



Figure S2. Peak broadening of the ^1H - ^{15}N HSQC spectrum of [U - ^{15}N] γD -crystallin with diluted lysate is consistent with the presence of $\sim 5 \mu\text{M}$ of ribosomes in the sample. Overlay of the amide envelopes of ^1H - ^{15}N HSQC NMR spectra of $10 \mu\text{M}$ purified [U - ^{15}N] γD -crystallin in buffer containing no ribosomes (yellow); $2 \mu\text{M}$ ribosomes (purple); $4 \mu\text{M}$ ribosomes (green); $6 \mu\text{M}$ ribosomes (red); diluted lysate (blue). The data were collected at RT on a Bruker Avance II spectrometer operating at a ^1H frequency of 700 MHz with 512 scans per transient; 1024 and 128 complex points were collected in ^1H and ^{15}N dimensions. The first transient of each spectrum was extracted by using “rser 1” command and multiplied by a cosine-bell window function and zero-filled to 2048 points prior to Fourier transformation. The corresponding sweep-widths were 12 ppm and 35 ppm in ^1H and ^{15}N dimensions, respectively.