Certificate of Analysis
TYRO3 (RSE), 10 µg

TYRO3 Protein Tyrosine Kinase, GST-tagged

Part Number: PV3828
Lot Number: 1868084V
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 protein, catalytic domain (amino acids 451-890) GST-tagged, expressed in insect cells. Activated *in-vitro* via autophosphorylation.

Specific Activity:

2,910 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 0.83 µg/mL.

Concentration:

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

Calculated **6,140 nM**.

Aliases:

DKT, BRT, TIF

Storage and Handling:

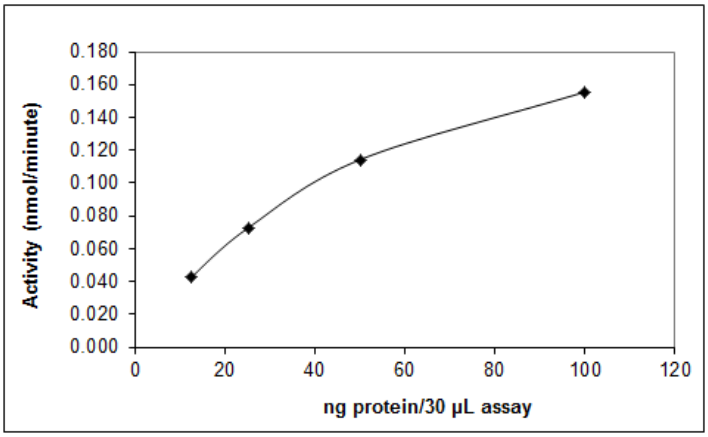
For maximum recovery please spin prior to use. Unless noted below, aliquots of the 5 ug, 10ug and 20ug sizes of kinase are not recommended as materials can be used in original packaging until exhausted. For larger sizes, the number of freeze/thaws may be reduced by preparing aliquots, aliquots below 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

TYRO3 (RSE) 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 Na_3VO_4 and 10% Glycerol.

Assay Conditions:

TYRO3 (RSE) was pre-diluted in enzyme dilution buffer and assayed in 25 mM Tris (pH 7.5), 10 mM $MgCl_2$, 0.5 mM EGTA, 0.5 mM Na_3VO_4, 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 [^{32}P]-γ-ATP for 10 minutes at 30°C.

Gel Information for TYRO3 (RSE)

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

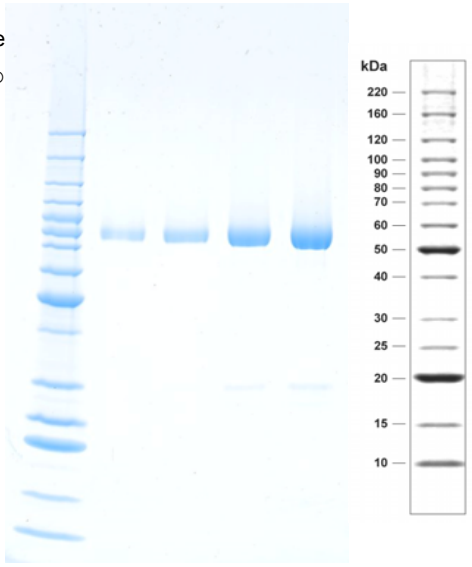
Lane 1: Invitrogen™ BenchMark™ Protein Ladder (Catalog #: 10747-012).

Lane 2: 0.4 µg TYRO3 (RSE)

Lane 3: 0.8 µg TYRO3 (RSE)

Lane 4: 2 µg TYRO3 (RSE)

Lane 5: 4 µg TYRO3 (RSE)



Purity:

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

Molecular Weight:

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

Mass Spectrometry:

TYRO3 (RSE) was subjected to proteolytic digest followed by mass spec analysis. The resulting MS/MS data verified TYRO3 (RSE) identity by comparison against the amino acid sequence(s) of the recombinant protein.

Protein sequence alignment with reference sequence(s)

GenBank Accession Number: NP_006284

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   1 MAPILGYWKI KGLVQPTRLL LEYLEEKYEE HLYERDEGDK WRNKKFELGL EFPNLPYYID GDVKLTQSMA IIRYIADKHN MLGGCPKERA EISMLEGAVL GST TAG
   1 MAPILGYWKI KGLVQPTRLL LEYLEEKYEE HLYERDEGDK WRNKKFELGL EFPNLPYYID GDVKLTQSMA IIRYIADKHN MLGGCPKERA EISMLEGAVL IVGN TYRO3
 451 ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- NP_006284

 101 DIRYGVSRIA YSKDFETLKV DFLSKLPEML KMFEDRLCHK TYLNGDHVTH PDFMLYDALD VVLYMDPMCL DAFPKLVCFK KRIEAIPQID KYLKSSKYIA
 101 DIRYGVSRIA YSKDFETLKV DFLSKLPEML KMFEDRLCHK TYLNGDHVTH PDFMLYDALD VVLYMDPMCL DAFPKLVCFK KRIEAIPQID KYLKSSKYIA
 451 ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------

 201 WPLQGWQATF GGGDHPPKSD LVPR
 201 WPLQGWQATF GGGDHPPKSD LVPRHNQTSL YKKAGTLRKR RKETRFGQAF DSVMARGEPA VHFRAARSFN RERPERIEAT LDSLGISDEL KEKLEDVLIP
 451 ---------- ---------- ---------- ------LRKR RKETRFGQAF DSVMARGEPA VHFRAARSFN RERPERIEAT LDSLGISDEL KEKLEDVLIP

 224
 301 EQQFTLGRML GKGEFGSVRE AQLKQEDGSF VKVAVKMLKA DIIASSDIEE FLREAACMKE FDHPHVAKLV GVSLRSRAKG RLPIPMVILP FMKHGDLHAF
 515 EQQFTLGRML GKGEFGSVRE AQLKQEDGSF VKVAVKMLKA DIIASSDIEE FLREAACMKE FDHPHVAKLV GVSLRSRAKG RLPIPMVILP FMKHGDLHAF

 224
 401 LLASRIGENP FNLPLQTLIR FMVDIACGME YLSSRNFIHR DLAARNCMLA EDMTVCVADF GLSRKIYSGD YYRQGCASKL PVKWLALESL ADNLYTVQSD
 615 LLASRIGENP FNLPLQTLIR FMVDIACGME YLSSRNFIHR DLAARNCMLA EDMTVCVADF GLSRKIYSGD YYRQGCASKL PVKWLALESL ADNLYTVQSD

 224
 501 VWAFGVTMWE IMTRGQTPYA GIENAEIYNY LIGGNRLKQP PECMEDVYDL MYQCWSADPK QRPSFTCLRM ELENILGQLS VLSASQDPLY INIERAEEPT
 715 VWAFGVTMWE IMTRGQTPYA GIENAEIYNY LIGGNRLKQP PECMEDVYDL MYQCWSADPK QRPSFTCLRM ELENILGQLS VLSASQDPLY INIERAEEPT

 224
 601 AGGSLELPGR DQPYSGAGDG SGMGAVGGTP SDCRYILTPG GLAEQPGQAE HQPESPLNET QRLLLLQQGL LPHSSC.
 815 AGGSLELPGR DQPYSGAGDG SGMGAVGGTP SDCRYILTPG GLAEQPGQAE HQPESPLNET QRLLLLQQGL LPHSSC
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* highlighted residues denote differences from the reference protein sequence(s).

Anita Targosz, Associate Director Date: 01/Mar/2017