Table 1 List of differentially expressed protein after CIP2A knockdown in H1299 cells.

Spot No.	**Protein Name**	**Accession No.**	**MW/pI**	**Coverage (Score)**	**No. of unique peptides**	**Folds of change (*p value*)** ^{a,b}	**MS/MS fragment** ^{c}
Metabolism							
5	Glucosidase II	gi|2274968	107,289 /5.74	1% (242)	5	1.56±0.08 (0.04)	^{52}SIRPGLSPYR^{61} ^{174}GLLEFEHQR^{182} ^{438}YFTWDPSR^{445} ^{559}DAQHYGGWEHR^{569} ^{603}AFFAGSQR^{610}
9	UDP-N-acteylglucosamine pyrophosphorylase 1	gi|3273316	57,421 /5.92	10% (313)	5	1.73±0.12 (0.03)	^{52}AIEGFNQSSHQK^{63} ^{133}KTLFQIQAER^{142} ^{134}TLFQIQAER^{142} ^{283}TNPTEPVGVVCR^{294} ^{340}DVVNVYEPQLQHHVAQK^{356}
15, 16	α-enolase	gi|693933	47,421 /7.01	18% (420)	5	1.99±0.20 (0.01)	^{33}AAVPSGASTGIYEALLR^{50} ^{133}HIADLAGNSEVILPVPAFNVINGGSHAGNK^{162} ^{240}VVIGMDVAASEFFR^{253} ^{359}LAQANGWGVMVSHR^{372} ^{407}YNQLLR^{412}
20	glyceraldehyde-3-phosphate dehydrogenase	gi|7669492	36,201 /8.57	9% (269)	3	-2.12±0.33 (0.02)	^{67}LVINGNPITIFQER^{80} ^{67}LVINGNPITIFQERDPSK^{84} ^{310}LISWYDNEFGYSNR^{323}
24	L-lactate dehydrogenase	gi|4557032	36,900 /5.71	14% (313)	4	-2.32±0.31 (0.01)	^{8}LIAPVAEEEATVPNNK^{23} ^{92}IVVVTAGVR^{100} ^{159}VIGSGCNLDSAR^{170} ^{320}SADTLWDIQK^{329}
26	dimethylarginine dimethylaminohydrolase 2	gi|7524354	29,911 /5.53	12% (267)	2	1.73±0.24 (0.04)	^{114}IVEIGDENATLDGTDVLFTGR^{134} ^{158}DFAVSTVPVSGPSHLR^{173}
32	glutathione S-transferase	gi|2204207	23,595 /8.91	21%(318)	3	-1.73±0.13 (0.02)	^{1}PPYTVVYFPVR^{11} ^{55}FQDGDLTLYQSNTILR^{70} ^{103}YISLIYTNYEAGKDDYVK^{120}
34	Phosphoglycerate mutase 1	gi|4505753	28,900 /6.67	24% (344)	4	1.74±0.34 (0.04)	^{11}HGESAWNLENR^{21} ^{22}FSGWYDADLSPAGHEEAK39 ^{118}SYDVPPPPMEPDHPFYSNISK^{138} ^{181}VLIAAHGNSLR^{191}
37	nucleoside diphosphate kinase A	gi|35068	20,740 /5.83	26% (305)	5	-2.15± 0.02 (0.019)	^{35}TFIAIKPDGVQR^{46} ^{47}GLVGEIIKR^{55} ^{78}EHYVDLKDRPFFAGVK^{94} ^{85}DRPFFAGLVK^{94}

