ABSTRACT

The present application provides a method for predicting the functional site of a protein using data of the entire proteins of an organism of which genome data or cDNA data is known, comprising the steps of calculating the frequency of occurrence of an oligopeptide in the entire proteins, calculating the value of each amino-acid residue contributing to the frequency of occurrence as the representative value of the function, and predicting the protein functional site by using the representative value of function as an indicator. The present invention also provides a system for predicting a functional site for automatically performing said methods. Additionally, the present application provides a method for preparing a function-modified protein comprising subjecting the amino-acid residues composing the functional site identified by the method described above to artificial mutation, and a novel thermophilic DNA polymerase prepared by the method.