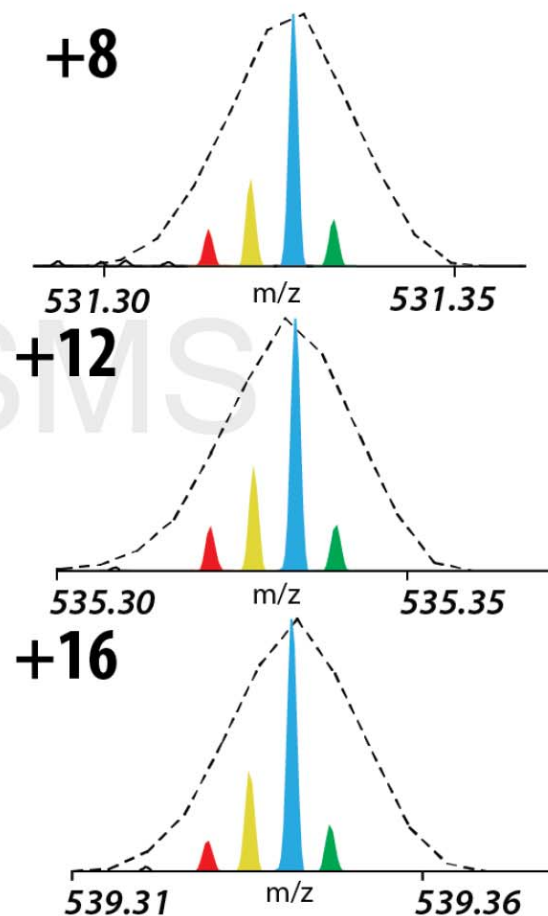
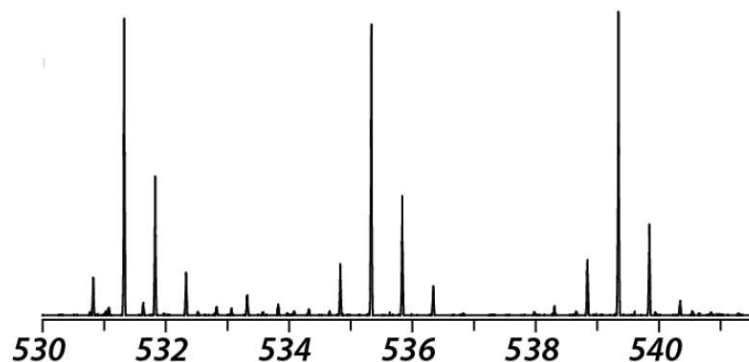
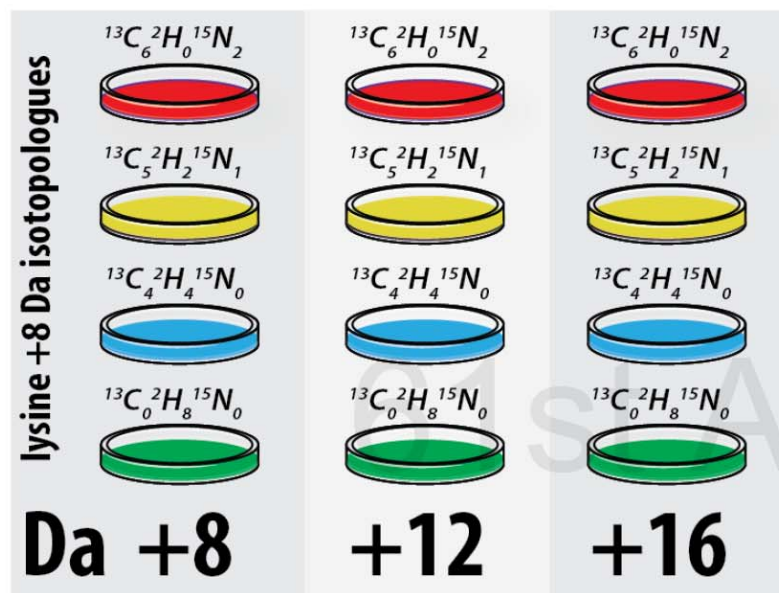
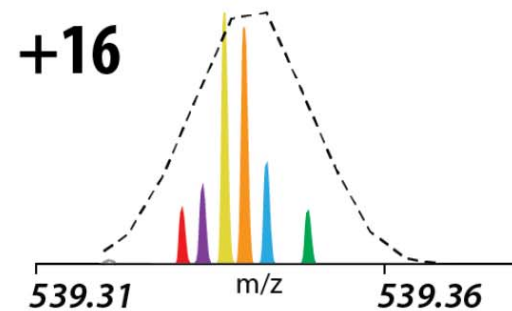
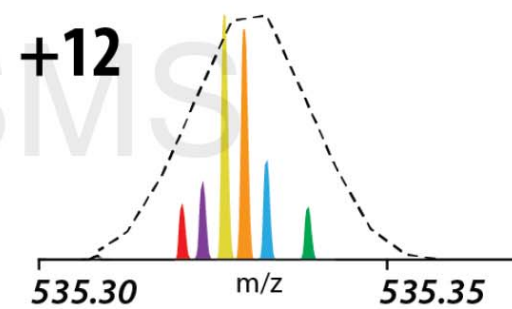
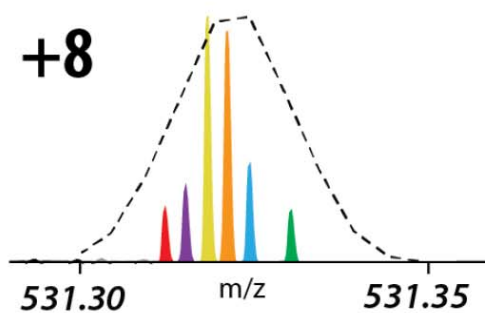
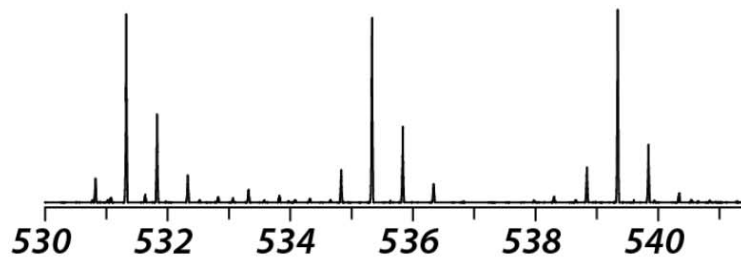
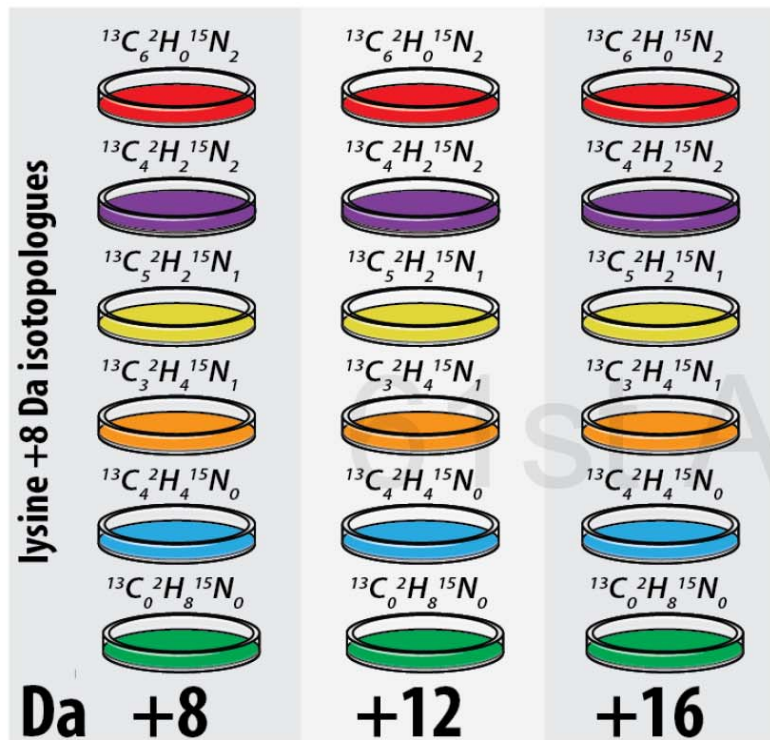


