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METHOD OF CONSTRUCTING STEREOSTRUCTURE OF PROTEIN HAVING PLURAL (54)**NUMBER OF CHAINS**

(57)A method is provided of constructing a tertiary structure of a protein composed of plural chains having given arbitrary amino acid sequences by extending an comparative modeling method of constructing a tertiary structure of a protein composed of a single chain having a given arbitrary amino acid sequence (extended modeling method). In this method, an input file format of the plural chains in a computer software program is each corrected so as to present a form of a temporary single chain (correction of sequence alignment) and the tertiary structure is constructed based on the modeling method while assuming that the structure has plural chains in calculation of a potential formula by the computer software program, thereby constructing the tertiary structure of the target protein.

Namely, a method is provided of constructing the tertiary structure of an arbitrary protein having plural chains, which serves as a particularly important key factor in developing drugs or the like, highly accurately and much more efficiently than by a conventional method.

FIG 9 TARGET ANING ACID SEQUENCE OF PROTEIN WITH UNKNOWN
STRUCTURE: ARBITRARY NUMBER OF PLURAL CHAINS HOMOLOGY SEARCH AND SEQUENCE ALIGNMENT BY ALIGNMENT SOFTWARE STEP 20 SELECTION OF ANIMO ACID SEQUENCES OF ONE OR MORE REFERENCE PROTEINS FROM SEARCH RESULTS 1 STEP 30 1 CONSTRUCTION AND OPTIMIZATION OF Ca ATOMIC COORDINATES STEP 50 CONSTRUCTION AND OPTIMIZATION OF SIDE-CHAIN ATOMIC COORDINATES VALIDATION OF MODEL STRUCTURE CONSTRUCTION OF FINAL STRUCTURE: PREDICTION OF 3-D STRUCTURE

FLOW CHART SHOWING PREDICTION OF 3-D STRUCTURE OF PROTEIN ACCORDING TO THE INVENTION (EXAMPLE)