

ProQinase™ PDGFR-alpha V561D

platelet-derived growth factor receptor, alpha polypeptide

Recombinant Human Active Protein Kinase

HGNC Symbol: PDGFRA

Synonyms: PDGFR2, CD140a, RHEPDGFRA

Product No.: 1056-0000-1

Lot: 002

Description: Human PDGFR-alpha, C-terminal fragment, amino acids Q₅₅₁-L₁₀₈₉ (as in [NCBI/Protein](#) entry NP_006197.1) with a V561D mutation, N-terminal GST-HIS6 fusion protein with a 3C cleavage site, expressed in Sf9 insect cells

Product identity: PDGFR-alpha V561D Lot 002, has been verified by mass spectrometry LC-ESI-MS/MS

Theoretical MW_{Fusion Protein}: 89908 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 10 µl are not advisable. Avoid repeated freeze-thaw cycles!

Protein concentration: 0.105 µg/µl

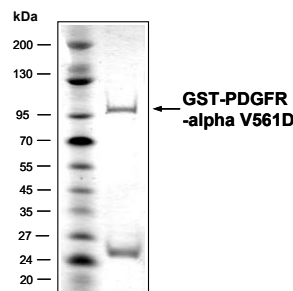
(Bradford method using BSA [Sigma, cat# A-7638, Lot 79H7641] as standard protein)

Biochemical Parameters:

Specific kinase activity (P_i transfer): 28 pmol/µg*min

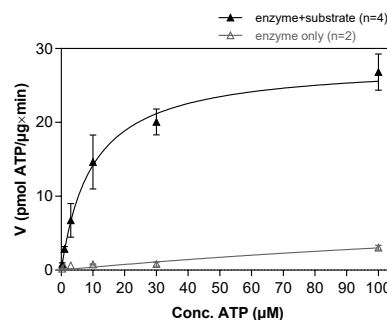
ATP-K_M: 9.8 µM

PDGFR-alpha V561D Lot 002
Coomassie stain



2.0 µg GST-PDGFR-alpha V561D

PDGFR-alpha V561D Lot 002
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 80 µg/ml
- Kinase: 4 µg/ml

Assay technology:

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

Sequence information

GST-PDGFR-alpha V561D Recombinant Fusion Protein Amino Acid Sequence							
1	MSPILGYWKI	KGLVQPTRLL	LEYLEEKYEE	HLIERDEGDK	WRNKKFELGL	EFPNLPYYID	60
61	GDVKLTQSMA	IIRYIADKHN	MLGGCPKERA	EISMLEGAVL	DIRYGVSRIA	YSKDFETLKV	120
121	DFLSKLPEML	KMFEDRLCHK	TYLNGDHVTH	PDFMLYDALD	VVLYMDPMCL	DAFPKLVCFK	180
181	KRIEAIPIQID	KYLKSSKYIA	WPLQGWQATF	GGGDHPPKSD	PMGHHHHHGG	RDSLEVLFGG	240
241	PLAMGQKPRY	EIRWRDIESI	SPDGHEYIYV	DPMQLPYDSR	WEFPRDGLVL	GRVLGSGAFG	300
301	KVVEGTAYGL	SRSQPVVMKVA	VKMLKPTARS	SEKQALMSEL	KIMTHLGPHL	NIVNLLGACT	360
361	KSGPIYIITE	YCFYGDLVNY	LHKNRDSFSL	HHPEKPKKEL	DIFGLNPADE	STRSYVILSF	420
421	ENNGDYMDMK	QADTTQYVPM	LERKEVSKYS	DIQRLSYDRP	ASYKKKSMLD	SEVKNLLSDD	480
481	NSEGLTLLDL	LSFTYQVARG	MEFLASKNCV	HRDLAARNVL	LAQGKIVKIC	DFGLARDIMH	540
541	DSNYVSKGST	FLPVKWMape	SIFDNLTYTL	SDVWSYGILL	WEIFSLGGTP	YPGMMVDSTF	600
600	YNKIKSGYRM	AKPDHATSEV	YEIMVKCWNS	EPEKRPSFYH	LSEIVENLLP	GQYKKSYEKI	660
661	HLDFLKSDHP	AVARMRVDS	NAYIGVTYKN	EEDKLKDWEG	GLDEQRLSAD	SGYIIPLPDI	720
721	DPVPEEEDLG	KRNRHSSQTS	EESALETGSS	SSTFIKREDE	TIEDIDMMDD	IGIDSSDLVE	780
781	DSFL						840

