Supplemental Table 1. PRG07 Results Compilation

						Added Protein[1]											
						Myoglobin	Ubiquitin	Cyt. *c*	Horseradish peroxidase	Serum albumin	Catalase	Glucose oxidase	Carbonic anhydrase I	Trypto-phanase	Glycero-kinase	Lacto-peroxidase	Hexokinase
					Quantity in sample B (pmol)	5.00	23.00	11.50	11.00	3.33	0.34	0.33	1.14	1.56	0.78	0.78	0.16
					Quantity in sample A (pmol)	0.50	5.00	2.50	5.00	5.00	0.50	0.50	2.50	5.00	2.50	2.50	0.50
					Ratio B/A	10.00	4.60	4.60	2.20	0.67	0.67	0.67	0.45	0.31	0.31	0.31	0.31
Identifier[2]	No. Prot. identified	TP[3]	FP[4]	Method[5]	Days[6]	Percent error of ratio[7]											
67483	10	10 (6)		LF	10	30.2	0.7	10.9	12.3	7.0	-19.4	-8.0	-1.3			-12.9	-316
19971v	8	8 (6)	1	LF-hrSRM	9	0.3	-10.7	-9.8	-13.6	-26.0	-7.5		-123			-148	
29850	8	8 (7)	6 (2)	iTRAQ	7	50.9	18.7	18.9	2.3	-11.0	-16.3		-16.7			-19.4	
60752v	9	9 (9)		LF	7	10.9	6.5	-3.7	10.0	22.0	29.9	28.0	18.5			6.5	
01606v	6	6 (5)		LF	7	13.3	3.5	-6.7	-1.8	-17.0			-7.9				
87037	7	6 (6)	5 (3)	18O	5	14.4	25.4	27.0	-6.8	-14.0					-63.2	-51.6	
40318	6	6		18O	7	38.4	-9.8	35.4	3.6	11.5			-299				
38057	7	7		iTRAQ	5	55.6	41.7	42.0	24.5	-20.0	4.5		-41.0				
27960v	4	4 (3)		ICPL	10		-17.2		-17.7	-18.5			-23.3				
00715	6	6 (4)	4 (3)	2D-S		93.6	46.1	78.9		-48.5			-1.3			6.5	
13036	6	6 (5)	2	iTRAQ	10	75.4	40.2	42.0	26.8	-15.5			-10.1				
78544	6	6 (6)	2	DIGE	2	97.2	92.2		69.5	-112	-7.5		-294				
66639	5	5 (5)	2	iTRAQ	4	55.8	63.0		36.4	-24.5			-25.6				
52666	3	3 (2)	8 (2)	DIGE	6					13.0			14.1		-156		
12114	3	3	8 (1)	iTRAQ	4			5.0	35.9	13.0							
05197	3	3	6	iTRAQ	8		33.0	29.1	8.2								
01043	3	3	12	iTRAQ	3			54.8	32.3				-25.6				
54864	4	4 (4)	10 (6)	iTRAQ	4	85.4	65.7	68.0		-26.0							
50768	3	3 (2)	12 (5)	iTRAQ	14		82.0		74.5					-47.2			
14359v	4	4 (3)	5	iTRAQ	5	80.0	60.2	60.2	26.8								
91919	2	2 (1)	13	iTRAQ	6				64.5					-732			
55649v	4	4 (3)	4	iTRAQ	4	79.7	58.9	55.9	27.7								
80053	1	1	13	LF-gel/LC	15	-60.0											
80329	1	1		DIGE	6				-31.8								
21543v	2	2	11	2D-Fl	21	28.6							29.5				
08999	1		10 (2)	LF-count+	10	-27.9											
70301	1	1 (1)	12	ICAT	8					-295							
21205	1		15 (10)	iTRAQ	4							41.5					
81279		3 (2)	1 (1)	iTRAQ	5												
88888			15	iTRAQ	6												
13056			8	DIGE	10												
23343			15 (14)	2D-C	3												
12114			2	2D-Fl	10												
21347			15 (14)	2D-Fl	25												
03280			7 (7)	DIGE	10												
11299			10 (3)	iTRAQ	7												

8 respondents did not return quantitative data; those entries were not included in this table

[1] The indicated quantities of proteins were added to an *E. coli* lysate as described in Methods; the quantities shown above for glycerokinase and tryptophanase (both are *E. coli* proteins) represent the amounts added to the mixture. Sample C contained the same quantities of protein as sample B.

[2] v, instrument vendor

[3] True positives, the number of proteins correctly identified as being present at different relative levels in samples A and B; the number of TP results considered to be "high confidence" by the respondent is shown in parenthesis.

[4] False positives, the number of proteins incorrectly identified as being present at different relative levels in samples A and B; the number of FP results considered to be "high confidence" by the respondent is shown in parenthesis.

[5] Methods: LF, label-free; LF-count+, label-free-spectral count+differential peptide ion intensity integration; iTRAQ, isobaric tags for relative and absolute quantitation; ICAT, isotope coded affinity tag; ICPL, isotope coded protein label; 18O, $^{16}O/^{18}O$ labeling; 2D-S, 2D PAGE/silver stain; 2D-C, 2D PAGE/Coomassie, 2D-Fl; 2D PAGE/fluorescent stain, DIGE, differential in-gel electrophoresis.

[6] The amount of time required for the study, as provided by participants in the results survey

[7] % error of ratio = [(observed ratio – expected ratio)/expected ratio] x 100; results that were greater than the expected ratio are shown as positive values; observed ratios that are less than expected are negative numbers.