



Figure 4. The helical characteristics of each peptide; AT1(●), AT2(■), AT3(▲), and AT4(◆)

antibody, almost no deviation was observed (Fig. 3B). A similar result was shown by anti-AT2 antibody (data not shown).

The CD spectra were measured on a J-725 Spectropolarimeter (Jasco), and the % contents of the secondary structures were calculated by SSE-338W protein secondary structure analysis program (Jasco). It was found that AT1 peptide is easy to adopt an α -helix structure. AT1 exhibited an extremely high content of α -helix (100% even in 10% TFE). AT3 peptide was found to adopt also a 100% α -helix structure, but only in 60% TFE. Almost no helical content was observed for AT2 peptide and a very low for AT4 peptide. These results indicated that the ability of antibody to sense the conformation change is well-related to the structural characteristics of each peptide fragment to adopt an α -helical conformation.

References

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