



## SUPPLEMENTARY ONLINE DATA Identification of autophosphorylation sites in eukaryotic elongation factor-2 kinase

Sébastien PYR DIT RUYS\*<sup>1</sup>, Xuemin WANG†‡<sup>1</sup>, Ewan M. SMITH†<sup>2</sup>, Gaëtan HERINCKX\*, Nusrat HUSSAIN\*, Mark H. RIDER\*, Didier VERTOMMEN\* and Christopher G. PROUD†‡<sup>3</sup>

\*Université catholique de Louvain and de Duve Institute, 75 Avenue Hippocrate, B-1200 Brussels, Belgium, †Department of Biochemistry and Molecular Biology, University of British Columbia, Vancouver, BC, Canada, V6T 1Z3, and ‡Centre for Biological Sciences, Life Sciences Building, University of Southampton, Southampton S017 1BJ, U.K.

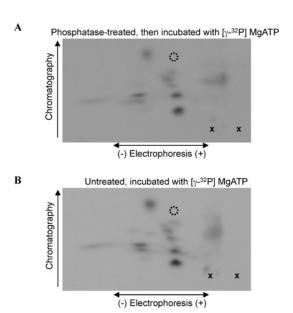


Figure S1 2D autophosphorylation peptide maps of alkaline-phosphatasetreated compared with untreated wild-type eEF2K

(A) Wild-type eEF2K was first dephosphorylated with alkaline phosphatase and subsequently allowed to undergo autophosphorylation in the presence of Ca<sup>2+</sup>/CaM as described in the Experimental section of the main text. (B) Wild-type eEF2K phosphorylated in the presence of Ca<sup>2+</sup>/CaM without pre-treatment. After tryptic digestion, phosphopeptides were resolved by 2D electrophoresis and chromatography (polarity and directions are indicated). The positions where the sample (larger 'X') and the DNP-lysine (smaller 'x') were applied, and the final migration position of the DNP-lysine marker (broken open circle) are also shown.

Received 15 September 2011/21 December 2011; accepted 4 January 2012 Published as BJ Immediate Publication 4 January 2012, doi:10.1042/BJ20111530

<sup>&</sup>lt;sup>1</sup> These authors contributed equally to this work.

<sup>&</sup>lt;sup>2</sup> Present address: MRC Toxicology Unit, Hodgkin Building, Lancaster Road, Leicester, LE1 9HN, U.K.

To whom correspondence should be addressed (email c.g.proud@soton.ac.uk).