

ESMFold

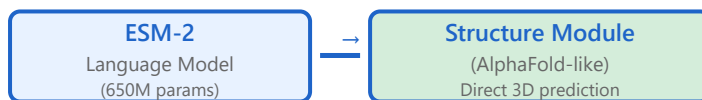
Language Model-Only Approach

Traditional (e.g., AlphaFold2):



⌚ Slow (minutes to hours)

ESMFold:



⚡ Fast (seconds)

Key Innovation: No MSA Required

- Evolutionary info learned directly from 250M+ protein sequences
- 60× faster than AlphaFold2 (seconds vs minutes)
- Enables metagenomic-scale structure prediction

Language model only

ESM-2 pretrained transformer

No MSA required

Single sequence input

Speed benefits

60× faster inference

Metagenomic applications

Unknown protein discovery

Limitations

Lower accuracy on orphan proteins