Table S1 - Peptide masses used for analysis from hibernation factors and bL31 & bL36 paralogs

Protein Name	Peptide Sequence	Ion Charge[a]	m/z (unlabeled)[a]	m/z (heavy labeled)[a]	m/z (medium-heavy labeled)[a]
bL31A	STVGHDLNLDVCSK	2	772.8723	776.8794	774.8849
	CHPFFTGK	2	497.2342	501.2413	499.2467
	VDRFNK	2	389.7139	398.7252	394.7366
	VDRFNKR	2	467.7645	481.7799	475.7972
bL31B	TVVFHDTSVDEYFK	3	562.9385	565.6099	564.2802
	IGSTIKTDREIELDGVTYPYVTIDVSSK	3	1033.8747	1042.5536	1038.5648
	TDREIELDGVTYPYVTIDVSSK	3	834.0866	840.0941	837.4350
	SHPFYTGK	2	468.7323	472.7394	470.7449
	LRTVASEGNVAR	2	636.8546	646.8628	642.8747
	TVASEGNVAR	2	502.2620	507.2661	505.2721
bL36A	VICSAEPK	2	452.2339	456.2410	454.2464
bL36B	VLNSLR	2	351.2189	356.2230	354.2289
	ERHPDCQIVKR	4	360.1899	367.1976	364.2063
Rmf	GYQAGIAGR	2	446.7354		
Hpf	LEQYFDR	2	485.7351		
	INQVYVVLK	2	538.3291		
Sra	HILGLDHK	2	466.7693		*
	KIVTEGDKSSVVNNPTGR	2	951.0080		
	IVTEGDKSSVVNNPTGR	2	886.9605		
RaiA	LAKLEK	2	351.2314		
	WQTHLINPHIILSK	2	850.4858		
	RAATSVKDANFVEEVEEE	2	1011.9844		
	AATSVKDANFVEEVEEE	2	933.9338		

Footnotes:

a) Ion charge and peptide m/z values are for precursor MS1 particles

* For proteins Hpf, Rmf, Sra, RaiA heavy and medium-heavy labeled peptide were not indentified/determined