

Full interpretation of the results requires you to look at the individual melt curves.

96% of curves were used in  $T_m$  estimations

Average estimation of error is **0.1 C**

Protein as supplied is **well behaved**

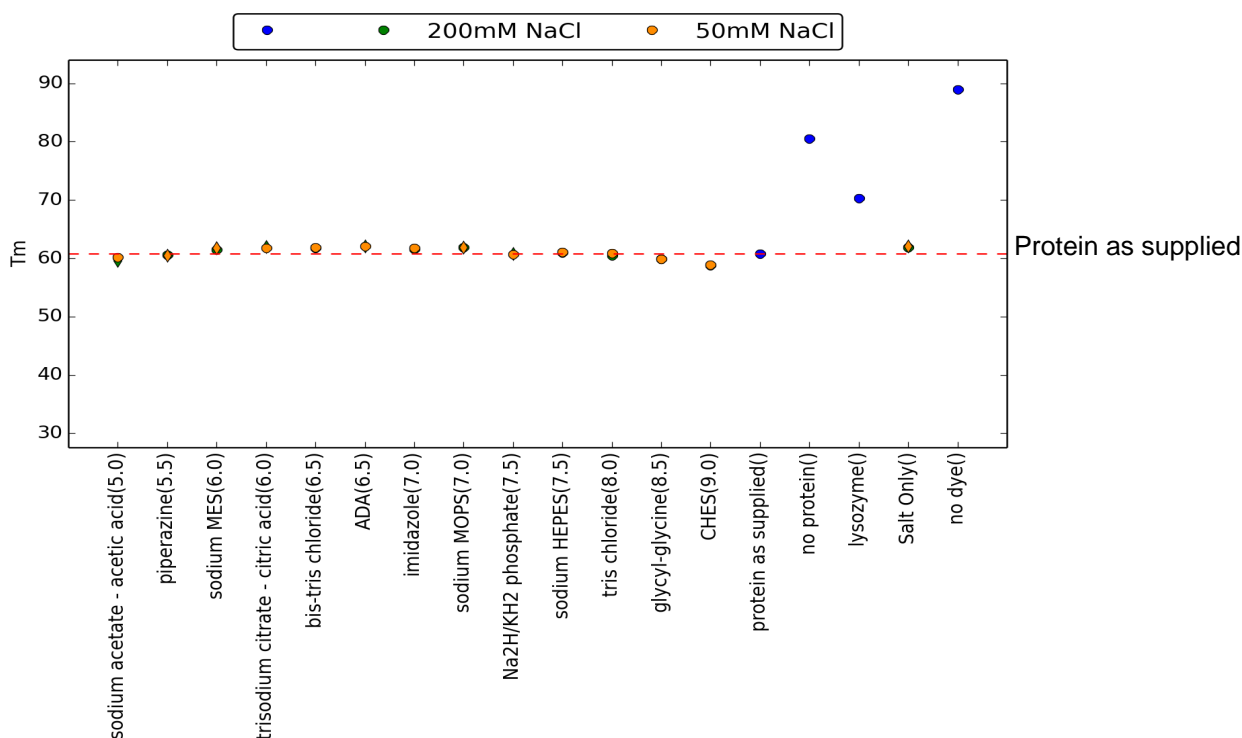
Protein as supplied:  $T_m = 60.78(+/-0.03)$

