



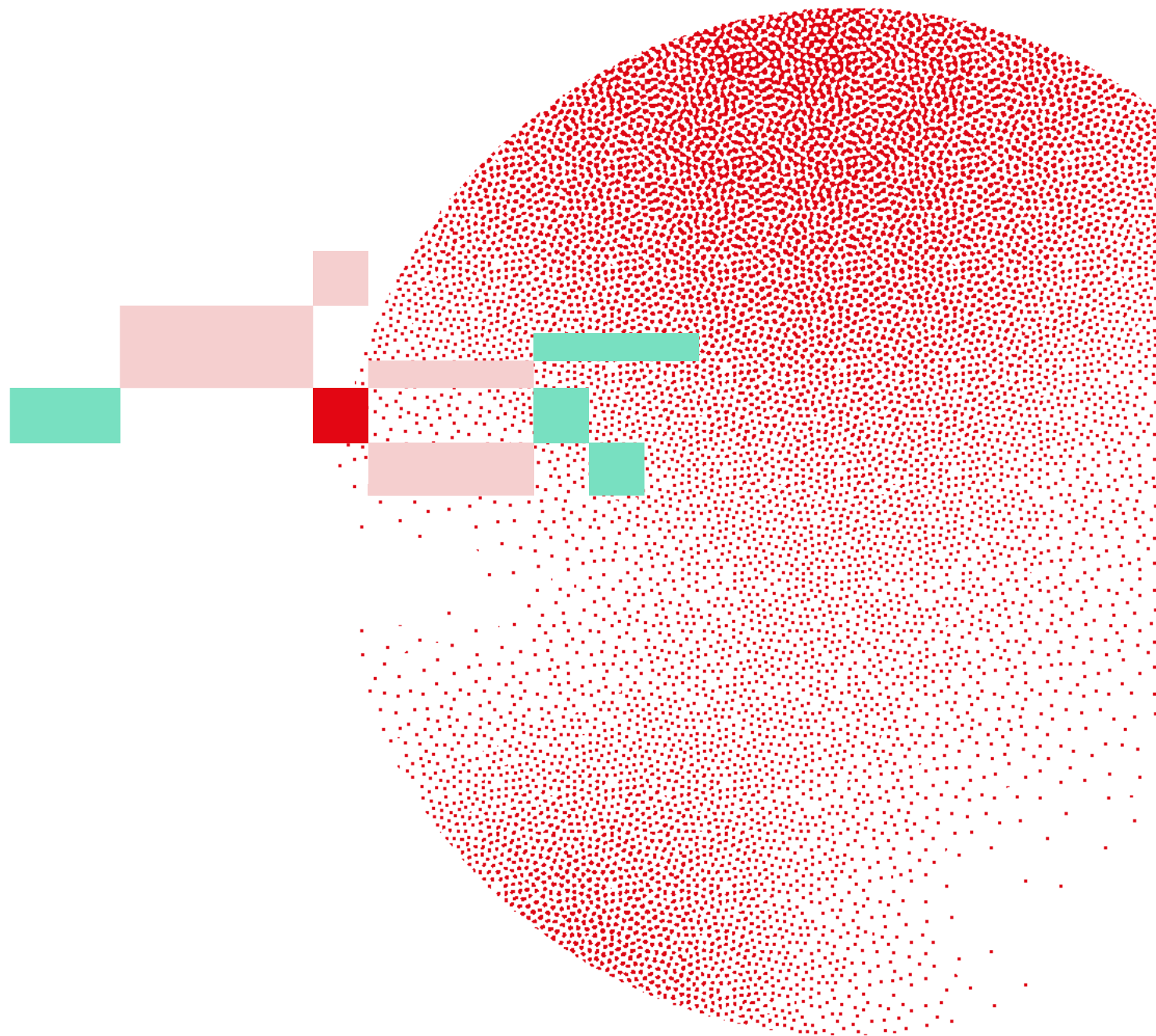
Swiss Institute of
Bioinformatics

DAY 2, PART 4

Bonus methods

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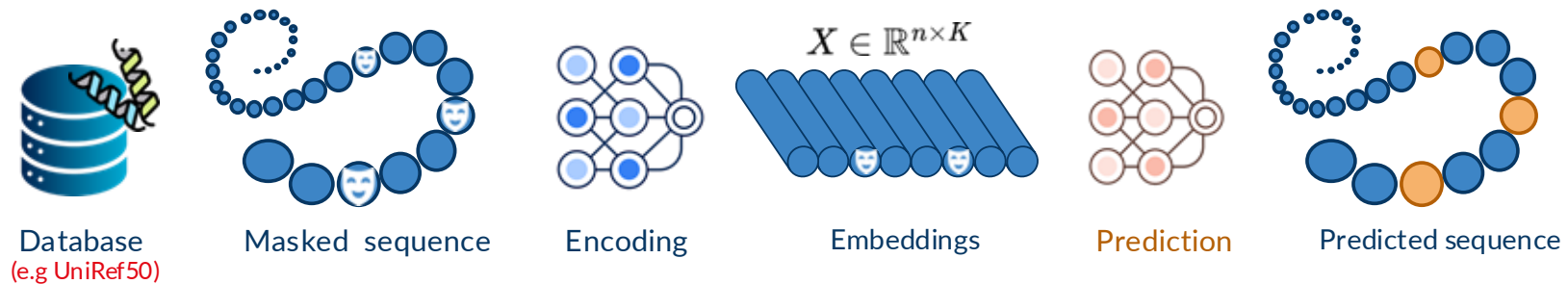
