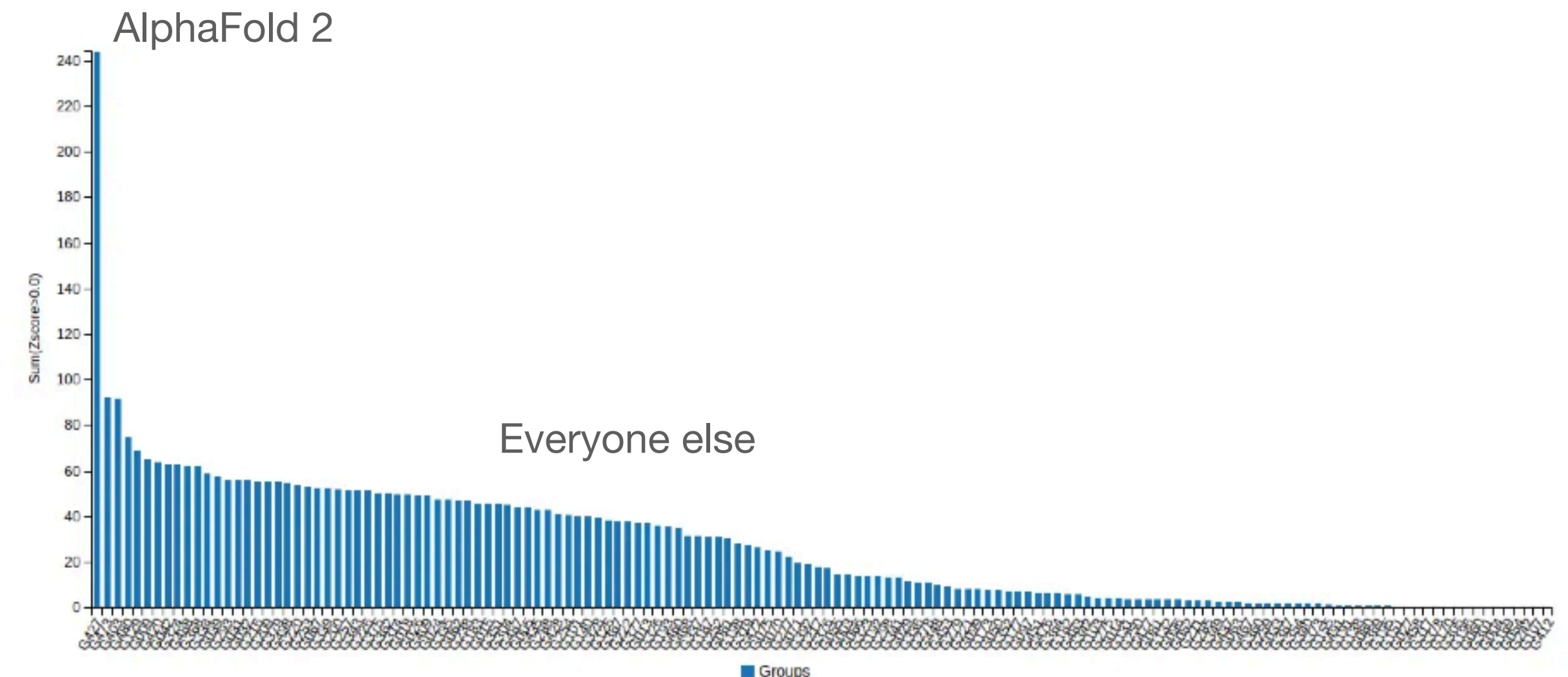