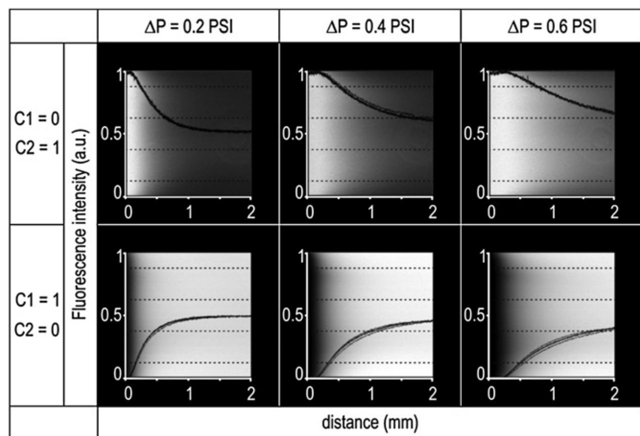
effects near walls <25% of area). Due to the binary branching of the inlets, the perfused area can be arbitrarily wide (here, 2 mm). This enables analyzing responses of large cell populations in parallel and acquiring rich statistics on single-cell variability.




**255-Pos Board B134**
**Detection and Identification of Virus Particles on a Microfluidic Platform**
**Louis Strong**, Clark Edson, Daniel B. Hall, Senerath Palamakumbura, Gyula Varadi.
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We have developed a nanoparticle-based assay to capture and detect targeted virus particles on a microfluidic platform. Antibody-decorated magnetic nanoparticles were used to capture virions and detection was afforded by measuring the change in magnetic birefringence relaxation rates. Vesicular Stomatitis Virus (VSV), a bullet-shaped, negative-strand RNA virus, is used as a model for air, water or blood-borne pathogenic viruses. Antibodies against the single envelope glycoprotein of either the Indiana or New Jersey strains of VSV were conjugated to 30nm superparamagnetic nanoparticles to generate the capturing reagent. The size distribution of the antibody-nanoparticle conjugates was determined using a CONTIN analysis of dynamic light scattering (DLS) data. Our results were confirmed by TEM analysis. Antibody-decorated nanoparticles were combined with one of the VSV strains and subjected to Ismagilov mixing, utilizing two immiscible phases in micro-channels to increase the speed of capture. Virus binding was determined by changes in hydrodynamic volume of the virus-nanoparticle complexes as measured by their birefringence relaxation rate under stopped flow conditions. In addition, the dynamics of particle complex formation and aggregation was studied by DLS at different scattering angles. We compared the results of these two methods for measuring time-dependent increases in the size of the nanoparticle/virus complexes. The birefringence relaxation method is more adaptable to field and other applications than DLS since it is relatively insensitive to particle concentration or to the presence of dust and sample impurities. Our approach is superior to existing techniques such as qPCR or ELISA assays due to the speed of detection and insensitivity to environmental contaminants. We are looking into the suitability of this assay for point-of-care applications.
This work was supported in part by NIH grant R44 ES012515.

**256-Pos Board B135**
**Phenotypic and Genotypic Heterogeneity of Cyanobacterial Populations in Hot Spring Microbial Mats Revealed by Microfluidic Single-Cell Analysis**
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The microbial mats found at Octopus Spring in Yellowstone National Park exhibit highly organized community structures. Thermophilic unicellular cyanobacteria (Synechococcus spp.), found in the 1-mm thick top layer of these hot spring mats, act as the primary producers in the microbial communities. The cyanobacterial population is an excellent model system for studying how environmental factors affect the structure of a microbial community because the system is relatively simple and formed under a well-defined set of environmental gradients such as temperature, oxygen and light levels. To obtain a detailed description of both phenotypic and genotypic structures of the population, we extended our microfluidic approach that has been previously developed for single-cell protein analysis of a similar type of cells [Huang et al., Science, 315, 81-84 (2007)]. First, a protein analysis chip was developed for simultaneous analysis of multiple single-cell lysates for higher throughput. We demonstrate that 16 cells can be analyzed individually during each round of analytical procedures to obtain phycobiliprotein distributions at the single-cell level. Second, a genetic analysis chip was designed to amplify genomic DNA from individual cyanobacteria cells via multiple displacement amplification. The presence of a selected set of genes was compared among populations under different environmental conditions. This type of single-cell genomic data is useful for elucidating the role of cyanobacterial species deduced from the metagenomic analysis of the microbial mat samples.

