

ProQinase™ ALK L1196M (GST-HIS-tag)

ALK receptor tyrosine kinase

Recombinant Human Active Protein Kinase

HGNC Symbol: ALK

Synonyms: CD246

Product No.: 1180-0000-1

Lot: 001

Description: Human ALK L1196M, internal fragment, amino acids L₁₀₆₆-S₁₄₃₇ (as in [NCBI/Protein](#) entry NP_004295.2), L1196M mutation, N-terminal GST-HIS₆ fusion protein with a 3C cleavage site, expressed in Sf9 insect cells

Product identity: ALK L1196M Lot 001, was confirmed as ALK with a L1196M mutation by mass spectroscopy LC-ESI-MS/MS

Theoretical MW_{Fusion Protein}: 70,477 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: 0.271 µg/µl

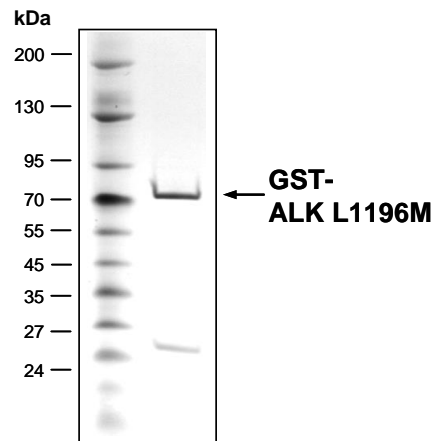
(Bradford method using BSA [Sigma, cat# A-7638, Lot 79H7641] as standard protein)

Biochemical Parameters:

Specific kinase activity (P_i transfer): 74 pmol/µg × min

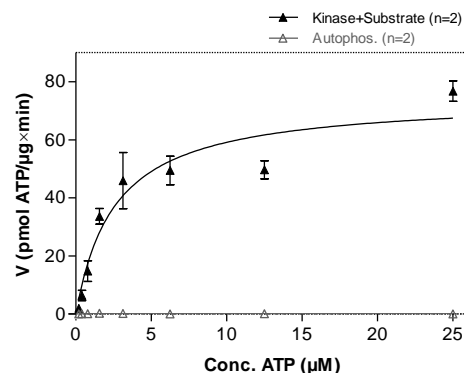
ATP-K_M: 2.6 µM

ALK L1196M Lot 001:
Coomassie stain



2.0 µg GST-ALK L1196M

ALK L1196M Lot 001:
Determination of V_{max} and K_M value for ATP



Determination of K_M value & Specific activity:

- Assay conditions:
 - 60 mM HEPES-NaOH, pH 7.5
 - 3 mM MgCl₂
 - 3 mM MnCl₂
 - 3 µM Na-orthovanadate
 - 1.2 mM DTT
 - 50 µg / ml PEG_{20,000}
 - ATP (variable)
 - Substrate: TRK-C derived peptide, 20 µg/ml
 - Kinase: 1 µg/ml
- Filter binding assay
- MSPH membrane (Millipore)

Additional assay technology:

ALK L1196M Lot 001 was also successfully tested by Reaction Biology for the use with the ADP-Glo™ Kinase assay from Promega ADP-Glo assay conditions may vary from radiometric assay conditions, please inquire for assay details

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GST-ALK L1196M Recombinant Fusion Protein Amino Acid Sequence							
1	MSPILGYWKI	KGLVQPTRL	LEYLEEKYEE	HLYERDEGDK	WRNKKFELGL	EFPNLPYYID	60
61	GDKVLTQSM	IIRYIADKHN	MLGGCPKERA	EISMLEGAVL	DIRYGVSRIA	YSKDFETLKV	120
121	DFLSKLP EML	KMFEDRLCHK	TYLNGDHVTH	PDFMLYDALD	VVLYMDPMCL	DAFPKLVCFK	180
181	KRIEAI PQID	KYLKSSKYIA	WPLQGWQATF	GGGDHPPKSD	PMG HHHHHG	RDS LEVLFCG	240
241	PLAMVLQAMQ	MELQSP EYKL	SKLRTSTIMT	DYNPNYCFAG	KTSSISDLKE	VPRKNITLIR	300
301	GLGHGAFGEV	YEQVSGMPN	DSPPLQVAVK	TLPEVCSEQD	ELDFLMEALI	ISKFNHQNIV	360
361	RCIGVSLQSL	PRFILMELMA	GGDLKSFLRE	TRPRPSQPSS	LAML DLLHVA	RDIACGCQYL	420
421	EENHF IHRDI	AARNCLL TCP	GPRVAKIGD	FGMARDIYRA	SYRKGCCAM	LPVKWMPPEA	480
481	FMEGIFTSKT	DTWSFGVLLW	EIFSLGYMPY	PSKSNQEVLE	FVTSGGRMDP	PKNCPGPVYR	540
541	IMTQCWQHQP	EDRPNFAILL	ERIEYCTQDP	DVINTALPIE	YGPLVEEEEK	VPVRPKDPEG	600
600	VPPLLV SQQA	KREEERS					660

