

Structural insights into the UbiD protein family from the crystal structure of PA0254 from *Pseudomonas aeruginosa*

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Supplementary Figure S1.

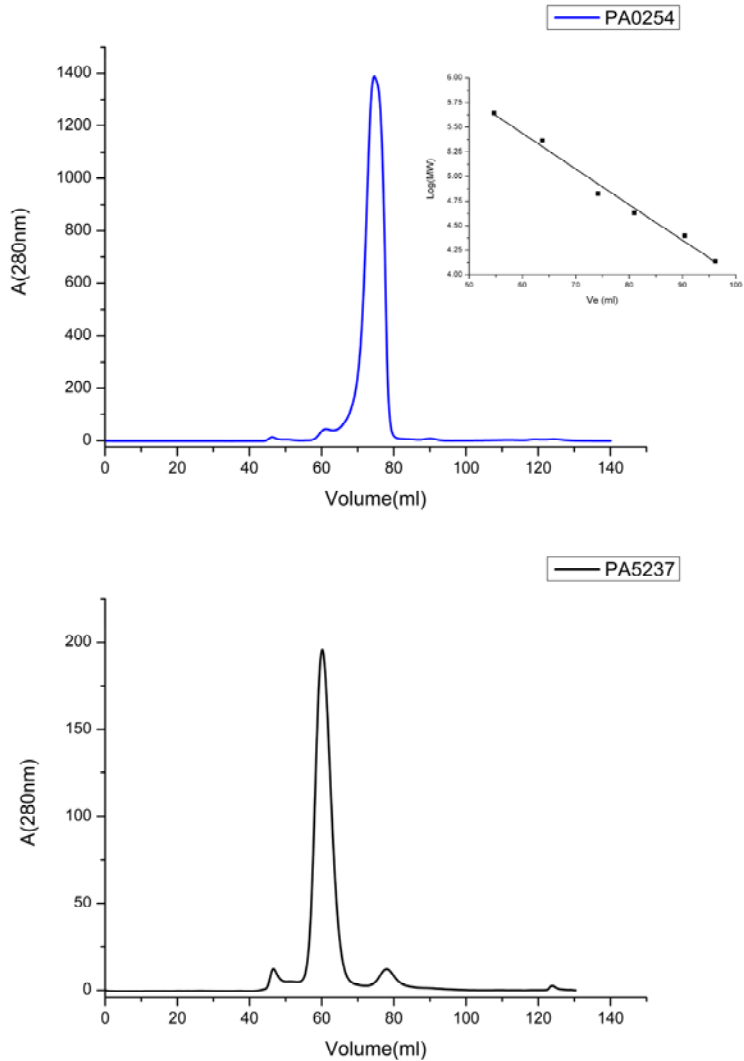


Figure S1. Elution profile of PA0254 (UbiD2, top panel) and PA5237 (UbiD1, lower panel) from size exclusion chromatography using a superdex-200 column (GE-Healthcare) calibrated with Ribonuclease-A (13,7 kDa) Chymotrypsinogen-A (25 kDa) Ovalbumin (43 kDa) Albumin (67 kDa) Catalase (232 kDa) and Ferretin (440 kDa). The data for the calibration curve is shown in the insert in the top-panel. The absorbance at 280 nm is displayed as mAU. The elution volume of PA0254 at 75 ml corresponds to a molecular weight of 85 kDa. The peak position of PA5237 at 57 ml indicates a mass of 353 kDa corresponding to a hexameric arrangement.

Supplementary Figure S2.

