

# PDGFR-alpha V561D

platelet-derived growth factor receptor, alpha polypeptide

Recombinant Human Active Protein Kinase

HGNC Symbol: PDGFRA

Synonyms: PDGFRA, PDGFR2, CD140a

Product No.: 1056-0000-1

Lot: 002

**Description:** Human PDGFR-alpha, C-terminal fragment, amino acids Q<sub>551</sub>-L<sub>1089</sub> (as in NCBI/Protein entry NP\_006197.1) with a V561D mutation, N-terminal GST-HIS<sub>6</sub> fusion protein with a 3C cleavage site, expressed in Sf9 insect cells

**Product identity:** PDGFR-alpha V561D Lot 002, was confirmed as PDGFR-alpha by mass spectroscopy LC-ESI-MS/MS

**Theoretical MW<sub>Fusion Protein</sub>:** 89,908 Da

**Expression:** Baculovirus infected Sf9 cells

**Purification:** GST-Affinity Chromatography

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

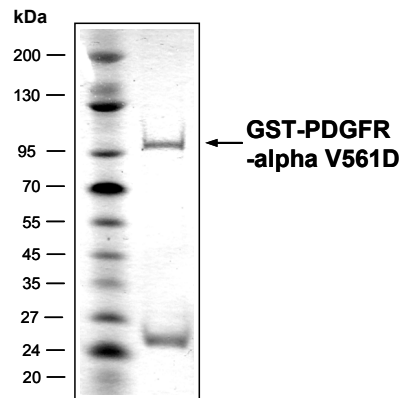
**Storage temperature:** -80°C  
Avoid repeated freeze-thaw cycles!

**Protein concentration:** 0.105 µg/µl  
(Bradford method using BSA [Sigma, cat# A-7638, Lot 79H7641] as standard protein)

**Biochemical Parameters:**

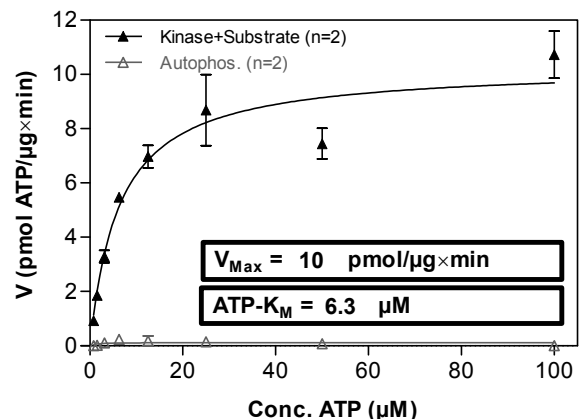
Specific activity: 10 pmol/µg×min  
ATP-K<sub>M</sub>: 6.3 µM

**PDGFR-alpha V561D Lot 002:  
Coomassie stain**



2.0 µg GST-PDGFR-alpha V561D


**PDGFR-alpha V561D Lot 002:  
Determination of V<sub>max</sub> and K<sub>M</sub> value for ATP**



**Determination of K<sub>M</sub> value & Specific activity:**

- 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
  - PDGFR-alpha V561D: 1.0 µg / ml
- Filter binding assay
  - MSFC membrane (Millipore)

**Additional assay technology:** PDGFR-alpha V561D Lot 002

was also successfully tested by ProQinase for the use with the ADP-Glo™ Kinase assay from 

## PDGFR-alpha V561D

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PDGFR-alpha V561D Recombinant Fusion Protein Amino Acid Sequence							
1	MSPILGYWKI	KGLVQPTRL	LEYLEEKYE	HLYERDEGDK	WRNKKFELGL	EFPNLPYYID	60
61	GDVKLTQSM	IIRYIADKHN	MLGGCPKERA	EISMLEGAVL	DIRYGVSRIA	YSKDFETLKV	120
121	DFLSKLP EML	KMFEDRLCHK	TYLNGDHVTH	PDFMLYDALD	VVLYMDPMCL	DAFPKLVCFK	180
181	KRIEAI PQID	KYLKSSKYIA	WPLQGWQATF	GGGDHPPKSD	PMGHHHHHHG	RDSLEVL FQG	240
241	PLAMGQKPRY	EIRWRDIESI	SPDGHEYIYV	DPMQLPYDSR	WEFPRDGLVL	GRVLGSGAFG	300
301	KVVEGTAYGL	SRSQPVMKVA	VKMLKPTARS	SEKQALMSEL	KIMTHLGPHL	NIVNLLGACT	360
361	KSGPIYIITE	YCFYGLVNY	LHKNRDSFLS	HHPEKPKKEL	DIFGLNPADE	STRSYVILSF	420
421	ENNGDYMDMK	QADTTQYVPM	LERKEVSKYS	DIQRSLYDRP	ASYKKKSM LD	SEVKNLLSDD	480
481	NSEGLTLLDL	LSFTYQVARG	MEFLASKNCV	HRDLAARNVL	LAQ GKIVKIC	DFGLARDIMH	540
541	DSNYVSKGST	FLPVKWM APE	SIFDNLYTTL	SDVWSYGILL	WEIFSLGGTP	YPGMMVDSTF	600
600	YNKIKSGYRM	AKPDHATSEV	YEIMVKCWNS	EPEKRPSFYH	LSEIVENLLP	GQYKKS YEKI	660
661	HLDFLKS DHP	AVARMRVDSD	NAYIGVTYKN	EEDKLDWEG	GLDEQR LSAD	SGYI I PLPI	720
721	DPVPEEEDLG	KRNRHSSQTS	EESA IETGSS	SSTFIKREDE	TIEDIDMDD	IGIDSSDLVE	780
781	DSFL						840