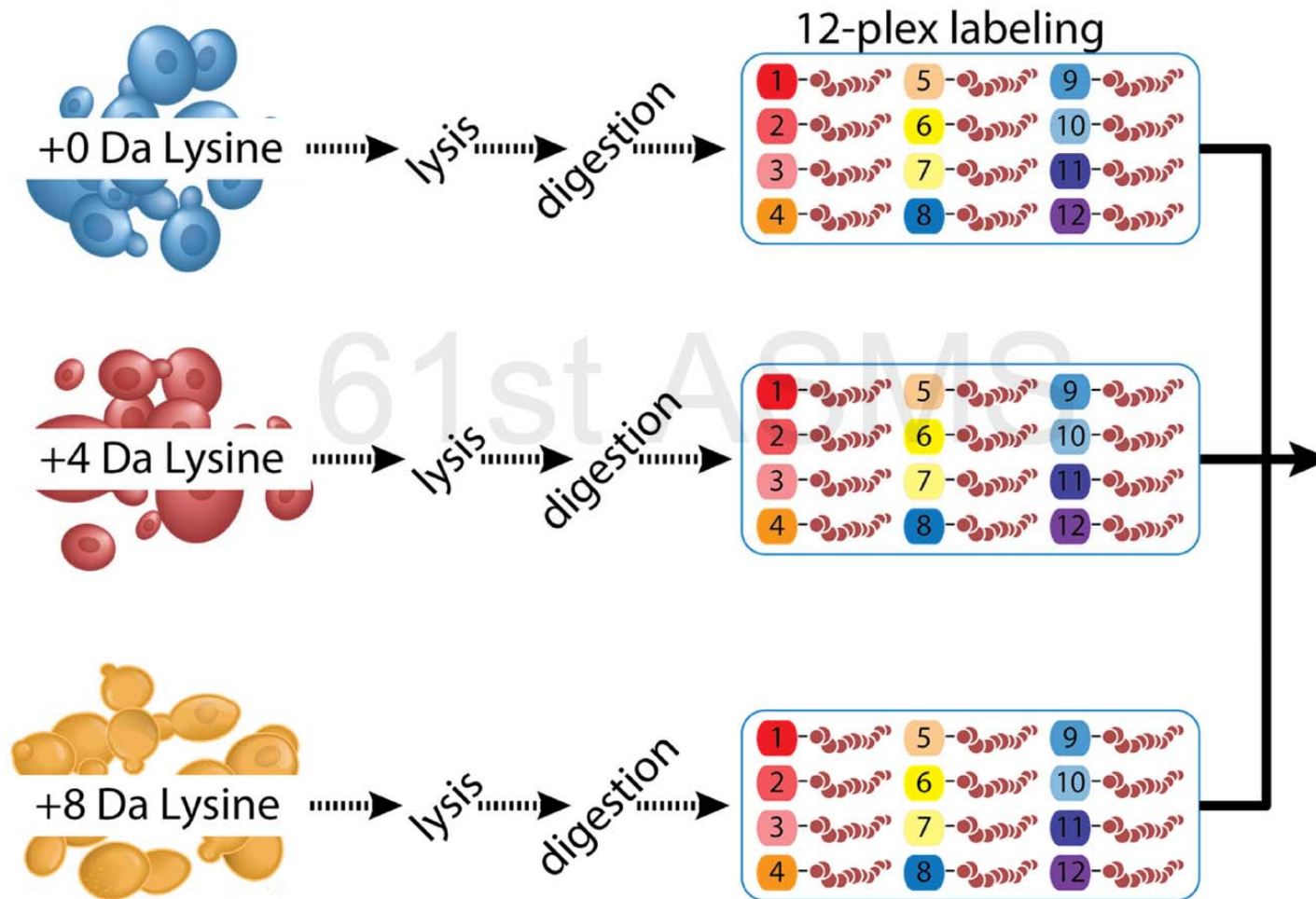
4 → 12-plex NeuCode SILAC Method

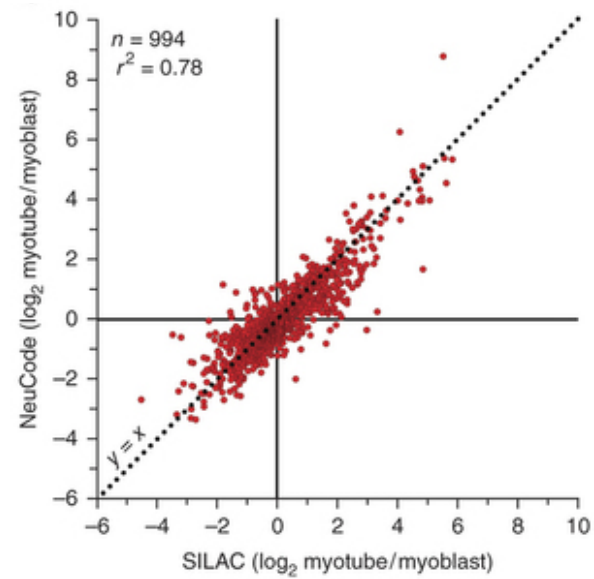
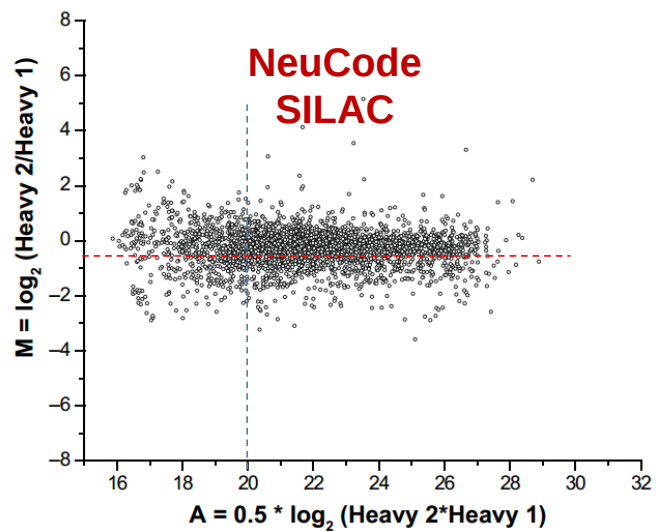
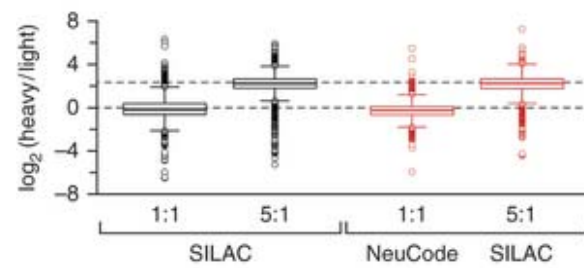
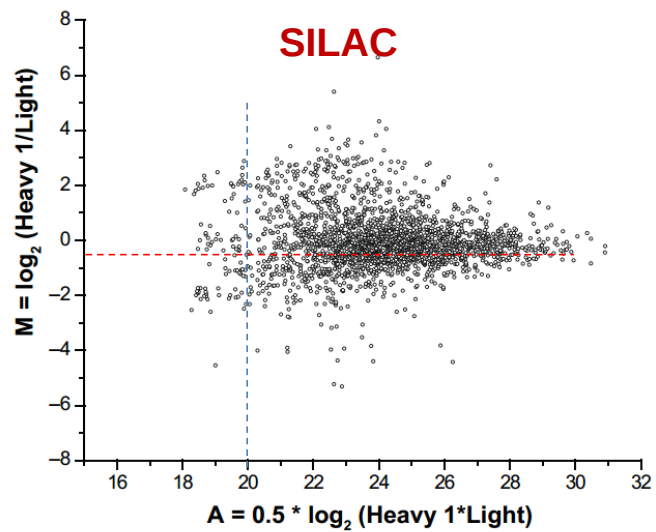


