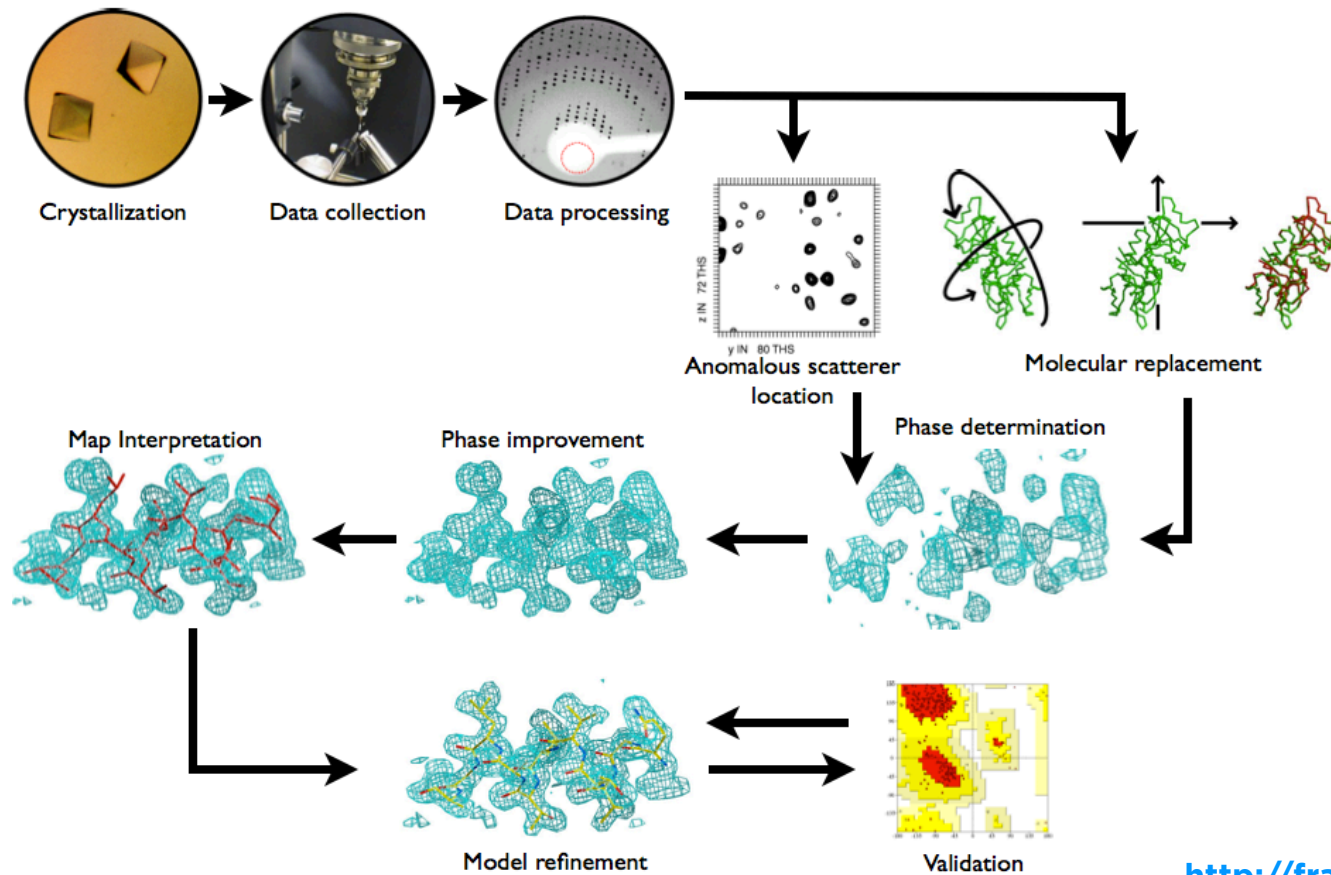


# X-ray Crystallography 101



# Key take-aways

1. X-ray crystallography results from an ensemble averaging of millions of molecules in the crystal
2. Models in the PDB are often sub-optimal and can contain errors
3. Intensity of “spots” dictated by the electron density (the probability distribution of molecules across unit cells)
4. Positions of “spots” relates to the arrangement of unit cells in the crystal
5. Every “spot” contains contributions from every part of the crystal. Every part of the map contains contributions from every “spot”