

AAA2003 Study

Table 1: Site Identification Key

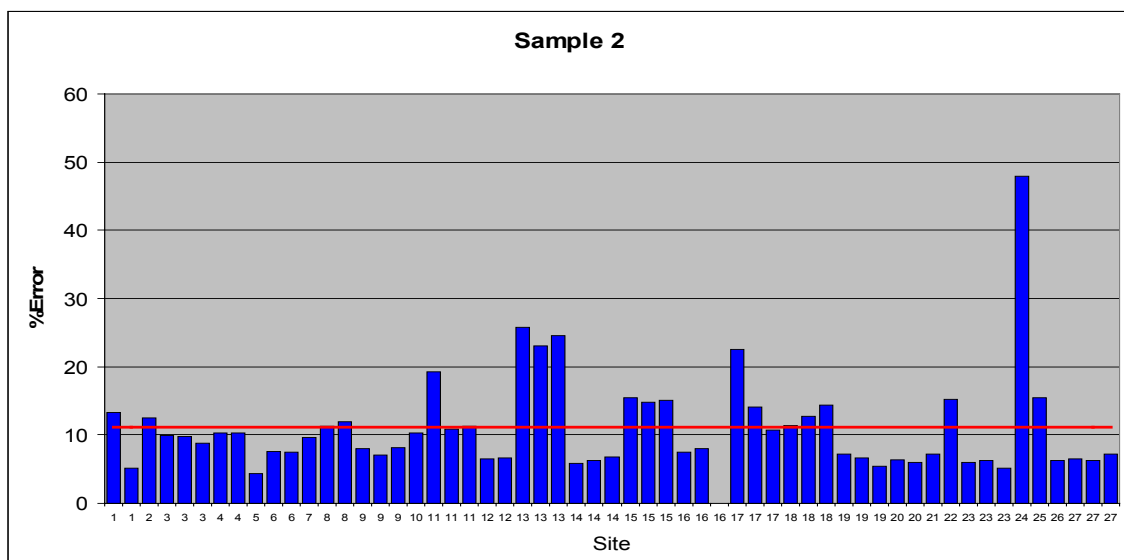
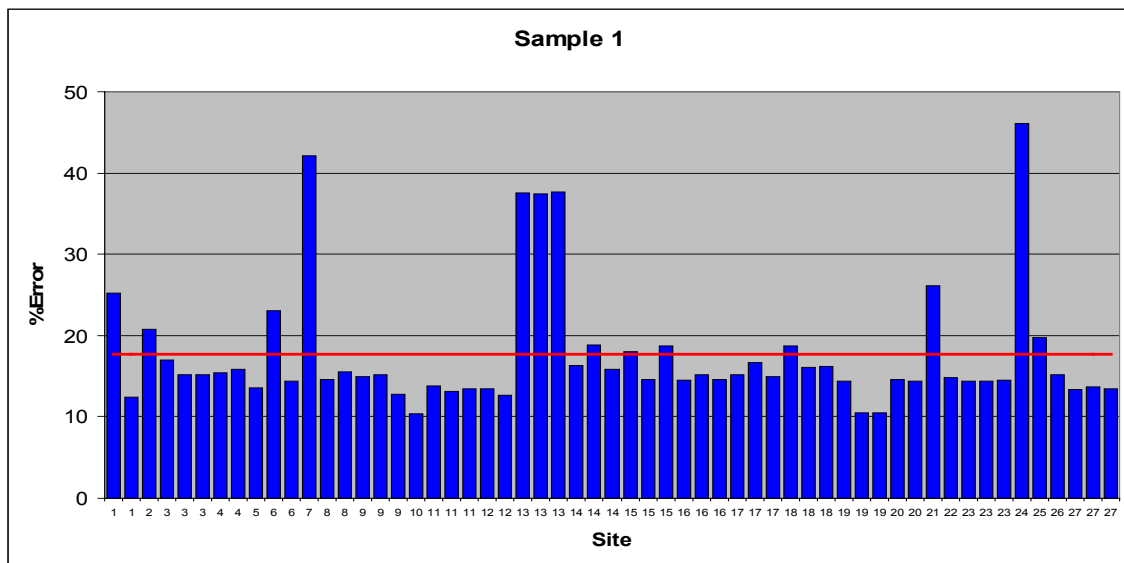
Site	Identification	Site	Identification	Site	Identification
1	715	10	200.02	19	46540
2	10023	11	20090	20	51840
3	10258	12	21322	21	53025
4	12080	13	2C-OH	22	53602
5	12345	14	30509	23	61001
6	13236	15	3383	24	88666
7	13445	16	34623	25	CBTBE
8	14220	17	40952	26	MAXY1
9	100.21	18	43072	27	pspna
				28	Kalibration advanced