6 → 18-plex NeuCode SILAC Method

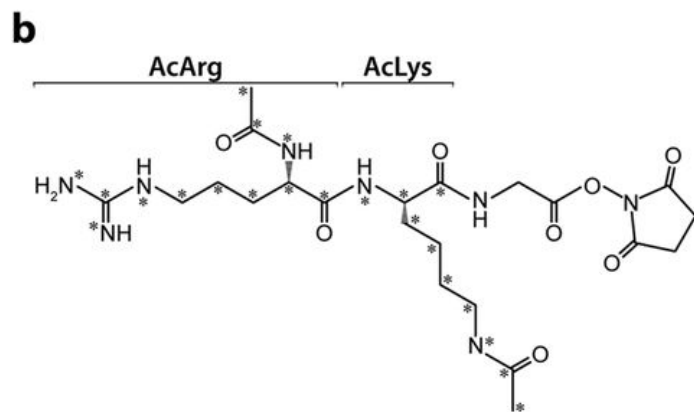
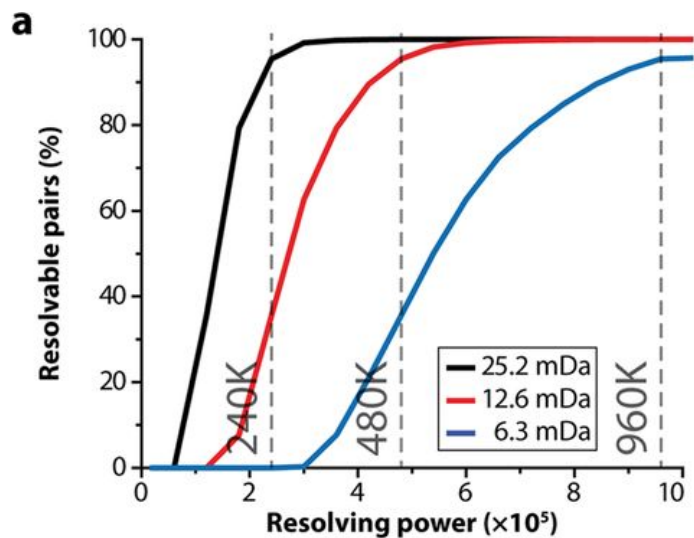


