field (TMF). Indeed, by properly selecting the phase shift between the signals sent to three or more heaters around the crucible, the magnetic field may be made "travelling" along the crucible. In this way the normal growth parameters of the melt growth (pulling/solidification rate, temperature gradient, rotations) are enriched with new degrees of freedom, namely intensity, frequency and direction of the non-stationary magnetic field. By choosing the right field parameters, the crystal grower has the possibility of either stimulating or damping the melt convection, acquiring in this way a good control over transport phenomena in the liquid phase. This in turn provides an efficient control of the solid-liquid interface shape.
In this presentation the concept of travelling magnetic field and the necessary hardware modification will be presented. The results of TMF applied to Czochralski growth of silicon and Vertical Gradient Freeze of germanium and silicon will also be reported. These examples also show that the use of this magnet-heater ensemble provides bulk crystals of superior quality.

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Discovery of post-Perovskite at high pressure and its geophysical implications

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Recent developments in X-ray diffraction (XRD) measurements at the synchrotron radiation source, combined with laser-heated diamond-anvil cell (LH-DAC) techniques, enables the crystal structure determinations at ultrahigh-pressure and -temperature (*P*-*T*) conditions expected for the deep Earth. $MgSiO_3$ perovskite is known to be a primary mineral in the Earth's lower mantle below 660-km depth and the most abundant mineral inside the Earth, but its stability and possible phase transition to a denser structure in the lowermost mantle has long been a matter of debate because large seismic anomalies found in this region are not reconciled with the known properties of perovskite. Recently we discovered a novel phase transition from $MgSiO_3$ perovskite to post-perovskite through a drastic change in the XRD pattern at high *P*-*T* conditions near the base of the mantle around 2600-km depth [1, 2]. Crystal structure of post-perovskite was determined with the aid of computer simulations of atomic positions using the XRD pattern. Unlike perovskite, $MgSiO_3$ post-perovskite is a strongly anisotropic crystal; it has an orthorhombic symmetry (space group: *Cmcm*) with a SiO_6-octahedral sheet-stacking structure along the *b*-axis. It is isostructural with $UFeS_3$ and $CaIrO_3$, which are stable at ambient condition. The Mg^{2+} site in post-perovskite is smaller than in perovskite, resulting in a volume reduction of 1.0-1.5%. The calculated [3, 4] and measured elastic properties [5] of post-perovskite now explain the seismic-wave velocity structure in the lowermost mantle. The high positive pressure/temperature slope (Clapeyron slope) of the perovskite/post-perovskite transition boundary destabilizes the thermal boundary layer at the bottom of the mantle and remarkably enhances the mantle convection. Recent measurements of transport properties demonstrated that both electrical and thermal conductivities of post-perovskite are much higher than those of perovskite. The electronically highly conductive post-perovskite layer in the lowermost mantle enhances the electromagnetic coupling between solid mantle and liquid core, which possibly changes the Earth's rotation speed [6].

In addition, we are now able to perform XRD measurements up to 377 GPa and 5700 K, corresponding to the center of the Earth [7]. With such techniques, hcp (hexagonal-close-packed) structure has been found to a stable form of iron in the Earth's solid inner core (5100 to 6400-km depth). While the effect of impurities such as nickel and some light alloying element(s) remains to be examined, the knowledge of crystal structure of inner core material helps to predict physical properties and interpret seismic structures.

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KN10

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Exploration of the Protein Universe with High Throughput Structural Biology

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The landscape of structural biology has changed significantly over the past decade due to the overwhelming amount of novel sequence data generated from genome sequencing projects and the increased automation and robotics that facilitate protein production through crystallization to structure determination. These advances have unleashed unparalleled opportunities for re-evaluation of the size and diversity of the protein universe via explorations into new environments, such as the human microbiome and, in general, for addressing more challenging biological questions. For over a decade, the Joint Center for Structural Genomics (http://jcsg.org) has been at the forefront of developing tools and methodologies that enable the application of HTP structural biology to a broad range of biological investigations. For example, in the previous phases of the NIH PSI (http://www.nigms.nih.gov/initiatives/psi), we explored structural coverage of uncharted regions of the protein universe [1] as well asa single organism that enabled a complete structural reconstruction of the metabolic network of *Thermotoga maritima*.[2] As we embark on PSI: Biology, the JCSG is leveraging its HTP platform to take on challenging targets in stem cells and T cells that capitalize on our extensive experience to develop the best strategies to enhance chances of success. The emerging field of metagenomics has been particularly enlightening, where the human gut microbiome sequencing projects have already uncovered fascinating new families and expansions of known families for adaptation to particular environments. These high-throughput approaches can be applied to important biological problems not only in large consortia, such as the JCSG, but also in individual laboratories to tackle fundamental biological questions. Examples of the types and range of biological problems that are being tackled by PSI:Biology, as well as examples from my own laboratory on influenza virus and the search for a universal vaccine will be discussed [3]. The JCSG is located at The Scripps Research Institute, the Genomic Institute of the Novartis Research Foundation, U.C. San Diego, Sanford-Burnham Medical Research Institute, and SSRL/Stanford University, and supported by U54 GM094586, and P01 AI058113 and HHSN272200900060C.

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