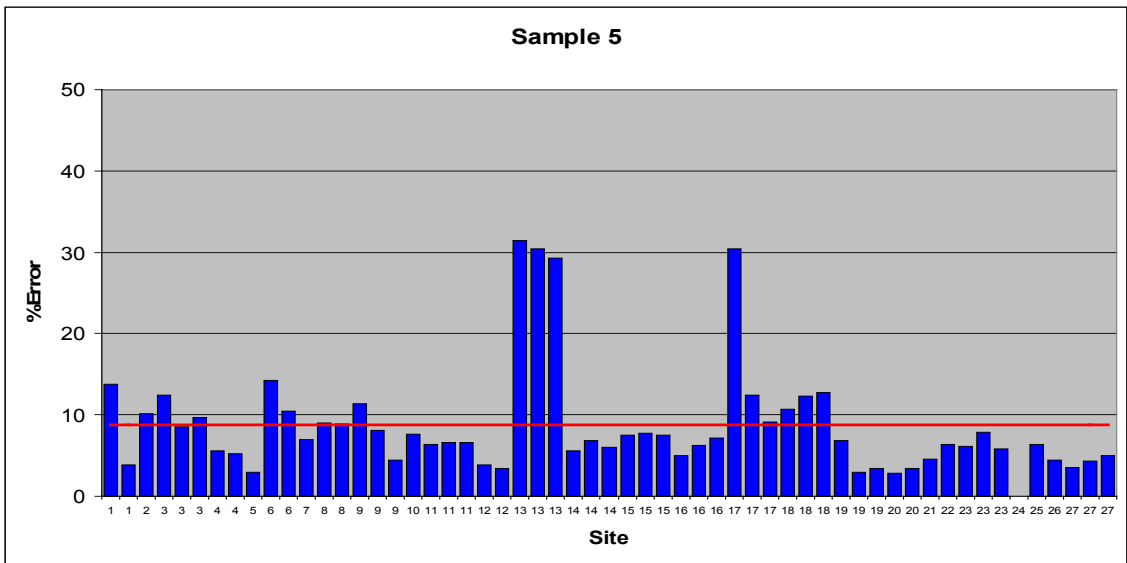
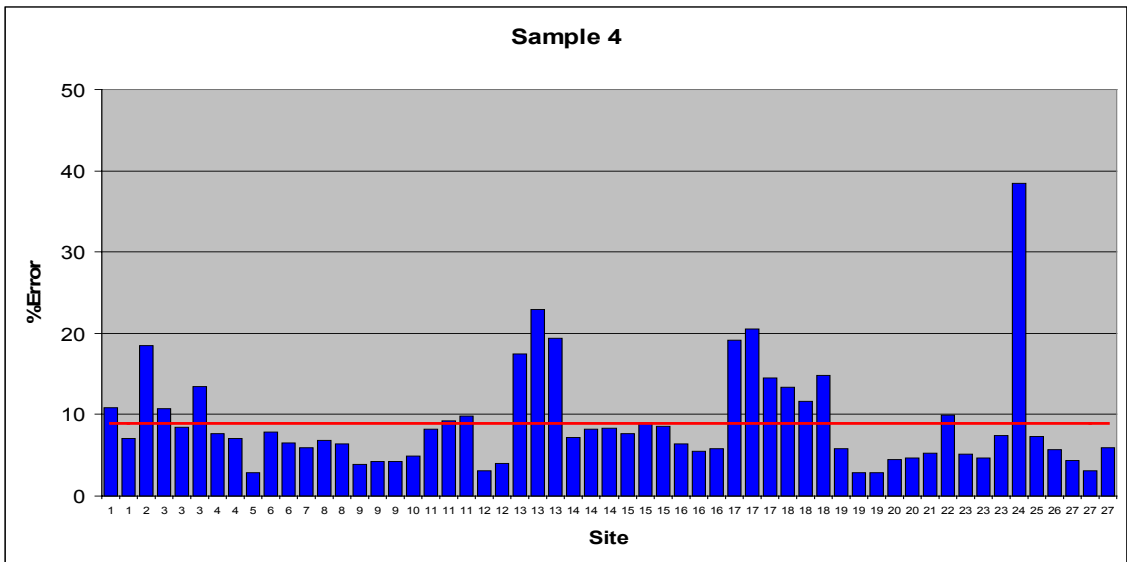
