MTORC2 is an *in vivo* hydrophobic motif kinase of S6 Kinase 1.

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Abstract

Ribosomal protein S6 kinase 1 (S6K1), a major downstream effector molecule of mTORC1, regulates cell growth and proliferation by modulating protein translation and ribosome biogenesis. We have recently identified eIF4E as an intermediate in transducing signals from mTORC1 to S6K1 and further demonstrated that the role of mTORC1 is restricted to inducing eIF4E phosphorylation and interaction with S6K1.This interaction relieves S6K1 auto-inhibition and facilitates its hydrophobic motif (HM) phosphorylation and activation as a consequence. These observations underscore a possible involvement of mTORC1independent kinase in mediating HM phosphorylation. Here, we report mTORC2 as an *in-vivo* HM kinase of S6K1. We show that S6K1 truncation mutant ∆NH∆CT, resistant to rapamycin mediated mTORC1 inhibition, continues to display HM phosphorylation with selective sensitivity toward torin-1. We also show that HM phosphorylation of wildtype S6K1and ∆NH∆CT depends on the presence of mTORC2 regulatory subunit-rictor. Furthermore, truncation mutagenesis analysis highlights the involvement of a conserved amino acid stretch of S6K1 in mediating mTORC2 dependent HM phosphorylation. We finally show that deletion of this amino acid stretch leads to complete loss of HM phosphorylation regardless of the presence of functional TOS motif. Our data identifies mTORC2 as a physiological HM kinase that can activate S6K1 after its auto-inhibition is overcome by mTORC1. We, therefore, propose a novel mechanism for S6K1 regulation where mTOR complex 1 and 2 act in tandem to activate the enzyme.

Introduction

The mechanistic target of rapamycin (mTOR) is a master regulator of cell growth and proliferation, whose deregulation is implicated in various pathological conditions including cancer, diabetes, arthritis and osteoporosis (Saxton and Sabatini, 2017; Zou et al., 2020). mTOR forms two structurally and functionally distinct complexes called the mTOR complex 1 (mTORC1) and mTOR complex 2 (mTORC2) (Loewith et al., 2002; Mossmann et al., 2018) . mTORC1 comprises of three core components viz the catalytic subunit-mTOR, the regulatory

subunit-raptor and GβL. In addition, PRAS40 and Deptor constitute the inhibitory subunits of mTORC1. On the other hand, mTORC2 also comprises of mTOR and GβL. However, instead of raptor, the regulatory component of mTORC2 is a 200 KDa protein -- rictor. The other components of mTORC2 are PRR5, Deptor, and SIN1(Yang et al., 2018). Among the two complexes, mTORC1 is extensively studied and implicated in integrating signals from multiple growth factors, nutrients, and energy supply to regulate cell growth and proliferation. One of the major downstream effector molecules of mTORC1 is Ribosomal protein S6 kinase 1 (S6K1)--a member of AGC family of protein kinases (Hay and Sonenberg, 2004; Majeed, S.T.; Majeed, R.; Shah, G.; Andrabi, 2019). S6K1 is shown to use special amino terminal sequence motif TOS to interact with mTORC1 regulatory subunit-raptor (Nojima et al., 2003). This interaction is believed to induce S6K1 phosphorylation at Thr-412, situated in a hydrophobic motif C-terminal to the catalytic domain. Accordingly, loss of Thr-412 phosphorylation, either due to mTORC1 inhibition or its impeded recruitment due to TOS mutation/disruption, endorses the dependence of hydrophobic motif (HM) phosphorylation on the activation state of mTORC1. However, continued display of HM phosphorylation in S6K1 mutants, harbouring mutations disrupting TOS function (Ali and Sabatini, 2005; Dennis et al., 2001) , suggest that mTORC1 regulates S6K1 in a manner that is distinct from the one that influences HM phosphorylation. The observations are consistent with our earlier data that highlight disconnect between HM phosphorylation and rapamycin response by S6K1, to foster the argument that loss of phosphorylation may be a consequence rather than a mechanistic basis of mTORC1 inhibition (Beigh et al., 2013, 2012). In addition, identification of new mTORC1 substrates without a consensus TOS motif also undermine the centrality of TOS in mediating raptor binding (Fonseca et al., 2018; Kim et al., 2011; Koren et al., 2010). The observations are further endorsed by recent data that demonstrate occurrence of S6K1 phosphorylation even in absence of raptor (Ahmed et al., 2019). Furthermore, we have recently demonstrated that the role of mTORC1 is restricted to engaging eIF4E with S6K1-TOS motif for relieving the auto-inhibition, due to carboxy terminal auto-inhibitory domain (CAD), to facilitate consequential HM phosphorylation and activation of S6K1. Altogether, these observations suggest that relieving auto-inhibition should render S6K1 active and independent of the regulation by mTORC1 and further point towards involvement of mTORC1 independent kinase in phosphorylating S6K1 at hydrophobic motif site (Majeed et al., 2021).

Here, we report mTORC2 as an *in vivo* HM kinase of S6K1.We identify a 19 amino acid sequence responsible for mediating HM phosphorylation of S6K1. Our data, therefore, proposes

a novel mechanism describing a stepwise action of mTOR complex 1 and 2 in regulating S6K1 activation.

Materials and Methods

Cell lines and Culture Conditions

HEK293 and HEK293T cells, described previously (Majeed et al., 2021), were maintained in Dulbecco's modified Eagles medium (DMEM) supplemented with 10% (v/v) foetal bovine serum (Invitrogen), 50 µg/ml penicillin and 100 µg/ml streptomycin (Sigma-Aldrich) at 37°C with 5% CO2.

Reagents and Antibodies

PVDF membrane (GE Healthcare/Millipore), Rapamycin (Sigma Aldrich), Torin-1 (Sigma Aldrich) and Protein G-Agarose beads (Genscript), Polyetheleneimine reagent (Polysciences, Inc.), Radioactive ATP (BRIT, Hyderabad-India). Antibodies against p-S6K1(T389/T412), Raptor, Rictor, S6 and Flag- tag were purchased from Cell Signaling Technologies (Beverly MA); HA-tag, myc-tag and GAPDH (Sigma- Aldrich); S6K1 (GenScript); rabbit and mouse secondary antibodies conjugated to IR Dye 800CW (LI-COR Biotechnology, Lincoln, Nebraska).

Expression Vectors and Transfections

A pMT2-based cDNA encoding an amino-terminal HA-tagged S6K1 (αI variant) and S6K1 truncation mutant ∆NH∆CT S6K1 were gifted by Prof. Joseph Avruch, Harvard Medical School Boston, USA. Truncation mutants of S6K1 *viz* 147-421, 110-421, 91-421 and 77-421 were constructed in pKMYC mammalian expression vector. A common reverse primer 5' GCCGAATTCCTAACTTTCAAGTACAGATGGAG3' and specific forward primers 5'GAGGATCCATGCTGGAGGAAGTAAAGCAT3'; 5'GCGGATCCATGAAAGTAACAGGAGCAAATACT3'; 5'GCGGATCCATGTTTGAGCTACTTCGGGTACTTG3'and 5' GCGGATCCATGACTAGTGTGAACAGAGGGCCA 3' were used for PCR amplification of the respective mutants. cDNA HA-Raptor (#8513), HA-Rictor ( ) were purchased from addgene. HA tagged S6K1 truncation mutant S6K1∆91-109 was generated using primers (1) 5'Phos-AAAGTAACAGGAGCAAATACTGGGAAGATA3' and (2)5'Phos-ACATTCTGGTCTGATTTTTTCTGGCCC3'. The mutations were verified by DNA sequence and restriction analysis. For transient transfection of cells, 1□×□106 cells were plated onto a 60-mm

dish 24 hr prior to transfection. 1-2 µg of Plasmid DNA along with transfection agents Lipofectamine (Invitrogen) or Polyetheleneimine, PEI (Polysciences, Inc.) were used to transfect the cells. Standard protocol was followed for cell transfection.

