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| **Figure 6–figure supplement 4. Comparison of Equilibrated Conformations Observed in DMD to Published Crystal Structures. A)** Steric occlusion of the PDZ3 ligand-binding pocket within the α-basin. The structure of PDZ3 bound to a short peptide (1TP3, yellow) is aligned with PDZ3 from a representative α-basin model (cyan). The ligand is shown as a beta strand (yellow) that overlaps with the SH3 HOOK insertion (orange). **B)** Lack of steric occlusion in the β-basin. The structure of GuK (yellow) bound to a MAP1A peptide (red) is aligned with a representative β-basin model (purple). The canonical ligand binding pockets of GuK and PDZ3 remain accessible in the β-basin. |