Impact of maltose modified poly(propylene imine) dendrimers on liver alcohol dehydrogenase (LADH) internal dynamics and structure

Michal Ciolkowski[a,*], Inessa Halets[b], Dzmitry Shcharbin[b], Dietmar Appelhans[c], Brigitte Voit[c], Barbara Klajnert[a], Maria Bryszewska[a]

[a] *Department of General Biophysics, University of Lodz, 141/143 Pomorska St., 90-236 Lodz, Poland*

[b] *Institute of Biophysics and Cell Engineering of Natl. Acad. Sci., Academicheskaja 27, 220072, Minsk, Belarus*

[c] *Leibniz Institute of Polymer Research Dresden, Hohe Strasse 6, 01069 Dresden, Germany*

Supplementary Material

Figure S1 reveals changes of horse liver alcohol dehydrogenase (LADH) CD spectra upon addition of G4 PPI, G4 PPI-OS and G4 PPI-DS dendrimers. Figures S2 and S3 give an insight into the spatial structure of LADH. Figure S2 shows the positions of tryptophan residues. Figure S3 shows the cleft between catalytic and coenzyme binding domains of LADH. Structures are based on a structure from Protein Databank (PDB ID: 6ADH)[1]. Visualizations of LADH were prepared with the use of DS Visualizer software (Accelrys).

[1] H. Eklund, J.-P. Samama, L. Wallen, C.-I. Branden, A. Akeson, T.A. Jones, Structure of a triclinic ternary complex of horse liver alcohol dehydrogenase at 2.9 Å resolution, J. Mol. Biol. 146 (1981) 561-587.

