

## ProQinase™ ALK R1275Q

ALK receptor tyrosine kinase

Recombinant Human Active Protein Kinase

HGNC Symbol: ALK

Synonyms: CD246

Product No.: 1181-0000-1

Lot: 006

**Description:** Human ALK R1275Q, internal fragment, amino acids L<sub>1066</sub>-S<sub>1437</sub> (as in [NCBI/Protein](#) entry NP\_004295.2), R1275Q mutation, N-terminal GST-HIS<sub>6</sub> fusion protein with a 3C cleavage site, expressed in Sf9 insect cells

**Product identity:** ALK R1275Q Lot 001, was confirmed as ALK by mass spectroscopy LC-ESI-MS/MS

**Theoretical MW<sub>Fusion Protein</sub>:** 70,431 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:** 0.139 µg/µl

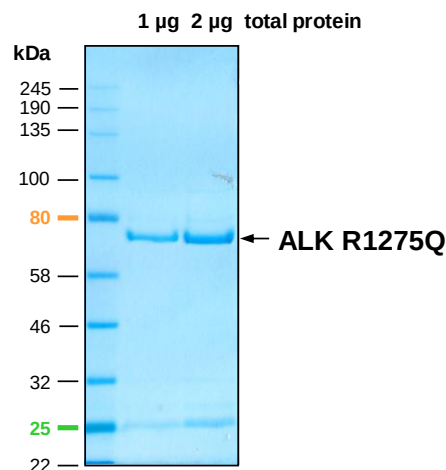
(Bradford method using BSA [Sigma, cat# A-7638, Lot 79H7641] as standard protein)

### Biochemical Parameters:

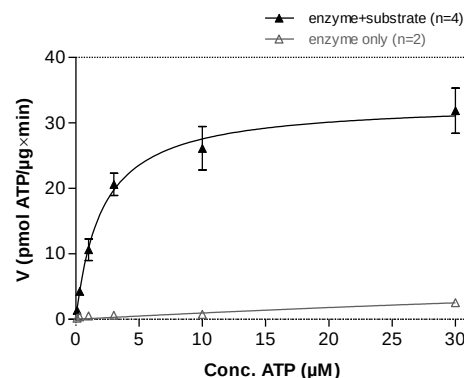
Specific kinase activity (P<sub>i</sub> transfer): 33 pmol/µg × min

ATP-K<sub>M</sub>: 2 µM

### ALK R1275Q Lot 006: Coomassie stain



### ALK R1275Q Lot 006: 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: TRK-C derived peptide 80 µg/ml  
Kinase: 2 µg/ml
- Filter binding assay  
MSPH membrane (Millipore)

### Additional assay technology:

ALK R1275Q Lot 006 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 R1275Q Recombinant Fusion Protein Amino Acid Sequence |            |            |            |            |             |            |     |
|---------------------------------------------------------------|------------|------------|------------|------------|-------------|------------|-----|
| 1                                                             | MSPILGYWKI | KGLVQPTRLL | LEYLEEKYEE | HLIERDEGDK | WRNKKFELGL  | EFNLPYYID  | 60  |
| 61                                                            | GDVKLTQSMA | IIRYIADKHN | MLGGCPKERA | EISMLEGAVL | DIRYGVSRIA  | YSKDFETLKV | 120 |
| 121                                                           | DFLSKLPEML | KMFEDRLCHK | TYLNGDHVTH | PDFMLYDALD | VVLYMDPMCL  | DAFPKLVCFK | 180 |
| 181                                                           | KRIEAIQID  | KYLKSSKYIA | WPLQGWQATF | GGGDHPPKSD | PMGHHHHHG   | RDSLEVLFGG | 240 |
| 241                                                           | GLAMVLQAMQ | MELQSPYKYL | SKLRTSTIMT | DYNPNYCFAG | KTSSISDLKE  | VPRKNITLIR | 300 |
| 301                                                           | GLGHGAFGEV | YEGQVSGMPN | DPSPLQVAVK | TLPEVCSEQD | ELDFLMEALI  | ISKFNHQNIV | 360 |
| 361                                                           | RCIGVSLQSL | PRFILLELMA | GGDLKSFLRE | TRPRPSQPSS | LAMLDLLHVA  | RDIACGCQYL | 420 |
| 421                                                           | EENHFIHRDI | AARNCLLTCP | GPGRVAKIGD | FGMAQDIYRA | SYRKGCCAM   | LPVKWMPPEA | 480 |
| 481                                                           | FMEGIFTSKT | DTWSFGVLLW | EIFSLGYMPY | PSKSNQEVLE | FVTSGGRMDP  | PKNCPGPVYR | 540 |
| 541                                                           | IMTQCWQHQP | EDRPNFAILL | ERIEYCTQDP | DVINTALPIE | YGPLVEEEEEK | VPVRPKDPEG | 600 |
| 600                                                           | VPPLLVSSQA | KREEERS    |            |            |             |            | 660 |

