cysteine content and high binding capacity for metals essential (e.g. Zn and Cu) and toxic (e.g. Cd and Hg) metals. MTs consist of two metal binding domains (α and β) that are assembled from cysteine clusters. Cysteine sulfhydryl groups participate in the coordination of heavy metals. Due to their high binding capacity for different metals, MTs are suitable for detoxification, remediation and recycling in applications in agricultural areas. Their potential use for development of metal biosensors for environmental and therapeutic purposes is also recognized. A Type 1 MT from *Triticum durum,* dMT, was expressed in *E. coli* cells as a GST-fusion protein (GSTdMT) [1]. Due to the aggregation propensity, instability in the presence of oxygen and susceptibility to proteolytic degradation applications involving native MTs are impractical. Some of these difficulties were circumvented with the GST fusion partner. In the present study structure of the model system GSTdMT was investigated with view of biosensor applications. GSTdMT was purified with Cd as a dimer in monodisperse solutions [2]. Structure of GSTdMT was investigated by small angle X-ray scattering (SAXS), circular dicroism (CD) and UV-vis spectrophotometric measurements. Inductively coupled plasma optical emission spectroscopy (ICP-OES) and EXAFS measurements showed that GSTdMT binds about 4 Cd^{2+}/protein in a tetrahedral arrangement. SAXS measurements revealed that GSTdMT has an elongated shape with a radius of gyration of 3.57 nm. dMT structure appears to be independent of GST in the GSTdMT fusion. In the investigations for biosensor activity the fusion protein (apo- and holo-foms) was immobilized onto epoxy- and thiol-modified surfaces. Immobilization was verified and attempts for quantification of the bound protein were carried out by GST antibody labeling. Results on detection and quantification of Cd-binding to the apo- and holo-protein will be presented.

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Keywords: metal-binding proteins; SAXS; biosensors

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Aspects of Crystallinity of High Grad Quartz Ores Using X-Ray Diffraction and Infrared Spectroscopy Diagnostic Their Chemical Reactivity. Mervat S. Hassan[a], Tafuk R. Boulos[a], Alia Adam[b]. [a]*Central Metallurgical R & D Institute, Egypt.* [b]*Physics Department, Faculty of science, Al-Azhar University, Girls Branch, Egypt.*
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This work aimed to find relationship between structural imperfection, physical properties and chemical reactivity of two Egyptian quartz ores employed in local production of sodium silicate. Quartz (A) is known to be the highly reactive sample in sodium silicate production than quartz (B). The powder diffraction data of the two quartz samples were refined on the basis of Rietveld method using the Fullprof program. Peak profile analysis of the single and multiple lines were performed applying the winFit program based on the Fourier methods of Waren-Averbach to calculate the crystal size and strain in the two samples. Infrared spectroscopy has been used to study the structure of quartz. Investigation is based on the assignment of infrared bands to certain structural groups of SiO_4 tetrahedra. Systematic investigations of structure have been carried out in between 1000 cm^{-1} and 500 cm^{-1} bands of silicates The crystallinity of samples has been ascertained by comparing the ratio of intensity of the characteristic peak at 778 and 695 cm^{-1}. For analytical band wavenumber close to 797cm^{-1} it was observed that the absorbance decreased as particle size increased. The opposite effect was noted for analytical bands wavenumber 693 and 506-513 cm^{-1}. For strongest diffraction lines of the two quartz samples, it was observed that the intensity increased with the diameter of the particles.

Keywords: quartz; crystallinity; structure imperfections

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Protein Crystallography: Counter Diffusion Crystallization Method and Its Potential for Room-Temperature Data Collection. Mehmet Aslantas[a], Engin Kendi[b], Vivian Stojanoff[c], Tuba Büyükdemirkıran[a]. [a]*K.S.U., Department of Physics, Kahramanmaras, Turkey.* [b]*Hacettepe University, Department of Physics Engineering, Ankara, Turkey.* [c]*BNL, NSLS, 11973 Upton, NY, USA.*
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High-resolution cryogenic synchrotron X-ray data collection is valuable to protein crystallography compare to room temperature data collection leading to serious radiation damage to the crystals, cryo-induced structural changes and freezing problems. However counter-diffusion method for crystallization can be applied to a wide range of molecules and complexes, and might be very useful for SESAME synchrotron users in Middle East. In this presentation, the potential benefits of Counter Diffusion technique, data collection at the optimum wavelength of lysozyme derivative crystals at room temperature, data quality and structure refinement results will be discussed.

Keywords: macromolecular synchrotron X-ray crystallography; crystallization; room-temperature data collection