



**Supplementary figure 1.** MALDI TOF/TOF MS analysis of two selected ions with  $m/z$  1247.6 (A) and  $m/z$  942.6 (B) found in extract from *dimm* (*c929*)-GAL4 enriched cells. Complementary sequence information resulting from ion fragmentation with retention of charge at the N-terminal (b-ions) or C-terminal (y-ions) side of the peptide bond were found showing an almost complete series for the  $m/z$  1247.6 ion. The amino acid sequence deduced is consistent with that of Dromyosuppressin. The tandem mass spectrum obtained from the precursor ion at  $m/z$  942.6 contains 3 b-ions consistent with the sequence of Tachykinin-like peptide. The fragments are labeled according to the nomenclature of Biemann<sup>97</sup>.

**Supplementary table 1.** The theoretical and observed monoisotopic m/z ratios of protonated peptides [M+H]<sup>+</sup> identified in adult *Drosophila melanogaster* brain extract by on-line LC-ESI-Q-TOF CID tandem MS and/or off-line HPLC accurate mass MALDI-FTMS measurement.

Peptide sequence <sup>a</sup>	ESI-Q-TOF MS						MALDI-FTMS <sup>c</sup>
	LC retention time (min)	Precursor ions		Monoisotopic Mass of [M+H] <sup>+</sup> ion		Mascot Score or PepSeq identification <sup>b</sup>	
		m/z	charge state	Measured m/z	Theoretical m/z		
DQWQKLHGGWa	n/d	n/d	n/d	n/d	n/d	-	+
pQTFQYSRGWTNa	n/d	n/d	n/d	n/d	n/d	-	+
AAMDRYa	31.64	725.41	1	725.42	725.34	PepSeq	n/d
PQRLRWa	23.44	854.51	1	854.51	854.51	PepSeq	n/d
LPVYNFGLa	34.10	921.55	1	921.55	921.52	PepSeq	n/d
SVPFKPRLa	23.79	942.69	1	942.70	942.59	PepSeq	n/d
APNGFLGMRa	35.19	481.14	2	961.51	961.27	PepSeq	+
SPSLRLRFa	27.32	487.81	2	974.61	974.59	PepSeq	+
KPMRLRWa	20.79	985.41	1	985.41	985.59	PepSeq	n/d
SAPQDFVRSa	35.44	503.23	2	1005.45	1005.55	PepSeq	n/d
PKQDFMRFa	28.59	534.33	2	1067.65	1067.62	PepSeq	n/d
APVNSFVGMRa	25.82	538.85	2	1076.69	1076.57	PepSeq	+
TDVDHVFLR	26.32	551.32	2	1101.64	1101.57	30	n/d
TPAEDFMRFa	36.95	556.69	2	1112.37	1112.52	24.6	n/d
pQLTFSPDWGK	35.05	1161.53	1	1161.53	1161.56	PepSeq	+
DPKQDFMRFa	30.11	591.73	2	1182.45	1182.57	PepSeq	n/d
FDDYGHMRFa	27.91	593.74	2	1186.46	1186.51	55	n/d
FDDYGHMoRFa	23.92	601.79	2	1202.58	1202.51	PepSeq	n/d
WFGDVNQKPI	31.88	602.26	2	1203.52	1203.62	PepSeq	+
SDPDMLNSIVE	28.51	1219.61	1	1219.62	1219.55	PepSeq	n/d
TDVDHVFLRFa	29.68	624.32	2	1247.64	1247.66	74	+
LTKAQGDFNEF	28.25	635.31	2	1269.60	1269.61	PepSeq	n/d
TTRPQPFNFGLa	30.10	638.88	2	1276.76	1276.68	PepSeq	+
FAQYRPTSYSA	25.39	645.71	2	1290.42	1290.61	PepSeq	n/d
YIGSLARAGGLMT	31.35	655.31	2	1309.62	1309.70	PepSeq	n/d
YRKPPFNGSIFa	29.66	662.89	2	1324.77	1324.72	20	n/d
AYRKPPFNGSIFa	29.72	698.41	2	1395.81	1395.76	-	+
NLGALKSSPVHGVQ	24.42	703.9	2	1406.80	1406.78	47	n/d
SVAALAAQGLLNAPK	33.62	712.43	2	1423.85	1423.83	70	+
GPSASSGLWFGPRLa	35.03	715.93	2	1430.86	1430.76	62	+
YIGSLARAGGLMTYa	28.54	736.32	2	1471.63	1471.78	20	n/d
YLRSPTYGNVNEL	29.68	763.24	2	1525.48	1525.77	PepSeq	n/d
TGPSASSGLWFGPRLa	45.77	766.43	2	1531.86	1531.80	-	+
NLGALKSSPVHGVQQ	24.17	767.95	2	1534.89	1534.84	47	n/d
RQAQGWNKFRGAWa	43.15	802.48	2	1603.95	1603.84	-	+
NVGTLARDFQLPIPNa	36.63	827.53	2	1654.06	1653.91	PepSeq	+
GGDDQFDDYGHMRFa	29.69	829.93	2	1658.46	1658.67	53	n/d
GTVLIQTDNTQYIRTa	28.56	861.36	2	1721.71	1721.92	PepSeq	n/d
NSVVLGKQRFHSHWGa	37.51	871.61	2	1742.21	1741.96	PepSeq	n/d
EESNPAQEFLTKAQGDF	37.26	955.91	2	1910.81	1910.88	PepSeq	n/d
NSELINSLSLPKNMNDAa	38.16	986.53	2	1972.02	1972.06	PepSeq	n/d
EESNPAQEFLTKAQGDFNEF	40.03	1150.85	2	2300.70	2301.03	PepSeq	n/d

<sup>a</sup>Previously unreported peptides and fragments are labeled in boldface; <sup>b</sup>Peptide identifications were made either with Mascot Search (scores are provided), manual and automatic matching using PepSeq, or exact mass measurements with FTMS (indicated by -); <sup>c</sup> +: detected in extract; n/d: not detected.

