

# Researchers find possible universal code of protein structure

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A Dartmouth College study finds there may be a universal code to predict protein structure, which could help to determine why certain mutations cause disease and how to fix them.

The findings appear in the journal *Structure*.

The [human genetic code](#) is a prescription for making proteins. Human cells follow this code to make individual protein molecules, which then fold up into 3D structures and carry out their function. So, in principle, a single gene (i.e., a sequence of DNA nucleotides) leads to a single protein molecule, which leads to a specific structure and function.

"If we could predict the final 3D structures of proteins from their genetic sequence, we would be one step closer to understanding the cell on a molecular level and curing disease," says co-author Gevorg Grigoryan, an assistant professor of computer science at Dartmouth.

In their new study, researchers analyzed this problem, called structure prediction. Their idea was that protein structures can be predicted by breaking them into 3D fragments, or pieces/building blocks they call TERMS (tertiary motifs). TERMS from natural proteins, they found, are often reused by many unrelated proteins. It further turns out that by looking at the distributions of these TERMS in nature, the researchers can make models that connect sequence and structure. Thus, they can tell which parts of predicted structures are likely correct and which ones may be wrong.

"Our findings suggest that there may be a universal code for protein sequence-structure relationships, written on the level of local structural fragments," Grigoryan says. "If this is so, and we can use this code to predict [protein structure](#), we will gain a powerful tool for understanding how certain mutations cause disease and how to fix them."

Provided by Dartmouth College

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