

## ProQinase™ EIF2AK4

eukaryotic translation initiation factor 2 alpha kinase 4

### Recombinant Human Active Protein Kinase

**HGNC Symbol:** EIF2AK4

**Synonyms:** GCN2, KIAA1338

**Product No.:** 1932-0000-1

**Lot:** 001

**Description:** Human EIF2AK4, full length, amino acids M<sub>1</sub>-F<sub>1649</sub> (as in [NCBI/Protein](#) entry NP\_001013725.2), N-terminal GST-HIS<sub>6</sub> fusion protein with a 3C cleavage site, expressed in Sf9 insect cells

**Product identity:** EIF2AK4 Lot 001, was confirmed as EIF2AK4 by mass spectroscopy LC-ESI-MS/MS

**Theoretical MW<sub>Fusion Protein</sub>:** 214,998 Da

**Expression host:** Sf9 insect cells

**Purification:** GST-Affinity Chromatography

**Activation:** This kinase was not activated by special procedures

**Storage buffer:** 50 mM HEPES pH 7.5, 100 mM NaCl, 5 mM DTT, 15 mM reduced glutathione, 20 % glycerol

**Storage temperature:** -80°C

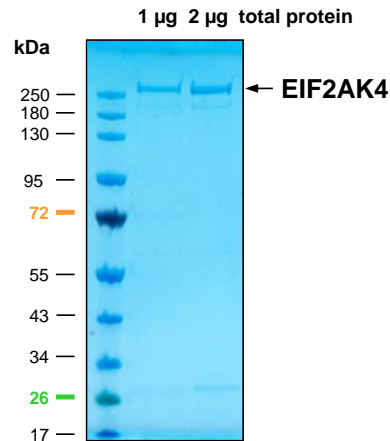
For complete recovery, mix well and spin before use. Product must not be stored in diluted solutions, aliquots below 10µl are not advisable. Avoid repeated freeze-thaw cycles!

**Protein concentration:** 0.229 µg/µl  
(Bradford method using BSA [Sigma, cat# A-7638, Lot 79H7641] as standard protein)

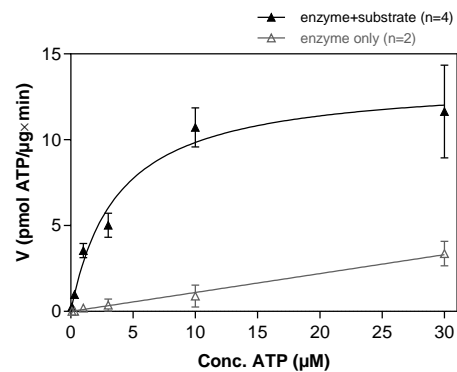
**Biochemical Parameters:**

Specific kinase activity (P<sub>i</sub> transfer): 14 pmol/µg x min  
ATP-K<sub>M</sub>: 3.7 µM

EIF2AK4 Lot 001:  
Coomassie stain



EIF2AK4 Lot 001:  
Determination of V<sub>max</sub> and K<sub>M</sub> value for ATP



- Assay conditions:
  - 60 mM HEPES-NaOH, pH 7.5
  - 3 mM MgCl<sub>2</sub>
  - 3 mM MnCl<sub>2</sub>
  - 3 µM Na-orthovanadate
  - 1.2 mM DTT
  - 50 µg/ml PEG<sub>20,000</sub>
  - ATP (variable)
  - Substrate: S6-derived peptide 5 µg/ml
  - Kinase: 0.3 µg/ml
- Filter binding assay  
MSIP membrane (Millipore)

