

# HASH License

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HASH is an automated program for predicting  $H^\alpha$  chemical shifts using the chemical shifts of nearby backbone atoms (i.e., adjacent atoms in the sequence). HASH combines a new fragment-based chemical shift search approach with a non-parametric regression model, called the generalized additive model, to effectively solve the prediction problem. HASH is developed in the lab of Prof. Bruce Donald at Duke University.

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<signature of Bruce Donald>, 01 May, 2012  
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- [a] Jianyang Zeng, Pei Zhou, and Bruce Randall Donald. HASH: a program to accurately predict protein Ha shifts from neighboring backbone shifts. *Journal of Biomolecular NMR*, 2013 (in press).

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