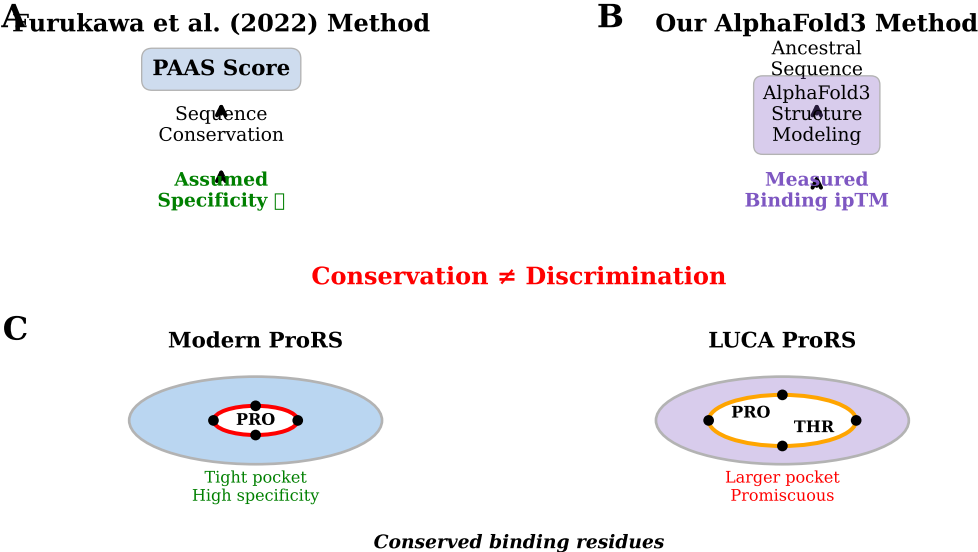


Figure 5: Methodological Comparison - Challenging Furukawa et al.



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Key Insight:

Furukawa et al. inferred ancestral specificity from sequence conservation. However, conserved residues can form a LARGER binding pocket in ancestors.

Our structural modeling reveals:

- LUCA ProRS: 89.7% promiscuity (THR binds at 89.7% of PRO affinity)
- Eukaryotic ancestor: 84.8% promiscuity
- Modern human: 97.5% promiscuity

Conclusion: Ancient translation systems tolerated high error rates. Conservation of residues does not imply conservation of specificity.