Drawing inspiration from ionic selectivity of biological channels, we have explored the nature of the transport of ions through single nanopores of diameters comparable to the transported ions. As a test system, we used single nanopores and ions of room temperature ionic liquids (RTILs). RTILs are liquids composed entirely of charged species and contain no solvent. Their constituent ions can be very bulky with diameters ranging from tenths of an angstrom to greater than 10 Å. In recent years, RTILs have garnered a wealth of attention, especially in regard to their physical and chemical properties; however, most, if not all, studies thus far have focused on bulk characteristics, leaving their properties on the nanoscale ripe for investigation.

Our study focused on a select few RTILs, and on how the size of their cations and anions affects the conductivity of the liquid through our pores. Single nanopores of controlled geometry and of various diameters, ranging from a few nanometers to a few hundred nanometers, were prepared in polyethylene terephthalate foils. High voltages (-5V to +5V) were applied across the membrane and the resulting ionic currents were recorded, allowing us to calculate the conductivity of the RTILs. Conductivity of the liquids in sub-10 nm pores was found several times smaller compared to the bulk values. Our results indicate that steric effects outweigh the contributions of electrostatic interactions of the ions with the pore walls in determining the conductivity of an RTIL in nanopores. While our experiments were motivated by biological channels whose openings are comparable in size to that of the ions in the system, they have allowed us to examine physical properties, primarily the conductivity, of certain RTILs. These studies represent important steps in the characterization of RTILs on the nanoscale.

3333-Pos Board B380

Fluidic Diodes in Nano- and Microscale Pores to Detect Drug Aggregation Erik C. Yusko, Ran An, Michael Mayer.

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We present a novel method of producing ion current rectification (ICR) in nano- and micro- scale pores that does not require electrical double layer overlap within a pore. ICR in nanopores has typically been constrained in two ways: i) at least one dimension or component of the channel must be on the order of the Debye screening length and ii) charge asymmetry must be induced within the pore. Asymmetric channel geometries, modified surface charges, and asymmetric bulk ion concentrations are commonly applied to produce the necessary charge asymmetry. In the method presented here, ICR is dependent on electroosmotic flow (EOF) to position two solutions of different conductance within a pore. Substrates containing pores with diameters of 10 nm, 30 nm, and 500 nm were used to separate the two different solutions. We have achieved rectification factors ranging from 2-15, as a function of solution properties, in conical and cylindrical pores with diameters much larger than the Debye screening length. Thus, ICR can be achieved at higher ionic strengths (here up to 300 mM), in pores with large diameters (here up to 3 μm), and in pores without patterned surface charges. We also present a phenomenon unique to the two-solution system that we introduce here. Dissolving a drug in one solution, which contains 75%, DMSO, and then moving the molecules through the pore into a purely aqueous solution leads to detectable aggregation of the drug in the pore. The aggregate typically proceeds to the point of blocking the pore (>85% reduction in current) and subsequently ejects from the pore. We have investigated the aggregation and subsequent clearance of the aggregate from the pore and propose a mechanism for the cyclic pro-

3334-Pos Board B381

Nanopipette surface modification for biosensing

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We have developed a sensitive nanopipette assay for the detection and functional analysis of proteins in a microbial sample. This unique, label-free biosensor is inexpensive, easy to fabricate and versatile. The nanopipette size, geometry, and surface chemistry for attaching a biomarker, antibody or protein probe were previously optimized using both experiments and modeling to provide detectable signals in real time, in a very small reaction volume (attoliters). In this phase, the goal was to modify the surface chemistry procedure so that only a restricted area of the nanopipette tip was functionalized for probe attachment. Preliminary experiments demonstrate the sensitivity and selectivity of the nanopipette with specific protein targets of yeast cells and fungi. We have further developed biophysical and kinetic models that help us to interpret and explain phenomena underlying the current signals obtained from the nanopipette system. These models characterize the physical, chemical, electrical and thermodynamic forces responsible for molecular interactions (ion-surface and probe-target) at the nanopipette tip. The models provide several feedback parameters related to actual experimental conditions, which are used for further improvements of the detection scheme. In the next phase, the functionalized nanopipette will be applied to the study of living cells as a diagnostic tool to detect protein expression.

3335-Pos Board B382

Detection Of Nerve Agent Hydrolytes In An Engineered Nanopore

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We report a stochastic nanopore sensing method for the detection of organophosphorus nerve agent hydrolysis products. By employing an engineered α -hemolysin single pore embedded in a planar lipid bilayer as the stochastic sensing element and β -cyclodextrin as a host molecule, trace amounts of soman and cyclosarin hydrolytes could be detected, with detection limits of 53 nM and 102 nM, respectively. Importantly, sarin, tabun, and VX hydrolysis products, as well as other common pesticides, do not interfere with detection of the analytes. The method offers the potential as a rapid and sensitive sensing technique for use in on-site analysis of nerve agents in environmental monitoring applications at the single-molecule level.

