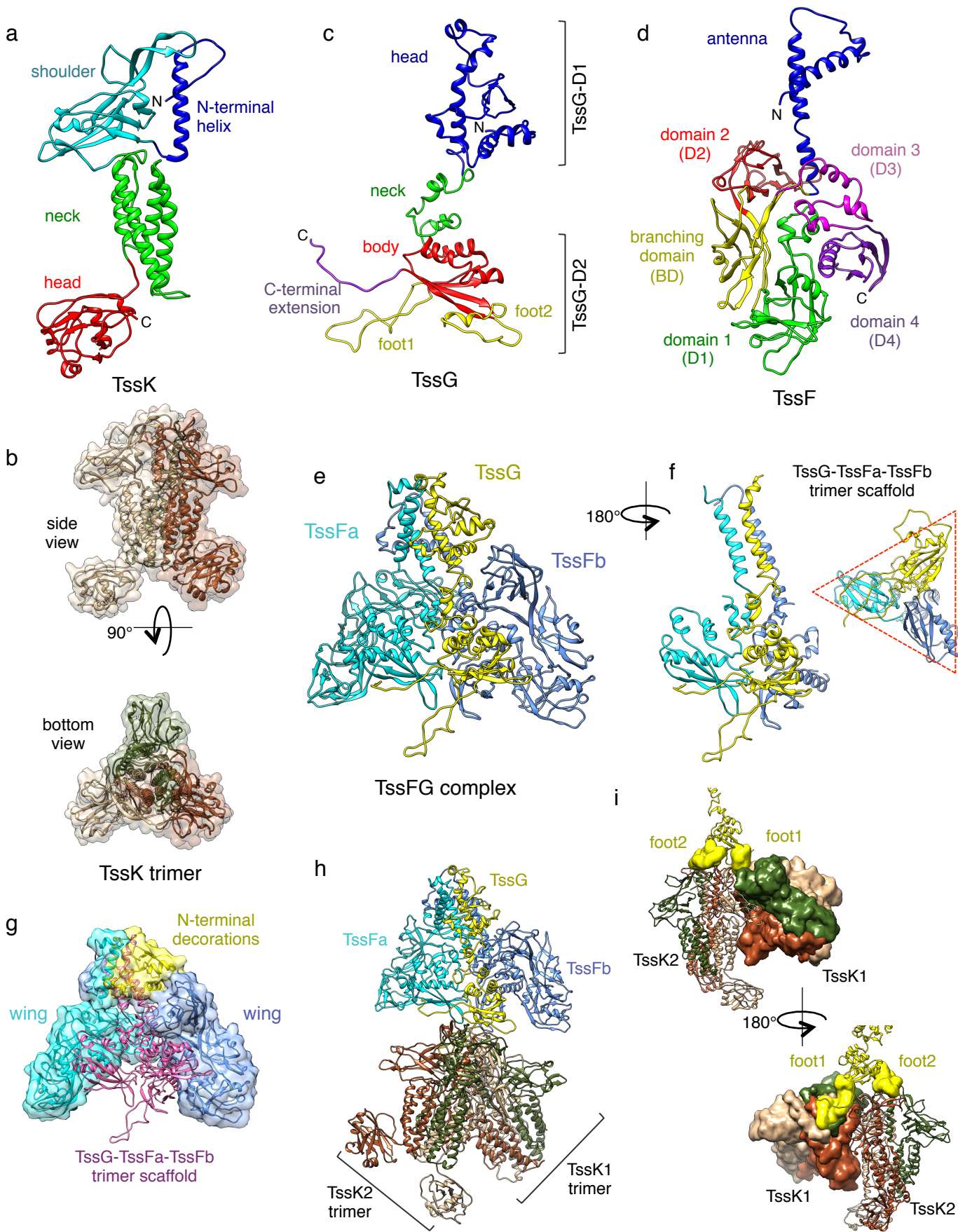


Figure 3

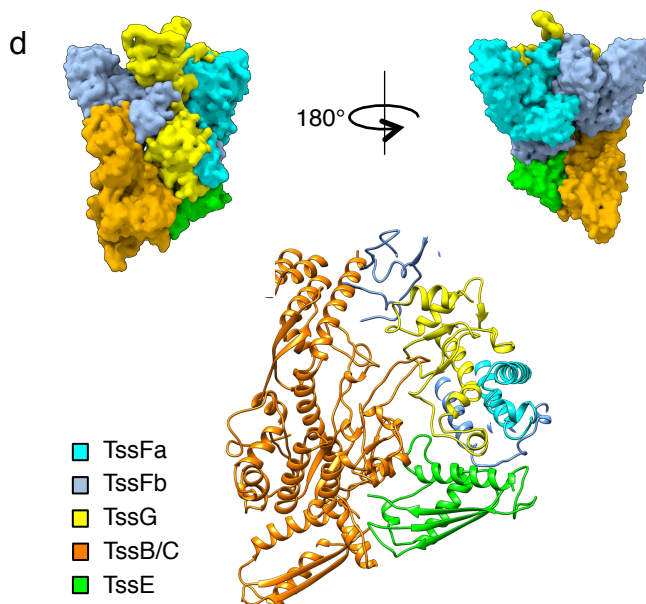
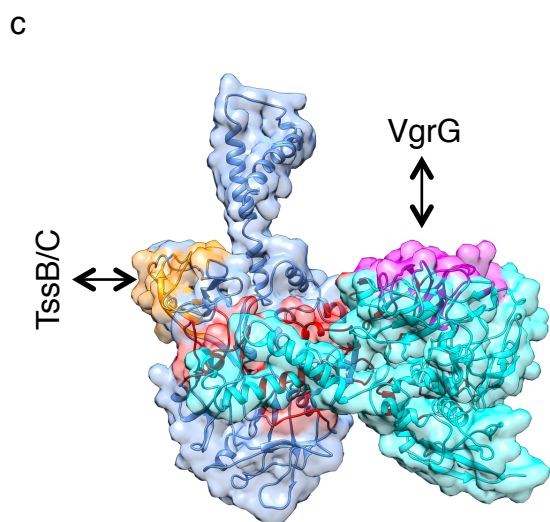
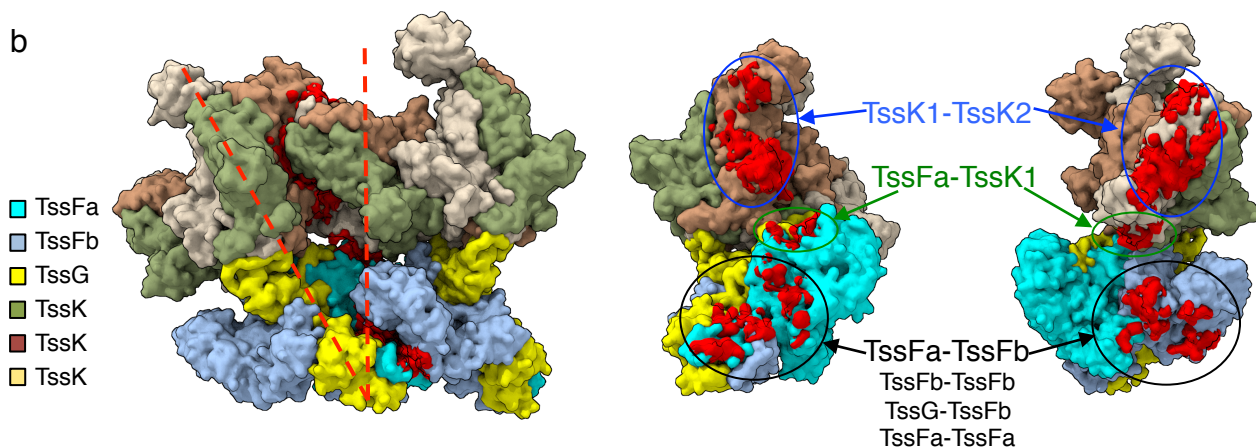
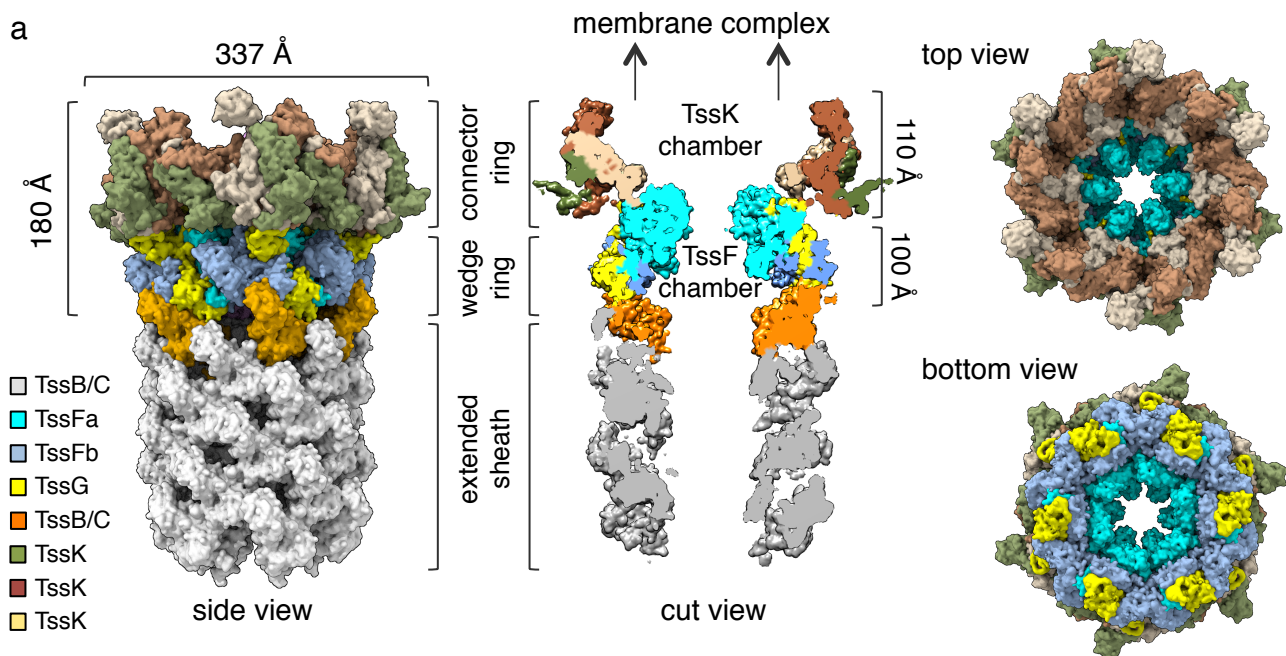
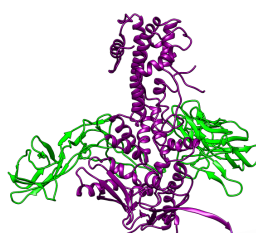


Figure 4

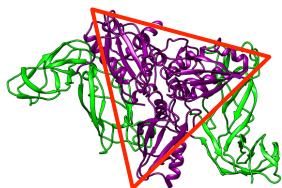
T6SS

bacteriophage T4

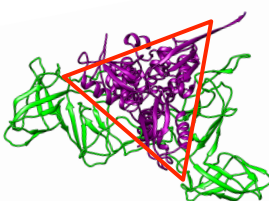
a



b

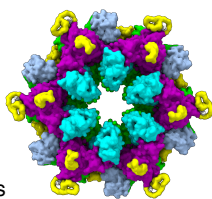


trifurcation
unit

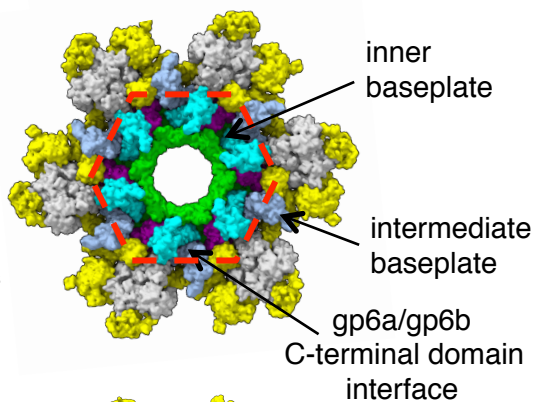


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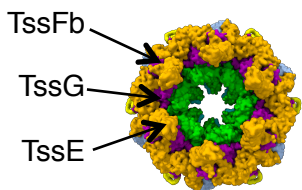
- TssFa
- TssFb
- TssG
- trimer scaffold
- TssF wing domains (D2/BD)



- gp8
- gp6a
- gp6b
- gp7
- trimer scaffold
- gp6 wing domains

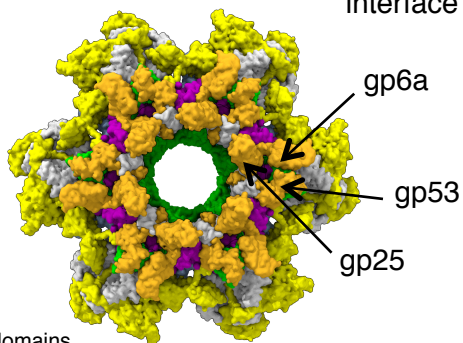


d



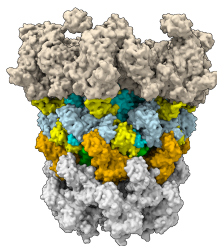
- TssFb
- TssG
- trimer scaffold
- TssF wing domains
- sheath interacting domains

- gp8/gp53
- gp7
- trimer scaffold
- gp6 wing domains
- sheath interacting domains



