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**Figure 2-figure supplement 2. Structure of Cel48S depicts the linker region** (A) The structure of the full-length Cel48S was determined by cryo-EM to a resolution of 3.4 Å (Supp. Fig. S3). The purple region is part of the linker that was structurally determined between the enzyme and the dockerin. (B) Ribbon representation of the cryo-EM structure (orange) overlayed with PDB:5YJ6 (yellow) (Liu et al., 2018). Slices through the structure (right, black and red indicated in B) show the quality of our reconstruction and the position of the random coil linker (purple) that follows the catalytic domain (C) Zooming into the random coil linker, overlayed with the density map, allows us to resolve the protein sequence (MTYKVPGTP) that bridges the catalytic domain to the dockerin (Dock). Tyr666 and Pro669 were used as anchors for modelling. (D) Backbone fit to the cryo-EM density map and the catalytic tunnel (asterisk). The black circle marks the position of Ser673 which immediately precedes the dockerin module, positioned ~1 nm away from the tunnel.