

The background features a light-colored mosaic pattern of irregular shapes. On the right side, there is a vertical arrangement of colorful spheres (red, green, yellow, blue) with a cracked, mosaic-like texture. Some of these spheres are connected by thin lines, resembling a molecular structure or a chain of beads.

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**BOOK OF
ABSTRACTS**



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molecules^[2]; iv) the activation of the human TLR4/MD-2 complex by natural under-acylated LPS^[3]. We have applied a combination of different computational techniques, such as MD simulations, NMA, docking calculations, virtual screening, and membrane simulations to address some of these questions. Other PRRs have also been studied (lectins) by means of computational techniques to address the design of glycomimetics with enhanced selectivity.

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P05-3

Design of novel glycopeptide-based cancer vaccines

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Cancer is currently one of the world's most serious public health problems. Significant efforts are being made to develop new strategies that can eradicate tumors selectively without detrimental effects to healthy cells. One promising approach is focused on the design of vaccines^[1] that contain partially glycosylated mucins in their formulation. Although some of these vaccines are in clinical trials, a lack of knowledge about the molecular basis that governs the antigen presentation, and the interactions between antigens and the elicited antibodies has limited their success thus far.

We are developing a multidisciplinary approach that combines synthesis, X-ray diffraction, nuclear magnetic resonance and molecular modeling to identify these features^[2,3] (Figure). Our results provide valuable hints for the design of efficacious cancer vaccines.

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P05-4

Using resurrected ancestral proviral proteins to engineer virus resistance

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We have recently reported that resurrected ancestral proviral factors prevent phage T7 propagation in *E. coli* (Delgado *et al.*, 2017, *Cell Reports* 19, 1247-1256). Here, we describe preliminary experiments addressed at using this system to explore repeatability of molecular evolution.

P05-5

Connexin43 is a pivotal regulator in controlling the chondrocyte phenotype in osteoarthritis

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Osteoarthritis (OA) is the most common degenerative rheumatic disease, being its etiology still poorly understood. OA is primarily characterized by articular cartilage degradation and joint degeneration. In early stages, osteoarthritic chondrocytes (OACs) undergo phenotypic changes increasing cell proliferation, cluster formation and production of matrix-remodelling enzymes. OACs contain high levels of Cx43, that together with increased gap junction intercellular communication (GJIC) and changes in Cx43 interaction network have been associated with development and progression of OA. The aim of this study was investigating the role of Cx43 in the dedifferentiation processes that suffer OACs. Human chondrocytes T/C-28a2 cell line was transfected with a plasmid containing the human Cx43 sequence. Cx43 overexpression and cellular localization was confirmed by western blot, qPCR, flow cytometry and immunofluorescence. Cx43 upregulation led to a significant increase in the expression of COX-2, IL-1 and MMP-3. Collagen type II levels were significantly diminished in Cx43 transfected OACs in comparison with control cells. Cell proliferation and GJIC increased significantly when Cx43 was upregulated. Flow cytometry analysis revealed an increase in the levels of stemness-like cell surface markers related with an immature state when Cx43 is overexpressed. Our results suggest that Cx43 upregulation is involved in the phenotypic changes and dedifferentiation processes detected in OACs responsible for degradation of cartilage and its predisposition to develop OA. In the light of these results, it is important to take into account Cx43 levels and function in the scope of designing more effective targeted therapies for prevention and treatment of OA.

P06. Biochemistry of Nutrition

P06-1

Mature adipose tissue contribution to disposal of excess glucose through its conversion to lactate, glycerol, alanine and pyruvate

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Adipose tissue (AT) as a disperse organ has a considerable size, which is considered to be rather inactive due to the large size of fat reserves. However, despite its the small "live" mass, its potential activity is very high, and its metabolic diversity (largely unexplored) is even higher. The tissue is able to actively participate in the synthesis of arginine-citrulline, oxidize branched-chain amino acids, produce alanine and glutamine and contains a complete functional urea cycle.