

Protein-protein Interactions (PPI) Library

PPI focused library contains about **142K** compounds, **2250** templates
 number of unique heterocycles: 810, diversity coefficient: 0,805, number of screens: 10669

Principles of Design:

- Diversity
- 3D-Shape
- Escape from flatland, High SP3
- Drug-likeness
- Natural product likeness
- Targeted Diversity

Structure of the library

- Library consists of several complementary parts:
 Nonpeptide Peptidomimetics (based on the PPI biased substructures) ~25K compounds
- Set of Recognition Elements (gamma-, beta-turns, dipeptide mimetics) ~30K compounds
- Tripeptide mimetics ~3K compounds
- Shape (helix, beta-sheet, strand, loop) mimetics ~10K compounds
- 3D-mimetics (single Isomers, caged compounds, etc.) ~3K compounds
- Set of Spiro-compounds ~5.5K compounds
- Set of Unusual compounds ~7K compounds
- Set of cyclic Ugi-compounds ~40K compounds
- Set "Escape from Flatland" ~30K compounds
- PDZ-domain inhibitors ~ 5K compounds
- MDM2 binding inhibitors ~8K compounds
- CD16a binding inhibitors ~2K compounds
- pGPCRs Focused sub-libraries:
- Chemokines ~10K compounds
- Hedgehog pathway ~10K compounds
- Neurotensin ~2K compounds

154 < MW < 863; 420 on average
 0 < H-bond acceptors < 15; 5 on average
 0 < H-bond donors < 9 1 on average
 0 < rotatable bonds < 20; 6 on average
 -8.0 < logD (pH 7.4) < 12.2; 3.7 on average
 -14.4 < log of solubility in water (pH 7.4) < 15.3;
 -3.9 on average 0 < percentSP3 < 100; 34.8 on average

