

## Supplementary Materials

<b>Kunitz_Lyd_34901 Frame 1: 93 aa</b>				
1	ATG TGG AAA ATT CTA TTC TTA TTT ACA TTA ATT ACA ATT TCT ATT	45		
1	Met Trp Lys Ile Leu Phe Leu Phe Thr Leu Ile Thr Ile Ser Ile	15		
46	GCA AAT GAT GAT CAA CAA GCT GAA GAA ACA CAA TTT ACA CTA AAT	90		
16	Ala Asn Asp Asp Gln Gln Ala Glu Glu Thr Gln Phe Thr Leu Asn	30		
91	GAT TGT AAA GAA GGT GCA GAA AAG AAC GAT AAA CAA CGT TGT CTA	135		
31	Asp Cys Lys Glu Gly Ala Glu Lys Asn Asp Lys Gln Arg Cys Leu	45		
136	GCT TAT TTC CGT GTC TAT AAT TGG AAT AAT GAA AAA CAA GCA TGC	180		
46	Ala Tyr Phe Arg Val Tyr Asn Trp Asn Asn Glu Lys Gln Ala Cys	60		
181	GAA CAA GTT ATC TAT GGT GGT TGT CAC AAA ACT CAC AAT AAT TTC	225		
61	Glu Gln Val Ile Tyr Gly Gly Cys His Lys Thr His Asn Asn Phe	75		
226	CAA ACA TTT GAA GAT TGT GAG AAA ATC GCT AAA CCG ATT TGT ACA	270		
76	Gln Thr Phe Glu Asp Cys Glu Lys Ile Ala Lys Pro Ile Cys Thr	90		
271	CAA AAA AAT TAA	282		
91	Gln Lys Asn End	94		
<b>Kunitz_Myl_37778 Frame 1:87 aa</b>				
1	ATG ATG AAA ATT TGC TTT CTG TTA TCA GTT TTA ATA ATT TCA ACA	45		
1	Met Met Lys Ile Cys Phe Leu Leu Ser Val Leu Ile Ile Ser Thr	15		
46	TTC GCT GAT AGT TCA GAA ATA GAA TTC ACC AAA GAA GAT TGT ACT	90		
16	Phe Ala Asp Ser Ser Glu Ile Glu Phe Thr Lys Glu Asp Cys Thr	30		
91	AAA GAT GTT CAA TTT GGC GAC ATT AGT TGT CTG GCT TTA ACT CCC	135		
31	Lys Asp Val Gln Phe Gly Asp Ile Ser Cys Leu Ala Leu Thr Pro	45		
136	GTT TAT CAT TAT AAT CAC ATA ACA AAA GAG TGT GAG AAT AAG AAT	180		
46	Val Tyr His Tyr Asn His Ile Thr Lys Glu Cys Glu Asn Lys Asn	60		
181	TAT GGT GGA TGT AAT GCT AGC AAC AAT AAT TTC GCT ACG AAA GAA	225		
61	Tyr Gly Gly Cys Asn Ala Ser Asn Asn Asn Phe Ala Thr Lys Glu	75		
226	CAG TGC GAG AAA ATC GCA TTT CCA GTT TGT CGA TCA TAA	264		
76	Gln Cys Glu Lys Ile Ala Phe Pro Val Cys Arg Ser End	88		
<b>Kunitz_Lyd_46461 Frame 1: 79 aa</b>				
1	ATG TTT AAT AAT AGC TIG AAT AAC ATT ATT ATT ATT ATT TTT	45		
1	Met Phe Asn Asn Ser Leu Asn Asn Ile Ile Ile Ile Ile Phe	15		
46	GTA GAT TGT AAC GAA GGT GCA GAA AAG AAC GAT AAA CAA CGT TGT	90		
16	Val Asp Cys Asn Glu Gly Ala Glu Lys Asn Asp Lys Gln Arg Cys	30		
91	CTA GCT TAT TTC CGT GTC TAT AAT TGG AAT AAT GAA AAA CAA GCA	135		
31	Leu Ala Tyr Phe Arg Val Tyr Asn Trp Asn Asn Glu Lys Gln Ala	45		
136	TGC GAA CAA GTT ATC TAT GGT GGT TGT CAC AAA ACT CAC AAT AAT	180		
46	Cys Glu Gln Val Ile Tyr Gly Gly Cys His Lys Thr His Asn Asn	60		
181	TTC CAA ACA TTT GAA GAT TGT GAG AAA ATC GCT AAA CCG ATT TGT	225		
61	Phe Gln Thr Phe Glu Asp Cys Glu Lys Ile Ala Lys Pro Ile Cys	75		
226	ACA CAA AAA AAT TAA	240		
76	Thr Gln Lys Asn End	80		

Figure S1. Transcript and protein sequence from three sequenced clones with Leu at P1 site. Yellow, leader peptide sequence; blue, Cys residues involved in disulphide bridges; green, P1 residue.



Figure S2. Alignment of Kunitz domain sequences from insects; green, Kunitz family signature sequence; blue, P1 site; red, Cys involved in disulphide bridges. \* (asterisk) indicates positions which have a single, fully conserved residue; : (colon) indicates conservation between groups of strongly similar properties.