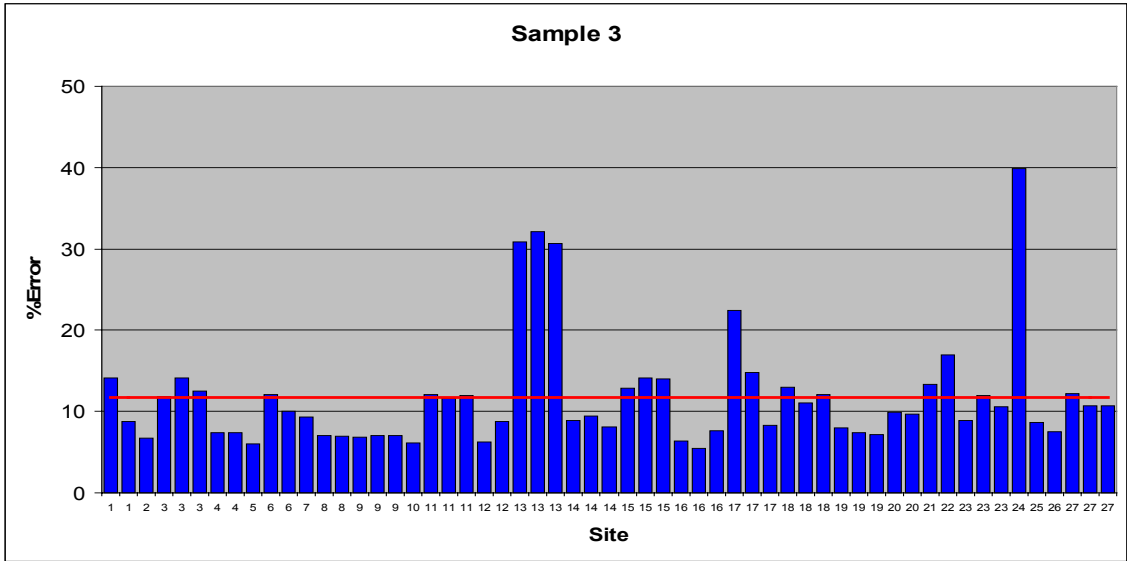
Table 2: Protein Identification Key

