

MBCD. Significant large-scale self-clustering of IgE-FcεRI occurs upon cross-linking with multivalent antigen, and we describe analytical methods to correct for multiple gold binding and quantify clustering in these stimulated cells. Our correlation function particle distribution approach is likely to have wide applicability in nanoscale image analysis.

#### 1490-Pos

##### Design of a Biologically Relevant Supported Bilayer Platform for the Study of Membrane Active Peptides

Janice Lin, John Szymanski, Peter C. Seanson, Kalina Hristova.

The Johns Hopkins University, Baltimore, MD, USA.

Membrane active peptides represent a class of soluble proteins that interact and disrupt the plasma membrane. Examples of these include antimicrobial peptides, cancer therapeutics, and cell-penetrating peptides. These peptides are amphiphilic and, in a concentration dependent manner, can self assemble to destabilize the lipid bilayer. These peptides are rich in positively charged lysine and arginine residues and thus have a strong preference for negatively charged bilayers. In order to study the insertion mechanism and kinetics of these peptides, we have designed a negatively charged, supported bilayer platform on silicon. The negative charge serves to electrostatically drive peptides to bind to the lipid bilayer interface. Furthermore, this platform is electrically addressable through electrochemical impedance spectroscopy, which yields bilayer resistance, thickness, and structural heterogeneity data. This platform consists of an asymmetrical bilayer with 10 mol% negatively charged POPS, cholesterol, and POPC in the upper leaflet and DPhPC lipids in the lower leaflet, all supported by a PEG cushion on a silicon wafer. Resistances up to  $2 \times 10^9 \Omega \mu\text{m}^2$  and capacitances of  $0.8 \mu\text{F cm}^{-2}$  have been measured for the platform. The high resistance allows for high accuracy in the detection of the activity of membrane active peptides of interest.

#### 1491-Pos

##### Staphylococcus aureus Enriched in Ordered Lipids Present Resistance Towards the Antibacterial Agent sPLA<sub>2</sub>-IIA: An Unusual Mechanism to Survive

Hector Jackson Ocampo Ariza, Johanna Paola, Chavez Escobar,

Jorge L. Romero Becerra, Martha J. Vives, Chad Leidy.

Universidad de los Andes, Bogota, Colombia.

Bacterial membranes present solid-ordered/liquid-disordered (*so/ld*) cooperative melting event close to physiological temperature. The cellular advantage of this thermotropic melting event is yet to be determined. We show that this thermal behavior provides resistance towards a membrane active antibacterial agent.

Phospholipase A<sub>2</sub> type IIA (sPLA<sub>2</sub>-IIA) is a hydrolytic enzyme which presents antibacterial properties towards Gram positive bacteria. The enzyme has higher activity in *ld* phase compared to *so* phase in anionic membranes. We show that the lipid phase behavior of Staphylococcus aureus (*S.aureus*) membranes as measured by FTIR modulates sPLA<sub>2</sub>-IIA by inducing a sharp drop in activity below the melting temperature of the membrane (centered at 15.3°C).

The effects of sPLA<sub>2</sub>-IIA treatment on cell viability are also investigated. While above the main melting event viability drops to 20% of the initial CFU after treatment, below the main melting event cell viability only drops to 60% under the same treatment. This strongly suggests that cells in the solid-ordered phase are better adapted to survive the enzymatic insult.

These results led us to explore if a subpopulation of *S.aureus* enriched in ordered lipids can be selected after repeated treatment with sPLA<sub>2</sub>-IIA at 37°C. After selecting for resistance at 37°C we measured growth curves, membrane order, and cell viability as a function of treatment temperature. The results suggest that at 37°C there is a bacterial subpopulation with increased membrane rigidity that insures survival of the colony to an insult by sPLA<sub>2</sub>-IIA. This subpopulation also presents a longer latency period which can be explained by the increased presence in ordered lipids, which are known to inhibit cell division. Even if the growth conditions are not optimal, the presence of this subpopulation ensures survival from the antibacterial insult.

