

Certificate of Analysis

TYRO3 (RSE), 100 µg

TYRO3 Protein Tyrosine Kinase, GST-tagged



Part Number: PR7480A
Lot Number: 1366162A
Immediate Storage: -80°C
Shipping Conditions: dry ice

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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:

3,660 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:

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

Calculated **3,520 nM**.

Aliases:

DKT, BRT, TIF

Storage and Handling:

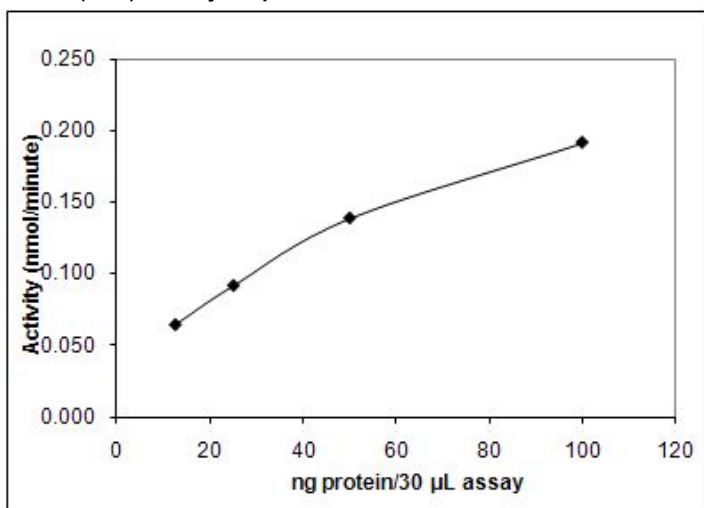
For maximum recovery please spin prior to use. Aliquots of the 5 µg, 10 µg and 20 µg sizes of kinase are not recommended as materials can be used in original packaging until exhausted. For larger sizes, the number of freeze/thaws may be reduced by preparing aliquots, aliquots below 20 µL are not recommended. **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 Na₃VO₄ 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 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 TYRO3 (RSE)

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

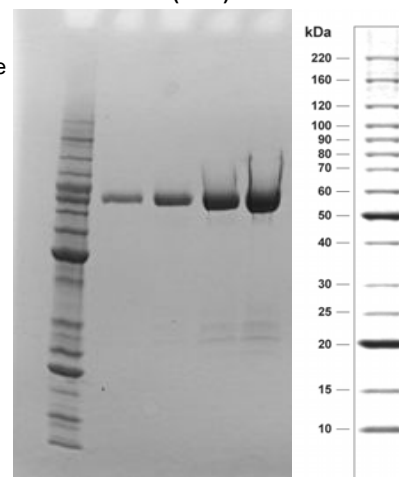
Lane 1: Invitrogen™ BenchMark™ Protein Ladder (Catalog #: 10747-012).

Lane 2: 0.8 µg TYRO3 (RSE)

Lane 3: 1.6 µg TYRO3 (RSE)

Lane 4: 4 µg TYRO3 (RSE)

Lane 5: 8 µg TYRO3 (RSE)



Purity:

90% 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  GDVKLTQSM  IIRYIADKHN  MLGGCPKERA  EISMLEGAVL  GST TAG
1  MAPILGYWKI  KGLVQPTRLL  LEYLEEKYEE  HLYERDEGDK  WRNKKFELGL  EFPNLPYYID  GDVKLTQSM  IIRYIADKHN  MLGGCPKERA  EISMLEGAVL  IVGN TYR03
451 -----
101 DIRYGVSRIA  YSKDFETLKV  DFLSKLP EML  KMFEDRLCHK  TYLNGDHVTH  PDFMLYDALD  VVLYMDP MCL  DAFPKLVCFK  KRIEAIQID  KYLKSSKYIA
101 DIRYGVSRIA  YSKDFETLKV  DFLSKLP EML  KMFEDRLCHK  TYLNGDHVTH  PDFMLYDALD  VVLYMDP MCL  DAFPKLVCFK  KRIEAIQID  KYLKSSKYIA
451 -----
201 WPLQGWQATF  GGGDHPPKSD  LVPR
201 WPLQGWQATF  GGGDHPPKSD  LVPRHNQTSL  YKKAGTLRKR  RKETRFQOAF  DSVMARGEPA  VHFRAAR SFN  RERPERIEAT  LDSLGISDEL  KEKLEDV LIP
451 -----
224
301 EQQFTLGRML  GKGEFGSVRE  AQLKQEDGSF  VKVAVKMLKA  DIIASSDIEE  FLREAACMKE  FDHPHVAKLV  GVSLRSRAGK  RLPIMVILP  FMKHGDLHAF
515 EQQFTLGRML  GKGEFGSVRE  AQLKQEDGSF  VKVAVKMLKA  DIIASSDIEE  FLREAACMKE  FDHPHVAKLV  GVSLRSRAGK  RLPIMVILP  FMKHGDLHAF
224
401 LLASRIGENP  FNLPLQLTIR  FMVDIACGME  YLSSRNFIHR  DLAARNCMLA  EDMTVCVADF  GLSRKIYSGD  YYRQGCASKL  PVKWLAL ESL  ADNLYTVQSD
615 LLASRIGENP  FNLPLQLTIR  FMVDIACGME  YLSSRNFIHR  DLAARNCMLA  EDMTVCVADF  GLSRKIYSGD  YYRQGCASKL  PVKWLAL ESL  ADNLYTVQSD
224
501 VWAFGVTMWE  IMTRGQTPYA  GIENAEIYNY  LIGGNRLKQP  PECMEDVYDL  MYQCWSADPK  QRPSFTCLRM  ELENILGQLS  VLSASODPLY  INIERAE EPT
715 VWAFGVTMWE  IMTRGQTPYA  GIENAEIYNY  LIGGNRLKQP  PECMEDVYDL  MYQCWSADPK  QRPSFTCLRM  ELENILGQLS  VLSASODPLY  INIERAE EPT
224
601 AGGSLELPGR  DQPYSGAGDG  SGMGAVGGTP  SDCRYILTPG  GLAEQPGQAE  HQPESPLNET  QRLLLLQOGL  LPHSSC
815 AGGSLELPGR  DQPYSGAGDG  SGMGAVGGTP  SDCRYILTPG  GLAEQPGQAE  HQPESPLNET  QRLLLLQOGL  LPHSSC
    
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* highlighted residues denote differences from the reference protein sequence(s).



Becky. Baker, QA Engineer III

Date: 17/Apr/2013

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