

Les protéines identifiées fournies par l'analyse MS sont classées par groupe d'interaction:

<input type="checkbox"/>	▲ ID	Molecules in Network	Score	Focus Molecu	Top Functions
<input type="checkbox"/>	1	14-3-3, 14-3-3 (β,ε,ζ), 14-3-3(β,γ,θ,η,ζ), ↓ALAD , ↑ANXA7 , ↑APOA1 , ↑ATP5B* , Calpain, ↑CALR , ↑CKB , Cofilin, Creatine Kinase, ↓DBT , ↑FGB , ↑FGG , Fibrin, Fibrinogen, ↑GFAP , ↑HSPA4 , ↑HSPB6 , Ldh, ↓LDHB , LDL, NFκB (complex), ↑P4HB , ↑PGM1 , ↑PRPH , ↑S100A1 , ↑SERPINA1* , ↑TGM2 , ↓TPI1 , ↑YWHAB , ↑YWHAE , ↑YWHAQ (includes EG:22630), ↑YWHAZ	48	24	Protein Trafficking, Genetic Disorder, Hematological Disease
<input type="checkbox"/>	2	↑ACTC1* , Actin, ↓ALDH2* , Alpha tubulin, ↑ANXA5* , Beta Tubulin, ↑CAPZB , ↑CCT2 , ↑CRYAB , ↑DES* , ↓DLST , ↑DPYSL2 , ERK1/2, Erm, ↑EZR* , EZR-MSN-RDX, F Actin, ↓FABP3* , HSP, Hsp90, ↑HSPA5 , ↑HSPB1 , ↓HSPD1 , Immunoglobulin, Insulin, ↑MSN* , Ras homolog, ↑RDX* , Rock, ↑TPM3 , ↑TUBA4A , ↑TUBB2C , Tubulin, ↓VDAC1 , ↑VIM	43	21	Cellular Assembly and Organization, Cellular Compromise, Genetic Disorder
<input type="checkbox"/>	3	26s Proteasome, ↑ACTR3* , Akt, Ap1, Caspase, Ck2, Cytochrome c, ↓ENO3 , ERK, ↓FKBP4 , ↓FTH1 , Histone h3, Hsp70, IgG, IL1, ↑INPP5E , Jnk, ↑MBD1 , MHC Class I (complex), ↑MVP , P38 MAPK, PDGF BB, ↑PDIA3 , PI3K (complex), Pka, Pkc(s), PLC, ↓PRDX3 , ↓PRDX6 , ↓PSMB4 , RNA polymerase II, ↑SERPINA3K , ↓SRL* , ↓UQCRC1 , ↑YWHAG	28	15	Small Molecule Biochemistry, Skeletal and Muscular System Development and Function, Lipid Metabolism
<input type="checkbox"/>	4	↓ALAD , ↓ALDH2* , ↓BCKDHA* , BCKDHB, butyric acid, C22ORF28, ↑COL6A1 , COL6A3, CR1, Creb, ↓DBT , ↓ECH1 , GSTM2, GSTM4, GSTM3 (includes EG:14864), ↓GSTM3 (includes EG:2947)*, HPX, HSP90AA2, ↓IDH3A* , IKBKG, LEP, LIN54, ↓LRPPRC , MAPK3, MAPKAPK5, ↑MVP , ↓MYL4 , ↑PNPLA2 , Rlc, SLC12A6, ↑SLMAP , TIAL1, TNF, ↓TUFM , ZAP70	26	14	Drug Metabolism, Glutathione Depletion In Liver, Genetic Disorder
<input type="checkbox"/>	5	acad, ↓ACADS , ↓ACADSB , ACOT1 (includes EG:26897), acyl-CoA dehydrogenase, ↓ATP5H (includes EG:10476), ATP5S, ATPase, ↓CLPP , CLPX, DDX1, HNF4A, ↓IVD , KIF1B, KIF20B, ↓MDH1 , MLH1, NDUFA9 (includes EG:4704), ↑NDUFAF3 , NDUFAF4, ↓NDUFS1 , NDUFS2, NDUFS3, NDUFS4, NDUFS8, ↓NDUFV2 , ↓NUDT2 , PPARA, ↑PSMD13 , ↑PYGB , ↑SEPT2* , SLC25A22, SNCA, ↓SUCLA2 , TMOD2	26	14	Genetic Disorder, Metabolic Disease, Cardiovascular Disease
<input type="checkbox"/>	6	↓ACOT2 , ↑ADK , ANKRD2, CAD, ↑COMT , DLAT, DLD, EHD1, ↑EHD2 , ↑EHD4 , F2, FHL1, ↓HDHD3 , IGF1R, KLK2, L-triiodothyronine, ↑MYBPC3 , MYOF, PACSIN1, PACSIN2, PDHA2, PDHA1 (includes EG:5160), ↓PDHB , ↓PDHX , ↓PDK2 , SDC4, ↓SELENBP1 , ↑SERPINA1* , ↑SERPINB6 , SNAP29, ↑TCAP , TRIM55, TRIM63, TRIP13, TTN	24	14	Lipid Metabolism, Nucleic Acid Metabolism, Small Molecule Biochemistry
<input type="checkbox"/>	7	ACTL6B, ANO8, ↓COQ9	2	1	Infection Mechanism, Genetic Disorder, Neurological Disease
<input type="checkbox"/>	8	CAV3, DYSF, ↑TRIM72 , UBE2I	2	1	Genetic Disorder, Skeletal and

Les protéines identifiées en MS sont en gras. Le caractère « sur ou sous-expression » est indiqué par la flèche de couleur reflétant le résultat de quantification s'il y a lieu. Les autres protéines sont proposées grâce aux données bibliographiques.