

## *Division of Signal Transduction Therapy*

### **Standard Operating Procedure**

#### **Preparation of active CSNK1G3 [1 – 423]**

**Enzyme description:-** CSNK1G3 [1 - 423]

**Clone number:-** DU 35305

**Source:-** Recombinant

**Expression system:-** *E.coli*

**Tag:-** N-terminal GST

**Purification method:-** GSH Sepharose

**Calculated molecular mass:-**

Monoisotopic 75, 674.27 daltons

Average Mass 75, 723.09 daltons

[cysteines reduced, methionines have not been oxidised]

**Theoretical pI:-** 8.61

**Purity:-** 85 %

**Activation protocol:-** Constitutively active

**Enzyme storage buffer:-**

50 mM Tris-HCl pH 7.5, 270 mM Sucrose, 150 mM NaCl, 0.1 mM EGTA,  
0.1 % 2-mercaptoethanol, 0.02 % Brij-35, 1 mM benzamidine, 0.2 mM PMSF

**Storage temperature:-** -70 °C

**Assay buffer:-**

50 mM Tris-HCl pH 7.5, 0.1 mM EGTA, 0.1 % 2-mercaptoethanol, 10 mM MgAc

**Substrate:-**

KRRRALS\*VASLPGL (where S\* is phospho Ser)

Final concentration: 300 µM

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**Clone Data Sheet**

**CSNK1G3 [1 - 423]**

<b><u>Protein</u></b>	CSNK1G3 [1 - 423]
<b><u>Clone number</u></b>	DU 35305
<b><u>Species</u></b>	Human
<b><u>Accession number</u></b>	AAH47567.1
<b><u>Tags</u></b>	N-terminal GST
<b><u>Bacterially expressed protein</u></b>	<p>MSPILGYWKIKGLVQPTRLLEYLEEKYEEHLYERDEGDKWRNKKFELG LEFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAETSMLEGA VLDIRYGVSR IAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGDH VTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKYLKSS KYIAWPLQGWQATFGGGDHPPKSDLEVLFGQPLGSMENKKKDKDKSDDR <b>MARPSGRSGHNTRGTGSSSSGVLMVGNFRVGGKIGCGNFGE LRLGKNL</b> <b>YTNEYVAIKLEPMKSRAPQLHLEYRFYEQLGSGDGIPOVYYFGPCGKYN</b> <b>AMVLELLGPSLEDLFDLCDRTFSLKTVLMIAIQ LISRMEYVHSKNLIYR</b> <b>DVKPENFLIGRPGNKTQQVIHIIDFGLAKEYIDPETKKHIPYREHKS LT</b> <b>GTARYMSINTHLGKEQSRDDLEALGHMFMYFLRGS LPWQGLKADTLKE</b> <b>RYQKIGDTRATPIEVL CENFPEMATYLRVRRLDFFEKPDYDYL RKL F</b> <b>TDLFDRKGYMFDYEYDWIGKQLPTPVGAVQODPALSSNREAHQHRDKMQ</b> <b>QSKNQVVSSTNGELNTDDPTAGRSNAPI TAPTEVEVMDETNCQKVLNMW</b> <b>CCCFKRRKRKTIQRHK</b></p>
<b><u>Native sequence</u></b>	<p>Amino acids M1 – K423 (end) of human CSNK1G3. Residue M232 of the fusion protein is equivalent to M1 of the native enzyme. The GST tag is located at residues 1 – 220.</p>
<b><u>Protease cleavage</u></b>	PreScission ( <u>LEVLFGQP</u> ) residues 221 - 229
<b><u>Cloning sites</u></b>	<i>Bam</i> H1 and <i>Not</i> 1 sites of pGEX 6P-1

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### Nucleotide Sequence of insert

ggatccATGGAAAATAAAAAGAAAGACAAGGACAAATCAGATGATAGAATGGCACGACC  
TAGTGGTCGATCGGGACACAACACTCGAGGAACTGGGTCTTCATCGTCTGGAGTTTTAA  
TGGTTGGACCTAACTTTAGAGTTGGAAAAAAAAATTGGATGTGGCAATTTTGGAGAATTA  
CGATTAGGGAAAAATTTATACACAAATGAATATGTGGCAATTAAGTTGGAGCCCATGAA  
ATCAAGAGCACCACAGCTACATTTGGAATACAGATTCTATGAGCAGTTAGGATCTGGAG  
ATGGTATACCTCAAGTTTACTATTTTCGGCCCTTGTGGTAAATACAATGCTATGGTGCTG  
GAACTGCTGGGACCTAGTTTTGGAAGACTTGTGTTGACTTGTGTGACAGAACATTTTCTCT  
TAAAACAGTTCTCATGATAGCTATAACAATGATTTCTCGCATGGAATATGTCCATTCAA  
AGAACTTGATATACAGAGATGTAAAACCTGAGAACTTCTTAATAGGACGACCAGGAAAC  
AAAACCCAGCAAGTTATTCACATTATAGATTTTGGTTTGGCAAAGGAATATATTGATCC  
GGAGACAAAGAAACACATACCATAACAGAGAACACAAGAGCCTTACAGGAACAGCTAGAT  
ATATGAGCATAAACACACATTTAGGAAAAGAACAAGTAGAAGAGACGATTTAGAAGCT  
TTAGGTCATATGTTTCATGTATTTTCTGAGAGGCAGTCTTCCTTGGCAAGGCTTAAAGGC  
TGACACATTAAGGAGAGGTATCAGAAAATTGGAGATACAAAACGGGCTACACCAATAG  
AAGTGTATGTGAAAATTTTCCAGAAATGGCAACATATCTTCGTTATGTAAGAAGGCTA  
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TCGAAAAGGATATATGTTTGATTATGAATATGACTGGATTGGTAAACAGTTGCCTACTC  
CAGTGGGTGCAGTTCAGCAAGATCCTGCTCTGTTCATCAAACAGAGAAGCACATCAACAC  
AGAGATAAGATGCAACAATCCAAAAACCAGTTGTAAGTTCTACAAATGGAGAGTTAAA  
CACAGATGACCCACCGCAGGACGTTCAAATGCACCCATCACAGCCCTACTGAAGTAG  
AAGTGTGATGGATGAAACCAACTGCCAGAAAGTGTGTAACATGTGGTGCTGCTGTTTTTTC  
AAACGAAGGAAAAGGAAAACCATACAGCGCCACAAAtgagcgccgc