43	inositol monophosphatase 1	gi|443382	30,437 /5.16	15%(283)	4	1.96± 0.21 0.03	^{134}GDFCIQVGR^{142} ^{59}EKYPSHSFIGEESVAAGEK^{77} ^{181}LFCIPVHGIR^{190} ^{264}EIQVIPLQR^{272} ^{264}EIQVIPLQRDDED^{276}
Transcriptional and translational regulation							
6	elongation factor 2	gi|4503483	96,246 /6.41	8% (395)	5	1.53±0.11 0.03	^{2}VNFTVDQIR^{10} ^{606}ARPFPDGLAEDIDKGEVSAR^{625} ^{634}YLAEKYEWDVAEAR^{647} ^{728}CLYASVLTAQPR^{739} ^{786}AYLPVNESFGFTADLR^{801}
7	far upstream element-binding protein 2	gi|119589502	77,060 /6.84	7% (449)	4	-2.13±0.25 0.03	^{41}GGGGPGGGGPGGGSAGGPSQPPGGGGPGIR^{70} ^{41}GGGGPGGGGPGGGSAGGPSQPPGGGGPGIRK^{71} ^{307}DQGGFGDRNEYGSR^{320} ^{449}AINQQTGAFVEISR^{462}
12	ruvB-like 1	gi|4506753	50,538 /6.02	17% (569)	5	1.82± 0.18 (0.03)	^{34}QAASGLVGQENAR^{46} ^{172}LDPSIFESLQKER^{184} ^{185}VEAGDVIYIEANSGAVKR^{202} ^{318}ALESSIAPIVIFASNR^{333} ^{379}AQTEGINISEEALNHLGEIGTK^{400}
13,17	heterogeneous nuclear ribonucleoprotein H1	gi|5031753	49,484 /5.89	12% (576)	4	1.57±0.02 (0.04)	^{17}GLPWSCSADEVQR^{29} ^{50}EGRPSGEAFVELESEDEVK^{68} ^{99}HTGPNSPDTANDGFVR^{114} ^{317}VHIEIGPDGR^{326}
21	nascent polypeptide-associated complex subunit alpha	gi|5031931	23,370 /9.6	15% (253)	2	-1.98±0.17 (0.03)	^{126}SPASDTYIVFGEAK^{139} ^{140}IEDLSQQAQLAAAEK^{154}
22	acidic leucine-rich nuclear phosphoprotein 32	gi|5453880	28,682 /3.99	13% (141)	2	-2.15±0.42 (0.03)	^{117}SLDLFNCEVTNLNDYRENVFK^{137} ^{138}LLPQLTYLDGYDR^{150}
29	prohibitin	gi|4505773	29,843 /5.57	25% (588)	5	-1.98±0.31 (0.02)	^{94}ILFRPVASQLPR^{105} ^{106}IFTSIGEDYDER^{117} ^{134}FDAGELITQR^{143} ^{220}AAELIANSLATAGDGLIELR^{239} ^{240}KLEAAEDIAYQLSR^{253}
33	SAP domain-containing ribonucleoprotein	gi|32129199	23,713 /6.1	23% (271)	4	1.54±0.21 (0.02)	^{13}LAELKQECLAR^{23} ^{29}GIKQDLIHR^{37} ^{93}ITSEIPQTER^{102} ^{181}FGIVTSSAGTGTTEDTEAK^{199}
35	protein DJ-1	gi|31543380	20,050 /6.33	33% (279)	3	-1.64±0.17 (0.01)	^{33}VTVAGLAGKDPVQCSR^{48} ^{64}EGPYDVVVLPGGNLG

