GO Biological process	**GO Cell. component**	**Total no. of peptides**	**Remarks**
chromatin modeling/modification transcriptional regulation	nucleus	289	ATPase-dependent chromatin remodeling, HDACs
Unknown		158	putative transcription factors, RNA binding proteins, nucleolar proteins, receptors etc.
mRNA processing	nucleus	139	splicing factors
DNA topological change	nucleus	130	topoisomerases
transcription regulation, DNA dependent	nucleus	105	Transcription factors
Metabolism	mitochondrion	54	carboxylases
protein biosynthesis	cytosol	53	ribosomal proteins
ribosome biogenesis	nucleolus	37	apoptotic chromatin condensation inducer in the nucleus
DNA repair	nucleus	28	XRCC1, Ku autoantigen
nucleolus biogenesis	nucleus	24	
cell proliferation	nucleus	23	Ki-67
DNA replication	nucleus	23	ORC
chromatin assembly	nucleus	21	histones
Cytoskeleton		18	tubulin
structural molecule	nucleus	11	NuMA1
protein targeting	nucleus	7	
Apoptosis	nucleus	4	CDC5
protein chaperone	nucleus	4	
cell cycle	nucleus	3	RCC1
signal transduction		2	GTP binding protein 3
Total # of peptides:		**>1100**	
Gel slices:		**~45**	
MW range:		**15-324kDa**	

Supplementary Table I: Classification by Gene Ontology (GO) criteria of proteins identified by mass spectrometry as co-purifying with GATA-1