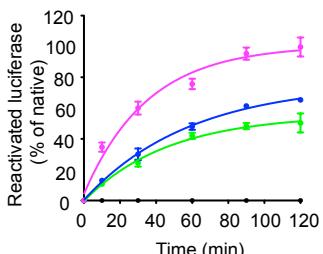
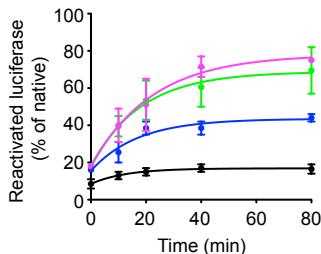


**A Ssa1, Sse1, Hsp104 (yeast)**

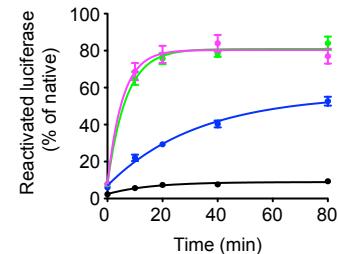
● +Ydj1 ● +1/2xYdj1+1/2xSis1  
● +Sis1 ● no chaperones

**B Ssa1, Sse1 (yeast)**

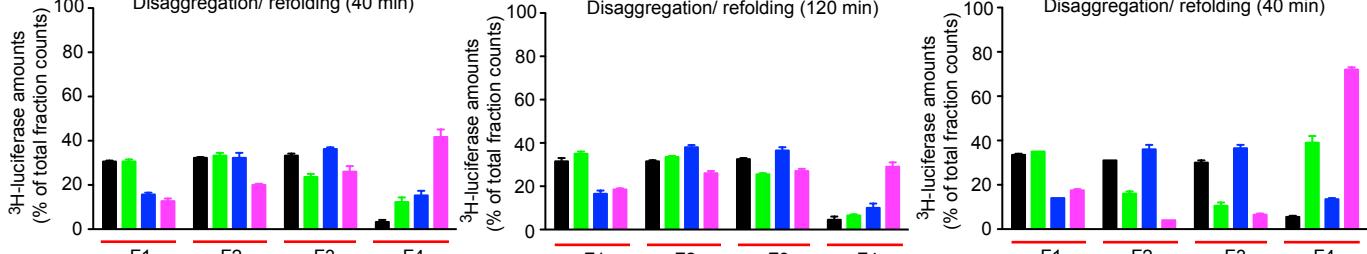
● +Ydj1 ● +1/2xYdj1+1/2xSis1  
● +Sis1 ● no chaperones

**C DnaK, GrpE (bacteria)**

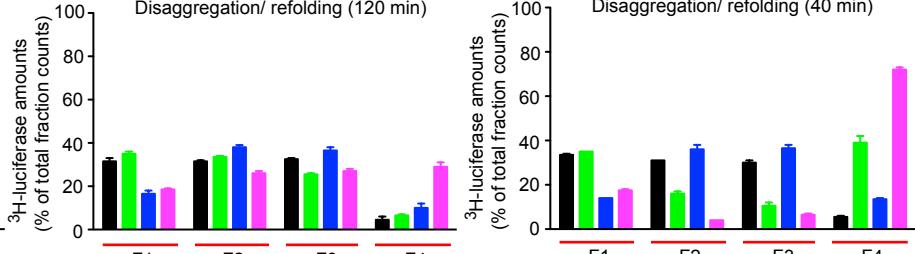
● +DnaJ ● +1/2xDnaJ+1/2xCbpA  
● +CbpA ● no chaperones

**D****Hsp104, Ssa1, Sse1**

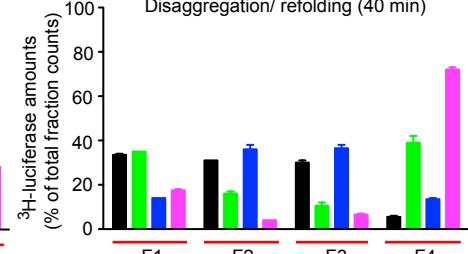
● +Ydj1 ● no chaperones  
● +Sis1 ● +0.5 Ydj1 + 0.5 Sis1  
Disaggregation/ refolding (40 min)

