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Effect of annealing on the microphase separation of polyurethane and polyurethaneurea elastomers

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It is well documented that the properties and performance of polyurethanes and polyurethaneureas are strongly dependent on the degree of microphase separation and ensuing morphologies [1,2]. The morphology of segmented polyurethanes is very complicated, not only because of their two-phase structure, but also because of other physical phenomena such as crystallization and hydrogen bond formation in hard and soft domains. These phenomena have been intensively studied over years, as they are relevant to understand and control the properties of the final product.
In this paper, two series of MDI and ethylene glycol adipate polyol-based polyurethane (PU) and polyurethaneurea (PUU) elastomers were examined, with emphasis on characterizing the effect of annealing on the morphology and microphase separation. Series I includes four PU samples where only aliphatic diol chain extenders were used while series II includes five PUU samples where a mixture of aliphatic diol and aromatic or heterocyclic diamine chain extenders were used. All samples were annealed at 100°C up to 14 days according to the ASTM 0573-99 method. TGA results show that annealing at 100°C does not result in any thermal degradation but mechanical characterizations show that the annealing causes a drop of the E-modulus, likely due to morphological changes. This conclusion is confirmed by SAXS, WAXD, DSC and DMA measurements where the annealed samples show different behaviour compared to the non annealed ones. Moreover, the differences are affected by the annealing time. During high temperature annealing SAXS measurements reveal that the micro phase separation gradually progresses. In addition, extra melting peaks appear in the DSC measurements together with sharp crystalline reflections in WAXD, pointing to additional crystallization.

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A model of the solution structure of human Pex5p obtained by small angle X-ray scattering

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Peroxisomal matrix proteins are synthesized by cytosolic ribosomes and posttranslationally imported into the peroxisome organelle. So far, two peroxisomal targeting signals (PTS1 and PTS2) that are required for the import of peroxisomal matrix proteins into the peroxisome, have been identi''6ed [1, 2]. Proteins belonging to this family possess a tripeptide with the sequence SKL located at the C- termini [3].
Specific targeting of these proteins to the peroxisome is mediated by one of two receptors, Pex5p or Pex7p. The majority of these proteins are recognized by Pex5p as PTS1 receptor, which have been described for species ranging from yeast to mammals [4, 5].
In the N-terminal half of Pex5p a number of conserved di-aromatic pentapeptide repeats (WxxxY/F motif) are present which speci''6cally bind to the cytosolic domain of the peroxisomal membrane protein Pex14p with high affinity [6]. The C- terminal half of Pex5p is responsible for recognition of the PTS1 tripeptide and contains six TPR domains in the C terminal half of the protein [7, 8]. The mechanism by which matrix proteins are translocated across the peroxisomal membrane is still poorly understood.
The solution structure of human Pex5p obtained by small angle scattering reveals that the N-terminus of Pex5p has an elongated, partially unfolded structure, whereas the C-terminus possesses a globular TPR domain. This result is discussed in relation to conformational flexibility, which is crucial for cargo protein transport regulation.

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