

ALK F1174L

ALK receptor tyrosine kinase

Recombinant Human Active Protein Kinase

HGNC Symbol: ALK

Synonyms: CD246

Product No.: 1178-0000-1

Lot: 001

Description: Human ALK F1174L, internal fragment, amino acids L₁₀₆₆-S₁₄₃₇ (as in [NCBI/Protein](#) entry NP_004295.2), F1174L mutation, N-terminal GST-HIS₆ fusion protein with a 3C cleavage site, expressed in Sf9 insect cells

Product identity: ALK F1174L Lot 001, was confirmed as ALK with a F1174L mutation by mass spectroscopy LC-ESI-MS/MS

Theoretical MW_{Fusion Protein}: 70,425 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: 0.323 µg/µl

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

Biochemical Parameters:

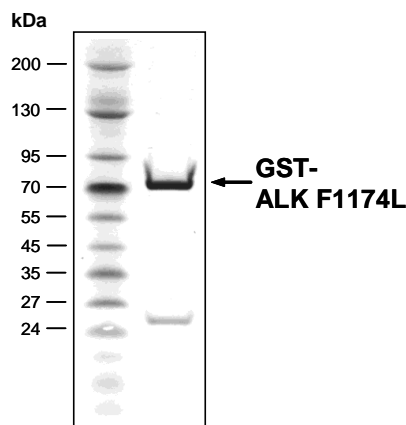
Specific kinase activity (P_i transfer): 94 pmol/µg × min

ATP-K_M: 2.2 µM

Additional assay technology:

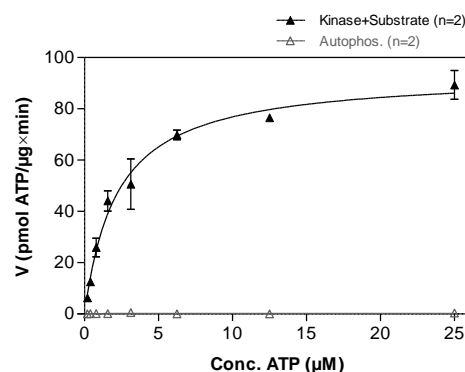
ALK F1174L Lot 001 was also successfully tested by ProQinase for the use with the ADP-Glo™ Kinase assay from Promega
ADP-Glo assay conditions may vary from radiometric assay conditions, please inquire for assay details

ALK F1174L Lot 001:
Coomassie stain



2.0 µg GST-ALK F1174L

ALK F1174L Lot 001:
Determination of V_{max} and K_M value for ATP



• 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 40 µg/ml

Kinase: 1 µg/ml

• Filter binding assay

MSPH membrane (Millipore)

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GST-ALK F1174L Recombinant Fusion Protein Amino Acid Sequence							
1	MSPILGYWKI	KGLVQPTRL	LEYLEEKYEE	HLYERDEGDK	WRNKKFELGL	EFPNLPYYID	60
61	GDKVLTQSM	IIRYIADKHN	MLGGCPKERA	EISMLEGAVL	DIRYGVSRIA	YSKDFETLKV	120
121	DFLSKLP	KMFEDRLCHK	TYLNGDHVTH	PDFMLYDALD	VVLYMDPMCL	DAFPKLVCFK	180
181	KRIEAI	PQID KYLKSSKYIA	WPLQGWQATF	GGGDHPPKSD	PMG HHHHHG	RDS LEVLFCG	240
241	PLAMVLQAMQ	MELQSP	SKLRTSTIMT	DYNPNYCFAG	KTSSISDLKE	VPRKNITLIR	300
301	GLGHGAFGEV	YEQVSGMPN	DSPPLQVAVK	TLPEVCSEQD	ELDFLMEALI	ISKLNHQNIV	360
361	RCIGVSLQSL	PRFILLEMA	GGDLKSFLRE	TRPRPSQSS	LAMLDLLHVA	RDIACGCQYL	420
421	EENHFIHRDI	AARNCLLTC	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**: F1174L

