



Figure S3: Individual amide backbone fits. Each subgraph is a residue (number indicated at top). Fit types are indicated by letter code: “e” (exponential fit), “f” (fast; exchange occurred too quickly for reliable fit); “s”: (slow, exchange occurred too slowly for reliable fit). x-axis is time (0-1500 min); y-axis is the peak intensity relative to intensity of the peak in an unexchanged protein (I/I₀). Lines represent best fit to the data. Colors indicate hS100A9 (black) or hS100A9/M63F (orange).