Cryo-EM Reconstruction
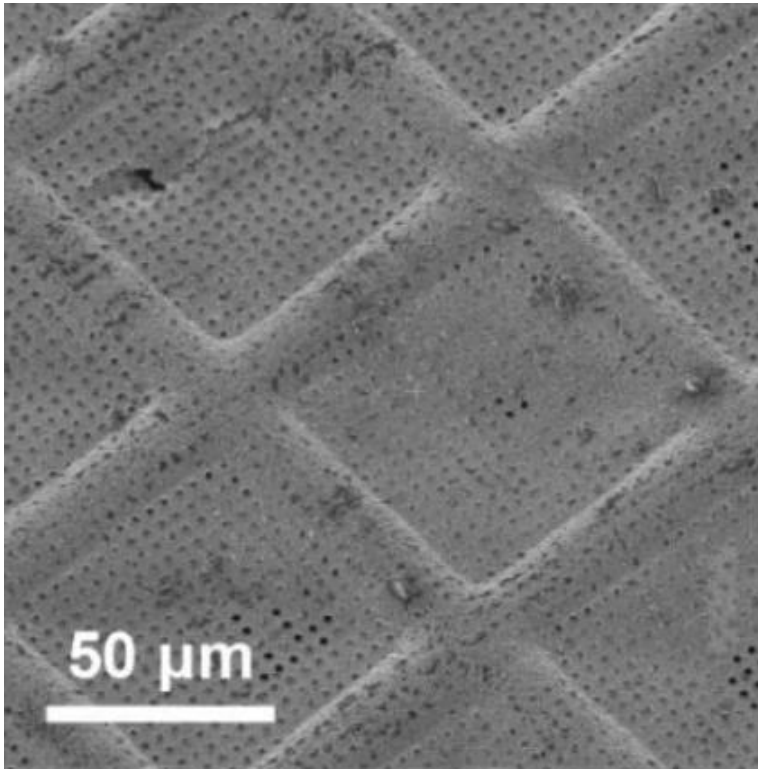
- Structural biology technique for protein visualization
  - Flash freeze protein and visualize using EM

Cryo-EM sample holder
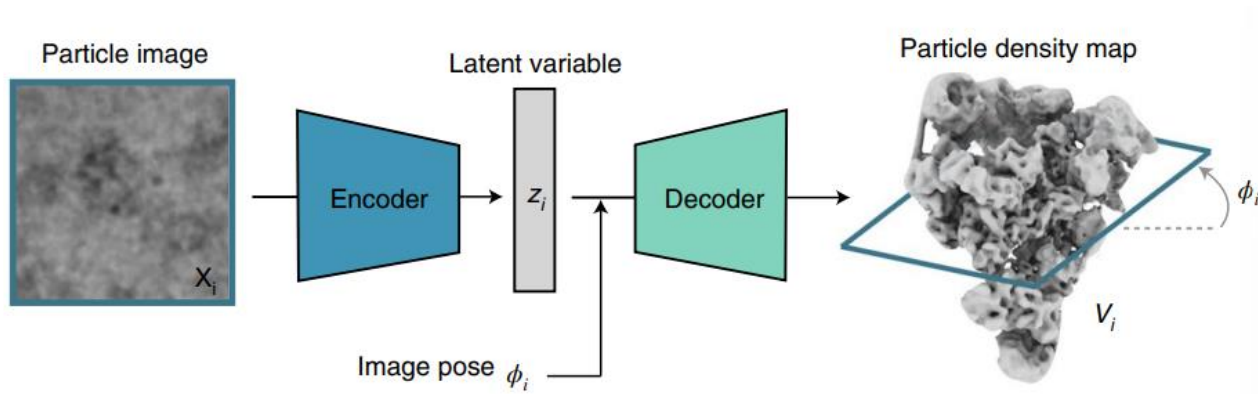
Issues:

- Protein heterogeneity is computationally difficult to visualize

- Current methods assume discrete conformations

How do we model continuous conformational changes?
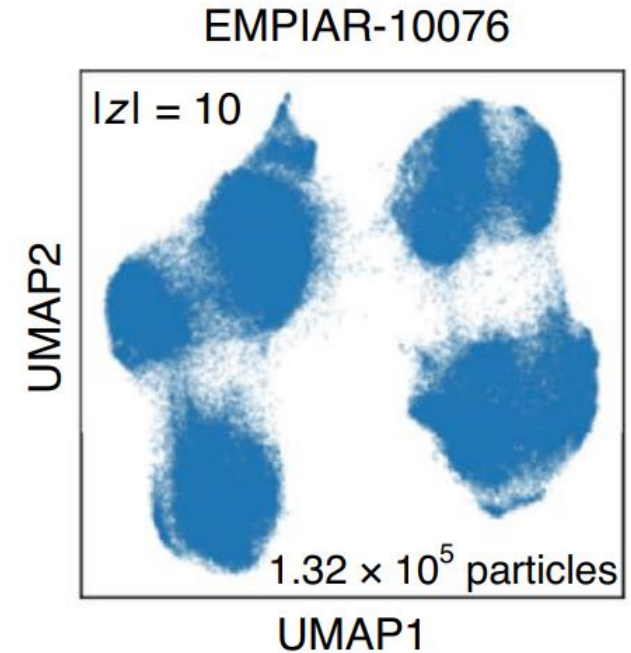
CryoDRGN: Neural Network Architecture

- Similar to **variational autoencoder** (**VAE**)
  - Unsupervised method that reconstructs images

Important Features:

- Two networks: Encoder and decoder

- Compressed latent variable

- Reconstruction Loss and KL Divergence:

$$\mathcal{L}(X; \xi, \theta) = E_{q_\xi(z|X)}(\log p(X|z)) - \beta KL(q_\xi(z|X)||p(z))$$

Generation of
continuous latent space

Zhong et al. *Nat. Methods.* **(2021)**