

## ProQinase™ FGFR1 V561M

fibroblast growth factor receptor 1

### Recombinant Human Active Protein Kinase

HGNC Symbol: FGFR1

**Synonyms:** BFGFR, FLT2, KAL2, H2, H3, H4, CEK, FLG, N-SAM, CD331

**Product No.:** 0890-0000-1

**Lot:** 003

**Description:** Human FGFR1, C-terminal fragment, amino acids M<sub>456</sub>-E<sub>765</sub> (as in [NCBI/Protein](#) entry NP\_056934.2), V561M point mutant, untagged, expressed in Sf9 insect cells

**Product identity:** FGFR1 V561M Lot 003, has been verified by mass spectrometry LC-ESI-MS/MS

**Theoretical MW<sub>Fusion Protein</sub>:** 35899 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, 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:** 0.14 µg/µl

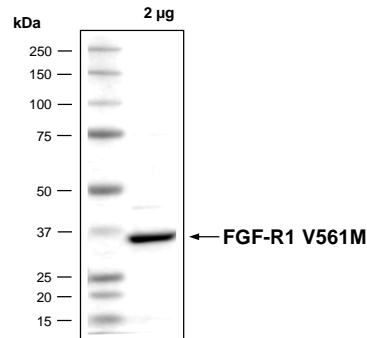
(Bradford method using BSA [Sigma, cat# A-7638, Lot 79H7641] as standard protein)

#### Biochemical Parameters:

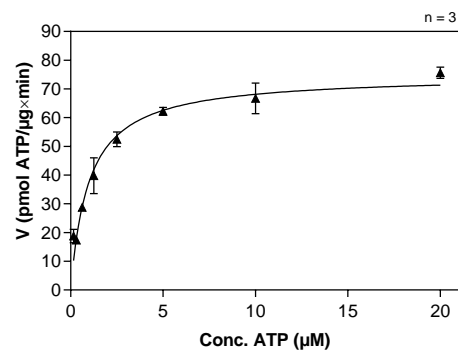
Specific kinase activity (P<sub>i</sub> transfer): 75 pmol/µg\*min

ATP-K<sub>M</sub>: 0.98 µM

#### FGFR1 V561M Lot 003: Coomassie stain



#### FGFR1 V561M Lot 003: 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: Poly(Ala:Glu:Lys:Tyr)<sub>6:2:5:1</sub> 20 µg/ml
- Kinase: 0.6 µg/ml

#### Assay technology:

- Radiometric filter binding assay
- MSFC membrane (96 well plate, Millipore)

Recombinant Proteins

Sequence information

| FGFR1 V561M Recombinant Protein Amino Acid Sequence |            |            |            |            |            |            |            |     |
|-----------------------------------------------------|------------|------------|------------|------------|------------|------------|------------|-----|
| 1                                                   | GPLAMG     | MLAG       | VSEYELPEDL | RWELPRDRLV | LGKPLGEGCF | GQVVLAEAIQ | LDKDKPNRVT | 60  |
| 61                                                  | KVAVKMLKSD | ATEKDLSDLI | SEMEMMKMIG | KHKNIINLLG | ACTQDGPLYV | IMEYASKGNL |            | 120 |
| 121                                                 | REYLQARRPP | GLECYNPSH  | NPEEQSSKD  | LVSCAYQVAR | GMEYLASKKC | IHRDLAARNV |            | 180 |
| 181                                                 | LVTEDNVMKI | ADFGIARDIH | HIDYKKTNTN | GRLPVKWMAP | EALFDRIYTH | QSDVWSFGVL |            | 240 |
| 241                                                 | LWEIFTLGGS | PYPGVPVEEL | FKLLKEGHRM | DKPSNCTNEL | YMMRDCWHA  | VPSQRPTFKQ |            | 300 |
| 301                                                 | LVEDLDRIVA | LTSNQE     |            |            |            |            |            | 360 |

1-6: legacy of tag cleavage **blue**: FGFR1 fragment **boxed**: V561M point mutation

| FGFR1 wt <sup>1</sup> Amino Acid Sequence |             |            |            |            |            |            |     |
|-------------------------------------------|-------------|------------|------------|------------|------------|------------|-----|
| 1                                         | MWSWKCLLFW  | AVLVTATLCT | ARPSPTLPEQ | AQPWGAPVEV | ESFLVHPGDL | LQLRCRLRDD | 60  |
| 61                                        | VQSINWLRDG  | VQLAESNRTR | ITGEEVEVQD | SVPADSGLYA | CVTSSPSGSD | TTYFSVNVSD | 120 |
| 121                                       | ALPSSSEDDDD | DDSSSEEKE  | TDNTKPNRMP | VAPYWTSPEK | MEKKLHAVPA | AKTVKFKCPS | 180 |
| 181                                       | SGTPNPTLRW  | LKNGKEFKPD | HRIGGYKVRY | ATWSIIMDSV | VPSDKGNYTC | IVENEYGSIN | 240 |
| 241                                       | HTYQLDVVER  | SPHRPILQAG | LPANKTVALG | SNVEFMCKVY | SDPQPHIQWL | KHIEVNGSKI | 300 |
| 301                                       | GPDNLPIVYQI | LKTAGVNTTD | KEMEVLHLRN | VSFEDAGEYT | CLAGNSIGLS | HHSAWLTVLE | 360 |
| 361                                       | ALEERPAMVT  | SPLYLEIIY  | CTGAFLISCM | VGSVIVYKMK | SGTKKSDFHS | QMAVHKLAKS | 420 |
| 421                                       | IPLRRQVTVS  | ADSSASMNSG | VLLVRPSRLS | SSGTPMLAGV | SEYELPEDLR | WELPRDRLVL | 480 |
| 481                                       | GKPLGEGCFG  | QVVLAEAIQL | DKDKPNRVTK | VAVKMLKSDA | TEKDLSDLIS | EMEMMKMIGK | 540 |
| 541                                       | HKNIINLLGA  | CTQDGPLYVI | VEYASKGNLR | EYLQARRPPG | LEYCYNPSHN | PEEQSSKDL  | 600 |
| 600                                       | VSCAYQVARG  | MEYLASKKCI | HRDLAARNVL | VTEDNVMKIA | DFGLARDIHH | IDYKKTNTNG | 660 |
| 661                                       | RLPVKWMAP   | ALFDRIYTHQ | SDVWSFGVLL | WEIFTLGGS  | YPGVPVEELF | KLLKEGHRMD | 720 |
| 721                                       | KPSNCTNELY  | MMRDCWHA   | PSQRPTFKQL | VEDLDRIVAL | TSNQEYLDLS | MPLDQYSPSF | 780 |
| 781                                       | PDTRSSTCSS  | GEDSVFSHEP | LPEEPCLPRH | PAQLANGGLK | RR         |            | 840 |

**blue**: FGFR1 sequence expressed in recombinant protein **Red**: variant in recombinant protein

<sup>1</sup>NCBI/Protein accession number NP\_056934.2

P467L: Sequence conflict: see UniProt P11362 and GenBank M37722.1