Ferritin is the universal iron storage protein utilized by most living cells to uptake and store iron, in a bio-available form via redox mechanisms. X-ray structural studies show that haem is able to bind horse spleen apoferritin in a site similar to that observed in bacterioferritin from Bacillus stearothermophilus.

The iron content of the protein is required for its activity. Ferritin is found in the liver, spleen, heart, and other tissues. Ferritin is the most abundant iron storage protein in mammals.

The crystal packing conesponds to a situation halfway between the well known hexagonal closest packing and the orthorhombic all-face centred one. Thus it is confirmed that the orthorhombic all-face centred one.

First, the orientation of the molecule has been successfully determined with a standard self-rotation followed by a locked self-rotation, then, the position in the unit cell, has been localized with the program AMoRe (Navaza, 1992). The model used was built from the coordinates of the tetragonal structure of cytochrome b 1 of Enterobacter coli. The asymmetric unit of the monoclinic crystal consists of twelve such dimers and a single haem. The haem is positioned in a special position on the two-fold axis of the dimer. The asymmetric unit of the monoclinic crystal of horse spleen apoferritin crystals of tetragonal and orthohombic forms, which differcct beyond 2.4 Å have been obtained. X-ray diffraction data were collected, on the three different crystal forms, with the LURE synchrotron radiation facilities.

We present a comparison of the structures of the three crystal forms: molecular packing and conformational differences will be discussed in relation with crystal symmetry differences.

The bacterial and mammalian 2-oxoacid dehydrogenase multienzyme complex families catalyse the oxidative decarboxylation of 2-oxoacids (pyruvate, α-ketoglutarate and branched-chain 2-oxoacids) to produce the corresponding acyl-CoA and NADH. A well known member of the family is pyruvate dehydrogenase (PDH), occurring at the end of the glycolysis and providing the tricarboxylic acid cycle with acetyl-CoA. The architectural design of PDH is composed of a central core enzyme, dihydrolipoamide acyltransferase (E2) with either octahedral (24-mer) or icosahedral (60-mer) symmetry, depending on the source of the enzyme. E2 binds the two peripheral enzymes, thiamin pyrophosphate (TPP) dependent decarboxylase (E1) and flavoenzyme lipoamide dehydrogenase (E3), leading to a molecular weight (M2) of these systems of 5 to 10 million Da. In mammals and yeasts, additional proteins are attached to the complex: the so-called protein X and a specific kinase and phosphatase. Deficiencies or malfunctioning of the complexes lead to severe pathological states such as numerous acidoses which are usually correlated with serious neurological dysfunctions.

The catalytic domain of E2 from B. stearothermophilus and Enterococcus faecalis PDH have been cloned, expressed in E. coli and purified. Of the former, crystals suitable for X-ray diffraction experiments grew within 10 days and diffract to about 4 Å resolution at cryo-temperatures. Here we describe the crystallisation of E2 from B. stearothermophilus and its preliminary analysis by X-ray crystallography.

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Bovine neurophysin II has been crystallized in eight distinct crystal forms containing 1, 2, 3, 4, 6 and 12 molecules per asymmetric unit. The mode of molecular aggregation observed in the crystal structures may be paradigms of how the neurophysin-hormone complexes are packaged in the neurosecretory granules (NSG).

The neurophysins (NP) are a family of disulfide rich proteins responsible for the packaging and transport of the posterior pituitary hormones oxytocin (OT) and vasopressin (VP). Two closely related classes of neurophysins are known, one complexed with VP and the other with OT, this association reflecting the synthesis of each hormone and its associated NP via a common precursor.

During transport, the hormone is cleaved from its neurophysin carrier but remains associated with the protein as a non-covalent complex. The neurophysin-hormone complex is then stored in NSG until release into the blood stream. Within the NSG, the NP-hormone complex concentration can be as high as 1000 mg/ml. Although the mode of NP aggregation within the NSG is unknown, it has been postulated based on the high concentrations observed in the NSG that the complexes exist as dimers, higher aggregates, or even amorphous or crystalline precipitates thus the mode of NP association observed in the crystal structures may serve as a model for neurophysin packaging through the NSG.

An analysis of the common modes of NP aggregation observed in the crystal structures will be presented.