1-218: GST Red: HIS6-tag Green: 3C cleavage site blue: ALK fragment boxed: R1275Q mutation

| ALK wt <sup>1</sup> Amino Acid Sequence |             |             |             |             |             |             |      |
|-----------------------------------------|-------------|-------------|-------------|-------------|-------------|-------------|------|
| 1                                       | MGAIGLLWLL  | PLLLSTA AVG | SGMG TGQRAG | SPAAGPPLQP  | REPLSYSRLQ  | RKSLAVDFVV  | 60   |
| 61                                      | PSLFRVYARD  | LLLPPSSSEL  | KAGRPEARGS  | LALDCAPLLR  | LLGPAPGVSW  | TAGSPAPAEA  | 120  |
| 121                                     | RTLSRVLKGG  | SVRKLRRAKQ  | LVLELGEEAI  | LEGCVGPPGE  | AAVGLLQFNL  | SELSFWWIRQ  | 180  |
| 181                                     | GEGRLRIRLM  | PEKKASEVGR  | EGRLSAAIRA  | SQPRLLFQIF  | GTGHSSLESP  | TNMPSPPSPDY | 240  |
| 241                                     | FTWNLTWIMK  | DSFPFLSHRS  | RYGLECSFDF  | PCELEYSPL   | HDLRNQSWSW  | RRIPSEEASQ  | 300  |
| 301                                     | MDLLDGP GAE | RSKEMPRGSF  | LLLNTSADSK  | HTILSPWMRS  | SSEHCTLA VS | VHRHLQPSGR  | 360  |
| 361                                     | YIAQLLP HNE | AAREIILLMPT | PGKHGWTVLQ  | GRIGRPDNP F | RVALEYISSG  | NRSLSAVDFE  | 420  |
| 421                                     | ALKNCSEGT S | PGSKMALQSS  | FTCWNGTVLQ  | LGQACDFHQD  | CAQGEDESQM  | CRKLPVGFYC  | 480  |
| 481                                     | NFEDGFCGWT  | QGTLSPTHPQ  | WQVRTLKDAR  | FQDHQDHALL  | LSTTDVPASE  | SATVTSATFP  | 540  |
| 541                                     | APIKSSPCEL  | RMSWLIRGVL  | RGNVSLVLVE  | NKTGKEQGRM  | VWHVAAYEGL  | SLWQWMVLPL  | 600  |
| 600                                     | LDVSDRFLWQ  | MVAWWGQGSR  | AIVAFDNISI  | SLDCYLTISG  | EDKILQNTAP  | KSRNLFERNP  | 660  |
| 661                                     | NKELKPGENS  | PRQTPIDFPT  | VHWFLLTTCGA | SGPHGPTQAQ  | CNNAYQNSNL  | SVEVGSEGPL  | 720  |
| 721                                     | KGIQIWKVPA  | TDTYSISGYG  | AAGGKGKNT   | MMRSHGVSVL  | GIFNLEKDDM  | LYILVGQQGE  | 780  |
| 781                                     | DACPSTNQLI  | QKVCIGENNV  | IIEEIRVNRS  | VHEWAGGGGG  | GGGATYVFKM  | KDGPVPLII   | 840  |
| 841                                     | AAGGGGRAYG  | AKTDTFHPER  | LENNSSVLGL  | NGNSGAAGGG  | GGWNDNTSLL  | WAGKSLQEGA  | 900  |
| 901                                     | TGGHSCPQAM  | KKWGWETRGG  | FGGGGGGCSS  | GGGGGGYIGG  | NAASNNDPEM  | DGEDGVSFIS  | 960  |
| 961                                     | PLGILYTPAL  | KVMEGHGEVN  | IKHYLNC SHC | EVDECHMDPE  | SHKVICFCDH  | GTVLAEDGVS  | 1020 |
| 1021                                    | CIVSPTPEPH  | LPLSLILSVV  | TSALVAALVL  | AFSGIMIVYR  | RKHQELQAMQ  | MELQSPYKYL  | 1080 |
| 1081                                    | SKLRTSTIMT  | DYNPNYCFAG  | KTSSISDLKE  | VPRKNITLIR  | GLGHGAFGEV  | YEGQVSGMPN  | 1140 |
| 1141                                    | DPSPLQVAVK  | TLPEVCSEQD  | ELDFLMEALI  | ISKFNHQNIV  | RCIGVSLQSL  | PRFILLELMA  | 1200 |
| 1201                                    | GGDLKSFLRE  | TRPRPSQPSS  | LAMLDLLHVA  | RDIACGCQYL  | EENHFIHRDI  | AARNCLLTCP  | 1260 |
| 1261                                    | GPGRVAKIGD  | FGMAQDIYRA  | SYRKGCCAM   | LPVKWMPPEA  | FMEGIFTSKT  | DTWSFGVLLW  | 1320 |
| 1321                                    | EIFSLGYMPY  | PSKSNQEVLE  | FVTSGGRMDP  | PKNCPGPVYR  | IMTQCWQHQP  | EDRPNFAILL  | 1380 |
| 1381                                    | ERIEYCTQDP  | DVINTALPIE  | YGPLVEEEEEK | VPVRPKDPEG  | VPPLLVSSQA  | KREEERS     | 1440 |
| 1441                                    | PPPLPTTSSG  | KAACKPTAAE  | ISVRVPRGPA  | VEGGHVNM AF | SQSNPPSELH  | KVHGSRNKPT  | 1500 |
| 1501                                    | SLWNPTYGSW  | FTEKPTKKNN  | PIAKKEPHDR  | GNLGLEGSCT  | VPPNVATGRL  | PGASLLLEPS  | 1560 |
| 1561                                    | SLTANMKEVP  | LFRLRHFP CG | NVNYGYQQQG  | LPLEAATAPG  | AGHYEDTILK  | SKNSMNQPGP  | 1620 |

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

<sup>1</sup>[NCBI/Protein](#) accession number NP\_004295.2