Stable cell lines

Stable cell lines of HEK293 overexpressing S6K1 were generated by retroviral transduction of pWZL-Neo-Myr-Flag-RPS6KB1 expression plasmid (addgene#20624). Stable cell lines of HEK293 overexpressing S6K1 mutant ∆NHT2 were generated by retroviral transduction of pWZL-Neo-Myr-Flag-∆NHT2 S6K1 plasmid, generated by gateway cloning ( ). Briefly, the PCR amplified ∆NHT2 S6K1 was sub-cloned into TOPO adapted entry vector using pENTR/TEV/D-TOPO Cloning Kit (Invitrogen). The entry vector was then recombined with pWZL-Neo-Myr-Flag-DEST Gateway-compatible retroviral destination vector (addgene# 15300) using LR Clonase™ II Enzyme mix (Invitrogen 11791020). The infected cells were selected and maintained with neomycin (500 µg/ml).

Gene Knock Down using shRNA

Non-target scrambled shRNA (SHC002) was purchased from Sigma Aldrich. shRNA to human raptor (plasmid#1857) and rictor (plasmid#1853) were purchased from Addgene. The preparation of shRNA infected HEK293 cells have been described previously ( ).

Immuno-precipitations and Western blotting

48 h post transfection, cells were starved overnight in serum-free DMEM. Cells were serum stimulated for 30 minutes in presence or absence of 50 nM of rapamycin or torin-1 as per the experimental requirements before lysis with ice cold NP40 lysis buffer (Kim et al., 2002). Centrifugation (micro centrifuge, 13,000 rpm at 4°C for 20 min) was carried out to remove the precipitated material to obtain a clear lysate. After clearing, the supernatant was added to 2µg each of either anti-HA, anti-Myc or anti- Flag antibodies (as per the experimental requirements) immobilized on 20 µl of a 50% slurry of protein G Agarose and rotated for 4 hours at 4°C. Immunoprecipitates were washed five times with lysis buffer. 2X Laemmli sample buffer was added to the immunoprecipitates. The samples were boiled at 100°C, centrifuged at 13,000 rpm for 2 minutes and resolved by SDS-PAGE. Proteins were transferred on PVDF membrane, probed with different antibodies at indicated concentrations and analysed using Odyssey infrared imager (LI-COR).

In vitro kinase assay

In Vitro Kinase assay has been described previously (Batool et al., 2020; Beigh et al., 2012) . Briefly, Proteins immobilized on either HA or Myc- beads were incubated with 1µg of the substrate and 5µCi 32PATP in a kinase reaction buffer containing 50mM Tris-Cl (pH 7.0), 10mM MgCl2, 0.5mM DTT, 50mM β-Glycero-phosphate, and 1mM ATP for 15 minutes at 37°C. Reaction was stopped by adding 5X loading buffer, run on an SDS-PAGE gel. Proteins were transferred on PVDF membrane, auto-radiographed and activity determined by standard protocol.

Statistical Analysis

Statistical analysis was performed using GraphPad software (Prism 8). All error bars represent SEM. For multiple group comparisons all groups from each experimental repeat were compared using 2way ANOVA. If the ANOVA test was significant ($p< 0.05$), Tukey's test was performed. The asterisks denote a significant p value defined as ** for $P <0.005$.

RESULTS AND DISCUSSION

MTORC1 is not a hydrophobic motif kinase of S6K1

To determine whether TOS motif is indispensable for mediating hydrophobic motif phosphorylation in S6K1 and whether relieving auto-inhibition renders S6K1 active and independent of-the-regulation by mTORC1, we created lines of HEK293 cells stably expressing Flag-tagged wild type S6K1 or its truncation mutant ∆NH∆CT and observed their state of T412 phosphorylation, present in the hydrophobic motif, in response to mTORC1 inhibition. We chose ∆NH∆CT S6K1 for the purpose because it bears truncations at TOS motif bearing -NH2 terminal domain and -COOH terminus auto inhibitory domain (Fig 1a). mTORC1 inhibition was achieved either by treating the cells with glycolytic inhibitor-2 deoxy glucose (2DG) or rapamycin or by growing in Earl's Balanced Salt Solution (EBSS) (Dennis et al., 2001). As seen, ∆NH∆CT HEK293 stable cells display T412 phosphorylation to an extent equivalent to their wild type counterpart that also correspond with its ability to phosphorylate GST-S6 *in vitro* (Fig 1b). The data, in agreement with published literature, reinforces the narrative of TOS motif redundancy in mediating HM phosphorylation of S6K1(Ali and Sabatini, 2005; Majeed et al., 2021).This is further substantiated by the data that demonstrates TOS-dysfunction is overcome by concomitant deletion of CAD (Ali and Sabatini, 2005). Furthermore, it was interesting to observe that, unlike wildtype S6K1, ∆NH∆CT S6K1 HEK293 cells exhibit complete resistance to

mTORC1 inhibition (Fig 1b).Taken together, the data clearly indicate that mTORC1 mediated regulation serves as a priming step for the occurrence of HM phosphorylation of S6K1, and mTORC1 by itself does not appear to be the HM kinase at least *in vivo.* However, it could still be argued that ΔNHΔCT S6K1, being an unnatural variant, may support raptor recruitment co-incidentally by virtue of some unknown sequence to facilitate HM-phosphorylation. We, therefore, downregulated the expression of raptor by lentivirally transducing HEK293 cells using raptor shRNA and transfected them with HA tagged ΔNHΔCT S6K1 or wild type S6K1 to assess whether ΔNHΔCT S6K1 still sustains HM phosphorylation. Fig 1c clearly demonstrates that raptor knock down induces loss of HM phosphorylation in wild type S6K1 only and no such loss was observed in ΔNHΔCT S6K1. Altogether, the data substantiates that the kinase other than mTORC1 was responsible for mediating HM phosphorylation in S6K1. Accordingly, we tried to ascertain the identity of a bonafide kinase that must mediate HM phosphorylation in S6K1. Strikingly, selective sensitivity of ΔNHΔCT S6K1 towards mTOR kinase inhibitor- torin 1 (Fig 1c), that was also reflected through *in vitro* kinase assay of ΔNHΔCT S6K1 stable HEK293 cells using GST-S6 as substrate (Fig 1d), highlights the prospect of mTORC2 as potential kinase. Pertinently, role of mTORC2 in mediating HM phosphorylation of S6K1 has also been reported by Sabatini group (Ali and Sabatini, 2005). However, their proposition that mTORC2 mediated HM phosphorylation is a non-physiological/random event does not reconcile with the data, including ours, that highlight the redundancy of TOS motif in mediating mTORC1 specific phosphorylation of S6K1 or other bonafide mTORC1 substrates, and therefore point towards alternative mechanism for S6K1 regulation (Batool et al., 2020; Fonseca et al., 2018; Kim et al., 2011; Koren et al., 2010; Majeed et al., 2021).