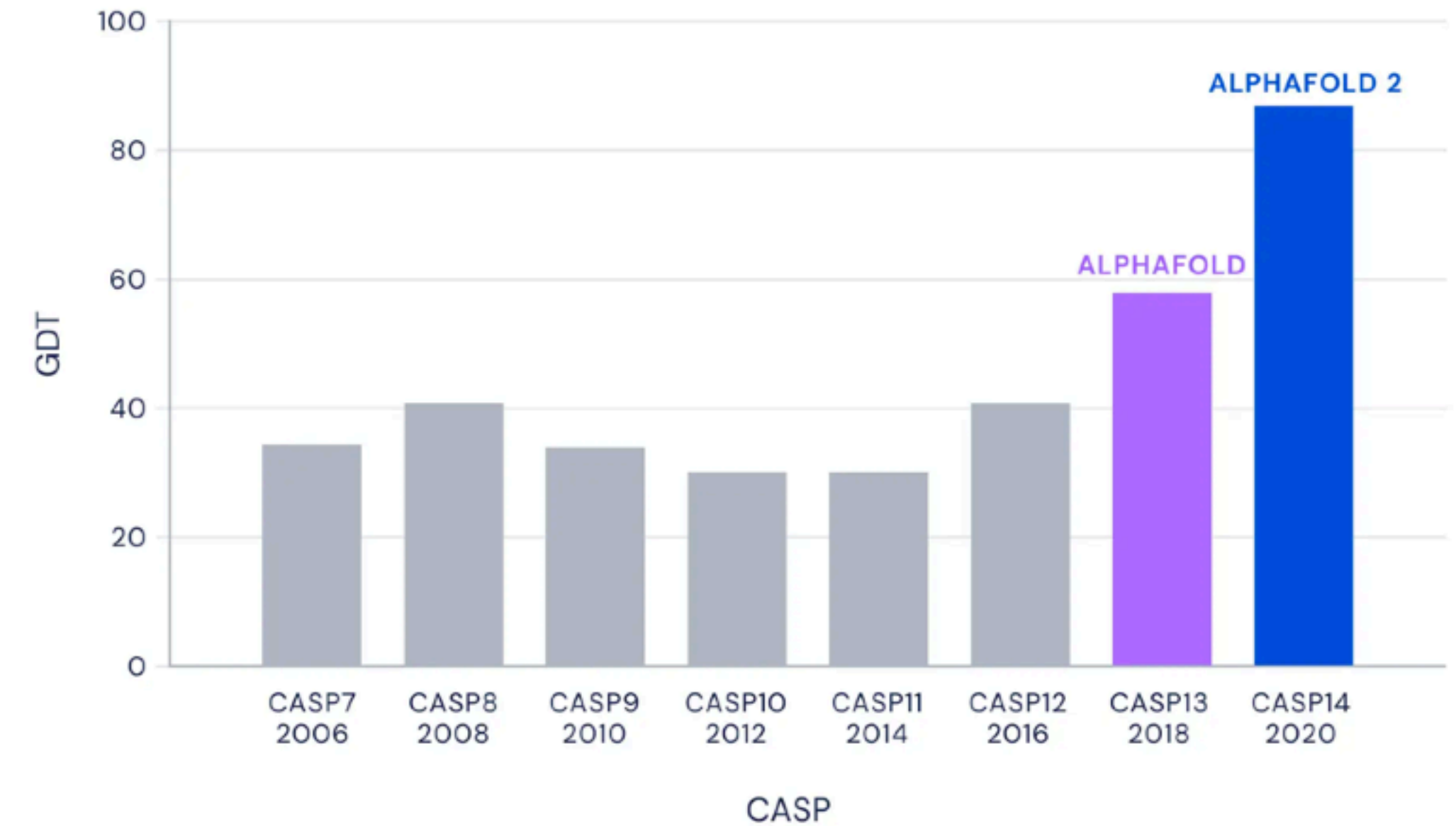# ML for protein folding

