

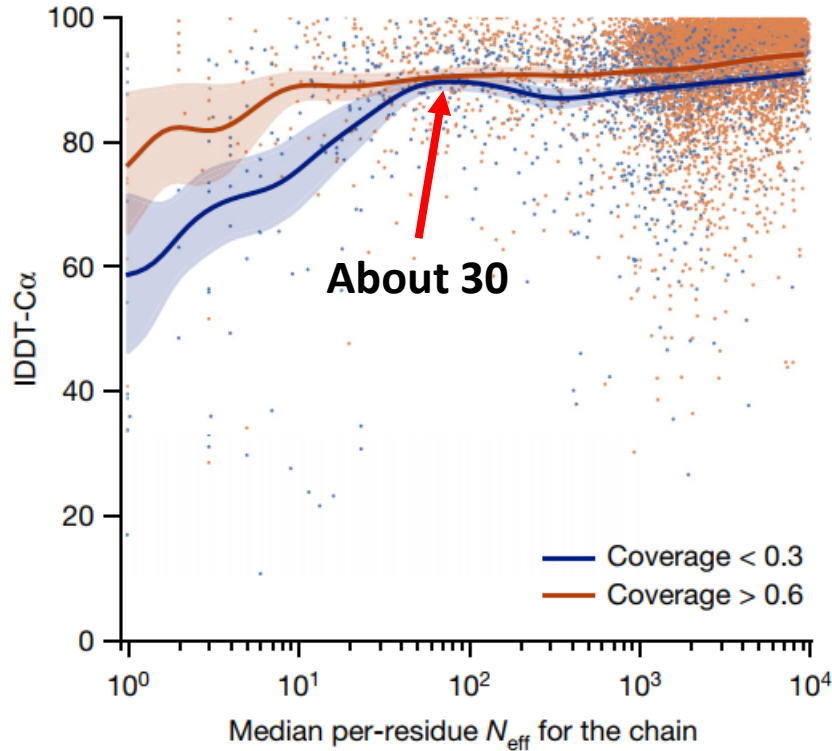
# Highly accurate protein structure prediction with AlphaFold

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# Influence of MSA depth



MSA information is needed to coarsely find the correct structure **within the early stages of the network**, but refinement of that prediction into a high-accuracy model does not depend crucially on the MSA information

# Summary

- What are the most important improvements for AF2 compared to other structure prediction tools?
- What does AF2 bring to the whole structural biology field?
- How will AF2 influence the techniques in structural biology, protein design, and drug development?
- What are the limitations of AF2?
  - Proteins that do not have enough template information...
  - Hetero-multimers...
  - ...