MTORC2 is an *in vivo* hydrophobic motif kinase of S6K1

In light of the above results that point towards the involvement of mTORC2 in mediating HM phosphorylation, we examined the state of HM phosphorylation of S6K1 and activation in backdrop of mTORC2 compromise, achieved in rictor knock-down HEK293 cells. Accordingly, we transfected wild type S6K1 in rictor shRNA or, alternatively, in control shRNA infected HEK293 cells to detect any change in the magnitude of T412 phosphorylation present in hydrophobic motif. As seen, T412 phosphorylation in rictor shRNA infected HEK293 cells decreases as compared to control shRNA HEK293 cells (Fig 2a). Interestingly, the decrease in T412 phosphorylation was more prominent upon treatment with increasing concentration of mTORC1 specific inhibitor-rapamycin (Fig 2a).Taken together, the results suggest that mTORC1 inhibition, due to addition of rapamycin, fails to relieve S6K1 auto-inhibition and

therefore prevents mTORC2 mediated HM phosphorylation of the enzyme. Although, the observation appears in tune with our previous finding that highlights the role of mTORC1 in relieving S6K1 auto-inhibition and priming it for HM phosphorylation and subsequent activation, we wanted to further substantiate the role of mTORC2 in mediating HM phosphorylation. Therefore, we used two different rapamycin resistant mutants ΔNHΔCT and F28AΔCT (Ali and Sabatini, 2005), for observing their state of T412 phosphorylation in rictor knock down HEK293 cells. While ΔNHΔCT mutant is described above, F28AΔCT shares the same –COOH terminal truncation as ΔNHΔCT but bears an inactivating mutation in the TOS motif instead of the -NH2 terminal truncation (Fig 1a) (Ali and Sabatini, 2005; Beigh et al., 2013). Both the mutants, despite being rapamycin resistant, exhibit significant loss of T412 phosphorylation in rictor knock down state (Fig 2b), indicating the involvement of mTORC2 in mediating T412 phosphorylation. The result further strengthens our viewpoint that the loss of T412 phosphorylation by rapamycin mediated mTORC1 inactivation in wild type S6K1 is due to persistent auto-inhibition, caused by CAD, which disallows mTORC2 the access to phosphorylate S6K1 at T412 site. We also evaluated the impact of serum stimulation on T412 phosphorylation in S6K1 transfected rictor shRNA HEK293 cells and observed that addition of serum does not induce T412 phosphorylation in rictor shRNA cells as compared to control shRNA cells (Fig 2c). Altogether, the data demonstrates that T412 phosphorylation is indeed mediated by mTORC2 after disinhibition or priming by mTORC1.

A 19 amino-acid region of S6K1 mediates mTORC2 phosphorylation.

Although the data presented above validates mTORC2 as an *in vivo* T412 kinase, we further wanted to ensure the specificity of mTORC2 in mediating this phosphorylation. We, therefore, argued if mTORC2 mediated T412 phosphorylation, observed in above discussed truncation mutants of S6K1, is a non-physiological/ random event as proposed by the Sabatini group, then a smaller mutant of S6K1 should also be phosphorylated in a similar manner by mTORC2. To address this, we examined the sequence of ΔNHΔCT S6K1, which comprises a total of 375 amino acids starting from amino acid 47 to 421 (see Fig 1a). A careful examination of the sequence revealed TOS like motif spanning the region from amino acid 154 to 158. Interestingly, the region is conserved among various species (Fig 3a). Therefore, we truncated 100 amino acids from -NH2 terminal end of ΔNHΔCT to generate a smaller mutant 147-421, which behaves like a TOS swap variant of S6K1 (Fig 3b). This mutant was important in two aspects as it would tell whether the presence of TOS like motif enhances its prospect of phosphorylation by mTORC1 as well as whether the smaller size of the mutant better facilitates

its non-physiological/random phosphorylation by mTORC2. Therefore, we transfected 147-421 S6K1 along with wild type and ΔNHΔCT in HEK293 cells and observed the T412 phosphorylation levels. Unlike wild type S6K1 and ΔNHΔCT S6K1, the mutant 147-421 failed to display any detectable phosphorylation at T412 (Fig 3b), indicating redundancy of TOS motif in mediating this phosphorylation on one hand as well as dispelling the notion that mTORC2 mediated T412 phosphorylation is a non-physiological event on the other. Instead, the results suggest involvement of a truncated region 47-146 in regulating T412 phosphorylation. Accordingly, we generated a series of smaller deletions across this amino acid stretch to identify the sequence imparting T412 regulation (Fig 3c), and transfected them in HEK293 cells. Fig 3d shows that while T412 phosphorylation was reasonably present in 77-421 and 91-421 truncation mutants of S6K1, no such phosphorylation was observed in 110-421 S6K1 mutant. The data, therefore, highlights the involvement of this 19 amino acid stretch, starting from amino acid 91 to 109, in imparting T412 regulation. Although we furthered our attempt to examine smaller deletions i.e.,91- 99 and 100-109 with in this stretch, but failed to gather any information due to the unreliable expression of these mutants. Next, we introduced this 19 amino acid deletion in wild type S6K1 to address whether the presence of TOS bearing amino and carboxy termini would help the mutant recover its T412 phosphorylation. As seen in Fig 3d, the mutant fails to display any detectable T412 phosphorylation to establish the 19 amino acid stretch as mTORC2 response site. Taken together, the data suggests that this 19 amino acid stretch mTORC2 dependent HM phosphorylation of S6K1.

The proposal that mTORC1 is an exclusive *in vivo* T412 kinase of S6K1 while mTORC2 mediated T412 phosphorylation is only a non-physiological event determined by the structure of S6K1, does not satisfactorily reconcile with the data that demonstrate T412 phosphorylation in TOS deficient S6K1 mutants (Ali and Sabatini, 2005; Dennis et al., 2001; Majeed et al., 2021). The findings contest the preposition that interaction between raptor and TOS motif of S6K1 is the basis for mTORC1 mediated T412 phosphorylation. Furthermore, absence of a consensus TOS motif in other mTORC1 substrates question the centrality of TOS in mediating mTORC1 specific substrate phosphorylation. The observation is further endorsed by our recent findings that identify eIF4E as mTORC1 substrate and an intermediate in transducing signals downstream of mTORC1 onto S6K1. The data, therein, demonstrates that the role of mTORC1 is restricted to engaging eIF4E with TOS motif of S6K1, required for relieving auto-inhibition and subsequently priming S6K1 for T412 phosphorylation in mTORC1 independent manner (Majeed et al., 2021). Based on these observations and the data presented here, mTORC2 appears to

be an *in vivo* T412 kinase. The experiments conducted in rictor shRNA infected cells, under serum-starved or serum-stimulated conditions, demonstrate that mTORC2 mediates T412 phosphorylation, subject to the priming by mTORC1.Therefore, our proposal, described in fig 4, that S6K1 requires priming by mTORC1 dependent TOS-eIF4E engagement before it exhibits mTORC2 mediated T412 phosphorylation, addresses the shortcomings that otherwise discredit mTORC2 as an *in vivo* T412 kinase. Notably, deletion analysis reveals 19 amino acid stretch of S6K1 responsible for mediating T412 phosphorylation by a torin sensitive kinase and therefore associates physiological specificity with mTORC2 mediated T412 phosphorylation. Furthermore, loss of T412 phosphorylation in S6K1 mutant deleted of this 19 amino acid stretch, despite the presence of a consensus TOS motif, unequivocally implicates the region in mediating T412 phosphorylation.

