Supporting Information

An *In Silico* Approach to Discovering Novel Inhibitors of Human Sirtuin Type 2

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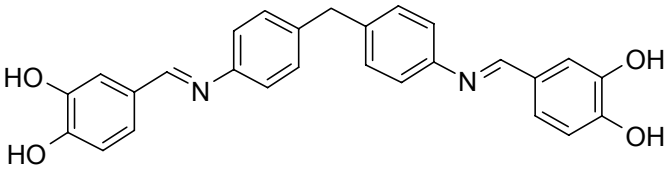
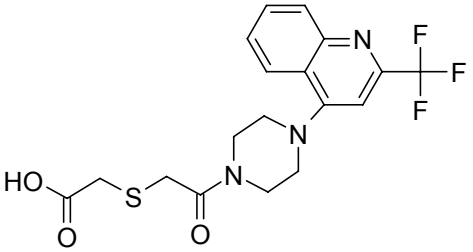
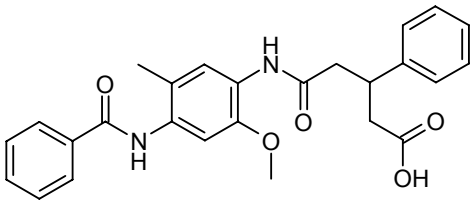
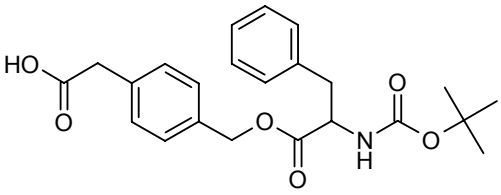
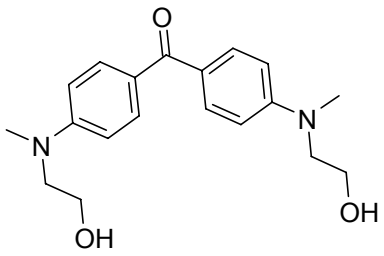
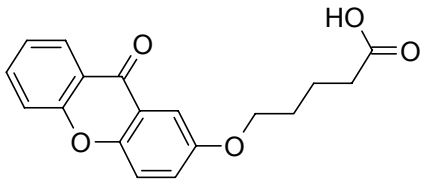
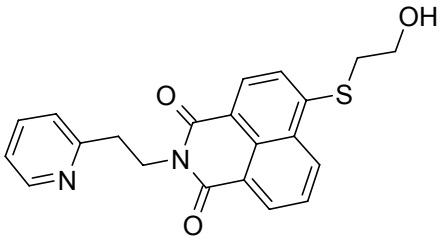
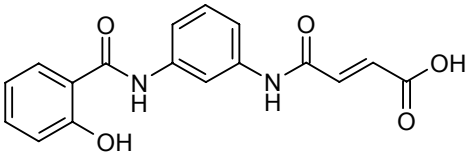
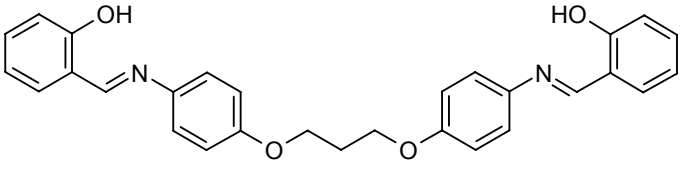
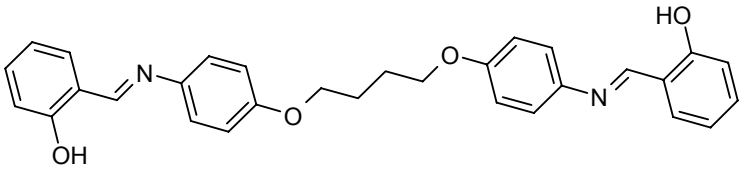
Table 1. Structures of the ten candidate hit compounds found to be inactive *in vitro*. The compounds had a measured inhibitory activity value (IC_{50}) over 1 mM for SIRT2.

