Supplementary Results

Human PLP α-decarboxylases share high identity and a common highly flexible catalytic loop (CL)

Sequence comparison of human PLP α-decarboxylases share high identity (**Table S1**) and a common evolutionary origin [1]. Structure comparison with other enzymes of the same structural family, (Fold-Type I [2] or aspartate aminotransferase family [3]), highlighted some common motifs and structural determinants [4]. Among these, the CL is always present and visible only in few structures. Human glutamate decarboxylase isoform GAD67 [5], human cysteine sulfinic acid decarboxylase (CSAD) (only deposited entry in the Protein Data Bank (PDB) as 2JIS; an analysis using this structure has been carried out in [4]) and human histidine decarboxylase (HDC) [6] show the CL of one monomer protruding into the active site of the other monomer. Interestingly, all the enzymes displaying a visible CL have been solved as dimers in the asymmetric unit. Although the crystal structures are snapshots at low potential energy states, it is evident that GAD67 and CSAD, evolutionary more correlated, display a superposition of the CL similar and slightly different from HDC [4]. Pig aromatic amino acid decarboxylase (AADC) (the only AADC mammalian structure solved until now) [7], human GAD65 [5], mouse CSAD [8] and mouse GADL1 [9] miss this flexible element. In the case of AADC a modeled structure has been built on the basis of the human HDC solved CL structure sharing 52.1% sequence identity and 82.6% sequence similarity by comparison of their mature forms [4] (the full-length amino acid sequences share 51% identity [10] and **Table S1** below).

Table S1-Identity of human PLP α-decarboxylases

#	identity (%)
AADC	--
HDC	51.88
GAD67	24.34
GAD65	22.81
CSAD	21.05

References

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