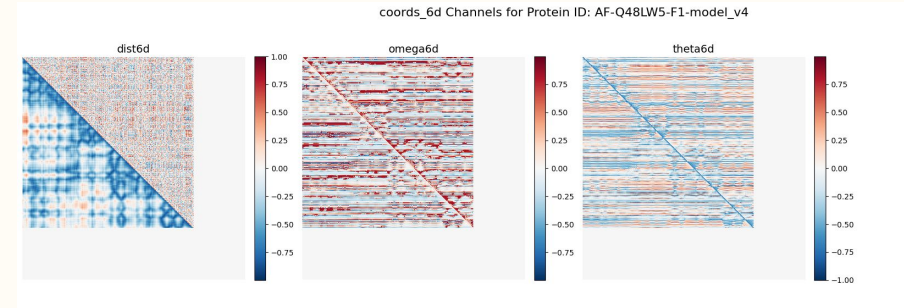
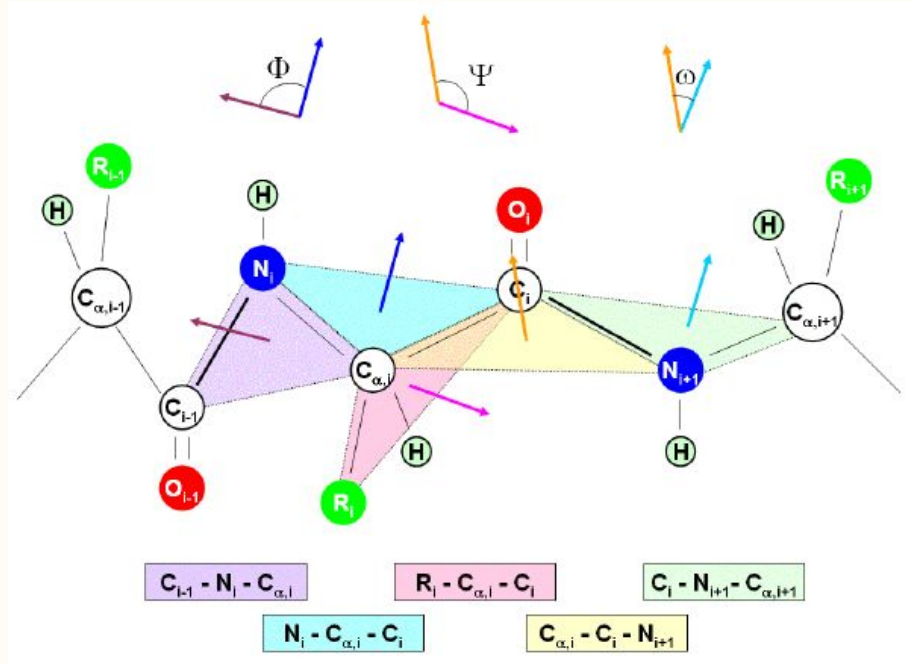
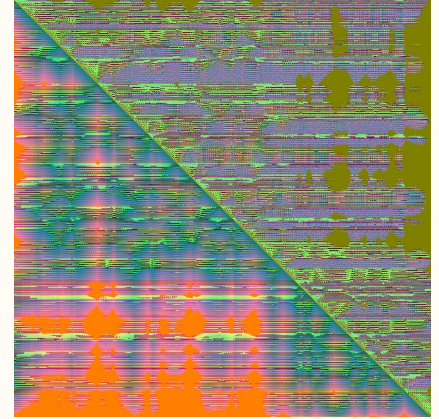
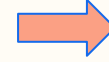
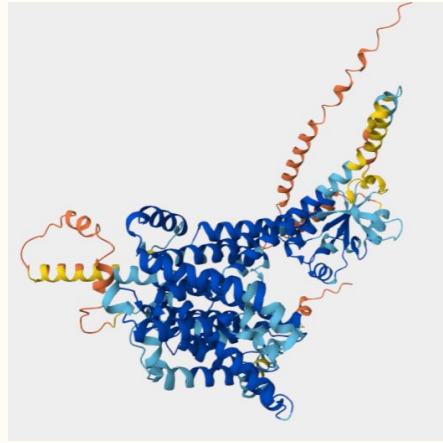
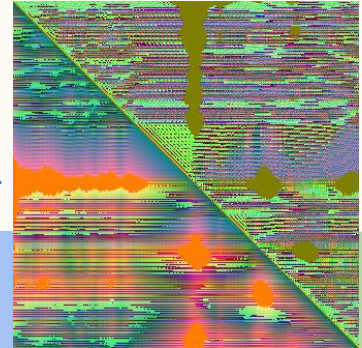
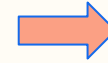
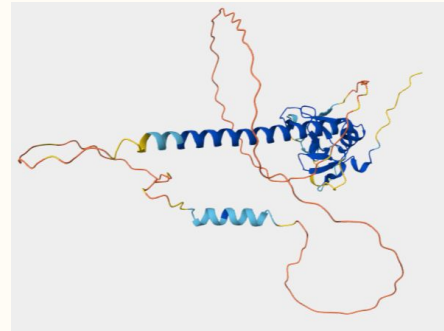


Protein Images





1. No need for equivariant methods, everything is relative
2. 3d coordinates are raw, extraction of some global and local features (inductive bias of protein geometry)



Reconstruction Quality

4096 codebook size

Mean reconstruction loss =
0.07

Trained on 2M protein
backbone structures

Input

Reconstruction

