s6.m20.o4 **Germanium Zeotypes**. M. Angeles Monge, E. Gutiérrez Puebla, N. Snejko, M. E. Medina and M. Iglesias, *Instituto de Ciencia de Materiales de Madrid, CSIC Cantoblanco. E-28049 Madrid (Spain). e-mail:amonge@icmm.csic.es*

Keywords: Germanium; Zeotypes; Structure,; Microporous Materials

In the earlier 1990s, two interesting germanates [1] were reported, but it was not until the end of the decade that the interest on the microporous germanium zeotypes appeared with great force [2,3], so that in the six later years about thirty paper on the purely Ge/O system have been reported. As it is known, in these zeotypes the secondary building unit (SBU) can be formed by Ge atom in tetrahedral, trigonal bypiramidal and octhahedral coordination, these plolyhedra being connected by sharing vertex, edges or faces. Anions (oxygen atoms or hydroxyl groups) being also frequently in 1-, 2-, or 3-coordination. This variability in coordinative modes allows for the generation of many different SBUs, different kinds of connection among them, and thus a plethora of structural possibilities. These compounds are obtained hydrothermally, by controlling a good number of variables, especially to obtain single crystals. Mild conditions are used (100 – 200°C, 1-20 atmospheres in the reactors of 40-120 ml volume), the time of reactions being varied from a few hours up to several weeks, depending on the material to obtain. Starting from germanium dioxide or germanium alkoxides in water or non-water media, different templates are chosen specially for each case (organic amines or transition metal complexes, basically). Results of synthesie, structures and catalytic properties of several new microporous germanium zeotypes obtained in our laboratory will be presented, as well as some structural relations established among them

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s6.m20.o5 **Designed Ankyrin Repeat Protein Libraries: A Valuable new Tool for the Crystallization of Biological Macromolecules.** Markus G. Grütter, Andreas Kohl, H. Kaspar Binz, Patrick Amstutz, Michael T. Stumpp, Christophe Briand, Guido Capitani, Patrick Forrer and Andreas Plückthun, *Department of Biochemistry, University of Zurich, Winterthurerstrasse 190, CH-8057 Zurich Switzerland, Gruetter@bioc.unizh.ch, phone: +41-1-635-5581, fax: +41-1-635-6834*

Keywords: Co-Crystallization; Protein-Protein Complex; Protein Design

Repeat proteins are ubiquitous protein-protein interaction molecules fundamental to many biological processes [1]. Their modular architecture is presumably the key to their evolutionary success. This architecture not only allows, in principle, to evolve their binding specificities by point mutations but also by insertion, deletion or shuffling of repeats. This evolutionary strategy might enable repeat proteins to acquire new functions by adjusting their surface without jeopardizing their overall topology.

We applied this concept *in vitro*, and designed ankyrin repeat proteins (ARP). By consensus sequence and structure analyses of ARPs, we derived a repeat module of 33 amino acids with fixed framework residues and randomized surface residues suitable for target binding. The random assembly of such modules yields combinatorial libraries of naive ARP's of varying length and diversities larger than 1010. Unselected library members are very well expressed, soluble, thermodynamically stable and show the correct fold [2].

By using ribosome display [3], an *in vitro* selection technique, we selected specific binders against a number of different protein targets with affinities in the low nanomolar range. This opens the possibility to crystallize a target protein in complex with a variety of ARPs and enhances the chances of obtaining structures of target proteins that are difficult to crystallize alone such as kinases and membrane proteins.

We have applied this technology to a variety of different proteins such as proteases, kinases and membrane proteins. The methodology and the structures of two unselected ARP's will be presented as well as the structures of two ARP-target protein complexes (ARP-maltose binding protein complex, ARP-kinase complex) proving the usefulness of selected ARP's in structural biology. The technology opens a new avenue in macromolecular crystallization and is an attractive alternative to antibodies in the crystallization of membrane proteins.

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