Can Folding Models Tell Binders from Bluffers?

Evidence from POISK: The Patent-Derived Antibody Dataset

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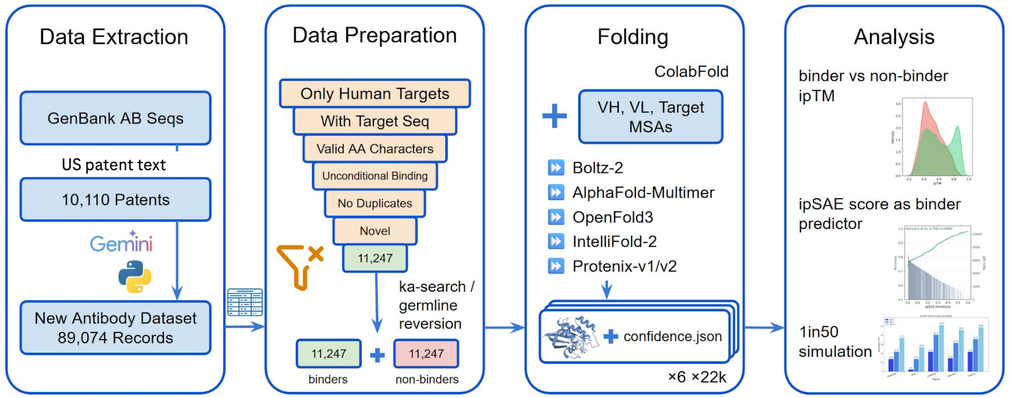
1 POISK: evidence beyond known structures

89,074 antibody–antigen records from 10,110 US patents,
covering >2,000 target sequences, with affinity and epitope annotations.

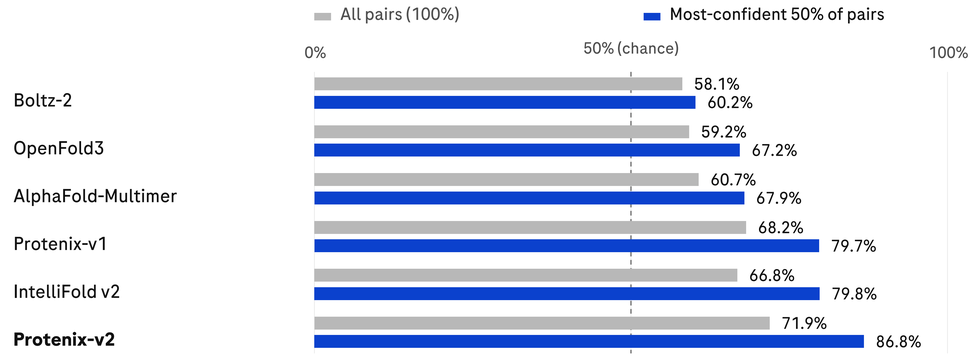


11,247 matched binder–decoy pairs; antibodies ≥95% identical to SAbDab excluded.
Shared MSAs; no templates. Decoys are putative negatives.

2 Useful enrichment, limited single-candidate recovery

Fv-target ipSAE separates binders from decoys better than ipTM.

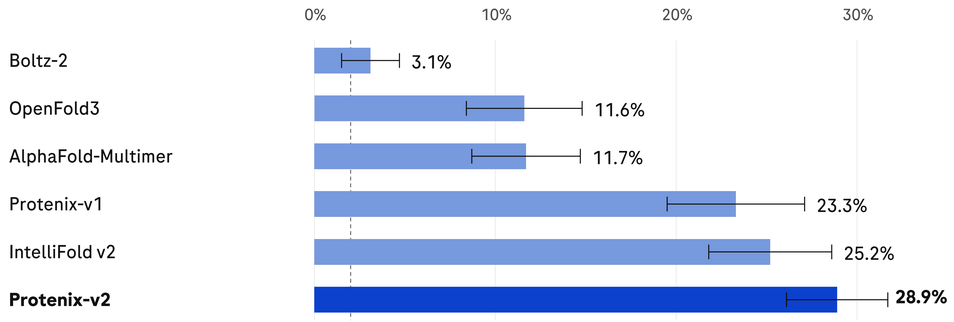
Binder–decoy pairwise accuracy



Higher ipSAE wins each pair; ties receive half credit. Dashed line: chance (50%).
50% coverage retains pairs with the highest max(binder, decoy) ipSAE.

Top-1 recovery among 50 candidates

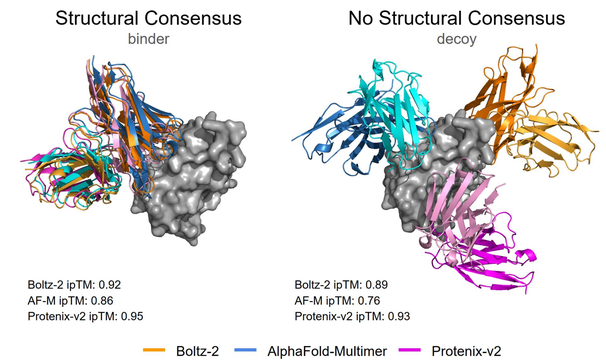
One binder + 49 decoys for the same antigen, ranked by ipSAE.



Dashed line: random (2%). Error bars: ±2 SD across 25 sampling runs;
540 trials/run across 27 antigen constructs.

Best top-1 recovery: 28.9% vs 2% random in the 1-in-50 benchmark.

3 Binding versus structural accuracy



Illustrative predictions for two antibodies against the same antigen.

Structural consensus

73.1% pairwise accuracy at 54.2% coverage when ≥3 models agree (DockQ ≥0.23).

Epitope localization remains limited

Protenix-v2 contacts ≥1 annotated epitope residue in 62.8% of 1,232 binders.

Contact: antibody–epitope heavy-atom distance ≤4Å.

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POISK: Patent-extracted Organization of Immunoglobulin Sequence Knowledge

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