	Identification
Sample 1	Aprotinin
Sample 2	Beta-lactoglobulin
Sample 3	Fetuin
Sample 4	Hemoglobin
Sample 5	Ubiquitin

Average compositional error

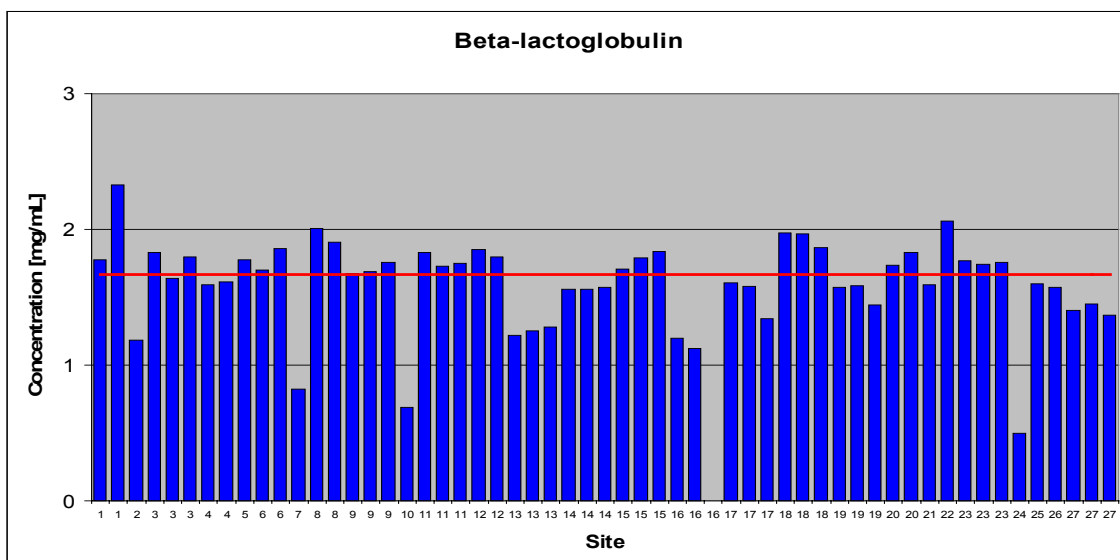
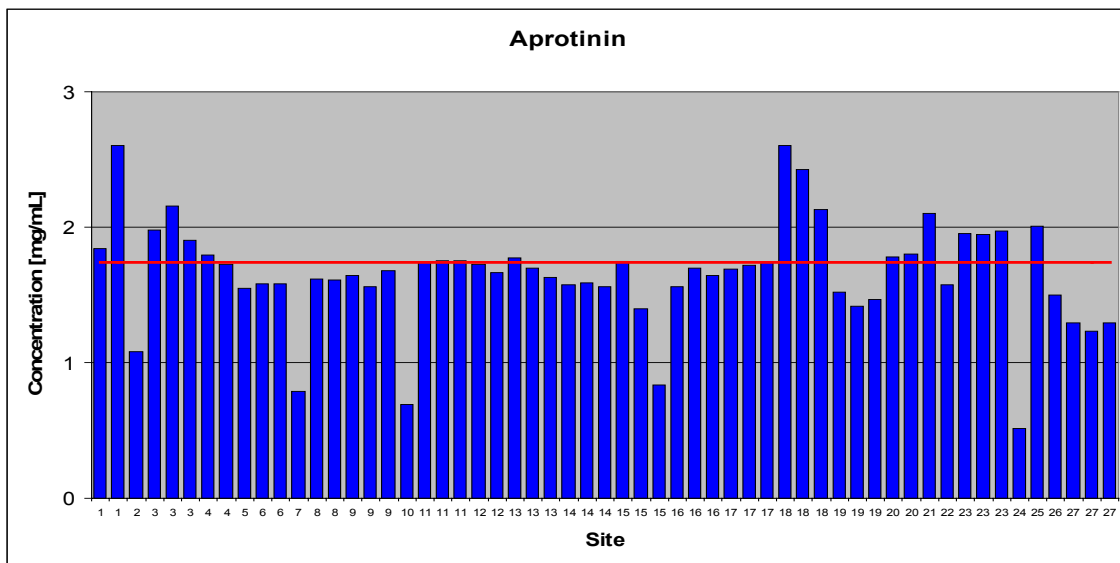
Average % errors (horizontal line) are: 17.7 ± 7.7 for sample 1, 11.1 ± 7.1 for sample 2, 11.7 ± 6.9 for sample 3, 8.9 ± 6.3 for sample 4 and 8.8 ± 6.7 for sample 5. The site identification key is shown in table 1. The identities of samples 1 - 5 are shown in table 2

