

Supplementary Table 1: Matrix effect for each peptide at two concentrations for an on-line SPE coupled with an LC-MS/MS method using a 4000 Triple Quad. (Six general functions: RF: Female reproduction; RM: male reproduction; I: Immunology; RH: Hormonal regulation; BM: General biomarker and Molting).

Protein name (type) – ID	Target peptide sequence	Matrix effect In %	
		QC 1 (250 ng/mL)	QC 3 (2500 ng/mL)
Vitellogenin (RF) - 64	HIEIFSPITK	4	1.9
Hemolymph clottable protein (RF) - 276	HAEFSVNPPLDSTQAV K	-2.3	5.1
	IYPAEALTIVIEK	-3.7	-5.6
Transglutaminase (RM/I) - 1917	GTLAVIPVQNR	2.5	2.6
Copine-8 (RM) - 2308	EVLEELPAQYMEFTR	6.7	8.2
Prophenoloxidase (RM/I) - 2562	APILEGYFSK	-2	-1.8
	GIDIIGDAFEADR	4.4	-2.3
	ATQPSYTVAQLELPGV NITR	-12.2	-8.7
	GIDFGTTQSVR	7.1	8.3
Ca transport ATPase sarcoplasmic/endoplasmic reticulum type-like isoform 1 (RM) - 4227	KAEIGIAMGSGTAVAK	-3.6	1.1
	LLEFEITGSTYEPDGVF LGGQR	-	-1.9
Transglutaminase (RM/I) - 7169	VLAVDILAK	-3.9	8.5
Hemolectin (I) - 11145	VEC[CAM]IAGFILPLEF K	1.6	0.9
Chitinase (Mue) - 12415	GGQWFGYDDISMIR	4.6	-1.6
Prophenoloxidase (RM/I) - 15561	IVIDLQQTVAQLR	-	-2.2
Clottable protein 2 (RF) – 17046	IATGMQSALPEYAGTG IK	5.3	4.2
	IFNVLQPIAESK	-3.8	-3.3

Protein name (type) – ID	Target peptide sequence	Matrix effect In %	
		QC 1 (250 ng/mL)	QC 3 (2500 ng/mL)
	ITMQEDGSGEVQLK	2.5	1.5
	TSEVFLPLTNELYQQTK	4.1	1.5
Copine-8 (RM) - 18473	KFLPSSGVDDLIK	-3.4	-1.1
	SYQILLITNGGLSDIDATKK	2.9	7.6
Epididymal sperm-binding protein 1 (RM) - 18609	VLSVVQNIITR	-2.2	-2.6
Na/K-ATPase a1 subunit (BM) - 32234	FVGLISLIDPPR	-1.6	2.2
	NLAFFSTNAVEGTAR	5.4	4.8
Copine-8 (RM) - 34845	AVAEIVQDYDSDGFFPALGFGGK	5.3	2.1
Clotting protein precursor (RF) - 39606	ISPLINSPDLPK	4.5	4.2
	NLPADQAAALASSDPDYAIR	-2.4	-2.1
Cytochrome P450 enzyme, CYP4C39 (Mue) - 100255	ILEDFVDVFNR	5.1	-1
	VYAEVIEVAGSGPIGLDQLR	2.5	1.6
Hemolectin (I) - 109695	NAGPVLLPSNTSPVLR	6.2	7.4
Na+/K+ ATPase (BM) - 110907	LGAIVAVTGDGVNDSPALK	-3.6	-1.2
	VIMVTGDHPITAK	4.5	8.5
Catalase (BM) - 110912	ADPALGQAIQER	-5.8	-5.2
	LADNIAGHVINTQEFIR	4.7	-1.4
Cytochrome P450 CYP12A2 (Mue) - 122081	FNNNLINTR	-5.3	-4
	TLEELSNEALR	-2.8	5
Farnesoic acid O-methyltransferase (RH) - 134275	EVFIGGWSNQNSAIR	11.7	9.1
Glutathion S transférase (BM) - 142711	LSAWLAAC[CAM]K	6.9	3.7

Protein name (type) – ID	Target peptide sequence	Matrix effect In %	
		QC 1 (250 ng/mL)	QC 3 (2500 ng/mL)
JHE-like carboxylesterase 1 (RH) - 144144	AFWGSPLR	16.6	7.7
	ILTTMWADFAR	-2.3	-0.8
	EFWIATDHNEVR	6.9	3.3
	LVLGTATYGR	3.9	6.3
Vitellogenin (RF) - 200426	ELTSAAEVVSSLLK	-1.3	-1.1
	TLGALELDVFSEAGK	2.8	1.2
Clotting protein precursor (RF) - 206469	AAIETAFVNHLK	-3.2	-4.1
Cellulase (BM) - 213317	ELDFADAHR	12.7	-3.5