m13.p34

Structure-based re-engineering of InlA - an invasin of Listeria monocytogenes

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The food-borne pathogen *Listeria monocytogenes* causes severe infections in immunocompromised patients. At 30% the mortality rate of this pathogen far exceeds that of other food-borne pathogens. The first step of listerial infection involves the uptake of bacteria into epithelial cells of the intestine. This uptake is mediated by the interaction of the major invasin Internalin (InlA) with its human receptor E-Cadherin.
We have previously investigated the recognition complex between InlA and human E-cadherin by crystallizing functional fragments of both proteins (InlA' and hEC1). The leucine-rich-repeat (LRR) protein InlA is found to bind the N-terminal domain of E-cadherin by its 15 unit LRR-domain. Nevertheless, despite a large interaction surface, the complex is surprisingly weak.
Presently, we have undertaken to investigate whether this low affinity is of biological relevance. For this purpose we have substituted individual amino acids in InlA' to increase the affinity for hEC1. We have identified two residues that, when suitably mutated, improve the binding strength 2500-fold. We have furthermore generated strains of *L. monocytogenes* that incorporate the InlA-mutations within the genome. This allows the effect of the higher affinity InlA-variants on the uptake of *L. monocytogenes* into human epithelial cells to be analyzed.

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Modulations in AlB_2-type Rare Earth Germanides and Silicides

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The AlB_2 structure type is present in a vast variety of binary and ternary intermetallic system. Also, many kinds of derivative structures can be found [1]. The structural study of compounds of the form AB_2 with A being a rare earth and B being either Si or Ge is as old as crystallography itself [2], but the last decade special interest have been directed towards these kind of systems, and a great amount of work have been put into these studies. [3-5]. The structures are very complicated, but in some special cases a good description can be achieved using a normal 3D approach [6-8]. We have made a full 3+1D description of the range AB_2 to A_2B_3 using the data from [4] and additional new data. The observed powder data gives $q = (\alpha 0 \gamma)$ and the space group $X2/m(\alpha 0 \gamma)0s$. The results show that the q-vector is a direct measure of the density of vacancies within the hexagonal network in the AlB_2 structure as AB_{2-qx}, and that special values of q_x gives periodic structures corresponding to superstructures of the basic unit cell. One of the observed structures is represented in figure 1.

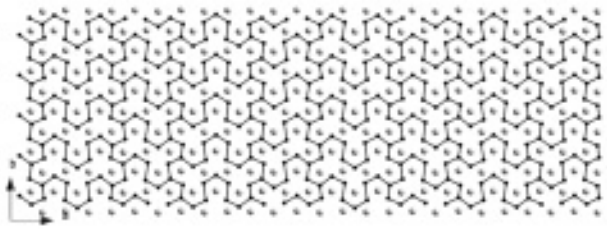

Figure 1: The structure of $DyGe_{1.58}$ viewed along the c-axis. Ge is indicated with black and Dy with grey.

[1] R.-D. Hoffmann and R. Pöttgen, Z. Kristallogr. 216 (2001) 127-145.
[2] W. H. Zachariasen Acta Cryst. (1949), 2, 94-99.
[3] F. P. Netzer, J. Phys. Condens. Matter, 7, (1995) 991-1022.
[4] I. Ijjaali, G. Venturini, B. Malaman, J. Alloys compd. 284 (1999), 237-242.
[5] P. Boulet, D. Bouëxière, J. Rebizant, F. Wastin J. Solid State Chem. 156, 313-320, (2001).
[6] G. S. Smith, Q. Johnson, A. G. Tharp, Acta Cryst. (1965), 18, 1085
[7] R. Pöttgen, R. -D. Hoffmann, D. Kuβmann, Z. Anorg. Allg. Chem. 624, (1998), 945-951.
[8] G. Venturini, I. Ijjaali, B. Malaman, J. Alloys Compd. 289, (1999), 116-119.