Crystal Structures of 1) Protein Tyrosine Phosphatase IB and 2) Ser/Thr Protein Kinase

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1) A truncated version (34KDa) of PTP1B, which only consists of residues 1-299 but has catalytic activity indistinguishable from 37KDa protein, has been overexpressed, purified and crystallized. Intensity data were collected from one crystal (0.2 x 0.2 x 0.3 mm^3) at 100 K with a R-AXIS IV at BL24XU. The crystal belongs to a new trigonal space group $P3_221$ with cell dimensions a=88.1Å, c=71.3 Å. Up to 96.5% unique reflections were significantly measured in a range of 50-1.4 Å resolution with the following intensity statistics: redundancy=3.0, <I/sigma>=27.5, Rmerge= 3.67. The crystal structure has been solved by molecular replacement, and crystallographic refinement is now in progress.

2) Two datasets of a Ser/Thr protein kinase have been collected - both crystals diffracted to better than 1.9 Å and both structures were refined at 2.0 Å. Apo-2 data were collected at room temperature, processed with PROCESS and the structure refined with 10 - 2 Å data to R=0.206, R(free)=0.299. This crystal was remarkable for its size = 0.01 x 0.04 x 0.1 mm^3. Apo-1 data were collected at 100 K, processed with ipmosflm and the structure refined with 10 - 2 Å data to R=0.215, R(free)=0.275. Apo-1 and -2 are two different crystal forms, apo-1 with 65% solvent content and apo-2 with 45% solvent content.