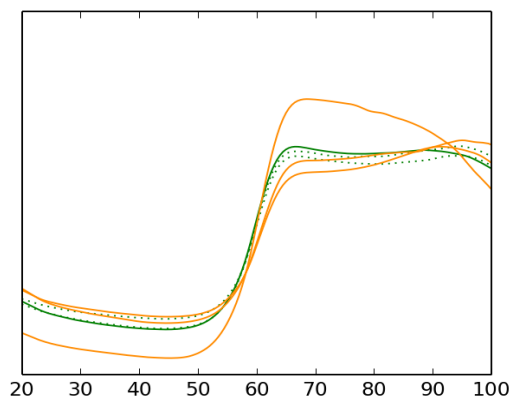
Lysozyme Control: Passed

No Dye Control: Failed

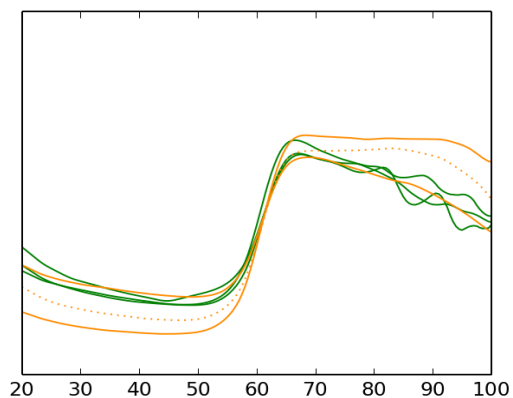
No Protein Control: Failed

$T_m$ s drawn in diamonds may be unreliable

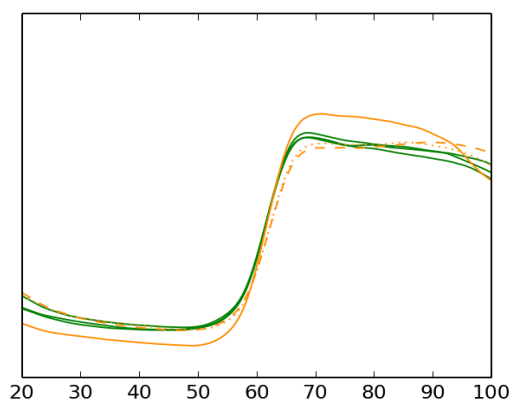




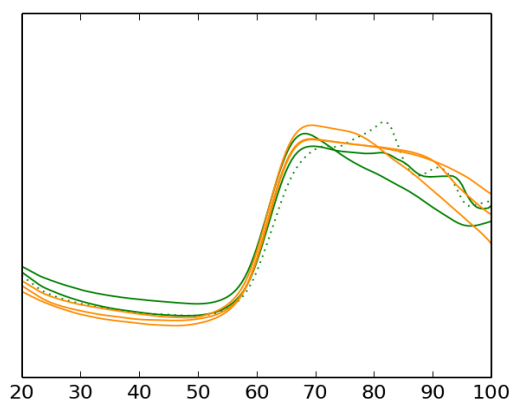
sodium acetate - acetic acid (5.0)  
Grouped by Tm