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Author Contributions

S.T.M. designed and performed the experiments, generated S6K1 stable cell lines, constructed S6K1 mutants, analysed and interpreted the data and wrote the manuscript. R.M. performed experiments, constructed rictor, raptor knockdown cell lines. M.A.Z. supervised the project. K.I.A conceived and supervised the project, designed the experiments, interpreted the data and wrote the manuscript.

Declaration of Interests

The authors declare no competing interests.

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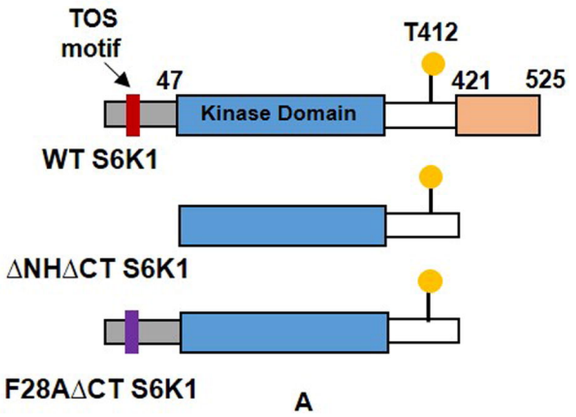
Legends

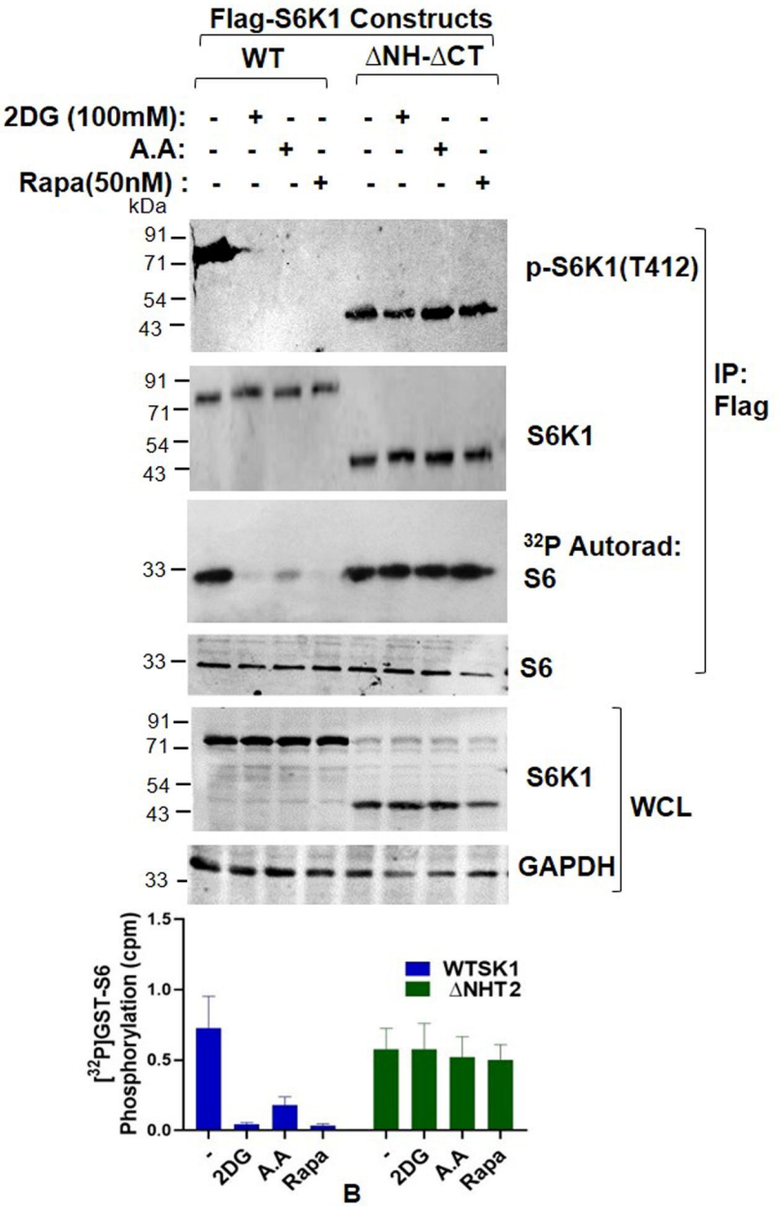
Fig 1 mTORC1 does not phosphorylate hydrophobic motif of S6K1. (A) S6 Kinase 1 domain structure. Representative picture demonstrates the structure full length S6K1 along with the location of TOS motif. Also shown are the truncation mutant ΔNHT2 and F28AΔCT used in the study. (B) Release of auto-inhibition renders S6K1 independent of mTORC1 regulation. Flag-WTS6K1 and Flag-ΔNHT2 S6K1 stable HEK293 cells were either lysed directly or after incubation with agents known to inhibit mTORC1 input (100 mM 2-Deoxy Glucose or 50 nM rapamycin for 30 minutes). Alternatively, mTORC1 inhibition was achieved by growing cells in amino acid free media (EBSS).The lysates obtained were Flag immunoprecipitated and probed for T412 levels of S6K1. Furthermore, S6K1 kinase activity was monitored using GST-S6 as a substrate in an *in vitro* kinase assay. Quantitation represents average results of three independent experimental series. Error bars denote SEM. (C) Raptor is not involved in mediating hydrophobic motif phosphorylation of S6K1. Raptor or scrambled shRNA infected HEK293 cells were transfected with wild type S6K1 or truncation mutant ΔNHT2. Before lysis, the cells were treated with increased concentration of torin in indicated manner for 30 minutes. The lysates obtained were HA immunoprecipitated and probed for T412 levels of S6K1. (D) S6K1 amino and carboxy termini truncation mutant ΔNHT2 is sensitive to torin. Flag-WTS6K1 and Flag-ΔNHT2 S6K1 stable HEK293 cells were either lysed directly or after 30 minutes incubation with 50nM torin. The lysates obtained were Flag immunoprecipitated and probed for T412 levels of S6K1 and S6K1 activity as described in (B).