**E****Ssa1, Sse1**

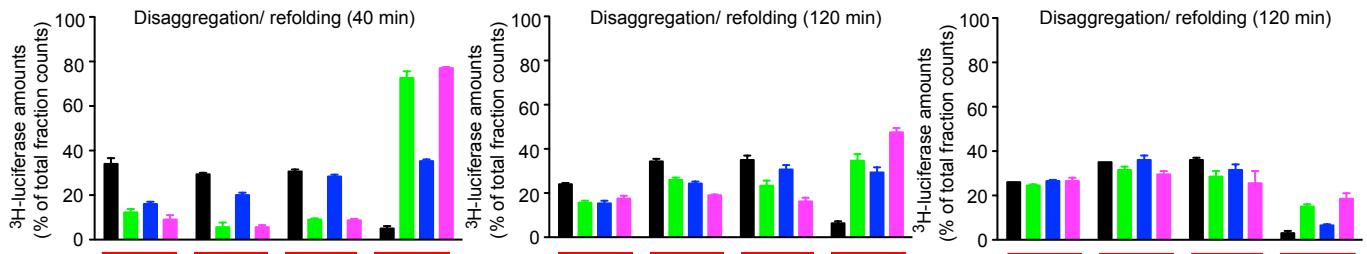
● +Ydj1 ● no chaperones  
● +Sis1 ● +1/2xYdj1+1/2xSis1  
Disaggregation/ refolding (120 min)

**F****HSPA8, Sse1**

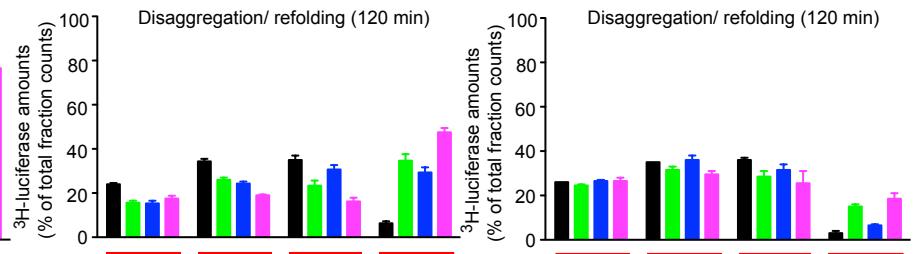
● +Ydj1 ● no chaperones  
● +Sis1 ● +1/2xYdj1+1/2xSis1  
Disaggregation/ refolding (40 min)

**G****ClpB, DnaK, GrpE**

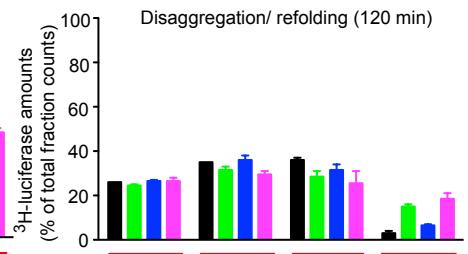
● +DnaJ ● no chaperones  
● +CbpA ● +0.5 DnaJ + 0.5 CbpA  
Disaggregation/ refolding (40 min)

**H****DnaK, GrpE, ClpB**

● +DnaJ ● no chaperones  
● +CbpA ● +1/2xDnaJ+1/2xCbpA  
Disaggregation/ refolding (120 min)

**I****DnaK, GrpE**

● +DnaJ ● no chaperones  
● +CbpA ● +1/2xDnaJ+1/2xCbpA  
Disaggregation/ refolding (120 min)

**J** $\varnothing$  distance [Å]

CbpA <sup>JD</sup> - DnaJ <sup>CTD</sup>	6/22 (-23.8 to -21.8)	44.1
DNAJB1 <sup>JD</sup> - DNAJ <sup>CTD</sup>	5/26 (-21.0 to -20.2)	41.4
DNAJB1 <sup>JD</sup> - DNAJA2 <sup>CTD*</sup>	2/4 (-24.3 to -24.0)	0.0

\* data taken from ref. Nillegoda et al., 2015

**Figure 4 - figure supplement 1**