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

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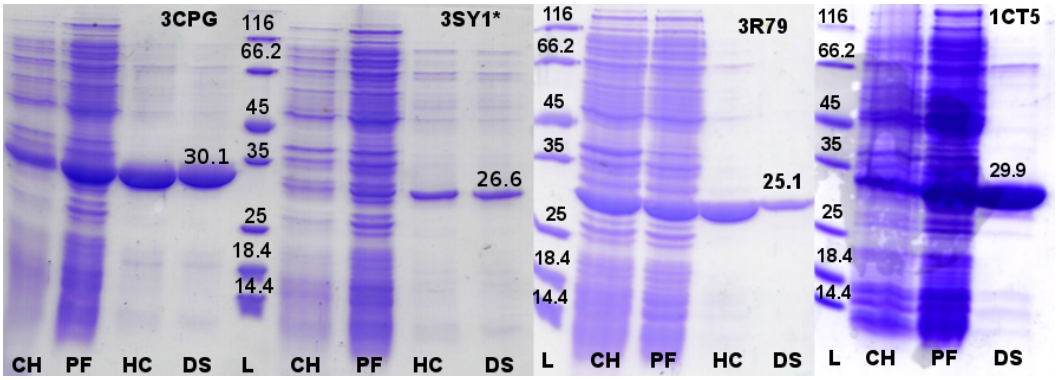

Figure S1.

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_6-tagged protein fraction after elution from Ni-column; DS, His_6-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

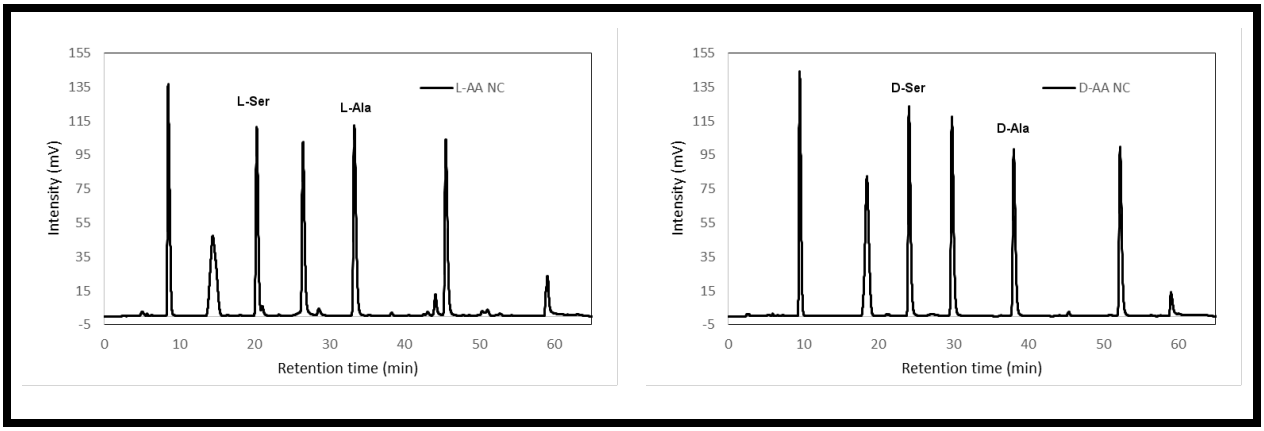

Figure S2. HPLC-chromatogram for the simultaneous analysis of racemization by the orphan protein templates of 6 different L-amino-acids (left) and D-amino-acids (right).

