

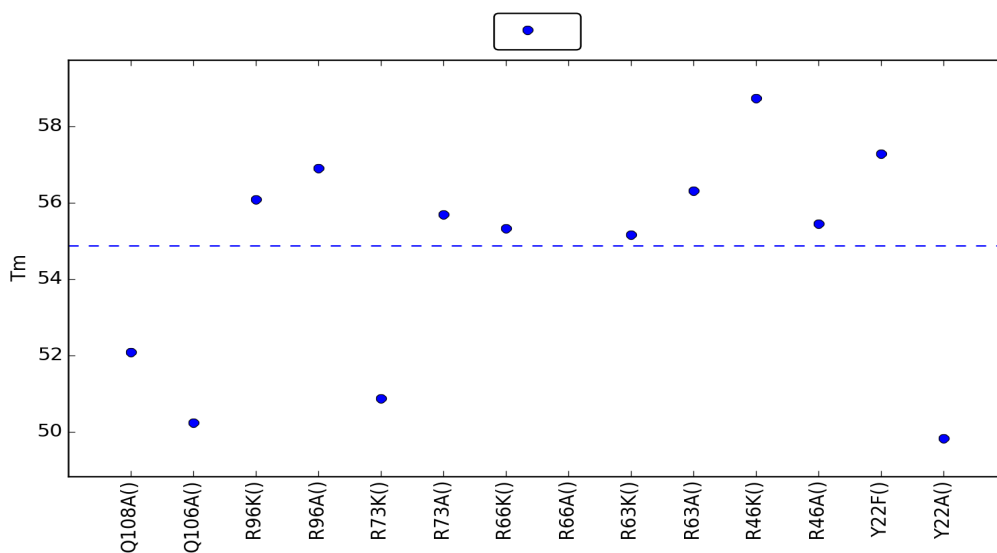
Full interpretation of the results requires you to look at the individual melt curves.

Curves used in Tm estimations (ideally 100%): **85%**

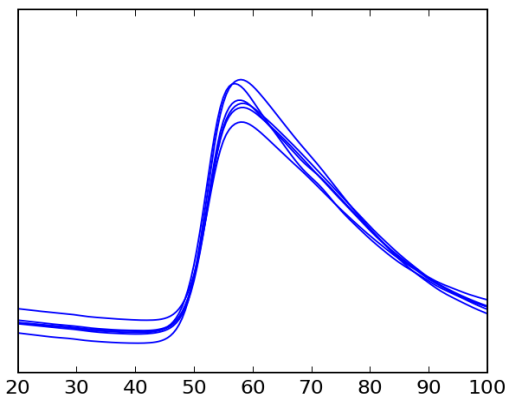
Average estimation error: **0.1°C**

Protein as supplied:
Tm = 54.87(+/-0.05)

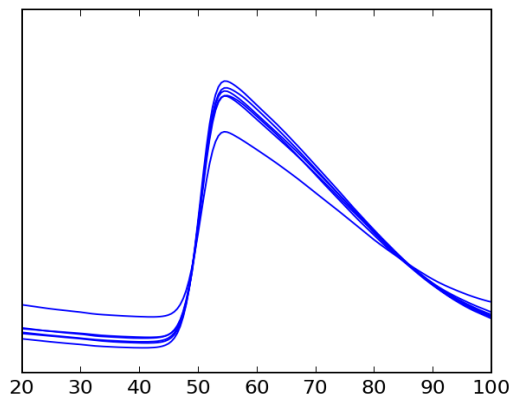
Lysozyme Control: Passed
No Dye Control: Not Found
No Protein Control: Not Found



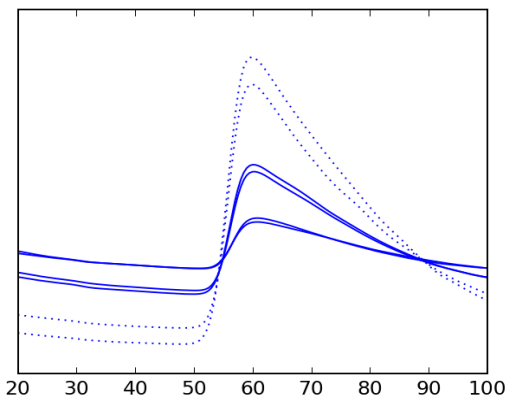
Highest Tm = 58.74 +/- 0.14
(R46K /)