							AQNLSESAAVK^{89} ^{90}EGPYDVVVLPGGNLGAQNLSESAAVK^{98}
40	eukaryotic translation initiation factor 3	gi|10801345	25,329 /4.72	6% (156)	2	-1.57±0.23 (0.03)	^{17}GIDRYNPENLATLER^{31} ^{21}YNPENLATLER^{31}
48	chromobox protein homolog 1	gi|5803076	21,519 /4.85	15%(237)	2	1.97±0.14 (0.04)	^{9}KVEEVLEEEEEEYVVEK^{25} ^{156}CPQVVISFYEER^{167}
Signal transduction and protein degradation							
14	erbB3 binding protein EBP1	gi|4099506	38,320 /6.13	14% (292)	4	2.13±0.31 (0.01)	^{102}LVKPGNQNTQVTEAWNK^{118} ^{210}AFFSEVER^{217} ^{210}AFFSEVERR^{218} ^{279}ITSGPFEPDLYKSEMEVQDAELK^{301}
27	14-3-3 protein epsilon	gi|5803225	29,326 /4.63	14% (297)	3	-2.15±0.16 (0.01)	^{95}LICCDILDVLDKHLIPAANTGESK^{118} ^{131}YLAEFATGNDR^{141} ^{131}YLAEFATGNDRK^{142}
28	proteasome subunit alpha type-1 isoform 2	gi|4506179	29,822 /4.24	17% (246)	3	-1.56±0.14 (0.03)	^{4}NQYDNDVTVWSPQGR^{18} ^{97}FVFDRPLPVSR^{107} ^{244}AQPAQPADEPAEKADEPMEH^{263}
30	ubiquitin carboxy-terminal hydrolase L1	gi|4185720	23,354 /5.33	29% (447)	4	-1.75±0.24 (0.04)	^{9}LGVAGQWR^{16} ^{125}NEAIQAAHDAVAQEGQCR^{142} ^{143}VDDKVNFHFILFNNVDGHLYELDGR^{167} ^{192}EFTEREQGEVR^{202}
31	proteasome subunit beta type-4	gi|22538467	29,242 /4.21	18%(442)	4	-1.57±0.37 (0.04)	^{59}VNNSTMLGASGDYADFQYLK^{78} ^{101}AIHSWLTR^{108} ^{166}EVLEKQPVLSQTEAR^{180} ^{171}QPVLSQTEAR^{180}
39	translationally-controlled tumor protein	gi|15214610	19,759 /4.84	13%(177)	3	-1.83±0.24 (0.04)	^{6}DLISHDEMFSDIYK^{19} ^{101}GKLEEQRPER^{110} ^{103}LEEQRPER^{110}
41	annexin A5	gi|4502107	35,971 /4.94	19%(581)	5	2.03±0.16 (0.02)	^{6}GTVTDFPGFDER^{17} ^{126}QVYEEEYGSSLEDDVVGDTSGYYQR^{150} ^{186}WGTDEEKFITIFGTR^{200} ^{193}FITIFGTR^{200} ^{276}SEIDLFNIR^{284}
42	proteasome subunit alpha type-3	gi|4506183	28,643 /4.26	12% (202)	3	-1.91±0.21 (0.01)	^{58}LYEEGSNKR^{66} ^{87}SLADIAREEASNFR^{100} ^{101}SNFGYNIPLK^{110}
49	ubiquitin-conjugating enzyme E2 K	gi|4885417	22,507 /5.33	19% (235)	3	1.63±0.17 (0.04)	^{29}VDLVDENFTELR^{40} ^{41}GEIAGPPDTPYEGGR^{55} ^{62}IPETYPFNPPK^{72}
Protein trafficking							

1	nuclear autoantigenic sperm protein isoform 2	gi|27262628	85,471 /4.26	11% (493)	5	-2.31±0.32 (0.02)	^{377}DGAVNGPSVVGDQTPIEPQTSIER^{400} ^{418}LVPSQEETKLSVEESEAAGDGVDTK^{442} ^{536}EAQLYAAQAHLK^{547} ^{638}EIEELKELLPEIR^{650} ^{698}KPTDGASSSNCVTDISHLVR^{717}
19	annexin A1	gi|119582950	40,475 /6.57	19% (607)	5	2.34±0.42 (0.01)	^{30}GGPGSAVSPYPTFNPSSDVAALHK^{53} ^{114}TPAQFDADELR^{124} ^{186}GDRSEDFGVNEDLADSDAR^{204} ^{189}SEDFGVNEDLADSAR^{204} ^{215}GTDVNVFNTILTTR^{228}
23	Clathrin chain A	gi|4502899	23,704 /4.43	14%(243)	3	-1.84±0.17 (0.03)	^{139}AIKELEEWYAR^{149} ^{142}ELEEWYAR^{149} ^{163}AAEEAFVNDIDESSPGTEWER^{183}
44	Ran-specific GTPase-activating protein	gi|542991	23,610 /5.19	6% (144)	2	-1.23±0.08 (0.04)	^{58}FASENDLPEWK^{68} ^{58}FASENDLPEWKER^{70}
47	endoplasmin precursor	gi|4507677	92,696 /4.76	5% (379)	4	2.03±0.34 (0.01)	^{76}FAFQAEVNR^{84} ^{385}SILFVPTSAPR^{395} ^{396}GLFDEYGSK^{404} ^{512}FQSSHHPTDITSLDQYVER^{530}
Cytoskeletal proteins							
2	Drebrin	gi|18426913	72,078 /5.02	13% (336)	4	-2.27± 0.16 (0.01)	^{150}LREDENAPVGTTYQK^{165} ^{272}SESEVEEAAAIIAQRPDNPR^{291} ^{337}SPSDSSASTPVAEQIER^{354} ^{355}ALDEVTSSQPPPLPPPPPPAQETQEPSPILDSEETR^{390}
18	septin-2	gi|4758158	41,689 /6.15	14% (342)	5	2.1±0.24 (0.03)	^{78}TVQIEASTVEIEER^{91} ^{97}LTVVDTPGYGDAINCR^{112} ^{117}TIISYIDEQFER^{128} ^{129}YLHDESGLNR^{138} ^{129}YLHDESGLNRR^{139}
25	F-actin-capping protein subunit beta	gi|4826659	30,952 /5.36	17% (407)	5	-2.1 ±0.07 (0.02)	^{15}RLPPQQIEK^{23} ^{95}KLEVEANNAFDQYR^{108} ^{96}LEVEANNAFDQYR^{108} ^{146}GCWDSIHVVEVQEK^{159} 226STLNEIYFGK235
38	Stathmin 1/oncoprotein 18	gi|5031851	17,292 /5.76	24% (255)	3	-2.31± 0.22 (0.02)	^{15}ASGQAFELILSPR^{27} ^{28}SKESVPEFPLSPPK^{41} ^{86}AIEENNNFSK^{95}
46	microtubule-associated protein	gi|6912494	30,151 /5.02	20%(314)	3	1.79±0.05 (0.01)	^{114}FFDANYDGKDYDPVAAR^{130}

