

## Protein folding computed from evolutionary information

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The talk will describe the use of evolutionary information in protein sequences, either from natural evolution or from deep and broad evolution experiments, to determine protein 3D folds and functional interactions. The EVfold method was the first computational method to compute many correct protein 3D structures from multiple sequence alignments. The 3Dseq method is a the fourth experimental method (after crystallography, NMR and cryoEM) for the determination of protein structures, via repeated cycles of mutation and selection that generate hundreds of thousands of isofunctional/isostructural sequences from which residue contacts and then structures are determined.