

Figure 1: Wedges for domain angle values set to 60 (top), 180 (middle), and 300 (bottom) degrees. Important are the rod like protein in the foreground and the more partially blue protein in the background.

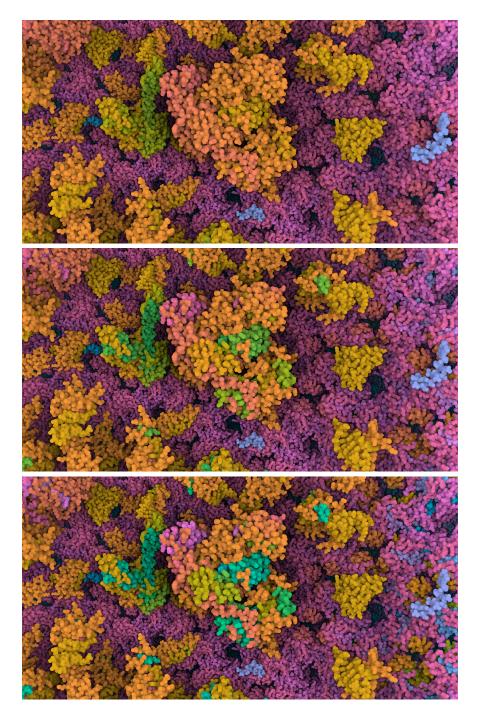


Figure 2: Wedges for secondary structure angle values set to 60 (top), 180 (middle) and 300 (bottom) degrees. Important are the rod like protein in the foreground and the more partially blue protein in the background. Domain angles were calculated as normal with max 180 degrees.

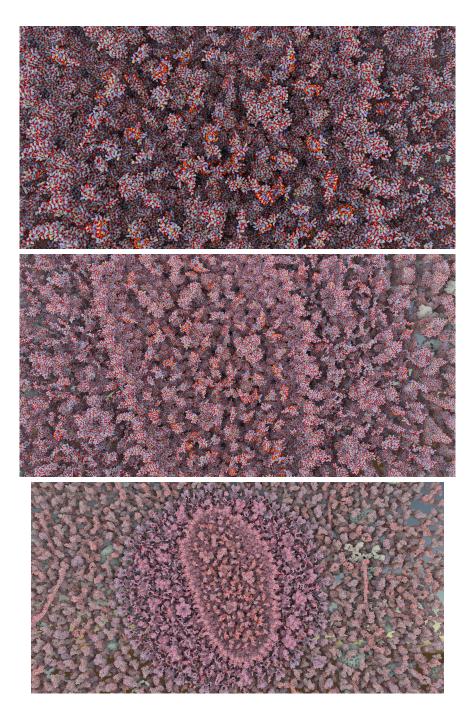


Figure 3: display of visualization using only colors for atoms at different zoom levels.

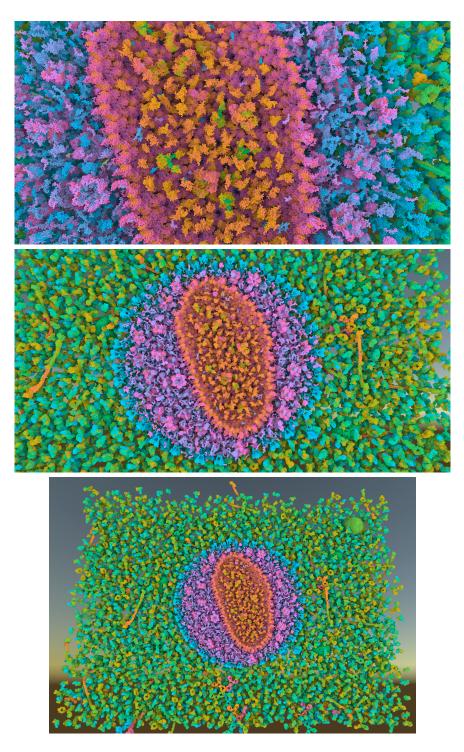


Figure 4: display of visualization using only secondary structure colors at different zoom levels.

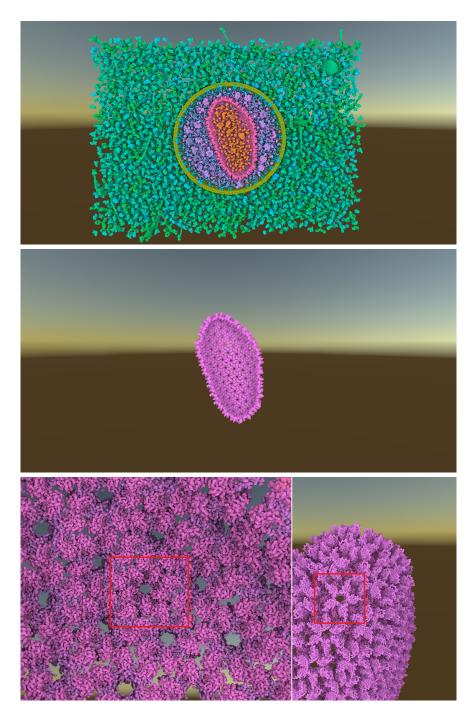


Figure 5: User study search task. Top: complete visualization. Middle: capsid only. Bottom: pentamer, from interior (left) and exterior (right), in red box.

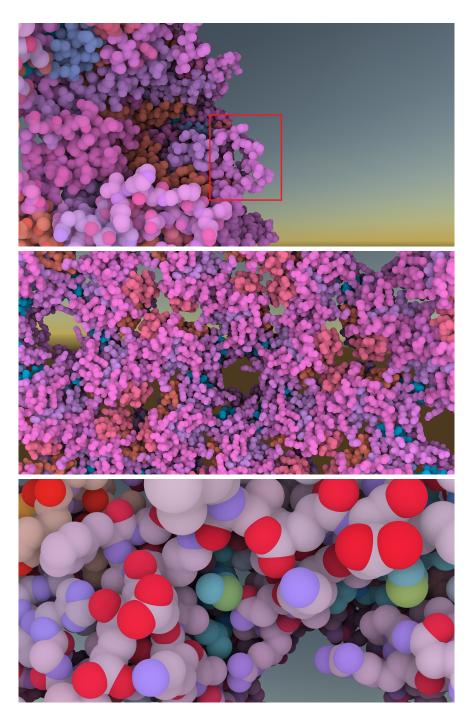


Figure 6: User study search task. Top: Cyclophilin A binding site (red box). Middle: Alpha helices (blue). Bottom: Sulfur (yellow).