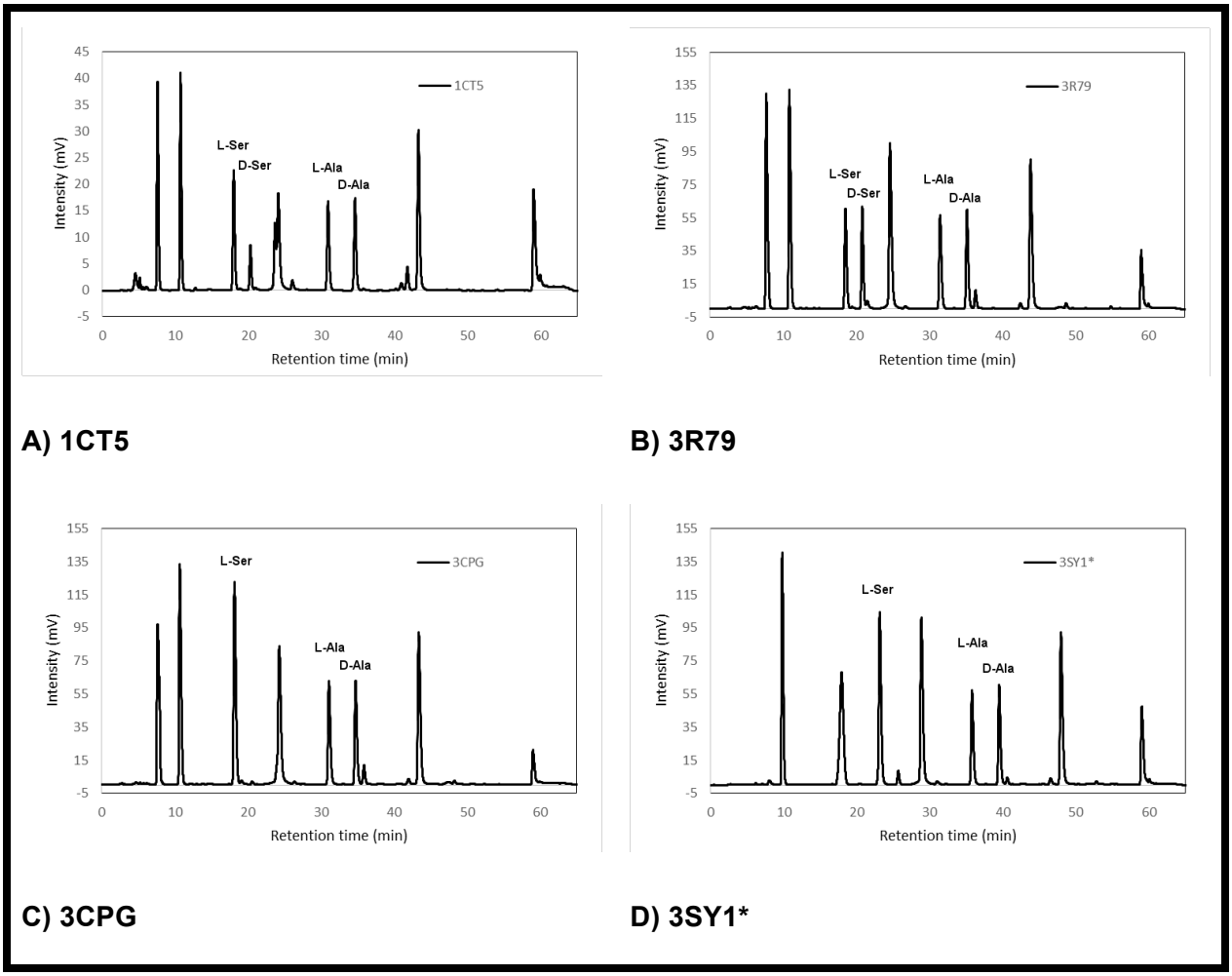

Figure S3. Substrate profile for each of the orphan protein tested in the racemization of L-amino acids to their D-counterpart.

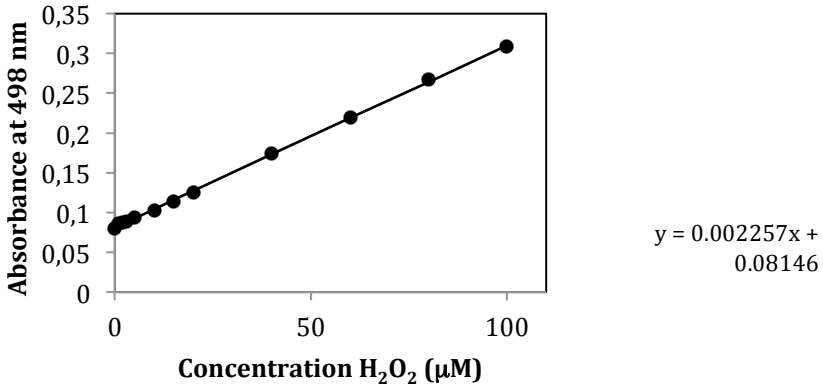

Figure S4. Calibration curve for quinoenimine dye formation as a function of hydrogen peroxide concentration.