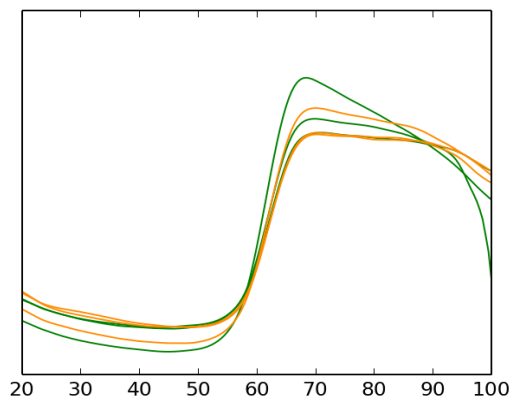
piperazine (5.5)  
Grouped by Tm



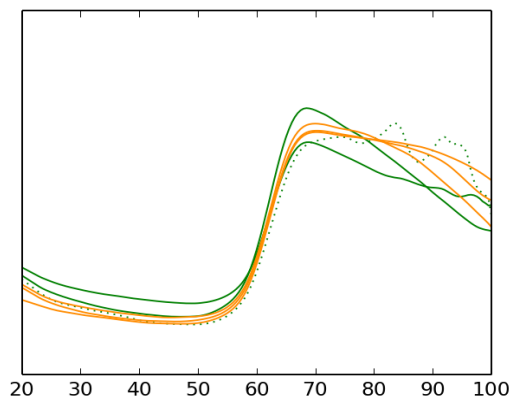
sodium MES (6.0)  
Grouped by Tm



trisodium citrate - citric acid (6.0)  
Grouped by Tm

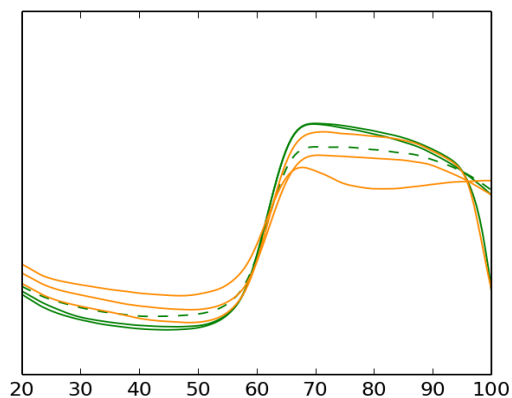


bis-tris chloride (6.5)  
Grouped by Tm



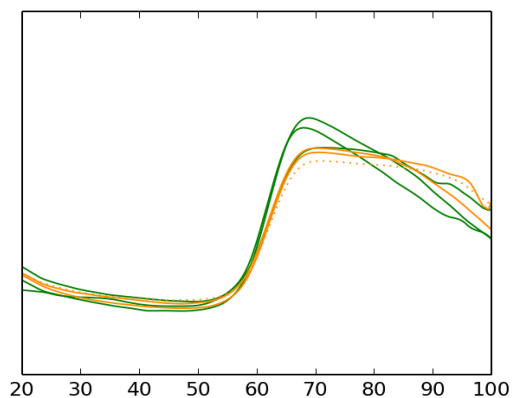
ADA (6.5)  
Grouped by Tm

Curves drawn with dashed lines are unable to be analysed (monotonic, saturated, in the noise, and outliers) and are excluded from Tm calculations  
Curves drawn with dotted lines have unreliable estimates for Tms



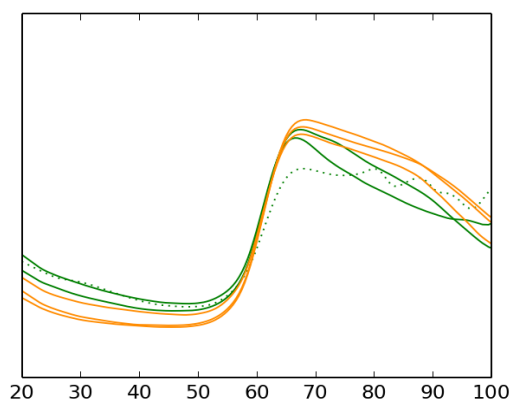
imidazole (7.0)

Grouped by Tm



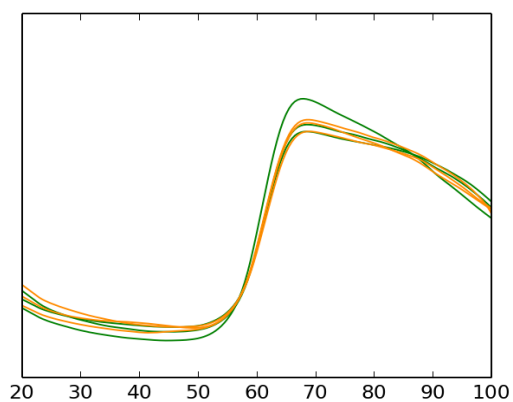
sodium MOPS (7.0)

Grouped by Tm



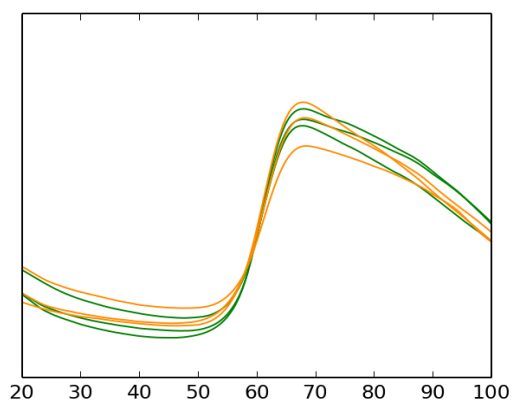
Na<sub>2</sub>H/KH<sub>2</sub> phosphate (7.5)

Grouped by Tm



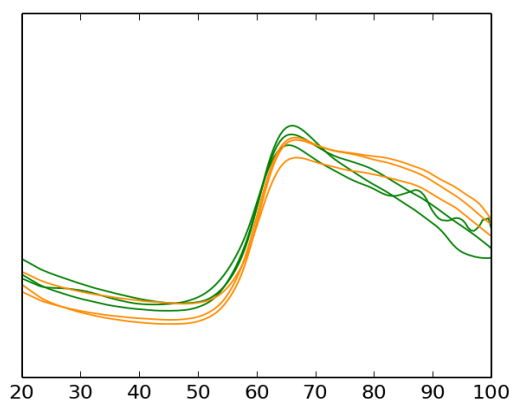
sodium HEPES (7.5)

Grouped by Tm



tris chloride (8.0)

Grouped by Tm

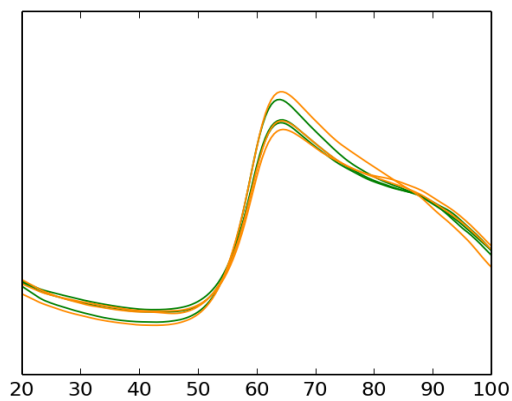


glycyl-glycine (8.5)

