Phy 27 (1988) 169.

Keywords: activity, MBE, gallium nitrides

MS.49.6

Acta Cryst. (2008). A**64**, C89

Contrast of dislocations in 4H-SiC by SR topography in grazing-incidence geometry

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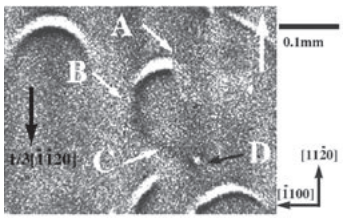
Dislocations near surface of 4H-SiC were observed using synchrotron radiation topography in the Bragg case with grazing-incidence geometry. Figure is an image of basal-plane dislocation half-loop at **g**=11-28, λ=0.15nm on Si-face. The (0001) plane is tilted towards the [-1-120] direction by 8 degrees from the surface. In this condition, lattice defects within 10 μm depth are observed. Along this dislocation line, bright contrast at A, dark and bright asymmetric line at B, and dark contrast at C are observed. Absence in contrast can be seen at B at **g**=1-108, and so that B is a screw dislocation part. We have observed migrations of dark dislocations in specimens after forward-bias degradation effect, in which Si-core dislocations are known to move. Thus we concluded that C is Si-core, A is C-core edge dislocation, and the Burgers vector is 1/3[-1-120]. The observed dark and bright contrast is discussed to be similar effect described by Ando and Kato (1970). By applying this rule we could identify uniquely 6 different Burgers vectors for all basal-plane dislocations and threading edge dislocations at only one diffraction condition.
Ando and Kato: J. Appl. Cryst. **3** (1970) 74.



Keywords: wide-bandgap semiconductors, dislocations, topography X-ray

MS.50.1

Acta Cryst. (2008). A**64**, C89

Decoding homophilic recognition specificity of Dscam, a neuronal receptor with thousands isoforms

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The Dscam gene gives rise to thousands of diverse cell surface receptors thought to provide homophilic and heterophilic recognition specificity for neural development and immune responses. Mutually exclusive splicing allows for the generation of sequence variability in three immunoglobulin (Ig) ecto-domains (D2, D3, D7). X-ray structures of the N-terminal four Ig domains (D1-D4) of four distinct Dscam isoforms have been determined. The structures reveal a horseshoe configuration, with variable residues of D2 and D3 constituting two independent surface-epitopes on either side of the receptor. All these four isoforms engage in homo-dimerization coupling variable domains D2 with D2 and D3 with D3 using the same epitope. The recognition specificity has been analyzed to decode how sequence and local conformation of these two variable domains contribute to homophilic interaction. The structure of the third Ig-like domain D7 has also been determined in the form of D7-D8 fragment for several isoforms. A general view of how these variable Ig domains embedded in thousands receptor isoforms offer hemophilic recognition for neuronal wiring has been provided.

Keywords: dscam receptor, decoding recognition specificity, thousand isoforms

MS.50.2

Acta Cryst. (2008). A**64**, C89

Crystal structure of the [2Fe-2S] transcriptional activator SoxR bound to DNA

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SoxR functions as a sensor of oxidative stress such as superoxide and nitric oxide. It exists as a dimer with each subunit containing a [2Fe-2S] cluster. Reversible oxidation of the [2Fe-2S] cluster activates SoxR to enhance the production of various antioxidant proteins through the *soxRS* regulon. SoxR belongs to the MerR family of transcriptional activators, target promoters of which have an unusual 19 or 20 bp spacer between the -35 and -10 operator elements. In the active state, SoxR and other MerR family proteins activate transcription from unique promoters by distorting the DNA conformation. In order to elucidate structural features of the iron-sulfur cluster of SoxR and the transcriptional activation mechanism, we have determined the crystal structures of SoxR and its complex with DNA in the oxidized (active) state [1]. The overall structure of SoxR consists of a DNA binding domain, a dimerization helix and an Fe-S cluster binding domain. The dimerization helix forms an antiparallel coiled-coil, stabilizing the SoxR dimer. The structures reveal that the [2Fe-2S] cluster of SoxR is unusually solvent-exposed and surrounded by an asymmetric environment, suggesting that the asymmetrically charged environment is a key factor of redox-dependent conformational changes of SoxR and the target promoter. The DNA structure is shown to be sharply bent at the middle and unwound by 3-bp, compared to a B-form DNA. Based on comparison of the target promoter sequences of the MerR family, the present structures shows an activated promoter conformation with a 20-bp spacer in the MerR family.
[1] Watanabe S, Kita A, Kobayashi K, Miki K., Proc Natl Acad Sci USA, 2008, 105, 4121.

Keywords: SoxR protein, MerR family, transcription factors

MS.50.3

Acta Cryst. (2008). A**64**, C89–90

Hybrid LRR technique and crystal structures of the toll-like receptor complexes

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