

**Electronic Supplementary Material for Publication in *Appl. Microbiol. Biotechnol.***

**Bioinformatic Analysis of Fold Type III PLP-dependent Enzymes  
Discovers Multimeric Racemases**

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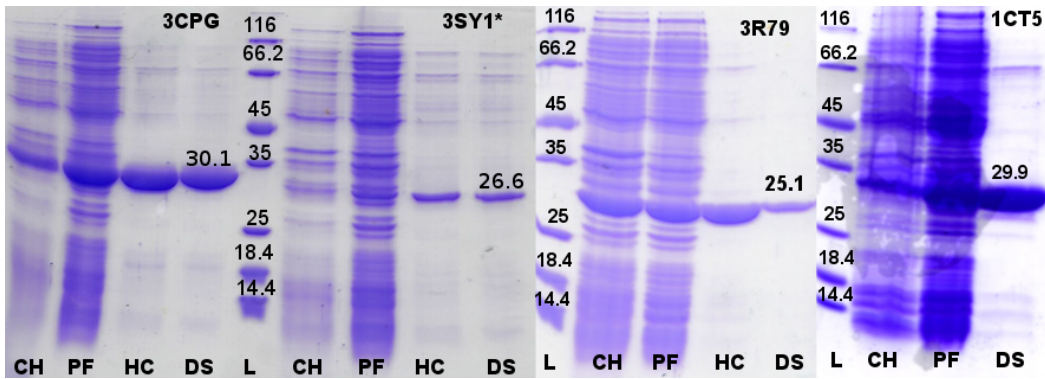
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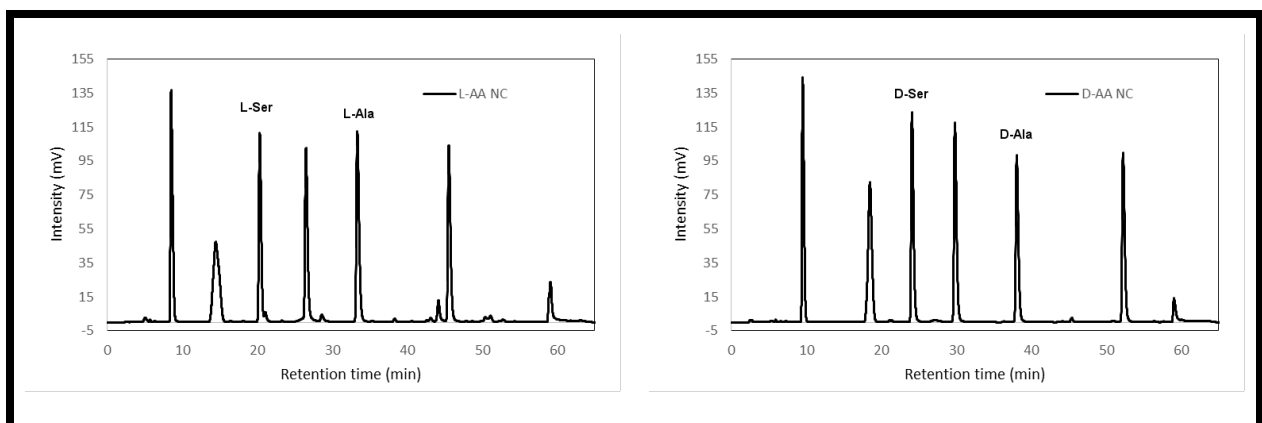


