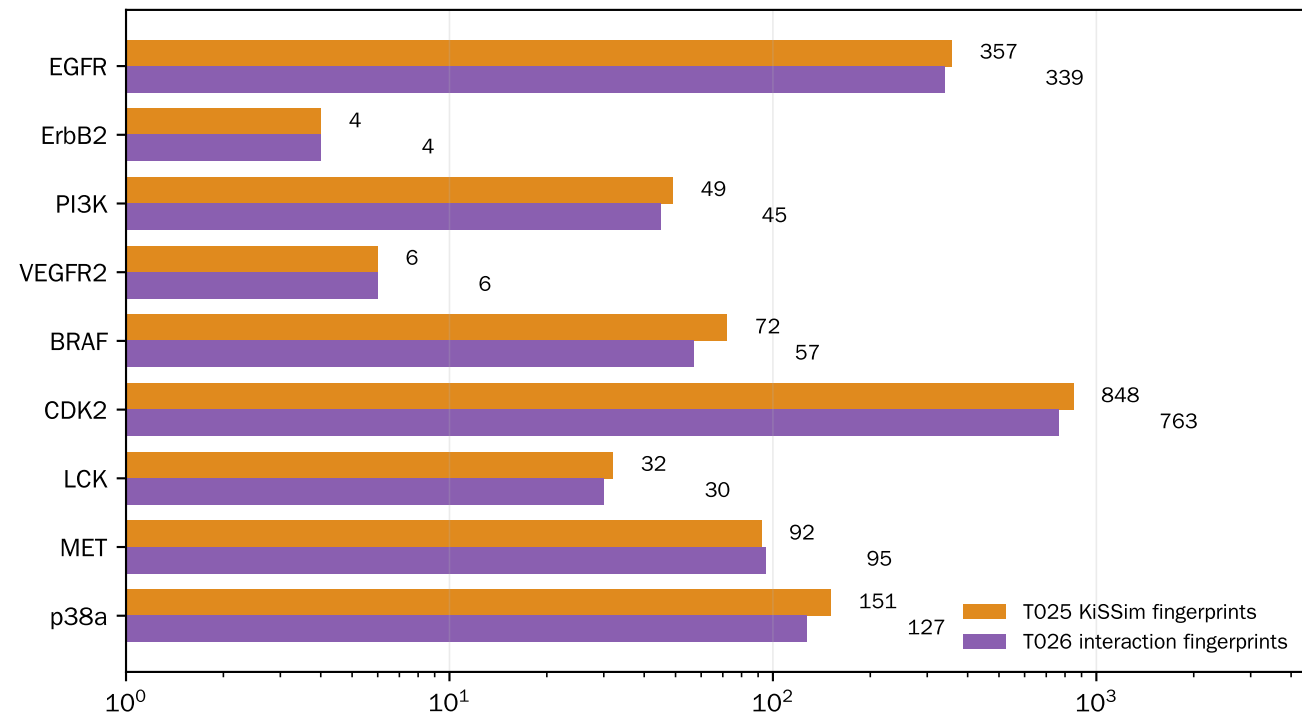


Cohort and per-view coverage - the 9-kinase TeachOpenCADD cohort

A Structural evidence per kinase is very uneven



structures with a published descriptor (log scale)
 Cohort = the 1620 frozen KLIFS structure IDs of T023-T027. T025 retains 1611 structures with a shipped KiSSim fingerprint; T026 retains 1466 with a published KLIFS interaction fingerprint (154 returned no fingerprint - that is a missing annotation, not an absence of interactions). T024 compares one canonical 85-position pocket sequence per kinase. T027 ships only a derived matrix, so the number of jointly measured compounds behind it cannot be recovered from the pack.

B What each view compares, and what it cannot

