feasible in the present case, since the transition pressure is 10 GPa, within the reach of hydrostatic pressure.

The subtle nature of the transition as reflected in the Raman results and the observed optical property changes would fit in the above picture. It is very likely that multiple twinning occurs during the transition and the domains are a direct consequence of it. Twinning would also explain the fact that the sample does not regain its original single-crystal character on release of pressure after the 10 GPa transition. The other possibility is that they are ferroelastic domains. The optical observations under a polarizing microscope demonstrate the power of this technique in revealing subtle phase transitions.

Our picture then for the high-pressure transformation sequence in $A^{2+}B^{6+}O_4$ compounds is scheelite to wolframite, or wolframite-like phase and then to a phase with truly octahedrally coordinated BO_6 units. There are other monoclinic structures closely related to wolframite for ABO_4 compound[5] and they are a possibility as intermediate high-pressure phases, before the transformation to the phase involving a change to octahedral coordination.

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Analysis of a conformation-specific epitope of the alpha subunit of human chorionic gonadotropin: Study using monoclonal antibody probes

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Monoclonal antibodies (MAbs) have been used extensively for identification of sequence-specific epitopes using either the ELISA or/and IRMA methods. However, attempts to use MAbs for identification of conformation-specific epitopes have been very few as they are considered very labile. We have investigated the stability of conformation-specific epitopes of human chorionic gonadotropin (hCG) using a quantitative solid-phase radioimmunoassay (SPRIA) technique. Several epitopes are stable to mild modification (chemical and proteolytic) conditions, and epitopes show differential stability for these modifications. Based on these observations, a monoclonal antibody (MAb 16) for an α-subunit-specific epitope of hCG has been used to monitor changes at the epitopic site (identified as epitope 16) on modification of hCG, using SPRIA with immobilized MAb 16. Modifications of amino groups, hydroxyl group of tyrosine as well as carboxyl group of Asp/Glu all bring about sufficient changes in the epitope integrity. Peptide bond hydrolysis at lysine residues damages the epitope, but not at arginine residues. Hydrolysis at tyrosine does not affect the epitope, though modification of the side-chain of tyrosine inactivates the epitope. Destruction of the epitope occurs on reduction of the disulphide bonds. Partial retention of the epitope activity is seen on modification of carboxyl or the ε-amino groups of lysine. Based on these results four to six amino acids have been identified to be at the epitopic site, and the data suggest that two peptide segments are brought together by the disulphide bond Cys10–Cys60 to form the epitope.

EPITOPES form a very important and specific immunochemical feature of a protein or a macromolecular antigen, and this feature of the antigen is used extensively in the development of specific radioimmunoassays, immunodiagnostics, vaccines etc.[1–4]. Epitopes are classified into sequence-specific (contiguous) and conformation-

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