Grouped by Tm

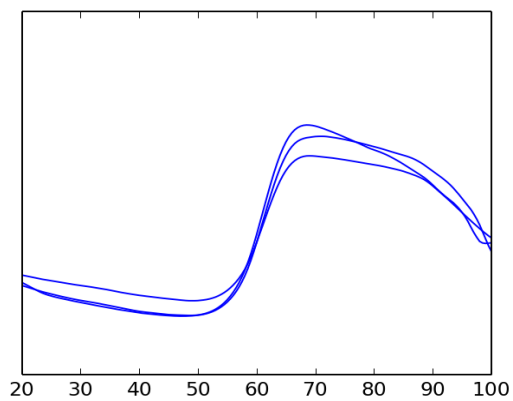
Curves drawn with dashed lines are unable to be analysed (monotonic, saturated, in the noise, and outliers) and are excluded from Tm calculations

Curves drawn with dotted lines have unreliable estimates for Tms



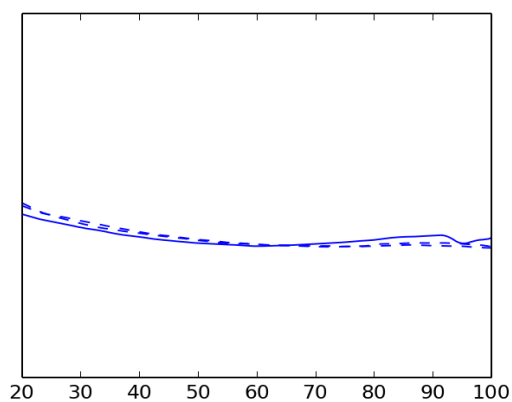
CHES (9.0)

Grouped by Tm



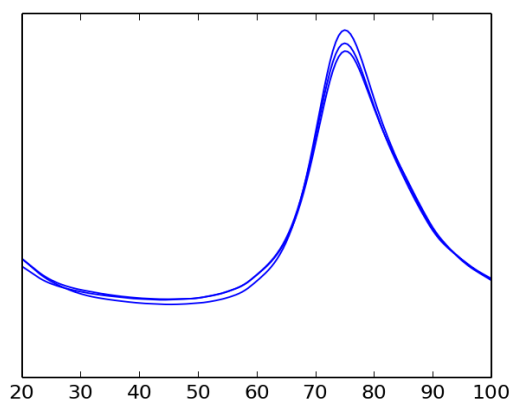
protein as supplied ( )

Grouped by Tm



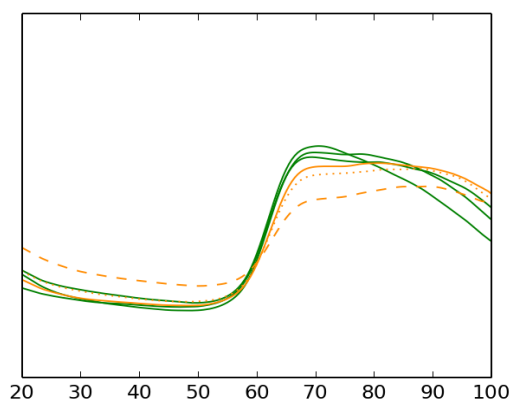
no protein ( )

Grouped by Tm



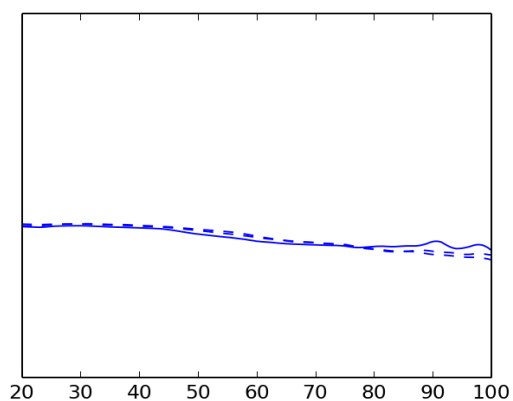
lysozyme ( )

Grouped by Tm



Salt Only ( )

Grouped by Tm



no dye ( )

Grouped by Tm

Curves drawn with dashed lines are unable to be analysed (monotonic, saturated, in the noise, and outliers) and are excluded from Tm calculations

Curves drawn with dotted lines have unreliable estimates for Tms