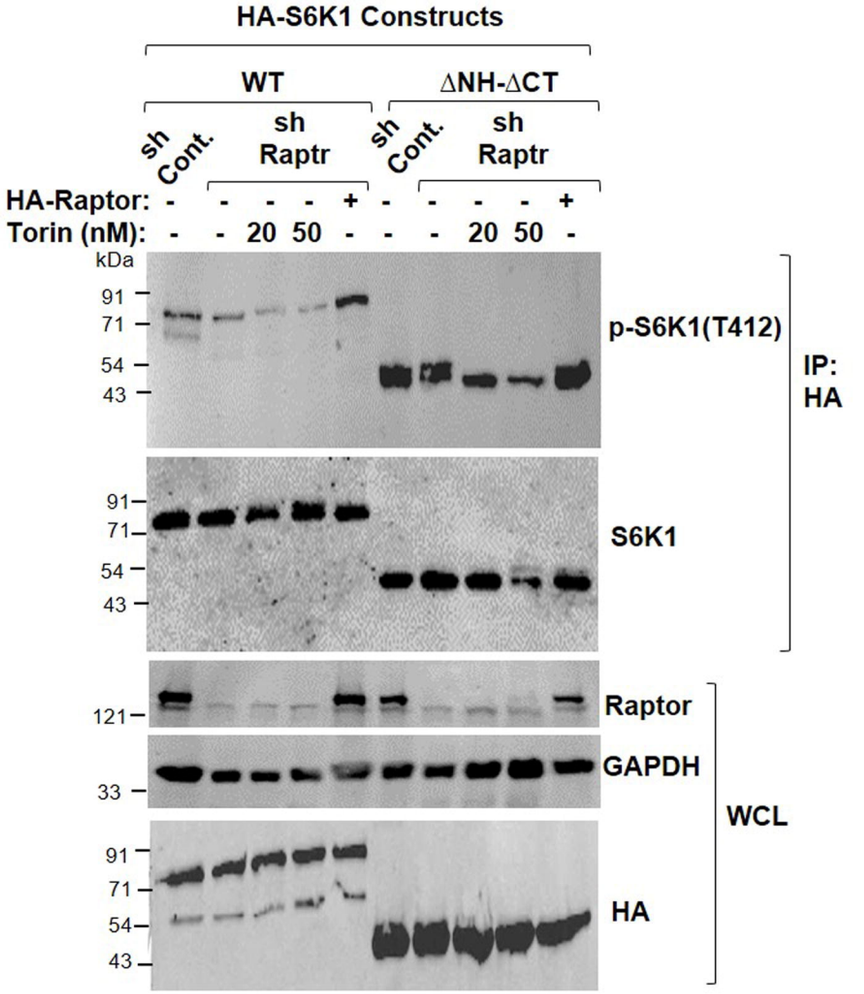
Fig 2 mTORC2 is an *in vivo* T412 kinase of S6K1. (A and B) S6K1 loses T412 phosphorylation in rictor knock down cells. HEK293 cells were infected with rictor shRNA to generate rictor knockdown cell line. Scrambled shRNA was used as control. The cells were transfected with HA tagged WT-S6K1. Before lysis, the cells were treated with increased concentration of rapamycin for 30 minutes in indicated manner. The lysates obtained were HA immunoprecipitated and probed for T412 levels of S6K1. Quantitation showingT412 phosphorylation levels represents average result of three independent experimental series normalized to their respective protein content. Error bars denote SEM. p value denoted as ** indicates $P < 0.005$ (A). HA tagged rapamycin resistant S6K1 mutants F28AΔCTand ΔNHT2 were transfected in rictor or scrambled shRNA infected HEK293 cells in indicated manner. Additionally, 2 µg of myc-rictor encoding plasmid was transfected in rictor shRNA cell line to rescue its knock down effect. Prior to lysis, the cells were treated with 50nM of rapamycin for 30 minutes. The lysates obtained were HA immunoprecipitated and probed for T412 levels (B). (C) S6K1 T412 phosphorylation does not respond to serum stimulation in rictor knock down cells. HA tagged wild type S6K1 was transfected in rictor or scrambled shRNA infected HEK293 cells in indicated manner. Additionally, 2 µg of myc-rictor encoding plasmid was transfected in rictor shRNA cell line to rescue its knock down effect. The cells were grown in serum supplemented DMEM for 48 hours and then serum starved for 12 hours. Prior to lysis, cells were serum stimulated for 30 minutes in indicated manner. The lysates were HA immunoprecipitated and probed for T412 levels.

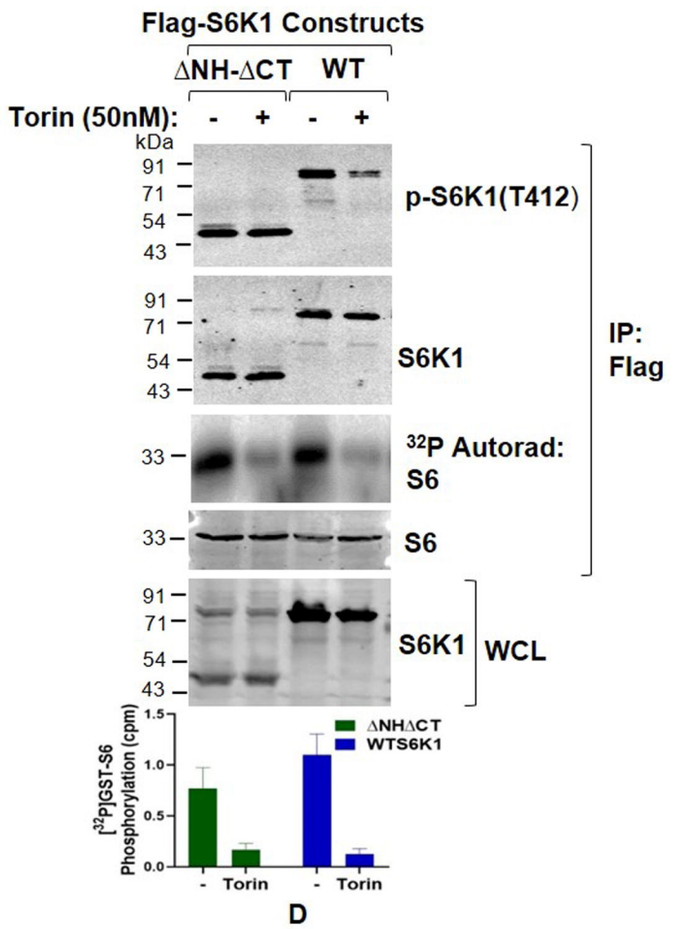
Fig 3 S6K1 harbors mTORC2 responsive site. (A) S6K1 harbors a TOS like motif in kinase domain. Sequence alignment shows a TOS like motif in catalytic kinase domain of S6K1 and its conserved nature across the species. (B) Structure of truncation mutants of S6K1 used in the study. (C-E) A 19 amino acid region is responsible for mediating mTORC2 dependent T412 phosphorylation of S6K1. HEK293 cells were transfected with HA tagged wild type S6K1 or truncation mutant ∆NHT2 or myc tagged 147-421 S6K1 as indicated (C) or with myc tagged S6K1 truncation mutants 77-421, 91-421 and 110-421 (D) or with HA tagged wild type S6K1 and ∆91-109 (E). Prior to lysis, cells were treated with 50nM of torin-1 (C and D) or with 50 nM of rapamycin (E) for 30 minutes. The lysates obtained were epitope immunoprecipitated and probed for T412 levels. Furthermore, S6K1 kinase activity was monitored using GST-S6 as a substrate in an *in vitro* kinase assay (E). Quantitation represents average results of three independent experimental series. Error bars denote SEM.