e

connector
ring



- TssB/C
- TssFa
- TssFb
- TssG
- TssB/C
- TssK

- gp8/gp53/gp18
- gp6a
- gp6b
- gp7
- gp18
- gp9/gp10/gp11/gp12

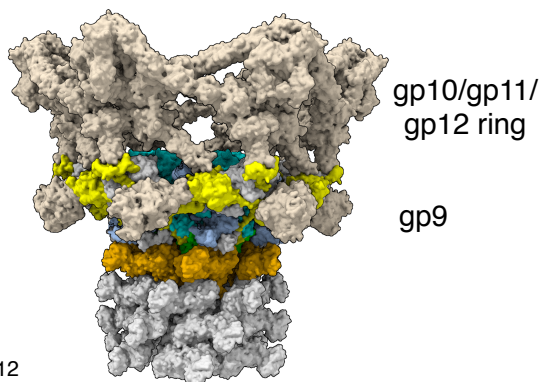


Figure 5

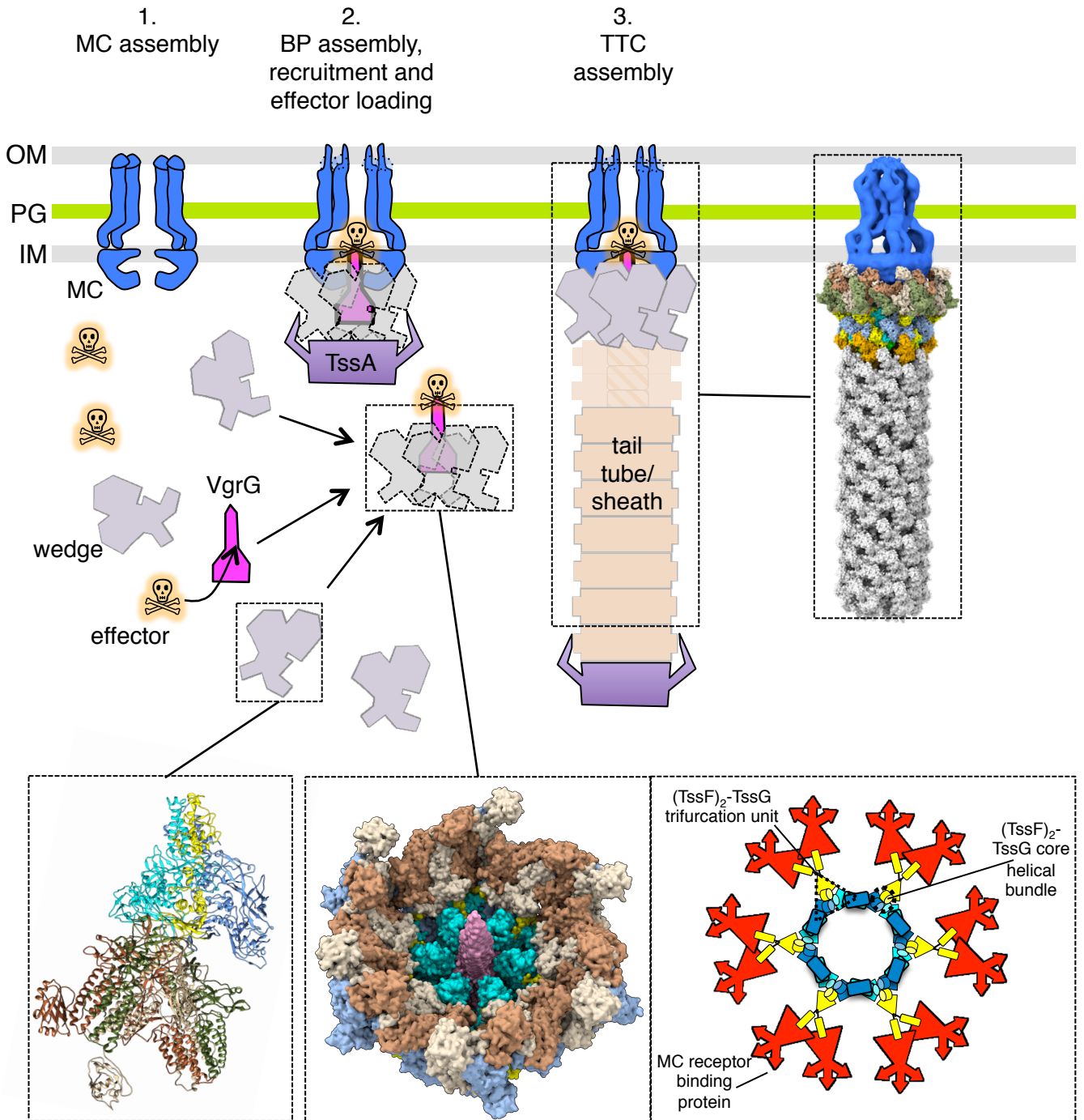


Figure 6

Supplementary Results

Native mass spectrometry.

Native mass spectrometry (Native MS) was used to measure the mass of the intact protein complex from which the stoichiometry can be deduced¹. The molecular mass of each individual subunit was firstly checked in denaturing conditions. A molecular mass of $499,490 \pm 200$ Da was obtained for the complex indicating that the TssKFGE complex comprises six TssK, two TssF, one TssG and one TssE subunits (TssK₆F₂G₁E₁; theoretical mass: 498,905 Da) (**Supplementary Fig. 3b**). The difference from the measured and theoretical masses arises from the presence of numerous salt adducts, which is a common phenomenon in native MS. A similar stoichiometry was obtained for the purified TssKFG complex (TssK₆F₂G₁; measured mass: $481,916 \text{ Da} \pm 200 \text{ Da}$, theoretical mass: 481,520 Da; **Supplementary Fig. 3c**). For TssF, TssG and TssE, this stoichiometry is in agreement with previous studies, indicating the conserved nature of the T6SS wedge among various species. Interestingly, native MS analyses confirmed the peripheral and weaker association of TssE in the TssKFGE complex, as TssE dissociates first when the TssKFGE complex is submitted to collisional activation (**Supplementary Fig. 3d**). Only 3 TssK monomers per wedge complex were found in *Serratia marcescens* and uropathogenic *E. coli*²⁻⁴. These discrepancies could be explained by the different approaches used to purify or assess the stoichiometry of the complex, or by differences in T6SS baseplate composition in these various bacterial species.

Segmentation of the CryoEM map

Our native MS and biochemical analyses of the purified TssKFGE complex unambiguously showed that TssE is present with a stoichiometry of one TssE per complex. At lower density thresholds, the cryo-EM map reveals a density that could be attributed to TssE at the tip of the TssFG. In agreement with this hypothesis, a model of the EAEC TssE generated based on the gp25 crystal structure (PDB: 5IW9;²) fits into the identified density (**Fig. 2h**).

Dominant-negative approach by “small domain interference” (SDI)

First, to validate this approach, we performed SDI with TssK sub-domains. It was previously shown that the TssK N-terminal shoulder domain is anchored into the baseplate whereas the TssK C-terminal head domain binds the membrane complex⁵. We reasoned that overproduction of TssK shoulder (TssK_S) or TssK shoulder and neck (TssK_{SN}) sub-domains should interfere with T6SS wedges assembly, and by lacking the head domain will prevent proper association with the membrane complex. *In vivo*, overproduction of TssK_{SN} and, to a lower extent, TssK_S in wild-type cells impacts the assembly of T6SS wedges, blocks T6SS sheath dynamic and prevents T6SS activity (**Supplementary Fig. 5a-c**). The difference in the negative effect observed between TssK_{SN} and TssK_S could be explained by the stabilization of the TssK trimer by the helix packing of the neck domains⁵ that results in a better incorporation of TssK_{SN} compared to TssK_S into the TssKFGE complex *in vitro* (**Supplementary Fig. 5d**). We then hypothesized that overproduction of the TssG domain which mediates the recruitment of TssK, should have a dramatic negative effect on T6SS function. Our competition experiments showed that only the overproduction of TssG-D2 has a negative effect on the T6SS-dependent killing of *E. coli* target cells (**Supplementary Fig. 5e**). This result confirms that TssG-D2 has a central role for T6SS wedge assembly. To provide further evidence for the position of TssG-D2 at the interface between TssF and the two TssK trimers, we used the EVcomplex program (Hopf et al., 2014) to predict inter-molecular interactions between TssG and TssK using evolutionary covariance analysis (see Methods section). First, the algorithm confirmed our previous findings, showing that the TssG-D2 domain is the major interface with the TssK shoulder domain. Second, the algorithm predicted a number of potential TssK_S-TssG-D2 interfacial residue pairs with high scores (**Supplementary Fig. 6a**). The corresponding TssG-D2 residues, Pro-240 and Leu-255 were substituted, and these TssG-D2 variants (P240A and L255A and P240A-L255A) were assayed by SDI in interbacterial competition experiments. Although these TssG-D2 variants were produced at levels comparable to the wild-type TssG-D2 (see insets in **Supplementary Fig. 6b**), the TssG-D2 P240A and L255A mutants were drastically affected in their ability to inhibit T6SS-function. Combining the P240A and L255A mutations decreases even further the T6SS-inhibitory effect of TssG-D2 overproduction (**Supplementary Fig. 6b**).

The TssK-TssFG interface

To rationalize the results of the Alanine mutation analysis discussed above, we mapped the positions of TssG Pro-240 and TssG Leu-255 on the TssKFG structure. Only Pro-240 is proximal to the TssKG interface, being directly in contact to TssK Leu-14. Thus, its mutation is compatible with a TssKG interface destabilization. On the other hand, TssG Leu-255 is far from the interface, and its mutation probably destabilized the fold of the C-terminal region. When compared with the structure, the Alanine mutational study above has revealed some key residues important for the stability of the TssK-G interaction stability, although the molecular mechanism remains to be addressed.

Supplementary Discussion

The T6SS baseplate - membrane complex connection

As mentioned in recent publications, there is a symmetry mismatch between the 5-fold symmetric TssJLM membrane complex and the 6-fold symmetric baseplate⁴⁻⁶. In this configuration, the 36 copies of TssK (6 per individual wedge) could contact the 10 copies of TssLM. However, our cryo-EM structure shows that the TssK_H domains within each TssK trimer are in different orientations. We thus suggest that the flexibility of the TssK_H domains is key to adapt to the symmetry mismatch and that only a subset of these TssK_H domains engages with the membrane complex. This symmetry mismatch is likely to be important for T6SS function. It may maintain the system under a metastable conformation, allowing a higher turnover rate of ejection of the Hcp tube. It may also accommodate the large conformational changes expected between the baseplate and the membrane complex during sheath contraction. Finally, it may play a critical role in the controlled dissociation of the baseplate after firing, as suggested for the dissociation of V-ATPases⁷.

Comparison between T6SS and bacteriophage baseplates.

Analogy between the T6SS baseplate and the “simple contractile baseplate” from the Mu phage – The architecture and stability of the TssKFGE wedge complex is reminiscent to the Mu phage baseplate wedge⁸. Although sequence identity between the T6SS and Mu phage protein is very low, their respective overall structural organization suggests that the T6SS and Mu phage wedge complexes are highly similar. The Mu phage wedge is formed by the proteins Mup46, Mup47, and Mup48. Mup46 is a gp25 homolog, like TssE. Mup47 is homologous to the gpJ wedge protein of *E. coli* phage P2, like TssF⁹. Mup48 is homologous to the gpI wedge protein of *E. coli* phage P2, like TssG⁹. Mup47 and Mup48 form a stable complex, a behavior comparable with the T6SS TssF-TssG complex⁹. However, the relative stoichiometry of both wedge complexes differs significantly: 2:2:2 for Mup46/47/48 and 6/2/1/1 for TssK/F/G/E. The whole Mu phage baseplate is formed by the attachment of dimers of the Mup46/47/48 wedge (BW1, BW2 and BW3, according to the standard nomenclature previously proposed⁸) on the Mup43/44 hub complex (BH1 and BH2). However, the predicted T6SS baseplate does not seem to contain such BH1/BH2 hub complex. The T6SS proteins share many structural characteristics with “simple” contractile baseplates, even though TssK has no equivalent in Mu phage proteins. We have previously demonstrated that TssK is homologous to lactococcal siphophage receptor binding proteins (RBP) proteins⁵ and we have shown in this work that TssF and TssG are partly a T4 phage gp6 and gp7 homologs. Therefore, the T6SS wedge complex and baseplate seem to be an evolutionary “patchwork”, rooted in T4 bacteriophage, siphophage and Mu phage.

TssF and TssG are gp6 and gp7 counterparts in the T4 phage baseplate – Previous structural studies on the T4 bacteriophage have reported the moderate to high-resolution structures of the whole baseplate^{2,10-12}. Despite no sequence conservation, it was proposed that TssF and TssG could be the structural counterparts of gp6 and gp7 respectively^{2,9}. Gp6 and gp7 are subunits of the T4 phage inner baseplate in which they interact tightly to form the T4 phage wedge complex. The TssG and gp7 structures are not readily superimposable. However, TssG and the central part of gp7 (residues 640-900) display the same domain organization with an N-terminal antenna followed by a helical neck domain and an α/β body (**Supplementary Fig. 9a**). The rest of the gp7 structure is specific to the T4 baseplate. By contrast, based on secondary structure predictions⁹, TssF shares much higher structural homology with the N-terminal region of gp6 (**Supplementary Fig. 9b**). The domain from residue 1 to 410 of gp6 is composed of an N-terminal antenna followed by two consecutive β -sandwich domains (called the wing domains) and an α/β domain (called the trifurcation domain). These domains resemble the TssF antenna, D2, BD and D4

domains, respectively (**Supplementary Fig. 9b**). The C-terminal region of gp6 structure is not present in TssF and is not found in any protein of the T6SS baseplate. Strikingly, not only TssF and TssG adopt a similar structure to portions of gp6 and gp7, but the structural organization of the T4 (gp6)₂-gp7 heterotrimeric unit is conserved in the T6SS wedge complex (**Fig. 5a-b**). In the T4 baseplate, the backbone of the wedge domain is made of a heterotrimeric helical bundle and a trifurcation unit, which are made of the gp6/gp7 antennas and of the gp6/gp7 α/β domains, respectively. This trimeric scaffold, which tightly connects gp7 and the two gp6, is very similar to that of the TssFG complex (**Fig. 5a-b**). Although the organization is identical, it is interesting to note that the T4 phage trifurcation unit comprises three equivalent domains made of two helices and one three-strands β sheet while the TssFG trimeric scaffold contains two helices and one four-strands β sheet (**Fig. 5a-b**).

Inter-wedge contacts are different in the T4 and T6SS baseplates – The multimerization of T6SS wedges into the hexagonal baseplate diverge from the bacteriophage counterpart. In the T6SS baseplate, we showed that the inter-wedge contacts are mostly mediated by TssFa-TssFb interactions that spread in different domains of both protomers (**Fig. 4b**). In the T4 baseplate, the inter-wedge contacts are also mediated by gp6a/gp6b interactions. However, these interactions are restricted to the dimerization of a T4-specific gp6 C-terminal domain (residues 412-659) (**Fig. 5c**). Within each T4 wedge complex, these C-terminal domains are directly connected to the trifurcation unit. Therefore, a continuous ring of alternating trifurcation units and dimers of gp6 C-terminal domains stabilize the T4 inner baseplate^{2,12,13}. The T4 phage baseplate also comprises an additional subunit, absent from the T6SS baseplate, gp8, that interacts with the N- and C- terminal domains of gp7 and thus reinforces the overall structure.

Interaction of the T4 and T6SS baseplates with the spike – Both T4 and T6SS baseplates contain a constriction at the center of the wedge ring that is delineated by gp6b and TssFa respectively. In the T6SS baseplate, TssFa wing domains exclusively cover the cavity that receives the VgrG gp27-like hub domain (**Fig. 5c-d**, **Supplementary Fig. 9c**). In the T4 baseplate, the gp6a wing domain mostly contributes to the central constriction but the gp27 hub position is stabilized in the cavity by a T4-specific component, gp53 (**Fig. 5c**, **Supplementary Fig. 9c**).

Interaction of the T4 and T6SS baseplates with the contractile sheath – The structure of the sheath component of the T4 phage gp18 is known (PDB: 3FOH; ¹⁴). Based on the cryo-EM structure of the native T4 phage tail in the extended conformation (EMD-1126; ¹⁵) determined at 12 Å, it is possible to fit gp18 in the sheath density and to reconstitute the extended sheath structure. The contacts between the sheath and the baseplate subunits can be inferred after docking to the T4 phage baseplate structure². These contacts are in agreement with previously published biochemical and genetics data^{12,16,17}. Overall the structures of the T4 and T6SS sheath building blocks (gp18 and TssBC complex respectively) are different (**Supplementary Fig. 9d-e**). However, they can be split in similar domains: an N-terminal antenna domain, a central globular domain and an α/β domain that protrudes from the central domain (**Supplementary Fig. 9d-e**). Strikingly, TssE and gp25 interact similarly with the sheath α/β domain and share the same fold as these TssBC and gp18 domains (**Supplementary Fig. 9d-e**). The baseplate-sheath connections in phage T4 and T6SS have conserved features but are stabilized by specific contacts. The N-terminal domains of gp18 and of TssBC interact with one of the wing domains of gp6b or TssFb respectively (**Supplementary Fig. 9d-e**). In the T4 phage, the central domain of gp18 interacts with a T4-specific protein, gp53 (**Supplementary Fig. 9e**). In the T6SS, this interaction is replaced by the interaction with the N-terminal head domain of TssG, which is T6SS-specific (**Supplementary Fig. 9d**).

