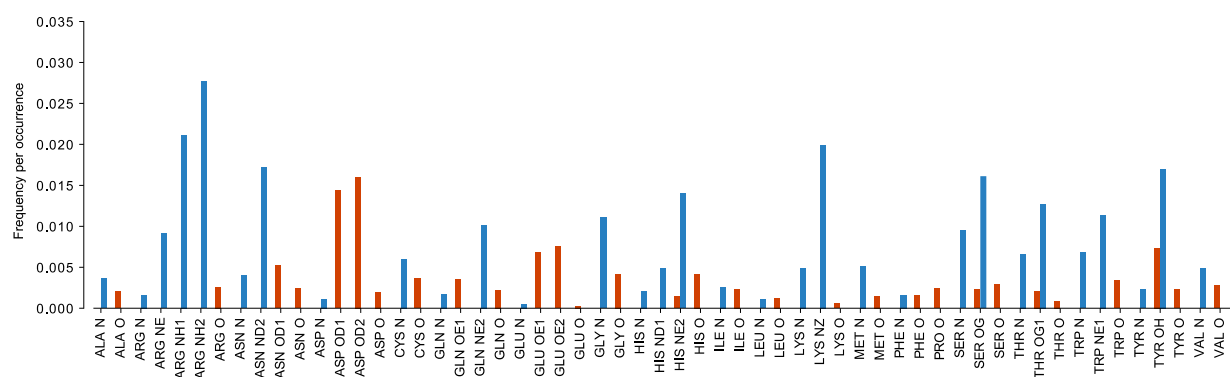


## Supplementary Material for

"Protein-ligand interfaces are polarized:

Discovery of a strong trend for intermolecular hydrogen bonds to favor donors on the protein side with implications for predicting and designing ligand complexes" by Sebastian Raschka, Alex Wolf, Joseph Bemister-Buffington, and Leslie A. Kuhn, *Journal of Computer-Aided Molecular Design*



**Fig. S1** Intermolecular H-bonds formed by each amino acid atom type in ligand binding sites. Similar to Fig. 6 (b), but instead of normalizing by binding site occurrence, the frequency is normalized by the total number of times each amino acid atom type occurs in the whole protein