

# Certificate of Analysis

## CLK4, 10 µg

Recombinant Human CDC-Like Kinase 4, GST-tagged



**Part Number:** PV3839

**Lot Number:** 827665B

**Immediate Storage:** -80°C

**Shipping Conditions:** dry ice

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### Description:

Recombinant Human Full-Length protein, GST-tagged, expressed in insect cells. No special measures were taken to activate this kinase.

### Specific Activity:

26 nmoles of phosphate transferred to RS domain derived peptide substrate (GRSRSRSRSR) per minute per mg of total protein at 30°C. Activity determined at a final protein concentration of 8.33 µg/mL.

### Concentration:

0.30 mg/mL total protein as measured using the Bradford protein assay with BSA as a standard.

Calculated **3,530 nM**.

### Storage and Handling:

Store at -80°C. At first use, aliquot and store at -80°C to avoid multiple freeze-thaws. If properly stored at -80°C, this product is guaranteed for 6 months from date of purchase.

### Storage Buffer:

50 mM Tris (pH 7.5), 150 mM NaCl, 0.5 mM EDTA, 0.02% Triton® X-100, 2 mM DTT and 50% Glycerol.

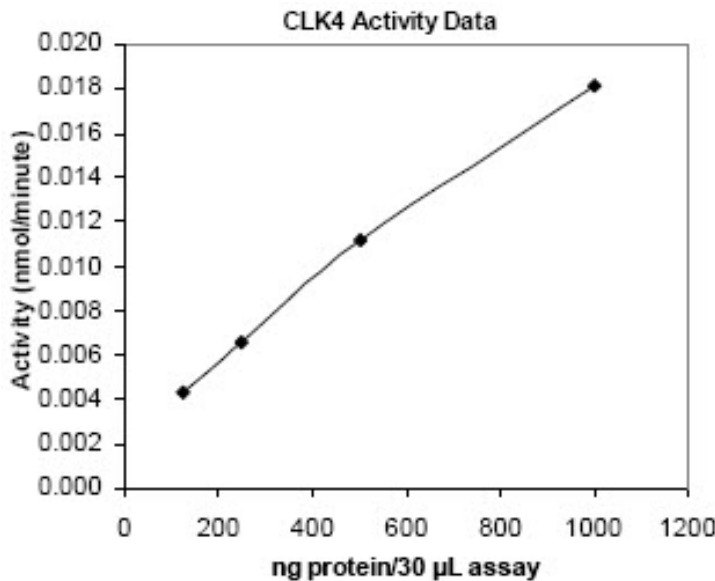
### Dilution Buffer\*:

20 mM Tris (pH 7.5), 0.02% Triton® X-100, 0.1 mg/mL BSA, 2 mM DTT, 0.5 mM Na<sub>3</sub>VO<sub>4</sub> and 10% Glycerol.

\* Note: The dilution buffer described above is used for the radiometric assay format only. For high throughput applications such as LanthaScreen®, Adapta® and Z-LYTE® refer to the associated product literature for the recommended buffer.

## QUALITY ASSURANCE

CLK4 Activity Graph



### Assay Conditions:

CLK4 was pre-diluted in enzyme dilution buffer and assayed in 25 mM Tris (pH 7.5), 10 mM MgCl<sub>2</sub>, 0.5 mM EGTA, 0.5 mM Na<sub>3</sub>VO<sub>4</sub>, 5 mM β-glycerophosphate, 2.5 mM DTT, 0.01% Triton® X-100, 200 µM ATP, 100 µM RS domain derived peptide substrate (GRSRSRSRSR) and trace [<sup>32</sup>P]-γ-ATP for 10 minutes at 30°C.

Gel Information for CLK4

**Page Description:** The SDS-PAGE and/or Native PAGE were run on 4-20% Tris-Glycine Novex® gels (Catalog #: EC6025BOX).

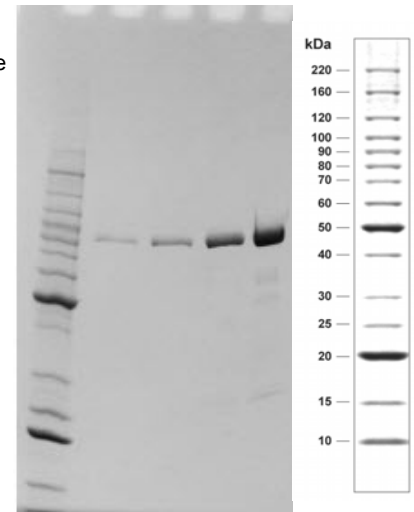
**Lane 1:** Invitrogen™ BenchMark™ Protein Ladder (Catalog #: 10747-012).

