A monoclinic polymorph of malonamide is considered. The compound was purchased from Sigma-Aldrich. Crystallization from water in a room temperature by a slow evaporation yielded good crystals for high-resolution X-ray measurements (see next paragraph). The preliminary results based on a spherical refinement (see figure 1) confirmed that the refined structure is in agreement with those published by Chieh et al. [1]. To get the quantitative description of the electronic structure of title compound the multipole refinement is intended and a full topological analysis will be a subsequent step of our work.

High-resolution X-ray diffraction data were collected at beamline F1 of the storage ring DORIS III at HASYLAB/DESY, Hamburg, Germany. Beamline F1 is equipped with a kappa-axis four-circle Huber diffractometer and a MAR165 CCD detector. The temperature for the experiment was maintained at 100 K with an Oxford Cryosystem N2 gas stream cooling device. Two ‘zero’ runs with exposure times of 2 and 4 seconds and three ‘high’-order runs with angle settings of 2θ, ω, χ: −45, 0, 0; −50, −30, 60; −50, 20, 60° and a scan time of 60 s were measured. This setting gave 91 117 collected reflections up to a resolution of sin θ/λ = 1.25 Å⁻¹ (d = 0.40 Å) and overall completeness 94%. The XDS program [2] was used for integration of frames and for preliminary data reduction. Final sorting, merging and application of the oblique incidence correction [3] for the dataset were performed with the programs SADABS and XPARP [4]. During merging procedure 4137 outliers were downweighted and finally 13 726 unique reflections were obtained with an internal agreement factor of 3.78%.

![Figure 1: The molecular structure of malonamide with atom numbering scheme](image)

**References**