

Certificate of Analysis

LTK (TYK1), 100 µg

Leukocyte Tyrosine Kinase, GST-tagged

ThermoFisher
SCIENTIFIC

Part Number: PR8108A

Lot Number: 1879717G

Immediate Storage: -80°C

Shipping Conditions: dry ice

5781 Van Allen Way

Carlsbad, CA 92008

Phone: 760.603.7200

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Description:

Recombinant human, Catalytic Domain (amino acids 450-864), GST tagged, expressed in insect cells. No special measures were taken to activate this kinase.

Specific Activity:

460 nmoles of phosphate transferred to Abl1 peptide substrate (EAIYAAPFAKKK) per minute per mg of total protein at 30°C. Activity determined at a final protein concentration of 1.67 µg/mL.

Concentration:

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

Calculated **4,070 nM**.

Aliases:

TYK1

Storage and Handling:

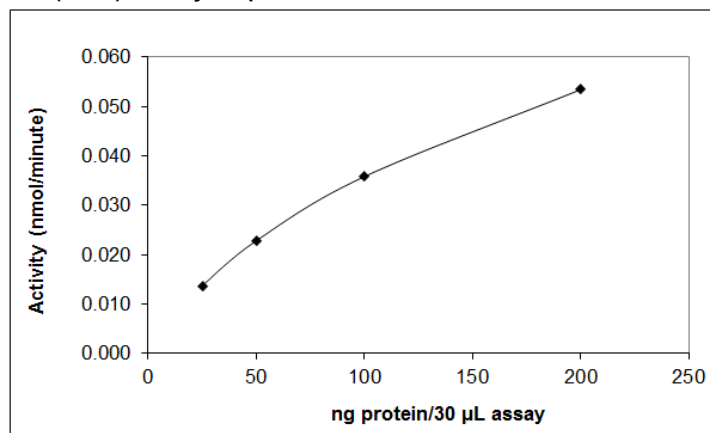
For maximum recovery please spin prior to use. Unless noted below, aliquots of the 5 µg, 10µg and 20µg sizes of kinase are not recommended as materials can be used in original packaging until exhausted. For larger sizes, the number of freeze/thaws may be reduced by preparing aliquots, aliquots below 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 (pH 7.5), 150 mM NaCl, 0.5 mM EDTA, 0.02% Triton® X-100, 2 mM DTT and 50% Glycerol.

QUALITY ASSURANCE

LTK (TYK1) Activity Graph



Dilution Buffer:

20 mM Tris (pH 7.5), 0.02% Triton® X-100, 0.1 mg/mL BSA, 2 mM DTT, 0.5 mM Na₃VO₄ and 10% Glycerol.

Assay Conditions:

LTK (TYK1) was pre-diluted in enzyme dilution buffer and assayed in 25 mM Tris (pH 7.5), 10 mM MgCl₂, 0.5 mM EGTA, 0.5 mM Na₃VO₄, 5 mM β-glycerophosphate, 2.5 mM DTT, 0.01% Triton® X-100, 200 µM ATP, 200 µg/mL Abl1 peptide substrate (EAIYAAPFAKKK) and trace [³²P]-γ-ATP for 10 minutes at 30°C.

Gel Information for LTK (TYK1)

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

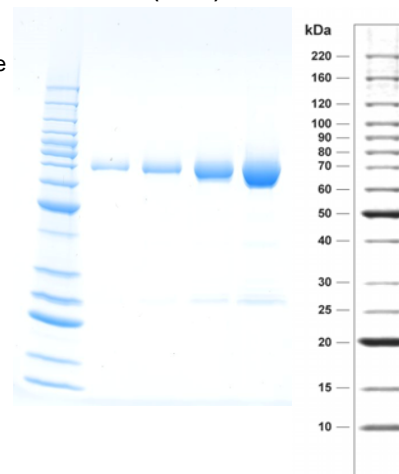
Lane 1: Invitrogen™ BenchMark™ Protein Ladder (Catalog #: 10747-012).

