

Certificate of Analysis

CDK2/cyclin A, 1 mg

Cyclin-Dependent Kinase 2/cyclin A complex, Histidine-tagged

ThermoFisher
SCIENTIFIC

Part Number: PR4448A

Lot Number: 2098464D

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 full length CDK2/cyclin A complex, Histidine-tagged, expressed in insect cells. No special measures were taken to activate this kinase.

Specific Activity:

2,070 nmoles of phosphate transferred to Histone H1 peptide substrate (PKTPKKAKKL) per minute per mg of total protein at 30°C. Activity determined at a final protein concentration of 0.5 µg/mL.

Concentration:

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

Calculated **4,160 nM**.

Storage and Handling:

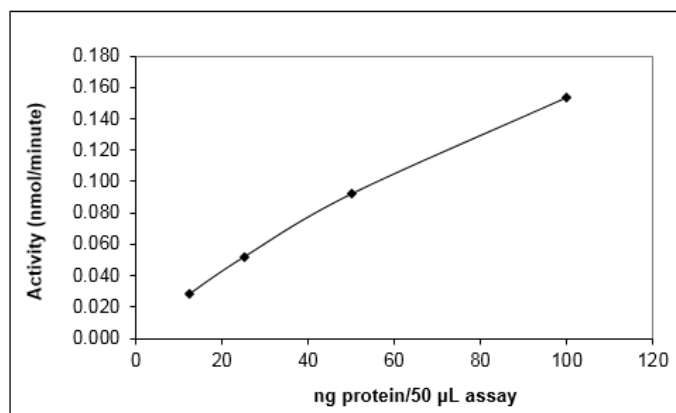
For maximum recovery please spin prior to use. Unless noted below, aliquots of the 5 µg, 10 µg and 20 µg sizes of kinase are not recommended as materials can be used in original packaging until exhausted. For larger sizes, the number of freeze/thaws may be reduced by preparing aliquots, aliquots below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

20 mM Tris (pH 7.5), 150 mM NaCl, 0.5 mM EDTA, 0.01% Triton® X-100, 2 mM DTT, 20% Glycerol.

QUALITY ASSURANCE

CDK2/cyclin A Activity Graph



Dilution Buffer:

20 mM Tris (pH 7.5), 0.05% Triton®X-100, 10% Glycerol, 1 mM DTT, 0.1 mg/mL BSA.

Assay Conditions:

CDK2/cyclin A was pre-diluted in enzyme dilution buffer and assayed in 20 mM Tris (pH 7.5), 5 mM MgCl₂, 100 µM ATP 100 µM Histone H1 peptide substrate (PKTPKKAKKL) and trace [³²P]-γ-ATP for 10 minutes at 30°C.

Gel Information for CDK2/cyclin A

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

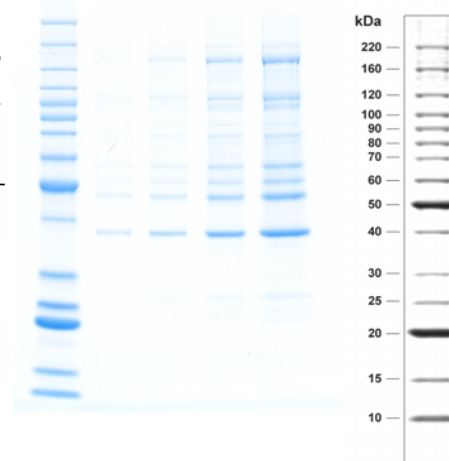
Lane 1: Invitrogen™ BenchMark™ Protein Ladder (Catalog #: 10747-012).

Lane 2: 0.5 µg CDK2/cyclin A

Lane 3: 1.0 µg CDK2/cyclin A

Lane 4: 2.5 µg CDK2/cyclin A

Lane 5: 5.0 µg CDK2/cyclin A



Purity:

85% as determined by a Coomassie® blue stained SDS-PAGE gel and Western Blot analysis.

Molecular Weight:

38.5 / 52.8 kDa.

Mass Spectrometry:

CDK2/cyclin A was subjected to proteolytic digest followed by mass spec analysis. The resulting MS/MS data verified CDK2/cyclin A identity by comparison against the amino acid sequence(s) of the recombinant protein.

