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## EXPERIMENT REPORT

We tested for the first time crystals of bacterial FmtA and *Arabidopsis thaliana* uracil phosphotransferase (UPP). We diffracted 76 crystals grown in different conditions, with different morphologies and frozen under different cryogenic conditions. All in all, we collected 64 datasets.

Best FmtA crystals diffracted to 2.2 – 2.5 Å resolution. We found the automatic data processing with various programs very useful. The structure was determined on the fly by molecular replacement using a pre-existing protein structure at lower resolution as search model.

Best UPP crystals diffracted to 2.5 – 3 Å resolution, which was sufficient to determine the structure by molecular replacement using the structure of *Toxoplasma* UPRT as search model.

Overall, the session was very successful since we determined the first structures of two new proteins. These data will be completed with future structural studies of the proteins in complex with ligands to characterize the active site and catalytic mechanisms. We expect that, along 2023, these results will be the subjects of two research articles.

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