

	Signal peptide	
TKDP4	--MNRLCLSAALLLLLVILVDS	TPVYEHTQDQGLETSHGRRLEKRSVTDLISAFMDAMV 58
TKDP5	MKMSRLCLSAALLFLPVILVDS	TPVYEQNTQDQGLV----- 36
TKDP3	--MNRLCLSAALLFLLVILVDS	TLVNIHHIQDEGLETSHRRGPKKHSTKDMIKNIIRGVA 58
TKDP1	--MRQLCLSSALLFLLVILVDS	TPLNIHHIQDEGVETSHRRGPEKRSVIDVVTSIIDGVA 58
TKDP2	--MSRLCLSAALLFLLVILVDS	TPVYEHTQDQGLETSHRRGPEKRSIIDVISHVIDGVV 58
PTI	MKMSRLCLSVALLVLLGTLAASTP	----- 24
STI	MKMSRLCLSIALLVLLGTLAASTP	----- 24
CTI	--MKLSCLLALCLTPCLVGLASSGE	----- 23
SPINT4	--MKLIELGLLGLFTSLLTTPLMG	----- 23
	* * *	
TKDP4	I V AELLKG-----	66
TKDP5	-----	
TKDP3	T G AKIANAGSGF-----	70
TKDP1	T G TKIVKNGAGLLTGLAEIITKAIK G VMISRIQFD N HTQEELPTLNIEYSTLSEENK G V	118
TKDP2	K G TKIFHG-----	66
PTI	-----	
STI	-----	
CTI	-----	
SPINT4	-----	
TKDP4	-----	
TKDP5	-----	
TKDP3	-----	
TKDP1	ETSHRK G PEKRSVIDVVTSIIDGVAT G TKIVTKGASILTGLAEIINKAIR G VMISRIQF	178
TKDP2	-----	
PTI	-----	
STI	-----	
CTI	-----	
SPINT4	-----	
TKDP4	-----	
TKDP5	-----	
TKDP3	-----	
TKDP1	N HTLEEFPKLNIEYSTLSEDNT G VETSRRRGPEKRSVIDVVTSIIDGVAT G TKIVK K G	238
TKDP2	-----	
PTI	-----	
STI	-----	
CTI	-----	
SPINT4	-----	
	Kunitz domain-encoding exon	
TKDP4	--VGFD E LKGLPQ T MSQMMISGRQLENH A VEVFPTQ-----TLREENK A DSKPA F CLE P K	119
TKDP5	-----MISG K QLEKRSVKELPTA-----VLQ E ENK A TSRPA F CLE H K	73
TKDP3	--IREVV K AMREG N K G HVK T SGAQL K N HTVEESPTFNTQQLILSEK N K A DSRPA F CLE P K	128
TKDP1	SIL T GLAEIINKA I K G VMISGIQ F N HTLE E YQTLKIEYSALNEEN K AASKPALC L EP K	298
TKDP2	--LKGLADII S NGIQ G VMISGTQ L E N HTVEEFL T QIL K H-----AASKPE F CME P E	116
PTI	-----GCDTS N Q A K-----AQR P DFC L EP P	44
STI	-----GCDTS N Q A K-----AQR P DFC L EP P	44
CTI	-----TSD N LKQ E ASQ D -----LFQ T PPD L CQ L PQ	48
SPINT4	-----GMTQITDMI-----CKK F K D RCK M PL	44
	▲▲▲▲ ▲ Ti site * BPTI KUNITZ 2 (PS50279) BPTI KUNITZ 1 (PS00280)	
TKDP4	VTGHSKSSWPRYFYNA E T G H C EQFTYGG L GGN K NNF I TE E E C M K T C GQ G AG S I R EHAK S G	179
TKDP5	FSG P C IT P EIRYFYNA K T G H C EHFIY G C NG K KNNFL T E E D C I K T C GQ G AG S P-----	126
TKDP3	VVG H GT K M P RYFYDA K T G H C EPFY G SLGGN K NNFL T IE D C M K T C GQ G AG S I-----	181
TKDP1	VTG G C NA V MTRYFYNAQ N GL C EQFVY D C EGN G NNF E K L E D C M K T C SQ E AG S I-----	351
TKDP2	LKG P C KD M TRYFYNA K TRY C EPFVY G C EGN K NNF Q TL S H C IV T C CPVP V TM-----	169
PTI	YTGP C KAKMIRYFYNA K AG F C ETFVY G C AK S NNF R SA E D C M R T C GGAIG P E N L ----	100
STI	YTGP C KAKMIRYFYNA K AG F C ETFVY G C AK S NNF R SA E D C M R T C GGAIG P E N L ----	100
CTI	ARG P C K A ALLRYFY N ST S SA C EPFY G C Q G N D NNF E TT E M C L R I C Q P P E T E D K S-----	103
SPINT4	N F GS C Y D IO F RYFY N IT S GL C ESFVY T G C D G N L NNY R L K I E C OM T C E K Y I K ER-----	98
	* P-P ****: *: * * . : : **: * *	
TKDP4	PQ K P 183	
TKDP5	----	
TKDP3	----	
TKDP1	----	
TKDP2	----	
PTI	----	
STI	----	
CTI	----	
SPINT4	----	

Additional file 7 - Figure S4. Alignment of the bovine CTI, PTI, STI, TKDP1-5 and SPINT4 precursor proteins