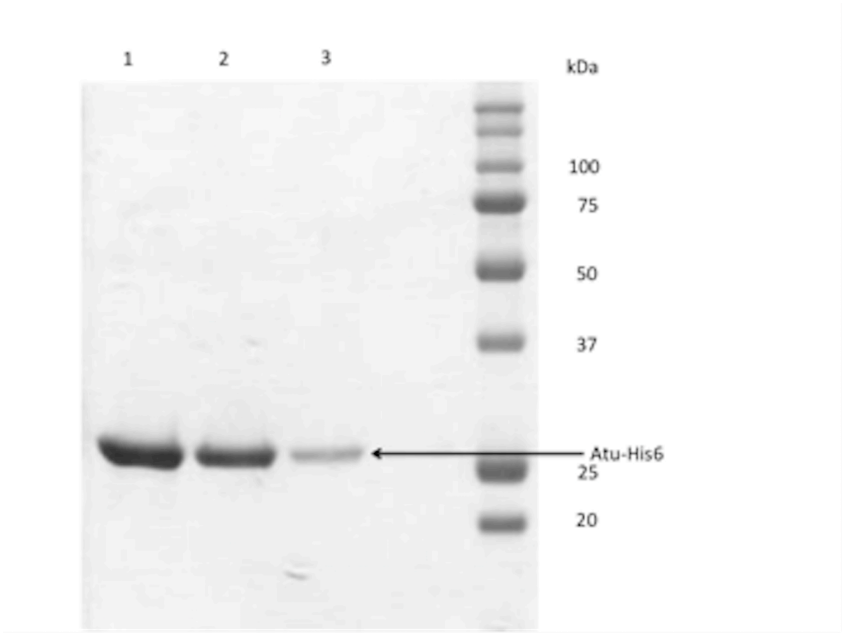
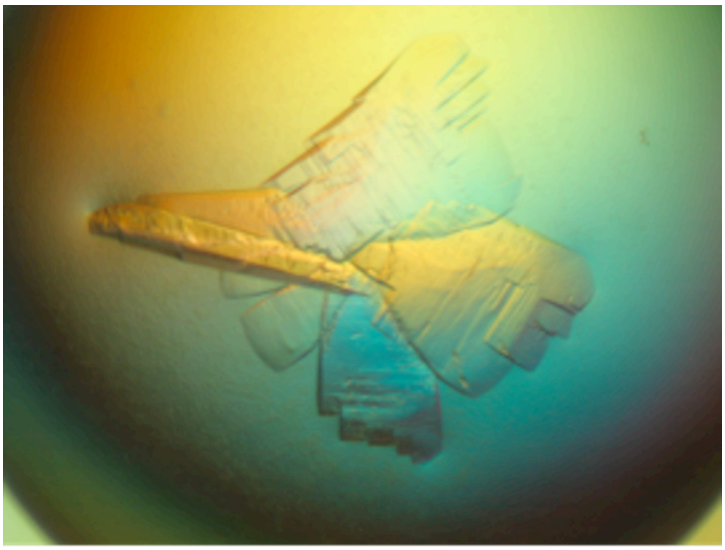
Supplementary data set S1

