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## Certificate of Analysis

### PI3 Kinase (p120 $\gamma$ )

(Recombinant enzyme expressed in Sf21 insect cells)

Catalogue # 14-558M

Lot # D8CN080U

**Product Description:** N-terminal 6His-tagged recombinant full-length human PI3 kinase (p120 $\gamma$ ) expressed by baculovirus in Sf21 insect cells. Purified using Ni<sup>2+</sup>/NTA-agarose. Purity 90.1% by SDS-PAGE and Coomassie blue staining. MW = 130kDa.

**Specific Activity (lot# D8CN080U):** 63U/mg, where one unit of PI3 Kinase (p120 $\gamma$ ) activity is defined as 1nmol phosphatidylinositol 3,4,5-trisphosphate formed per minute at 22°C with a final ATP concentration of 100 $\mu$ M.

**Formulation:** 250 $\mu$ g of enzyme in 117.7 $\mu$ l of 50mM Tris/HCl pH7.5, 150mM NaCl, 10% glycerol, 0.1mM EGTA, 2mM DTT.

**Storage and Stability:** Store at -70°C from date of shipment. For maximum recovery of product, centrifuge original vial prior to removing the cap.

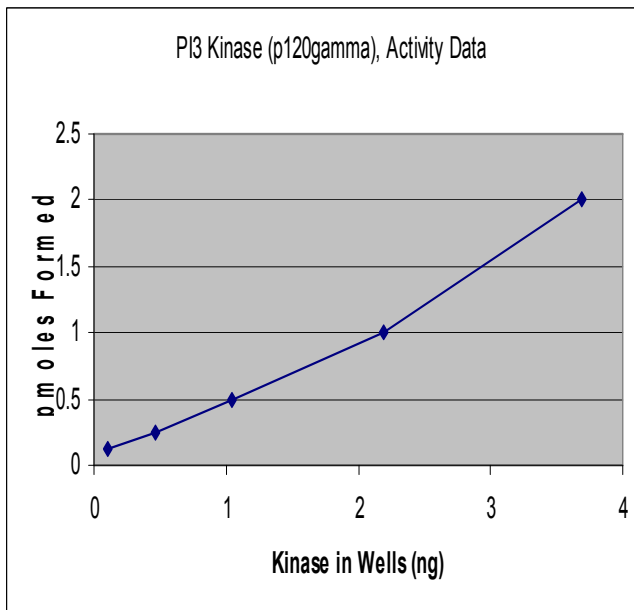
**Handling Recommendations:** Rapidly thaw the vial under cold water and immediately place on ice. Aliquot unused material into pre-chilled microcentrifuge tubes and immediately snap-freeze the vials in liquid nitrogen prior to re-storage at -70°C.

FOR IN VITRO RESEARCH USE ONLY  
NOT FOR USE IN HUMANS OR ANIMALS

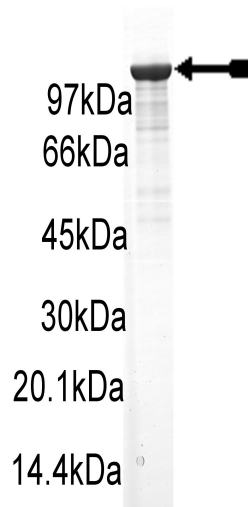
### Quality Control Testing

**Kinase Assay:** 0.125–2.0ng of this lot of PI3 Kinase (p120 $\gamma$ ) was assayed in a 30 minute reaction using the PIPProfiler™ protocol (see <http://www.upstate.com/features/pipprofiler>).

**MS Tryptic Fingerprint:** Confirmed identity as PI3 Kinase (p120 $\gamma$ ) with 23% amino acid coverage of the translated sequence listed on page two.



**SDS-PAGE and Coomassie Stain:** Purity was assessed by SDS-PAGE and Coomassie blue staining using 3 $\mu$ g of active PI3 kinase (p120 $\gamma$ ).



### P13 Kinase (p120 $\gamma$ ) Sequence Information

<b>Protein</b>	human P13 Kinase (p120 $\gamma$ )
<b>Tags</b>	N-terminal 6His
<b>Native sequence</b>	M34 of the recombinant protein is equivalent to M1 of human P13 Kinase (p120 $\gamma$ ).
<b>Accession number</b>	GenBank AF327656. The recombinant protein contains the amino acid substitution R459Q with respect to this accession number. This conflict is reported in GenBank XM_027912. The residue coordinates in the native sequence are given.

