

The crystals diffracted to 2.4 angstrom resolution at ESRF. We have tried to collect SAD data-sets of zinc signal in DBD domain, but due to the small size of the crystals and serious radiation damage, the data-sets with weak anomalous signal were not good enough to solve the starting phase. There are lots of methionines in this protein. So the data from the Se-met crystals will be used to get starting phase with SAD/MAD method.