1EXS: Structure Of Porcine Beta-Lactoglobulin

JournalArticle (Originalarbeit in einer wissenschaftlichen Zeitschrift)

ID 4531073
Author(s) Abrahams, J. P.; Hoedemaeker, F. J.
Author(s) at UniBasel Abrahams, Jan Pieter ;
Year 2000
Title 1EXS: Structure Of Porcine Beta-Lactoglobulin
Journal Worldwide Protein Data Bank
Pages / **Article-Number** 1EXS
Keywords Lipid-binding protein
Mesh terms Science & TechnologyLife Sciences & BiomedicineBiochemistry & Molecular BiologyBiochemistry & Molecular Biology
beta-Lactoglobulin (BLG) is a lipocalin and is the major protein in the whey of the milk of cows and other ruminants, but not in all mammalian species. The biological function of BLG is not clear, but a potential role in carrying fatty acids through the digestive tract has been proposed. The capability of BLG to aggregate and form gels is often used to thicken foodstuffs. The structure of the porcine form is sufficiently different from other known BLG structures that SIRAS phases had to be measured in order to solve the crystal structure to 2.4 A resolution. The r.m.s. deviation of C(alpha) atoms is 2.8 A between porcine and bovine BLG. Nevertheless, the typical lipocalin fold is conserved. Compared with bovine BLG, the tilted alpha-helix alters the arrangement of surface residues of the porcine form, completely changing the dimerization behaviour. Through a unique pH-dependent domain-swapping mechanism involving the first ten residues, a novel dimer interface is formed at the N-terminus of porcine BLG. The existence of this novel dimer at low pH is supported by gel-filtration experiments. These results provide a rationale for the difference in physicochemical behaviour between bovine and porcine BLG and point the way towards engineering such dimerization motifs into other members of the lipocalin family.

Digital Object Identifier DOI 10.2210/pdb1exs/pdb
ISI-Number 2012135001716630
Document type (ISI) Data set