## Errata

Table 1., page 40

## **Table 1.** Review of the Experiments Performed:

We performed several experiments in two cell lines gathering more than 100 000 hits. Data was organized and processed as described in Methods. Samples of incubation containing bait protein or an antibody specific to bait protein are noted "Positive control", "Negative control" are noted samples of incubation with untreated resin or other antibody (as described previously).

Source	Procedure	Number of samples		Number of protein hits	
		Positive	Negative	Positive	Negative
LNCaP	immunoprecipitation	9	9	36547	38772
LNCaP	pull-down	13	12	12896	9977
HUVEC	pull-down	3	2	6912	4079

## Errata

A comparison of the hit list obtained after new data processing (27.6. 2013, table 3, page 42) with the previous one suggests that a heavy chain of myosin was present in both negative and positive control and therefore is a contaminant. Hornerin, rather than myosin, seems to stick to GCPII.

## Table 3. First 21 Positive Hits from All Immunoprecipitations with GCPII-08 in LNCaPs:

Throughout all immunoprecipitations in LNCaP cells, a best sequence coverage in each run for given accession number (coverage) in positive control (+) was chosen as well as the highest number of peptides found (peptides). Coverage or peptides of the negative controls were subtracted numerically obtaining "difference". FOLH1 is the gene of our bait protein (positive control). Hits in the list are sorted according to "peptide difference". Data from these experiments suggest that GCPII might specifically bind to hornerin or collagen type I.

Accession Number	Gene	Peptides (+)	Coverage (+)	Peptides Difference	Coverage Difference
sp P02452 CO1A1_HUMAN	COL1A1	132	56,3	99	23,6
sp P05 GCPII	FOLH1	97	62,1	93	37,3
sp Q04609 FOLH1_HUMAN	FOLH1	97	62,1	93	37,3
tr D3DTX7 D3DTX7_HUMAN	COL1A1	90	53,6	84	45,5
sp Q04609-6 FOLH1_HUMAN	FOLH1	67	60,3	63	33,5
sp Q04609-7 FOLH1_HUMAN	FOLH1	67	58,4	63	33,1
sp S01 AviEXST	AviEXST	67	58,1	63	30,6
tr A4UU13 A4UU13_HUMAN	FOLH1	67	56,9	63	31,6
sp P35908 K22E_HUMAN	KRT2	121	88,1	53	1,3
tr H6VRG3 H6VRG3_HUMAN	KRT1	140	72,0	47	0,6
sp P13645 K1C10_HUMAN	KRT10	133	73,5	46	-5,39
sp A6NCN2 KT81L_HUMAN	KRT121P	44	32,1	42	15,2
sp S01 AviEXST	AviEXST	44	36,7	40	9,2
tr Q2VPJ0 Q2VPJ0_HUMAN	FOLH1	43	47,27	39	20,6
tr F5H299 F5H299_HUMAN	COL1A2	47	34,0	33	14,0
sp P08123 C01A2_HUMAN	COL1A2	47	34,0	33	14,0
tr H6VRG2 H6VRG2_HUMAN	KRT1	129	72,7	29	1,2
tr Q5DT20 Q5DT20_HUMAN	HRNR	36	39,1	29	24,0
sp Q86YZ3 HORN_HUMAN	HRNR	36	39,1	29	24,0