36-plex



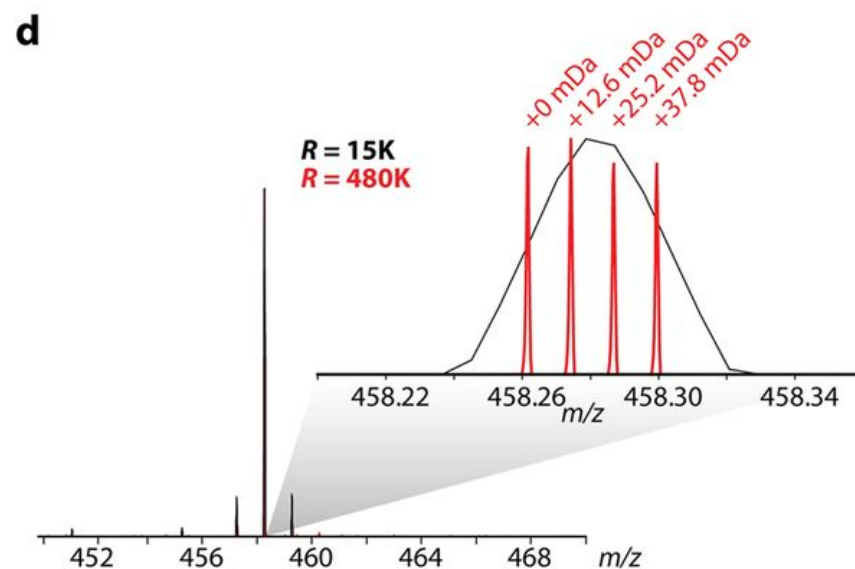


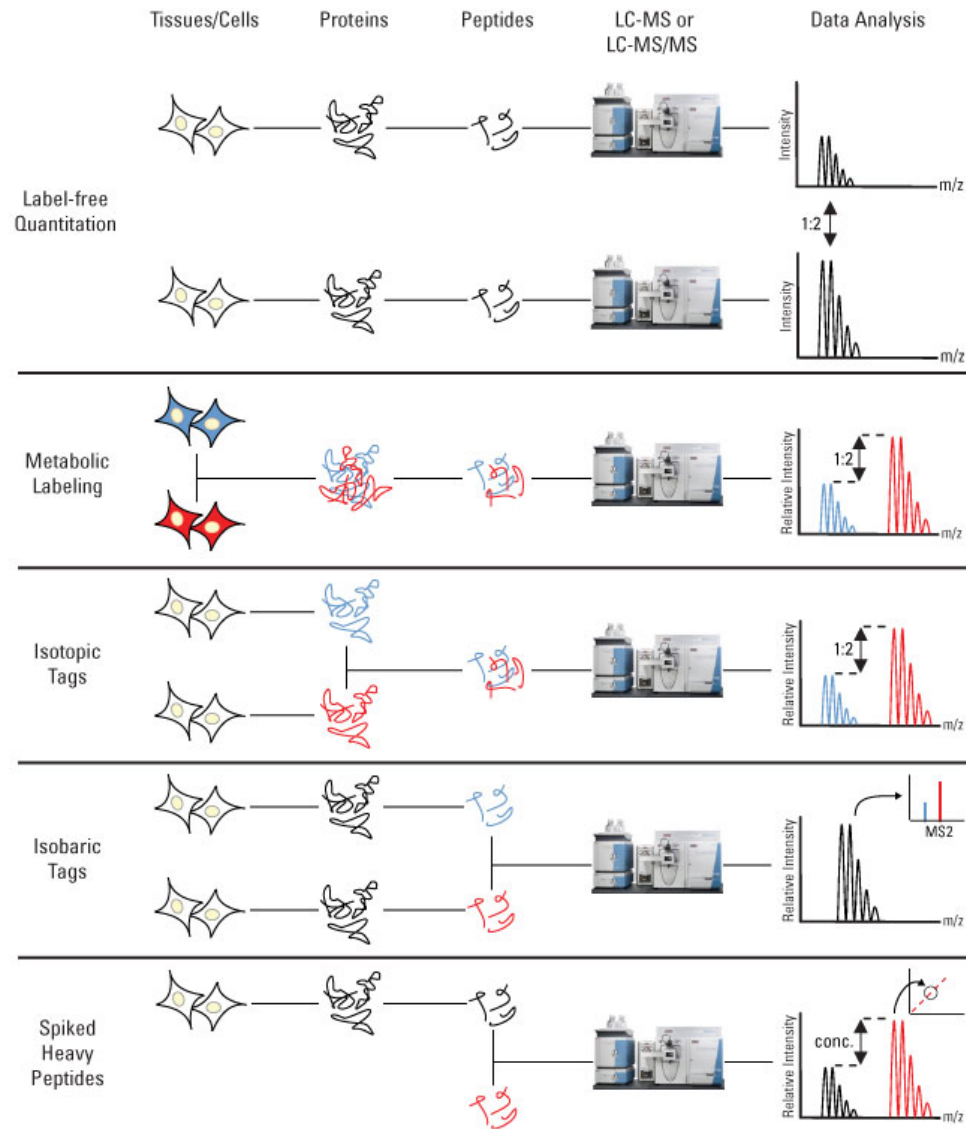
Neucode chemical labeling

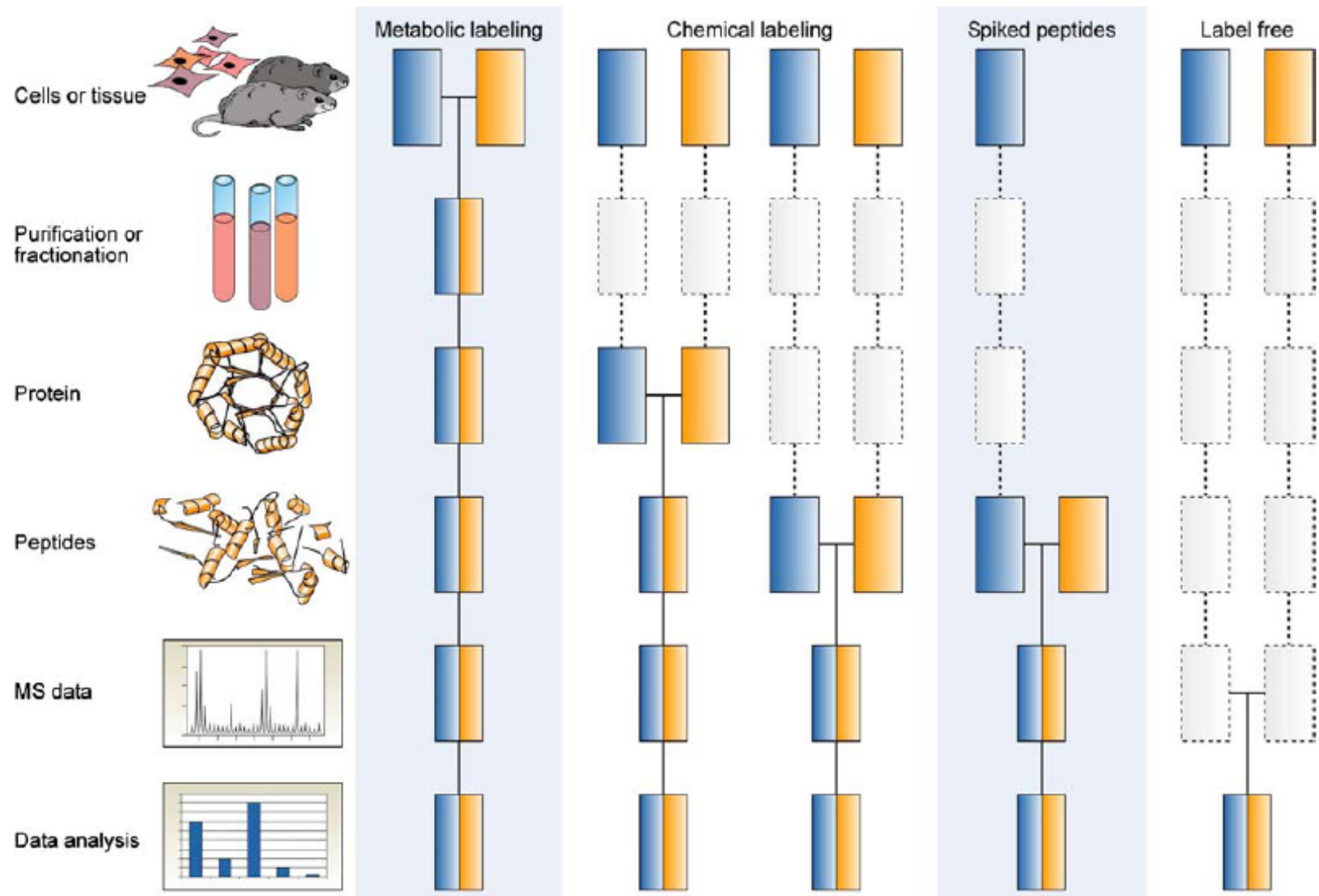


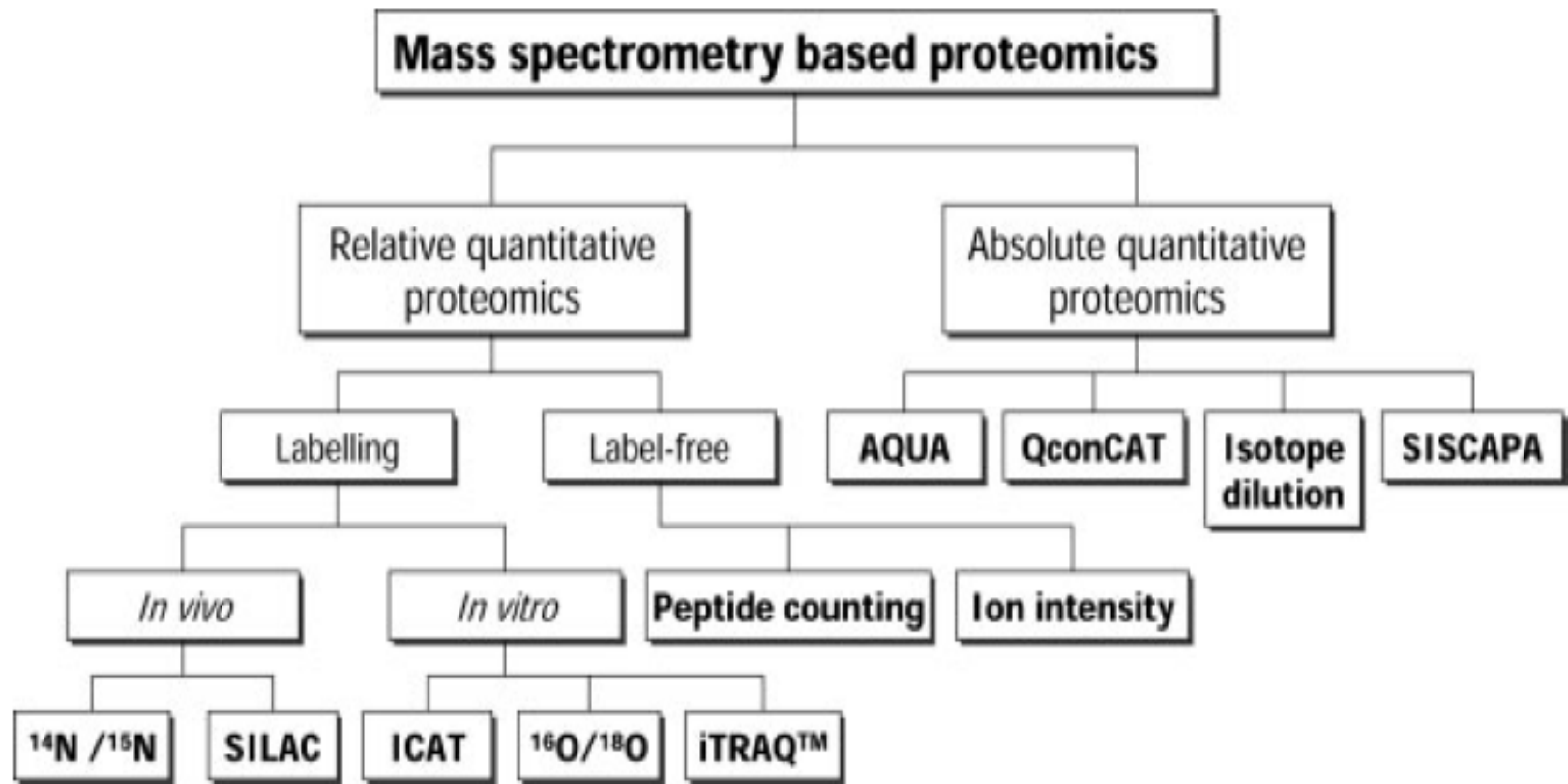
c

Label	AcArg		AcLys		Total		Isotope mass
	^{13}C	^{15}N	^{13}C	^{15}N	^{13}C	^{15}N	
1	0	4	0	2	0	6	5.9822
2	0	4	2	0	2	4	5.9948
3	2	0	2	2	4	2	6.0075
4	6	0	0	0	6	0	6.0201