Specialization of the apical part of the T4 and T6SS baseplates – The T4 phage and the T6SS baseplates are specialized molecular machines that interact with different targets. The T4 phage baseplate interacts with the bacterial surface prior to infection, while the T6SS baseplate interacts with the T6SS membrane complex. To achieve this specialization, the T4 and T6SS baseplates contain dedicated adaptor proteins recruited by gp7 and its TssG counterpart (**Fig. 5c**). In T4, the N- and C- terminal domains of gp7 interact with gp9 and gp10, which in turn assemble the short tail fiber proteins gp12 (**Fig. 5c-f**)¹⁷⁻²⁰. In T6SS, the TssG foot domains recruit two TssK trimers, which then interact with the T6SS membrane complex to anchor the T6SS contractile device to the bacterial cell envelope (**Fig. 5c-f**).

Assembly mechanism and stability of the T4 and T6SS baseplates – In the T4 bacteriophage the wedge complex appears to be transient or less stable preventing its purification. By contrast, the T6SS wedge complex is much more stable and prone to purification, as shown by the isolation of TssKFG or TssKFGE complexes in EAEC, *S. marcescens* and uropathogenic *E. coli* (this work; ^{2,3}) This higher stability of a preformed T6SS baseplate intermediate may reflect an adaptation to the secretion process. One hypothesis is that a subset of toxin effectors needs to be loaded onto VgrG ²¹⁻²³, hence delaying the polymerization of the wedge around the VgrG hub. By contrast, the fully assembled T4 phage baseplate is much more stable than the T6SS baseplate, since we did not succeed to purify the T6SS hexagonal baseplate. At the molecular level, TssF-TssF inter-domain interactions appear to be less tightly connected in the fully assembled T6SS baseplate, involving a limited contact surface area, as compared to bacteriophage T4 gp6-gp6 contacts. Consequently, the connection between individual T6SS wedges seems to be weaker, in agreement with the lower stability of the T6SS baseplate compared to that of bacteriophage T4. In addition, this could be explained by the presence of the T4-specific gp53 subunit that has been shown to promote polymerization of the wedges to form a hubless baseplate ¹⁹. This difference may have functional implications. In phage T4, the hubless baseplate needs to remain stably associated during the transport of the phage genome. By contrast, after firing, the T6SS baseplate needs to dissociate, releasing individual wedges that will presumably assemble a new baseplate at the membrane complex. This reversible association would allow a recycling of the individual T6SS wedges.

Supplementary Table 1. Reagents and resources

REAGENT or RESOURCE	SOURCE	IDENTIFIER
Antibodies		
Mouse monoclonal anti-VSVG, clone P5D4	Sigma-Aldrich	Cat# A5977; RRID:AB_439710
Mouse monoclonal anti-FLAG, clone M2	Sigma-Aldrich	Cat# F3165; RRID:AB_259529
Mouse monoclonal anti-HA, clone HA-7	Sigma-Aldrich	Cat# H3663; RRID:AB_262051
Mouse monoclonal anti-StrepII, clone GT661	lba	Cat# 2-1507-001 RRID:AB_513133
Mouse monoclonal anti-polyHistidine, clone HIS-1	Sigma-Aldrich	Cat# H1029; RRID:AB_260015
Alkaline phosphatase-conjugated goat anti-mouse secondary antibody	Millipore	Cat# AP503A; RRID:AB_805353
Bacterial Strains		
DH5 α	New England Biolabs	Cat# C2987I
W3110	Laboratory collection	N/A
BL21 (DE3)	New England Biolabs	Cat# C2527I
Enteroaggregative <i>E. coli</i> strain 17-2	Laboratory collection	N/A
Enteroaggregative <i>E. coli</i> strain 17-2- <i>tssK</i> -sfGFP	²⁵	N/A
Enteroaggregative <i>E. coli</i> strain 17-2- <i>tssK</i> -sfGFP- Δ <i>tssF</i>	This paper	N/A
Enteroaggregative <i>E. coli</i> strain 17-2- <i>tssK</i> -sfGFP- Δ <i>tssG</i>	This paper	N/A
Enteroaggregative <i>E. coli</i> strain 17-2- <i>tssK</i> -sfGFP- Δ <i>tssE</i>	This paper	N/A
Enteroaggregative <i>E. coli</i> strain 17-2- <i>tssK</i> -sfGFP- Δ <i>vgrG</i>	This paper	N/A
Enteroaggregative <i>E. coli</i> strain 17-2- <i>tssK</i> -sfGFP- Δ <i>tssA</i>	This paper	N/A
Enteroaggregative <i>E. coli</i> strain 17-2- <i>tssK</i> -sfGFP- Δ <i>tssM</i>	²⁵	N/A
Enteroaggregative <i>E. coli</i> strain 17-2 TssB-mcherry	²⁶	N/A
Enteroaggregative <i>E. coli</i> strain 17-2 TssB-mcherry- Δ <i>tssM</i>	⁹	N/A
Chemicals, Peptides, and Recombinant Proteins		
HisTrap high performance (5mL)	GE Healthcare	Cat# GE17-5248-01
StrepTrap high performance (5mL)	GE Healthcare	Cat# GE28-9075-47
Superose 6 increase 10/300 GL	GE Healthcare	Cat# GE29-0915-96
Superdex 200 increase 3.2/300	GE Healthcare	Cat# GE28-9909-46
cOmplete™ ULTRA Tablets, EDTA-free, glass vials Protease Inhibitor Cocktail	Roche	Cat# 05892953001
DNase I	Roche	Cat# 10104159001
rLysozyme solution	Merck	Cat# 71110
Ammonium Acetate	Sigma-Aldrich	Cat# A1542
Imidazole	Sigma-Aldrich	Cat# 56750
Hepes	Sigma-Aldrich	Cat# H3375
NativeMark unstained protein standard	Invitrogen	Cat# LC0725
NativePAGE Sample Buffer (4X)	Invitrogen	Cat# BN2003
Mini-PROTEAN TGX Precast gel (4-15%)	Bio-Rad	Cat# 456-1084
4X Laemmli Sample Buffer	Bio-Rad	Cat# 161-0747
2-Mercaptoethanol	Sigma-Aldrich	Cat# M3148
Acrylamide/Bis-Acrylamide 37.5:1, 40%	Biosolve	Cat# 001422335BS
Nitro blue tetrazolium (NBT)	Apollo Scientific	Cat# BIMB1019
5-Bromo-4-chloro-3-indolyl phosphate disodium (BCIP)	Apollo Scientific	Cat# BIMB1018
Recombinant DNA		

pKD4	27	Addgene Plasmid #45605
pKOBEG	28	N/A
pBAD33	29	N/A
pBAD33-TssK _S ^{VSVG}	5	N/A
pBAD33-TssK _{SN} ^{VSVG}	5	N/A
pBAD33-TssK _C ^{VSVG}	5	N/A
pBAD33-TssG-D1 ^{lag}	This paper	N/A
pBAD33-TssG-D2 ^{Flag}	This paper	N/A
pCDF-Duet1	Novagen	Novagen Plasmid #71340-3
pRSF-Duet1	Novagen	Novagen Plasmid #71341-3
pET-Duet1	Novagen	Novagen Plasmid #71146-3
pACYC-Duet1	Novagen	Novagen Plasmid #71147-3
pCDF-TssK ^H -F-G ^{Flag-HA} E	This paper	N/A
pCDF-TssK ^H -F-G ^{Flag}	5	N/A
pCDF-F-G ^{Flag-HA} E	This paper	N/A
pCDF-K ^{His} -F-HA ^E	This paper	N/A
pCDF-F-G ^{Flag}	This paper	N/A
pCDF-K ^H	This paper	N/A
pRSF-K ^H	This paper	N/A
pCDF-K ^{HA}	This paper	N/A
pCDF-F	This paper	N/A
pCDF-G ^{Flag}	This paper	N/A
pCDF-G ^{(Δ1-32)Flag}	This paper	N/A
pRSF-G ^{(1-144)Flag}	This paper	N/A
pRSF-G ^{(168-end)Flag}	This paper	N/A
pCDF-HA ^E	This paper	N/A
pRSF-HA ^E	This paper	N/A
pRSF-H ^E	This paper	N/A
pRSF-H ^E (Δ1-24)	This paper	N/A
pETDuet-VgrG ^{HA}	This paper	N/A
pETDuet-VgrG	This paper	N/A
pACYC-FlagTssA	This paper	N/A

Software and Algorithms

ARIA	30	http://aria.pasteur.fr
Coot	31	https://www2.mrc-lmb.cam.ac.uk/personal/pemsley/coot/
Coot trimmings	32	https://github.com/olibclarke/coot-trimmings
Cryosparc 0.6	33	https://cryosparc.com/
Csparc2star.py	34	https://github.com/asarnow/pyem/blob/master/csparc2star.py
DeepCNF	35	http://raptorx.uchicago.edu/StructurePropertyPred/predict/
EMRinger	36	http://emringer.com/
EVcomplex program	37	https://evcomplex.hms.harvard.edu
gCTF	38	https://www.mrc-lmb.cam.ac.uk/kzhang/Gctf/
Gremlin	39	http://gremlin.bakerlab.org
i-TASSER	24	https://zhanglab.ccmb.med.umich.edu/I-TASSER/
ImageJ	40	https://imagej.net/ImageJ
MapAlign	41	https://github.com/sokrypton/map_align
MicrobeJ	42	http://www.microbej.com/index.html
MolProbity	43	http://molprobity.biochem.duke.edu/

MotionCor2	44	http://msg.ucsf.edu/em/software/motioncor2.html
Phenix	45	https://www.phenix-online.org/
Phenix real-space refine	46	https://www.phenix-online.org/
Phyre2	47	http://www.sbg.bio.ic.ac.uk/phyre2/html/page.cgi?id=index
PISA	48	http://www.ebi.ac.uk/pdbe/pisa/
RaptorX	24	http://raptorx.uchicago.edu/ContactMap/
RELION 2.1	49	http://www2.mrc-lmb.cam.ac.uk/relion/index.php/Download_%26_install
REP	50	https://github.com/rkms86/REP
Rosetta	51	https://www.rosettacommons.org/software
UCSF Chimera	52	https://www.cgl.ucsf.edu/chimera

Protein accession numbers

TssE	WP_061358700.1	type VI secretion system baseplate subunit TssE [Escherichia coli]
TssF	WP_000342463.1	type VI secretion system baseplate subunit TssF [Escherichia coli]
TssG	WP_000553781.1	type VI secretion system baseplate subunit TssG [Escherichia coli]
TssK	WP_000708638.1	type VI secretion system baseplate subunit TssK [Escherichia coli]

Other

Titan Krios	Thermo scientific	https://www.fei.com/krios-g3i/
K2 Summit camera	Gatan, Pleasanton, USA	http://www.gatan.com
Vitrobot	FEI - Thermo Fisher	https://www.fei.com/products/vitrobot/
ÄKTAmicro	GE Healthcare Life Sciences	https://www.gelifesciences.com/en/at/shop/aktamicro-p-02952
Synapt G2Si HDMS	Waters	www.waters.com
Triversa Nanomate	Advion	https://advion.com/products/triversa-nanomate/

Deposited Data

EAEC TssKFG complex	This paper, deposited at EMdatabank	EMD-0008
EAEC TssK root-like domains	This paper, deposited at EMdatabank	EMD-0010
EAEC TssFG wings and stalk domain	This paper, deposited at EMdatabank	EMD-0009
EAEC TssKFG model	This paper, deposited at PDB	PDB 6GIY
EAEC TssK model	This paper, deposited at PDB	PDB 6GJ3
EAEC TssFG model	This paper, deposited at PDB	PDB 6GJ1

Supplementary table 2. Cryo-EM data collection, refinement and validation statistics

	TssKFG (EMDB-0008) (PDB 6GIY)	TssK (EMDB-0010) (PDB 6GJ3)	TssFG (EMDB-0009) (PDB 6GJ1)
Data collection and processing			
Magnification	130,000X	130,000X	130,000X
Voltage (kV)	300	300	300
Electron exposure (e-/Å ²)	45	45	45
Defocus range (μm)	0.4 to 3 μm	0.4 to 3 μm	0.4 to 3 μm
Pixel size (Å)	1.1 Å	1.1 Å	1.1 Å
Symmetry imposed	C1	C1	C1
Initial particle images (no.)	167,825	167,825	167,825
Final particle images (no.)	32,504	32,504	32,504
Map resolution (Å)	4.6Å	4.3Å	4.7Å
FSC threshold	0.143	0.143	0.143
Map resolution range (Å)	3.9 and 18 Å	3.8-33 Å	4.3-8Å
Refinement			
Initial model used (PDB code)	6GJ1 and 6GIY	5M30	-
Model resolution (Å)	4.6Å	4.3Å	4.7Å
FSC threshold	0.143	0.143	0.143
Model resolution range (Å)			
Map sharpening <i>B</i> factor (Å ²)	81.97	87.66	188.97
Model composition			
Non-hydrogen atoms	28969	17405	13013
Protein residues	3649	2194	1638
Ligands	N/A	N/A	N/A
<i>B</i> factors (Å ²)			
Protein	35.09-358.02	39.53-247.92	79.33-427.4
Ligand	N/A	N/A	N/A
R.m.s. deviations			
Bond lengths (Å)	0.28	0.39	0.52
Bond angles (°)	0.62	0.63	0.76
Validation			
MolProbity score	1.94	1.91	2.36
Clashscore	5.95	5.11	13
Poor rotamers (%)	0.32	0.37	0.31
Ramachandran plot			
Favored (%)	87.06	86.23	80.28
Allowed (%)	12.66	13.45	19.52
Disallowed (%)	0.28	0.32	0.2

Supplementary Table 3. Agreement of model contacts with predicted contact maps.

#Consistent: number of predicted contacts consistent with the final structure.

#Inconsistent: number of predicted contacts inconsistent with the final structure.

