Certificate of Analysis
RPS6KA1 (RSK1), 10 µg

Ribosomal Protein S6 Kinase, Polypeptide 1, Histidine-tagged

Part Number: PV3680
Lot Number: 880119J
Immediate Storage: -80°C
Shipping Conditions: dry ice

5791 Van Allen Way
Carlsbad, CA 92008
Phone: 760.603.7200
Fax: 760.602.6500
www.lifetechnologies.com

Description:

Recombinant human full-length protein, Histidine-tagged, expressed in insect cells. Co-expressed with untagged PDK1 and activated *in vitro* by GST-tagged MAPK1.

Specific Activity:

500 nmoles of phosphate transferred to S6 peptide substrate (AKRRRLSSLRA) 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 **3,390 nM**.

Aliases:

RSK, HU-1, RSK1

Storage and Handling:

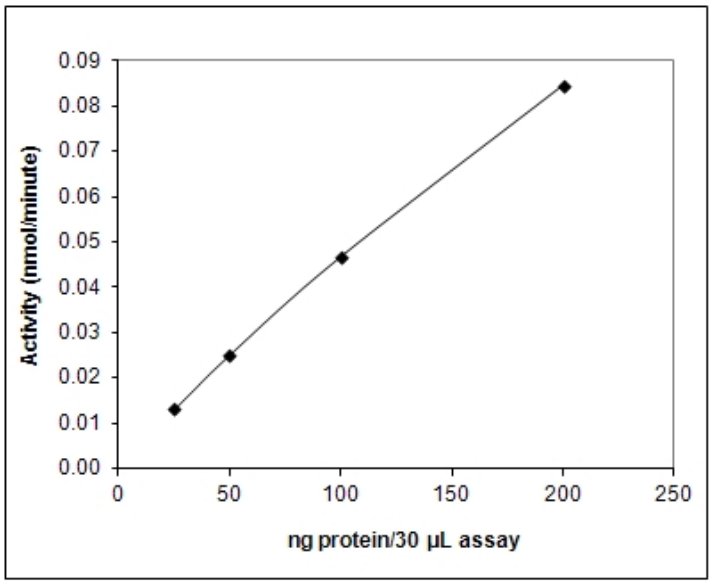
For maximum recovery please spin prior to use. Aliquots of the 5 ug, 10ug and 20ug sizes of kinase are not recommended as materials can be used in original packaging until exhausted. For larger sizes, the number of freeze/thaws may be reduced by preparing aliquots, aliquots below 20 µL are not recommended.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

RPS6KA1 (RSK1) Activity Graph



Gel Information for RPS6KA1 (RSK1)

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

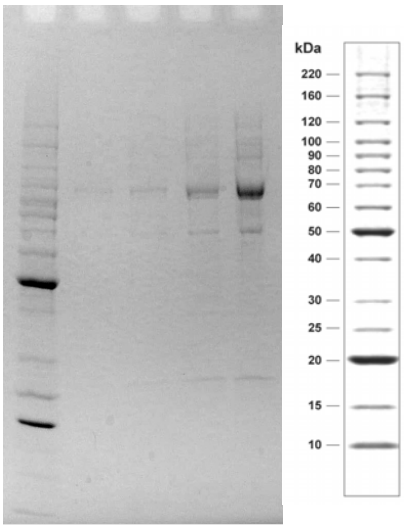
Lane 1: Invitrogen™ BenchMark™ Protein Ladder (Catalog #: 10747-012).

Lane 2: 0.6 µg RPS6KA1 (RSK1)

Lane 3: 1.2 µg RPS6KA1 (RSK1)

Lane 4: 3 µg RPS6KA1 (RSK1)

Lane 5: 6 µg RPS6KA1 (RSK1)



Dilution Buffer:

20 mM Tris (pH 7.5), 0.05% Triton® X−100, 0.1 mg/mL BSA, 2 mM DTT, 0.5 mM Na_3VO_4 and 10% Glycerol.

Assay Conditions:

RPS6KA1 (RSK1) 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, 133 µg/mL S6 peptide substrate (AKRRRLSSLRA) and trace [^{32}P]-γ-ATP for 10 minutes at 30°C.

Purity:

50% as determined by a Coomassie® blue stained SDS-PAGE gel.