1-218: GST **Red**: HIS6-tag **Green**: 3C cleavage site **blue**: ALK fragment **boxed**: L1196M

ALK wt ¹ Amino Acid Sequence							
1	MGAIGLLWLL	PLLLSTA AVG	SGMG TGQRAG	SPAAGPPLQP	REPLSYSRLQ	RKSLAVDFV	60
61	PSLFRVYARD	LLLPPSSSEL	KAGRPEARGS	LALDCAPLLR	LLGPAPGVSW	TAGSPAPAEA	120
121	RTLSRVLKG	SVRKLRRAKQ	LVLELGEEAI	LEGCVGPPGE	AAVGLLQFNL	SELSFWWIRQ	180
181	GEGRLRIRLM	PEKKASEVGR	EGRLSAAIRA	SQPRLLFQIF	GTGHSSLESP	TNMPPSPDY	240
241	FTWNLTWIMK	DSFPFLSHRS	RYGLECSFDF	PCELEYSPL	HDLRNQSWSW	RRIPSEEASQ	300
301	MDLLDGP GAE	RSKEMPRGSF	LLLNTSADSK	HTILSPWMS	SSEHCTLAVS	VHRHLQPSGR	360
361	YIAQLLP HNE	AAREILLMPT	PGKHGWTVLQ	GRIGRPDNP	RVALEYISSG	NRSLSAVDF	420
421	ALKNCSEGTS	PGSKMALQSS	FTCWNGTVLQ	LGQACDFHQD	CAQGEDESQM	CRKLPVGFYC	480
481	NFEDGFCGWT	QGTLSPTHPQ	WQVRTLKDAR	FQDHQDHALL	LSTTDVPASE	SATVTSATFP	540
541	APIKSSPCEL	RMSWLIRGVL	RGNVSLVLE	NKTGKEQGRM	VWHVAAYEGL	SLWQWMVLP	600
600	LDVSDRFWLQ	MVAWWGQGS	AIVAFDNISI	SLDCYLTISG	EDKILQNTAP	KSRNLFERNP	660
661	NKELKPGENS	PRQTPIFDPT	VHWFLLTTCGA	SGPHGPTQAQ	CNNAYQNSNL	SVEVGSEGPL	720
721	KGIQIWKVPA	TDTYSISGYG	AAGGKGGKNT	MMRSHGVSVL	GIFNLEKDDM	LYILVGQQGE	780
781	DACPSTNQLI	QKVCIGENNV	IEEEEIRVNRS	VHEWAGGGGG	GGGATYVFKM	KDGVVPLII	840
841	AAGGGGRAYG	AKTDTFHPER	LENNSSVLGL	NGNSGAAGGG	GGWNDNTSLL	WAGKSLQEGA	900
901	TGGHSCPQAM	KKWGWETRGG	FGGGGGGCSS	GGGGGGYIGG	NAASNNDPEM	DGEDGVSFIS	960
961	PLGILYTPAL	KVMEGHGEVN	IKHYLNCSHC	EVDECHMDPE	SHKVICFCDH	GTVLAEDGVS	1020
1021	CIVSPTPEPH	LPLSLILSVV	TSALVAALVL	AFSGIMIVYR	RKHQELQAMQ	MELQSP EYKL	1080
1081	SKLRTSTIMT	DYNPNYCFAG	KTSSISDLKE	VPRKNITLIR	GLGHGAFGEV	YEQVSGMPN	1140
1141	DSPPLQVAVK	TLPEVCSEQD	ELDFLMEALI	ISKFNHQNIV	RCIGVSLQSL	PRFILMELMA	1200
1201	GGDLKSFLRE	TRPRPSQPSS	LAML DLLHVA	RDIACGCQYL	EENHF IHRDI	AARNCLL TCP	1260
1261	GPRVAKIGD	FGMARDIYRA	SYRKGCCAM	LPVKWMPPEA	FMEGIFTSKT	DTWSFGVLLW	1320
1321	EIFSLGYMPY	PSKSNQEVLE	FVTSGGRMDP	PKNCPGPVYR	IMTQCWQHQP	EDRPNFAILL	1380
1381	ERIEYCTQDP	DVINTALPIE	YGPLVEEEEK	VPVRPKDPEG	VPPLLV SQQA	KREEERS PAA	1440
1441	PPPLPTTSSG	KAACKPTAAE	ISVRVPRGPA	VEGGHVNMAF	SQSNPPSELH	KVHGSRNKPT	1500
1501	SLWNPTYGSW	FTEKPTKKN	PIAKKEPHDR	GNLGLGESC	VPPNVATGRL	PGASLLLEPS	1560
1561	SLTANMKEVP	LFRLRHFP	CG NVNYGYQQG	LPLEAATAPG	AGHYEDTILK	SKNSMNQPGP	1620

blue: ALK sequence expressed in recombinant protein **Red**: variant in recombinant protein

¹[NCBI/Protein](https://www.ncbi.nlm.nih.gov/protein/42952) accession number NP_004295.2