Accuracy: $\#consistent / (\#inconsistent + \#consistent)$

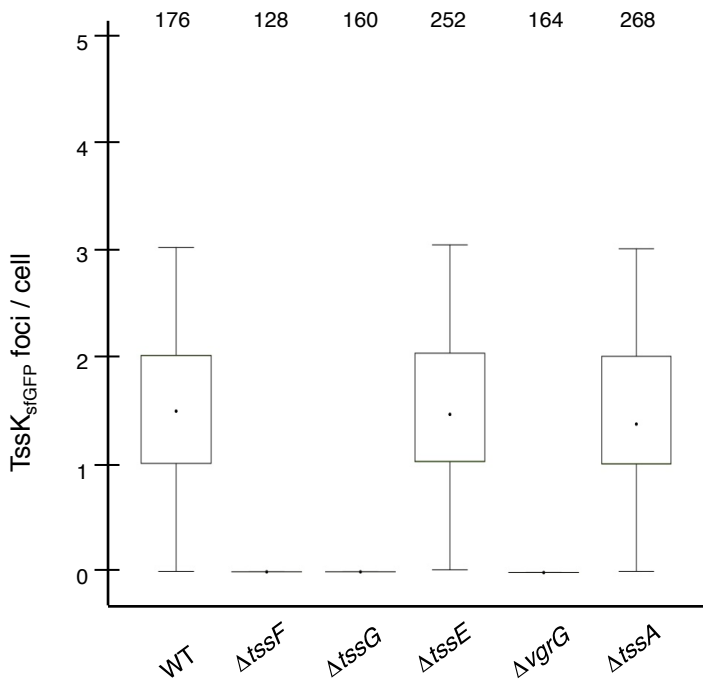
	#Consistent	#Inconsistent	Accuracy
TssK	1696	54	0.97
TssG	1180	180	0.87
TssF	2554	432	0.85

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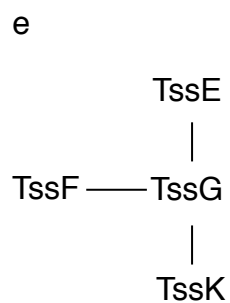
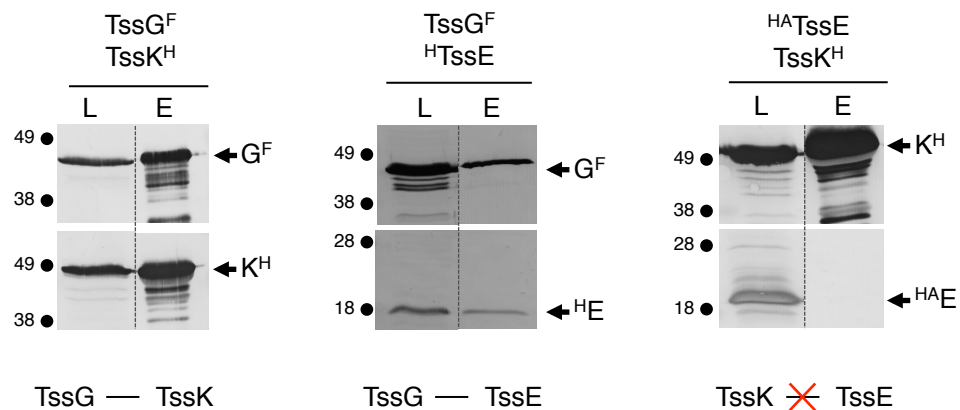
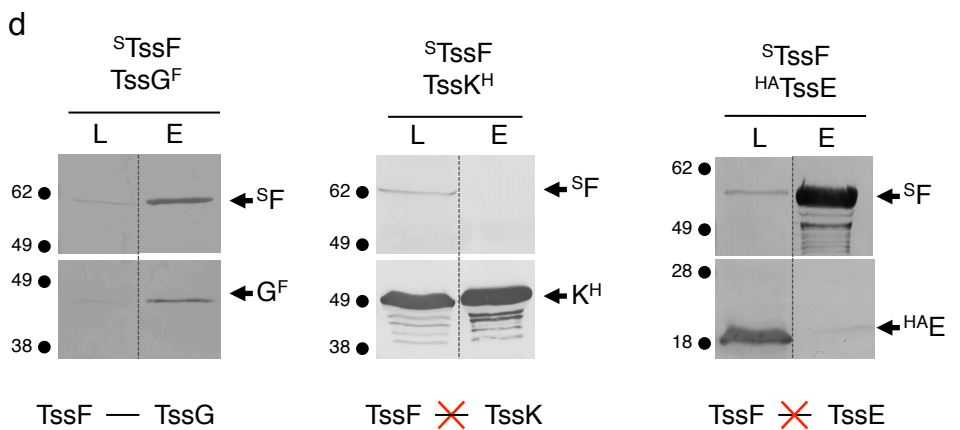
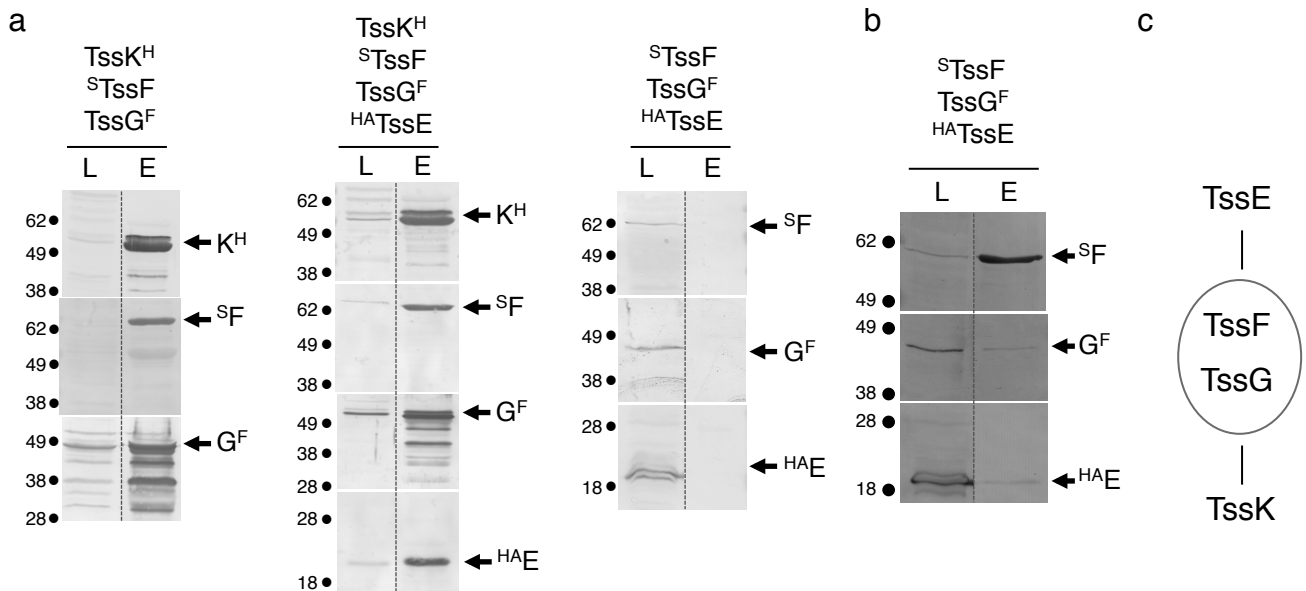
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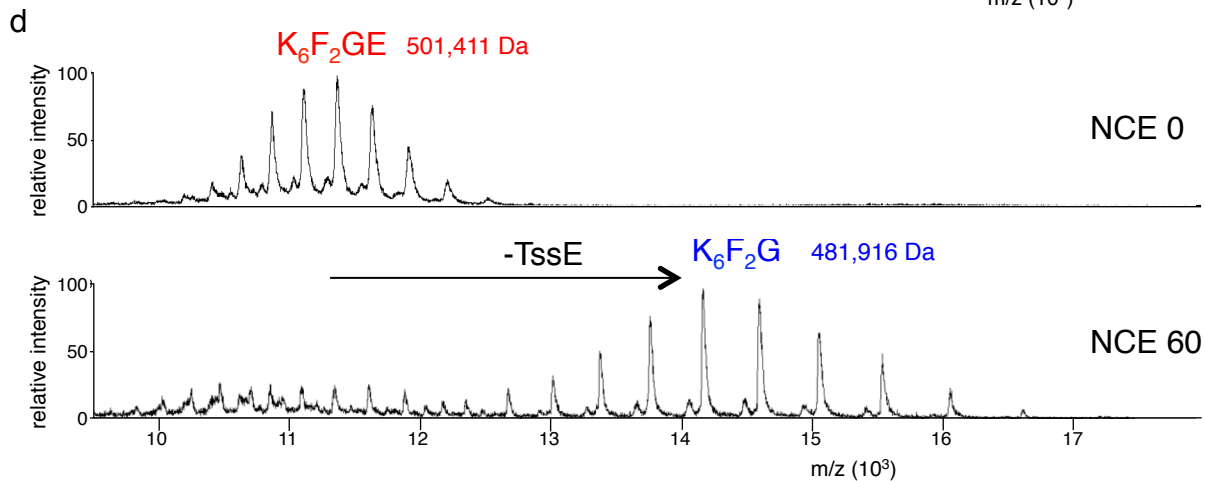
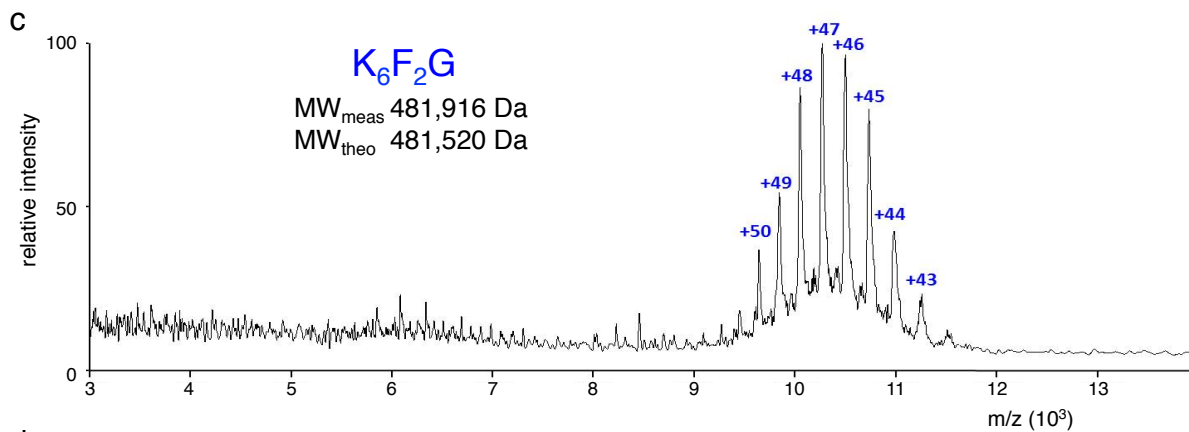
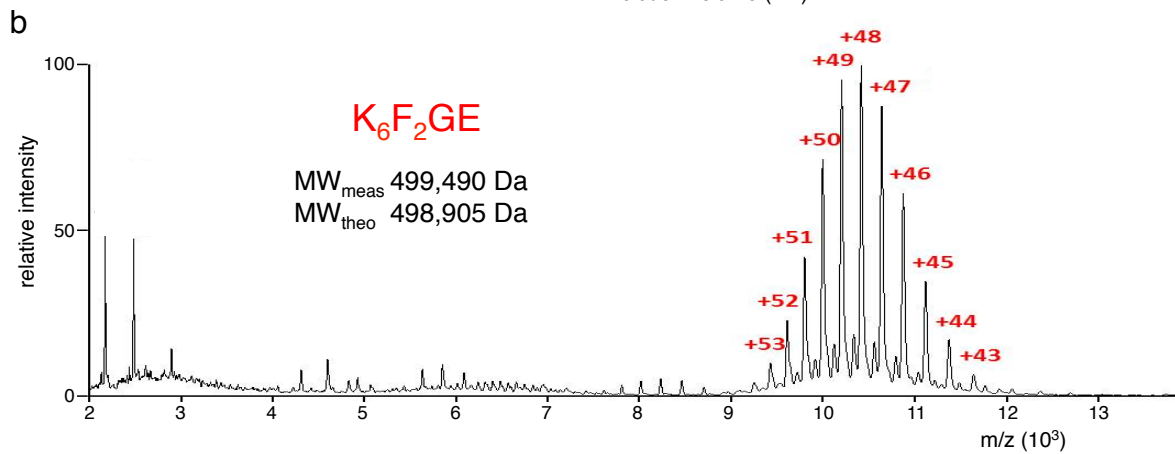
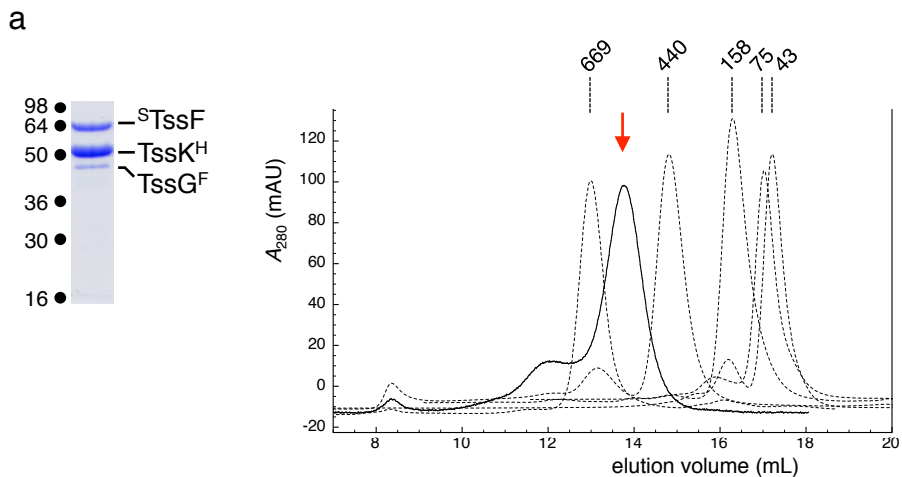
Supplementary Figure 1. Statistical analysis of TssK_{sfGFP} foci formation. Related to Figure 1.

Statistical analysis of TssK_{sfGFP} foci formation in various T6SS mutant backgrounds. Shown are the box-and-whisker plots of the measured number of TssK_{sfGFP} foci per cell for each indicated strain with the lower and upper boundaries of the boxes corresponding to the 25th and 75th percentiles respectively (black dot, the median values for each strain; whiskers, the 10th and 90th percentiles); The number of cells analyzed for each strain is indicated on top.



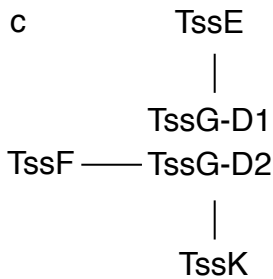
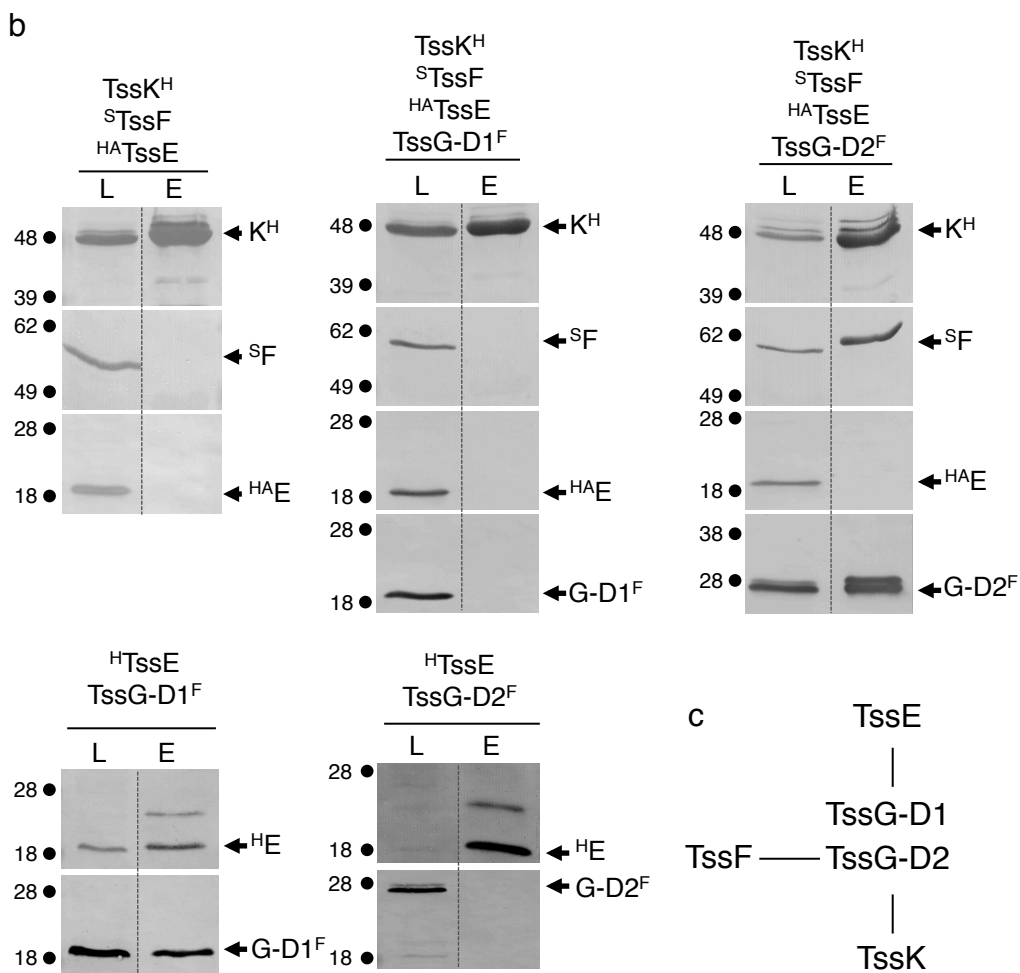
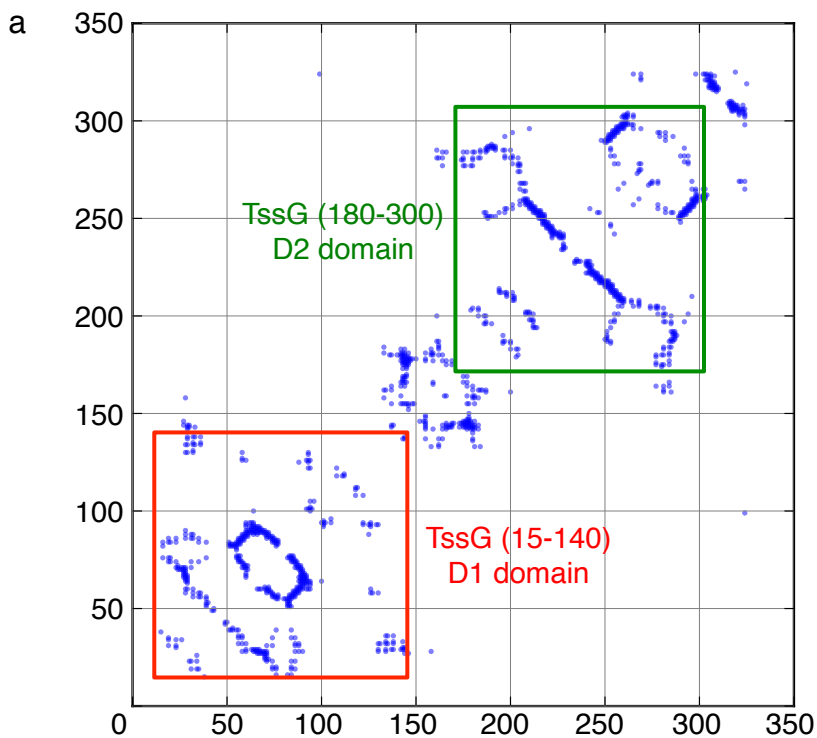
Supplementary Figure 2. Protein-protein interaction network between the TssKFGE complex. Related to Figure 1.

