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The gene encoding for outer membrane phospholipase A (OMPLA) is wide spread among Gram-negative bacteria, of which many are pathogenic. OMPLA is one of the few enzymes in the outer membrane of these bacteria. This 31 kDa protein hydrolyses phospholipids, displays broad substrate specificity, is strictly calcium dependent and shows no sequence homology with water soluble (phospho)lipases or with the structurally related porins. This phospholipase is surrounded by its own substrate but is dormant in normally growing cells. Perturbations of the membrane trigger the hydrolysis of phospholipids by forming active dimers.

The crystal structure of the monomer reveals a 12 stranded anti-parallel ß-barrel architecture. The active site is located at the end of a ß-strand and it harbors a unique catalytic triad comprising an asparagine, histidine and a serine.

Dimerisation results in formation of substrate binding pockets and functional oxyanion holes (that stabilizes the transition state). Monomer-monomer contacts are almost exclusively confined to the membrane embedded part of the protein and they comprise polar interactions in an otherwise hydrophobic environment.

All structural and biochemical evidence leads to an activation model of this membrane enzyme. Perturbation of the membrane results in phospholipid presentation to the outer leaflet. This triggers most likely dimerisation resulting in active complexes that hydrolyze the phospholipids. Production of lyso-phospholipid and fatty acids further destabilizes the outer membrane. This destabilization facilitates export of proteins, colicins or toxins out of the bacterium.
