AlphaFold Revolution

AlphaFold 2 Architecture

Input: Protein Sequence

Evoformer
(MSA Processing)

Pair Representation
(Residue Interactions)

Structure Module
IPA (Invariant Point Attention)

3D Protein Structure
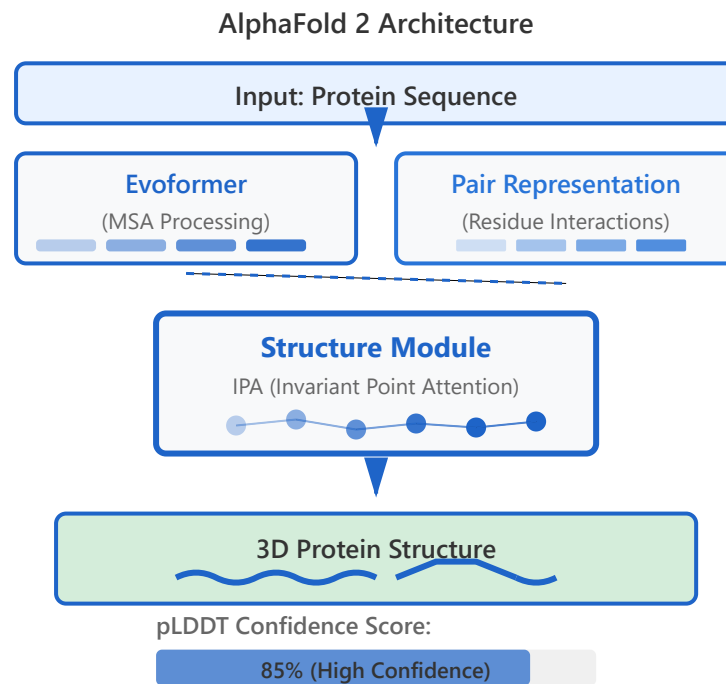
pLDDT Confidence Score:

85% (High Confidence)

Architecture innovations
Evoformer + Structure module

MSA processing
Evolutionary information extraction

Structure module
IPA: SE(3)-equivariant attention

Confidence metrics
pLDDT per-residue scores

Database impact
200M+ structures predicted