#### Recombinant P13 Kinase (p120 $\gamma$ ) amino acid sequence:

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1 MSYYHHHHHH DYDIPTTENL YFQGAMGSGI RPCMELENYK QPVVLRDNC RRRRRMKPRS
61 AAASLSSMEL IPIEFVLPTS QRKCKSPETA LLHVAGHGNV EQMKAQVWLR ALETSSVAADF
121 YHRLGPHHFL LLYQKKGQWY EIYDKYQVVQ TLDCLRYWKA THRSPGQIHL VQRHPPSEES
181 QAFQRQLTAL IGYDVTDVSN VHDDELEFTR RGLVTPRMAE VASRDPKLYA MHPWVTSKPL
241 PEYLWKKIAN NCIFIVIHRN TTSQTIKVSP DDTPGAILQS FFTKMAKKKS LMDIPESQSE
301 QDFVLRVCGR DEYLVGETPI KNFQWVRHCL KNGEEIHVVV DTPDPALDE VRKEEWPLVD
361 DCTGVTGYHE QLTIHGKDHE SVFTVSLWDC DRKFRVKIRG IDIPVLPNT DLTVFVEANI
421 QHGQQVLCQR RTSPKPFTEE VLWNVWLEFS IKIKDLPKGA LLNLQIYCGK APALSSKASA
481 ESPSSSESKGK VQLLYYVNL LIDHRFLLRR GEYVLHMWQI SGKGEDQGSF NADKLT SATN
541 PDKENSMSIS ILLDNYCHPI ALPKHQPTPD PEGDRVRAEM PNQLRKQLEA IIATDPLNPL
601 TAEDKELLWH FRYESLKHPK AYPKLFSSVK WQQQEIVAKT YQLLARREVV DQSALDVGLT
661 MQLLDCNFSD ENVRAIAVQK LESLEDDV LHYLLQLVQAV KFEFPHDSAL ARFLLKRGRLR
721 NKRIGHFLFW FLRSEIAQSR HYQQRFAVIL EAYLRGCGTA MLHDFTQQVQ VIEMLQKVTL
781 DIKLSAEEKY DVSSQVISQL KQKLENLQNS QLPESFRVPY DPGLKAGALA IEKCKVMASK
841 KKPLWLEFKC ADPTALSNET IGIIFKHGDD LRQDMLILQI LRIMESIWET ESLDLCLLPY
901 GCISTGDKIG MIEIVKDATT IAKIQQSTVG NTGAFKDEV LNHWLKEKSPT EEKFQAAVER
961 FVYSCAGYCV ATFVLGIGDR HNDNIMITET GNLFHIDFGH ILGNYKSFLG INKERVPFVL
1021 TPDFLFVMTG SGKKTSPHFQ KFQDICVKAY LALRHHTNLL IILFSMMLMT GMPQLTSKED
1081 IEYIRDALTV GKNEEDAKKY FLDQIEVCRD KGWTVQFNWF LHLVLGKIQG EKHSA
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#### Recombinant P13 Kinase (p120 $\gamma$ ) nucleotide sequence:

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1 atgtcgtact accatcacca tcaccatcac gattacgata tccaacgac cgaaaacctg
61 tattttcagg gcgcatggg atccggaatt cgcccttgca tggagctgga gaactataaa
121 cagcccgtgg tgctgagaga ggacaactgc cgaaggcgcc ggaggatgaa gccgcgcagt
181 gctgcggcca gcctgtctc catggagctc atccccatcg agttcgtgct gccaccacgc
241 cagcgcaaat gcaagagccc cgaaacggcg ctgctgcacg tggccggcca cggcaacgtg
301 gagcagatga aggccaggt gtggctgcga gcgctggaga ccagcgtggc ggcggaactc
361 taccaccggc tgggaccgca tcacttctc ctgctctatc agaagaagg ggcaggttac
421 gagatctacg acaagtacca ggtggtgcag actctggact gcctgcgcta ctggaaggcc
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541 caagccttcc agcggcagct cacggcgctg attggctatg acgtcactga cgtcagcaac
601 gtgcacgacg atgagctgga gttcacgctc cgtggcttgg tgaccccgcg catggcggag
661 gtggccagcc gcgacccaa gctctacgcc atgcaccctg gggtgacgct caagcccctc
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901 caggattttg tgctgcgcgt ctgtggccgg gatgagtacc tgggtgggca aacgcccctc
961 aaaaacttcc agtgggtgag gcaactgcctc aagaacggag aagagattca cgtggtactg
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