

**Circular Dichroism Unit Conversion**

When comparing the Circular Dichroism spectra of different constructs, or the same construct at different concentrations, or when using to use the data to estimate secondary structure content, it is usual to normalise the machine units of millidegrees ellipticity by conversion to mean residue molar ellipticity using the following equation (where  $n$  is the number of peptide bonds in the protein and *Ellipticity* is the raw data from the instrument):

$$\theta(\text{deg.cm}^2.\text{dmol}^{-1}) = \frac{\text{Ellipticity(mdeg).10}^6}{\text{Pathlength(mm).}[Protein](\mu\text{M}).n}$$