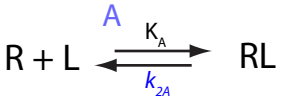
1:1 binding mechanisms

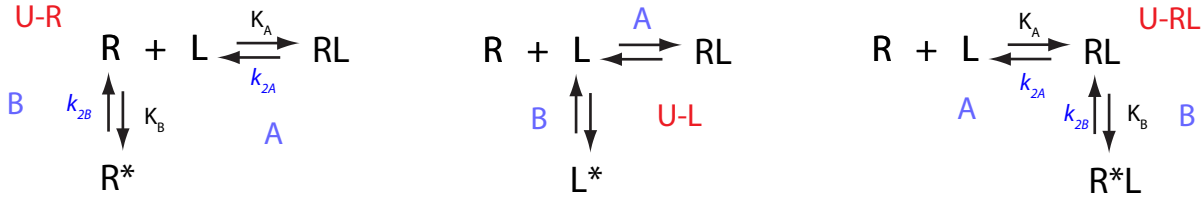
General convention:
R - receptor, NMR observable species;
L- ligand, NMR invisible
My code (molecularity-highest order species)
Transition name: A, B, C...

Generic 1:1 binding



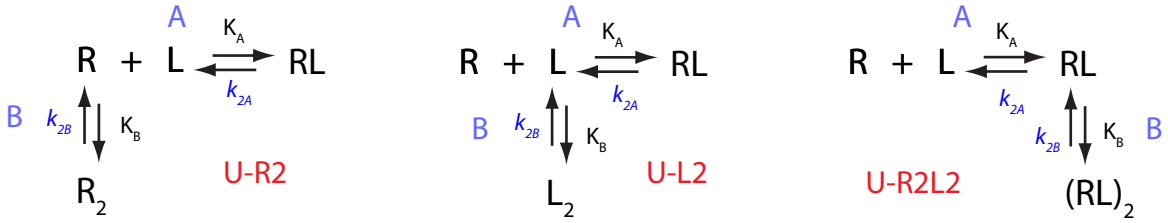
U

1:1 binding coupled with a unimolecular dead-end interconversion



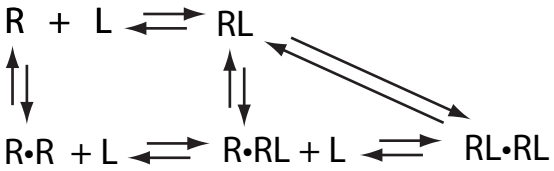
In these reactions we have concentration-independe isomerization that simply equilibrium concentration may only manifest itself th rate-limitation phenomen producing 'linear' populat changes on titration.

1:1 binding coupled with a dead-end dimerization reaction



In these reactions the dead-end complex formation depends on concentration so will both influence population profiles (ITC) as well as kinetic behavior through rate-limitation.

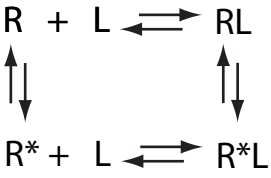
1:1 binding coupled with a binding-competent dimer formation



B-R2-R2L2

U-RL-RL reaction scheme includes dimeriza- tion steps described above and adds a balance between the dimeric species through parallel ligand binding equilibria. We should see both non-linear population changes in the course of titration as well as rate-limitation phenomena.

Parallel 1:1 binding reactions coupled via unimolecular receptor isomerization

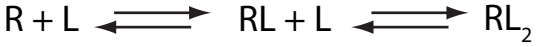


U-R-RL

U-R-RL reaction scheme includes concentration-independent isomerization steps and adds a balance between the isomers through parallel ligand binding equilibrium. Equilibrium concentration of species will be scaled by isomerization reactions, which will only manifest themselfs in rate-limitation phenomena.

1:2 binding mechanisms

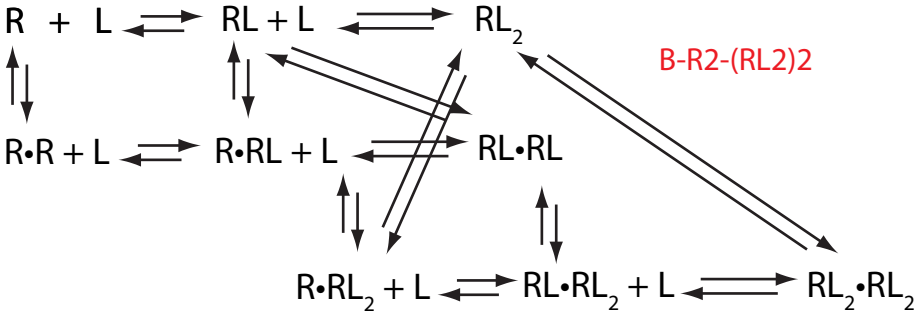
Generic 1:2 binding



B

B mechanism will produce both non-linear population changes and rate-limitation steps.

1:2 binding coupled with a dimerization reaction



B-R2-(RL2)2

B-R2-(RL2)2 reaction scheme includes dimerization steps as well as second ligand binding steps. The scheme is overly complicated and only useful in some of its limiting cases . Which cases are related to real world?