a, b, and d. Soluble extracts of *E. coli* BL21(DE3) cells producing the indicated protein were submitted to an affinity purification step on HisTrap or StrepTrap. The lysate (total soluble material, L), and eluate (E) were subjected to denaturing 12.5%-acrylamide polyacrylamide gel electrophoresis (PAGE) and immunodetected with the appropriate antibody. Immunodetected proteins are indicated in the right. Molecular weight markers (in kDa) are indicated in the left. Tags: H, 6×His; S, Strep-tag; F, FLAG; HA, hemagglutinin. In panel **d**, the result of the pairwise interaction is schematized (red cross indicates that no interaction is observed). Schematic summaries of panels **a-b** and **d** are shown in panels **c** and **e** respectively. Protein-protein interaction experiments have been performed independently twice and a representative result is shown.



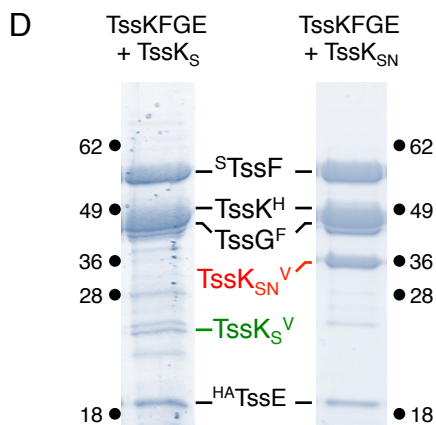
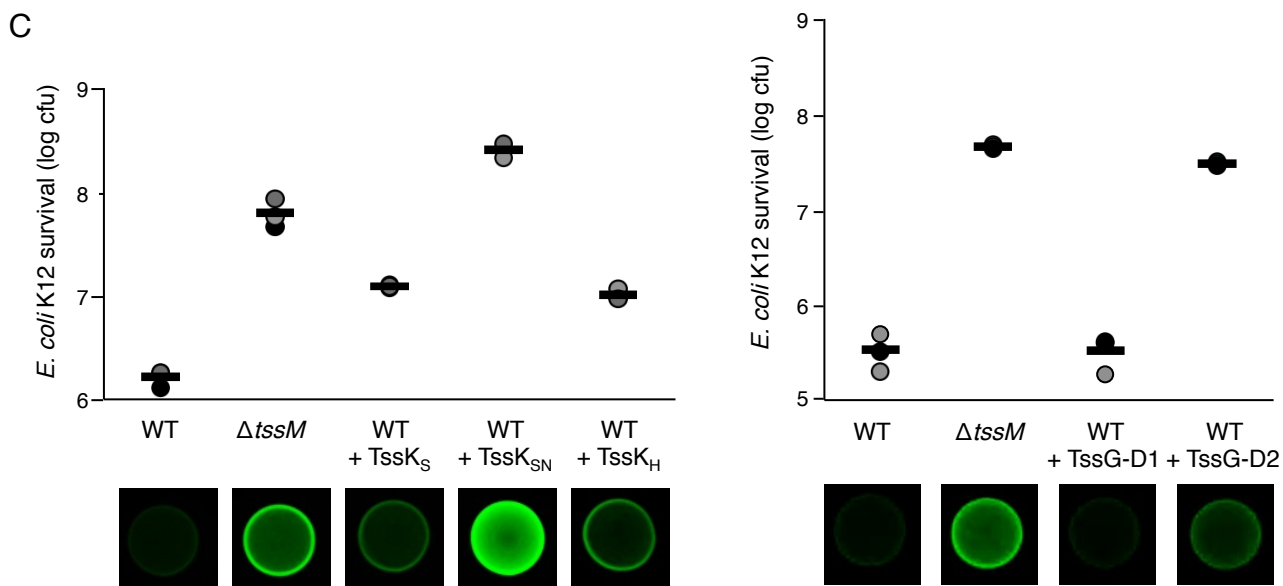
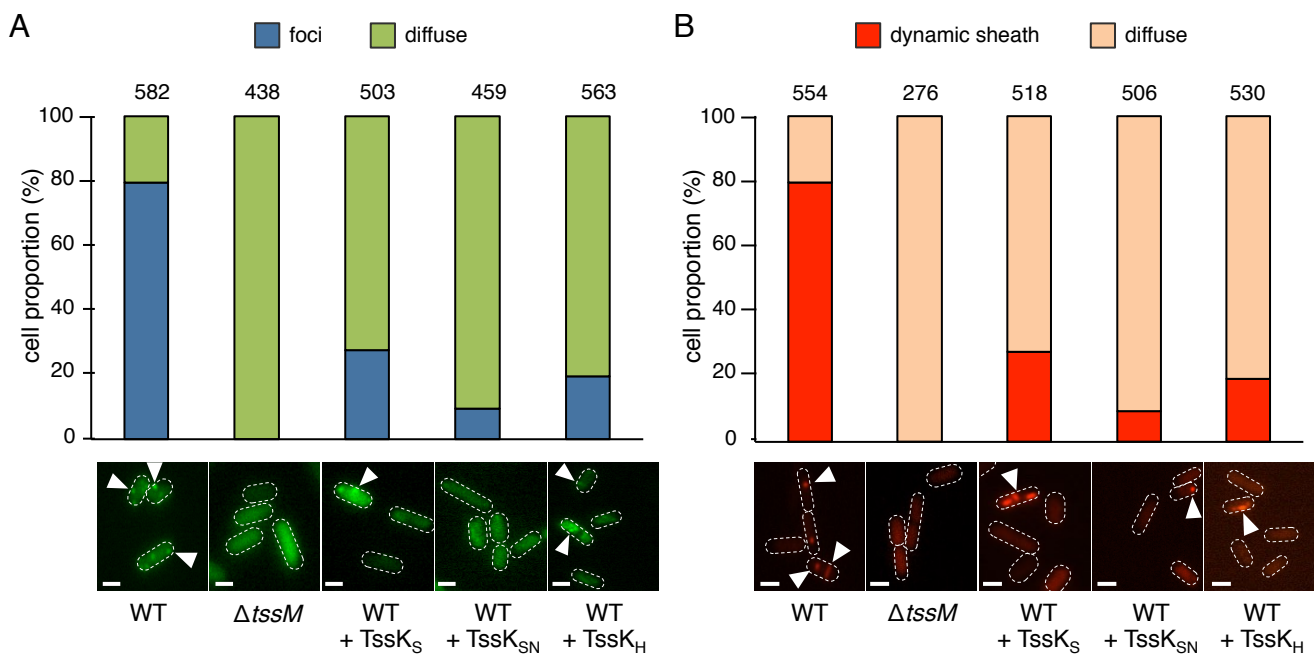
Supplementary Figure 3. Purification, biochemical characterization and stoichiometry analyses of the TssKFG and TssKFGE complexes. Related to Figure 1.

a. Left panel: Purified TssKFG complex subjected to sodium dodecyl sulfate 12.5%-acrylamide PAGE and Coomassie staining. The different proteins are indicated on the right, whereas molecular weight markers are indicated on the left. Right panel. Biochemical characterization of the TssKFG complex. Analytical size-exclusion chromatography analysis of the purified TssKFG complex (continuous line) on a Superose 6 column, calibrated with 43-, 75-, 158-, 440- and 660-kDa molecular mass markers (dotted lines). The molecular mass of each marker (in kDa) is indicated on the top of the corresponding peak. An arrow indicates the position of the peak fraction corresponding to the TssKFG complex. TssKFG complex purification and analytical size-exclusion chromatography analysis experiments were performed at least three times and a representative result is shown. **b-c.** Mass spectra of the TssKFGE (**b**) and TssKFG (**c**) complexes obtained in native conditions. The stoichiometry (indicated in red and blue for the TssKFGE and TssKFG complexes) were defined based on the comparison between theoretical (MW_{theo}) and measured (MW_{meas}) molecular weight markers. **d.** In-source dissociation (cone voltage: 150 V) of the TssKFGE complex obtained by collisional activation in native conditions. Native mass spectrometry and collisional activation experiments were performed 3 times and a representative result is shown.



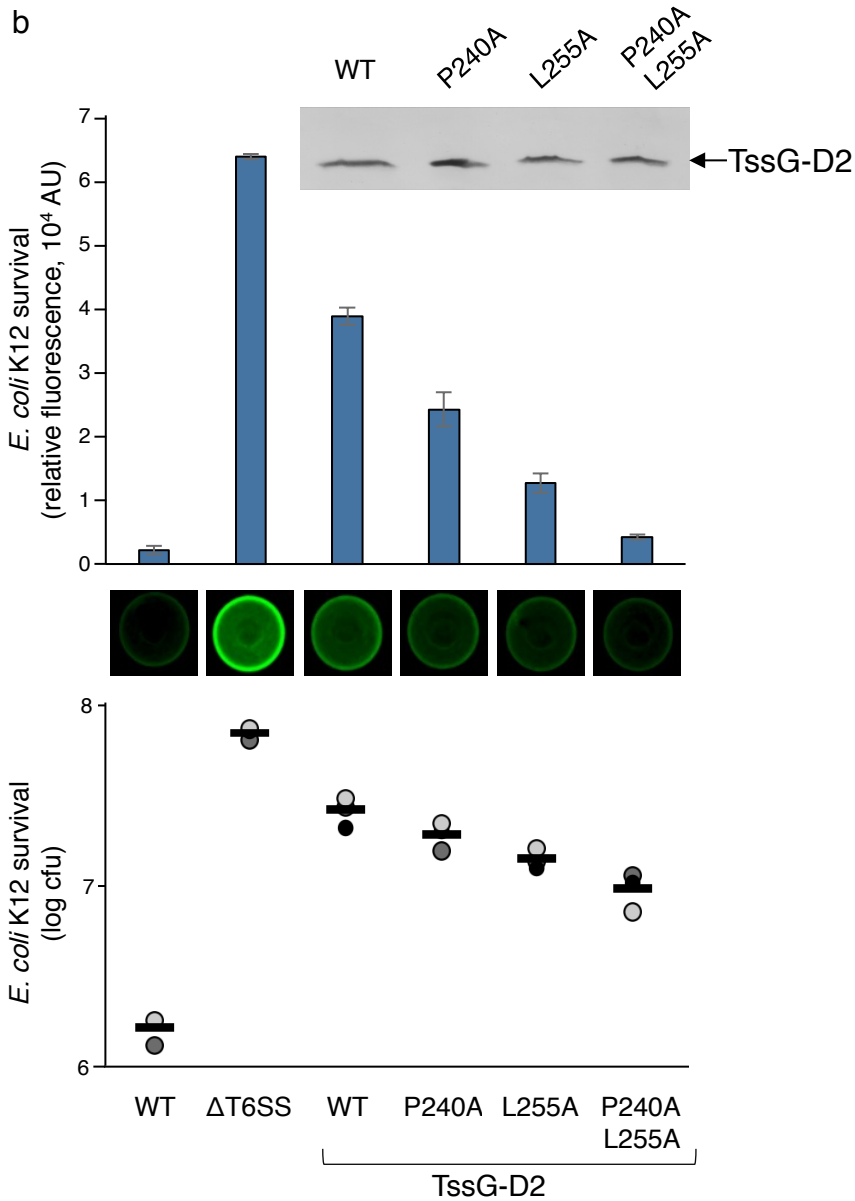
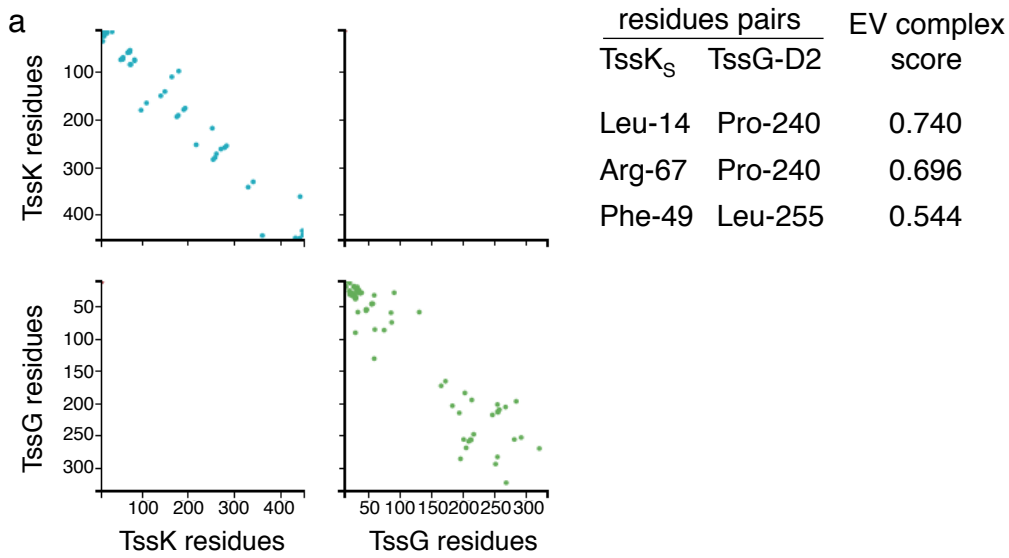
Supplementary Figure 4. TssG domain organization and interactions. Related to Figure 1.

a. TssG residue contacts predicted by RaptorX²⁴ plotted into a contact map. X and Y axis are the residue indexes of TssG. Each blue dot is a predicted contact. The map is organized into two blocks of dense contacts located at the N- (TssG-D1, red, residues 15-140) and C-terminus (TssG-D2, green, residues 180-300). **b.** Soluble extracts of *E. coli* BL21(DE3) cells producing the indicated protein or domains were submitted to an affinity purification step on HisTrap. The lysate (total soluble material, L), and eluate (E) were subjected to denaturing 12.5%-acrylamide polyacrylamide gel electrophoresis (PAGE) and immunodetected with the appropriate antibody. Immunodetected proteins are indicated in the right. Molecular weight markers (in kDa) are indicated in the left. Tags: H, 6×His; S, Strep-tag; F, FLAG; HA, hemagglutinin. Protein-protein interaction experiments have been performed independently twice and a representative result is shown. **c.** Schematic summary of the interactions of TssG-D1 and -D2 with the TssKFE proteins.