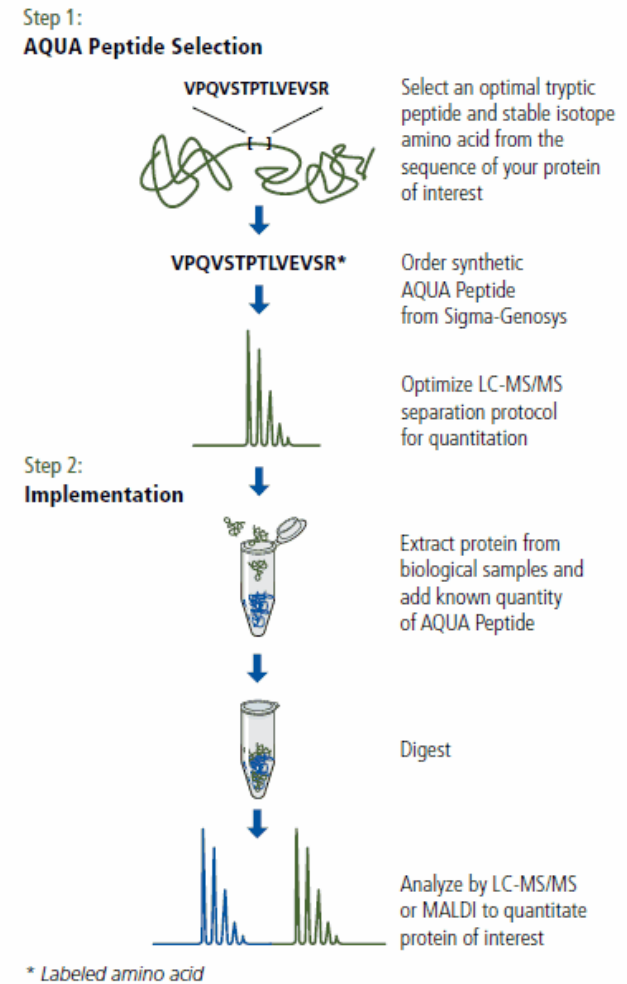
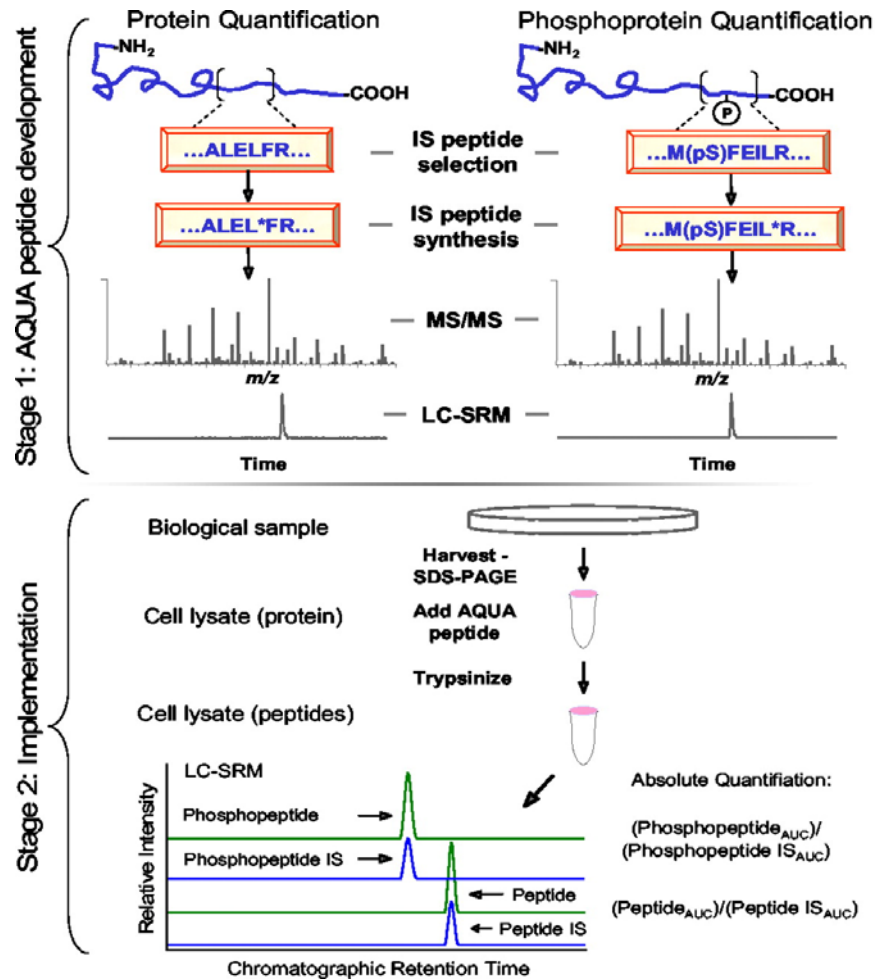




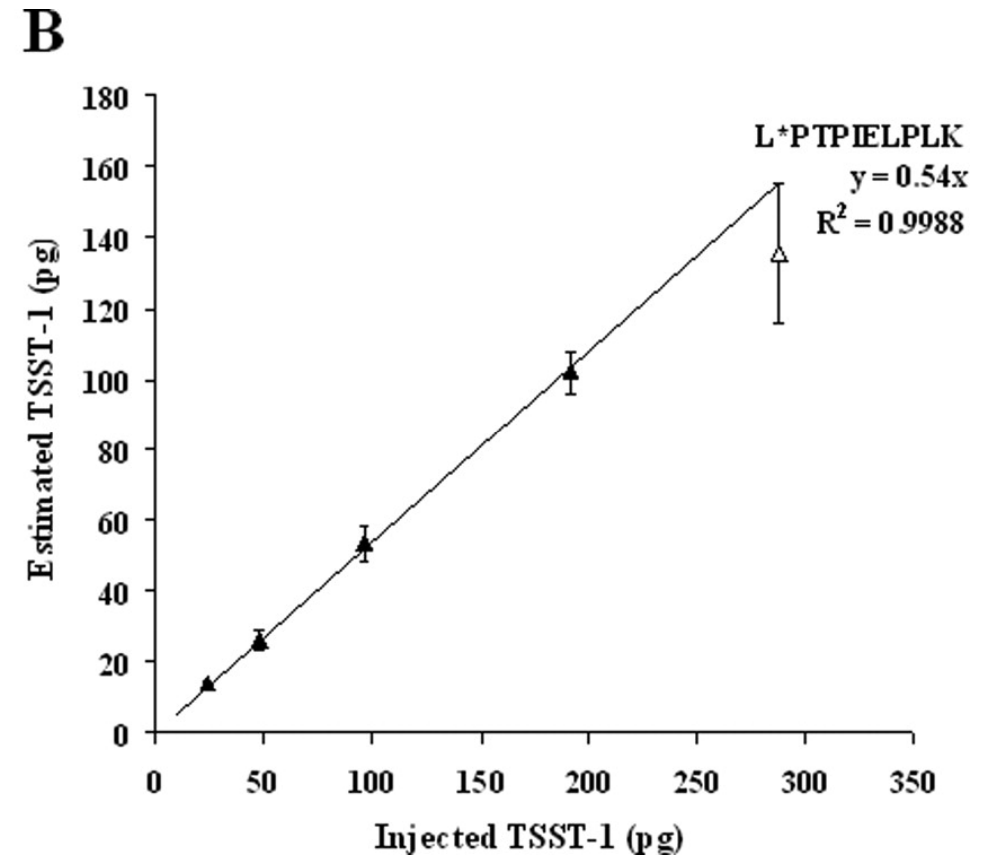
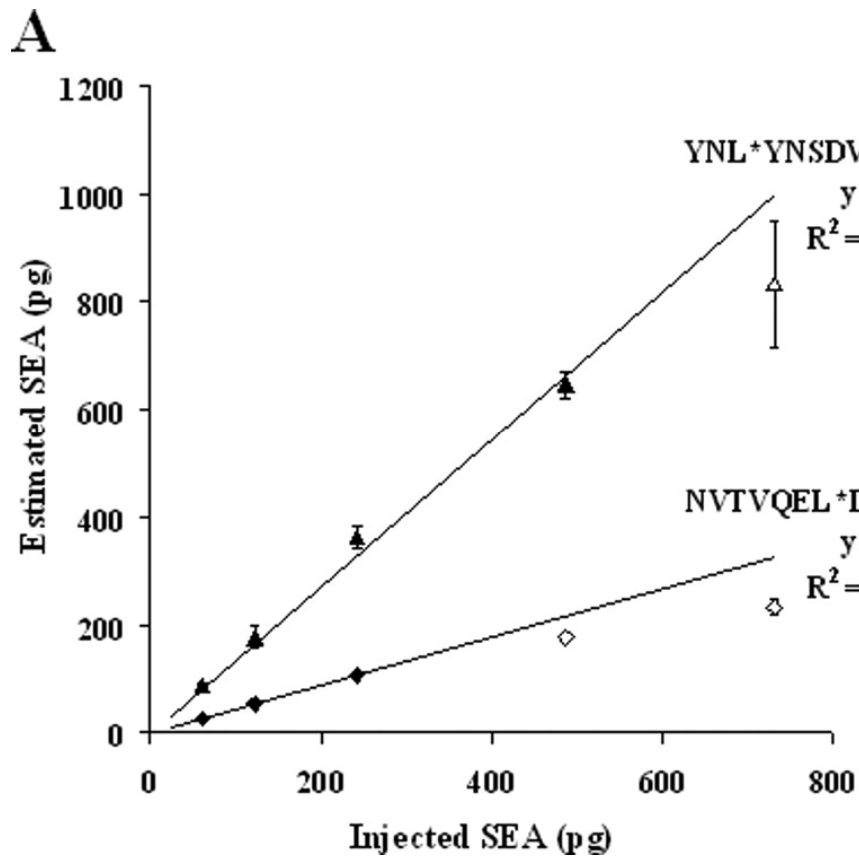


