

## CHAPTER V

### CONCLUSION

Proteins from *Sesbania grandiflora* flowers, leguminous plant, were characterized by using electrophoresis, chromatography and mass spectrometry. Crude proteins from *Sesbania grandiflora* flowers were extracted and fractionation precipitated with ammonium sulfate. The amount of protein is higher when using the higher amount of ammonium sulfate, the most concentration was found in 60% precipitation and the lowest concentration was found in 20% precipitation. Biological activity tests of these proteins found that 60% and 90% crude protein show hemagglutination and  $\alpha$ -glucosidase inhibitory activity. For 60% crude protein, 13.5 mg of SGF60 was purified in only one step by using DEAE-cellulose anion exchange chromatography. This protein show 31 HU/mg of specific hemagglutination activity with rabbit red blood cell and 82% inhibition of  $\alpha$ -glucosidase inhibitory activity. Approximate molecular weight of SGF60 from SDS-PAGE electrophoresis is 40 kDa. To identify this protein, tandem mass spectrometry using ESI-Q-TOF has been use. Peptide sequencing shows that partial amino acid sequence of SGF60 matched with p27SJ, a novel protein inhibited HIV-1, from *Hypericum perforatum* and DING protein from *Solanum tuberosum*. For 90% crude protein characterization, 2.16 mg SGF90 can be purified in two steps. Gel filtration chromatography using Superdex-200 has been used in first step and DEAE-cellulose anion exchange chromatography was used in second step. Molecular weight of this protein is 63 kDa. To identify amino acid sequences of this protein, ESI-Q-TOF has been use. The database searching of peptide sequences show that partial amino acid sequence of SGF90 protein matched with the partial amino acid sequence of beta-glucosidase (At5g36890) and beta-glucosidase F8K4.3 protein from *Arabidopsis thaliana*. SGF90 can inhibit  $\alpha$ -glucosidase enzyme (74%inhibition) and agglutinate rabbit erythrocyte at 3.8 HU/mg. In addition, the protein profile of *Sesbania grandiflora* from 2D-gel electrophoresis presents at least six proteins. These proteins were analyzed by peptide mass mapping using MALDI-TOF MS. From the search results, there are no signification match between the results and proteins in database.