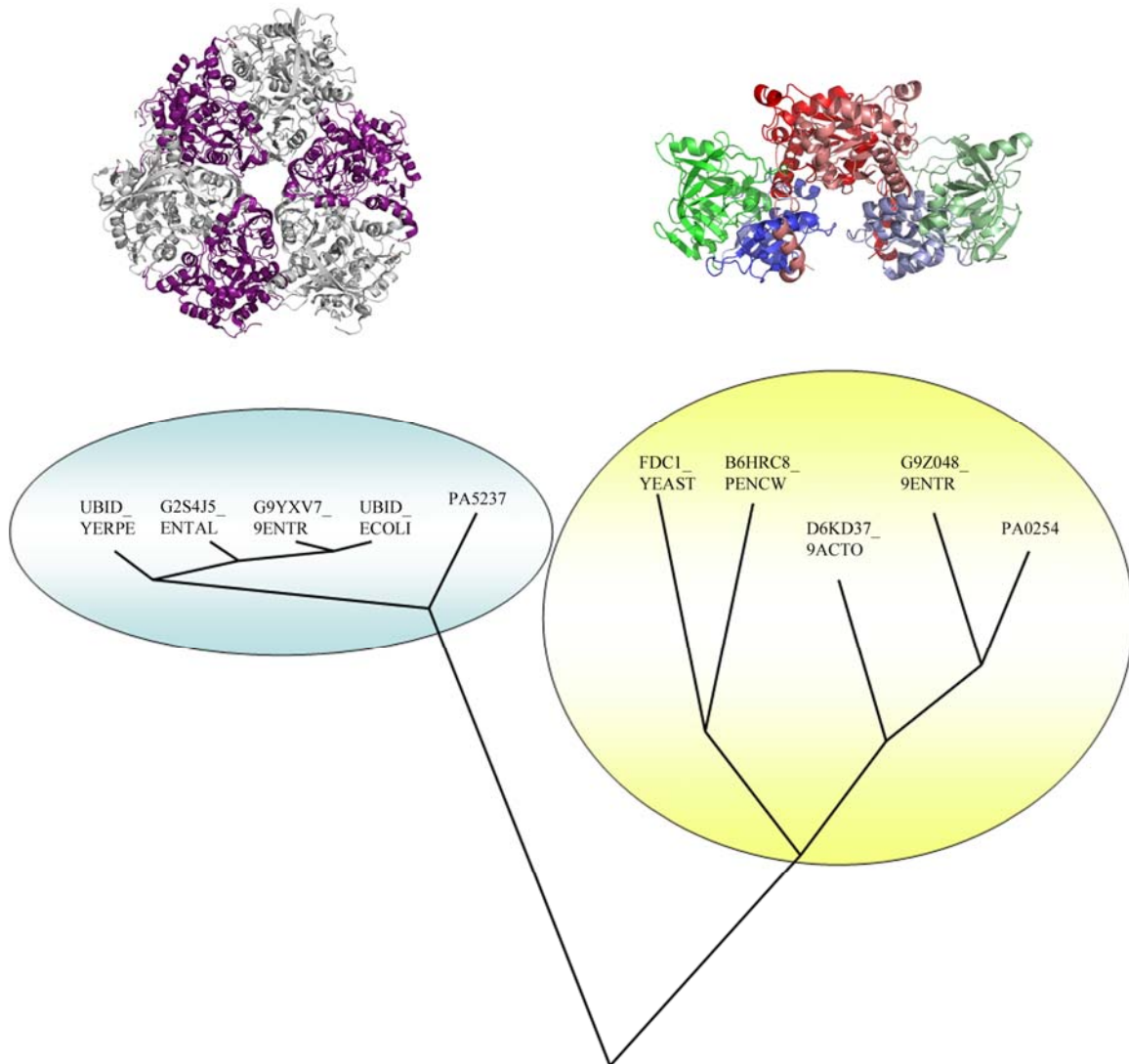


Figure S2. Phylogenetic tree generated at www.cbrg.ethz.ch/services/PhylogeneticTree based on the sequences of UbiD-like proteins used in the alignment in Figure 2. The members of this sequence family are clustered in two groups, one harboring the hexameric *bona fide* UbiD-like enzymes (to the left) exemplified by UbiD from *E. coli* (PDB code 2IDB). The second group comprises UbiD2-like proteins, represented by dimeric PA0254 described in this paper.

Supplementary Figure S3.

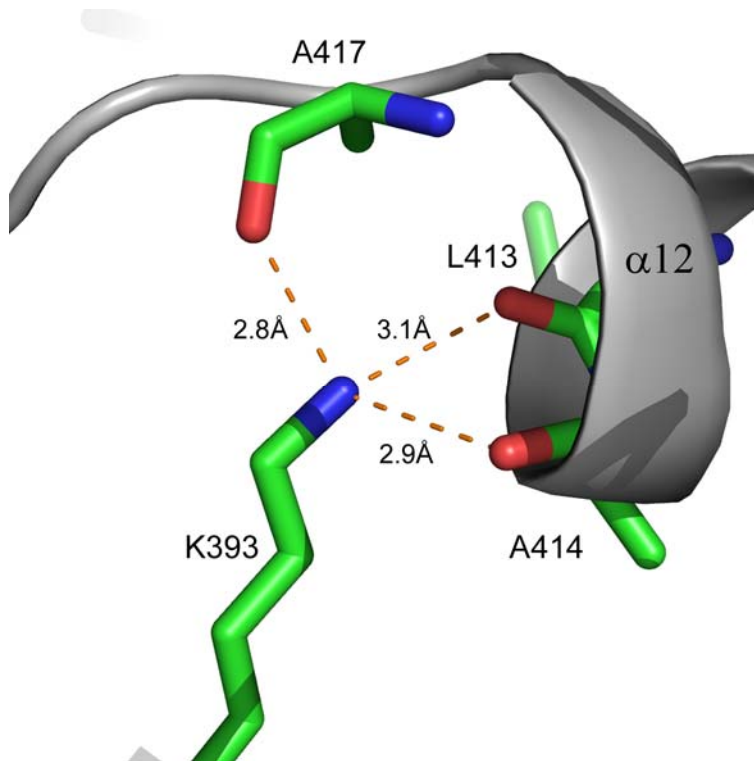


Figure S3. In the dimer interface Lys393 is engaged in interactions with the residues from helix $\alpha 12$ of the second subunit. The ϵ -amino group of Lys393 potentially forms hydrogen bonds with the carbonyl oxygen atoms of Ala414, Leu413 and Ala417. Hydrogen bonds are displayed as dashed lines with the distances indicated.