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Structural mapping of protein network aids us to unleash their evolutionary links and to design accurate drugs

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Functional annotation of a protein sequence and that too precisely for its every single encoded domain is challenging. As the number of protein sequences is rapidly growing, the overwhelming count of proteins can only be annotated computationally, although a high accuracy is always expected. Decade is gone when the protein sequence could be annotated through the statistical scoring of its similarity with the existing database of functionally understood protein sequences. A protein structure is naturally too robust over its primary sequence information. To decode the functional attributes of a protein, the task of modeling, assessing and comparing a best predicted protein model with the functionally understood protein or domain conformations becomes a promising exercise. Majority of these protein structure prediction algorithms fail to construct the accurate near-native model with the correct structural topology of each of the encoded domain and with an acceptable mutual orientation of these domains in the overall protein model. The improved protein modeling algorithm is hereby first presented to bridge the sequence-structure gap and the challenge of predicting the functional detail of a protein sequence is further resolved. Smooth mapping of the evolutionary link and biochemical network of protein sequences in a cell is thereby emphasized to develop the best set of composite drugs for effectively curing even the currently unresolved deadly diseases.

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Non-GMO genetically edited crop plants

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The availability of genome sequences of many crop plants accompanied with revolution of new genome editing tools provided a breakthrough in modulating novel traits with unprecedented control and accuracy. However, plasmid mediated delivery of these genome editing components into cells can results in uncontrolled, random integration of plasmid sequences, potential safety problems, possible GMO regulations and other social hurdles. Here, we would like to propose direct delivery of purified Cas9 protein with guide RNA into plant cells. This method has shown high efficiency, significantly reduced off-target effects and immediate genome editing after delivery compared to plasmid mediated genome editing. Furthermore, Cas9 protein-guide RNA complexes will be decomposed immediately after editing the gene of interest and thus there is huge possibility to be considered as Non-GMO crop plants.

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