CHAPTER VI
CONCLUSIONS

1. In this study, amino acid properties (hydropathy, amino acid side chain properties, hydrophobicity and helical tendencies) coded amino acid sequences were used for a prediction of the existence and percent of secondary structure (helix, sheet and turn) by neural networks.

2. The percent accuracy predictions of non-properties coded amino acid sequence were lower than the prediction when using the properties coded amino acids.

3. The prediction of the existence of helix, sheet and turn in the same network (from all properties code amino acid) had the prediction accuracy (25-50%) were lower than prediction of helix (80-100%), sheet (70-85%) and turn (45-60%) in separated networks (from all properties).

4. Different properties coding for amino acid sequence and different number of hidden units give different prediction accuracies.

5. For the existence of helix structure prediction, the network of 2 group hydropathy with 100 hidden units and the network of amino acid side chain with 7 hidden units gave highest prediction accuracy (100%).

6. For the existence of sheet structure prediction, the network of amino acid side chain properties with 100 hidden units gave the highest prediction accuracy (85.71%).

7. For the existence of turn structure prediction, the network of amino acid side chain properties with 7 hidden units gave the highest prediction accuracy (67.8%).

8. The percent helix, sheet and turn prediction was performed to helps the prediction of folding classes. For percent (6 groups), there were sixth possible outputs representing the percent value of 0%, 1-20%, 21-40%, 41-60%, 61-70%, 71-80% and 81-100%. For percent (3 groups), there were three possible outputs representing the percent value of 0%, 1-50% and 51-100%. For percent (2 groups), there were two outputs representing of percent value of 0-15% and 16-

100% which grouped by the definition of folding classes. The percent (2 groups) was the desire outputs of only helix and sheet.

9. For percent of helix prediction, the network of hydropathy (2 groups) with 35 hidden units gave the highest prediction accuracy (70.71%) for percent (6 groups) prediction and the network of the network of amino acid side chain properties with 70 and 100 hidden units gave the highest prediction accuracy (78.7%) for percent (3 groups) prediction.

10. For percent of sheet prediction, the network of hydropathy (2 groups) with 35 hidden units and hydropathy (7 groups) with 70 hidden units gave the highest prediction accuracy (50%) for percent (6 groups) prediction. While, the highest accuracy (78.57%) for percent (3 groups) prediction were the results of the network of hydropathy (7 groups) with 7 hidden units and amino acid side chain properties with 100 hidden units.

11. For percent turn prediction, the highest accuracy (46.43%) for percent (6 groups) prediction were resulted form the networks of hydropathy (7 groups) with 35 and 100 hidden units. While the highest accuracy (64.29%) for percent (3 groups) prediction resulted from the networks of hydropathy (2 groups) with 70 and 100 hidden units.

12. For percent (2 groups) of helix structure prediction, the highest (78.7%) accuracy resulted from the networks of amino acid side chain properties with 100 hidden units and hydrophobicity with 120 hidden units.

13. For percent (2 groups) of sheet structure prediction, the highest (75%) accuracy resulted from the networks of hydropathy (2 groups) with 35 hidden units.

14. The prediction of percent secondary structure especially helix and sheet structure can be used for the folding classes prediction