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# Pathway analysis with Metaboanalyst and KEGG

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Targeted  
 Metabolomics &  
 Proteomics  
 Laboratory

## Files in mummichog results folder

1531447106.01.Workshop_neg_out	Today, 3:52 PM	--	Folder
tsv	Today, 3:52 PM	--	Folder
_tentative_featurematch_Workshop_neg_out.xlsx	Jul 12, 2018, 9:03 PM	117 KB	Micros...(xlsx)
InspectedNodes_ActivityNetwork.tsv	Jul 12, 2018, 9:03 PM	20 KB	Plain Text
mcg_metabolite_works...t_Workshop_neg_out.tsv	Jul 12, 2018, 9:03 PM	67 KB	Plain Text
mcg_metabolite_works...Workshop_neg_out.xlsx	Jul 12, 2018, 9:03 PM	26 KB	Micros...(xlsx)
mcg_modularanalysis_Workshop_neg_out.xlsx	Jul 12, 2018, 9:03 PM	81 KB	Plain Text
mcg_modularanalysis_Workshop_neg_out.tsv	Jul 12, 2018, 9:03 PM	25 KB	Micros...(xlsx)
mcg_pathwayanalysis_Workshop_neg_out.xlsx	Jul 12, 2018, 9:03 PM	183 KB	Plain Text
mcg_pathwayanalysis_Workshop_neg_out.tsv	Jul 12, 2018, 9:03 PM	57 KB	Micros...(xlsx)
_tentative_featurematch_Workshop_neg_out.tsv	Jul 12, 2018, 9:03 PM	383 KB	Plain Text
mummichog.log	Jul 12, 2018, 9:03 PM	16 KB	Log File
result.html	Jul 12, 2018, 9:03 PM	163 KB	HTML
sif	Jul 12, 2018, 9:03 PM	--	Folder
web	Jul 12, 2018, 8:58 PM	--	Folder

Open the file. It's on your thumb drive.

## Identification of each observed ion

m/z	id	match_forr	mz_differen	name	pathway
73.0294	C00116	M-H2O-H[-]	0	Glycerol; G Phosphatidylinositol phosphate metabolism\$Galactose metabolism\$Fatty Acid Metabolism\$S	
73.0294	C00163	M-H[-]	-0.0001	Propanoate Bile acid biosynthesis\$Propanoate metabolism	
73.0294	C00207	M-H+O[-]	-0.0001	Acetone; D Pyruvate Metabolism\$Propanoate metabolism	
73.0294	C00418	M-2H[2-]	-0.0001	(R)-Mevalo Squalene and cholesterol biosynthesis	
73.0294	C00424	M-H[-]	-0.0001	(S)-Lactalide Pyruvate Metabolism	
73.0294	C00479	M-H+O[-]	-0.0001	Tryptophan metabolism	
73.0294	C00937	M-H[-]	-0.0001	(R)-Lactalide Pyruvate Metabolism\$Glycine, serine, alanine and threonine metabolism	
73.0294	C05235	M-H[-]	-0.0001	Hydroxyac Pyruvate Metabolism	
73.0294	C05999	M-H[-]	-0.0001	Lactaldehyde; 2-Hydroxypropionaldehyde; 2-Hydroxypropanal	
75.0101	C00385	M-2H[2-]	0.0007	Xanthine Purine metabolism	
87.0456	C00246	M-H[-]	0.0005	Butanoic ac Butanoate metabolism\$Fatty acid activation	
93.0353	C00116	M(S34)-H[-]	-0.0005	Glycerol; G Phosphatidylinositol phosphate metabolism\$Galactose metabolism\$Fatty Acid Metabolism\$S	
93.0353	C00146	M-H[-]	0.0007	Phenol; Bei Benzoate degradation via CoA ligation	
93.0353	C04221	M-H2O-H[-]	0.0008	trans-1,2-Dihydrobenzene-1,2-diol	
93.0353	C15584	M-H[-]	0.0007	Phenol	
93.0355	C00116	M(S34)-H[-]	-0.0003	Glycerol; G Phosphatidylinositol phosphate metabolism\$Galactose metabolism\$Fatty Acid Metabolism\$S	
93.0355	C00146	M-H[-]	0.0009	Phenol; Bei Benzoate degradation via CoA ligation	
93.0355	C15584	M-H[-]	0.0009	Phenol	
93.0374	C00116	M(Cl37)-H[-]	0.0002	Glycerol; G Phosphatidylinositol phosphate metabolism\$Galactose metabolism\$Fatty Acid Metabolism\$S	
99.0079	C00042	M-H2O-H[-]	-0.0008	Succinate; Valine, leucine and isoleucine degradation\$Phytanic acid peroxisomal oxidation\$Arginine and F	
99.0079	C01036	M-2H[2-]	-0.0009	4-Maleylac Tyrosine metabolism	
99.0079	C01061	M-2H[2-]	-0.0009	4-Fumaryl Tyrosine metabolism	
99.0079	C02170	M-H2O-H[-]	-0.0008	Methylmal Valine, leucine and isoleucine degradation	
99.0079	C05985	M+HCOO[-]	-0.0003	2-Propyn-1 Propanoate metabolism	