ALK wt ¹ Amino Acid Sequence								
1	MGAIGLLWLL	PLLLSTA	AVG SGMGTGQ	RAG SPAAGP	PPLQP REPLSYS	RQLQ RKS	LAVDFV	60
61	PSLFRVYARD	LLLPPSSSEL	KAGRPEAR	GS LALDCAP	LLR LLGPAP	GVSW TAG	SPPAAEA	120
121	RTLSRVLKGG	SVRKLRR	AQ LVLELGE	EAI LEGCVG	PPE AAVGLL	QFNL SEL	FSWIRQ	180
181	GEGRLRIRLM	PEKKASEVGR	EGRLSAAIRA	SQPRLLFQIF	GTGHSSLESP	TNMPSPSPDY		240
241	FTWNLTWIMK	DSFPFLSHRS	RYGLECSFDF	PCELEYSPL	HDLRNQSWSW	RRIPSEEASQ		300
301	MDLLDGP	GAE RSKEMPR	GSF LLLNTS	ADSK HTILSP	WMS SSEHCT	LAVS VHRHL	QPSGR	360
361	YIAQLLPHNE	AAREILLMPT	PGKHGWTVLQ	GRIGRPDNP	F RVALEYISSG	NRSLSAVDF		420
421	ALKNCSEGTS	PGSKMALQSS	FTCWNGTVLQ	LGQACDFHQD	CAQGEDESQM	CRKLPVGFYC		480
481	NFEDGFCGWT	QGTLSPHTPQ	WQVRTLKDAR	FQDHQDHALL	LSTTDVPASE	SATVTSATFP		540
541	APIKSSPCEL	RMSWLIRGVL	RGNVSLVLE	NKTGKEQGRM	VWHVAAYEGL	SLWQWMVLP		600
600	LDVSDRFLWQ	MVAWWGQGS	R AIVAFDN	ISI SLDCYLT	ISG EDKILQ	NTAP KSRNL	FERNP	660
661	NKELKPGENS	PRQTPIFDPT	VHWFLLTCGA	SGPHGPTQAQ	CNNAYQNSNL	SVEVGSEGPL		720
721	KGIQIWKVPA	TDTYSISGYG	AAGGKGGKNT	MMRSHGVS	VL GIFNLEK	DDM LYILV	QQQE	780
781	DACPSTNQLI	QKVCIGENNV	IIEEIRVNRS	VHEWAGGGG	GGGATYVFKM	KDGVVPLII		840
841	AAGGGGRAYG	AKTDTFHPER	LENNSSVLGL	NGNSGAAGG	GGWNDNTSLL	WAGKSLQEGA		900
901	TGGHSCPQAM	KKWGWETRGG	FGGGGGCSS	GGGGGGYIG	NAASNDPEM	DGEDGVSFIS		960
961	PLGILYTPAL	KVMEGHGEVN	IKHYLNC	SHC EVDECH	MDPE SHKVIC	FCDH GTVLA	EDGVS	1020
1021	CIVSPTPEPH	LPLSLILSVV	TSALVAALVL	AFSGIMIVYR	RKHQELQAMQ	MELQSP	SKLRTSTIMT	1080
1081	SKLRTSTIMT	DYNPNYCFAG	KTSSISDLKE	VPRKNITLIR	GLGHGAFGEV	YEQVSGMPN		1140
1141	DSPPLQVAVK	TLPEVCSEQD	ELDFLMEALI	ISKLNHQNIV	RCIGVSLQSL	PRFILLEMA		1200
1201	GGDLKSFLRE	TRPRPSQSS	LAMLDLLHVA	RDIACGCQYL	EENHFIHRDI	AARNCLLTC		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	VEGGHVMAF	SQSNPPSELH	KVHGSRNKPT		1500
1501	SLWNPTYGSW	FTEKPTKKN	PIAKKEPHDR	GNLGLG	ESCT VPPNVAT	GRL PGASLLLEPS		1560
1561	SLTANMKEVP	LFRLRHFP	CG NVNYGYQQQ	G LPLEAATA	PG AGHYEDTILK	SKNSMNP	QPGP	1620

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

¹[NCBI/Protein](#) accession number NP_004295.2

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