Directory	Sites	Ligands	Method	Notes
Cyp_CsA+	1	1	fluorescence intensity	**Basic protein-ligand Kd determination** ***Cyp*** = recombinant human cyclophilin ***CsA+*** = Cyclosporin A labeled with a fluorescent probe (+) This is the control experiment, a prerequisite for analysis of competitive displacement assay data using the unlabeled CsA (molecule of interest)
Cyp_CsA_CsA+	1	2	fluorescence intensity	**Competitive ligand displacement assay** ***Cyp*** = recombinant human cyclophilin **CsA** = Cyclosporin A **CsA+** = Cyclosporin A labeled with a fluorescent probe (+) Kd for the spectroscopically "invisible" ligand is determined by a competing out the "visible" ligand from the protein-ligand complex. Compare two methods of analysis: (1) determine Kd for CsA+ separately, or (2) determine both Kd's simultaneously.
RIZ1_H3pep	1	1	NMR	**NMR chemical shift titration to determine weak protein-protein Kd** ***RIZ1*** = tumor supporesor protein ***H3pep*** = synthetic peptide representing histone H3 Combine chemical shifts for multiple nuclei (^{1}H and/or ^{15}H) to increase overall sensitivity of Kd measurement.
TDG_16U11+	2	1	fluorescence polarization	**Two binding sites: one strong ("specific") and one weak ("nonspecific")** ***TDG*** = thymine DNA glycosylase ***16U11+*** = Texas Red (+) labeled 28 bp DNA fragment, U as target nucleotide Two-site vs. one-site model discrimination analysis.
ThT_22AG	4	1	ESI-MS	**Mass spectrometry titration: Four cooperative binding sites** ***ThT*** = Thioflavin T ***22AG*** = human telomeric G-quadruplex sequence dAGGG(TTAGGG)$_3$ "Progressive cooperativity": Each added ligand is causing the subsequent ligand to bind ever more strongly (up to four binding sites).
WIN61651_p56lck	2	2	^{32}P liquid scintillation counting	**Initial rate enzyme kinetics: determine mechanism / mode of inhibition** ***WIN61651*** = small molecule kinase inhibitor (Sterling Winthrop) ***p56lck*** = p56^{lck} kinase Determining the mode of inhibition (competitive, non-competitive, mixed type) is strongly affected by substrate inhibition.
Lig_Prot_BDom	1	2	(unspecified)	**Full-length protein and just the binding domain compete for a ligand of interest** ***Lig*** = some type of ligand (undisclosed) ***Prot*** = some type of protein (undisclosed) ***BDom*** = a binding domain taken out of this protein and expressed separately The purpose of this experiement is to determine the affinity (Kd) between the binding domain and the ligand. One big problem is that only the binding to the full-length protein can be observed, and -- most importantly -- the binding to the full length protein is approximately 50 times weaker than binding to the binding domain. This very large difference in binding affinities presents a significant challenge for experiment design.