23-24 June 2026





ESM-2

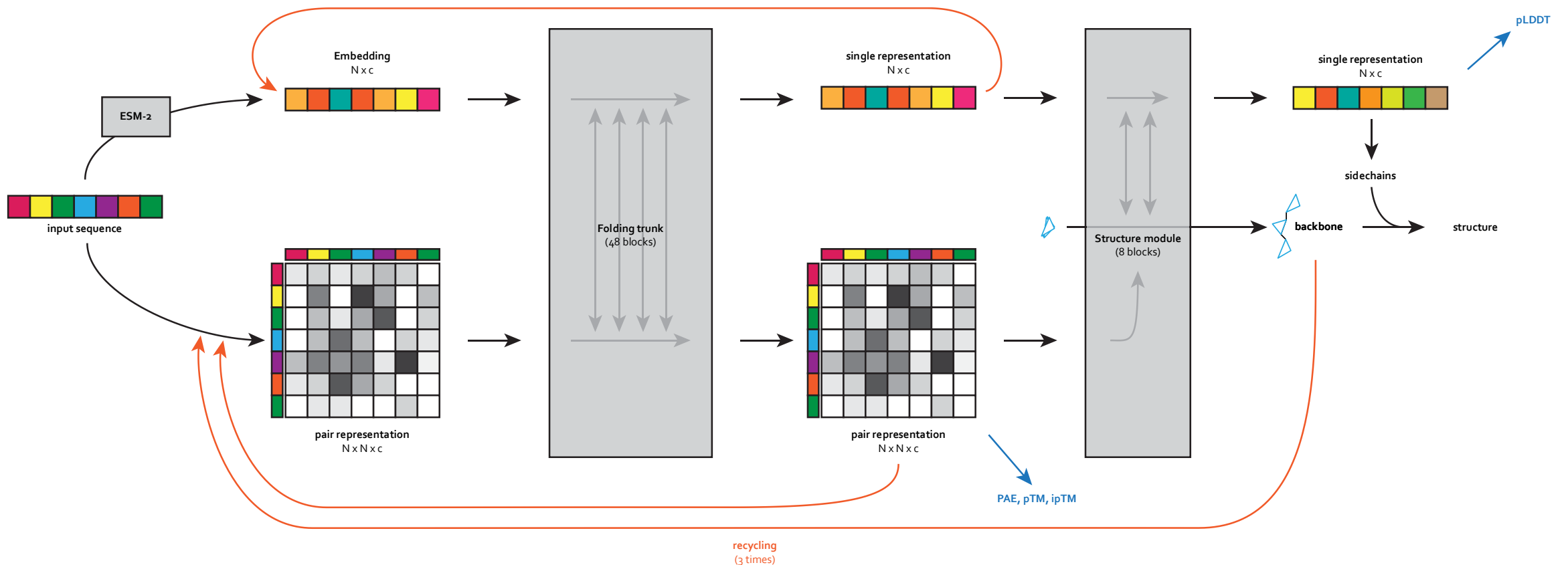
- Protein language model (pLM)
- Trained on 65 million sequences (compared to billions of sequences AlphaFold2 has access to when constructing an MSA)