Absolute quantification

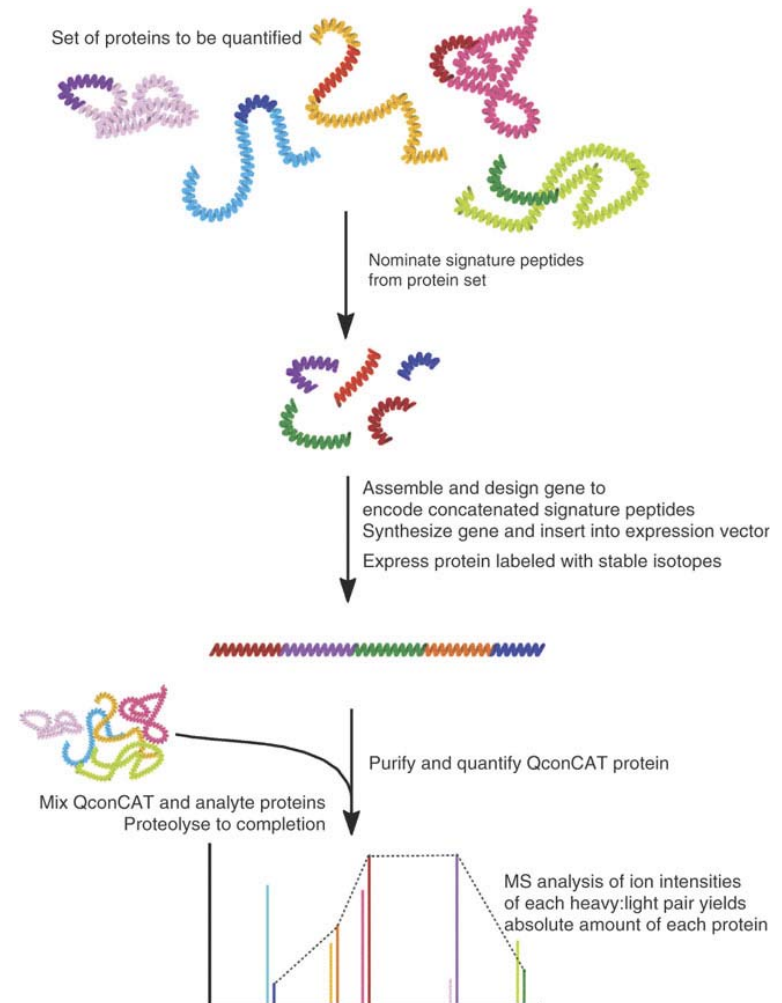
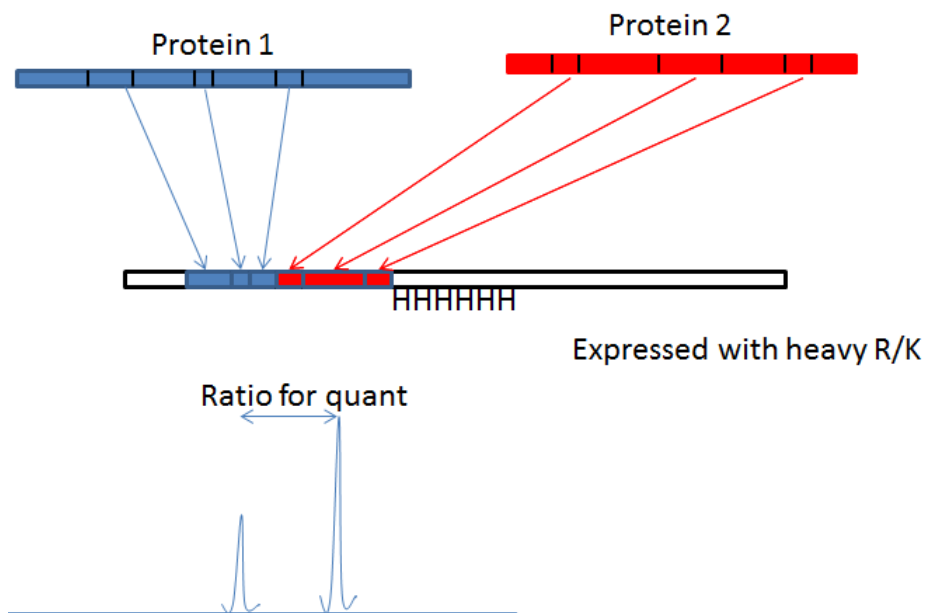
Absolute quantification : AQUA



Absolute quantification : AQUA

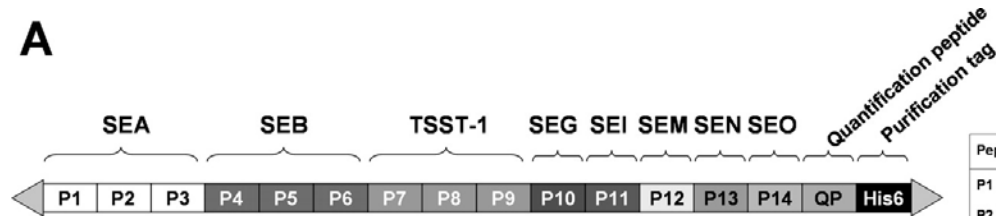


Absolute quantification : QconCAT



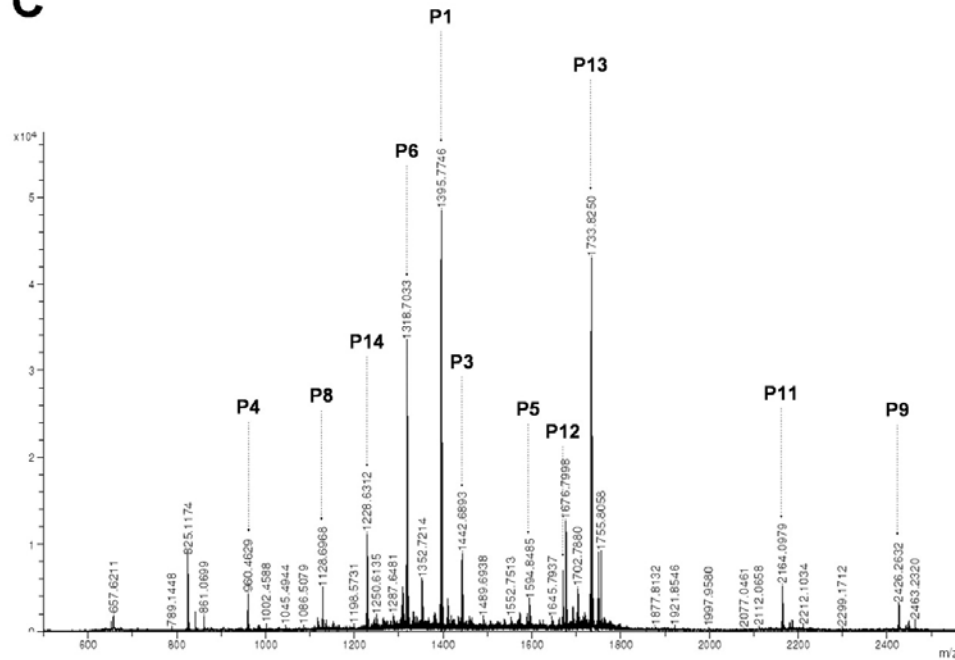
Absolute quantification : QconCAT

A

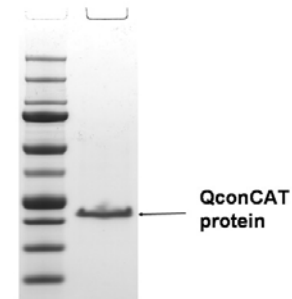


Peptide	Toxin	Sequence	Mass
P1	SEA	NVTQELDLQAR*	1395.5
P2	SEA	QNTVPLETVK*	1136.3
P3	SEA	YNLYNSDVFDGK*	1442.5
P4	SEB	LGNYDNVR*	960.0
P5	SEB	VLYDDNHVSAINVK*	1594.8
P6	SEB	VTAQELDYLR*	1318.5
P7	TSST-1	HQLTQIHGLYR*	1375.6
P8	TSST-1	LPTPIELPLK*	1128.4
P9	TSST-1	NTDGSISLIIFSPYSPAFTK*	2426.7
P10	SEG	NNTSFWDLPK*	1523.7
P11	SEI	SFSYDLFYTGDLVPSFLK*	2164.4
P12	SEM	YIYGGVTLAGDYLEK*	1669.9
P13	SEN	GSVGAEFFQFYSDNR*	1733.8
P14	SEO	TVDIYGVYYK*	1228.4
PQ		VICSAEGSK*	901.0
His6		PGGGSHHHHHH	1196.2

