

Publication

Methods used in the structure determination of bovine mitochondrial F-1 ATPase

JournalArticle (Originalarbeit in einer wissenschaftlichen Zeitschrift)**ID** 4531105**Author(s)** Abrahams, J. P.; Leslie, A. G. W.**Author(s) at UniBasel** [Abrahams, Jan Pieter](#) ;**Year** 1996**Title** Methods used in the structure determination of bovine mitochondrial F-1 ATPase**Journal** Acta Crystallographica. Section D, Biological Crystallography**Volume** 52**Pages / Article-Number** 30-42**Mesh terms** Science & TechnologyLife Sciences & BiomedicinePhysical SciencesBiochemical Research
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With a size of 372 kDa, the F-1 ATPase particle is the largest asymmetric structure solved to date. Isomorphous differences arising from reacting the crystals with methyl-mercury nitrate at two concentrations allowed the structure determination, Careful data collection and data processing were essential in this process as well as a new form of electron-density modification, 'solvent flipping'. The most important feature of this new procedure is that the electron density in the solvent region is inverted rather than set to a constant value, as in conventional solvent flattening. All non-standard techniques and variations on new techniques which were employed in the structure determination are described.

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