Recombinant Proteins

Sequence information

GST-EIF2AK4 Recombinant Fusion Protein Amino Acid Sequence							
1	MSPILGYWKI	KGLVQPTRL	LEYLEEKYEE	HLYERDEGDK	WRNKKFELGL	EFPNLPYYID	60
61	GDVKLTQSMA	IIRYIADKHN	MLGGCPKERA	EISMLEGAVL	DIRYGVSRIA	YSKDFETLKV	120
121	DFLSKLP EML	KMFKDR LCHK	TYLNGDHVTH	PDFMLYDALD	VVLYMDPMCL	DAFPKLVCFK	180
181	KRIEAI PQID	KYLKSSKYIA	WPLQG WQATF	GGGDHPPKSD	PMGHHHHHG	RDSLEVLFGG	240
241	MAGGRGAPG	RGRDEPPESY	PQRQDHELQA	LEAIYGADFQ	DLRPD ACPV	KEPPEINLVL	300
301	YPQGLTGEEV	YVKVDLRVVC	PPTYPDVVPE	IELKNAKGLS	NESVNLLKSR	LEELAKHKCG	360
361	EVMIFELAYH	VQSFLSEHNK	PPPKSFHEEM	LERRAQEEQQ	RLLEAKRKEE	QEOREILHEI	420
421	QRRKEEIKEE	KKRKEMAKQE	RLEIASLSNQ	DHTSKKDPGG	HRTAAILHGG	SPDFVGNKGH	480
481	RANSSGRSRR	ERQYSVCNSE	DSPGSCEILY	FNMGSPDQLM	VHKGKCI GSD	EQLGKLVYNA	540
541	LETATGGFVL	LYEVLQWQK	KMGPF LTSQE	KEKIDKCKKQ	IQGTETEFNS	LVKLSHPNVV	600
601	RYLAMNLKEQ	DDSIVVDILV	EHISGVSLAA	HLSHSGPIPV	HQLRRYTAQL	LSGLDYLHSN	660
661	SVVHKVLSAS	NVLVDAEGTV	KITDYSISKR	LADICKEDVF	EQTRVRFSDN	ALPYKTGKKG	720
721	DVWRLG LLLL	SLSQGECEGE	YPVTIPSDLP	ADFQDFLKKC	VCLDDKERWS	PQQLLKH SFI	780
781	NPQPKMPLVE	QSPEDSEGQD	YVETVIPSNR	LPSAAFFSET	QRQFSRYFIE	FEELQLLKGK	840
841	AFGAVIKVQN	KLDGCCYAVK	RIPINPASRQ	FRRIKGEVTL	LSRLHHENIV	RYYNAWIERH	900
901	ERPAGPGTPP	PDSGPLAKDD	RAARGQPASD	TDGLDSVEAA	APPPILSSSV	EWSTSGERSA	960
961	SARFPATGPG	SSDDEDDDED	EHGGVFSQSF	LPASDSESDI	IFDNEDENSK	SONQDEDCNE	1020
1021	KNGCHESEPS	VTTEAVHYLY	IQMEYCEKST	LRDTIDQGLY	RDTVRLWRLF	REILDGLAYI	1080
1081	HEKGM IHRDL	KPVNIFLDS	DHVKIGDFGL	ATDHLAFSAD	SKQDDQTGDL	IKSDPSGHLT	1140
1141	GMVGTALYVS	PEVQGSTKSA	YNQKVDL FSL	GIIFFEMSYH	PMVTASERIF	VLNQLRDPTS	1200
1201	PKFPEDFDDG	EHAQKSVIS	WLLNHDP AKR	PTATELLKSE	LLPPPQMEES	ELHEVLHHTL	1260
1261	TNVDGKAYRT	MMAQIFSQRI	SPAIDYTYDS	DILKGNFSIR	TAKMQQHVCE	TIIRIFKRHG	1320
1321	AVQLCTPLLL	PRNRQIYEHN	EAALFMDHSG	MLVMLPFDLR	IPFARYVARN	NILNLKRYCI	1380
1381	ERVFRPRKLD	RFHPKELLEC	AFDIVTSTTN	SFLPTAEI IY	TIYEIIQEFP	ALQERNYSIY	1440
1441	LNHTMLLKAI	LLHCGIPEDK	LSQVYI ILYD	AVTEKLTRRE	VEAKFCNLSL	SSNSLCRLYK	1500
1501	FIEQKGD LQD	LMPTINSLIK	QKTGIAQLVK	YGLKDLEEVV	GLLKKLGIKL	QVLINLGLVY	1560
1561	KVQQHNGIIF	QFVAFIKRRQ	RAVPEIL AAG	GRYDLLIPQF	RGPQALGPVP	TAIGVSI AID	1620
1621	KISA AVLNME	ESVTISSCDL	LVVSVGQMSM	SRAINLTQKL	WTAGITAEIM	YDWSQSQEEL	1680
1681	QEYCRHHEIT	YVALVSDKEG	SHVKVKSFEK	ERQTEKRVLE	TELVDHVLQK	LRTKVTDERN	1740
1741	GREASDNLAV	QNLKGSFSNA	SGLFEIHGAT	VVPIVSVLAP	EKLSASTRRR	YETQVQTRLQ	1800
1801	TSLANLHQKS	SEIEILAVDL	PKETILQFLS	LEWDADEQAF	NTTVKQLLSR	LPKQRYLKL V	1860
1861	CDEIYNIKVE	KKVSVLFLYS	YRDDYYRILF				1920