C

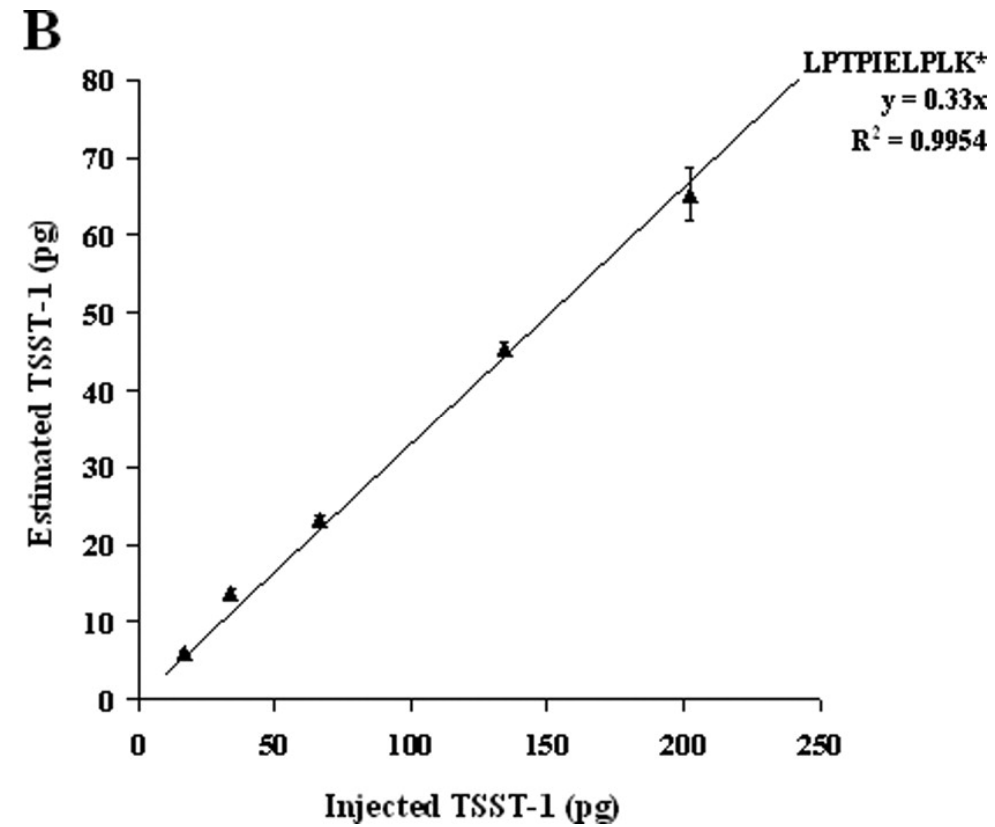
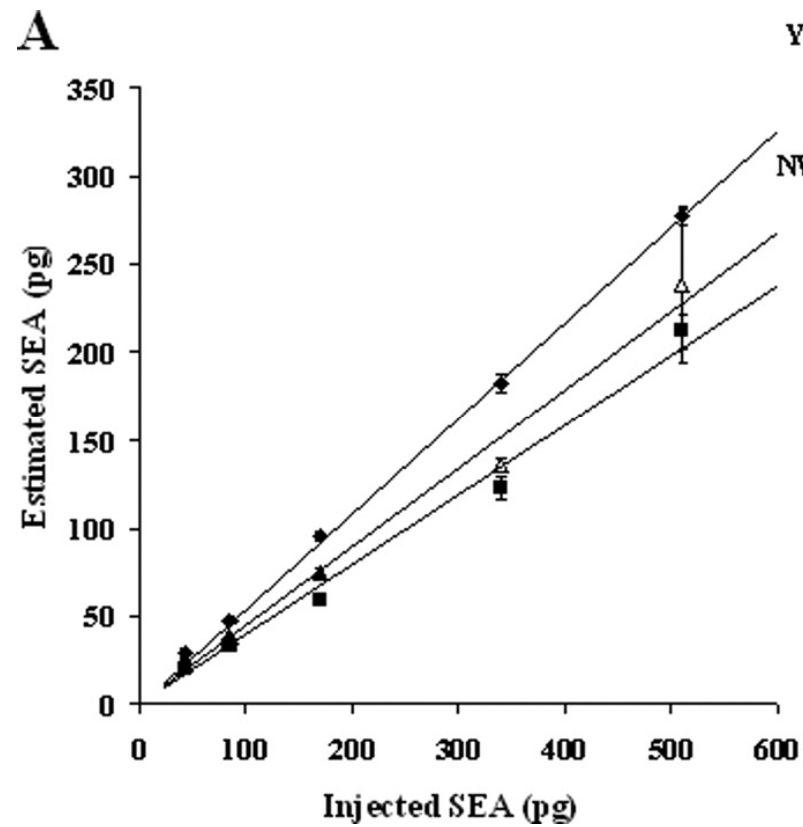


