MS1-P13 **Protein crystallization in gels: the better choice to grow crystals for structural determination.** A.E.S. Van Driessche, J.A. Gavira, L.A. González-Ramírez, E. Melero-García, F. Otálora, J.M. García-Ruiz. *Laboratorio de Estudios Cristalográficos, IACT, CSIC - U.Granada, Spain.*
E-mail: jmgruiz@ugr.es

In this work the quality of crystals of several model and non-model proteins, grown under convection-free conditions in gels on ground and from solution in microgravity, are compared. To ensure the validity of the comparison critical parameters such as the equivalence of diffusive mass-transport conditions, the use of common protein and reactants batches, and the thermal history and duration of the experiment were carefully controlled. The obtained diffraction data show that, from a structural resolution point of view, no obvious differences exist between crystals grown under reduced convective flow in space and crystals grown in convection free conditions on ground. Our data also confirm that if a protein does not produce suitable crystals on earth it will surely not do so just by sending it to space for crystallization in microgravity. Based on our, and previous results, and taking into account the large economical and logistic costs associated to space-based experiments, and the constant technological advances on X-ray sources for diffraction experiments, we conclude that crystallization in gels on Earth should be the first method of choice to improve the quality of protein crystals for structural determination.

Keywords: gels; microgravity; protein crystal quality

MS1-P14 **Insulin Analogues for Insulin Receptor Studies and Medical Applications.** Christopher J. Watson[a] Jiří Jiráček[b], Lenka Žáková[b], Emília Antolíková[b], , Johan P. Turkenburg[a],Guy G. Dodson[a], and Andrzej M. Brzozowski[a], *[a]York Structural Biology Laboratory, Department of Chemistry, The University of York, Heslington, York, YO10 5YW, United Kingdom and [b]Institute of Organic Chemistry and Biochemistry, Academy of Sciences of the Czech Republic, v.v.i., Flemingovo nám. 2, 166 10 Prague 6, Czech Republic*
E-mail: cjw502@york.ac.uk

Diabetes affects 194 million people worldwide and costs an estimated Ł9bn in the UK each year. Diabetes occurs in two distinctive types I and II. Type I is the result of insufficient insulin being produced by the beta cells in the pancreas, whilst type II is characterised by the hosts' cells being immune to the effects of insulin completely. The discovery of insulin started in 1869 when Paul Langerhans identified tissue clumps in the pancreas. Frederick Banting in 1920 discovered the insulin molecule, which lead to Frederick Sanger determining the primary sequence of bovine insulin in 1951. Dorothy Hodgkin brought about the most recent discovery of insulin, its crystal structure in 1969. The structure of the insulin molecule and its receptor binding though has yet to be determined. We have created various semi-synthetic insulin analogues [1] that are designed to expose the binding core of the insulin molecule. It has been shown that in some cases binding affinity towards its receptor can be as high as 400% of that of wild type insulin. The crystal structure of these analogues possesses a â-turn that has not been previously seen [2], that exposes the binding epitope of the insulin molecule to the insulin receptor, making binding between the two tighter.

[1] Žáková, L. et al (2007) *J Pept Sci* **13**, 334-341
[2] Jirácek, J. et al (2010) *PNAS* **107**, 1966-1970

Keywords: β-turn; diabetes; peptide bond isomerisation