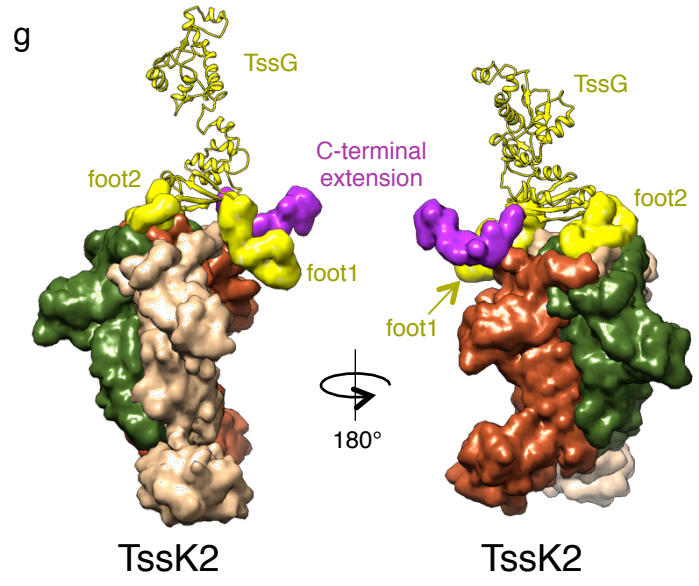
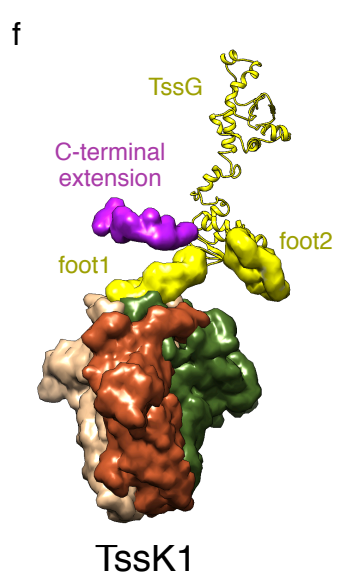
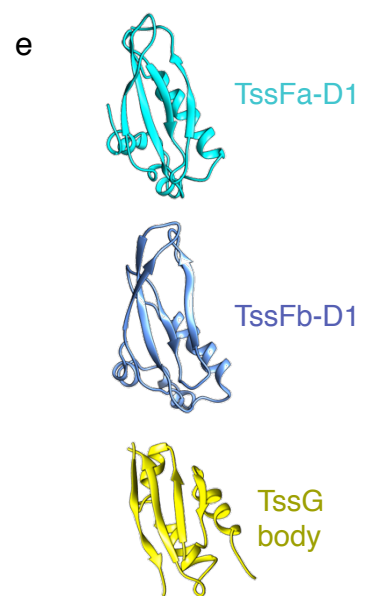
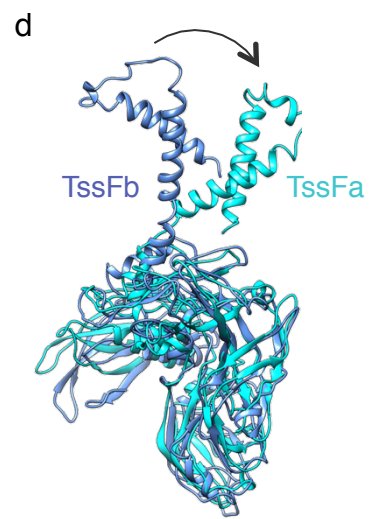
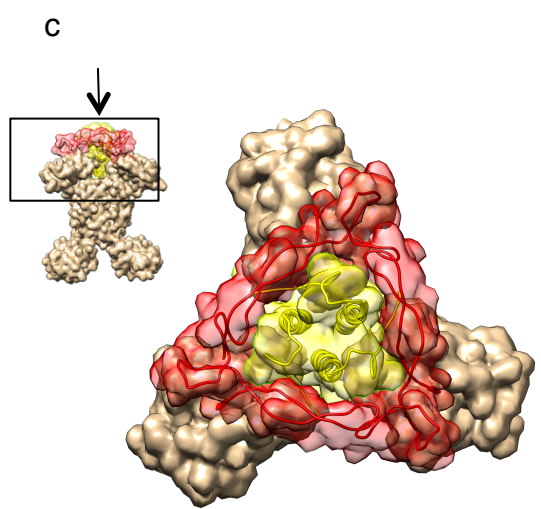
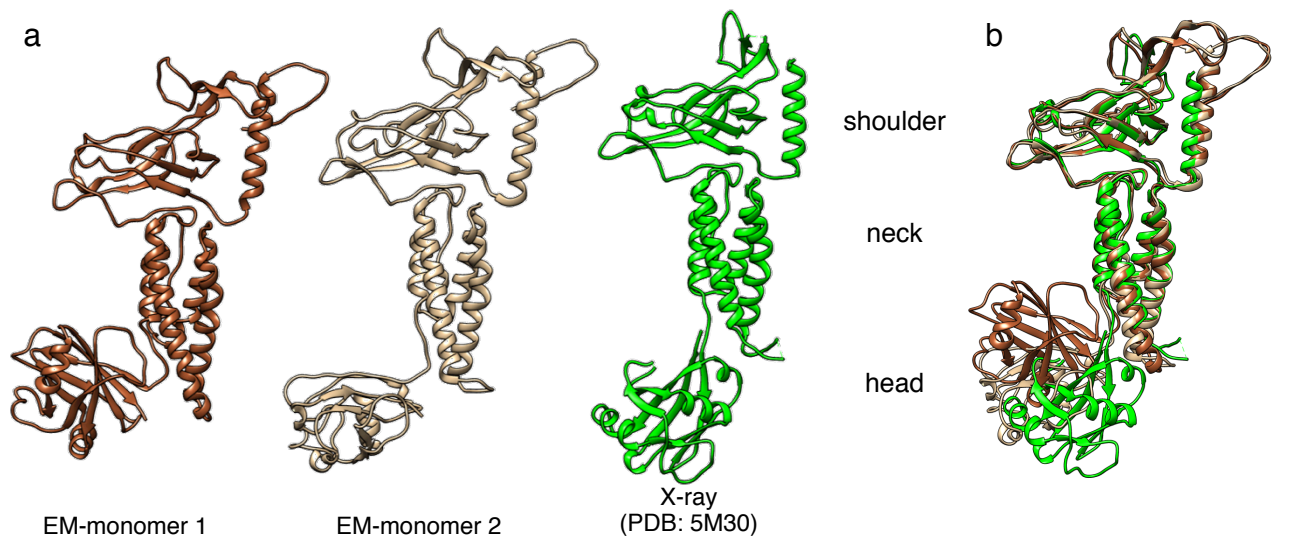
Supplementary Figure 5. Small Domain Interference analyses. Related to Figure 2.

a-c. Overproduction of TssK domains inhibits T6SS activity. **a.** Fluorescence microscopy recordings and statistical analyses of TssK_{sfGFP} foci formation upon overproduction of TssK domains (TssK_S, shoulder; TssK_{SN}, shoulder and neck; TssK_H, head). A representative image is shown on the bottom (white arrowheads indicate TssK_{sfGFP} foci). The graph representing the percentage of cells with diffuse (green), and foci (blue) patterns is indicated on top (number of cells analyzed indicated on top of each bar). **b.** Fluorescence microscopy recordings and statistical analyses of TssB_{mCherry} dynamics upon overproduction of TssK domains. A representative image is shown at the bottom (white arrowheads indicate dynamic TssB_{mCherry} sheaths). The graph representing the percentage of cells with diffuse (light orange) and dynamic (orange) patterns is indicated on top (number of cells analyzed indicated on top of each bar). Microscopy analyses were performed independently three times, each in technical triplicate, and a representative experiment is shown. Scale bars, 1 μ m. **c.** Antibacterial assay. Gfp⁺ kan^R *E. coli* K-12 recipient cells were mixed with the indicated attacker cells, spotted onto Sci-1-inducing medium (SIM) agar plates supplemented with 0.05% L-arabinose, and incubated for 4 h at 37°C. The image of a representative bacterial spot is shown on the bottom and the number of recovered *E. coli* recipient cells is indicated in the upper graph (in log¹⁰ of colony forming units (cfu)). The assays were performed from at least three independent cultures, with technical triplicates and a representative technical triplicate is shown. The circles indicate values from the technical triplicate, and the average is indicated by the bar. **d.** Purification of the TssKFGE complex upon overproduction of the TssK_S and TssK_{SN} domains. TssKFGE complexes were purified from cells overproducing TssK_S (left panel) or TssK_{SN} (right panel). The different proteins are indicated, as well as molecular weight markers (in kDa). Purification and sodium dodecyl sulphate 12,5%-acrylamide PAGE analysis were performed twice and a representative result is shown. **e.** The TssG-D2 domain interferes with T6SS antibacterial activity. Gfp⁺ kan^R *E. coli* K-12 recipient cells were mixed with the indicated attacker cells overproducing the indicated TssG domain, spotted onto Sci-1-inducing medium (SIM) agar plates supplemented with 0.05% L-arabinose, and incubated for 4 h at 37°C. The image of a representative bacterial spot is shown on bottom and the number of recovered *E. coli* recipient cells is indicated in the upper graph (in log¹⁰ of colony forming units (cfu)). The circles indicate values from three independent assays, and the average is indicated by the bar.



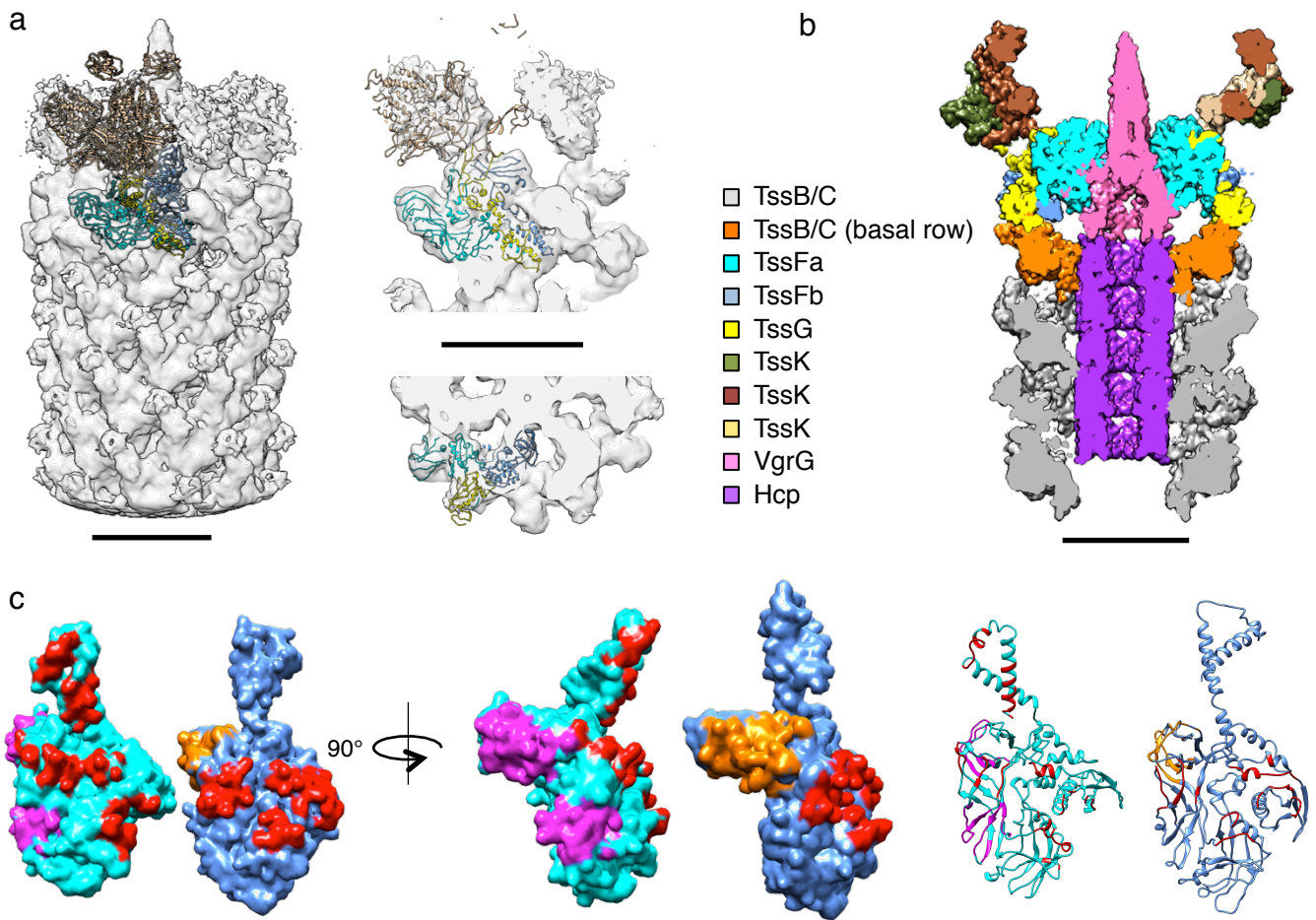
Supplementary Figure 6. TssG-TssK interaction. Related to Figure 2.

a. TssG-TssK residue contacts predicted by EVcomplex plotted into contact maps. X and Y axis are the residue indexes of TssG and TssK (as indicated). Each blue and green dot is a predicted contact in TssK and TssG respectively. The residue pairs with the higher EVcomplex scores are indicated on right. **b.** Gfp⁺ kan^R *E. coli* K-12 recipient cells were mixed with the indicated attacker cells overproducing the indicated TssG-D2 variants, spotted onto Sci-1-inducing medium (SIM) agar plates supplemented with 0.05% L-arabinose, and incubated for 4 h at 37°C. The image of a representative bacterial spot is shown on the middle, the relative fluorescence of the spot (in arbitrary units, AU) is shown on the top graph whereas the number of recovered *E. coli* recipient cells is indicated in the lower graph (in log¹⁰ of colony forming units (cfu)). The error bars represent the standard deviation across three independent assays. The circles indicate values from three independent assays, and the average is indicated by the bar. The levels of production of wild-type (WT) and mutant TssG-D2 variants is shown in the inset (SDS-PAGE and immunoblot analysis).



Supplementary Figure 7. Structures and domain interactions of the TssKFG proteins, Related to Figure 3

a. Comparison between cryo-EM and crystal structures of TssK. Each TssK protomer is represented in the same orientation. For the cryo-EM structure, two protomers with different orientations for the C-terminal domain are presented (in brown and beige). For the crystal structure, the protomer for which the terminal domain could be built is presented (in green). **b.** Superimposition of cryo-EM and crystal structures of TssK. The same protomers as in A. are superimposed. **c.** Triangular hub at the top of the TssK shoulder domains. The three loops located between residues 105 to 145 define a triangle (in red) that encompasses the loop 1-18 and α 1 helix bundle at the centre of the trimer (in yellow). **d.** Superimposition of the TssFa and TssFb protomers. TssFa and TssFb are represented as ribbons in cyan and blue respectively. Both protomers differ only by the position of the N-terminal antenna (indicated by the black arrow). **e.** Comparison between the TssFa and TssFb D1 domains and TssG body structures, shown in the same orientation. **f-g.** Interactions between the TssK1 (**f**) or TssK2 (**g**) trimer and TssG. The TssK protomers (green, beige and brown) and TssG feet and C-terminal extension are represented as surfaces. TssG antenna and body are represented as ribbons. TssG is in yellow with the exception of its C-terminal extension that is coloured in purple.

