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Folding region predictions by amino acid analysis of lysozyme superfamily proteins

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It is well known that the 3-D structure in lysozyme-like fold show wide variety but partially common topology. The aim of our research is to discuss whether common folding unit and common folding mechanism exist by analyzing c(chicken)-type lysozyme family which has folding mechanisms that have been investigated extensively, and its superfamily proteins i(invertabrate)-type, g(goose)-type, l(lambda-phage)-type lysozyme family. In order to achieve it, we mainly used Average Distance Map(ADM) analysis which predicts distribution of folding unit and F-value analysis which predicts the contact frequency of each residue. These methods are based on inter-residue average distance calculation with known 3-D structures. First we conducted BLAST search to get homologous proteins of each family. Then we got rid of the sequence of one of the pair which indicate more than 90% identity and sequence which causes large alignment gap on secondary structure. Finally we used 73 c-type, 52 i-type, 53 g-type and 100 l-type lysozyme proteins as objective proteins. Next we conducted the MAFFT alignment program and combined with our result of ADM analysis. As a result, we found that strongly conserved folding units exist in each family. Furthermore, we made use of combinatorial extension (CE) structural alignment program. As a result, the distribution of conserved units on 3-D structure within a family is partially conserved beyond family. These conserved regions included residues which indicate high contact frequency. That is, we can suggest the common folding mechanism among lysozyme superfamily.

Biography

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