ESMFold

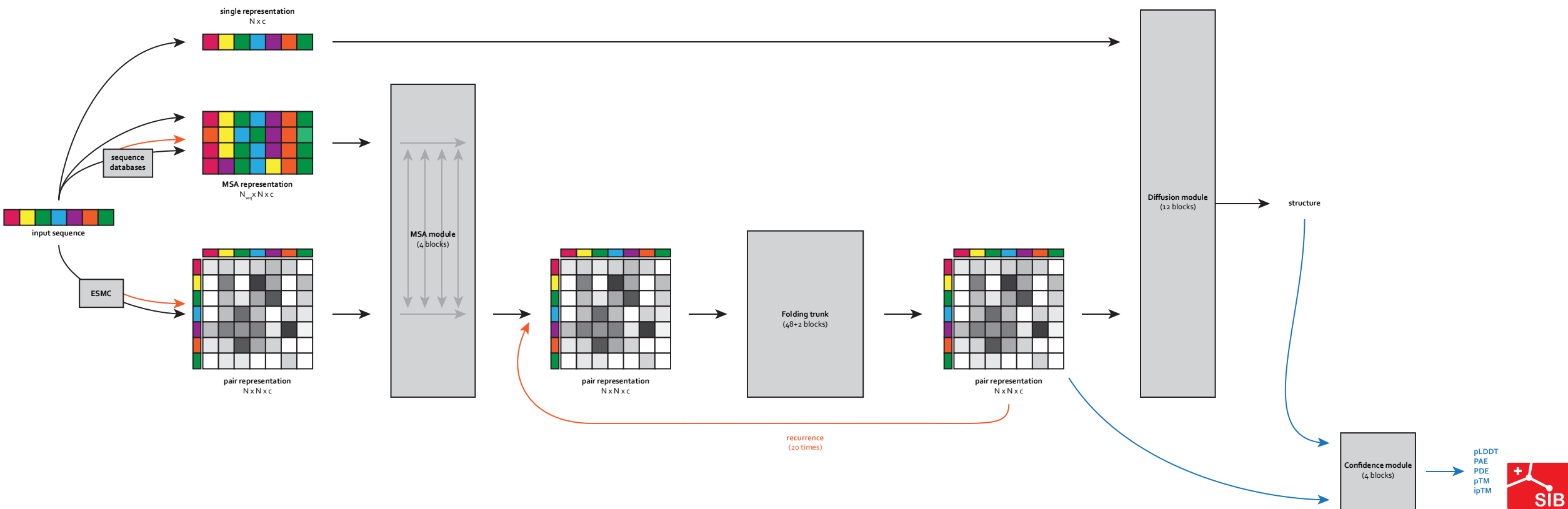
- Similar architecture as AlphaFold2, no templates and ESM-2 embedding instead of MSA → fast
- Doesn't perform as well as AlphaFold2





