

units of strongly coupled spins, whose relative orientation can vary easily involving noncollinearity of the spins. In a second example, an antiferromagnetic NiO/CoO thin layer over Pt, it was demonstrated that the soft-x-ray resonant magnetic reflectivity measured over a wide angular range provides a direct way to probe out-of-plane magnetic profiles [2]. Tonnerre *et al.* obtained the extension and structure of the magnetic ordering induced by an ultrathin Co FM layer, over a few oxide atomic layers in the antiferromagnetic layer.

[1] H.L. Meyerheim, J.-M. Tonnerre, L. Sandratskii, H.C.N. Tolentino, M. Przybylski, Y. Gabi, F. Yildiz, X.L. Fu, E. Bontempi, S. Grenier, J. Kirschner, *Physical Review Letters* **2009**, *103*, 267202. [2] J.M. Tonnerre, M.D. Santis, S. Grenier, H.C.N. Tolentino, V. Langlais, E. Bontempi, M. Garcia-Fernandez, U. Staub, *Physical Review Letters*, **2008**, *100*, 157202.

**Keywords:** X-ray resonant magnetic scattering, interfacial magnetism, metallic thin films

**MS.21.3**

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**High energy X-Ray surface and interface scattering**

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Using a focused high energy x-ray beam ( $E < 100$  keV) we have developed a dedicated instrument for High Energy MicroDiffraction (HEMD) for surface and interface scattering at beamline ID15A (ESRF, Grenoble, France). The high energy of the beam allows us to access deeply buried structures including interfaces. The instrument is also equipped with a beam deflector unit which allows us to incline the x-ray beam with respect to flat liquid surface and interfaces, sufficient to reach large perpendicular momentum transfer for atomic or molecular resolution [1].

The instrument has been used for a wide range of structural investigations on deeply buried interfaces. Examples including such diverse materials as ice, ionic liquids, alcohols, metal- semiconductor/insulator interfaces, hydrophobic interfaces, will be presented in order to demonstrate the high performance and capabilities of high energy microbeams in structural investigations of buried interfaces.

[1] V. Honkimaeki, H. Reichert, J.S. Okasinski, H. Dosch, *J. Synchrotron Rad.* **2006**, *13*, 426-431.

**Keywords:** surface, interface, high-energy x-rays

**MS.21.4**

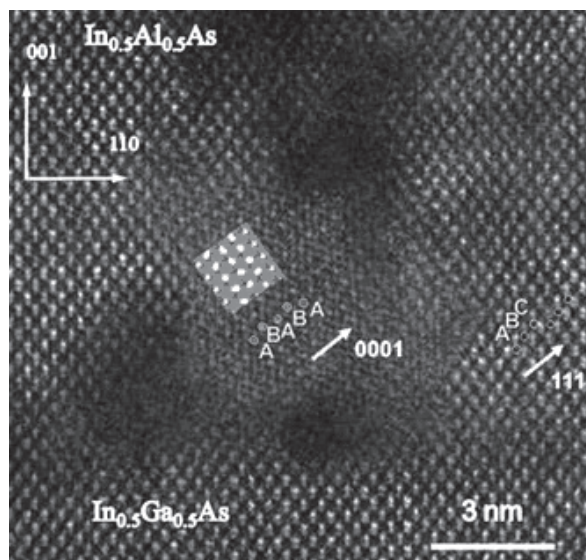
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**High resolution STEM study of InGaAs/InAlAs and Si/Ge heterostructures**

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Si/Ge and InGaAs/InAlAs based heterostructures are studied as perspective materials for high frequency generators, detectors and optoelectronic devices. Two types of heterostructures were investigated: a)  $\text{In}_x\text{Al}_{1-x}\text{As}/\text{In}_y\text{Ga}_{1-y}\text{As}/\text{In}_x\text{Al}_{1-x}\text{As}$  on InP substrate with different layer thickness and different content; b) Si/Ge heterostructures having 2 to 12 Ge layers thickness and deposited at low temperatures. The heterostructures were formed by MBE. In the present study we show an application of high-resolution scanning/transmission electron

microscopy for the determination of structural parameters and defects in heterostructures. The Cs corrected TITAN 80-300 TEM/STEM (FEI, US) equipped with HAADF detector (Fischione), EDXS (EDAX, US) and GIF (Gatan, US) systems were used in the study. In both systems the interfaces were atomically flat and tetragonal lattice distortions was the most typical mechanism of crystal lattices mismatch reduction. Low density of  $60^\circ$  misfit dislocations, microtwins (MTs), stacking faults (SFs) and second phase precipitates were found at  $\text{In}_x\text{Al}_{1-x}\text{As}/\text{In}_y\text{Ga}_{1-y}\text{As}$  interfaces Fig.1. These precipitates were identified as wurtzite inclusions in sphalerite matrix. The inverted pyramids started to form in the Ge layers associated with SFs, when thickness exceeded 10 monolayers. The MT and SF were revealed mostly by bright field HREM demonstrating poor contrast in HAADF STEM mode. The structure-properties relations were discussed.



**Fig. 1.** HR STEM image of  $\text{In}_{0.5}\text{Al}_{0.5}\text{As}/\text{In}_{0.5}\text{Ga}_{0.5}\text{As}$  interface. The model of wurtzite structure is in the insert. The sequence of layers typical for wurtzite (ABABAB) and sphalerite structures (ABCABC) are shown.