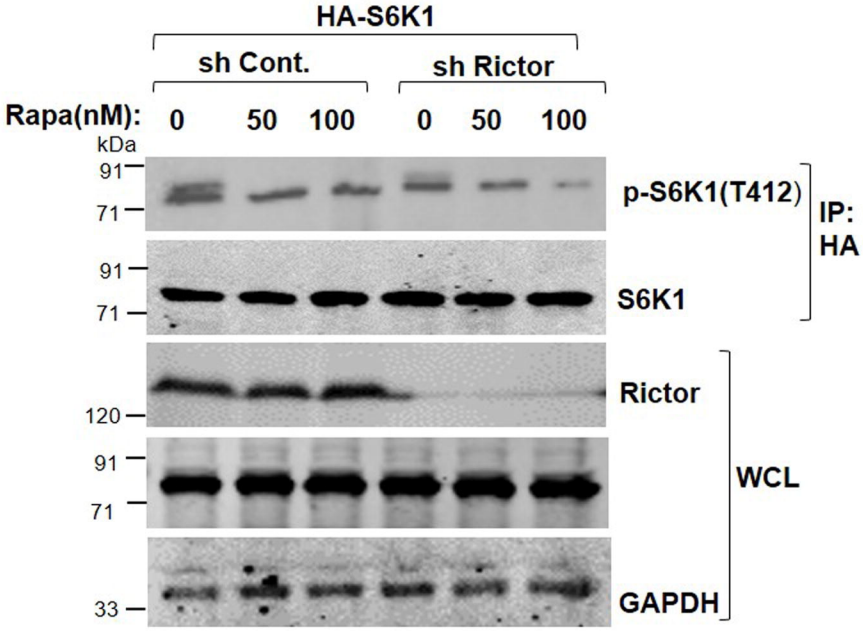
Fig 4 Illustration describing mTORC1, eIF4E and mTORC2 as participants for complete activation of S6K1.

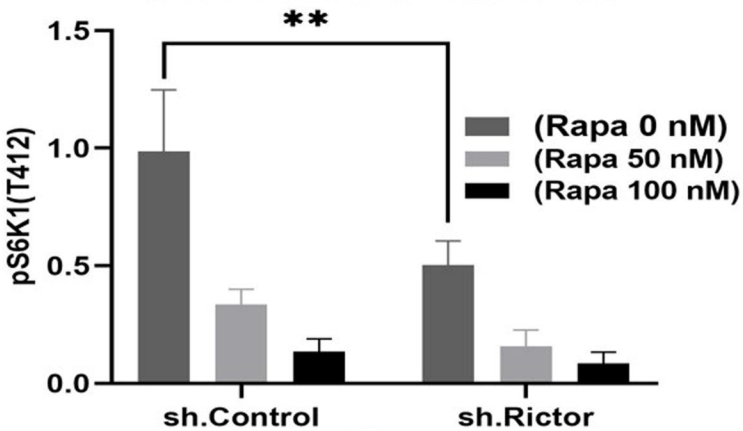

TOS motif
47
T412
421
525
Kinase Domain
WT S6K1
ΔNHΔCT S6K1
F28AΔCT S6K1
A


Flag-S6K1 Constructs
WT
ΔNH-ΔCT
2DG (100mM): - + - - - + - -
A.A: - - + - - - + -
Rapa(50nM) : - - - + - - - +
kDa
91
71
54
43
p-S6K1(T412)
S6K1
IP: Flag
33
32P Autorad: S6
S6
WCL
GAPDH
[32P]GST-S6 Phosphorylation (cpm)
1.5
1.0
0.5
0.0
WTSK1
ΔNHT2
-
2DG
A.A
Rapa
B

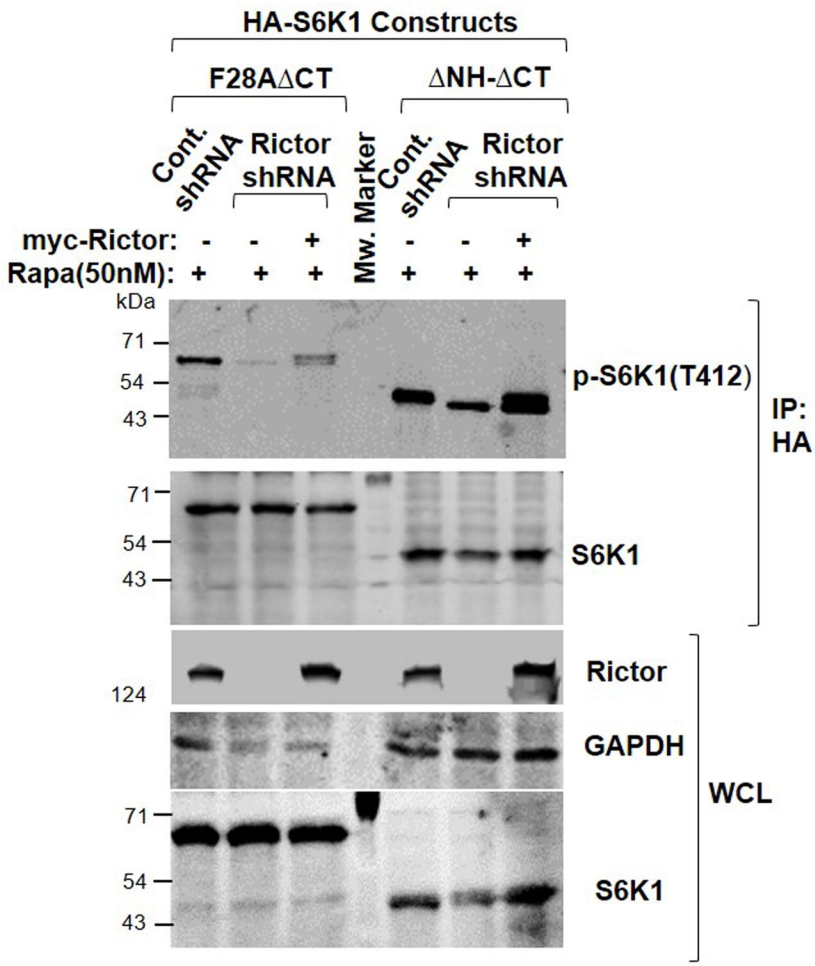

HA-S6K1 Constructs
WT
ΔNH-ΔCT
sh Cont.
sh Raptr
HA-Raptor: - - - - + - - - - +
Torin (nM): - - 20 50 - - - 20 50 -
kDa
91
71
54
43
p-S6K1(T412)
S6K1
IP: HA
121
Raptor
GAPDH
33
WCL
HA
C


Flag-S6K1 Constructs
ΔNH-ΔCT
WT
Torin (50nM): - + - +
kDa
91
71
54
43
p-S6K1(T412)
S6K1
IP: Flag
33
32P Autorad: S6
S6
WCL
[32P]GST-S6 Phosphorylation (cpm)
1.5
1.0
0.5
0.0
ΔNHΔCT
WTS6K1
-
Torin
D

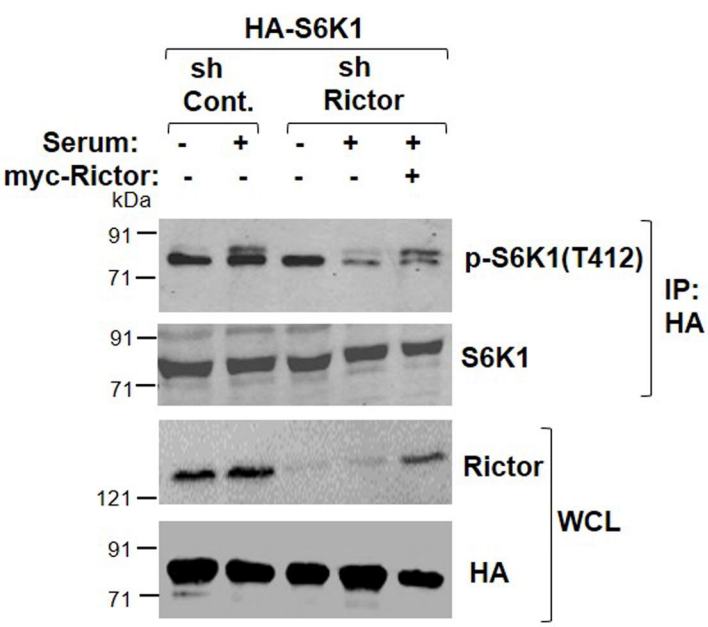

HA-S6K1
sh Cont.
sh Rictor
Rapa(nM): 0 50 100 0 50 100
kDa
91
71
p-S6K1(T412)
IP: HA
91
71
S6K1
120
Rictor
91
71
WCL
33
GAPDH


