

Certificate of Analysis

CSNK1E R178C (CK1 epsilon), 10 µg

Recombinant Human CSNK1E R178C (CK1 epsilon), GST-tagged



Part Number: A33498

Lot Number: 1965180

Immediate Storage: -80°C

Shipping Conditions: dry ice

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Description:

Recombinant human full-length CSNK1E R178C (CK1 epsilon) was expressed in insect cells using a N-terminal GST tag.

CSNK1E R178C (CK1 epsilon) is a member of the CK1 family of serine/threonine protein kinases which play an important role in diverse cell processes, including DNA replication and repair. CSNK1E is a regulator of Yes-associated protein (YAP) transcription coactivator which is a key regulator of organ size and a candidate human oncogene. CSNK1E is activated by CCK2R and this then phosphorylates PKD2 at Ser244. Phosphorylation of PKD2 leads to its nuclear accumulation and efficient phosphorylation of nuclear PKD2 substrates in human gastric cancer cells. CSNK1E can phosphorylate topoisomerase (topo) IIalpha at serine-1106 and this regulates the enzyme activity and sensitivity to topo II-targeted drugs.

Accession Number:

The gene accession number for CSNK1E R178C (CK1 epsilon) is NP_001885.1.

Specific Activity:

38 nmoles of phosphate transferred to dephosphorylated casein substrate per minute per mg of total protein at 30°C.

Concentration:

0.05 mg/mL as determined by densitometry of the kinase gel band(s).

Calculated **679 nM**.

Aliases:

HCKIE, CK1 epsilon

Storage and Handling:

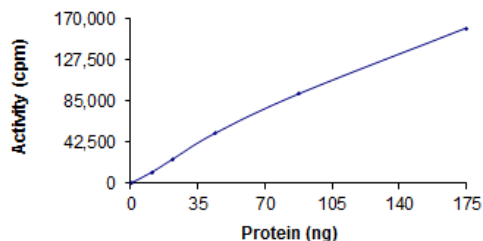
For maximum recovery please spin prior to use. Unless noted below, aliquots of the 5 µg, 10µg and 20µg sizes of kinase are not recommended as materials can be used in original packaging until exhausted. For larger sizes, the number of freeze/thaws may be reduced by preparing aliquots, aliquots below 20 µL are not recommended. **Please never store a kinase diluted.** If properly stored at -80°C, this product is guaranteed for 6 months from date of purchase.

Storage Buffer:

50 mM Tris-HCl (pH 7.5), 150 mM NaCl, 10mM glutathione, 0.1 mM EDTA, 0.25 mM DTT, 0.1 mM PMSF and 25% Glycerol.

QUALITY ASSURANCE

CSNK1E R178C (CK1 epsilon) Activity Graph



Dilution Buffer:

5 mM MOPS (pH 7.2), 2.5 mM β-glycerol-phosphate, 5 mM MgCl₂, 1 mM EGTA, 0.4 mM EDTA, 0.05mM DTT and 50 ng/µL BSA.

Assay Conditions:

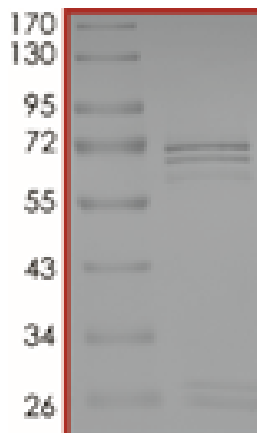
CSNK1E R178C (CK1 epsilon) was pre-diluted in enzyme dilution buffer and assayed in 5 mM MOPS (pH 7.2), 2.5 mM β-glycerol-phosphate, 5 mM MgCl₂, 1 mM EGTA, 0.4 mM EDTA, 0.05 mM DTT, with 50 µM ATP, trace [³²P]-γ-ATP and 200 µg/mL dephosphorylated casein substrate for 15 minutes at 30°C.

Gel Information for CSNK1E R178C (CK1 epsilon)

Page Description: Run on an SDS-PAGE gel and stained with Coomassie®.

Lane 1: Molecular Weight markers as labeled.

Lane 2: CSNK1E R178C (CK1 epsilon)



Purity:

> 70% as determined by a Coomassie® blue stained SDS-PAGE gel, excluding endogenous GST.

Molecular Weight:

73.6 kDa. Calculated from the protein sequence(s).

Protein sequence alignment with reference sequence(s)

GenBank Accession Number: NP_001885.1

1 MSPILGYWKIKGLVQPTRLLLEYLEEKYEHLVERDEGDKWRNKKFELGLEFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAIEISMLEGAVL GST
1 MSPILGYWKIKGLVQPTRLLLEYLEEKYEHLVERDEGDKWRNKKFELGLEFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAIEISMLEGAVL Life CSNK1E R178C
1 M-----NP_001885.1

101 DIRYGVSRIAYSKDFETLKVDLFLSKLPEMLKMFEDRLCHKTYLNGDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPIQIDKYLKSSKYIA
101 DIRYGVSRIAYSKDFETLKVDLFLSKLPEMLKMFEDRLCHKTYLNGDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPIQIDKYLKSSKYIA
2 -----

201 WPLQGWQATFGGGDHPKSD
201 WPLQGWQATFGGGDHPKSDLVPRGSMELRVGNKYRLGRKIGSGSFGDIYLGANIASGEEVAIKLECVKTKHPQLHIESKFYKMMQGGVGIPSIKWCGAE
2 -----ELRVGNKYRLGRKIGSGSFGDIYLGANIASGEEVAIKLECVKTKHPQLHIESKFYKMMQGGVGIPSIKWCGAE

220
301 GDYNVMVMELLGPSLEDLNFCSRKFSLKTVLLADQMISRIEYIHSKNFIHRDVKPDNFMGLGKKGNLVYIIDFGLAKKYRDARTHQHIPPYRENKNLT
75 GDYNVMVMELLGPSLEDLNFCSRKFSLKTVLLADQMISRIEYIHSKNFIHRDVKPDNFMGLGKKGNLVYIIDFGLAKKYRDARTHQHIPPYRENKNLT

220
401 GTAGYASINTHLGIEQSRDDLESGLGYLMYFNGLSLPWQGLKAATKRQKYERISEKKMSTPIEVLCKGYPSEFSTYLNFCRSLRFDDKPDYSYLRQLFR
175 GTARYASINTHLGIEQSRDDLESGLGYLMYFNGLSLPWQGLKAATKRQKYERISEKKMSTPIEVLCKGYPSEFSTYLNFCRSLRFDDKPDYSYLRQLFR

220
501 NLFHRQGFSDYVFDWNMLKFGAARNPEDVDREHEREERMGQLRGSATRALPPGPPTGATANRLRSAAEPVASTPASRIQPAGNTSPRAISRVDRE
275 NLFHRQGFSDYVFDWNMLKFGAARNPEDVDREHEREERMGQLRGSATRALPPGPPTGATANRLRSAAEPVASTPASRIQPAGNTSPRAISRVDRE

220
601 KVSMLRHRGAPANVSSDLTGRQEVSRIPASQTSVPFDHLGK
375 KVSMLRHRGAPANVSSDLTGRQEVSRIPASQTSVPFDHLGK

* highlighted residues denote differences from the reference protein sequence(s).

Anita Targosz

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Date: 27/Feb/2018

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