**Supplementary table 2.** The theoretical and observed monoisotopic m/z values of protonated peptides identified using MALDI-TOF MS analysis of extract or acetylated extract enriched from adult *D. melanogaster* expressing either *dim* (*c929*)-GAL4 or *Ddc*-GAL4 with UAS-*mCD8-GFP*.

Predicted peptide sequence	Calculated mass of [M+H] <sup>+</sup> ion <sup>a</sup>	Observed mass of [M+H] <sup>+</sup> ion			
		<i>dim</i> - GAL4 enriched cells	<i>Ddc</i> - GAL4 enriched cells	<i>dim</i> - GAL4 acetylated extract	<i>Ddc</i> - GAL4 acetylated extract
SRPYSFGLa	925.49	925.83		967.68	
SVPFKPRLa	942.59	942.72	942.98	1026.76	1082.04
APLAFVGLRa	942.59	942.72	942.98	984.80	984.94
PFCNAFTGCa	958.39	958.37			
APNGFLGMRa	961.50	961.91		1002.92	
SPSLRLRFa	974.59	974.65	974.93	1016.76	1016.97
KPQRLRWa	982.61	982.60	982.91	1066.80	1066.03
KPMRLRWa	985.59	985.64	985.96	1069.80	1069.96
APTSSFIGMR	1065.55	1065.81	1065.79	1107.71	1107.91
APVNSFVGMRa	1076.58	1076.72			
DPKQDFMRFa	1182.57	1182.61	1182.62	1266.67	1266.93
TDVDHVFLRFa	1247.65	1247.62	1247.64	1289.78	1289.99
TTRPQPFNGLa	1276.68	1276.61	1276.57	1318.82	1319.01
FDDyGHmRFa	1282.47	1282.64	1282.53	1324.79	1324.99
GANMGLYAFPRFa	1294.67	1294.60			
AQRSPSLRLRFa	1329.79	1329.69		1371.90	
qTFQYSRGWNa	1369.63	1369.56		1369.73	
AYRKPPFNGSIFa	1395.75	1395.68	1395.42	1479.85	1480.11
SVAALAAQGLLNAPK-OH	1423.84	1423.72		1507.92	
GPSASSGLWFGPRLa	1430.75	1430.62		1472.87	
YIGSLARAGGLMTYa	1471.77	1471.66	1471.28	1513.83	1514.10
TGPSASSGLWFGPRLa	1531.80	1532.04		1574.82	
RQAQGWNKFRGAWa	1603.84	1603.74	1603.15	1687.96	1688.17
NVGTLARDFQLPIPNa	1653.91	1653.73	1653.14	1695.92	1696.21
IDLSRLYGHMANPIV-OH	1698.90	1698.87	1699.07	1740.90	1741.18
GGDDQFDDyGHMRF	1738.63	1738.40		1780.91	
qVRYRQCYFNPISCF-OH	1906.87	1904.56 <sup>^</sup>	1904.58 <sup>^</sup>	1904.84 <sup>^</sup>	1905.16 <sup>^</sup>
QVRYRQCYFNPISCF-OH	1923.90	1921.58 <sup>^</sup>	1921.62 <sup>^</sup>	1963.88 <sup>^</sup>	1964.14 <sup>^</sup>
NSELINSLLSLPKNMNDa	1972.02	1971.86	1972.02	*	*

<sup>a</sup>Monoisotopic mass. m: oxidized Met residue; q: pyroglutamic acid; y: sulfated Tyr; <sup>^</sup>: The difference of 2 Da between the theoretical and observed m/z values is accounted for by the presence of a disulfide bond formed between the Cys residues; \*: neither the original nor the derivatized form of the ion was observed following acetylation.

**Supplementary table 3.** The theoretical and observed monoisotopic  $m/z$  values of protonated peptides found in the extract from the *dimm (c929)*-GAL4 line using off-line HPLC MALDI FTMS analysis.

Peptide sequence	Monoisotopic mass	
	Calculated mass of [M+H] <sup>+</sup> ion	Observed mass of [M+H] <sup>+</sup> ion
SPSLRLRFa	974.59	974.55
DPKQDFMRFa	1182.57	1182.55
TDVDHVFLRFa	1247.65	1247.64
TTRPQPFNFGLa	1276.68	1276.68
AYRKPPFNGSIFa	1395.75	1395.77
GPSASSGLWFGPRLa	1430.75	1430.78
YIGSLARAGGLMTYa	1471.77	1471.79
TGPSASSGLWFGPRLa	1531.80	1531.85
NVGTLARDFQLPIPNa	1653.91	1653.96