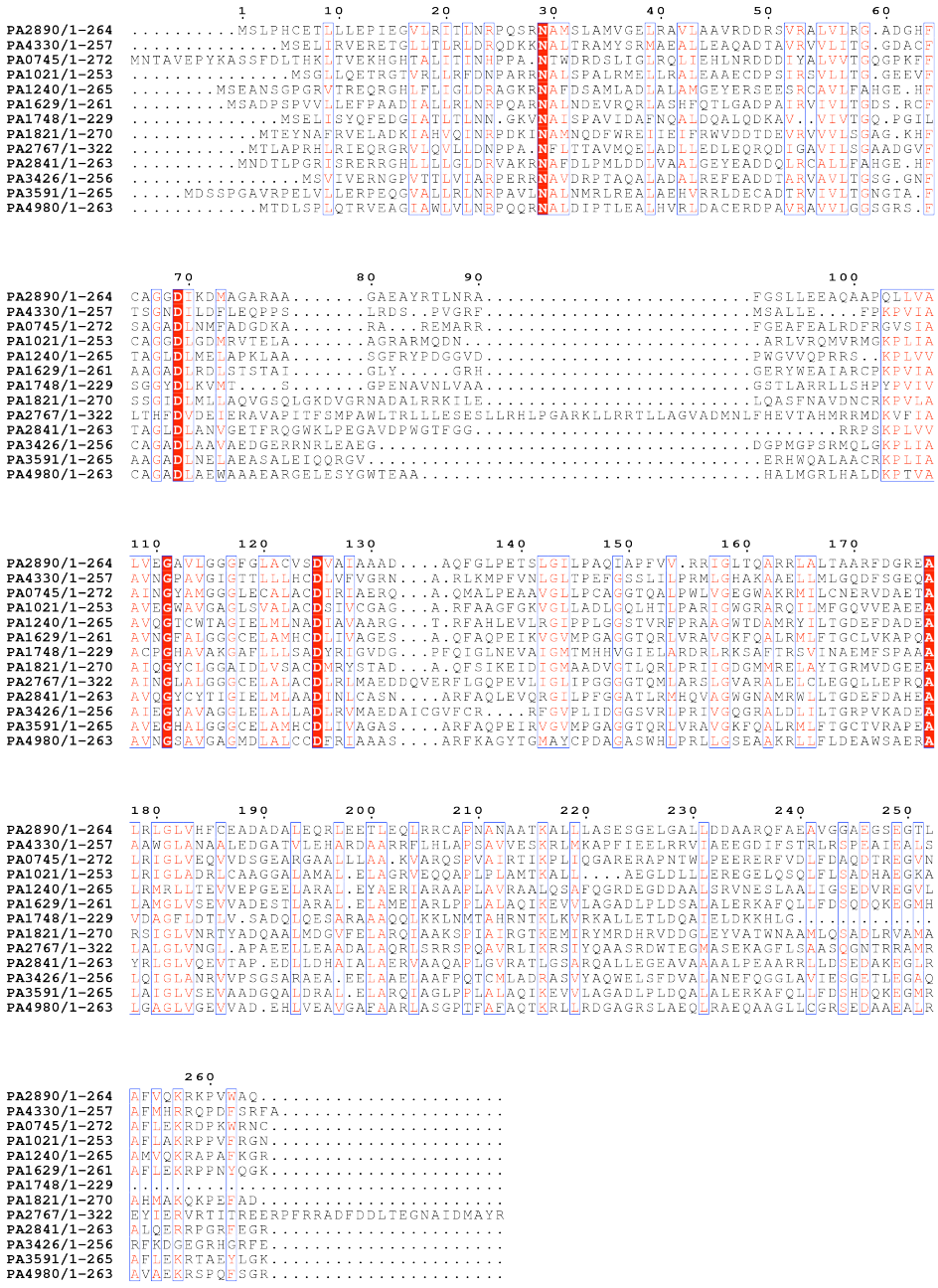


A



B

Supplementary Figure S1. (**A**) Purification of AtuE-His6. Lanes 1-3 show different amounts of purified AtuE-His6 on a 12% SDS-PAGE and subsequent staining with Coomassie brilliant blue. Note the absence of any visible impurities even at higher protein concentrations (35) (**B**) Cluster of AtuE crystals.



Supplementary Figure S2. Sequence alignment of *P. aeruginosa* putative hydratases.

Supplementary data set: *P. aeruginosa* proteins identified in the GeLC-MS/MS approach. Results from the GeLC-MS/MS experiment are shown on different Excel sheets as indicated at the bottom: all identified proteins, proteins that showed a significantly increased abundance in the presence of octanoate, proteins that showed a significantly increased abundance in the presence of citronellate. Proteins exhibiting a change in abundance ≥ 3 and a p-value ≤ 0.05 were considered as differentially abundant.

The tables show the fold-change, p-value and the "number of peptides used for quantification" as well as identifiers (Locus-Tag, NCBI accession number, gene name) for each protein identified. In addition metadata like subcellular localization, putative function, MW and pI as retrieved from the "Pseudomonas Genome Database" are given for each protein. Only proteins with 80% peptide- and 99% protein-probability (see materials and methods) and a minimum number of two peptides per protein are listed.