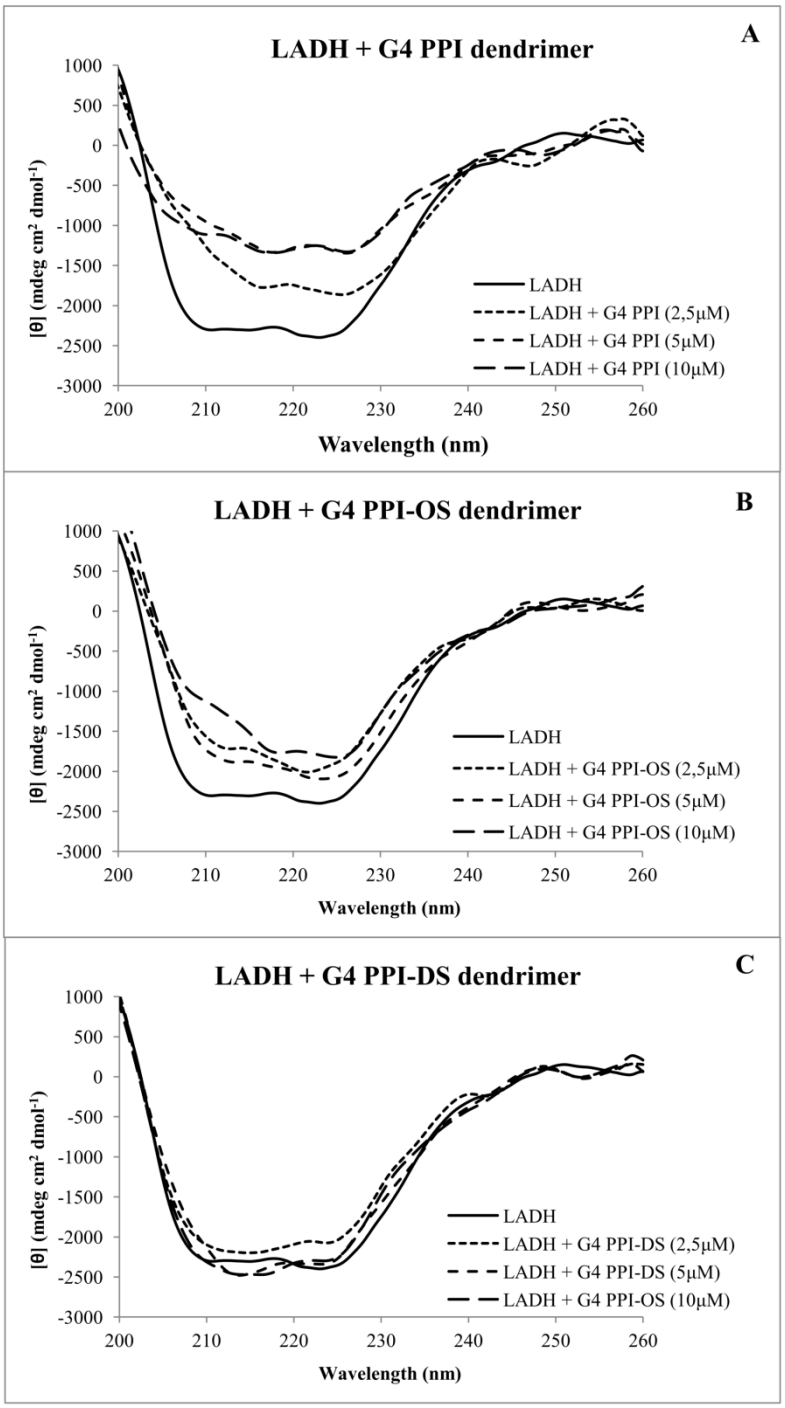

Figure S1. Changes in a CD spectrum of LADH upon addition of G4 PPI (**A**), G4 PPI-OS (**B**) and G4 PPI-DS (**C**) dendrimers.

