Molecular modeling contribution to the elaboration of a 3D model for lecithin cholesterol acyl transferase (LCAT).

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From its involvement in the reverse cholesterol transport, lecithin cholesterol acyl transferase (LCAT) is a key enzyme in the transport and the elimination of cholesterol. Therefore, one has focussed on the structure of this enzyme ; this paper describes the strategy followed to create a plausible 3D model for LCAT.

Firstly, by homology with other lipases and esterases of known 3D structure, some essential elements involved in the folding have been underlined : similar sequences, secondary structures, 3D motifs, environment of the catalytic site.

Secondly, different secondary structures prediction have been used to define a consensus model for LCAT, localising α-helices and β-strands along the sequence in accordance with experimental results.

Thridly, the threading methods have led to the elaboration of a 3D model for LCAT. The sequence has been divided in two parts : LCAT 1 (1-97 amino acids) and LCAT 2 (98-416 amino acids).The 3D models obtained allowed to identify essential elements described earlier and are compatible with the proposed mechanism fo LCAT. Moreover, this models enabled to visualise the localisation of essential residue in the enzyme's activity.