Literature Review

1 Introduction

Many different approaches are needed to enable an expansion of the industry for drug design. Focusing on (membrane-)protein-ligand interactions it is of interest to know the structure of the target molecule, as it is known that the proteins and especially the side-chains of the proteins are the key-players to the functions in our organisms [5,6].
Dealing with the challenges of predicting the protein structures, there are various problems that occur [1]. These problems can be categorized in five main problems these are: “errors in side-chain packing”, “distortions and shifts in correctly aligned regions”, “errors in regions without template”, “errors due to misalignments” and “incorrect templates” [1,2].

2 Methods

The following literature review will deal further with the errors in side-chain packing, focusing on different approaches that proved their efficiency in predicting the placement of the side-chains and ways that impact the functionalities [5]. The papers used in the literature review have been extracted from Web of Science and the main page from PubMed, using the queries “predicting protein structure”, “functional side-chain placement in proteins” and ”functional side-chains”. Then only 6 of the listed papers from the first page were chosen, which abstracts included the word “side-chain”.

3 Results

The approaches used to predict the main side-chain structure, can be sectioned into three main groups [5]. One of the main approaches, that has been proved to be fast and efficient is the comparison of unknown protein structures to previously determined protein structures [1,2,5]. To do this different softwares are used that categorize the unknown protein structure, giving information about its possible three-dimensional structure and packing of the side-chain [1,2,5].
The second main approach, that has proven its efficiency throughout the years, is the usage of stochastic methods [3,5]. Therefore it is of importance to include the most probable energetic lowest conformations, that a given protein backbone can form [5]. This can be further worked into algorithms [3].
The third main approach, refereed to as the systematic approach, also deals with low energy conformations a side-chain of a protein can take in. The systematic approach and the stochastic approach however is, that the systematic approach does not use stochastically given information [5].

4 Conclusion

As mentioned in the introduction, the prediction of the side-chain in proteins and especially membrane protein is important, for the expansion of the industry for drug design[4,6]. As different ligands bind differently to different side-chains, it is not only of importance to know the structure of the side-chain, but also of the ligand binding to it [6]. A fast and efficient method is the modulation of the ligand in silicio docking, which is a method to perform a protein-ligand interaction using softwares [4].

5 References

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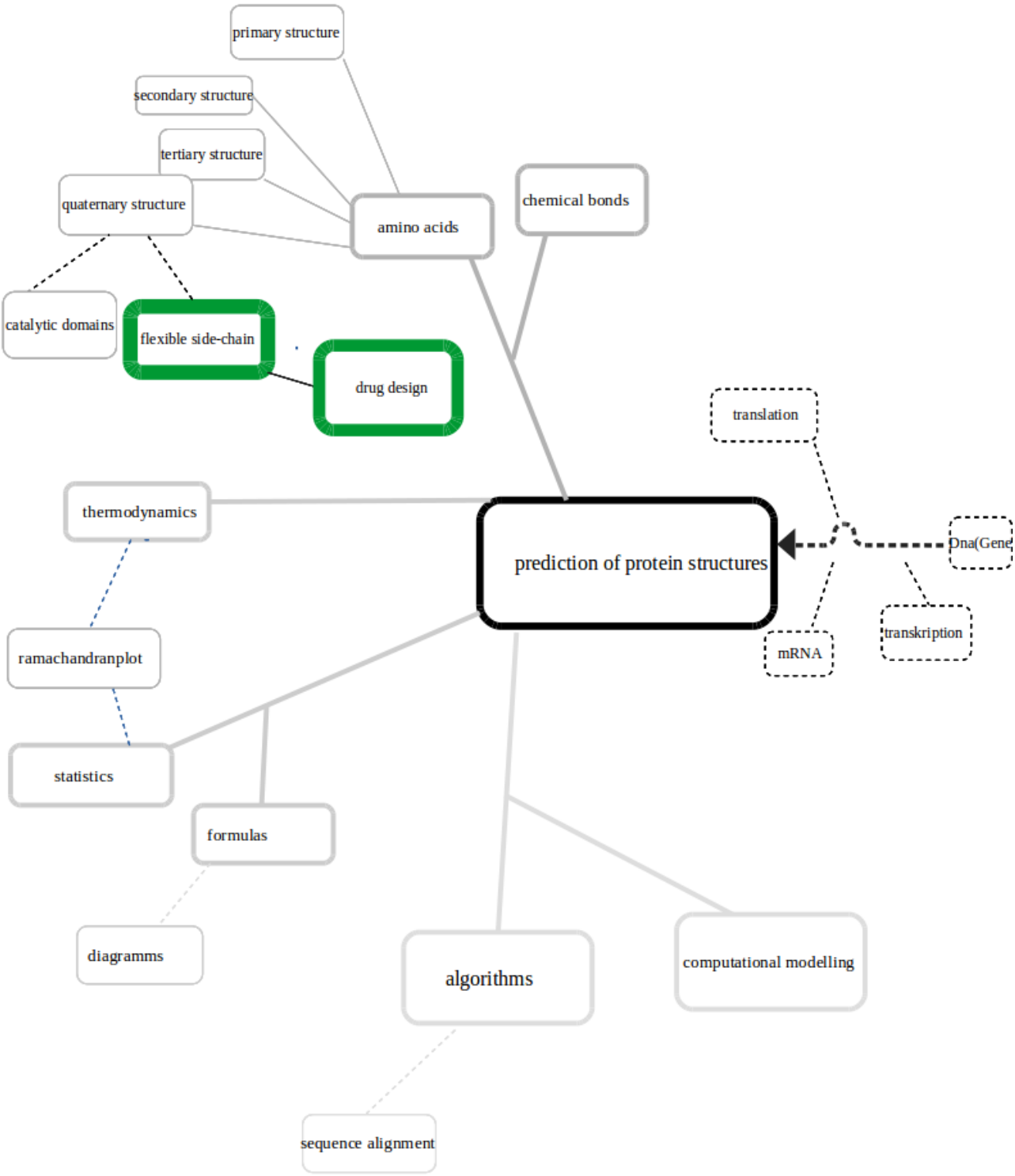
primary structure
secondary structure
tertiary structure
quaternary structure
amino acids
chemical bonds
catalytic domains
flexible side-chain
drug design
translation
thermodynamics
prediction of protein structures
Dna(Gene
transkription
mRNA
ramachandranplot
statistics
formulas
diagramms
algorithms
computational modelling
sequence alignment