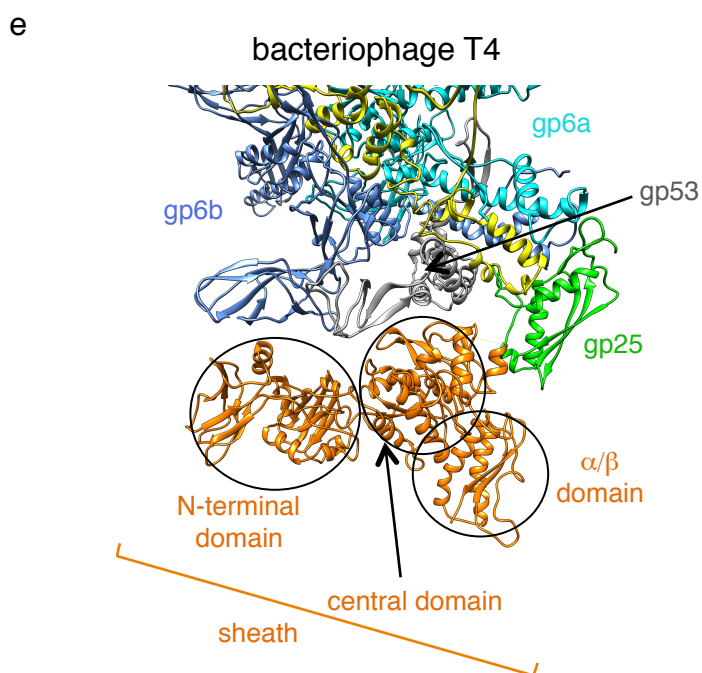
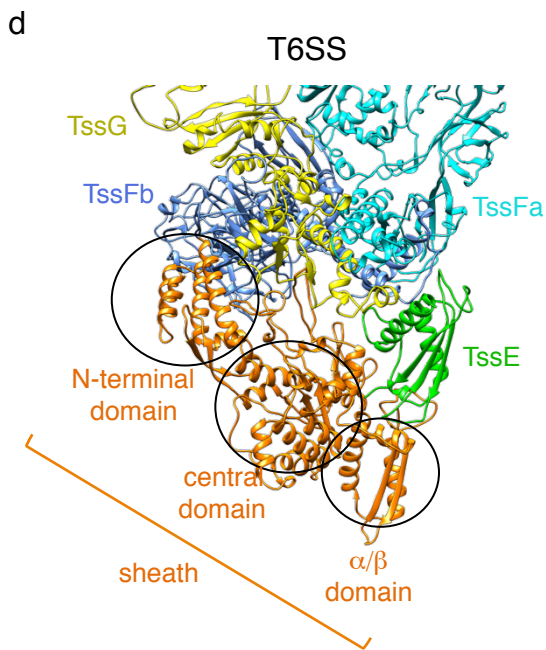
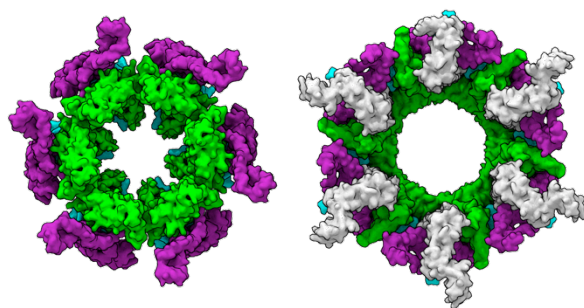
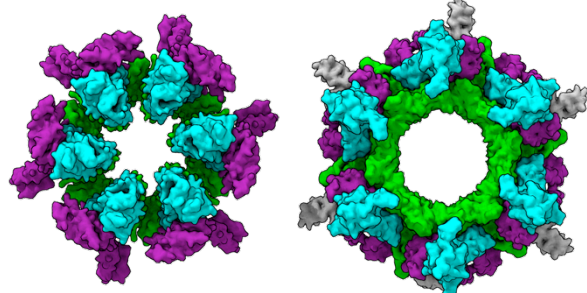
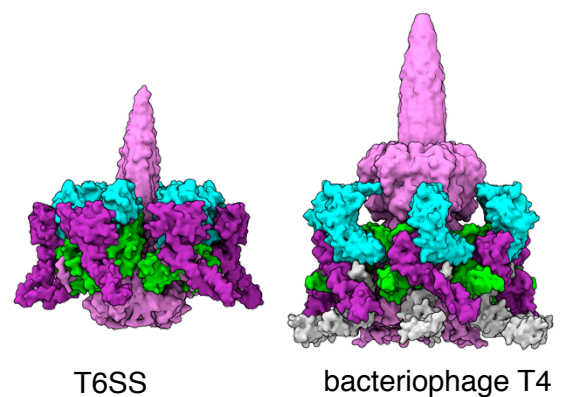
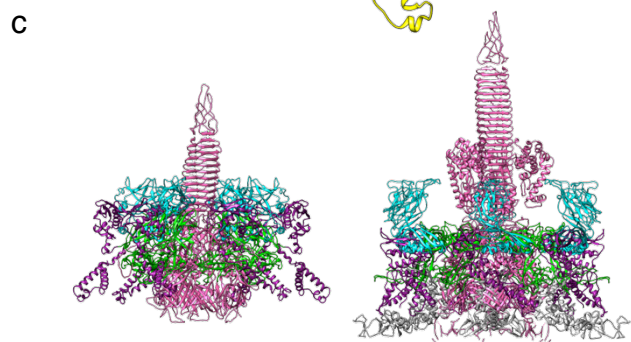
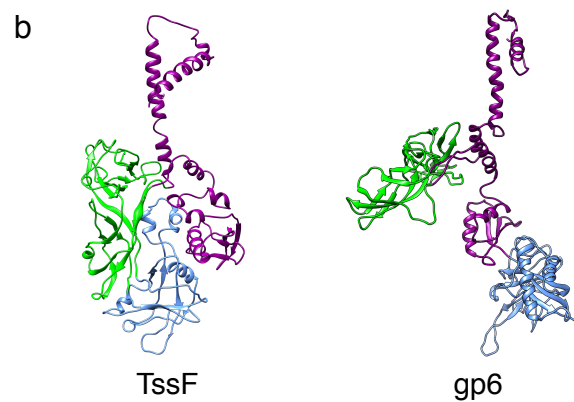
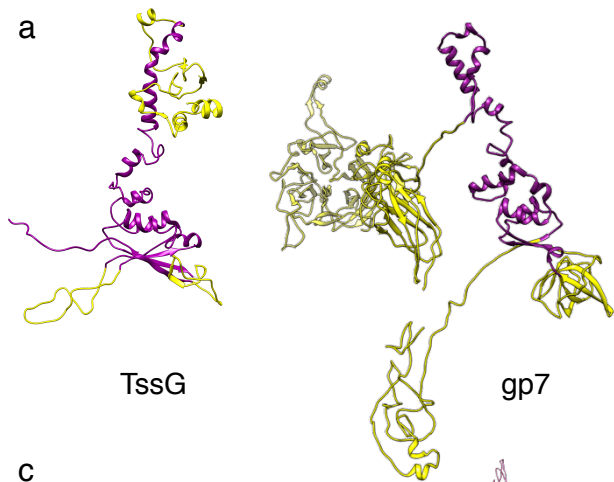


Supplementary Figure 8. T6SS extended sheath bound to the baseplate. Related to Figure 4

a. Fitting of the structure of the EAEK TssKFGE complex into the cryo-EM structure of the *V. cholerae* baseplate associated to a non-contractile sheath (EMD-3879). Left panel: side view highlighting one TssKFGE complex (ribbon diagram) fitted into the baseplate/sheath density (surface representation). Right panels: side (top) and bottom (bottom) slice of the TssKFGE complex fitted into the baseplate/sheath density. The bars correspond to 100 Å

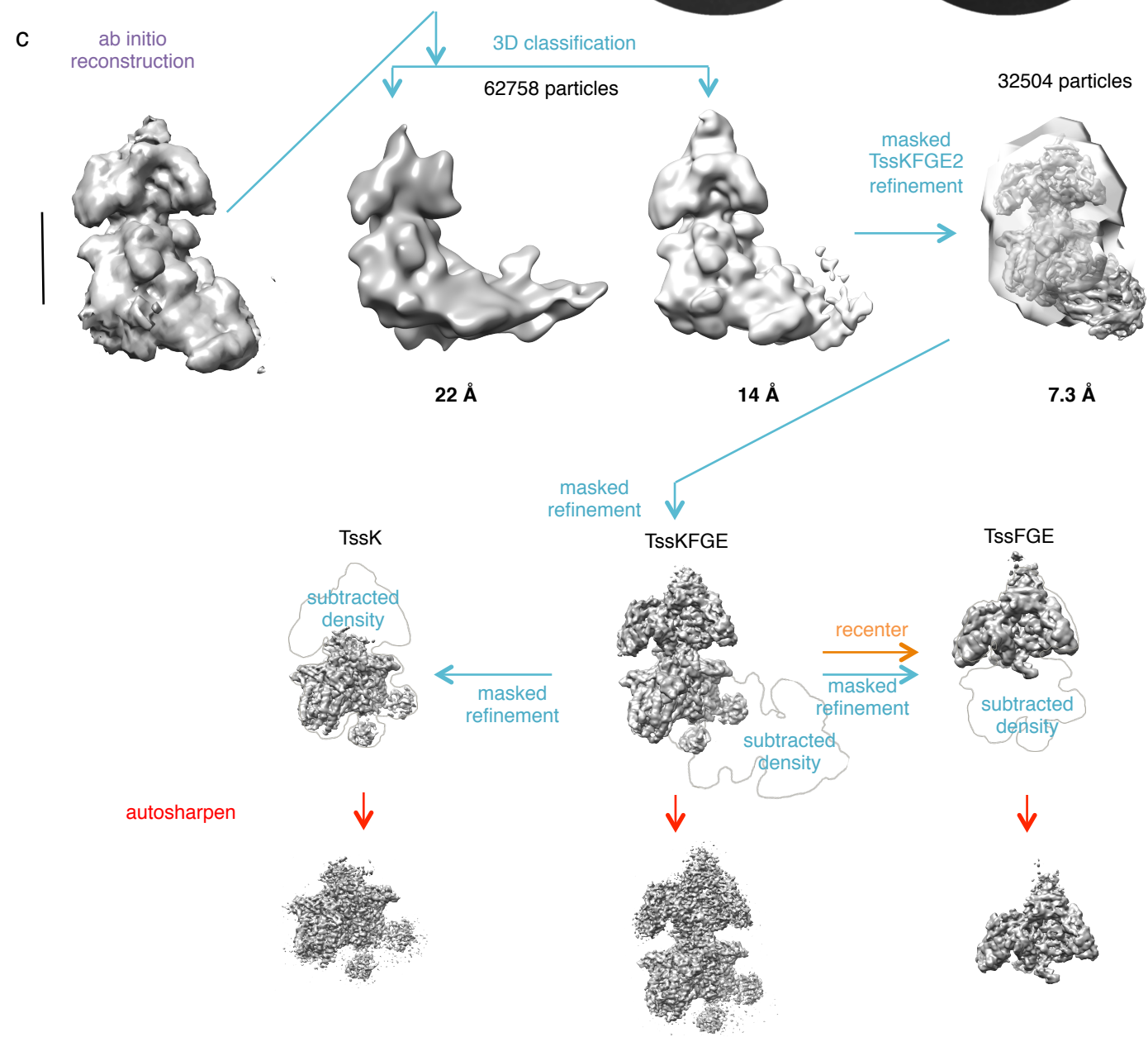
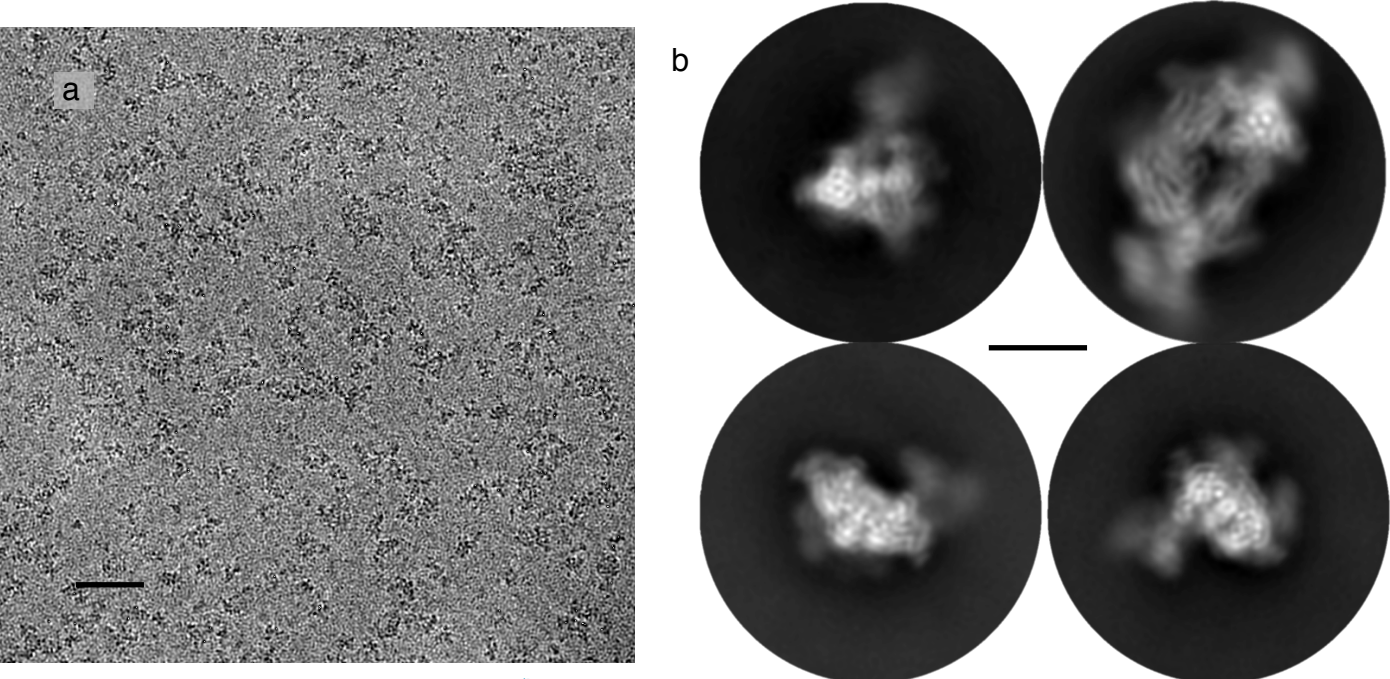
b. Same representation of the EAEK baseplate and sheath models as in Figure 4a, with the location of the Hcp tube and VgrG spike from *V. cholerae*. The bar corresponds to 100 Å

c. Ribbon diagram and surface representation of TssFa-TssFb belonging to two adjacent wedge complexes (main interface between wedge complexes within the T6SS baseplate). TssFa and TssFb are represented in cyan and blue respectively. The TssFa/Fb seen in Figure 4c is split open and the two protomers are placed in the same orientation. Within each subunit, the regions interacting with VgrG and TssBC are coloured in magenta and orange respectively. Left and middle panels display the same protomers rotated by 90° around their long axis. In the right panel, the protomers in ribbon diagram are shown in the same orientation as in the left panel.