**257-Pos Board B136**
**Adsorption and Stability of Streptavidin on Cluster-Assembled Nanostructured TiO*x* Films**
**Pasquale Emanuele Scopelliti**[1], Luca Giorgetti[2], Gero Bongiorno[3], Alessandro Podestá[3], Giuseppe Berlanda[3], Roberta Carbone[4], Paolo Milani[3].
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The study of the adsorption of proteins on nanostructured surfaces is of fundamental importance to understand and control cell-surface interactions and, notably, cell adhesion and proliferation; it can also play a strategic role in the design and fabrication of nanostructured devices for postgenomic and proteomic applications. We have recently demonstrated that cluster-assembled nanostructured TiO*x* films produced by supersonic cluster beam deposition [1] possess excellent biocompatibility and that these films can be functionalized with streptavidin, allowing the immobilization of biotinylated retroviral particles and the realization of living-cell microarrays for phenotype screening [2,3].
Here we present a multitechnique investigation of the adsorption mechanisms of streptavidin on cluster-assembled TiO*x* films. We show that this nanostructured surface provides an optimal balance between adsorption efficacy and protein functionality. By using low-resolution protein arrays, we demonstrate that a layer of adsorbed streptavidin can be stably maintained on a cluster-assembled TiO*x* surface under cell culture conditions and that streptavidin retains its biological activity in the adsorbed layer. The adsorption mechanisms are investigated by atomic force microscopy in force spectroscopy mode and by valence-band photoemission spectroscopy, highlighting the potential role of the interaction of the exposed carboxyl groups on streptavidin with the titanium atoms of the nanostructured surface.
[1] Barborini E. et al., J Phys D: Appl Phys 1999;32:L105-9.
[2] Carbone R. et al., Biomaterials 2006;27(17):3221(9).
[3] Carbone R. et al., Biomaterials 2007;28(13):2244(53).

**258-Pos Board B137**
**A "Microfluidic Nose": Detection of Olfactory Sensory Neuron Responses to Odorants Across the Whole Olfactory Receptor Space**
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In vertebrates, odorant molecules are detected by olfactory sensory neurons (OSNs) present in the nasal epithelium. A large, G-protein coupled receptor gene family is responsible for transducing the detection of a cognate molecule for a given receptor. Each OSN appears to express only one of thousands of olfactory receptor (OR) genes in rodents. Odorants are perceived by combinatorial activation of a number of ORs (it is specific to a subset of odorants); each OR recognizes a range of odorants and odorants are typically recognized by a number of ORs. Given the approximately thousand OSN/OR types and the hundreds of thousands of potential ligands, measuring individual OSN activation with the usual *in-vivo* and *in-vitro* methods is a laborious task that is not suitable for interrogating the whole OR space. Hence a microfluidic and high-throughput system was developed to analyze these cells.
Utilizing the techniques of soft-lithography, we developed a microwell array of ~32,000 wells (20 um diameter, 10 um depth) to capture dissociated olfactory epithelia (OE) cells and sequentially exposing them to different odorants. Cell response was detected using the Fluo4AM calcium binding dye. By imaging the fluorescence change in each well, a response profile to each odorant can be constructed for thousands of individual OSNs simultaneously.

**259-Pos Board B138**
**SOI Nanofet Devices For Ultra-Sensitive Detection of Biomolecules**
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In this work the fabrication and fluidic testing of silicon-on-insulator (SOI) field effect devices for the label-free detection of biological molecules are presented.