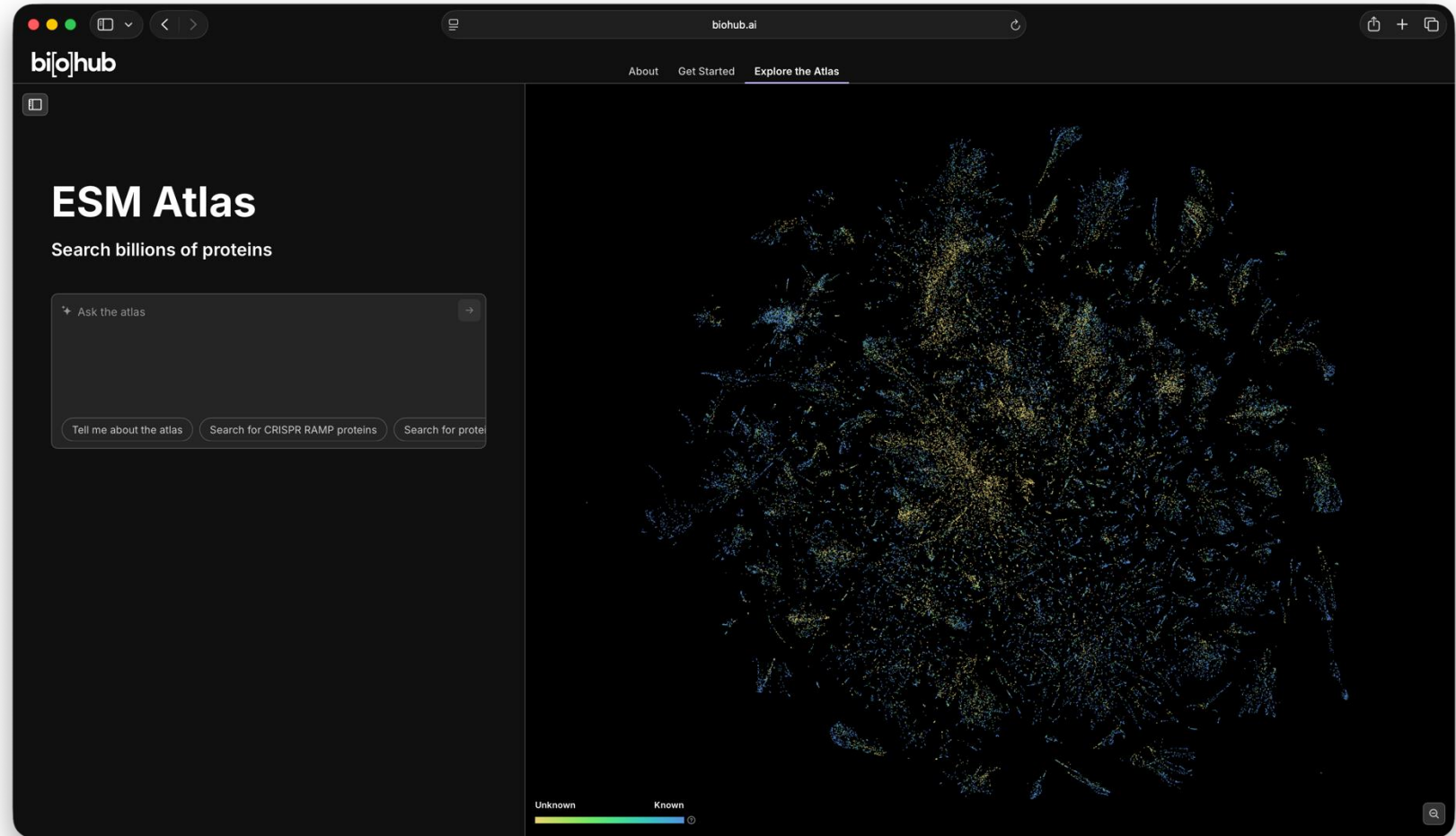
ESMC, ESMFold2

- Protein language (ESMC) trained on 2.8 billion sequences
- Different folding architecture (ESMFold2)
- Better at antibodies and protein-protein interactions; there is also a fast version

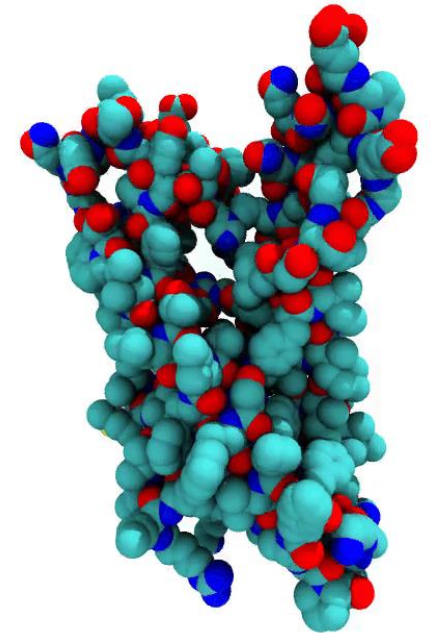


ESM Atlas

- 1.1 billion structures
- Using ESMFold2

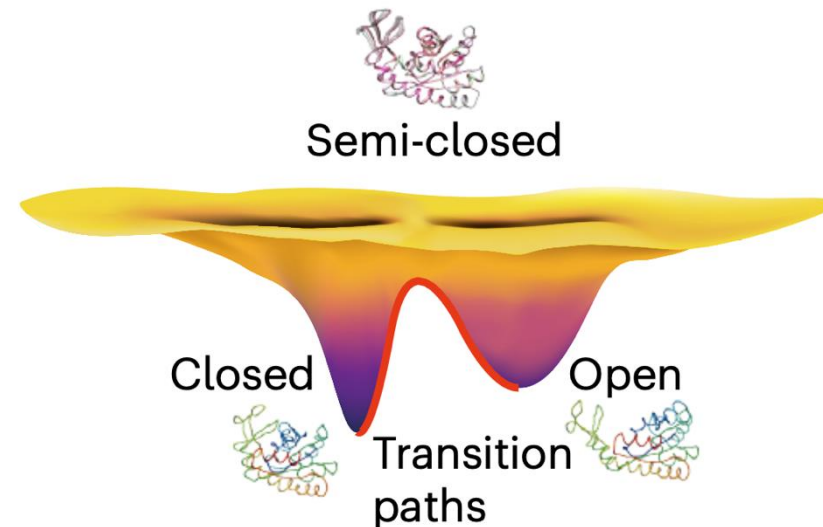


- AlphaFold is trained to predict only one conformation (crystal structure)
- Proteins are very dynamic in their native environment (solution, temperature, concentration)
- Methods to simulate protein dynamics:
 - MD – Molecular dynamics (physics based, takes a lot of time to simulate a few microseconds)





- Similar architecture to AlphaFold2
 - Replaces the structure module with a denoising diffusion model
- Trained to predict ensembles of conformations
 - Static structures, MD simulations, equilibrium distributions





Useful links

AlphaFold: A practical guide from EMBL-EBI:

<https://www.ebi.ac.uk/training/online/courses/alphafold/>

AlphaFold 3 guide:

<https://www.ebi.ac.uk/training/online/courses/alphafold/>

AFDB tutorial:

<https://www.ebi.ac.uk/training/events/accessing-and-interpreting-predicted-protein-structures-alfafold-database/>

ColabFold guide:

<https://doi.org/10.1038/s41596-024-01060-5>