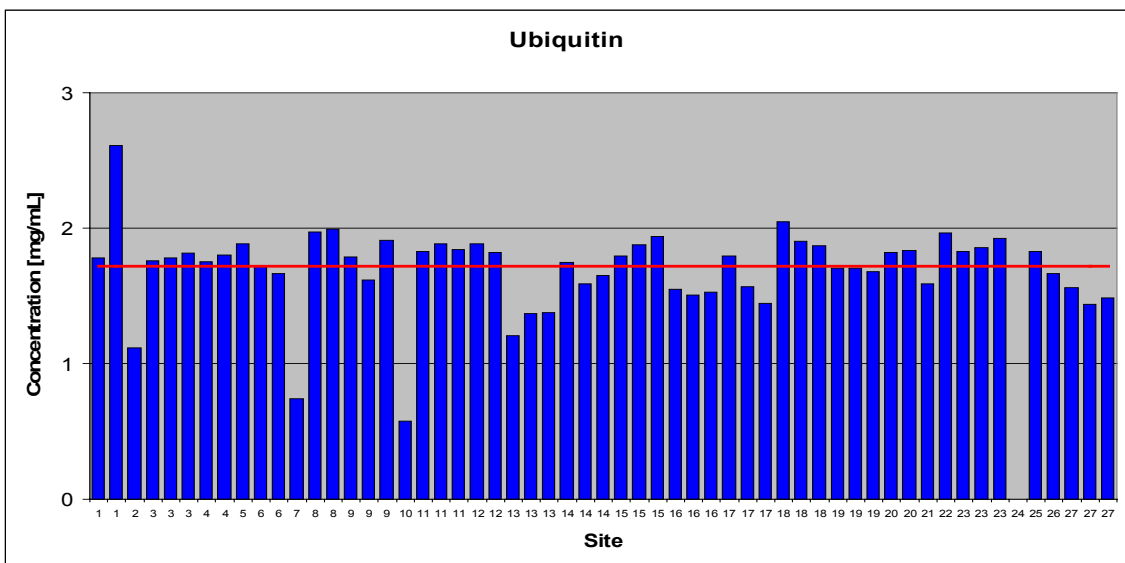
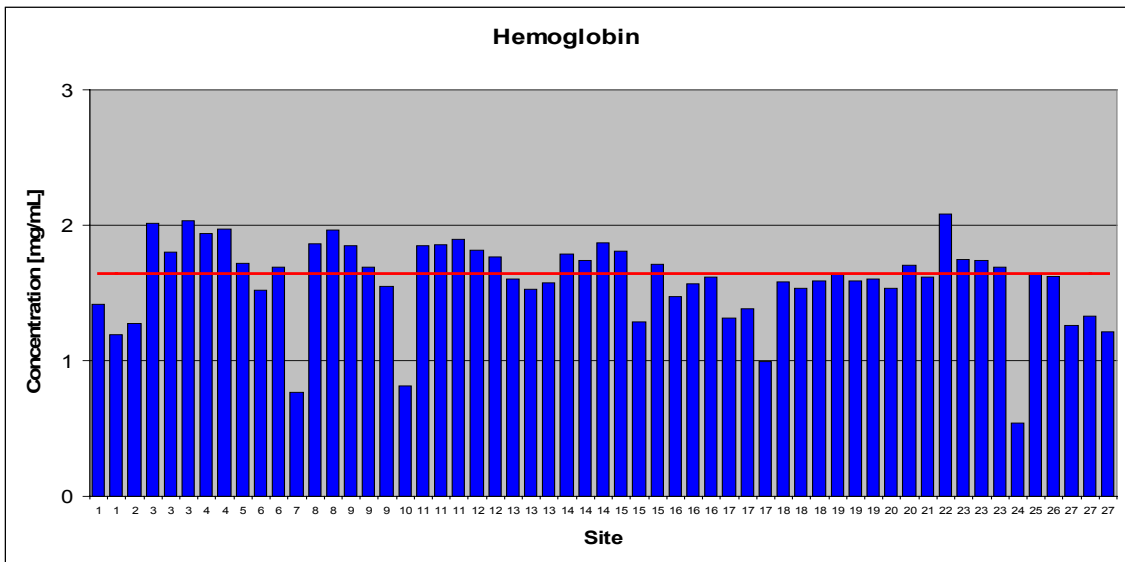
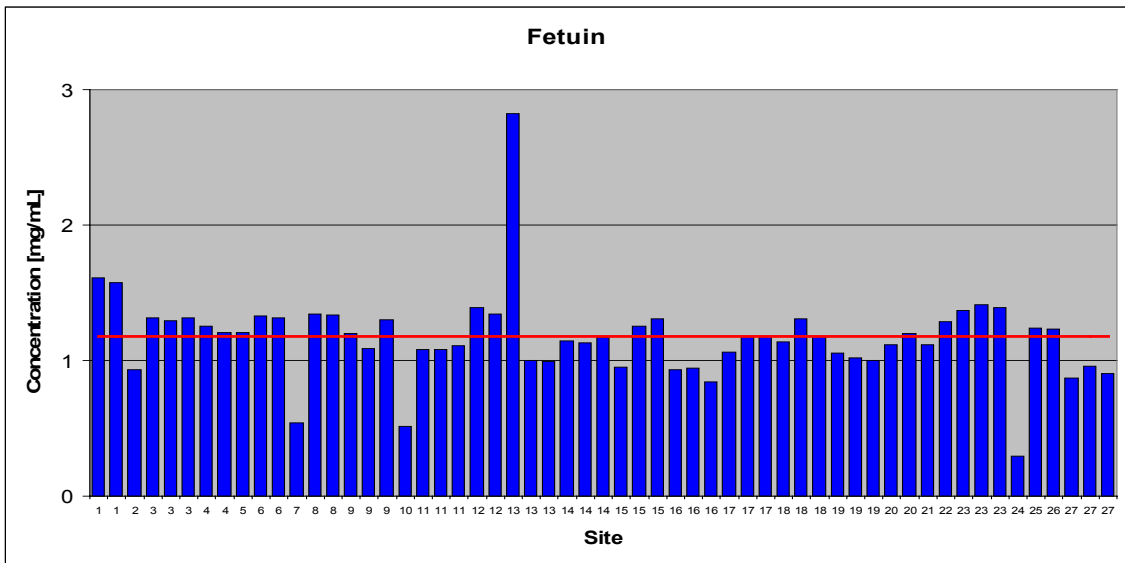