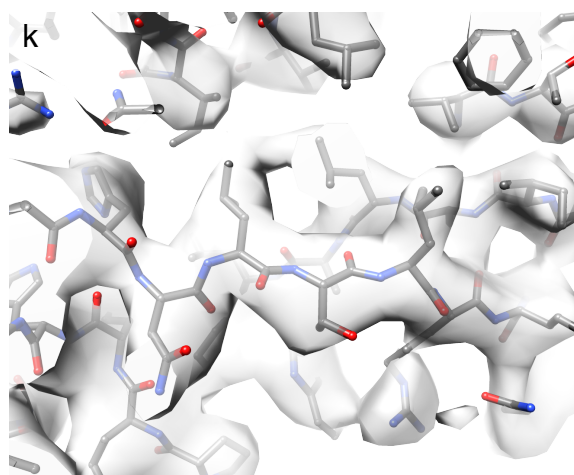
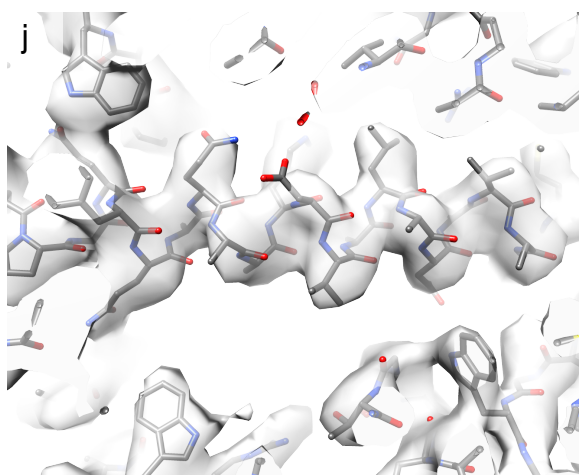
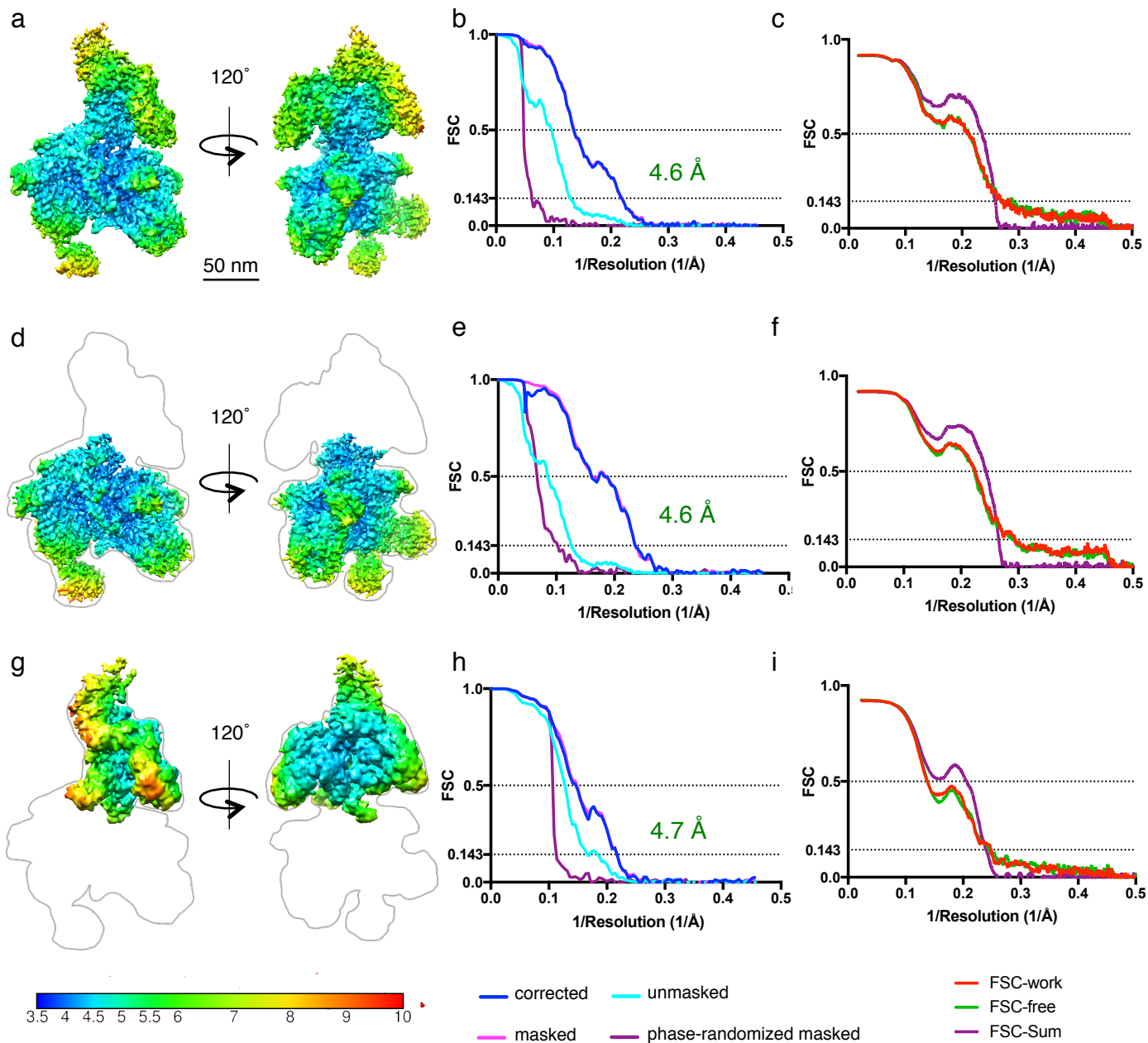
Supplementary Figure 9. Comparison of the bacteriophage T4 and T6SS baseplates. Related to Figure 5.

a. Comparison between TssG and gp7 structures (ribbon diagram). The structural features conserved in both structures are represented in purple. The structural elements specific to each protein are represented in yellow. **b.** Comparison between TssF and gp6 structures (ribbon diagram). The structural features conserved in both structures are represented in purple (trimer scaffold) and green (wing domain). The structural elements specific to each protein are represented in blue. **c.** Interaction between TssFa and gp6a with the spike. For TssFa and gp6a, the same colour code as in panel B is used. Top row: for the T6SS, TssFa and VgrG are represented. For the T4 bacteriophage, gp6a, gp53 (grey) and gp27-gp5 are represented. For each, a ribbon diagram and surface representation of the same view (side view) is displayed on the left and right part respectively. Bottom row: surface representation of the same assemblies but without the spike (Top and bottom views on left and right respectively). **d.** Ribbon diagram of the T6SS wedge-TssBC interaction. The colour code used to identify the various subunits is the same as in Figure 4D (TssFa, cyan; TssFb, blue; TssG, yellow; TssE, green; TssBC, orange). The different protomers and domains are identified. **e.** Ribbon diagram of the bacteriophage T4 wedge-gp18 interaction. The different protomers and domains are identified.



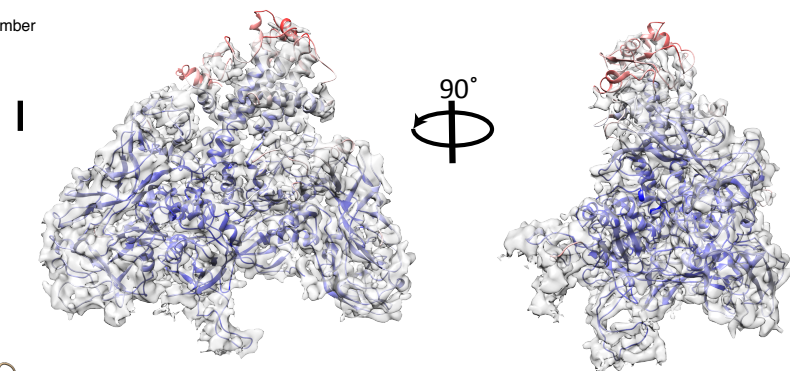
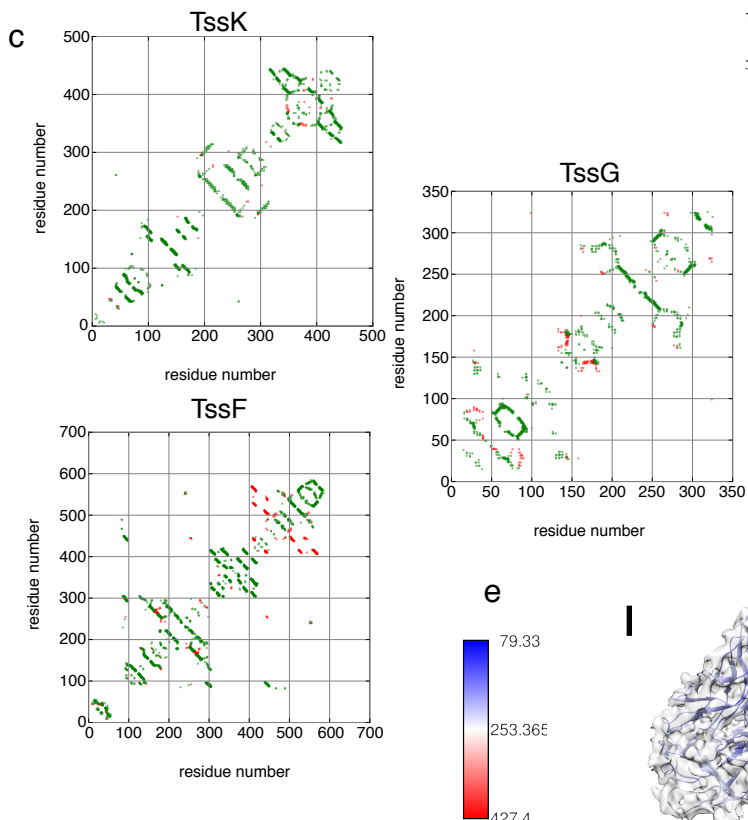
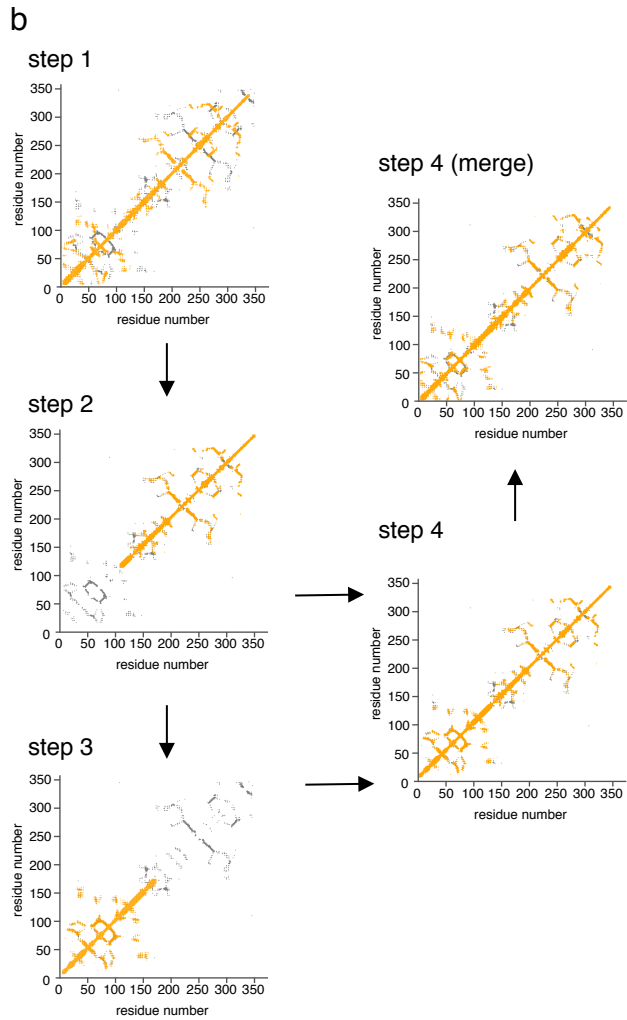
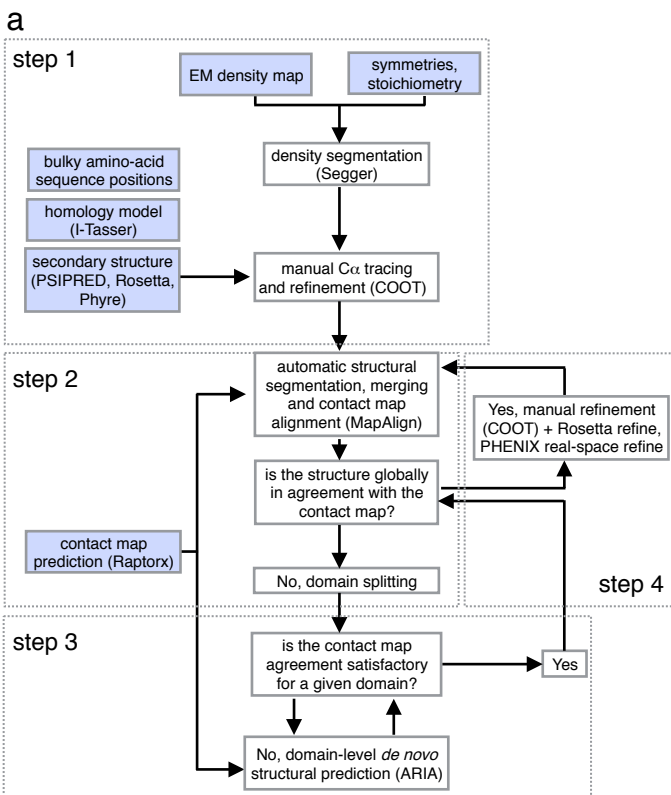
Supplementary Figure 10. Structure determination. Related to Figure 2.

a. Representative cryo-micrograph of the purified TssKFGGE complex. The scale bar corresponds to 50 nm **b.** Typical 2D classes of the 4 different views of the complex in ice (scale bar, 100 nm). **c.** Flowchart of the cryo-EM processing procedure. The colour of the arrows represents the different software packages used (light blue, Relion; red, Phenix; violet, Cryosparc; orange, REP).



Supplementary Figure 11. Analysis of model quality and refinement. Related to Figure 2.

a, d, and g. Local resolution of the TssKFGE (**a**), TssFGE (**d**) and TssK (**g**) auto-sharpened densities. **b, e, and h.** Fourier shell correlation (FSC) of the final reconstruction of TssKFGE (**b**), TssFGE (**e**) and TssK (**h**). The resolution limit was calculated at the cut-off 0.143. **c, f, and i.** Model validation by comparison of the Fourier shell correlation (FSC) between model and half map 1 (work), model and half map 2 (free), and model versus full sharpened map (sum) plotted in red, green and purple respectively for of the TssKFGE (**c**), TssFGE (**f**) and TssK (**i**). **j.** Representative local density of an α -helix (residues 19-33 of TssK chain H). **k.** Representative local density of a β -strand (residues 147-152 of TssK chain H).



TssG-D1

TssG-D2

TssF (495-585)

Supplementary Figure 12. Structural modeling of TssF and TssG. Related to Figure 2.

a. Flowchart of the structural modelling of TssG and TssF. **b.** Example of TssG contact map fit progressing with the different steps of the pipeline. The grey and orange dots are the predicted and model contacts, respectively, as defined in the supplementary methods text. **c.** Contact maps of the final TssK, TssG, and TssF structures compared to the corresponding predicted contact maps of the modelling pipeline. Green and red dots are predicted contacts in agreement and in disagreement with the structure, respectively. **d.** Ensemble of models for TssG-D1, TssG-D2 and TssF-D1 obtained from the predicted contacts and the ARIA modelling software (Step 3 of the pipeline). **e.** Fitting of the TssF and TssG structures in the postprocessed cryo-EM density (TssFGE), coloured according to B-factor values. The scale bar corresponds to 10 Å.