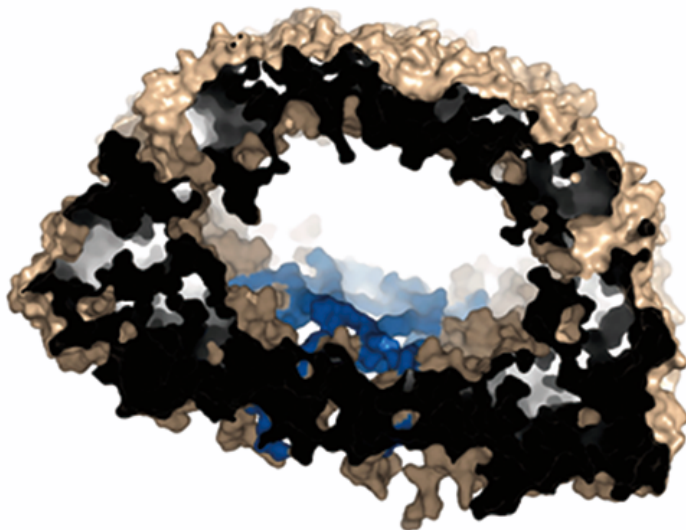
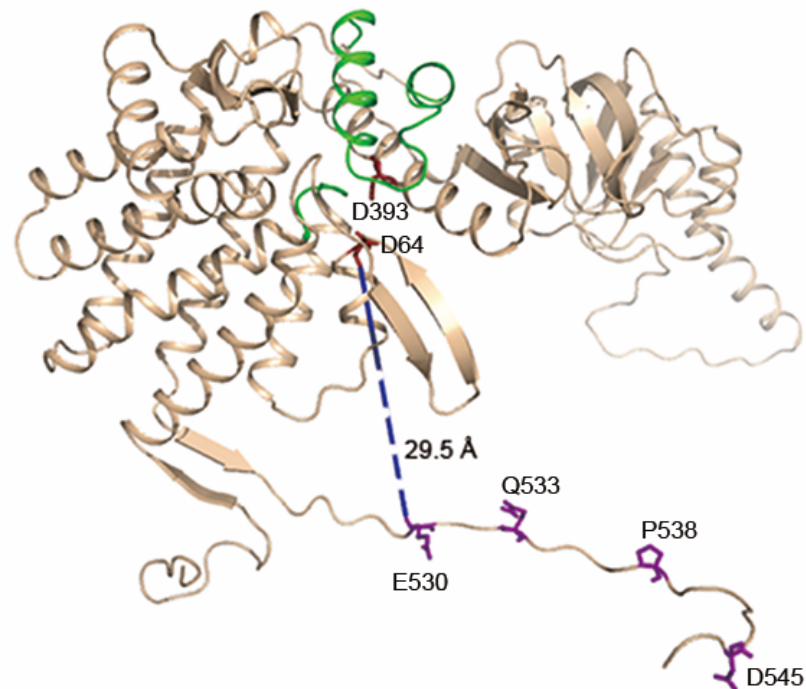


A



B



SUPPLEMENTAL FIGURE 2. 3D structural model of a CpkA octamer. The full-length CpkA octamer was built in MODELLER 9.12 using 1Q2V as a template. The structure of a single CpkA chain was then extracted from the octamer model. (A) Inner view of the surface of CpkA; the C-terminal region is shown in blue. (B) Ribbon model of a single chain of CpkA. The distance between Asp64 and Glu530 is shown. Catalytic residues Asp64 and Asp 393 are shown in red, and the four mutation sites are shown in magenta. The areas potentially involved in the functional movements of nucleotide-binding site mentioned in (43) are shown in green.