

## 1 Supplemental Information

## 2 Supplemental Figures





**Figure S1.** Stability studies of *Kl*Glk1 protein using Thermal Shift Assay (panels **a** and **b**) and Tycho (panels **c** and **d**). Panels (**a**) and (**c**) represent the raw fluorescence data, panels (**b**) and (**d**) show the corresponding first derivative.

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Figure S2. Kinetic analysis of *Kl*Glk1 activity. (a) Lineweaver-Burk linearization (reciprocal plot).
Datapoints for low ATP concentrations obey linear trend and were considered for fitting of a
linear model (solid line, R<sup>2</sup>=0.98). V<sub>max</sub> was determined from the Y-intercept, X-intercept is equal
to -1/Km. Error bars correspond to SD, N=3. (b) Comparative fit of classical Michaelis-Menten
plot (R<sup>2</sup>=0.96) and a Hill plot (R<sup>2</sup>=0.99, h=1.97). (c) Hill Plot. Error bars correspond to SD, N=3.





- 16 *Kl*Glk1 dimer in the solution with calculated molecular weight of 100 kDa (second peak). Refractive
- 17 index (mV) and corresponding calculated molecular weight (Da) are represented as a red and green
- 18 line, respectively.



- 20 Figure S4. Complete topology of KlGlk1 protein. Side view (a) and front view (b) of KlGlk1. H
- 21 indicates helices, S indicates strands.



23 **Figure S5.** 2D topology map of *Kl*Glk1 monomer.



Figure S6. Amino acid sequence alignment of *Kl*Glk1 and KlHxk1 glucose kinases from
 *Kluyveromyces lactis*. Amino acid sequence identity between *Kl*Glk1 and KlHxk1 is 37%.
 Sequence Secondary structures for both proteins are indicated.



- 30 Figure S7. Coloured representation of normalized B-factors in KlGlk1 protein structure. Red parts
- 31 represent high, white middle, blue low B factors.

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34 Figure S8. SDS-PAGE gel showing purity of the *Kl*Glk1 after final step of purification.