



**Appendix 1:** Human protein-protein interaction network

**Appendix 2: Gene Ontology functional enrichment analysis by Web Gestalt**

<b>Gene Ontology ID</b>	<b>Gene Ontology Name</b>	<b>The number of genes in the category</b>	<b>The number of overlapped genes between the sub network and the category</b>	<b>Adjusted p-value</b>	<b>Candidate Gene name</b>
<b>GO:1900034</b>	regulation of cellular response to heat	43	3	0.02	<i>MTOR, HSPA8, RPTOR</i>
<b>GO:0045945</b>	positive regulation of transcription by RNA polymerase III	10	2	0.03	<i>MTOR, RPTOR</i>
<b>GO:0071233</b>	cellular response to leucine	10	2	0.03	<i>MTOR, RPTOR</i>
<b>GO:0019886</b>	antigen processing and presentation of exogenous peptide antigen via MHC class II	93	3	0.03	<i>CLTC,DNM2,HLA-DRB</i>
<b>GO:0034605</b>	cellular response to heat	94	3	0.03	<i>MTOR, HSPA8, RPTOR</i>
<b>GO:0002495</b>	antigen processing and presentation of peptide antigen via MHC class II	95	3	0.03	<i>CLTC,DNM2,HLA-DRB</i>
<b>GO:0002504</b>	antigen processing and presentation of peptide or polysaccharide antigen via MHC class II	96	3	0.03	<i>CLTC,DNM2,HLA-DRB</i>
<b>GO:0043201</b>	response to leucine	13	2	0.04	<i>MTOR, RPTOR</i>
<b>GO:0002478</b>	antigen processing and presentation of exogenous peptide antigen	116	3	0.05	<i>CLTC,DNM2,HLA-DRB</i>
<b>GO:0019884</b>	antigen processing and presentation of exogenous antigen	123	3	0.05	<i>CLTC,DNM2,HLA-DRB</i>
<b>GO:0048002</b>	antigen processing and presentation of peptide antigen	128	3	0.05	<i>CLTC,DNM2,HLA-DRB</i>
<b>GO:0010592</b>	positive regulation of lamellipodium assembly	18	2	0.05	<i>DNM2, MTOR</i>
<b>GO:0009408</b>	response to heat	133	3	0.05	<i>MTOR, HSPA8, RPTOR</i>
<b>GO:0009267</b>	cellular response to starvation	141	3	0.05	<i>MTOR, HSPA8, RPTOR</i>

**Appendix 4: Gene Ontology enrichment of 17 target gene lists, 8 clusters, by DAVID**

Annotation cluster	Enrichment score	Gene ontology term	Count	p-value
1	4.83	Lysosome	6	0.000011
		Lysosome	6	0.000013
		macroautophagy	3	0.0023
2	2.45	focal adhesion	6	0.000016
		receptor-mediated endocytosis	4	0.00067
		Coated pit	3	0.00071
3	1.82	Golgi membrane	5	0.0015
		Endoplasmic reticulum	5	0.0079
		positive regulation of gene expression	3	0.025
4	1.57	plasma membrane	11	0.00073
		Membrane	13	0.0059
		disulfide bond	8	0.014
		Cell membrane	8	0.018
		Disulfide bond	8	0.018
		topological domain: Extracellular	7	0.044
		calcium ion binding	4	0.044
		integral component of plasma	5	0.031
		membrane glycosylation site: N-linked (GlcNAc...) signal peptide	8	0.035
		topological domain: Cytoplasmic	7	0.038
		Glycoprotein	7	0.044
		Transmembrane	8	0.044
		extracellular region	9	0.046
		integral component of membrane	5	0.047
			9	0.05
5	1.53	phosphatidylinositol-mediated signaling	3	0.0045
		PI3K-Akt signaling pathway	4	0.03

6	1.48	protein kinase binding	4	0.0049
		cytosol	8	0.016
		Phosphoprotein	12	0.019
		Cytoplasm	8	0.05
7	1.05	Endocytosis	4	0.012
		Nucleotide-binding	5	0.044
		ATP-binding	5	0.047
8	0.88	calcium ion binding	4	0.028