1-218: GST Red: HIS6-tag Green: 3C cleavage site blue: EIF2AK4

Recombinant Proteins

EIF2AK4 wt<sup>1</sup> Amino Acid Sequence

1	MAGGRGAPGR	GRDEPPESYP	QRQDHELQAL	EAIYGADFQD	LRPDACGPVK	EPPEINLVLY	60
61	PQGLTGEEVY	VKVDLRVKCP	PTYPDVVPEI	ELKNAKGLSN	ESVNULLKSRL	EELAKKHCGE	120
121	VMIFELAYHV	QSFLSEHNKP	PPKSFHEEML	ERRAQEEQQR	LLEAKRKEEQ	EQREILHEIQ	180
181	RRKEEIKEEK	KRKEMAKQER	LEIASLSNQD	HTSKKDPGGH	RTAAILHGGS	PDFVGNKGRH	240
241	ANSSGRSRRE	RQYSVCNSED	SPGSCEILYF	NMGSPDQLMV	HKGKCGSDE	QLGKLVYNAL	300
301	ETATGGFVLL	YEWVLQWQKK	MGPFLTSQEK	EKIDKCKQI	QGTETEFNSL	VKLSHPNVVR	360
361	YLAMNLKEQD	DSIVVDILVE	HISGVSLAAH	LSHSGPIPVH	QLRRYTAQLL	SGLDYLHSNS	420
421	VVHKVLSASN	VLVDAEGTVK	ITDYSISKRL	ADICKEDVFE	QTRVRFSDNA	LPYKTGKKGD	480
481	VWRLGLLLLS	LSQGQECGEY	PVTIPSDLPA	DFQDFLKKCV	CLDDKERWSP	QQLLKHSFIN	540
541	PQPKMPLVEQ	SPEDSEGQDY	VETVIPS NRL	PSAAFFSETQ	RQFSRYFIEF	EELQLLGKGA	600
601	FGAVIKVQNK	LDGCCYAVKR	IPINPASRQF	RRIKGEV TLL	SRLHHENIVR	YINAWIERHE	660
661	RPAGPGTPPP	DSGPLAKDDR	AARGQPASDT	DGLDSVEAAA	PPILSSSVE	WSTSGERSAS	720
721	ARFPATGPGS	SDEDDDEDE	HGGVFSQSFL	PASDSEDI I	FDNEDENSKS	QNQEDCNEK	780
781	NGCHESEPSV	TTEAVHYLYI	QMEYCEKSTL	RDTIDQGLYR	DTVRLWRLFR	EILDGLAYIH	840
841	EKGMIHRDLK	PVNI FLDSDD	HVKIGDFGLA	TDHLAFSADS	KQDDQTGDLI	KSDPSGHLTG	900
901	MVGTALYVSP	EVQGSTKSAY	NQKVDL FSLG	I IFFEMSYHP	MVTASERIFV	LNQLRDP TSP	960
961	KFPEDFDDGE	HAKQKSVISW	LLNHDP AKRP	TATELLKSEL	LPPPQMEESE	LHEVLHHTLT	1020
1021	NVDGKAYRTM	MAQIFSORIS	PAIDYTYSD	ILKGNFSIRT	AKMQQHV CET	IIRIFKRHGA	1080
1081	VQLCTPLLLP	RNRQIYEHNE	AALFMDHSGM	LVMLPFDLRI	PFARYVARNN	ILNLKRYCIE	1140
1141	RVFRPRKLR	FHPKELLECA	FDIVTSTTNS	FLPTAEI IYT	IYEIIQEFPA	LQERNYSIYL	1200
1201	NHTMLLKAIL	LHCGIPEDKL	SQVYIILYDA	VTEKLTREV	EAKFCNLSLS	SNSLCRLYKF	1260
1261	IEQKGDLDLQ	MPTINSLIKQ	KTGIAQLVKY	GLKDLEEVG	LLKKG IKLQ	VLINLGLVYK	1320
1321	VQQHNGIIFQ	FVAFIKRRQR	AVPEILAAGG	RYDLLIPQFR	GPQALGPVPT	AIGVSIADK	1380
1381	ISAAVLN MEE	SVTISSCDLL	VVSVGQMSMS	RAINLTQKLW	TAGITAEIMY	DWSQSQEELQ	1440
1441	EYCRHHEITY	VALVSDKEGS	HVKVKSFEKE	RQTEKRVLET	ELVDHVLQKL	RTKVTDERNG	1500
1501	READSNLAVQ	NLKGSFSNAS	GLFEIHGATV	VPIVSVLAPE	KLSASTRRRY	ETQVQTRLQT	1560
1561	SLANLHQKSS	EIEILAVDLP	KETILQFLSL	EWDAEQAFN	TTVKQLLSRL	PKQRYLKLVC	1620
1621	DEIYNIKVEK	KVSVLFLYSY	RDDYYRILF				1680

blue: EIF2AK4 sequence expressed in recombinant protein

<sup>1</sup>NCBI/Protein accession number NP\_001013725.2