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Correction: Single glucose molecule transport process revealed by force tracing and molecular dynamics simulations

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Correction for 'Single glucose molecule transport process revealed by force tracing and molecular dynamics simulations' by Yangang Pan *et al.*, *Nanoscale Horiz.*, 2018, **3**, 517–524, <https://doi.org/10.1039/C8NH00056E>.

The authors regret an error in Fig. 5A of the original article, whereby the white field image for E426A was identical to the white field image for K38A. This error most likely occurred due to a mislabelling of the white field image for E426A. The new Fig. 5 provided below replaces the originally published figure and contains new GFP and white field data for the blank, WT, K300A, E426A and K38A in Fig. 5A. The new data were obtained from a repeated set of imaging.

An independent expert has viewed the corrected figure and confirmed that it is consistent with the discussions and conclusions presented in the original article.

The Royal Society of Chemistry apologises for these errors and any consequent inconvenience to authors and readers.

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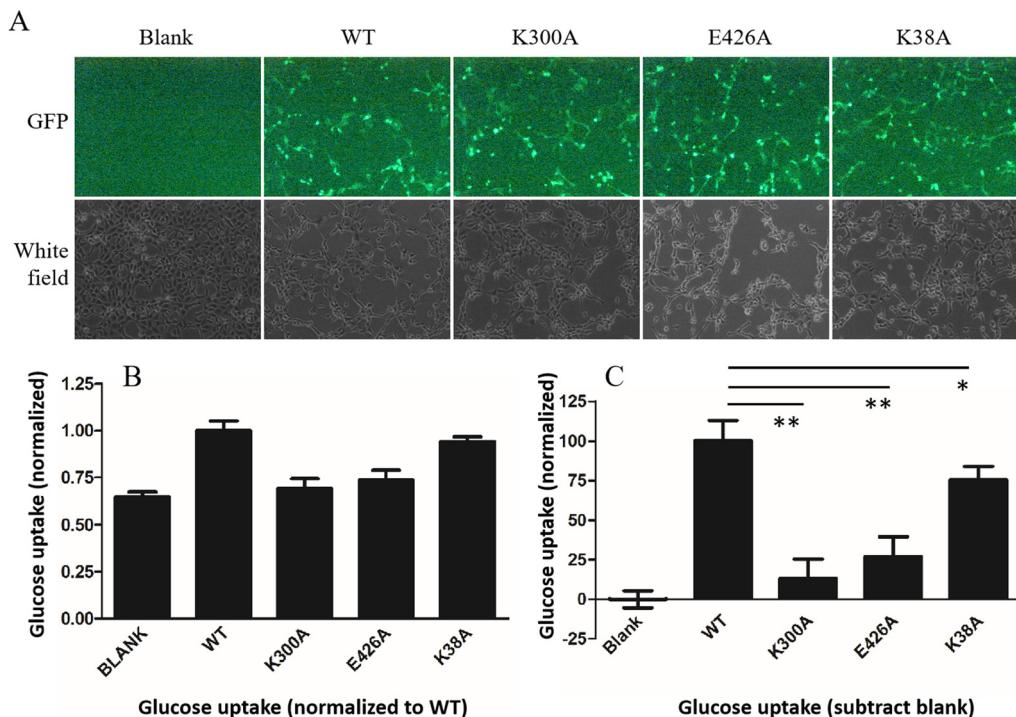


Fig. 5 Mutations of the K38, K300 or E426 residues of GLUT1 that blunted the uptake of glucose into the cells. (A) Representative images of the HEK293 cell expression of the WT or the K38A, K300A or E426A mutant versions of GLUT1-GFP. (B) Total glucose uptake into the cells. The data were normalized to the WT. (C) Percentage of glucose uptake inhibition observed by expressing the mutants or the WT GLUT1 in the cells. The data were subtracted from the blank and were normalized to the WT. The inhibition values caused by the K300A, E426A or K38A mutants are 86.84%, 72.92% and 24.43%, respectively. The data were subtracted from the blank and were normalized to the WT from B. * $P < 0.05$, ** $P < 0.01$.