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# INTERPRETATION OF ELECTRON MICROSCOPIC IMAGES OF CRYSTALLINE AGGREGATION OF LEUCINE AMINOPEPTIDASE

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Leucine aminopeptidase (LAP) is an enzyme-hydrolyzing peptide with a free amino group at the N-terminal amino acid residue. It has a molar mass of 326 000 and consists of six identical subunits with a molar mass of 54 000 $\pm$ $\pm$ 4 000 each.

The arrangement of the identical subunits inside the LAP molecule is described differently in the literature: while hexagonal packages in one plane appear to be unlikely, arrangements in the form of trigonal prisms or octahedrons are generally accepted /1, 2/.

In order to obtain more conclusive data on the spatial organization of crystalline LAP, electron-microscopic studies were carried out and the micrographs interpreted by means of optical and mathematical methods.

The electron microscopic studies were done proceeding from LAP solution in 0.1 Tris HCL buffer at pH 7.2 and 8.2 and at a concentration of 0.12 mg/ml. Negative staining with ammonium molybdate and methyl wolframate, respectively, yielded reproducible LAP molecule aggregates that were large enough for the interpretation of the micrographs. As carriers for the objects to be investigated, thin carbon films (20 - 40 Å) supported by Triafol microgrids were used /3/.

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