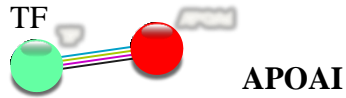


## Supplementary file-6

Protein networks and Gene ontology of serotransferrin and apolipoprotein-A1 by STRING - V 11.0



Number of nodes: 2

Number of edges: 1

Average node degree:1

Avg. local clustering coefficient: 1

Expected number of edges:0 PPI enrichment p-value: 0.0486 your network has significantly more interactions than expected (what does that mean?)

### Biological Process( GO)

GO-term	Description	Count in gene set	False discovery rate
GO:0002576	Platelet degranulation	2 of 129	0.0201
GO:0031647	Regulation of protein stability	2 of 251	0.0377

### Cellular Component (GO)

GO-term	Description	Count in gene set	False discovery rate
GO:0034774	Secretory granule lumen	2 of 323	0.0172
GO:0030139	Endocytic vesicle	2 of 275	0.0172
GO:0009986	Cell surface	2 of 690	0.0172
GO:0005788	Endoplasmic reticulum lumen	2 of 299	0.0172
GO:0005769	Early endosome	2 of 341	0.0172

**Molecular function analysis by panther**  
**15.0**

Family ID	Mapped IDs	Family Name	PANTHER GO-Slim Molecular Function
PTHR18976:SF11	HUMAN  HGNC=600 UniProt KB=P02647	APOLIPOPROTEIN A-I	Cholesterol binding
			O-acyltransferase activity
			Enzyme activator activity
			Phospholipid binding

**Reactome pathways**

Pathways	Description	Count in gene set
False discovery rate		
HSA-8957275 0.0013	Post-translational protein phosphorylation	2 of 106
HSA-381426 0.0013	Regulation of Insulin-like Growth Factor (IGF) transport	2 of 123
HSA-114608 0.0013	Platelet degranulation	2 of 125
HSA-5653656 0.0068	Vesicle-mediated transport	2 of 649
HSA-382551 0.0070	Transport of small molecules	2 of 706

