

>PDGF1_peptide

KIEIVRKKPIF

>PDGF2_peptide

LIDRTNANFL

>Human_PDGFNP_002599.1

MNRCWALFLSLCCYLRLVSAEGDPIPEELYEMLSDHSIRSFDDLQRLRHGDPGEEDGAELDLNMTRSHSG
GELESLARGRRSLGSLTIAEPAMIAECKTRTEVFQISRRLIDRTNANFLVWPPCVEVQRCSGCCNNRNVQ
CRPTQVQLRPVQVRKIEIVRKKPIFKKATVTLEDHLACKCETVAAARPVTRSPGGSQEQRAKTPQTRVTI
RTVRRRPPKPKHRKFKHDKTALKETLGA

>Mouse_PDGFNP_035187.2

MNRCWALFLPLCCYLRLVSAEGDPIPEELYEMLSDHSIRSFDDLQRLRHRSVDEDGAELDLNMTRAHSG
VELESSSRGRRSLGSLAAAEPAVIAECKTRTEVFQISRNLIDRTNANFLVWPPCVEVQRCSGCCNNRNVQ
CRASQVQMRPVQVRKIEIVRKKPIFKKATVTLEDHLACKCETVVTPRPVTRSPGTSREQRAKTPQARVTI
RTVRIIRPPKPKHRKFKHDKAALKETLGA

Human_PDGFNP_002599.1 MNRCWALFLsLCCYLRLVSAEGDPIPEELYEMLSDHSIRSFDDLQRLRHgDpgEEDGAEL
PDGF1_peptide -----
Mouse_Pdgfb MNRCWALFLpLCCYLRLVSAEGDPIPEELYEMLSDHSIRSFDDLQRLRHrDsvDEDGAEL
PDGF2_peptide -----

Human_PDGFNP_002599.1 DLNMTRSHSGgELES1ARGRRSLGSLtiAEPAMIAECKTRTEVFQISRrLIDRTNANFLV
PDGF1_peptide -----
Mouse_Pdgfb DLNMTRAHSGvELESsSRGRRSLGSLaaAEPAVIAECKTRTEVFQISRnLIDRTNANFLV
PDGF2_peptide -----LIDRTNANFLI-----

Human_PDGFNP_002599.1 WPPCVEVQRCSGCCNNRNVQCRpTQVQLRPVQVRKIEIVRKKPIFKKATVTLEDHLACKC
PDGF1_peptide -----KIEIVRKKPIF-----
Mouse_Pdgfb WPPCVEVQRCSGCCNNRNVQCRaSQVQMRPVQVRKIEIVRKKPIFKKATVTLEDHLACKC
PDGF2_peptide -----

Human_PDGFNP_002599.1 ETVaaaRPVTRSPGgSQEQRAKTPQtRVTIRTVRRRPPKPKHRKFKHDKtALKETLGA
PDGF1_peptide -----
Mouse_Pdgfb ETVvtpRPVTRSPGtSREQRAKTPQaRVTIRTVRIIRPPKPKHRKFKHDKaALKETLGA
PDGF2_peptide -----

Human_PDGFNP_002599.1 A
PDGF1_peptide -
Mouse_Pdgfb A
PDGF2_peptide -

Supplementary Figure S9. Sequence alignment of mouse and human PDGFB proteins and the PDGF1 and PDGF2 peptides. The sequence alignment was carried out using the MUSCLE program.^{S1}

Supplementary Table S1. High-performance liquid chromatography analysis of compounds

Compound	Retention Time (min)	Purity (%)
PDGF1	4.47	97.8
PDGF2	4.76	98.2
PDGF2-HTT	5.57	98.6

The purity of the peptides was verified by analytical UPLC with Nexera X2 (Schimadzu) on the C8 Kinetex 2.6 μ m 100 Å column (2.1 \times 100 mm; Phenomenex). The following eluents were used: A=0.1% TFA in water and B=0.1% TFA and 80% ACN in H₂O. The flow rate was 0.5 mL/min, and UV detection at λ =223 nm was performed. A linear gradient of 5 \rightarrow 100% B over 15 min was used. The percentage purity of peptides was determined as the % of area under the peak.

ACN, acetonitrile; HTT, head-to-tail cyclization methodology; PDGF, platelet-derived growth factor; TFA, trifluoroacetic acid.

Supplementary Table S2. Quantitative PCR primers

Gene	Forward/Reverse	Sequence
ACTB	Forward	CATGGGTCAGAAGGATTCT
ACTB	Reverse	ACACGCAGCTCATTGTAGAA
CDKN1A	Forward	CTGGCACCTCACCTGCTCTG
CDKN1A	Reverse	CGGATTAGGCTTCCTCTTGG
MYC	Forward	ATAGCAGCGGGCGGGCA
MYC	Reverse	CGAGGTCATAGTTCCTGTGGT
POU5F1	Forward	TCAGCCACATCGCCCA
POU5F1	Reverse	AGACCCAGCAGCCTCAA
TBP	Forward	TCCACAGTAATCTTGGTTGTA
TBP	Reverse	CACCATTTTCCCAGAACTGA
TGFB3	Forward	CGTGAGTGGCTGTTGAGAAG
TGFB3	Reverse	GATTAGATGAGGTTGTGGTGA
TP53	Forward	GCTTTGAGGTGCGTGTGGT
TP53	Reverse	AGTGGTTCTCTTTGGCTGGG
KIT	Forward	CTGCGTTCTGCTCCTACTGCTT
KIT	Reverse	CCTGGATGGATGGATGGT