Compd	Structure	Code[a]
1		CD01000
2		HTS01146
3		HTS06057
4		JFD01599
5		JFD02724
6		JFD03169

7		PHG01042
8		RDR01526
9		RDR01977
10		RDR01978

[a] Compound code numbers from Maybridge database.

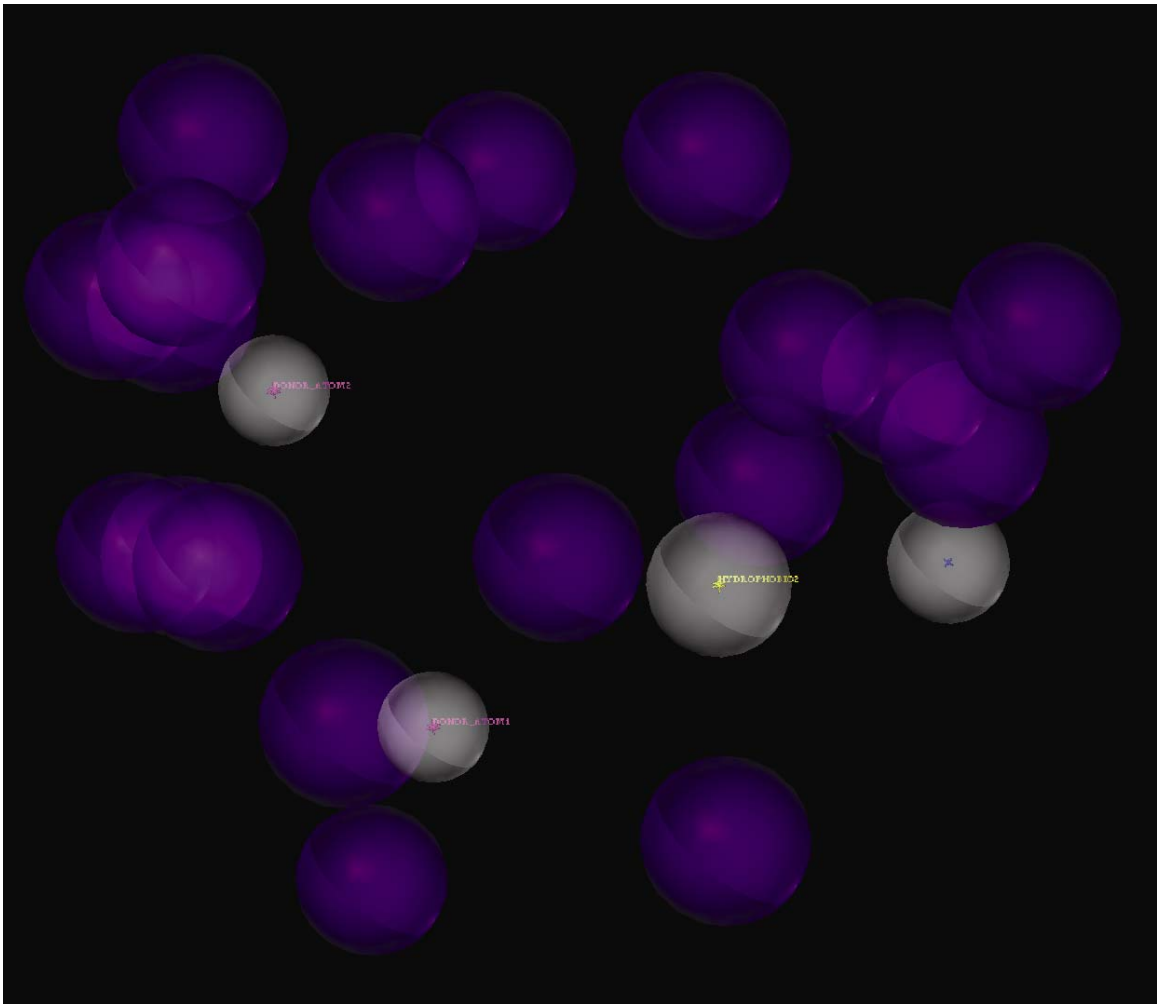


Figure 1. Graphical representation of the first database search query. Violet balls represent excluded volumes for outlining the putative SIRT2 active site. Gray balls with a magenta notation represent a donor atom at a tolerance of 1.0 Å. Candidate hit compounds were required to have at least one of these two donors. A gray ball with a yellow notation represents a hydrophobic feature at a tolerance of 1.3 Å. A gray ball without a notation represents an OH or SH group at a tolerance of 1.1 Å.

