

Supplementary Table 1. List of Protein Identified as N-346-binding Proteins

Spot no.	Protein name	Acc. no. ^a	PMF			MS/MS (MALDI)			MS/MS (nano-LC)		
			Seq. cov. (%)	Peptides ^b	Score ^c	Seq. cov. (%)	Peptides ^d	Score ^e	Distinct Peptides ^e	Seq. cov. (%)	Score ^f
1	Merozoite surface protein 7 precursor	15808773	29	10 (18)	126	3	K.EVQKPAQGGESTFR.K	56	19 (32)	50	292.1
2	Rhoptry-associated membrane antigen	237859953			N.D.			N.D.			75.31
3	14-3-3 protein, putative	296005038			Not id ¹			Not id ²	3 (4)	14	33.9
4	14-3-3 protein, putative	296005038			N.D.			N.D.	8 (12)	37	107.37
	Heat shock 70 kDa protein	124512406			N.D.			N.D.	3 (6)	4	35.92
	Tropomyosin alpha-1 chain (Human)	P09493			N.D.			N.D.	12 (17)	29	180.24
5	Not Identified				Not id ¹			Not id ²			N.D.
6	Tropomyosin alpha-3 chain (Human)	P06753	19	10 (39)	70			Not id ²			N.D.
7	Not Identified				Not id ¹	Not id ²	N.D.				
8	Not Identified				Not id ¹			Not id ²			N.D.
9	Not Identified				Not id ¹			Not id ²			N.D.
10	Endoplasmic reticulum-resident calcium binding protein	124803623			N.D.			N.D.	11 (18)	36	169.77
	Glideosome-associated protein 45	124806088			N.D.			N.D.	4 (6)	17	42.22
11	Endoplasmic reticulum-resident calcium binding protein	124803623	50	16 (26)	203	9	K.LNDDQVKDILGLK.I K.IAVTSLTDYGDVIR.Y K.IAVTSLTDYGDVIRYPEDFK.L	123	9 (19)	30	136.74
12	Rhoptry-associated membrane antigen	237859953									
13	Not Identified				Not id ¹			Not id ²			N.D.
14	Not Identified				Not id ¹			Not id ²			N.D.

Acc.no., accession number; Seq. cov., sequence coverage; N.D., Not done;

Not id¹, Not identified by PMF.

Not id², Not identified by MS/MS ion search.

^aAccession number from NCBI in the case of *P. falciparum* or Swiss-Prot in the case of human.

^bNumber of m/z values matching between that in the an in silico digest and that experimentally determined.

^cMASCOT probability-based MOWSE (molecular weight search) score calculated for PMF and MS/MS result: Score = $-10 \times \log_{10} P$ where p is the absolute probability that the given hit is a random event.

Protein scores greater than 55 (PMF) are significant ($p < 0.05$) and individual ions scores > 28 (MS/MS) indicate identity or extensive homology ($p < 0.05$) when searching the NCBI protein database.

Protein scores greater than 56 (PMF) are significant ($p < 0.05$) and individual ions scores > 28 (MS/MS) indicate identity or extensive homology ($p < 0.05$) when searching the Swiss-Prot protein database.

^dPeptides analyzed by PSD and high energy CID experiments; charge state, always +1.

^eNumber of matched peptides vs. number of searched peptides given in the bracket.

^fMill MS proteomic workbench probability-based peptide score calculated for MS/MS results.

The combined peptide mass fingerprint and LIFT MS/MS spectra were searched against the NCBI protein database (released 20120415; 17848406 sequences; 6126535335 residues)

using Biotoool 3.2 software (Autoflex III, Bruker Daltonics).