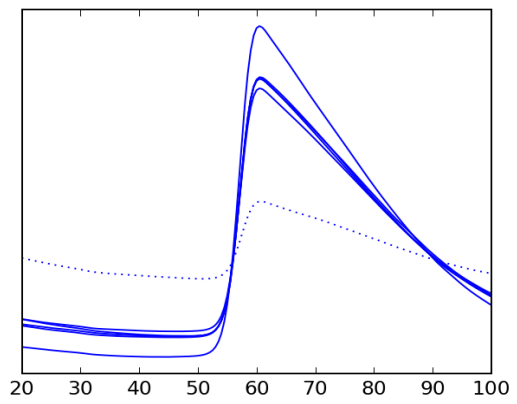
Q108A ()
 Grouped by Tm
 52.08 (+/-0.07)



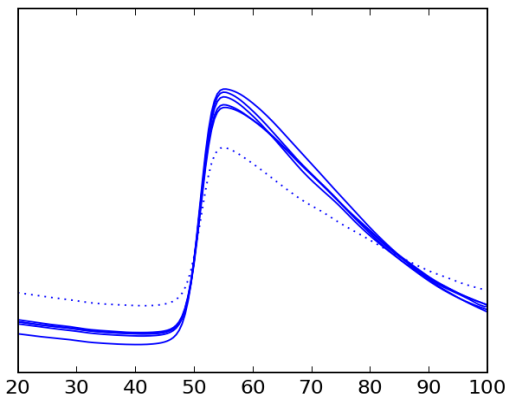
Q106A ()
 Grouped by Tm
 50.25 (+/-0.05)



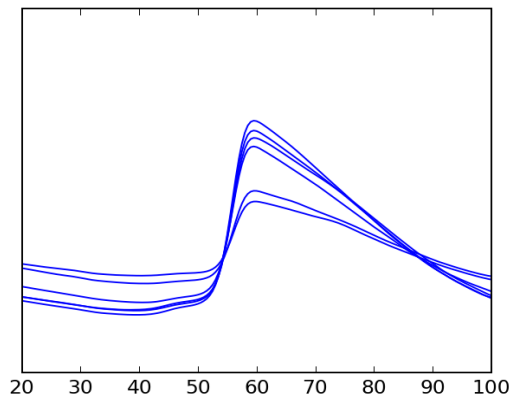
R96K ()
 Grouped by Tm
 56.09 (+/-0.18)



R96A ()
 Grouped by Tm
 56.91 (+/-0.03)

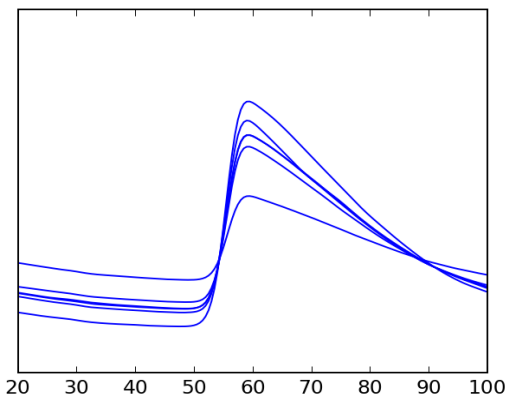


R73K ()
 Grouped by Tm
 50.88 (+/-0.04)

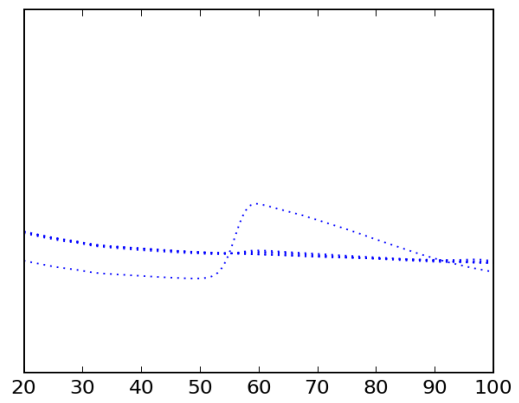


R73A ()
 Grouped by Tm
 55.69 (+/-0.07)

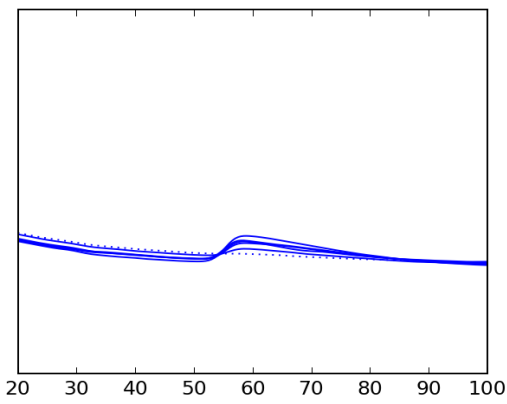
Monotonic, saturated, in the noise, and outlier curves are dotted, and excluded from Tm calculations
 Curves drawn with dashed lines have unreliable Tm estimates