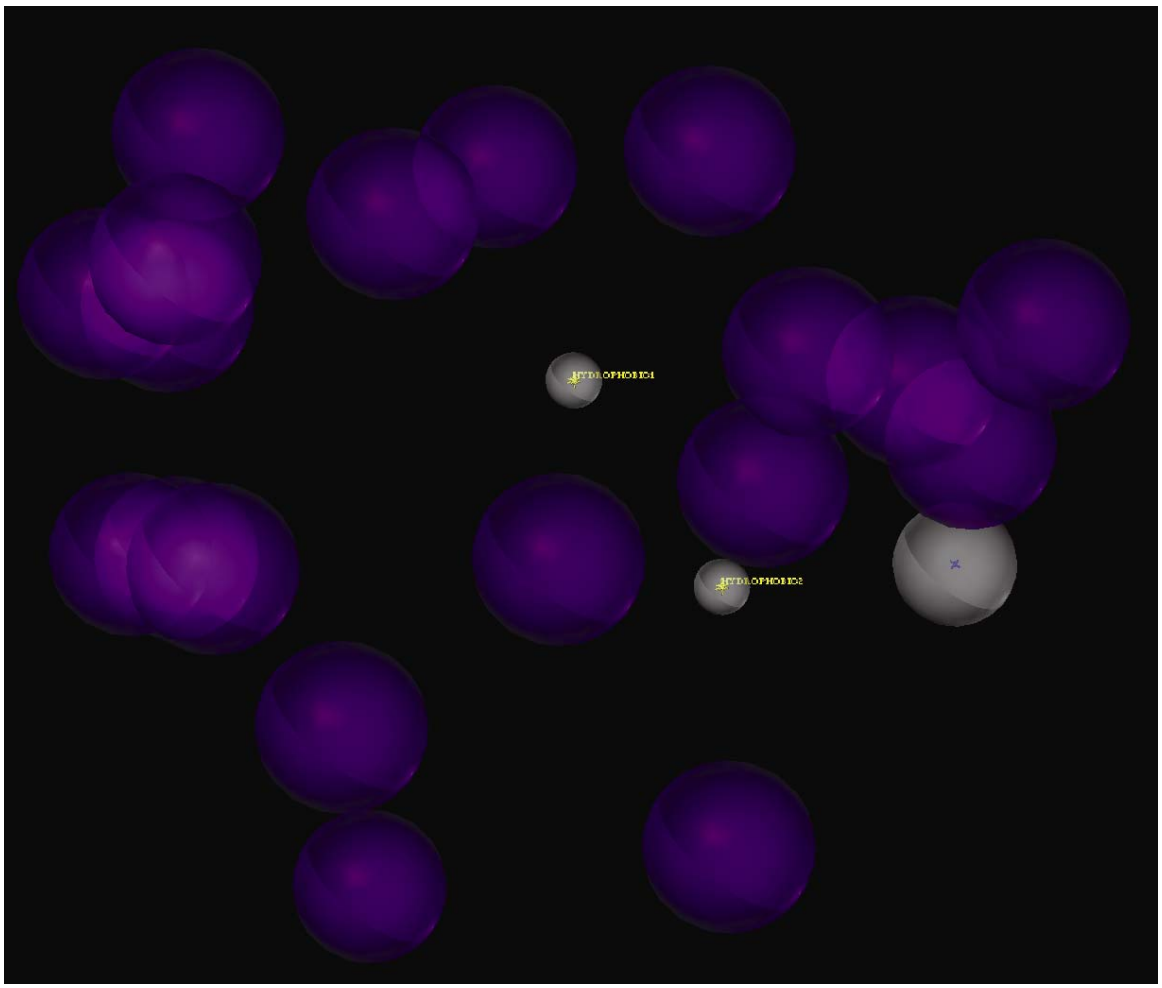


Figure 2. Graphical representation of the second database search query. Violet balls represent excluded volumes for outlining the putative SIRT2 active site. Gray balls with a yellow notation represent a hydrophobic feature at a tolerance of 0.5 Å. A gray ball without a notation represents an OH or SH group at a tolerance of 1.1 Å.