1-218: GST **Red**: HIS6-tag **Green**: 3C cleavage site **blue**: PDGFR-alpha fragment **boxed**: V561D mutation

PDGFR-alpha wt ¹ Amino Acid Sequence							
1	MGTSHPAFLV	LGCLLTGLSL	ILCQLSLPSI	LPNENEKVQ	LNSSFSLRCF	GESEVSWQYP	60
61	MSEEESSDVE	IRNEENNSGL	FVTVLEVSSA	SAAHTGLYTC	YNNHTQTEEN	ELEGRHIYY	120
121	VPDPDAFVFP	LGMTDYLIV	EDDDSAIIPC	RTTDPETPVT	LHNSEGVPVA	SYDSRQGFNG	180
181	TFTVGPYICE	ATVKGKKFQT	IPFNVYALKA	TSELDLEMEA	LKTVYKSGET	IVVTCAVFNN	240
241	EVVDLQWTYP	GEVKGKGITM	LEEIKVPSIK	LVYTLTVPEA	TVKDSGDYEC	AARQATREVK	300
301	EMKKVTISVH	EKGFIIEIKPT	FSQLEAVNLH	EVKHFVVEVR	AYPPPRISWL	KNNLTLIENL	360
361	TEITTDVEKI	QEIRYRSKLK	LIRAKEEDSG	HYTIVAQNED	AVKSYTFELL	TQVPSSILDL	420
421	VDDHHGSTGG	QTVRCTAEGT	PLPDIEWMIC	KDIKKCNET	SWTILANNVS	NIITEIHSRD	480
481	RSTVEGRVTF	AKVEETIAVR	CLAKNLLGAE	NRELKLVAPT	LRSELTVAAG	VLVLLVIVII	540
541	SLIVLVVIWK	QKPRYEIRWR	VIESISPDGH	EYIYVDPML	PYDSRWEFPR	DGLVLGRVLG	600
600	SGAFGKVVVEG	TAYGLSRSQP	VMKVAVKMLK	PTARSSEKQA	LMSELKIMTH	LGPLNIVNL	660
661	LGACTKSGPI	YIITEYCFYG	DLVNYLHKNR	DSFLSHHPEK	PKKELDIFGL	NPADESTRSY	720
721	VILSFENNGD	YMDMKQADTT	QYVPMLEKE	VSKYSIDIQS	LYDRPASYYK	KSMLDSEVKN	780
781	LLSDDNSEGL	TLLDLLSFTY	QVARGMEFLA	SKNCVHRDLA	ARNVLLAQGK	IVKICDFGLA	840
841	RDIMHDSNYV	SKGSTFLPVK	WMAPESIFDN	LYTTLSDVWS	YGILLWEIFS	LGSTPYPGMM	900
901	VDSTFYNKIK	SGYRMAKPDH	ATSEVYEIMV	KCWNSEPEKR	PSFYHLSEIV	ENLLPGQYKK	960
961	SYEKIHLDFL	KSDHPAVARM	RVDSDNAYIG	VTYKNEEDKL	KDWEGLDEQ	RLSADSGYII	1020
1021	PLPDIDPVPE	EEDLGKRNHR	SSQTSEESAI	ETGSSSSTFI	KREDETIEDI	DMMDDIGIDS	1080
1081	SDLVEDSFL						1140

blue: PDGFR-alpha sequence expressed in recombinant protein **Red**: variant in recombinant protein

¹[NCBI/Protein](https://www.ncbi.nlm.nih.gov/Protein) accession number NP_006197.1

Recombinant Proteins