Molecular Weight:

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

Mass Spectrometry:

RPS6KA1 (RSK1) was subjected to proteolytic digest followed by mass spec analysis. The resulting MS/MS data verified RPS6KA1 (RSK1) identity by comparison against the amino acid sequence(s) of the recombinant protein.

Protein sequence alignment with reference sequence(s)

GenBank Accession Number: NP_002944

```
   1 MSYYHHHHHH DYDIPTTENL YFQGITSLYK KAGSAAAVLE ENLYFQGSFT MPLAQLKEPW PLMELVPLDP ENGQTSGEEA GLQPSKDEGV LKEISITHHV IVGN RPS6KA1
   1 ---------- ---------- ---------- ---------- ---------- MPLAQLKEPW PLMELVPLDP ENGQTSGEEA GLQPSKDEGV LKEISITHHV NP_002944

 101 KAGSEKADPS HFELLKVLGQ GSFGKVFLVR KVTRPDSGHL YAMKVLKKAT LKVRDRVRTK MERDILADVN HPFVVKLHYA FQTEGKLYLI LDFLRGGDLF
  51 KAGSEKADPS HFELLKVLGQ GSFGKVFLVR KVTRPDSGHL YAMKVLKKAT LKVRDRVRTK MERDILADVN HPFVVKLHYA FQTEGKLYLI LDFLRGGDLF

 201 TRLSKEVMFT EEDVKFYLAE LALGLDHLHS LGIIYRDLKP ENILLDEEGH IKLTDFGLSK EAIDHEKKAY SFCGTVEYMA PEVVNRQGHS HSADWWSYGV
 151 TRLSKEVMFT EEDVKFYLAE LALGLDHLHS LGIIYRDLKP ENILLDEEGH IKLTDFGLSK EAIDHEKKAY SFCGTVEYMA PEVVNRQGHS HSADWWSYGV

 301 LMFEMLTGSL PFQGKDRKET MTLILKAKLG MPQFLSTEAQ SLLRALFKRN PANRLGSGPD GAEEIKRHVF YSTIDWNKLY RREIKPPFKP AVAQPDDTFY
 251 LMFEMLTGSL PFQGKDRKET MTLILKAKLG MPQFLSTEAQ SLLRALFKRN PANRLGSGPD GAEEIKRHVF YSTIDWNKLY RREIKPPFKP AVAQPDDTFY

 401 FDTEFTSRTP KDSPGIPPSA GAHQLFRGFS FVATGLMEDD GKPRAPQAPL HSVVQQLHGK NLVFSDGYVV KETIGVGSYS ECKRCVHKAT NMEYAVKVID
 351 FDTEFTSRTP KDSPGIPPSA GAHQLFRGFS FVATGLMEDD GKPRAPQAPL HSVVQQLHGK NLVFSDGYVV KETIGVGSYS ECKRCVHKAT NMEYAVKVID

 501 KSKRDPSEEI EILLRYGQHP NIITLKDVYD DGKHVYLVTE LMRGGELLDK ILRQKFFSER EASFVLHTIG KTVEYLHSQG VVHRDLKPSN ILYVDESGNP
 451 KSKRDPSEEI EILLRYGQHP NIITLKDVYD DGKHVYLVTE LMRGGELLDK ILRQKFFSER EASFVLHTIG KTVEYLHSQG VVHRDLKPSN ILYVDESGNP

 601 ECLRICDFGF AKQLRAENGL LMTPCYTANF VAPEVLKRQG YDEGCDIWSL GILLYTMLAG YTPFANGPSD TPEEILTRIG SGKFTLSGGN WNTVSETAKD
 551 ECLRICDFGF AKQLRAENGL LMTPCYTANF VAPEVLKRQG YDEGCDIWSL GILLYTMLAG YTPFANGPSD TPEEILTRIG SGKFTLSGGN WNTVSETAKD

 701 LVSKMLHVDP HQRLTAKQVL QHPWVTQKDK LPQSQLSHQD LQLVKGAMAA TYSALNSSKP TPQLKPIESS ILAQRRVRKL PSTTL.
 651 LVSKMLHVDP HQRLTAKQVL QHPWVTQKDK LPQSQLSHQD LQLVKGAMAA TYSALNSSKP TPQLKPIESS ILAQRRVRKL PSTTL
```

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

Becky. Baker, QA Engineer III Date: 06/Apr/2012