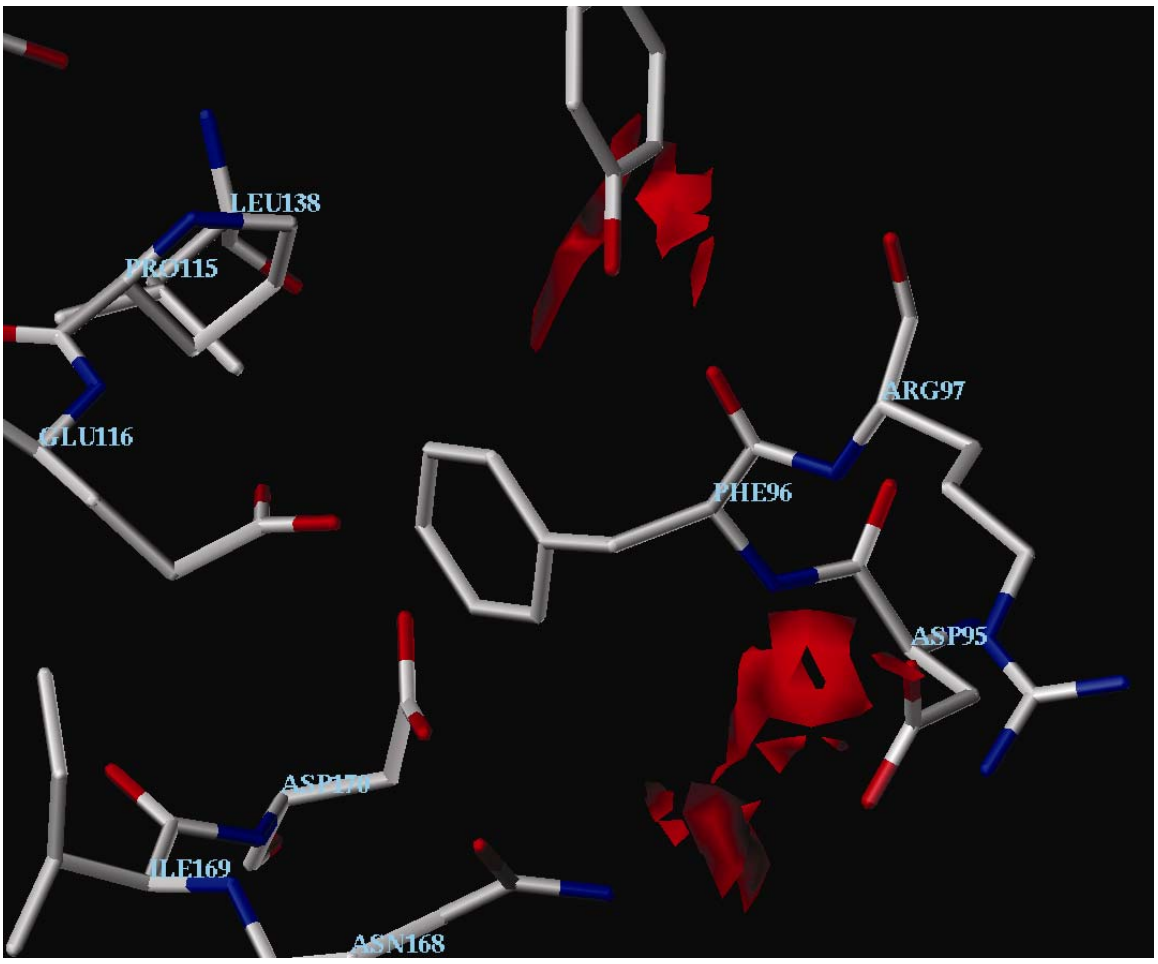


Figure 3. GRID interaction fields of the phenolic and carboxy hydroxyl group probe (OH) within the putative SIRT2 active site. The fields are visualized at an interaction energy level of −11.0 kcal/mol. Hydrogens of the amino acids are omitted for clarity.

