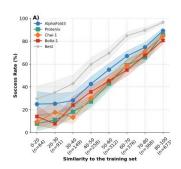
## Introducing OpenBind: Ed Griffen

**OpenBind** 

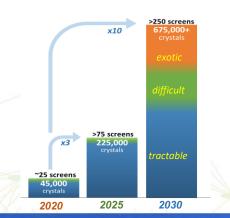


Cofolding methods are good where there are similar pockets and ligands – but not where there isn't the background data

Škrinjar, P.; Eberhardt, J.; Tauriello, G.; Schwede, T.; Durairaj, J. Have Protein-Ligand Cofolding Methods Moved beyond Memorisation? bioRxiv August 4, 2025, p 2025.02.03.636309. https://doi.org/10.1101/2025.02.03.636309.

- Goal: double/ treble PDB over 2 years with affinity data for every protein ligand pair; ultimately to increase PDB by 10x in 5-7 yr
- Centered at the UK Diamond Light Source with international partners
  - Seed funding (£8M) from UK Sovereign AI fund
- Building industrial partner group
- Recruiting

Ultra-High Throughput Crystallography



Automated Chemistry + Affinity

## measurements

- 3000 compounds3000 structures
- 3000 structure
   3000 affinities
- Design Make
  Algorithmic Robotic
  Analyze Test
  FEP, ML HT biophysics XChem

Use Model Rebuilding and Blind Challenges to drive up quality of Models







Open Data → Models → Challenges