	RP/EB family member						^{151}KPLTSSAPQRPISTQR^{168} ^{223}NIELICQENEGENDPVLQR^{241}
Protein synthesis							
10	transfer RNA-Trp synthetase	gi|340368	53,396 /5.32	9% (263)	5	1.65±0.21 (0.03)	^{97}GIDYDKLIVR^{106} ^{123}ATGQRPHHFLR^{133} ^{135}GIFFSHR^{141} ^{154}KPFYLYTGR^{162} ^{257}HVTFNQVK^{264}
Channel protein							
45	nuclear chloride channel	gi|4588526	27,249 /5.09	22%(480)	5	1.78±0.20 (0.02)	^{21}IGNCPFSQR^{29} ^{139}VLDNYLTSPLPEEVDETSAEDEGVSQR^{165} ^{194}YRGFTIPEAFR^{204} ^{196}GFTIPEAFR^{204} ^{209}YLSNAYAR^{216}
Chaperon							
3	Hsp90AA1	gi|83699649	98,652 /4.94	9% (449)	4	-1.77±0.18 (0.02)	^{154}HNDDEQYAWESSAGGSFTVR^{173} ^{186}VILHLKEDQTEYLEER^{201} ^{328}HFSVEGQLEFR^{338} ^{346}RAPFDLFENR^{355}
4	heat shock cognate 71	gi|62897129	71, 083 /5.37	9% (527)	4	-1.68±0.36 (0.04)	^{37}TTPSYVAFTDTER^{49} ^{138}TVTNAVVTVPAYFNDSQR^{155} ^{221}STAGDTLGGEDFDNR^{236} ^{300}ARFEELNADLFR^{311}
8	calreticulin precursor	gi|4757900	48,283 /4.29	8% (243)	2	-1.54±0.11 (0.03)	^{25}EQFLDGDGWTSR^{36} ^{163}CKDDEFTHLYTLIVRPDNTYEVK^{185}
11	T-complex protein 1 subunit beta	gi|5453603	57,794 /6.01	10% (589)	5	1.72±0.10 (0.03)	^{90}VQDDEVGDGTTSVTVLAAELLR^{111} ^{120}KIHPQTIIAGWR^{131} ^{121}IHPQTIIAGWR^{131} ^{285}HGINCFINR^{293} ^{377}GATQQILDEAER^{388}
36	prostaglandin E synthase 3	gi|23308579	18,971 /4.35	8% (80)	2	-1.79±0.21 (0.02)	^{79}KGESGQSWPR^{88} ^{80}GESGQSWPR^{88}

[a] p values were generated by analyzing the gel images with thr`ee replicates. These values are representative of CIP2A shRNA1 treated compared to control shRNA samples. Differences were considered significant at $p < 0.05$.

[b] we expressed the up-regulation as “+”, and downregulation as “-” after CIP2A knockdown.

[c] Protein scores greater than 56 are significant. All the proteins validated should have at least one peptide identified by MS/MS spectra with an individual ion score >28 indicated identity or extensive homology at $p < 0.05$. The charge state of each peptide is “+1.”