Docking protocols and scoring functions for structure-based virtual screening and ligand design are aiming at identifying the preferred ligand orientations and conformations (poses) within a protein and estimating the protein-ligand binding affinities. Classical force field approaches perform quite well in pose prediction, i.e. they provide binding energies suitable to compare different conformations and poses of one ligand. However, force field energies are too inaccurate to reliably compare complexes with different ligands. Moreover, solvent effects are usually taken into account as corrections to the force field terms at the cost of significantly more computational effort and/or additional inaccuracies. We present a virtual screening protocol which uses an empirical pose generator and a classical force field for refining and filtering the poses. The poses are then scored with our novel scoring function HYDE. HYDE evaluates hydrogen bonds and solvent effects solely based upon solvent accessible surfaces, exp. logP values of small molecules and a new water theory. HYDE parameters are not fitted towards experimental protein-ligand binding energies. Nonetheless, our docking protocol provided superior hit enrichments in various validation runs.