- Critical Assessment of protein Structure Prediction (CASP) bi-annual competition

- Predicting protein structures from amino acid sequences

- In the past two competitions, Google DeepMind used machine learning in their AlphaFold system to great success

AlphaFold 1 System

- The AlphaFold 1 System [2] consists of multiple components

- Specifically, the ML sub-component contains a supervised learning task

  - Input: amino acid sequence

  - Output: a matrix of inter-residue distances and torsion angles
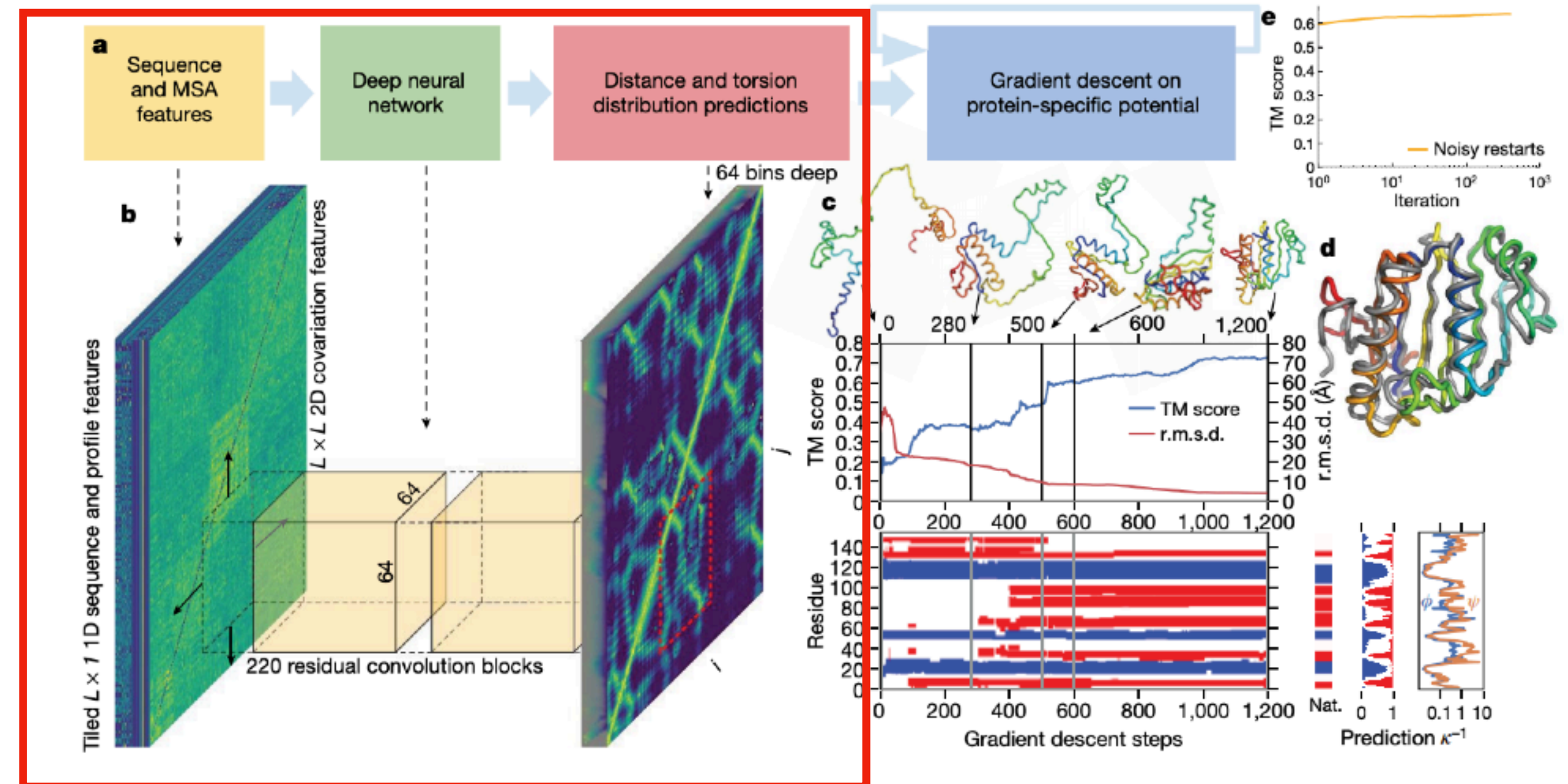
Machine learning portion of the AlphaFold 1 System

[2] Improved protein structure prediction using potentials from deep learning

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