3336-Pos Board B383

Transport Of Antibiotics Through OmpF Mutants Studied By Proteoliposome Swelling And Single-channel Reconstitution Techniques

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Mathias Winterhalter², Sergey M. Bezrukov¹

¹NICHD, NIH, Bethesda, MD, USA, ²Jacobs University, Bremen, Germany. We use site directed mutagenesis to study molecular mechanisms of beta-lactam antibiotic transport facilitated by the bacterial porin OmpF. First, we measure interaction of antibiotics with OmpF mutants, D113A, R82A, R42A, and E117A, reconstituted as single channels in bilayer lipid membranes (BLM). Second, we estimate antibiotic diffusion rates through these channels by measuring the swelling rates of proteoliposomes whose membranes contain wild type OmpF or these mutants.

Just as a wild type, R82A and R42A mutants studied by the BLM technique interact with OmpF showing clear time-resolved blockages of the current through their trimeric pores. D113A and E117A mutants demonstrate no time-resolved blockages but show some high-frequency excess noise. Two most probable explanations for the origin of this high-frequency noise component are that it is generated by: (i) fast irresolvable antibiotics transport events or (ii) events of antibiotic binding to the channel somewhere close to the opening of the channel without subsequent antibiotic translocation. In order to distinguish between these two scenarios we compare antibiotic translocation rates through OmpF mutants using reconstituted proteoliposomes. With this approach we are able to rule out the "fast transport event" scenario. D113Aand E117A-containing liposomes show significantly smaller swelling rates compared with the liposomes containing wild type and R82A and R42A mutants. These results are in accord with our theoretical rationalization of the constructive role of solute-channel interactions in channel-facilitated membrane transport.

3337-Pos Board B384

Mechanisms Of Selective Transport Through Nano-channels: Theory Vs. Experiment

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Functioning of living cells requires selective molecular transport, which is provided by transport channels that are able to selectively transport certain molecular species while filtering others, even similar ones. Such channels can selectively transport their specific molecules in the presence of vast amounts of non-specific competition. In many biological channels, efficient and selective transport occurs without direct input of metabolic energy and without transitions from an 'open' to a 'closed' state during the transport event. Examples include selective permeability of porins and transport through the nuclear pore complex. Mechanisms of selectivity of such channels have inspired design of artificial selective nano-channels, which mimic the selective biological channels and are built upon the same principles(e.g [3]).

Precise mechanisms of selective transport through such nano-channels are still unknown. I present a theoretical model to explain the of selectivity of transport through nano-channels, which contains only two essential ingredients: i) transient trapping of the cargoes inside the channel (e.g. due to binding inside the channel) ii) competition between the transported molecules for the limited space inside the channel [1,2]. The theory provides a mechanism for selectivity based on the differences in the kinetics of transport through the channel between different molecules. The theory explains how the specific molecules are able to filter out the non-specific competitors - and proposes a mechanism for sharp molecular discrimination. The theoretical predictions [1,2] account for previous experimental results [3] and have been verified in ongoing experiments.

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- [2] A. Zilman, Effects of inter-particle interactions on selective transport in narrow channels, Biophys J (2008), to appear.
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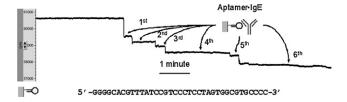
3338-Pos Board B385

Aptamer-Encoded Nanopore For Single-Molecule Detection In Sensing Of Biomedical And Bioterrorist Agents

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Various solid nanopores have been constructed with the advantage of changeable pore size over the protein nanopore. In principle, these solid nanopores, once functionalized in the lumen, should be able to capture individual target molecules. One should be able to observe this process from the binding-produced discrete current blocks. However, direct observation of single molecule binding to solid nanopores has been rarely reported. Here we for the first time report the aptamer encoded nanopore for single-molecule biosensing. Aptamers are short DNA or RNA sequences that can fold into specific conformations to bind their target proteins with high affinity and high selectivity. Comparing with antibodies, aptamers are durable in severe environment such as high temperature and extreme pH values. In particular, aptamers are advantageous in nanopore applications due to their smaller volume than their target proteins, allowing target-generated current block to be visualized. In this report, we demonstrate an aptamer-encoded nanopore for single molecule detection of IgE and bioterrorist agent ricin.



3339-Pos Board B386

Label-Free Electrical Biosensing Using Functionalized Nanopipettes Senkei Umehara^{1,2}, Paolo Actis¹, Adam R. Rogers¹, Ronald W. Davis², Miloslav Karhanek¹, Nader Pourmand^{1,2}.

