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X-ray diffraction and topographic studies of silicon epitaxial layers grown on the substrate with introduced porous silicon layer

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Recent applications of porous silicon in technology of solar cells concern manufacturing of exfoliated silicon epitaxial layers [1]. The samples prepared for obtaining exfoliated layers, containing two layers with different porosity were studied in the present case. Similarly as in [2] the investigation included white beam Bragg-case projection and section topography and monochromatic beam topography with recording of local rocking curves at HASYLAB. The samples were also studied with conventional HRD and reflectometric methods.

The porous layers without epitaxial deposition provided strong and narrow maximum at low angle side of the substrate maximum. After the deposition we observed the decrease of lattice parameter in the top layer with lower porosity while the layer with higher porosity still contained the material with larger lattice parameter. The topographic investigation in practically all samples revealed irregular contrasts which can be the dislocations generated at the annealed porous substrate. Other common defects were craters in the annealed porous layer overgrown and filled in the epitaxy. In layers of large thickness, we also observed narrow black and white stripes along <110>, most probably stacking faults with imperfect dislocation loops.

The exfoliated layers exhibited significant curvature. The most effective method of revealing defects in such layers were Bragg-case projection topographs and "zebra" pattern monochromatic beam topographs providing a map of sample curvature.

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Structure in solution of HopQ1 protein, type three effector from *Pseudomonas syringae*

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Many bacterial pathogens have evolved ingenious mechanisms to overcome the host defense response, and these methods include the delivery of type III effectors into host cells. HopQ1 (also known as HopQ1-1) represents one of 59 type III effector protein families identified in *Pseudomonas syringae*, a Gram-negative plant pathogenic bacterium [1].

The aim of this study was to characterize the structure of the monomeric form of HopQ1 protein from *Pseudomonas syringae* pv. *phaseolicola 1448A* and the complex of HopQ1 with 14-3-3a protein from *Nicotiana tabacum* as well as to analyze the interactions stabilizing different oligomeric forms of HopQ1

We decided to study the structure of HopQ1 in solution by the use of small angle scattering of synchrotron radiation (SAXS) technique supported by molecular modeling, confocal microscopy and circular dichroism.

The low resolution structure in solution of HopQ1 monomeric and dimeric forms determined by two independent programs DAMMIN [2] and GASBOR [3] as well as the HopQ1 complex with 14-3-3 protein will be presented. The overall shape of HopQ1 chain-like model resembles bulky and slightly flattened bottle and the predicted (by bioinformatics) structure fits perfectly to this model.

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