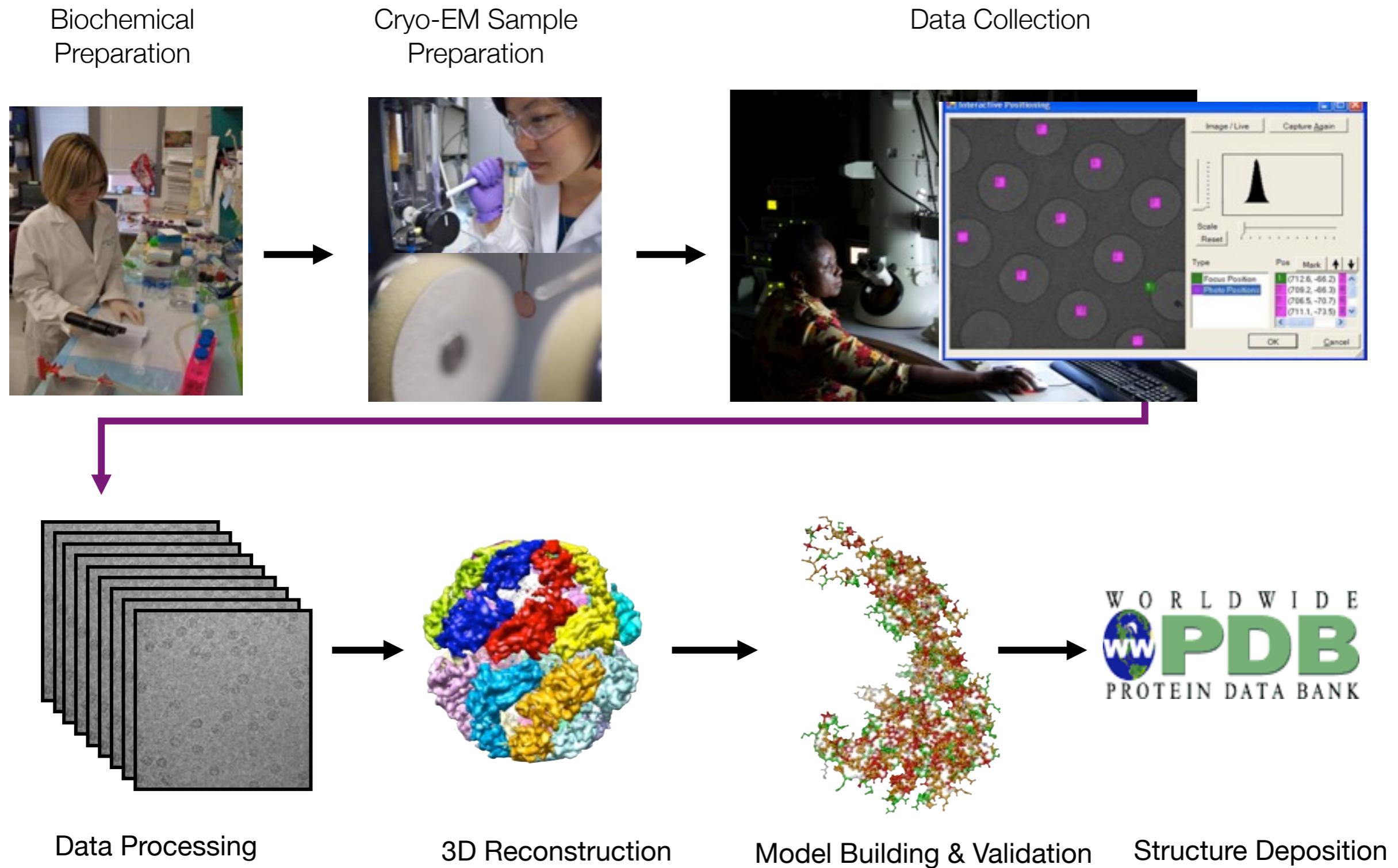
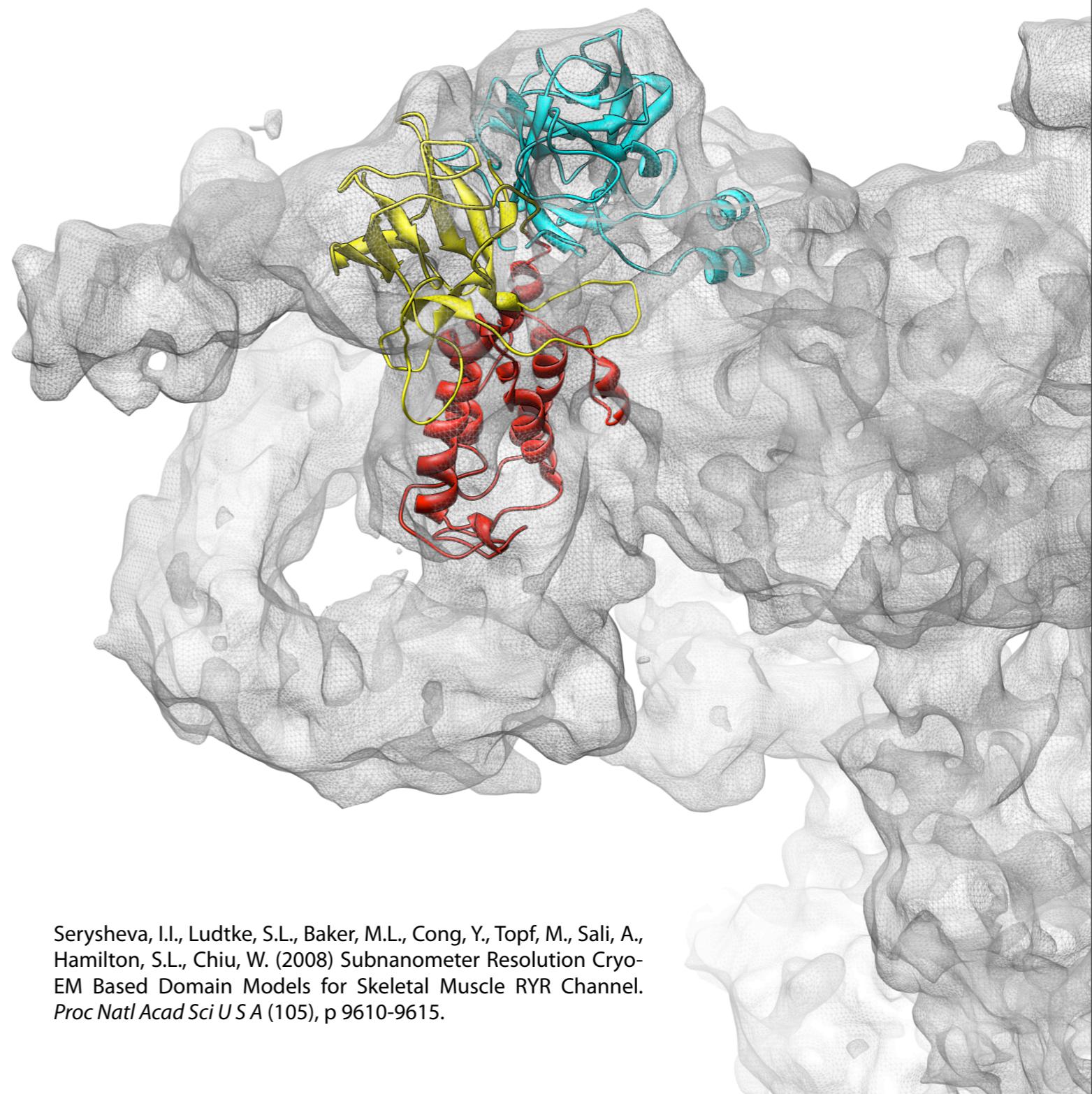


THE CRYO-EM “EXPERIMENT”



MODELING WITH KNOWN STRUCTURES

- Fitting atomic models
- Homology modeling
- Flexible fitting



Serysheva, I.I., Ludtke, S.L., Baker, M.L., Cong, Y., Topf, M., Sali, A., Hamilton, S.L., Chiu, W. (2008) Subnanometer Resolution Cryo-EM Based Domain Models for Skeletal Muscle RYR Channel. *Proc Natl Acad Sci U S A* (105), p 9610-9615.

NEAR ATOMIC RESOLUTIONS (3.5Å)

Features

- Subunit interfaces
- Helix visible
- strand separation
- Protrusions at bulky amino acid positions
- Traceable with *de novo* methods
- Secondary structure element anchors

Limitations

- “Lost in the forest”: complicated segmentations
- Difficult to distinguishing between features and noise
- Limited sidechain density
- Modeling depends on accuracy of secondary structure prediction