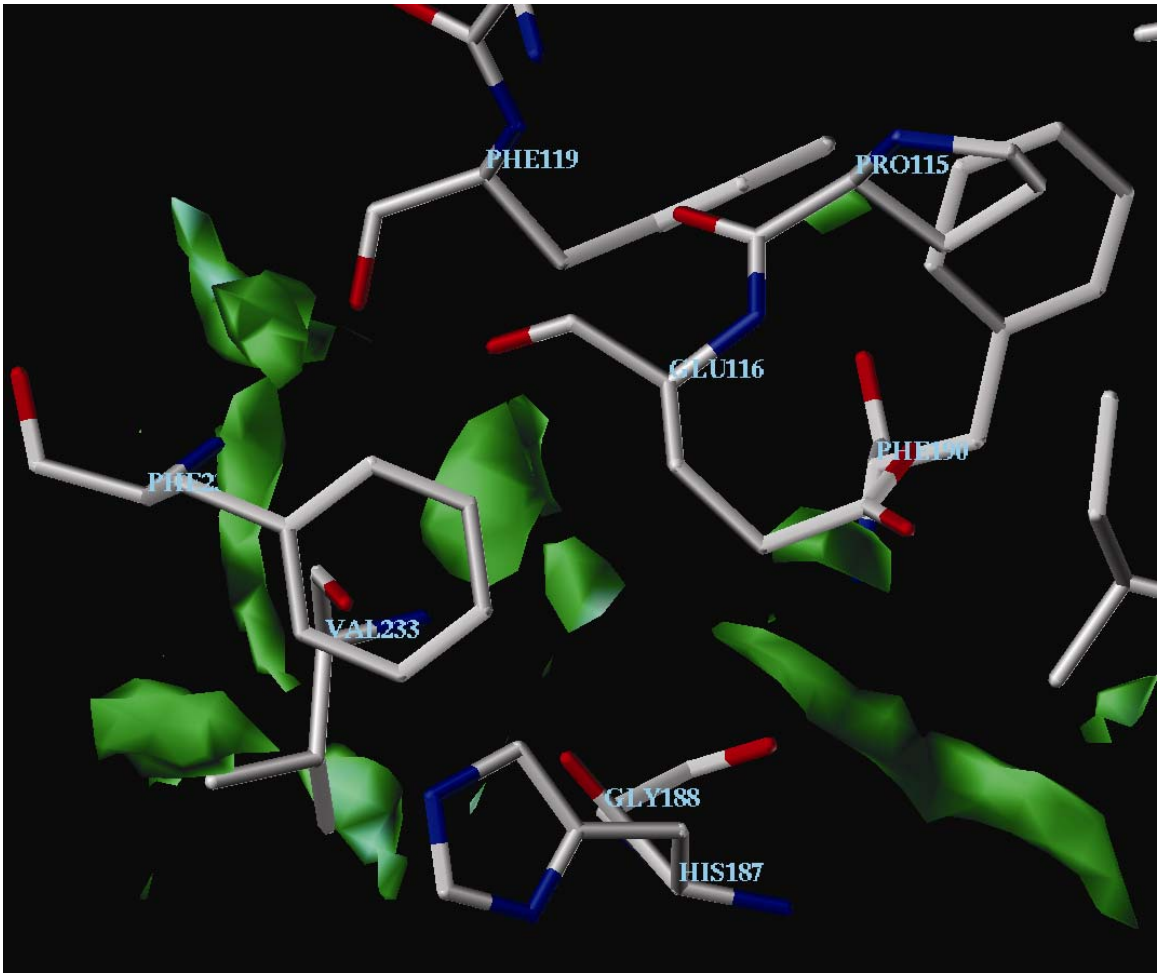


Figure 4. GRID interaction fields of the tetrahedral cationic NH_2 group probe (NH_2^+) within the putative SIRT2 active site. The fields are visualized at an interaction energy level of −13.0 kcal/mol. Hydrogens of the amino acids are omitted for clarity.

