

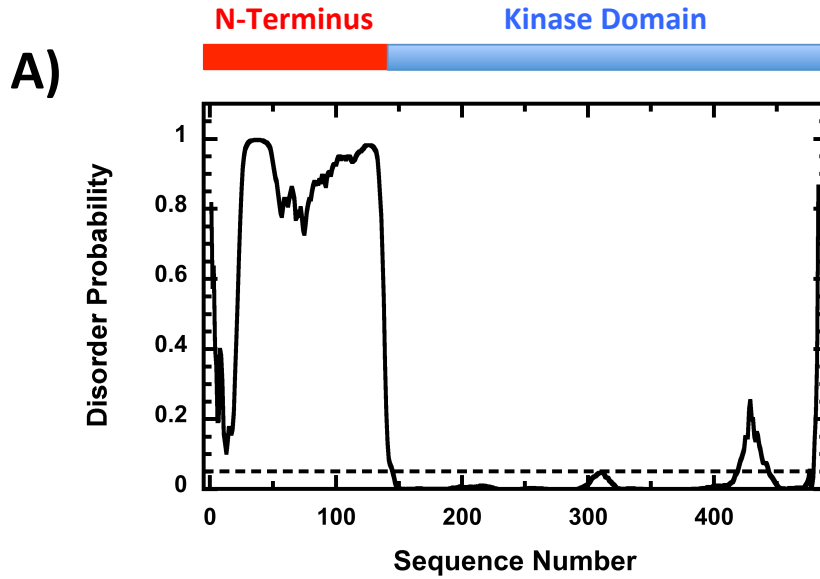
Supplementary Information for:

N-Terminus of the Protein Kinase CLK1 Induces SR Protein Hyper-Phosphorylation

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Fig.S1: Structure Predictions for CLK1 N-Terminus: A) Disorder prediction. The sequence for mouse CLK1 was obtained from NCBI (Accession NP 001036099) and run using DISOPRED. The dashed line represents the order/disorder threshold for the default false positive rate of 5%. Sequences with values above this threshold are considered disordered while those beneath this threshold are considered ordered. Most sequences within the kinase domain are ordered while all residues in the N-terminus are predicted to be disordered. B) Secondary structure prediction. CLK1 sequences are run using PSIPRED and structure propensities are labeled (helix, sheet, disordered). All residues in the N-terminus are predicted to be disordered with the exception of one tripeptide region (ARE).

Supplementary Figure S1 (Aubol et. al.)



B)

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1  M R H S K R T Y C P D W D E R D W D Y G T W R S S S S H K R K K R S H S S A R E Q K R C R Y D H S K 50
51  T T D S Y Y L E S R S I N E K A Y H S R R Y V D E Y R N D Y M G Y E P G H P Y G E P G S R Y Q M H S 100
101 S K S S G R S G R S S Y K S K H R S R H H T S Q H H S H G K S H R R K R S R S V E D D E E G H L I C 150
151 Q S G D V L S A R Y E I V D T L G E G A F G K V V E C I D H K V G G R R V A V K I V K N V D R Y C E 200
201 A A Q S E I Q V L E H L N T T D P H S T F R C V Q M L E W F E H R G H I C I V F E L L G L S T Y D F 250
251 I K E N S F L P F R M D H I R K M A Y Q I C K S V N F L H S N K L T H T D L K P E N I L F V K S D Y 300
301 T E A Y N P K M K R D E R T I V N P D I K V V D F G S A T Y D D E H H S T L V S T R H Y R A P E V I 350
351 L A L G W S Q P C D V W S I G C I L I E Y Y L G F T V F P T H D S R E H L A M M E R I L G P L P K H 400
401 M I Q K T R K R R Y F H H D R L D W D E H S S A G R Y V S R R C K P L K E F M L S Q D A E H E L L P 450
451 D L I G K M L E Y D P A K R I T L K E A L K H P F F Y P L K K H T
    
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Key Annotations

Helix	Sheet	Disordered
M	L	E