abcam

Product datasheet

Modified EIF2S peptide ab204868

Description

Product name Modified EIF2S peptide

Purity > 95 % HPLC.

Animal free No

Nature Synthetic

Sequence Modified-CILLSELSRRRIR

Additional sequence information The peptide is derived from human EIF2S1; aa46-57.

Specifications

Our Abpromise guarantee covers the use of ab204868 in the following tested applications.

The application notes include recommended starting dilutions; optimal dilutions/concentrations should be determined by the end user.

Applications HPLC

Functional Studies

Form Liquid

Additional notes The Modified EIF2S peptide sequence (Modified-CILLSELSRRRIR) is derived from human

EIF2S1 (46-57) and is suitable for use as the substrate for EIF2AK kinase family and MNK1.

ab204868 (Modified EIF2S peptide) can be utilized as a substrate for the following active protein

kinases:

ab125635 (Active human MNK1 full length protein)

Preparation and Storage

Stability and Storage Shipped at 4°C. Store at -20°C. Avoid freeze / thaw cycle.

pH: 7.5

General Info

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Relevance

Eukaryotic translation initiation factor 2 (eIF-2) functions in the early steps of protein synthesis by forming a ternary complex with GTP and initiator tRNA. This complex binds to a 40S ribosomal subunit, followed by mRNA binding to form a 43S preinitiation complex. Junction of the 60S ribosomal subunit to form the 80S initiation complex is preceded by hydrolysis of the GTP bound to eIF-2 and release of an eIF-2-GDP binary complex. In order for eIF-2 to recycle and catalyze another round of initiation, the GDP bound to eIF-2 must exchange with GTP by way of a reaction catalyzed by eIF-2B. Post-translational modification: Substrate for at least 4 kinases: EIF2AK3/PERK, GCN2, HRI and PKR. Phosphorylation stabilizes the eIF-2/GDP/eIF-2B complex and prevents GDP/GTP exchange reaction, thus impairing the recycling of eIF-2 between successive rounds of initiation and leading to global inhibition of translation. In case of infection by vaccinia virus or rotavirus A, eIF2S1 phosphorylation state is modulated. Subunit structure: Heterotrimer composed of an alpha, a beta and a gamma chain. Component of an EIF2 complex at least composed of CELF1/CUGBP1, CALR, CALR3, EIF2S1, EIF2S2, HSP90B1 and HSPA5. Interaction with METAP2 protects EIF2S1 from inhibitory phosphorylation. Interacts with ABCF1 isoform 2. Associates with ribosomes.

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