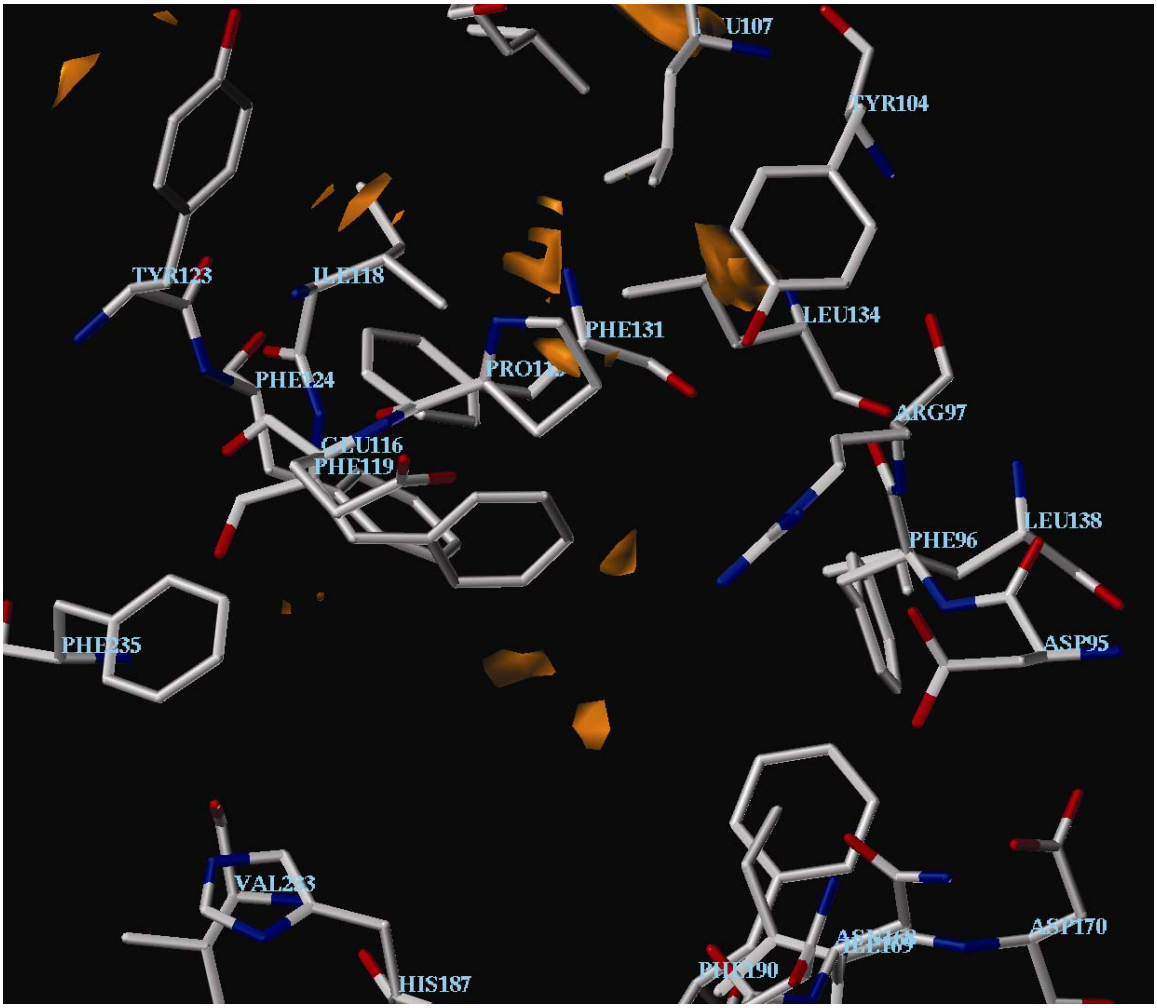


Figure 5. GRID interaction fields of the hydrophobic DRY probe within the putative SIRT2 active site. The fields are visualized at an interaction energy level of −1.5 kcal/mol. Hydrogens of the amino acids are omitted for clarity.

