

# Structural Dynamics of IRE1 and its Interaction with Unfolded Peptides

## Supplementary File 3

|                                          | hIRE1 $\alpha$ LD wild-type | hIRE1 $\alpha$ LD E102R | hIRE1 $\alpha$ LD Y161R |
|------------------------------------------|-----------------------------|-------------------------|-------------------------|
| $K_D$ [ $\mu$ M]                         | 2.14                        | 6.35                    | 5.433                   |
| $K_D$ 95% confidence interval [ $\mu$ M] | 1.809 to 2.528              | 5.835 to 6.959          | 4.296 to 7.095          |
| $R^2$                                    | 0.9918                      | 0.9992                  | 0.9851                  |

Goodness-of-fit parameters of binding curves of MPZ1-N-2X peptide to hIRE1 $\alpha$  LD for fluorescence anisotropy experiments.