

## Results from Metabolomic Data Analysis with MetaboAnalyst 5.0

## A) PLASMA

	Total	Expected	Hits	Raw p	$-\log_{10}(p)$	Holm adjust	FDR	Impact
Aminoacyl-tRNA biosynthesis	48	0.38	4	3.68E-04	3.43E+00	3.09E-02	3.09E-02	0.00
Valine, leucine and isoleucine biosynthesis	8	0.06	2	1.58E-03	2.80E+00	1.31E-01	6.62E-02	0.00
Phenylalanine, tyrosine and tryptophan biosynthesis	4	0.03	1	3.14E-02	1.50E+00	1.00E+00	6.40E-01	0.50
Arginine and proline metabolism	38	0.30	2	3.46E-02	1.46E+00	1.00E+00	6.40E-01	0.08
Valine, leucine and isoleucine degradation	40	0.32	2	3.81E-02	1.42E+00	1.00E+00	6.40E-01	0.00
Taurine and hypotaurine metabolism	8	0.06	1	6.19E-02	1.21E+00	1.00E+00	8.67E-01	0.00
Phenylalanine metabolism	12	0.10	1	9.15E-02	1.04E+00	1.00E+00	1.00E+00	0.36
Primary bile acid biosynthesis	46	0.37	1	3.11E-01	5.08E-01	1.00E+00	1.00E+00	0.02
Purine metabolism	66	0.52	1	4.16E-01	3.81E-01	1.00E+00	1.00E+00	0.00

## B) MILK

	Total	Expected	Hits	Raw p	$-\log_{10}(p)$	Holm adjust	FDR	Impact
Lysine degradation	25	0.12	1	1.10E-01	9.57E-01	1.00E+00	1.00E+00	0.00
Porphyrin and chlorophyll metabolism	30	0.14	1	1.31E-01	8.82E-01	1.00E+00	1.00E+00	0.05
Glycerophospholipid metabolism	36	0.17	1	1.56E-01	8.08E-01	1.00E+00	1.00E+00	0.00
Tryptophan metabolism	41	0.19	1	1.75E-01	7.56E-01	1.00E+00	1.00E+00	0.14
Aminoacyl-tRNA biosynthesis	48	0.22	1	2.03E-01	6.94E-01	1.00E+00	1.00E+00	0.00
Purine metabolism	66	0.31	1	2.69E-01	5.71E-01	1.00E+00	1.00E+00	0.00

**Total** is the total number of compounds in the pathway.

**Hits** is the actually matched number from the user uploaded data.

**Raw p** is the original *P*-value calculated from the enrichment analysis.

**Holm p** is *P*-value adjusted by Holm-Bonferroni method.

**FDR p** is *P*-value adjusted using False Discovery Rate.

**Impact** is the pathway impact value calculated from pathway topology analysis.