

Poster presentation

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## EAI-TupletScore, a pharmacophore and shape driven ligand-based de-novo design algorithm

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We describe a ligand-based de-novo design algorithm EAI-TupletScore and studies that demonstrate its ability to successfully generate lead hops between different classes of active ligands from the DUD dataset [1]. EAI-TupletScore uses the de-novo design engine EA-Inventor with a Pareto-Borda [2][3] scoring method that employs pharmacophore and steric tuples [4], as well as UNITY fingerprint similarities to a set of lead compounds to design novel ligands that maximize pharmacophore and shape similarity, while maintaining a certain level of structural dissimilarity, to these lead compounds. EAI-TupletScore, can be used to design novel ligand scaffolds (lead generation or lead hopping) or to optimize attachments on a fixed scaffold (lead optimization).

### References

1. Good AC, Oprea TI: *J Comput Aided Mol Des* 2008, **22**(34):169-178.
2. Alberto I, Azcarate C, Mallor F, Mateo PM: *Monografias del Semin Matem Garcia de Galdeano* 2003, **27**:27-35.
3. Coello CAC, Van Veldhuizen DA, Lamont GB: *Evolutionary algorithms for solving multi-objective problems* Springer, New York; 2007.
4. Abrahamian E, Fox PC, Nærum L, Christensen IT, Thøgersen H, Clark RD: *J Chem Inf Comput Sci* 2003, **43**(2):458-46.