The prediction of protein-ligand binding sites is an important task, allowing us to understand protein-ligand interactions, the understanding of which is essential in drug design and the development of certain areas of biology. Although machine learning tools for binding site prediction have been developed, the methods developed so far have only been interested in prediction from the 3D structure of the protein, which is unknown for most proteins. Therefore, in our work we are interested in prediction from knowledge of the mere sequence of residues representing the protein. Here we compare possible approaches to solve this problem. We compare the representation of residues using their chemical and physical properties with a representation using methods from natural language recognition. Furthermore, we compare the chosen machine learning methods. Finally, we compare our results with the P2Rank method, as a state-of-the-art method using 3D structure to predict protein-ligand binding sites.