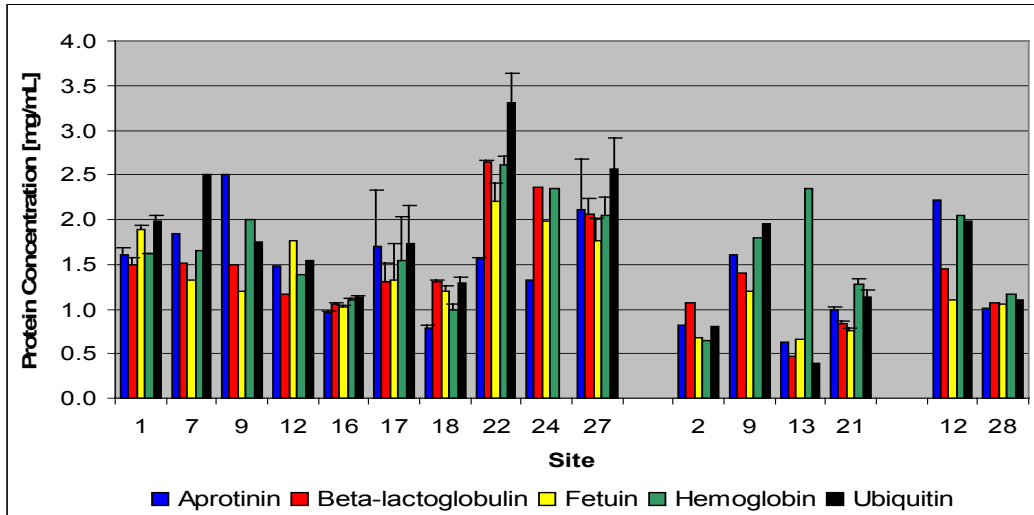


Protein concentration determined by AAA

The protein concentration for each data set was calculated as indicated in the Methods section. Mean concentrations (horizontal line) are: 1.74 ± 0.28 for aprotinin, 1.67 ± 0.23 for beta-lactoglobulin, 1.18 ± 0.17 for fetuin, 1.64 ± 0.23 for hemoglobin and 1.72 ± 0.20 for ubiquitin. The site identification key is shown in table 1.







Protein concentration determined by dye-binding assay

Others: Lowry assay (site 12), home made assay (site 28). Data from sites 2, 24, 13, and 28 are single measurements. All other sites performed multiple analysis (BCA assay: Site 1: n=10, site 7: n=7, site 9: n=2, site 12: n=2-3, site 16: n=9, site 17: n=3, site 18: n=3, site 22: n=2, site 27: n=9-15. Bradford assay: Site 9: n=3, site 21: n=4. Others: site 12: n=2). Data were reported as mean values but some of the laboratories have not indicated the standard deviation of their multiple measurements.