

Figure 1: A) 2D classes from the closed state dimer (left) and a low-pass filtered (12 Å) cryoEM map (right). One monomer is colored in blue and the other in yellow. B) 2D classes (left), SAXS envelope (middle), and cryoEM map (right) of the mixed state dimer which forms in the presence of calcium. In both A and B, the reconstructions are limited in resolution and completeness due to an orientation bias that needs to be corrected in future studies.

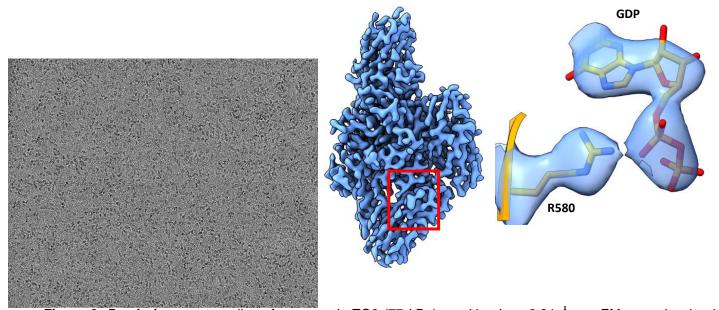


Figure 2: Proof of concept studies of monomeric TG2 (77 kDa) resulting in a 3.24 Å cryoEM map showing high resolution details of TG2 bound to GDP. The data was collected by tilting the stage 30° to overcome the orientation bias observed in preliminary studies of the monomer. A representative micrograph is included (left). The GDP binding site is shown indicated with a red box (middle) and R580 and GDP are shown docked into the cryoEM map (right).