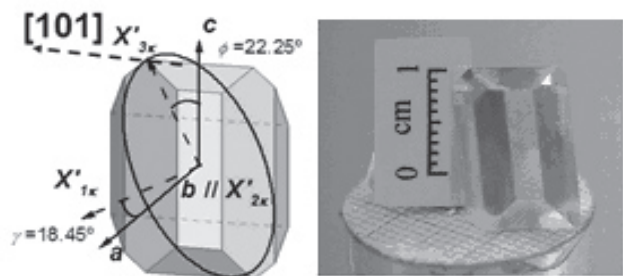


which are  $N_g$ ,  $N_m$  and  $N_p$ .  $N_p$  corresponds to the  $b$  crystallographic directions, and  $N_g$  and  $N_m$  are located in the (010) plane;  $N_g$  is located 18.5° clockwise from  $c$  crystallographic direction.

Such a thermal anisotropy in the monoclinic double tungstates leads to thermal lensing at high power operating levels. Focusing of the light in the crystal provokes high intensities so that the temperature increases significantly producing a mechanical deformation of the crystal, which in consequence, leads to a self-lensing material.

The laser experiments for power scaling carried out with Yb:KLuW in the thin disk configuration at high pump powers reached 9 W in cw regime showing a significant improvement in the thermal management due to the one-dimensional heat flow. This could be known thanks to the deep knowledge on the thermal properties of the monoclinic double tungstate crystals.



**Keywords:** thermal anisotropy, double tungstate crystals, high power lasers

## MS.28.5

*Acta Cryst.* (2011) A67, C75

### The optical spectra of $\text{Sr}_2\text{SiO}_4:\text{Eu}^{2+}$ nanocrystals

Young Jin Kim, Jun Seong Lee, *Department of Materials Science and Engineering, Kyonggi University, Suwon 443-760 (Korea)*. E-mail: yjkim@kyonggi.ac.kr

$\text{Sr}_2\text{SiO}_4$  has two polymorphs:  $\beta$ - $\text{Sr}_2\text{SiO}_4$  (monoclinic) and  $\alpha'$ - $\text{Sr}_2\text{SiO}_4$  (orthorhombic). There are two  $\text{Sr}^{2+}$  sites of ten-coordinated Sr(I) and nine-coordinated Sr(II) by oxygen atoms, which result in two emission bands at around 490 nm and 560 nm by doping  $\text{Eu}^{2+}$  ions. The various synthesizing methods such as a solid-state reaction and chemical preparations have been widely reported.

In this work,  $\text{Sr}_2\text{SiO}_4:\text{Eu}^{2+}$  nanocrystals were prepared by a co-precipitation method using metal nitrates and 3-aminopropyltriethoxysilane (APTES) as a silicon source.  $\text{NH}_4\text{Cl}$  was used as a flux. The as-prepared powders were annealed with different temperatures under  $\text{H}_2$  atmosphere in an electric tube furnace. The particle size and morphology were observed by a field-emission scanning electron microscope. X-ray diffractometer (XRD) and photoluminescence (PL) system were used to determine the crystal structure and the photoluminescence spectra, respectively. The effects of the preparation parameters on the structure of the nanocrystals and luminescent properties were investigated. With increasing the annealing temperature the crystallinity was enhanced, showing thin nanorod with the high aspect ratio. The PL spectra exhibited two emission bands at around 485 and 540 nm, indicating that  $\text{Eu}^{2+}$  ions were successfully substituted for two cation sites of Sr(I) and Sr(II). The preference of  $\text{Eu}^{2+}$  ions for Sr(I) or Sr(II) strongly depended on the preparing parameters such as the amount of a flux, firing temperature/time, and the  $\text{Eu}^{2+}$  concentration.

**Keywords:** luminescence, strontium, silicate

## MS.29.1

*Acta Cryst.* (2011) A67, C75

### Perspectives on the crystal structure of human adenovirus

Vijay S. Reddy, S. Kundhavai Natchiar, Tina-Marie Mullen, Glen R. Nemerow *The Scripps Research Institute, 10550 North Torrey Pines Road, La Jolla, California, 92037, (USA)*.

Replication-defective and conditionally replicating adenovirus (AdV) vectors are currently being utilized in ~25% of human gene transfer clinical trials. Rational development of adenovirus vectors for therapeutic gene transfer is hampered by the lack of accurate structural information. The recently determined X-ray structure of an adenovirus vector at 3.5 Å resolution of the 150-MDa virion containing nearly 1 million amino acids represents a milestone as the biggest bio-molecular structure yet determined using X-ray diffraction methods (Reddy et al., 2010). The crystal structure revealed interactions between the major capsid protein (hexon) and characteristic structural elements of several accessory molecules that stabilize the AdV capsid. Interestingly, the virus structure also showed an altered association, a symmetry mismatch, between the 5-fold symmetric penton-base proteins and the 3-fold symmetric fiber proteins, where the trimeric shaft of the fiber proteins was seen buried deep inside pore formed by the penton base subunits at the particle vertices. The near atomic resolution structure highlights significant advances in understanding the stabilizing interactions, virus assembly and cell entry mechanisms of a large dsDNA virus and provides new opportunities for improving adenovirus-mediated gene transfer.

V.S. Reddy, S.K. Natchiar, P.L. Stewart, G.R. Nemerow *Science* **2010**, 329(5995), 1071-5.

**Keywords:** adenovirus, capsid, structure

## MS.29.2

*Acta Cryst.* (2011) A67, C75-C76

### Structures of porcine adenovirus type 4 and bacteriophage T4 long tail fibres

Mark J. van Raaij,<sup>a</sup> Pablo Guardado-Calvo,<sup>b</sup> Sergio G. Bartual,<sup>b</sup> José M. Otero,<sup>b</sup> Carmela Garcia-Doval,<sup>a</sup> Antonio L. Llamas-Saiz,<sup>c</sup> Gavin C. Fox,<sup>d</sup> <sup>a</sup>*Departamento de Estructura de Macromoléculas, Centro Nacional de Biotecnología, CSIC, Madrid (Spain)*. <sup>b</sup>*Departamento de Bioquímica y Biología Molecular, Universidad de Santiago de Compostela (Spain)*. <sup>c</sup>*Unidad de Rayos X, RAIDT, Universidad de Santiago de Compostela (Spain)*. <sup>d</sup>*Laboratoire de Proteines Membranaires, Institut de Biologie Structurale, Grenoble (France)*. E-mail: mjvanraaij@cnb.csic.es

Certain viruses and bacteriophages use fibre proteins to bind to their host receptors. Examples are adenovirus, reovirus, and the T-even bacteriophages. These trimeric fibres have been shown to contain novel triple-stranded beta-structures. Here we present structures of porcine adenovirus type 4 fibre and of the tip of the bacteriophage T4 long tail fibre.

Adenovirus isolate NADC-1, a strain of porcine adenovirus type 4, has a fibre containing an N-terminal virus attachment region, shaft and head domains, and a C-terminal galectin domain connected to the head by an RGD-containing sequence. The crystal structure of the head domain is similar to previously solved adenovirus fibre head domains, but specific residues for binding the coxsackievirus and adenovirus receptor (CAR), CD46, or sialic acid are not conserved. The structure of the galectin domain reveals an interaction interface between its two