Supporting information for article:

Structural studies of a surface-entropy reduction mutant of O-GlcNAcase

Alexandra Males and Gideon J. Davies
Figure S1  Purification of HsOGA_{E602A605A}. The red boxes correspond to the identical fractions on the chromatogram and the gel that contain the purest sample, hence the fractions that were pooled. (a) Elution from a Superdex S200 column (GE Healthcare) resulted in a narrow peak after ~ 70 mL of elution buffer had passed through the column. (b) The resulting SDS-PAGE gel, 12%, showed two distinct bands for the two domains. * is the N-terminal catalytic domain that has a molecular weight of 46.6 kDa. † is the C-terminal stalk domain that has a molecular weight of 23.8 kDa. The protein ladder was Bio-Rad unstained low-range SDS-PAGE standards.

Figure S2

Table S1  Estimation of the secondary structure content of the constructs

| Construct          | HsOGA_{FL} | HsOGA_{11-396+535-715} | HsOGA_{E602A605A} |
|--------------------|------------|------------------------|-------------------|
| Predicted α (%)    | 9.89       | 16.33                  | 16.33             |
| Predicted β (%)    | 38.33      | 34.68                  | 34.68             |
| Max error          | 0.38       | 0.4                    | 0.4               |