1-218: GST    Red: HIS6-tag    Green: 3C    blue:PDGFR-alpha fragment    D: V561D mutation

PDGFR-alpha wt <sup>1</sup> amino acid sequence							
1	MGTSHPAFLV	LGCLLTGLSL	ILCQLSLPSI	LPNENEKV VQ	LNSSFSLRCF	GESEVSWQYP	60
61	MSEEESSDVE	IRNEENNSGL	FVTVLEVSSA	SAAHTGLYTC	YYNHTQTEEN	ELEGRHIYIY	120
121	VPDPDVA FVP	LGMTDYL VIV	EDDDSAIIPC	RTTDPETPVT	LHNSEGVVPA	SYDSRQGFNG	180
181	TFTVGPYICE	ATVKGKKFQT	IPFNVYALKA	TSELDLEMEA	LKTVYKSGET	IVVTCAVFNN	240
241	EVVDLQW TYP	GEVKGKGITM	LEEIKVPSIK	LVYTLTVPEA	TVKDSGDYEC	AARQATREVK	300
301	EMKKVTISVH	EKGFIEIKPT	FSQLEAVNLH	EVKHFVVEVR	AYPPPRISWL	KNNLTLIENL	360
361	TEITTDVEKI	QEIRYRSK LK	LIRAKEEDSG	HYTIVAQNE D	AVKSYTFELL	TQVPSSILDL	420
421	VDDHHGSTGG	QTVRCTAEGT	PLPDIEWMIC	KDIKKCNET	SWTILANNVS	NIITEIHSRD	480
481	RSTVEGRVTF	AKVEETI AVR	CLAKNLLGAE	NRELKLVAPT	LRSELTVA AA	VLVLLVIVII	540
541	SLIVLVVIWK	QKPRYEIRWR	VIESISPDGH	EYIYV DPMQL	PYDSRWEFPR	DGLVLRV L G	600
600	SGAFGKVVEG	TAYGLSRSQP	VMKVAVKMLK	PTARSSEKQA	LMSELKIMTH	LGPHLNIVNL	660
661	LGACTKSGPI	YIITEYCFYG	DLVNYLHKNR	DSFLSHHPEK	PKKELDIFGL	NPADESTRSY	720
721	VILSFENNGD	YMDMQADTT	QYVPMLEK E	VSKYSDIQRS	LYDRPASYKK	KSMLDSEVKN	780
781	LLSDDNSEGL	TLLDLLSFTY	QVARGMEFLA	SKNCVHRDLA	ARNVLLAQ GK	IVKICDFGLA	840
841	RDIMHDSNYV	SKGSTFLPVK	WMAPE SIFDN	LYTTLSDVWS	YGILLWEIFS	LG GTPYPGMM	900
901	VDSTFYNKIK	SGYRMAKPDH	ATSEVYEIMV	KCWNSEPEKR	PSFYHLSEIV	ENLLPGQYKK	960
961	SYEKIHLDFL	KSDHPAVARM	RVDSDNAYIG	VTYKNEEDKL	KDWEGGLDEQ	RLSADSGYII	1020
1021	PLPIDIPVPE	EEDLGKRRNH	SSQTSEESA I	ETGSSSSTFI	KREDETIEDI	DMMDDIGIDS	1080
1081	SDLVEDSFL						1140

blue: PDGFR-alpha sequence expressed in fusionprotein    Red: variant in fusionprotein

<sup>1</sup>NCBI/Protein accession number NP\_006197.1