Type IV secretion systems (T4SSs) are molecular machines used for the transport of macromolecules across the bacterial cell envelope in Gram-negative bacteria. Conjugative T4SSs translocates DNA from a donor to a recipient bacterium and contribute to bacterial genome plasticity, spread of antibiotic resistance genes or other virulence traits. In some bacteria such as *Helicobacter pylori*, *Brucella suis* etc., T4SSs are directly involved in secretion of virulence factors into host cells. The archetypal T4SS, the VirB/D system was defined in *Agrobacterium tumefaciens* where it is naturally responsible for the delivery of the T-DNA to the plant host-cell. The *A. tumefaciens* VirB/D system comprises 12 proteins (VirB1 to 11 and VirD4). Atomic structures of isolated components such as VirB11, VirB5, virB8, virB10 and virB9 are available. However, no structural data was available concerning the assembly of the complex, particularly at the level of both bacterial membranes where the T4SS is supposed to form pores/channels allowing the substrate to cross the membranes. We present the cryoEM structure of a 1 MDa core complex composed of virB7, virB9 and virB10 homologues from the *E. coli* conjugative plasmid pKM101 T4SS. We also present the crystal structure of the outer-membrane complex (sub-complex of this core) at 2.6 Å resolution. The molecular characterization of these complexes provides key insights into the nature, structure and assembly of the type IV secretion core complex and the outer-membrane pore.