**Figure S1.**

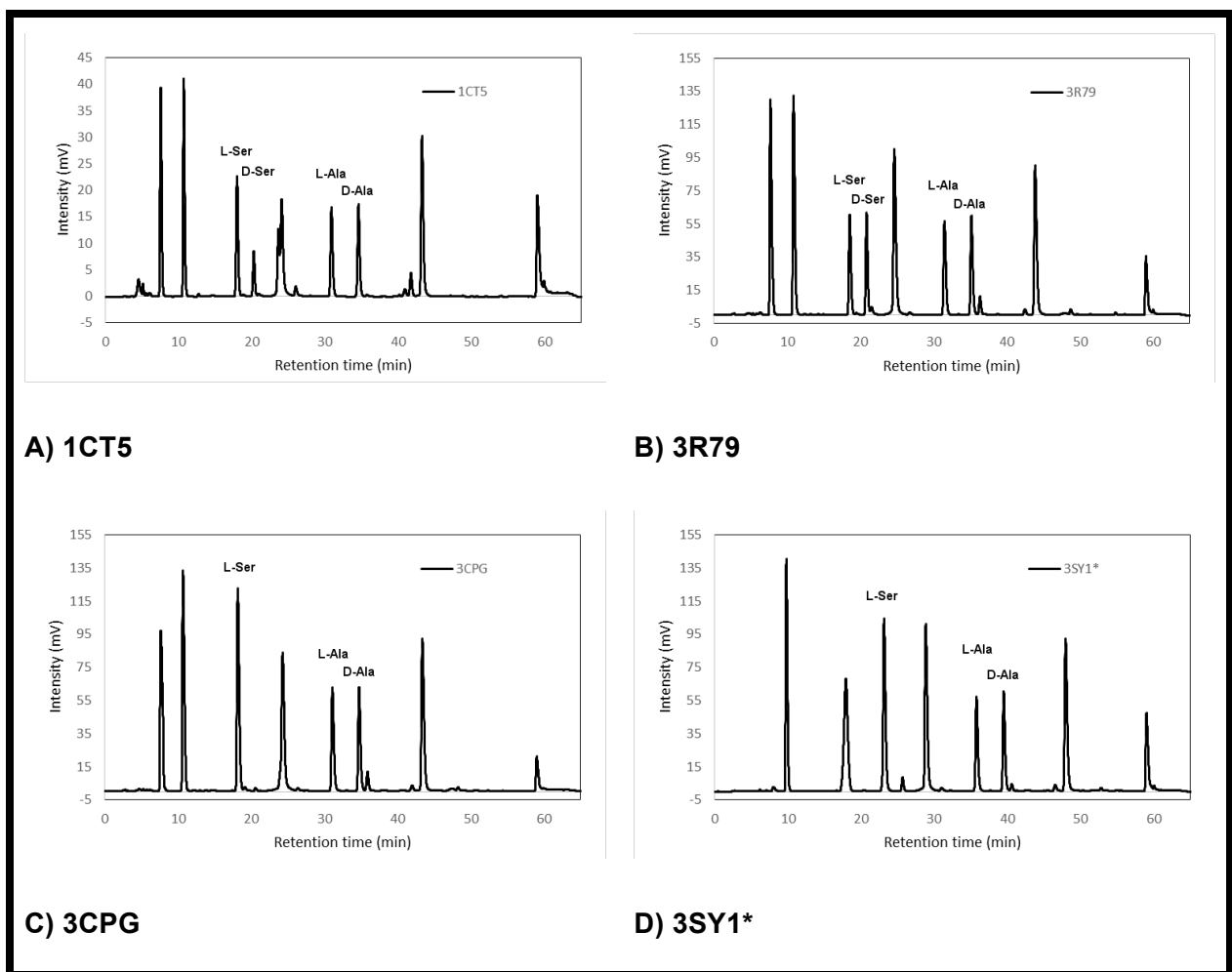
SDS-PAGE with Coomassie stain of the purified orphan proteins (from left to write: 3CPG, 3SY1\*, 3R79 and 1CT5). The sizes of the purified fractions and of the molecular markers are indicated above each band of the ladder (Pierce™ Unstained Protein MW Marker, Thermo Scientific). For each protein the following samples were compared to follow the protein concentration during purification: CH, cell harvest; PF, post-filtration crude cell extract; HC, His<sub>6</sub>-tagged protein fraction after elution from Ni-column; DS, His<sub>6</sub>-tagged protein after desalting.

**Table S1.** Retention times of amino acid enantiomers on a 7-47% gradient

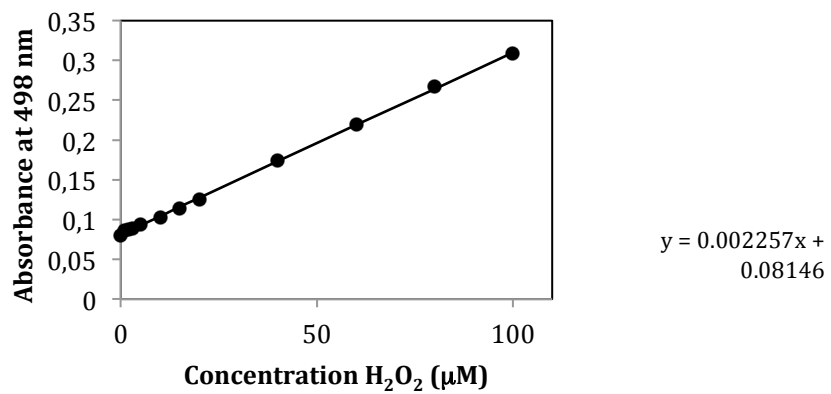
| Amino acid | Retention time |      |
|------------|----------------|------|
|            | [min]          |      |
|            | L              | D    |
| Asp        | 7.6            | 8.5  |
| Glu        | 10.8           | 14.6 |
| Ser        | 18.2           | 20.4 |
| Thr        | 24.3           | 26.5 |
| Ala        | 31.2           | 34.1 |
| Val        | 43.5           | 45.5 |



**Figure S2.** HPLC-chromatogram for the simultaneous analysis of racemization by the orphan protein templates of 6 different L-amino-acids (left) and D-amino-acids (right).



**Figure S3.** Substrate profile for each of the orphan protein tested in the racemization of L-amino acids to their D-counterpart.



**Figure S4.** Calibration curve for quinoenimine dye formation as a function of hydrogen peroxide concentration.