INTERACTION OF POLYETHYLENEOXYDE WITH BIO-MATERIAL, Jindrich HASEK, *Institute of Macromolecular Chemistry, AV CR, Heyrovskeho nam.2, 162 06 Praha 6, Czech Republic*. E-mail: hasek@imc.cas.cz

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X-ray structure analysis is very effective tool for determination of interaction between polymers and biological material. Polymers with molecular weight up to several tenth thousands can be incorporated into large cavities in the protein crystals. Segments of polymer with specific adhesion to the protein are fixed relative to the crystal lattice and can be determined with high accuracy with standard protein crystallography. Polyethyleneoxyde (POE) competes successfully for adhesion at protein surface with other molecules because due to its flexibility it can form a high number efficient interactions from multiple coordination bonds and hydrogen bridges to hydrophobic interactions. Total 284 observed configurations found in the PDB was classified into 20 interaction types summarized in this paper. The length of the adhering polymer segments observed in the protein crystals varies from two to twenty monomer units. Short polymer segments can be seen linear namely when their interactions to protein clefts are formed by polar residues only. More stable conformation and longer polymer chains are observed when the end of polymer chain is anchored in highly charged sites (Arg, Lys, His) near the surface of protein. In this case, the POE chain embedding the cation (ends of lysine or arginine) forms a number of other energetically convenient bonds. In some cases, POE winds around cations (Lys, Arg or cations from solution) to form cycles of 5-7 monomers with multiple coordination to the central ion. The examples include an embeding of the cation complexed POE inside a partly hydrophobic area of protein. POE molecule is anchored between His and Lys, winds arounds the NH_3^+ ion of Lys and leaves the protein with the seventh monomer already dissolved in solvent. Interesting is an embeding of the copolymer of poly(ethyleneoxyde) and poly(ethylene) (POE-PE) inside the fully hydrophobic area of protein forming thus a deep cleft between adjacent proteins.

Conclusion. Poly(ethyleneoxyde) is very competitive and universal ligand for proteins. It forms direct coordination contacts to the charged lysines, arginines and histidines, hydrogen bonds to polar and charged side chains and hydrogen bonds to the main chain NH groups. It can form 5-7 member rings by embedding the cation from buffer. The hydrophobic strands at the outer side of the ring envelope have high propensity to bind to the protein hydrophobic surface. Copolymerization of PEO with polyethylene can result in its binding to the larger hydrophobic protein surface.