Green lacewing flies (Chrysopidae) are predatory insects. They lay their eggs on the end of proteinaceous stalks that are typically 15-20μm thick and up to 1 cm long. Previous X-ray diffraction work in the 1957 has shown that the stalks are made from a cross beta structure that gives a well-defined diffraction pattern. The analysis of these data was given in terms of a structure in which the chain axis was normal to the stalk axis. Geddes et al. (1968) proposed a structure to explain the X-ray diffraction pattern of the cross-beta fibrous protein. The well-oriented fibers contain ribbon-like micelles about 25Å thick with their longest dimension parallel to the fiber axis. The ribbons are packed face to face with a variable interfacial separation around a mean of 15 ± 4Å. The inner structure of the ribbons was assumed to be that of the polyaniline as described by Arnott, but in the cross-beta conformation the extended parts of the polypeptide chains run at right angles to the fiber axis. In the protein studied these extended parts are linked together by short "bend" regions to form continuous folded polypeptide chains which lie in planes normal to the surface of the ribbon-like micelles and parallel to their long axis.

We will describe recent X-ray and neutron scattering work that extend this analysis of the eggstalk cross beta structure. X-ray data has been recorded to a resolution of better than 2Å, using the microfocus beamline on ID23-2 at the ESRF, and neutron diffraction tests are in progress on the new D19 diffractometer at the Institut Laue Langvin. Sequence information that may be vital to this analysis is being sought through N-terminal and internal sequencing.