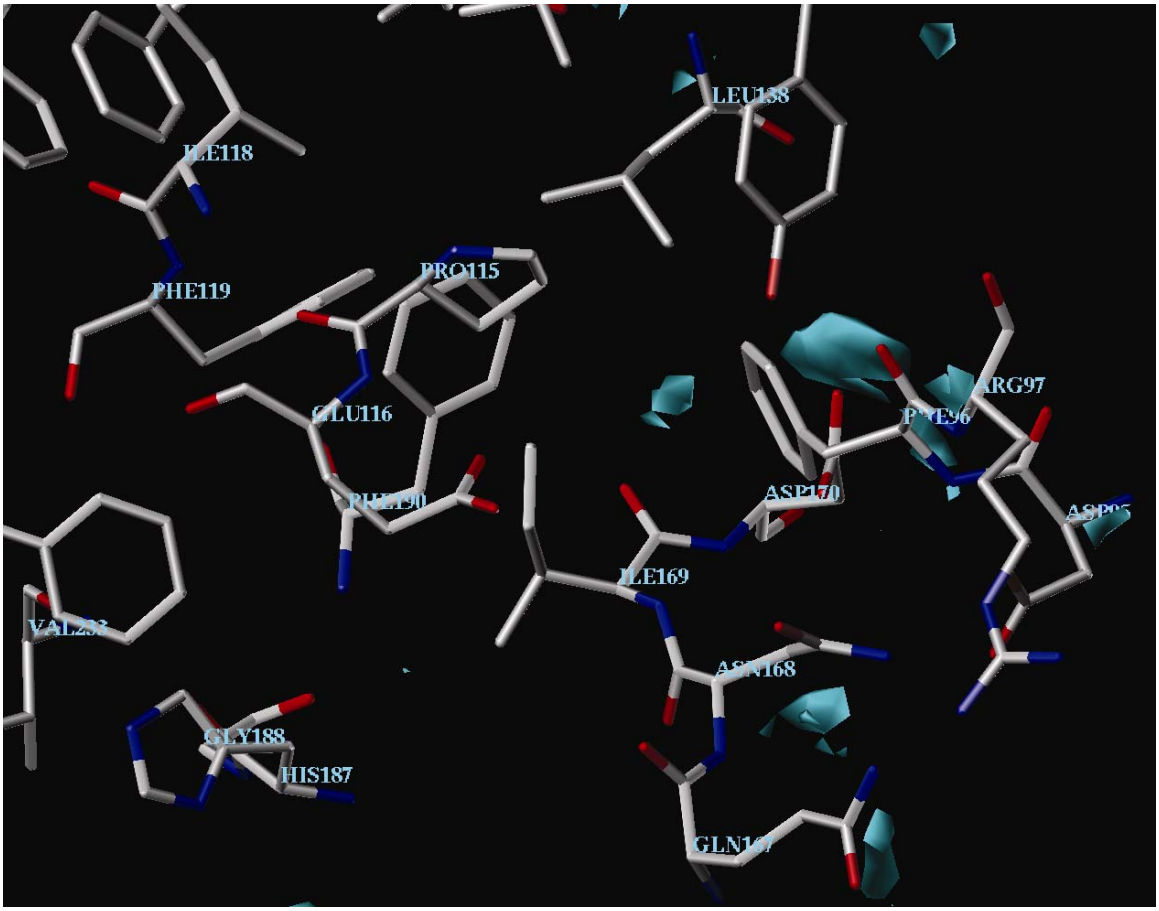


Figure 6. GRID interaction fields of the water probe within the putative SIRT2 active site. The fields are visualized at an interaction energy level of −16.0 kcal/mol. Hydrogens of the amino acids are omitted for clarity.