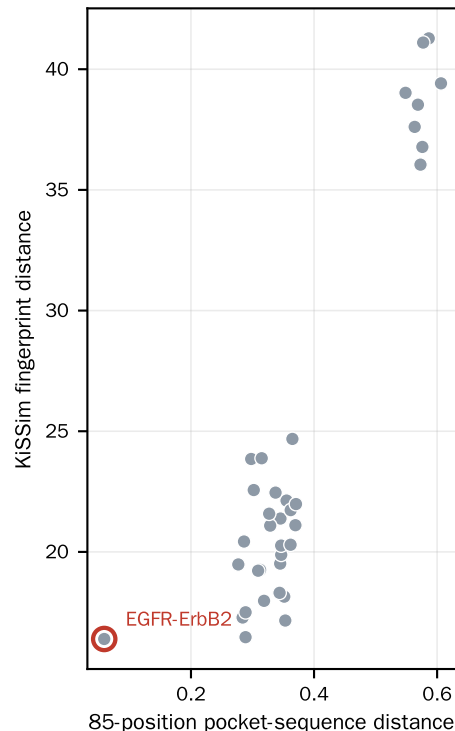


All six view pairs correlate positively ($r = 0.31-0.73$); 3 of 6 reach $p < 0.05$; T027 is the weakest

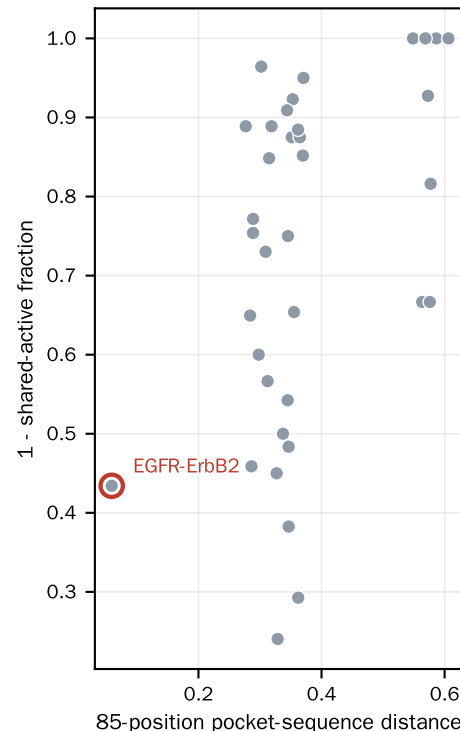
A Do the views rank pairs alike?

T024 sequence		0.70 $p=0.003$	0.50 $p=0.046$	0.43 $p=0.068$
T025 pocket geometry	0.70 $p=0.003$		0.73 $p=0.002$	0.31 $p=0.222$
T026 interaction fingerprint	0.50 $p=0.046$	0.73 $p=0.002$		0.36 $p=0.154$
T027 ligand profile	0.43 $p=0.068$	0.31 $p=0.222$	0.36 $p=0.154$	
	T024	T025	T026	T027

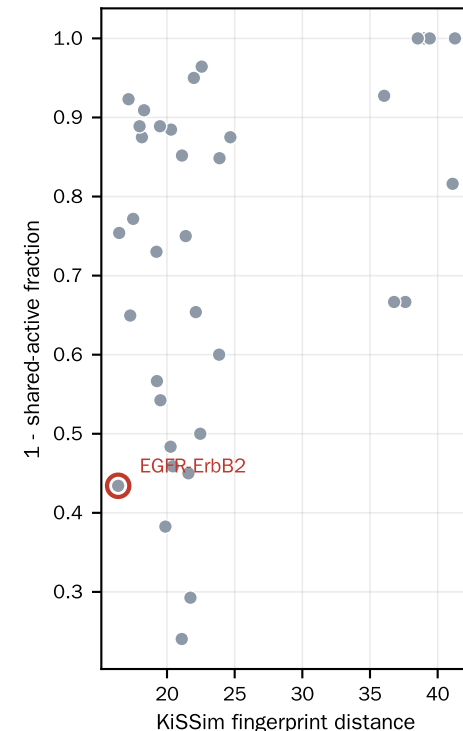
B Spearman $r = 0.70$



C Spearman $r = 0.43$



D Spearman $r = 0.31$



Spearman r over the 36 off-diagonal kinase pairs (no fixed agreement threshold is applied: the six values range 0.31-0.73 and three of them reach $p < 0.05$). Mantel p is the finite-sample estimator $(\text{extreme count} + 1)/(20000 + 1)$, seed 42, raw counts saved in results/agreement_extreme_count.csv. These 36 pairwise distances are derived from 9 kinases, so they are NOT 36 independent biological samples and the p -values are descriptive only - they support 'the rankings are related', not a confirmatory hypothesis test about targets. Panels B-D are the same 36 pairs; the ring marks EGFR-ErbB2, the pair with the smallest x -value in every panel.