## Select and copy the KEGG IDs

m/z	id	match_forr	mz_differen	name	pathway
73.0294	C00116	M-H2O-H[-]	0	Glycerol; G Phosphatidylinositol phosphate metabolism\$Galactose metabolism\$Fatty Acid Metabolism\$S	
73.0294	C00163	M-H[-]	-0.0001	Propanoate Bile acid biosynthesis\$Propanoate metabolism	
73.0294	C00207	M-H+O[-]	-0.0001	Acetone; D Pyruvate Metabolism\$Propanoate metabolism	
73.0294	C00418	M-2H[2-]	-0.0001	(R)-Mevalo Squalene and cholesterol biosynthesis	
73.0294	C00424	M-H[-]	-0.0001	(S)-Lactalide Pyruvate Metabolism	
73.0294	C00479	M-H+O[-]	-0.0001	Tryptophan metabolism	
73.0294	C00937	M-H[-]	-0.0001	(R)-Lactalide Pyruvate Metabolism\$Glycine, serine, alanine and threonine metabolism	
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73.0294	C05999	M-H[-]	-0.0001	Lactaldehyde; 2-Hydroxypropionaldehyde; 2-Hydroxypropanal	
75.0101	C00385	M-2H[2-]	0.0007	Xanthine Purine metabolism	
87.0456	C00246	M-H[-]	0.0005	Butanoic ac Butanoate metabolism\$Fatty acid activation	
93.0353	C00116	M(S34)-H[-]	-0.0005	Glycerol; G Phosphatidylinositol phosphate metabolism\$Galactose metabolism\$Fatty Acid Metabolism\$S	
93.0353	C00146	M-H[-]	0.0007	Phenol; Bei Benzoate degradation via CoA ligation	
93.0353	C04221	M-H2O-H[-]	0.0008	trans-1,2-Dihydrobenzene-1,2-diol	
93.0353	C15584	M-H[-]	0.0007	Phenol	
93.0355	C00116	M(S34)-H[-]	-0.0003	Glycerol; G Phosphatidylinositol phosphate metabolism\$Galactose metabolism\$Fatty Acid Metabolism\$S	
93.0355	C00146	M-H[-]	0.0009	Phenol; Bei Benzoate degradation via CoA ligation	
93.0355	C15584	M-H[-]	0.0009	Phenol	
93.0374	C00116	M(Cl37)-H[-]	0.0002	Glycerol; G Phosphatidylinositol phosphate metabolism\$Galactose metabolism\$Fatty Acid Metabolism\$S	
99.0079	C00042	M-H2O-H[-]	-0.0008	Succinate; Valine, leucine and isoleucine degradation\$Phytanic acid peroxisomal oxidation\$Arginine and F	
99.0079	C01036	M-2H[2-]	-0.0009	4-Maleylac Tyrosine metabolism	
99.0079	C01061	M-2H[2-]	-0.0009	4-Fumaryl Tyrosine metabolism	
99.0079	C02170	M-H2O-H[-]	-0.0008	Methylmal Valine, leucine and isoleucine degradation	
99.0079	C05985	M+HCOO[-]	-0.0003	2-Propyn-1 Propanoate metabolism	