**Keywords:** heterostructures, STEM, defects.

**MS.21.5**

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**Spatial resolution of electronic structure through modeling reflectivity spectra**

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X-ray absorption spectroscopy has become an important tool in understanding the electronic structure of materials. Resonant absorption edges in the soft x-ray regime are especially interesting as they allow the study of the lighter elements, such as in organic or organo-metallic substances, as well as important L-edges of the 3d transition metals important in magnetic and oxide systems. Measurements of soft x-ray absorption spectra are inherently surface sensitive, and are plagued by issues such as extinction (in electron yield measurements) or self absorption (in fluorescence yield measurements), which make accurate determination of the optical constants difficult. More accurate optical constants can be obtained by modeling the reflectivity spectra, while being somewhat less surface sensitive compared to electron yield.

Soft x-ray reflectivity from single crystals, thin films, or superlattice structures contains depth dependent information that can be exploited

to determine the optical constants in a depth dependent manner. By modeling the reflectivity spectra, in combination with angular resolved reflectivity, we show that it is possible to extract accurate optical constants in cases intractable with current techniques. Due to the large number of parameters inherent in such free-form modeling, we use the maximum entropy method to refine the underlying model in fitting the measured reflectivity data.

**Keywords:** spectrometry, XAS, reflectivity

## MS.22.1

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### Evolution and dynamics of protein complexes

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There is an abundance of data on protein interactions and protein complexes, both from conventional small-scale experiments collected over the decades, including three-dimensional structures, and more recently by large-scale functional genomics experiments. We can draw on this information to ask whether (i) non-functional protein interactions constrain protein sequences and (ii) whether protein structures harbor information about conformational changes upon binding to each other.

In order to answer the first question, we project evolutionary and systems information onto 397, 196, and 701 proteins of known structure from *E. coli*, *S. cerevisiae* and *H. sapiens* respectively. We find that the propensity of proteins to interact in a non-specific manner with other proteins is inversely correlated with their abundance in *E. coli* and *S. cerevisiae*. This tendency is most pronounced at surface residues, suggesting that high abundance proteins have evolved to have a less sticky surface. In *E. coli* and *S. cerevisiae*, we also find that the evolutionary conservation of an amino acid is positively correlated with the stickiness of the surface environment around it. Thus, residues in sticky surface patches are evolutionarily more constrained, possibly because they are more likely to trigger non-functional interactions if they mutate. Although significant, the impact of protein stickiness is comparatively small in shaping the physico-chemical properties and evolution of *H. sapiens* proteins. This suggests that promiscuous protein-protein interactions are freer to accumulate in species with a small effective population size; a phenomenon akin to junk DNA accumulation.

While non-functional interactions shape protein sequence and structure, functional protein interactions require not just sequence but also structural complementarity, which often involves conformational changes. We have analyzed the relationships between the structures of proteins and the conformational changes that they undergo upon binding. We find that the relative solvent accessible surface area of both free and bound subunits can be used to predict the magnitude of binding-induced conformational changes. We demonstrate that the relative solvent accessible surface area of monomeric proteins is useful as a simple proxy for intrinsic flexibility and for predicting conformational changes upon binding. In addition to the predictive power of this correlation, it reveals a strong connection between the flexibility of unbound proteins and their binding-induced conformational changes, consistent with the conformational selection model of molecular recognition.

**Keywords:** bioinformatics, protein complexes, protein interactions

## MS.22.2

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### Structural insight into the regulation of AMP-activated protein kinase

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The energy sensor AMP-activated protein kinase (AMPK) plays a central role in regulating cellular metabolism and energy homeostasis and is thus a major drug target for obesity, type 2 diabetes and related metabolic disorders. AMPK is a heterotrimeric enzyme composed of catalytic  $\alpha$ -subunit and regulatory  $\beta$ - and  $\gamma$ -subunits and characterized by its ability to undergo allosteric activation upon AMP binding to the  $\gamma$ -subunit. However, the molecular basis for this allosteric regulation remains unclear.

The catalytic  $\alpha$ -subunit contains an N-terminal Ser/Thr kinase domain (KD) and an autoinhibitory domain (AID). We determined the crystal structures of an unphosphorylated fragment of the AMPK  $\alpha$ -subunit (KD-AID) from *S. pombe* and of a phosphorylated kinase domain from *S. cerevisiae* (Snf1-pKD). Structural analyses indicate that AID binds, from the 'backside', to the hinge region of its kinase domain and constrains the mobility of helix  $\alpha$ C, hence resulting in an autoinhibited KD-AID with much lower kinase activity than that of the kinase domain alone. Further *in vitro* kinetic studies demonstrate that disruption of the KD-AID interface reverses the autoinhibition and these AMPK heterotrimeric mutants no longer respond to the change in AMP concentration.

Structural studies on AMPK core provide information on the heterotrimer formation, but the competitive binding of ATP or AMP results in little, if any, conformational changes. In contrast to previous results, our co-crystallized core structures of mammalian AMPK, in complex with either two ATP or three AMP, exhibit different nucleotide/protein stoichiometries and significant conformational differences on the  $\gamma$ -subunit. We set up a minimal kinetic model for AMPK regulation with two functional nucleotide binding sites and demonstrated that the predominant regulatory site on the  $\gamma$ -subunit binds AMP 125-fold more tightly than ATP. Together, our structural and biochemical data have shown the primary mechanism of AMPK autoinhibition and provide a relatively comprehensive view for its allosteric regulation by AMP/ATP exchange.

**Keywords:** AMP-activated protein kinase, autoinhibition, allosteric activation

## MS.22.3

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### A pseudokinase mediates cell wall integrity in *Mycobacterium Tuberculosis*

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