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## January 15, 2015

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<signature of Bruce Donald>, Mar 1, 2012
Bruce Donald, Professor of Computer Science

# 2 Citation Requirements

The citation requirements for the various different modules of our software are:

- For a general citation, please use:
  - C. Chen, I. Georgiev, A. C. Anderson, and B. R. Donald. Computational structure-based redesign of enzyme activity. *PNAS USA*, 106(10):3764–3769, 2009.
  - P. Gainza, K. E. Roberts, I. Georgiev, R. H. Lilien, D. A. Keedy, C. Chen, F. Reza, A. C. Anderson, D. C. Richardson, J. S. Richardson, and B. R. Donald. OSPREY: Protein design with ensembles, flexibility, and provable algorithms. *Methods in Enzymology*, 523:87-107, 2013.

#### • iMinDEE:

P. Gainza, K.E. Roberts, and B.R. Donald. Protein Design using Continuous Rotamers *PLoS Computational Biology*, (1): e1002335. doi:10.1371/journal.pcbi.1002335, 2012.

### • Protein:Protein Interactions:

K.E. Roberts, P.R. Kushing, P. Boisguerin, DR Madden, and B.R. Donald. Design of protein-protein interactions with a novel ensemble-based scoring algorithm. *Research in Computational Molecular Biology.*, volume 6577 of Lecture Notes in Computer Science. Heidelberg: Springer Berlin. pp. 361376. 2011

K.E. Roberts, P.R. Kushing, P. Boisguerin, DR Madden, and B.R. Donald. Computational Design of a PDZ Domain Peptide Inhibitor that Rescues CFTR Activity. *PLoS Computational Biology*., 8.4:e1002477, 2012.

## • MinDEE:

I. Georgiev, R. Lilien, and B. R. Donald. The minimized dead-end elimination criterion and its application to protein redesign in a hybrid scoring and search algorithm for computing partition functions over molecular ensembles. *J Comput Chem*, 29(10):1527–42, 2008.

## • BD:

I. Georgiev and B. R. Donald. Dead-end elimination with backbone flexibility. *Bioinformatics*, 23(13):i185–94, 2007. Proc. International Conference on Intelligent Systems for Molecular Biology (ISMB), Vienna, Austria (2007).

#### • Brdee:

I. Georgiev, D. Keedy, J. S. Richardson, D. C. Richardson, and B. R. Donald. Algorithm for backrub motions in protein design. *Bioinformatics*, 24(13):i196–204, 2008. Proc. International Conference on Intelligent Systems for Molecular Biology (ISMB), Toronto, Canada (2008).

#### • *DACS*:

I. Georgiev, R. Lilien, and B. R. Donald. Improved pruning algorithms and divide-and-conquer strategies for dead-end elimination, with application to protein design. *Bioinformatics*, 22(14):e174–183, 2006. Proc. International Conference on Intelligent Systems for Molecular Biology (ISMB), Fortaleza, Brazil (2006).

## • $K^*$ (current implementation):

I. Georgiev, R. Lilien, and B. R. Donald. The minimized dead-end elimination criterion and its application to protein redesign in a hybrid scoring and search algorithm for computing partition functions over molecular ensembles. *J Comput Chem*, 29(10):1527–42, 2008.

To cite the general idea of  $K^*$ , you can also cite:

R. Lilien, B. Stevens, A. Anderson, and B. R. Donald. A novel ensemble-based scoring and search algorithm for protein redesign, and its application to modify the substrate specificity of the Gramicidin Synthetase A phenylalanine adenylation enzyme. *J Comp Biol*, 12(6–7):740–761, 2005.

## • DEEPer:

M. A. Hallen, D. A. Keedy, and B. R. Donald. Dead-End elimination with perturbations (DEEPer): A provable protein design algorithm with continuous sidechain and backbone flexibility. *Proteins*, 81(1):18-39, 2013.

#### • COMETS:

M. A. Hallen and B. R. Donald. COMETS (Constrained Optimization of Multistate Energies by Tree Search): A provable and efficient algorithm to optimize binding affinity and specificity with respect to sequence. *Research In Computational Molecular Biology (RECOMB)* proceedings, in press, 2015.

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To do so, attach the following notices to the program. It is safest

to attach them to the start of each source file to most effectively state the exclusion of warranty; and each file should have at least the "copyright" line and a pointer to where the full notice is found.

<one line to give the program's name and a brief idea of what it does.>
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