**
1.5
1.0
0.5
0.0
pS6K1(T412)
(Rapa 0 nM)
(Rapa 50 nM)
(Rapa 100 nM)
sh.Control
sh.Rictor

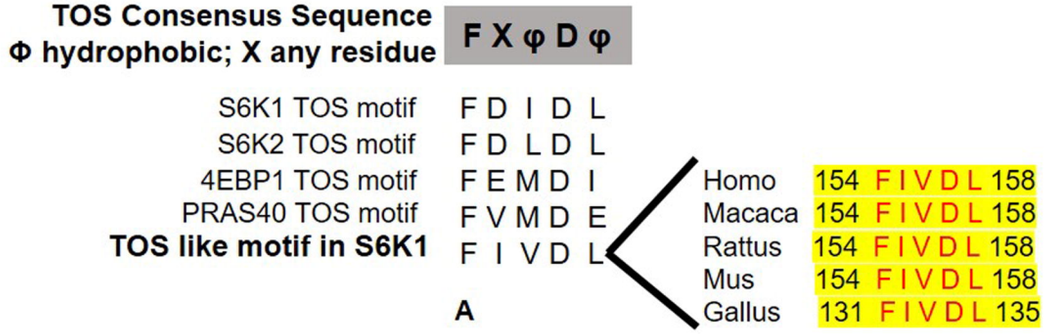
A

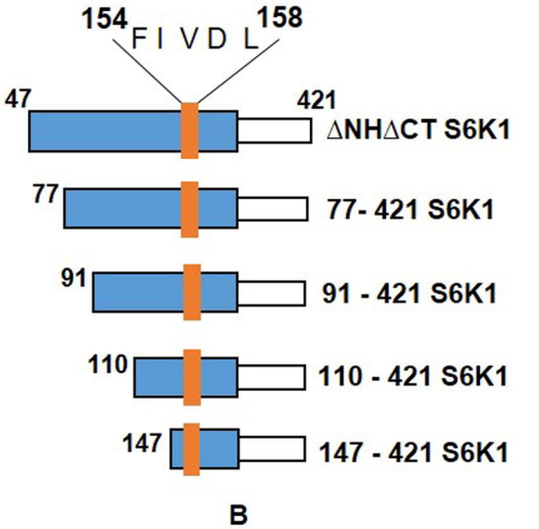

HA-S6K1 Constructs
F28AΔCT
ΔNH-ΔCT
Cont. shRNA
Rictor shRNA
Mw. Marker
Cont. shRNA
Rictor shRNA
myc-Rictor: - - + - - +
Rapa(50nM): + + + + + +
kDa
71
54
43
p-S6K1(T412)
IP: HA
71
54
43
S6K1
124
Rictor
GAPDH
WCL
71
54
43
S6K1

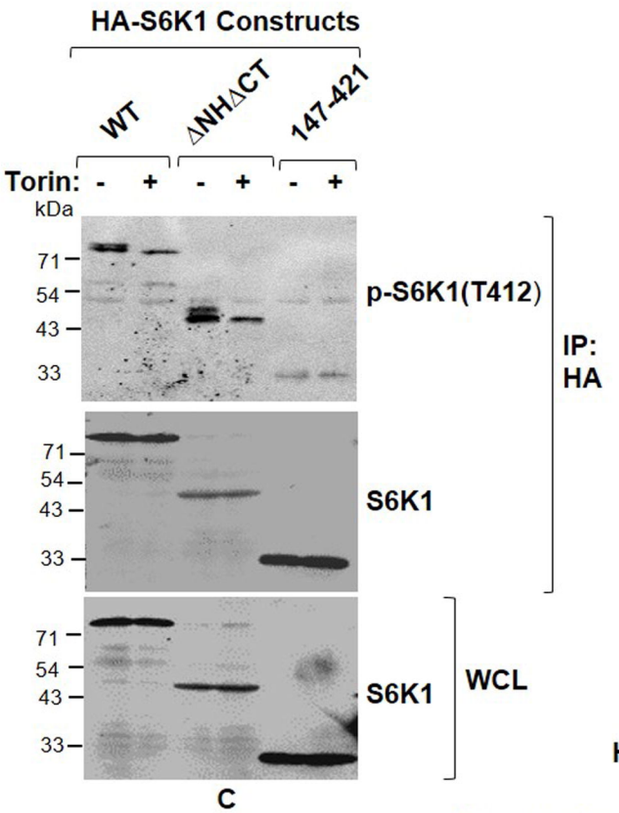
B

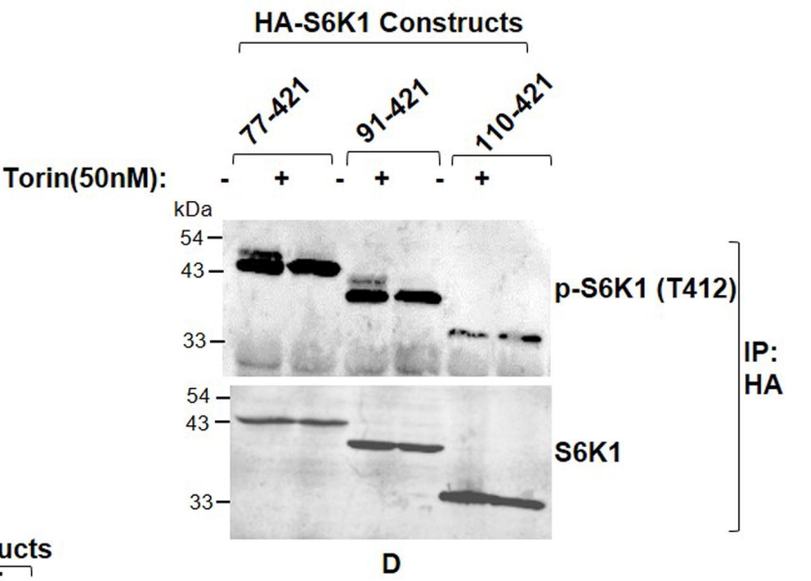

HA-S6K1
sh Cont.
sh Rictor
Serum: - + - + +
myc-Rictor: - - - - +
kDa
91
71
p-S6K1(T412)
IP: HA
91
71
S6K1
121
Rictor
WCL
91
71
HA

