Light:Heavy Ratios from MSQC1, Lot # 081M6281

Protein	SIL Peptide	Theoretical	Reported on Sigma Certificate of Analysis	Average of 27 Labs from ProteoRED Study* (CV)
CAH1	GGPFSDSY[R]	1	1.0	1.0 (4.8%)
	VLDALQAI[K]	2	2.0	2.0 (10.7%)
CAH2	AVQQPDGLAVLGIFL[K]	10	8.4	8.5 (10.9%)
	SADFTNFDP[R]	50	55.0	56.3 (12.7%)
NADPH	EGHLSPDIVAEQ[K]	1	0.9	0.9 (11.6%)
	ALIVLAHSE[R]	2	0.9	0.9 (7.9%)
CRP	ESDTSYVSL[K]	10	9.4	9.3 (7.4%)
	GYSIFSYAT[K]	50	38.0	37.4 (9.0%)
PPIA	VSFELFAD[K]	1	0.5	0.6 (14.7%)
	TAENF[R]	2	0.9	N/A
	FEDENFIL[K]	0.5	0.3	0.3 (15.9%)
CATA	FSTVAGESGSADTV[R]	10	4.9	5.5 (11.5%)
	NLSVEDAA[R]	50	49.0	34.0 (13.0%)
	GAGAFGYFEVTHDIT[K]	0.2	0.16	0.04 (24.3%)

* Data taken from 27 Labs (30 data sets). Sample (E) prepared by spiking 1 vial of MSQC1 into 100 µg yeast lysate digest.

* F. Canals et al., Proteored Multicentric Experiment 8: Quantitative Targeted Analysis in Proteomics. An Assessment Study. (PME8-QTAPAS), EUPA 2013.