Over the last 3-4 years Electron cryo Microscopy (cryoEM) has transformed structure biology. CryoEM increased the turnover for unique structures with near-atomic resolution drastically. Improvements in instrumentation and technique have delivered structures at resolutions between >1.9 and 4 Å for a number of years. It is becoming clear that EM is now limited by the ability to provide a sample with suitable quality rather than cryoEM instrumentation. In particular structural biology at the membrane interface is a largely uncharted territory. Unlike other high resolution techniques, cryoEM images both proteins and membranes. Visualizing proteins in the context of the lipid bilayer is essential to understand the chemistry and function of membrane proteins. But proteins are not passive bystanders; they are able to shape membranes, generate compartments and shuttle membrane proteins in and out of membranes. Once at the membrane, integral membrane proteins and their scaffolding/trafficking proteins form signalling platforms. Here we present the structures of membrane-protein complexes like clathrin coated vesicles isolated from animal tissues. The structure gives us a working model how steric hindrances help to time the loading of the enclosed vesicles with neurotransmitters. Another example for the versatility of cryoEM is the elucidation of the structure-function relationship of membrane bending proteins, such as endophilin, which forms the necks of clathrin coated buds during endocytosis.