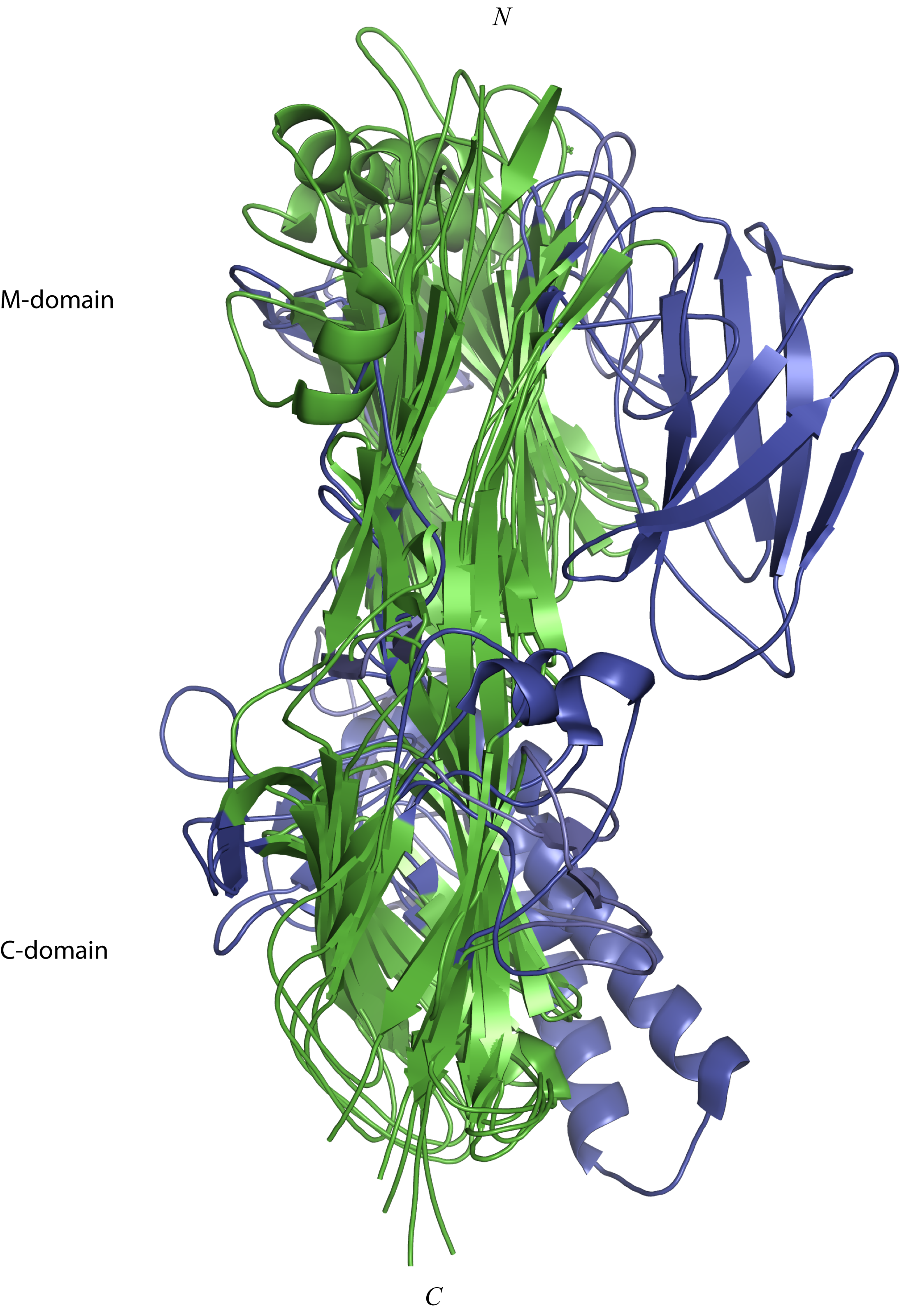

FIG S1 Structural alignment of Gram-positive backbone pilins highlights the conserved M-C domain core (Green) from T6 (*S. pyogenes*), RrgB (*S. pneumonia*), SpaA (*C. diptheriae*), FimP (*A. oris*) and GBS80 (*S. agalactiae*). The core Ig-like fold of the CnaA M-domain and a CnaB C-domain is decorated at conserved positions with extensions or variable regions (Blue). N = N-terminus. C = C-terminus.