#### 1492-Pos

##### Lifetime of Hyaluronan Containing Tethers Obeys a Generalized Bell Model

Marius C. Staiculescu<sup>1</sup>, Phillip Stein<sup>1</sup>, Mingzhai Sun<sup>2</sup>, Imre Derenyi<sup>3</sup>, Gabor Forgacs<sup>1</sup>.

<sup>1</sup>University of Missouri Columbia, Columbia, MO, USA, <sup>2</sup>Lewis-Sigler Institute for Integrative Genomics, Princeton, Princeton, NJ, USA,

<sup>3</sup>Department of Biological Physics, Eotvos Roland University, Budapest, Hungary.

Hyaluronan (HA), an unbranched non-sulfated glycosaminoglycan, is an important component of the extracellular and pericellular matrix of various cell types. It has key roles in many biological processes such as wound healing, angiogenesis, embryonic development, tumor progression and invasion. HA is especially abundant around tumor cells in malignant gliomas where it is associated with high invasivity and a poor prognosis. However it is unknown how malignancy is correlated with the biomechanical properties of the cellular glycocalyx and the lifetime of the chemical bonds formed by HA with its ligands. Here we introduce a method applicable to the study of biophysical properties of cellular glycocalyx through tether extraction. Specifically, we reveal the extent of the cellular ECM of a glioma cell line (HB), we demonstrate that tethers formed through non specific binding can be pulled from the cellular glycocalyx and by using a magnetic tweezers we determine the lifetime of these tethers. To calculate lifetime we simultaneously extract multiple tethers under constant force using paramagnetic beads as force transducer. We demonstrate that the stochastic lifetimes of these tethers and thus the bonds they are associated with are exponentially distributed and can be parametrized by a generalized Bell model. We determine the maximum likelihood estimates of the relevant parameters, such as force-free dissociation constant and reactive compliance. We test the consistency of our approach using computer simulations. This method could be employed in the development of therapies which interfere with HA organization and HA-receptor binding.

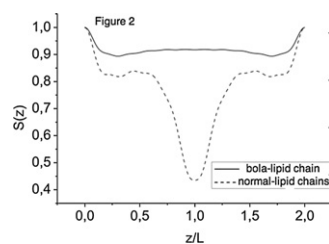
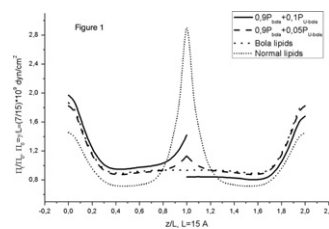
#### 1493-Pos

##### Analytical Derivation of Thermodynamic Properties of Bolalipid Membrane

Sergei I. Mukhin, Boris B. Kheyfets.

Moscow Institute for Steel and Alloys, Moscow, Russian Federation.

A model of bilayer lipid membrane with bola-lipids is studied. The bola-lipid is modeled by linking tails of the hydrophobic chains in the opposite monolayers within bilayer. We use for analytical derivations a flexible string model of hydrocarbon chain (Mukhin, Baoukina 2005) with modified condition at the linked chains ends. Calculated lateral pressure profiles are asymmetrical due to different concentrations of the U-shaped bolalipids in the opposite monolayers, Fig. 1, and orientational order parameters for linked and regular chains differ significantly at the monolayers interface, Fig. 2.



#### 1494-Pos

##### Highly Stable Poly(Lipid) Bilayers for Long-Term Ion Channel Recordings

Benjamin A. Heitz, Robert P. Cordero, S. Scott Saavedra,

Craig A. Aspinwall.

University of Arizona, Tucson, AZ, USA.

Long-term ion channel (IC) screening using cell-based assays is currently limited by throughput and cell to cell variability. ICs isolated and reconstituted into suspended lipid membranes offer an isolated view into IC structure and function, but IC recordings are limited by the short lifetime of the bilayer. Polymerizable lipids (poly(lipids)) offers one potential strategy for long-term