

Figure 2. A. Demonstrated conformational rearrangements of the dimer interface 2 and GTPase domain. B. High resolution features are observed in the BSE and stalk domains.

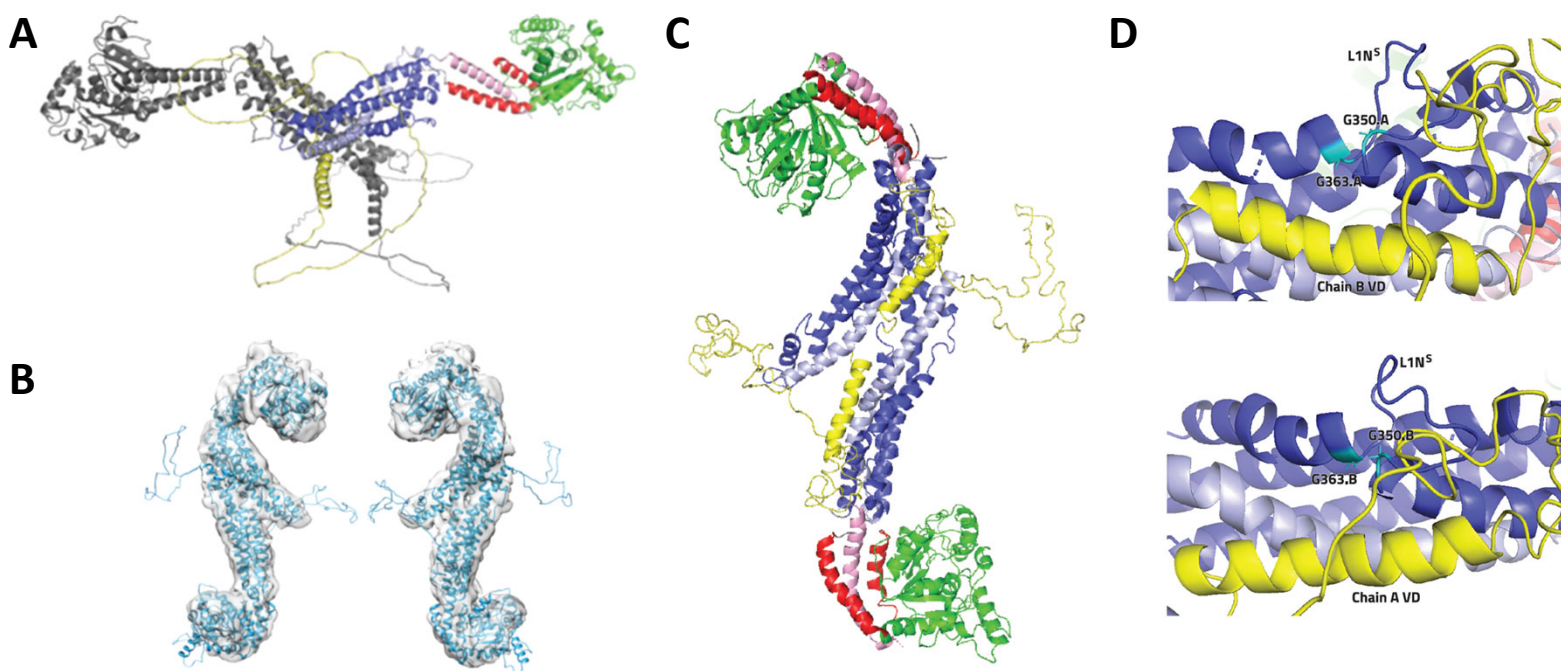


Figure 3. A. AlphaFold predicted structure includes a helix (yellow) that was believed to be intrinsically disordered. B. Using this model, the structure docked into a mid-resolution density of WT Drp1 that was fixed. C-D. Using MDFF flexible fitting the helix is observed to be docking near the G363 residue known to result in obligate dimers when a charge reversal is present.