¹University of California, Santa Cruz, Santa Cruz, CA, USA, ²Stanford Genome Technology Center, Stanford University, Palo Alto, CA, USA. Nanopipettes are recognized as a versatile tool for engineering and life science studies. Among a variety of applications of nanopipette technology, we are par-

studies. Annoting a variety of applications of nanopipette technology, we are particularly interested in developing a fully electrical sensing platform using nanopipette probes. The dimensions of our nanopipette, comparable to the size of many proteins and macromolecules, make it suitable for sensing biomolecules in general. Molecular interaction on the nanopipette tip are transduced into electrical signals based on changes in size, electrical charges and structures of the nanoscopic pore region.

Here we report the development of nanopipettes that specifically detect their non-labeled target molecules. To reliably identify the interacting molecules, the nanopipettes were individually functionalized by modifying the surface with antibodies. Then two different nanopipettes, one as a probe nanopipette with attached molecules specific to the target molecules (i.e. antigens) and the other as a control nanopipette, were immersed in the same bath solution to perform voltammetric measurement. The addition of target molecules tended to cause a lasting reduction in current flowing through the probe nanopipette, which was large enough to distinguish the probe nanopipette from the control. These results indicate that the target molecules were captured by antibodies specific to them, present only on the probe nanopipette surface, and that this process partially narrowed the pore. The tested target molecules included cancer biomarker proteins, therefore this system could be readily optimized for diagnostic use.

3340-Pos Board B387

Escape Dynamics of DNA from a Nanopore under the Influence of an AC Bias

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Monitoring the escape of ssDNA from a protein nanopore provides new insight into the dynamics of DNA translocation and a direct means of measuring prog-

ress of the escape. New instrumentation has been developed that allows for simultaneous application of an AC and DC bias across a protein nanopore. Initial measurements with the system have focused on the capture and release of ssDNA tails attached to DNA hairpins. Polynucleotide tails attached to 24 nucleotide DNA hairpins are threaded into the beta-barrel of an alpha-hemolysin channel under the influence of a strong DC driving voltage. After the capture of the hairpin, the DC voltage is turned off and the subsequent escape of the hairpin is directly monitored via an AC bias. Escape times were measured as a function of AC amplitude (20 to 250 mV), AC frequency (60-200 kHz), DC drive voltage (0 to 100 mV), and temperature (-10°C to 20°C). The applied AC voltage has been shown to play a significant role in the DNA/nanopore interaction. The results are well described by a one-dimensional diffusion model across an asymmetric, periodic potential.

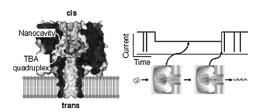
3341-Pos Board B388

Ion-Regulated Assembling Of The G-Quadruplex Aptamer - A Nanopore Single-Molecule Study

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Guanine-rich DNA and RNA can form high order G-quadruplexes through guanine-guanine base-pairs. G-quadruplexes in genome actively participate in gene regulation; and synthetic G-quadruplexes in vitro are potent pharmaceuticals, biosensors and bricks of nanostructures. Here we report on the development of a nanopore encapsulating single-molecule method for exploring how cations regulate the folding and unfolding of the G-quadruplex formed by the thrombin-binding aptamer (GGTTGGTGTGGTTGG). The signature blocks in the nanopore revealed that the G-quadruplex formation is cation-selective. The selectivity sequence is $K^+ > NH_4^+ \sim Ba^{2+} > Cs^+ \sim Na^+ > Li^+$, and G-quadruplex was not detected in Mg²⁺ and Ca²⁺. Ba²⁺ can form a longlived G-quadruplex with TBA, but the capability is affected by the cation-DNA interaction. This cation-selectivity is correlated with the G-quadruplex volume, which varies with cation species. Although the Na⁺- and Li⁺-quadruplexes feature similar equilibrium properties, they undergo radically different pathways. The Na⁺-quadruplex folds and unfolds most rapidly, while the Li⁺-quadruplex performs both reactions at the slowest rates. This research is beneficial for constructing fine-tuned G-quadruplex-based biosensors. The methodology in this work is also useful for investigating protein-G-quadruplex interactions.



3342-Pos Board B389

Folded and Unfolded Single Proteins Analyzed by Their Solid State Nanopore Translocation Dynamics

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The translocation of biological polymers through individual nanometer-scale pores is vital to cellular function and has great potential for technological applications in protein or nucleic acid measurements and identification. Research into this area has been focussed on characterizing the physics of translocation through voltage-biased nanopores and exploiting it to identify or sequence biological polymers. Here we show that the DNA-calibrated translocation signals of \(\mathcal{B} - lactoglobulin \) and histidine-containing phosphocarrier protein match