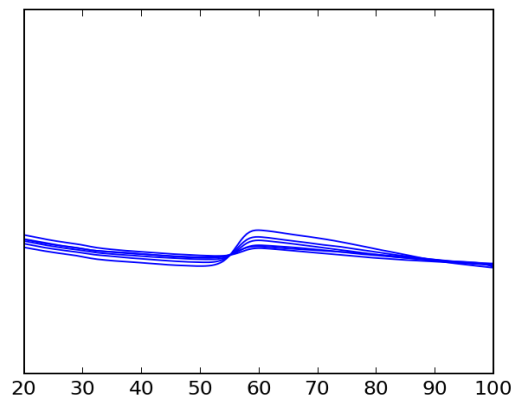
R66K ()
 Grouped by Tm
 55.33 (+/-0.08)



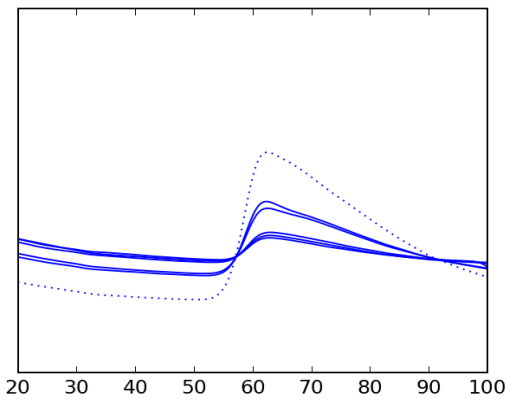
R66A ()
 Grouped by Tm
 None



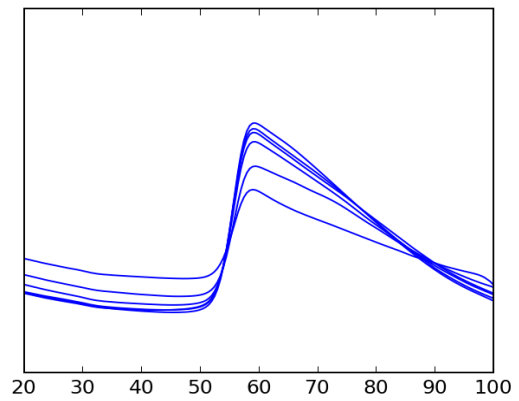
R63K ()
 Grouped by Tm
 55.17 (+/-0.25)



R63A ()
 Grouped by Tm
 56.32 (+/-0.27)

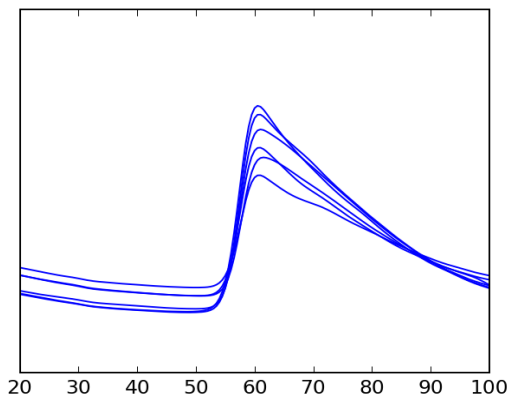


R46K ()
 Grouped by Tm
 58.74 (+/-0.14)



R46A ()
 Grouped by Tm
 55.45 (+/-0.03)

Monotonic, saturated, in the noise, and outlier curves are dotted, and excluded from Tm calculations
 Curves drawn with dashed lines have unreliable Tm estimates

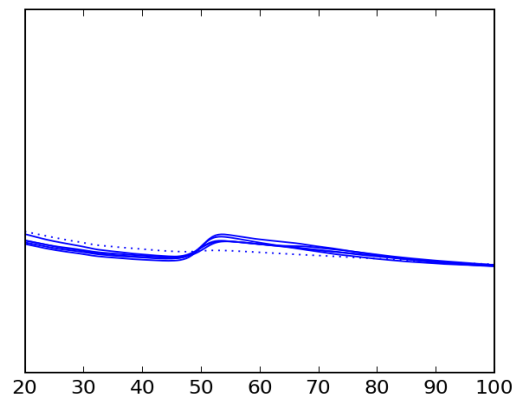


Y22F ()

Grouped by

Tm

57.29 (+/-0.12)



Y22A ()

Grouped by

Tm

49.83 (+/-0.29)