**Lane 2:** 0.5 µg CLK4

**Lane 3:** 1 µg CLK4

**Lane 4:** 2.5 µg CLK4

**Lane 5:** 5 µg CLK4



### Purity:

80% as determined by a Coomassie® blue stained SDS-PAGE gel.

### Molecular Weight:

85.0 kDa calculated from the protein sequence(s). Calculated from the protein sequence(s).

### Mass Spectrometry:

CLK4 was subjected to proteolytic digest followed by mass spec analysis. The resulting MS/MS data verified CLK4 identity by comparison against the amino acid sequence(s) of the recombinant protein.

Protein sequence alignment with reference sequence(s)

GenBank Accession Number: NP\_065717

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1 MAPILGYWKI KGLVQPTRLL LEYLEEKYEE HLYRDEGDK WRNKKFELGL EFPNLPYYID GDVKLTQ SMA IIRYIADKHN MLGGCPKERA EISMLEGAVL GST TAG
1 MAPILGYWKI KGLVQPTRLL LEYLEEKYEE HLYRDEGDK WRNKKFELGL EFPNLPYYID GDVKLTQ SMA IIRYIADKHN MLGGCPKERA EISMLEGAVL IVGN# PV3839
1 NP_065717
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101 DIRYGVSRIA YSKDFETLKV DFLSKLPEML KMFEDRLCHK TYLNGDHVTH PDFMLYDALD VVLYMDPMCL DAFPKLVCFK KRIEAIPOID KYLKSSSKYIA
101 DIRYGVSRIA YSKDFETLKV DFLSKLPEML KMFEDRLCHK TYLNGDHVTH PDFMLYDALD VVLYMDPMCL DAFPKLVCFK KRIEAIPOID KYLKSSSKYIA
2
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201 WPLQGWQATF GGGDHPPKSD LVPR
201 WPLQGWQATF GGGDHPPKSD LVPRHNQTSL YKKAGTMRHS KRTHCPDWDS RESWGHESYR GSHKRKRSSH SSTQENRHCK PHHQFKESDC HYLEARSLNE
2
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224
301 RDYRDRRYVD EYRNDYCEGY VPRHYHRDIE SGYRIHCSKS SVRSRRSSPK RKRNRHCSSH QSRSKSHRRK RSRSIEDDEE GHLICQSGDV LRARYEIVDT
65 RDYRDRRYVD EYRNDYCEGY VPRHYHRDIE SGYRIHCSKS SVRSRRSSPK RKRNRHCSSH QSRSKSHRRK RSRSIEDDEE GHLICQSGDV LRARYEIVDT
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224
401 LGEFAGFKV ECIDHGM DGM HVAVKIVKNV GRYREAAARSE IQVLEHLNST DPNSVFRVCVQ MLEWFDHHGH VCIVFELLGL STYDFIKENS FLPFQIDHIR
165 LGEFAGFKV ECIDHGM DGM HVAVKIVKNV GRYREAAARSE IQVLEHLNST DPNSVFRVCVQ MLEWFDHHGH VCIVFELLGL STYDFIKENS FLPFQIDHIR
-----
224
501 QMAYQICQSI NFLHHNKLTH TDLKPENILF VKSDYVVKYN SKMKRDERTL KNTDIKVVDF GSATYDDEHH STLVSTRHYR APEVILALGW SQPCDVWSIG
265 QMAYQICQSI NFLHHNKLTH TDLKPENILF VKSDYVVKYN SKMKRDERTL KNTDIKVVDF GSATYDDEHH STLVSTRHYR APEVILALGW SQPCDVWSIG
-----
224
601 CILIEYYLGF TVFQTHDSKE HLAMMERILG PIPQHMIQKT RKRKYFHNNQ LDWDEHSSAG RYVRRRCKPL KEFMLCHDEE HEKLFDLVRR MLEYPDQRI
365 CILIEYYLGF TVFQTHDSKE HLAMMERILG PIPQHMIQKT RKRKYFHNNQ LDWDEHSSAG RYVRRRCKPL KEFMLCHDEE HEKLFDLVRR MLEYPDQRI
-----
224
701 TLDEALQHPF FDLLKKK
465 TLDEALQHPF FDLLKKK
    
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\* highlighted residues denote differences from the reference protein sequence(s).



Marlene Johnson, Manager, QA/QC

Date: 10/Apr/2012

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