Lane 2: 0.4 µg LTK (TYK1)

Lane 3: 0.8 µg LTK (TYK1)

Lane 4: 2.0 µg LTK (TYK1)

Lane 5: 4.0 µg LTK (TYK1)



Purity:

90% as determined by a SDS-PAGE gel stained with SimplyBlue™ SafeStain.

Molecular Weight:

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

Mass Spectrometry:

LTK (TYK1) was subjected to proteolytic digest followed by mass spec analysis. The resulting MS/MS data verified LTK (TYK1) identity by comparison against the amino acid sequence(s) of the recombinant protein.

Protein sequence alignment with reference sequence(s)

GenBank Accession Number: NP_002335.2

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1  MAPILGYWKI  KGLVQPTRLL  LEYLEEKYEE  HLYERDEGDK  WRNKKFELGL  EFPNLPYYID  GDVKLTQSM  IIRYIADKHN  MLGGCPKERA  EISMLEGAVL  GST TAG
1  MAPILGYWKI  KGLVQPTRLL  LEYLEEKYEE  HLYERDEGDK  WRNKKFELGL  EFPNLPYYID  GDVKLTQSM  IIRYIADKHN  MLGGCPKERA  EISMLEGAVL  IVGN LTK
450 -----
101 DIRYGVSRIA  YSKDFETLKV  DFLSKLP EML  KMFEDRLCHK  TYLNGDHVTH  PDFMLYDALD  VVLYMDPMCL  DAFPKLVCFK  KRIEAIPQID  KYLKSSKYIA
101 DIRYGVSRIA  YSKDFETLKV  DFLSKLP EML  KMFEDRLCHK  TYLNGDHVTH  PDFMLYDALD  VVLYMDPMCL  DAFPKLVCFK  KRIEAIPQID  KYLKSSKYIA
450 -----
201 WPLQGWQATF  GGDHPPKSD  LVPR
201 WPLQGWQATF  GGDHPPKSD  LVPRHNQTSL  YKAGTKQKK  WQGLQEMRLP  SPELELSKLR  TSAIRTAPNP  YYCQVGLGPA  QSWPLPPGVT  EVSPANVTLL
450 -----
224
301 RALGHGAFGE  VYEGLVIGLP  GDSSPLQVAI  KTLPELCSPQ  DELDFLMEAL  IISKFRHQNI  VRCVGLSLRA  TPRLILLELM  SGGDMKSFLR  HSRPHLGQPS
514 RALGHGAFGE  VYEGLVIGLP  GDSSPLQVAI  KTLPELCSPQ  DELDFLMEAL  IISKFRHQNI  VRCVGLSLRA  TPRLILLELM  SGGDMKSFLR  HSRPHLGQPS
224
401 PLVMRDLLQL  AQDIAQGCHY  LEENHFHRD  IAARNCLLSC  AGPSRVAKIG  DFGMARDIYR  ASYYRRGDRA  LLPVKWMPPE  AFLEGIFTSK  TDSWSFGVLL
614 PLVMRDLLQL  AQDIAQGCHY  LEENHFHRD  IAARNCLLSC  AGPSRVAKIG  DFGMARDIYR  ASYYRRGDRA  LLPVKWMPPE  AFLEGIFTSK  TDSWSFGVLL
224
501 WEIFSLGYMP  YPGRTNQEV  LDFVVGGRMD  PPRGCPGVY  RIMTQCWQHE  PELRPSFASI  LERLQYCTQD  PDVLSLLPM  ELGPTPEEEG  TSGLGNRSLE
714 WEIFSLGYMP  YPGRTNQEV  LDFVVGGRMD  PPRGCPGVY  RIMTQCWQHE  PELRPSFASI  LERLQYCTQD  PDVLSLLPM  ELGPTPEEEG  TSGLGNRSLE
224
601 CLRPPQPEL  SPEKLKSWG  SPLGPWLSG  LKPLKSRGLQ  PQNLWNPTYR  S
814 CLRPPQPEL  SPEKLKSWG  SPLGPWLSG  LKPLKSRGLQ  PQNLWNPTYR  S
    
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* highlighted residues denote differences from the reference protein sequence(s).



Anita Targosz, Associate Director

Date: 09/Jun/2017

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