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 bacitracin in the X-ray crystal structure of bacitracin.

In the crystal structures, and whatever the studied metalloporphyrin, the protoporphyrin IX is always observed free of metal. However, in the crystal packing, both horse spleen apoferritin crystals of tetragonal and orthorhombic forms, which differ by 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 acytransferase (E2) with either octahedral (24-mer) or icosahedral (60-mer) symmetry, depending on the source of the enzyme. E2 binds two peripheral enzymes, thiamin pyrophosphate (TPP) dependent decarboxylase (E1) and flavoenzyme lipoamide dehydrogenase (E3), leading to a molecular weight (M) of these systems of 5 to 10 million Da. In mammals and yeast, 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. steaothermophilus 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-temperature. Here we describe the crystallisation of E2 from B. steaothermophilus and its preliminary analysis by X-ray crystallography.

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 paradigmatic 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.

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