1. Use Pfam HMM to find a homologous set of proteins and generate a protein alignment

2. Mark known active site positions in alignment

3. Compare sequences with experimental active site residues annotation and identify and complete any active site subpatterns

4. Extract all unique active site patterns and column positions in alignment

5. Look for active site patterns on sequences in alignment without active site annotation

6. If a sequence matches multiple active site patterns, resolve by choosing the active site pattern from the sequence with the greatest percentage identity