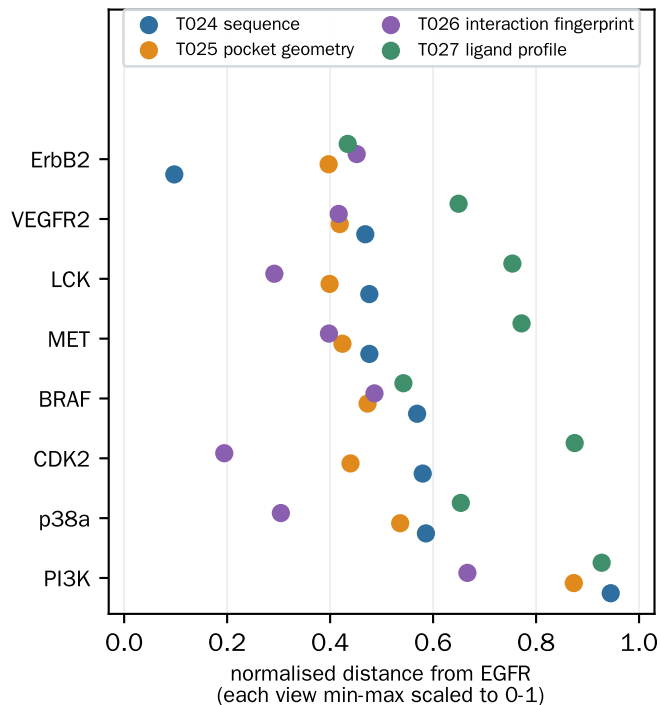


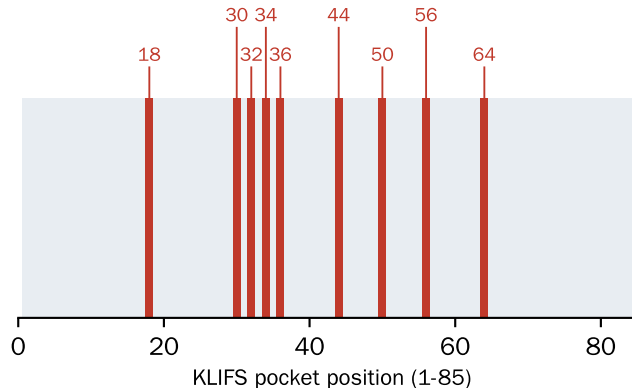
EGFR selectivity dossier: three views point to ErbB2, one points elsewhere

A EGFR's distance to every other kinase

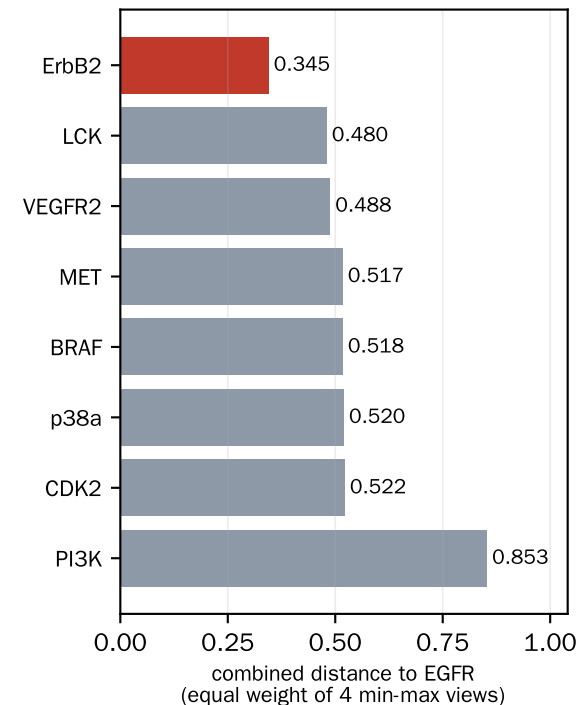


B Where the EGFR and ErbB2 pockets differ

position: EGFR > ErbB2
 18: E>V 30: S>G 32: D>G 34: H>Y 36: C>S
 44: I>V 50: F>Y 56: Y>H 64: R>V



C Combined view (ranked)



Panel A puts all four views on one axis by min-max normalising each view to 0-1 (raw units are NOT comparable: KiSSim distance runs ~16-41 while the other three run 0-1, so a shared raw axis would be misleading); the un-normalised values are in the companion CSV. Panel B marks the nine KLIFS pocket positions where the EGFR and ErbB2 pocket sequences differ, with the position numbers staggered and listed as a correspondence table because positions 30-36 are adjacent. Panel C is ranked by the actual combined distance, three decimals, so close pairs such as 0.480/0.488 stay distinguishable. Read together: the sequence, pocket-geometry and ligand-profile views place ErbB2 closest to EGFR, while the interaction-fingerprint view places CDK2 first - and that view covers ErbB2 with only 4 structures against CDK2's 763. These are similarity hypotheses, not measured selectivity.