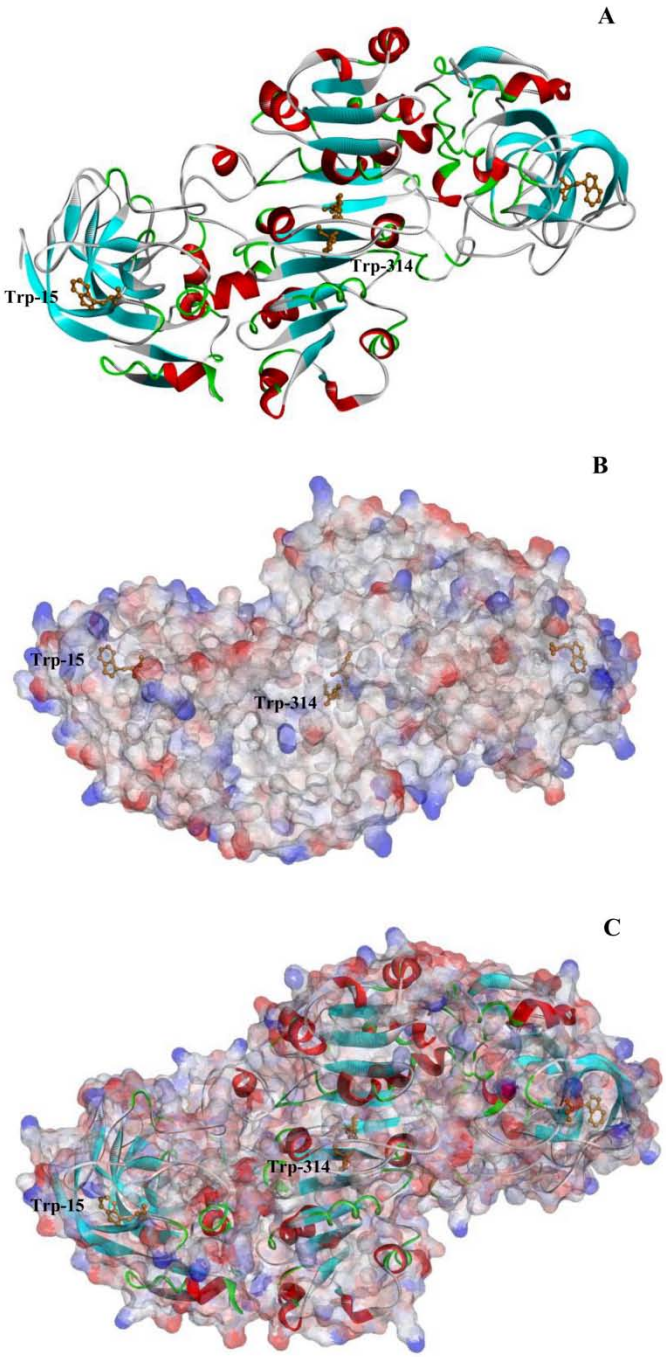

Figure S2. Positions of Trp-15 and Trp-314 residues in LADH. Tryptophan residues are marked in orange. Protein is depicted as secondary structure ribbon (**A**), solvent accessible surface (**B**) or secondary structure ribbon combined with solvent accessible surface (**C**).

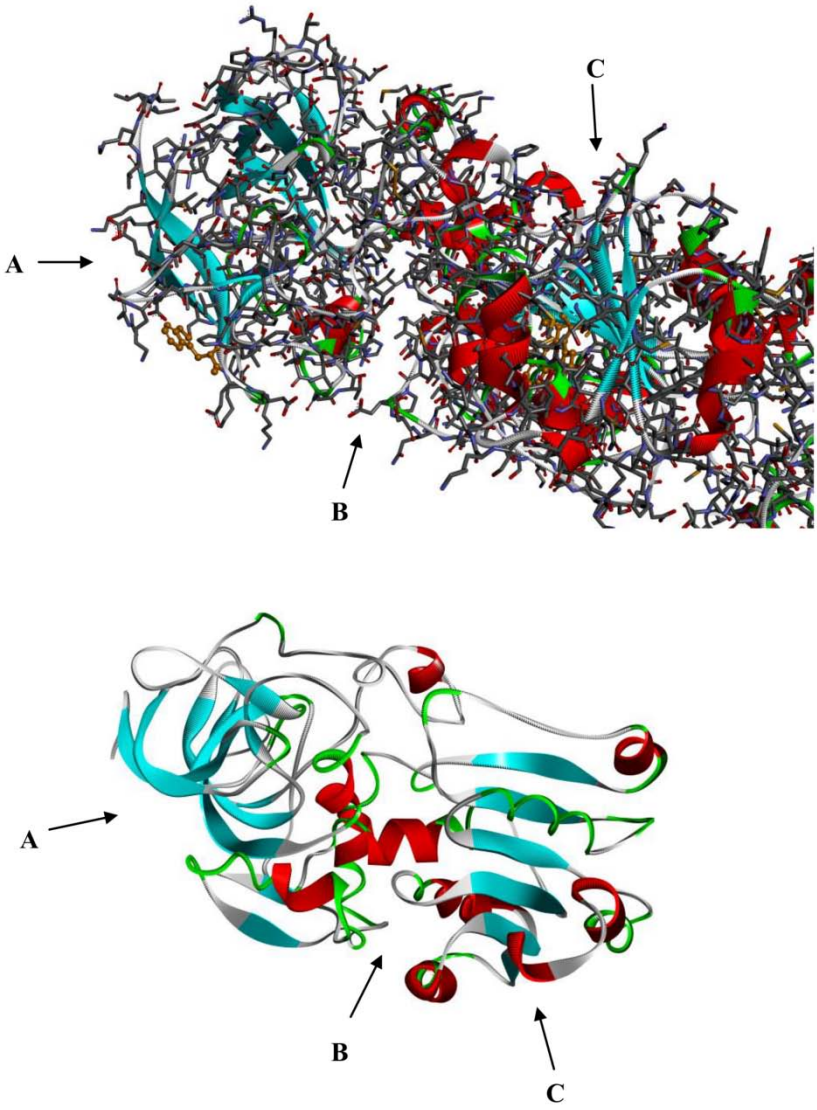

Figure S3. Subdomains of LADH. Upper diagram: spatial structure of LADH combined with its secondary structure; lower diagram: secondary structure of single LADH subunit. **A** – catalytic subdomain; **B** – cleft between catalytic and coenzyme binding subdomains; **C** – coenzyme binding subdomain.