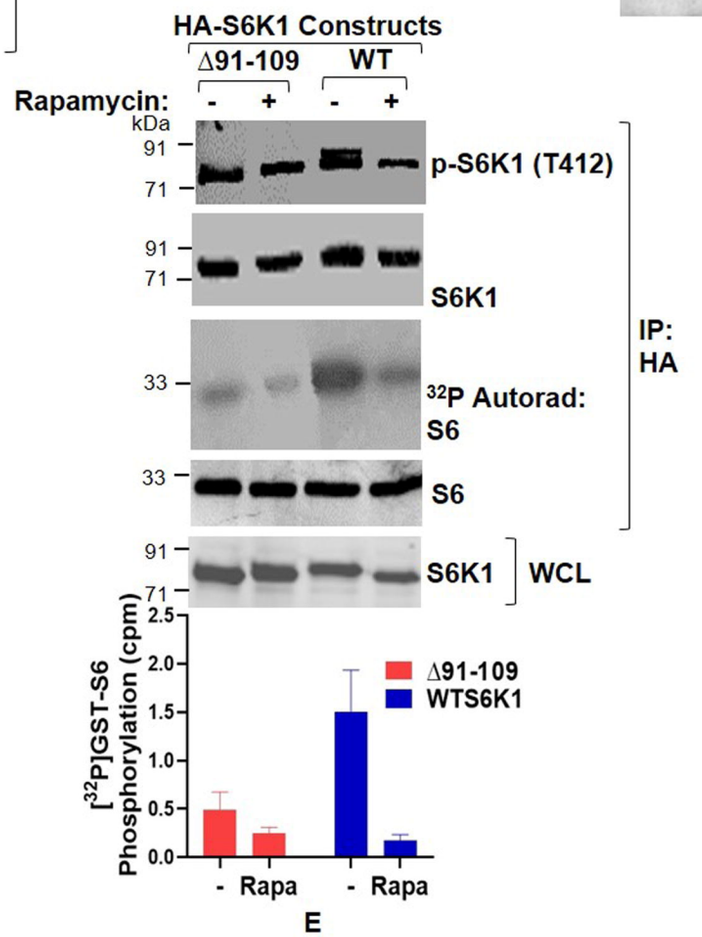
C

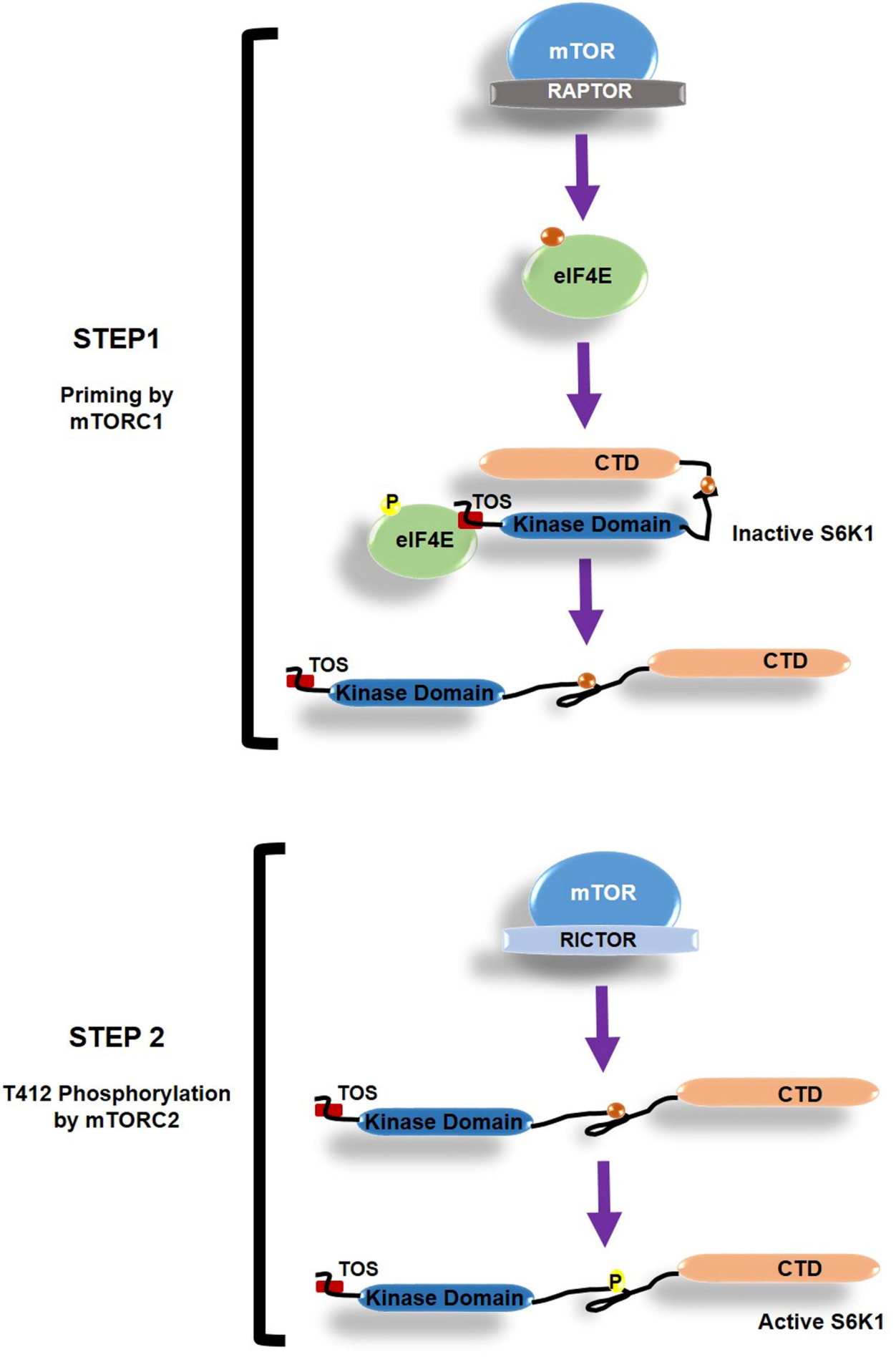

TOS Consensus Sequence
Φ hydrophobic; X any residue
F X φ D φ
S6K1 TOS motif F D I D L
S6K2 TOS motif F D L D L
4EBP1 TOS motif F E M D I
PRAS40 TOS motif F V M D E
TOS like motif in S6K1 F I V D L
Homo 154 F I V D L 158
Macaca 154 F I V D L 158
Rattus 154 F I V D L 158
Mus 154 F I V D L 158
Gallus 131 F I V D L 135
A


154 F I V D L 158
47
421
ΔNHΔCT S6K1
77
77- 421 S6K1
91
91 - 421 S6K1
110
110 - 421 S6K1
147
147 - 421 S6K1
B


HA-S6K1 Constructs
WT
ΔNHΔCT
147-421
Torin: - + - + - +
kDa
71
54
43
33
p-S6K1(T412)
S6K1
IP: HA
S6K1
WCL
C


HA-S6K1 Constructs
77-421
91-421
110-421
Torin(50nM): - + - + - +
kDa
54
43
33
p-S6K1 (T412)
S6K1
IP: HA
D


HA-S6K1 Constructs
Δ91-109
WT
Rapamycin: - + - +
kDa
91
71
p-S6K1 (T412)
S6K1
33
32P Autorad: S6
S6
IP: HA
S6K1
WCL
[32P]GST-S6 Phosphorylation (cpm)
2.5
2.0
1.5
1.0
0.5
0.0
Δ91-109
WTS6K1
- Rapa
- Rapa
E


STEP1
Priming by mTORC1
mTOR
RAPTOR
eIF4E
CTD
P
TOS
eIF4E
Kinase Domain
Inactive S6K1
TOS
Kinase Domain
CTD
STEP 2
T412 Phosphorylation by mTORC2
mTOR
RICTOR
TOS
Kinase Domain
CTD
TOS
Kinase Domain
P
CTD
Active S6K1