B

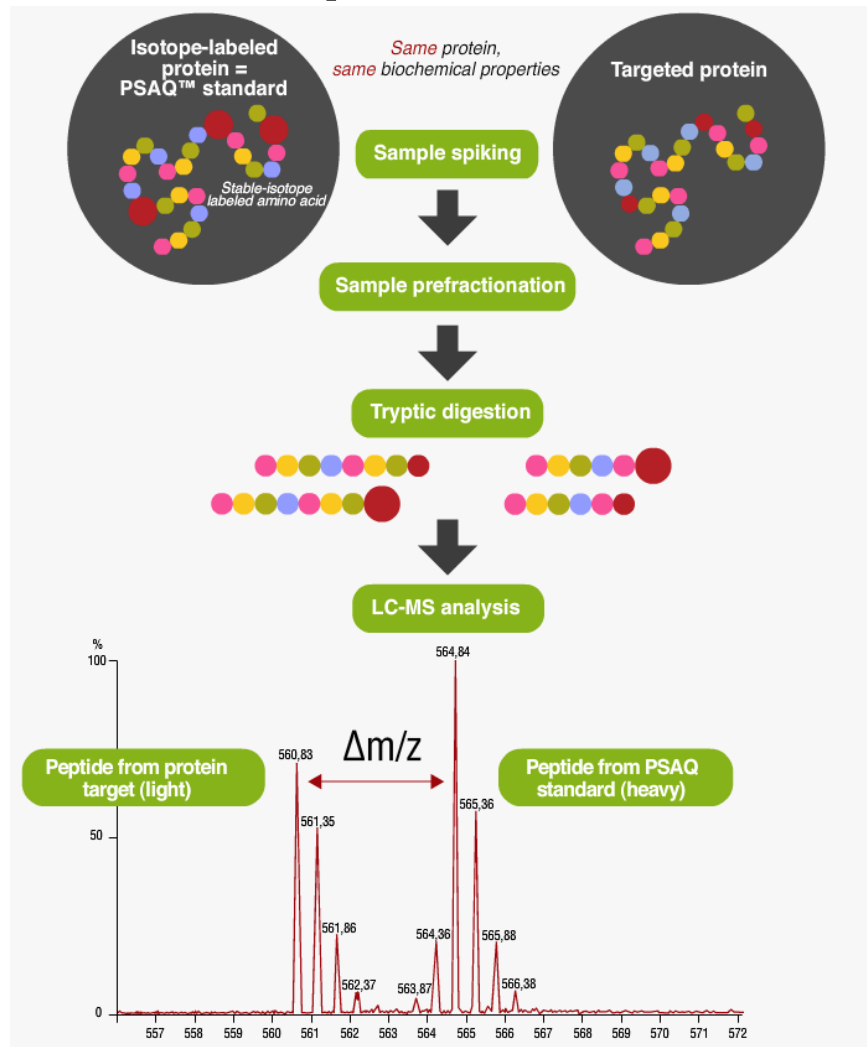


Mol Cell Proteomics. 2007 Dec;6(12):2139-49

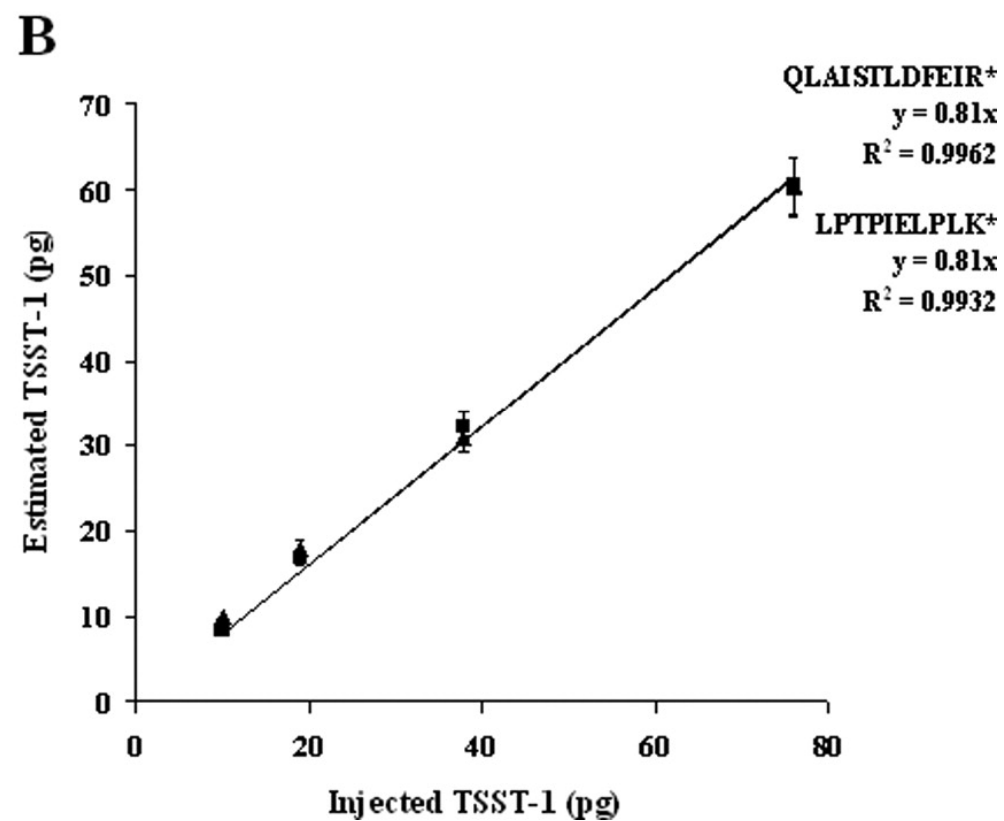
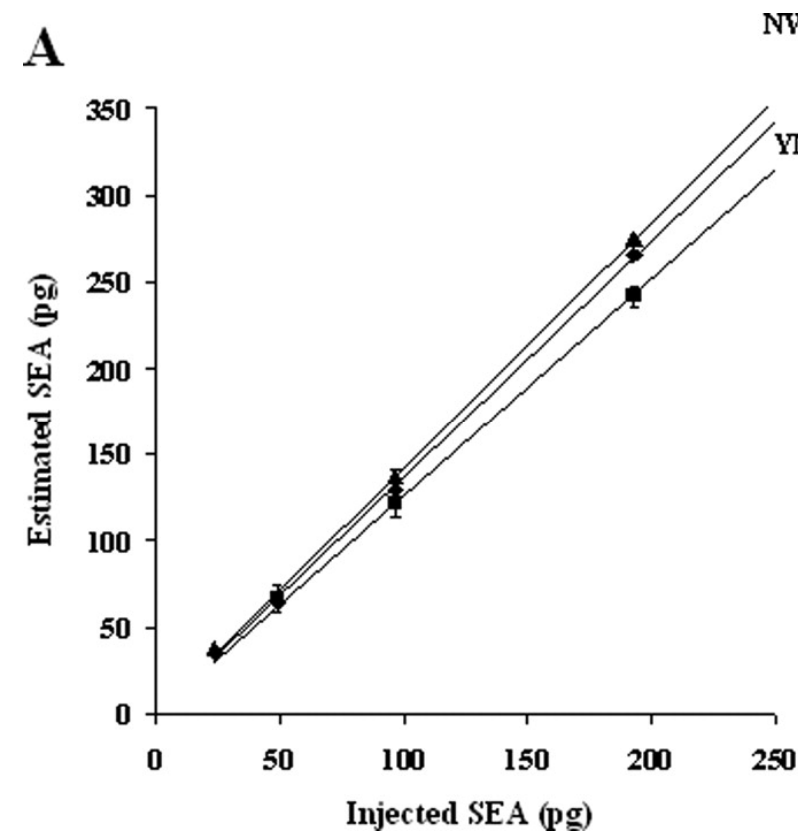
Absolute quantification : QconCAT



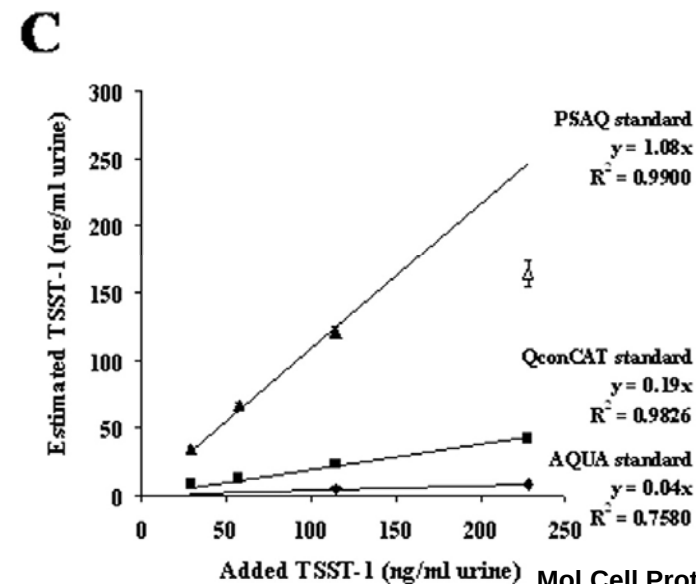
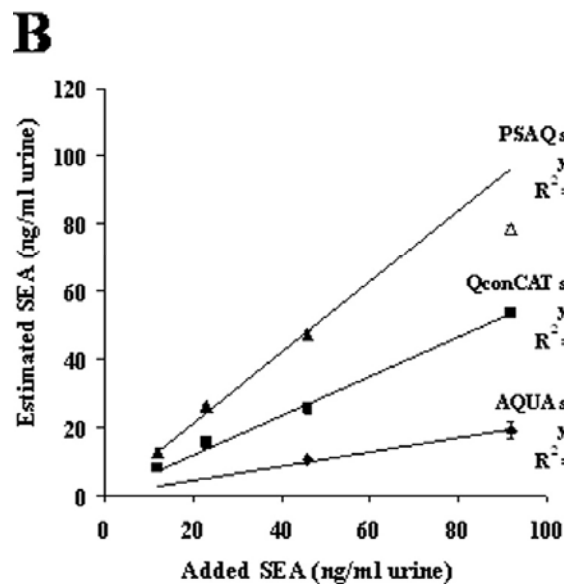
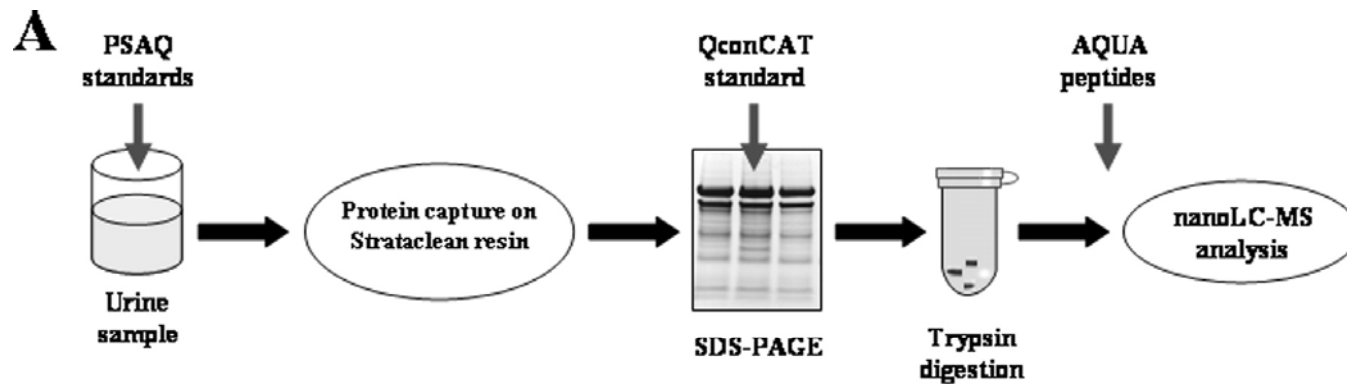
Absolute quantification : PSAQ



Absolute quantification : PSAQ



Absolute quantification : PSAQ



Absolute quantification : PSAQ