Protein sequence alignment with reference sequence(s)

GenBank Accession Number: NP_001789.2

CDK2 Alignment

1 MSYYHHHHH DYDIPTTENL YFQGAMLVPR GSPWDPEFME NFQKVEKIGE GTYGVVYKAR NKLTGEVVAL KKIRLDTETE GVPSTAIREI SLLKELNHPN IVGN CDK2
1 -----ME NFQKVEKIGE GTYGVVYKAR NKLTGEVVAL KKIRLDTETE GVPSTAIREI SLLKELNHPN NP_001789.2
101 IVKLLDVIHT ENKLYLVFEF LHQDLKKFMD ASALTGIPLP LIKSYLFQLL QGLAFCHSHR VLHRDLKPQN LLINTEGAIK LADFGLARAF GVPVRTYTHE
63 IVKLLDVIHT ENKLYLVFEF LHQDLKKFMD ASALTGIPLP LIKSYLFQLL QGLAFCHSHR VLHRDLKPQN LLINTEGAIK LADFGLARAF GVPVRTYTHE
201 VVTLWYRAPE ILLGCKYYST AVDIWSLGC I FAEMVTRRAL FPGDSEIDQL FRIFRTLGT P DEVVWPGVTS MPDYKPSFPK WARQDFSKVV PPLDEGRSL
163 VVTLWYRAPE ILLGCKYYST AVDIWSLGC I FAEMVTRRAL FPGDSEIDQL FRIFRTLGT P DEVVWPGVTS MPDYKPSFPK WARQDFSKVV PPLDEGRSL
301 LSQMLHYDPN KRISAKAALA HPFFQDVTKP VPHLRL.
263 LSQMLHYDPN KRISAKAALA HPFFQDVTKP VPHLRL

GenBank Accession Number: NP_001228.1

Cyclin A Alignment

1 MSYYHHHHH DYDIPTTENL YFQGAMLVPR GSPWGSM LGN SAPGPATREA GSALLALQQT ALQEDQENIN PEKAAPVQQP RTRAAALAVLK SGNPRGLAQQ IVGN Cyclin A
1 -----MLGN SAPGPATREA GSALLALQQT ALQEDQENIN PEKAAPVQQP RTRAAALAVLK SGNPRGLAQQ NP_001228.1
101 QRPKTRRVAP LKDLPVNDEH VTVPPWKANS KQPAFTIHVD EAEKEAQKKP AESQKIERED ALAFNSAISL PGPRKPLVPL DYPMDGSFES PHTMDMSIVL
65 QRPKTRRVAP LKDLPVNDEH VTVPPWKANS KQPAFTIHVD EAEKEAQKKP AESQKIERED ALAFNSAISL PGPRKPLVPL DYPMDGSFES PHTMDMSIVL
201 EDEKPVSVNE VPDYHEDIHT YLREMEVKCK PKVGYMKKQP DITNSMRAIL VDWLVEVGEE YKLQNETLHL AVNYIDRFLS SMSVLRGKLQ LVGTAAMLLA
165 EDEKPVSVNE VPDYHEDIHT YLREMEVKCK PKVGYMKKQP DITNSMRAIL VDWLVEVGEE YKLQNETLHL AVNYIDRFLS SMSVLRGKLQ LVGTAAMLLA
301 SKFEEIYPPE VAEFVYITDD TYTKKQVLRM EHLVLKVLTF DLAAPTQVNF LTQYFLHQQP ANCKVESLAM FLGELSLIDA DPYLKYLPSV IAGAAFHLAL
265 SKFEEIYPPE VAEFVYITDD TYTKKQVLRM EHLVLKVLTF DLAAPTQVNF LTQYFLHQQP ANCKVESLAM FLGELSLIDA DPYLKYLPSV IAGAAFHLAL
401 YTVTGQSWPE SLIRKTGYTL ESKPCLMDL HQTYLKAPQH AQQSIREKYK NSKYHGVSL NPPETLNL.
365 YTVTGQSWPE SLIRKTGYTL ESKPCLMDL HQTYLKAPQH AQQSIREKYK NSKYHGVSL NPPETLNL

* highlighted residues denote differences from the reference protein sequence(s).

Anita Targosz

Anita Targosz, Associate Director

Date: 01/Apr/2019

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