# Go to Metaboanalyst

MetaboAnalyst - statistical, functional and integrative analysis of metabolomics data

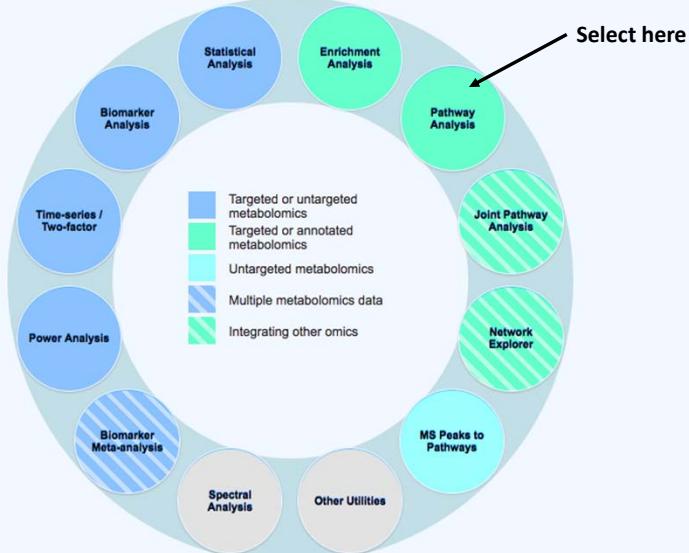
Welcome >> [click here to start](#) <<

## News & Updates

- Check out our latest paper on [MetaboAnalyst 4.0](#); [NEW](#)
- Check out our [OmicsNet](#) for flexible creation & 3D visualization of complex networks integrating metabolites, genes/proteins, miRNAs and transcription factors; [NEW](#)
- Fixed issue with name mapping in enrichment analysis (06/28/2018); [NEW](#)
- Fixed issue with pathway visualization (06/18/2018); [NEW](#)
- Enhanced pathway image generation to deal with concurrency issue (06/13/2018); [NEW](#)
- Fixed the issues for name mapping and node-click information in pathway visualization (06/12/2018); [NEW](#)
- Fixed the issue for data editor in biomarker analysis (05/28/2018); [NEW](#)
- Fixed the issue for sample hold-out analysis in biomarker analysis (04/23/2018); [NEW](#)
- Fixed the issue with time-series group ordering based on numeric values (04/19/2018); [NEW](#)
- Enhanced support for SVG export for KEGG global network (04/04/2018); [NEW](#)
- Check out our [MicrobiomeAnalyst](#) for comprehensive analysis of microbiome data;
- Release of MetaboAnalyst 4.0 together with a companion R package [MetaboAnalystR](#). You can still access [version 3.0 here](#) (01/29/2018);

MetaboAnalyst - statistical, functional and integrative analysis of metabolomics data

Click a module to proceed, or scroll down for more details:



Please enter a one-column compound list:

iC00116  
C00163  
C00207  
C00418  
C00424  
C00479  
C00937  
C05235  
C05999  
C00385  
C00246  
C00116  
C00146  
C04221  
C15584  
C00116  
C00116

**Transfer the KEGG IDs into the box, select the input type and submit**

**Input Type:**

Use our example data

## Listed metabolites

Compound Name/ID Standardization:

Please note:

- Greek alphabets are not recognized, they should be replaced by English names (i.e. alpha, beta)
- Query names in normal white indicate exact match - marked by "1" in the download file;
- Query names highlighted indicate no exact or unique match - marked by "0" in the downloaded file;
- For compound name, you should click the View link to perform approximate search and manually select the correct match if found;
- For KEGG ID, it is possible to have multiple hits, you should click the View link to manually select the correct match if found;

Query	Hit	HMDB	PubChem	KEGG	Details
C00116	Glycerol	<a href="#">HMDB0000131</a>	753	<a href="#">C00116</a>	
C00163	Propionic acid	<a href="#">HMDB0000237</a>	1032	<a href="#">C00163</a>	
C00207	Acetone	<a href="#">HMDB0001659</a>	180	<a href="#">C00207</a>	
C00418	Mevalonic acid	<a href="#">HMDB0000227</a>	449	<a href="#">C00418</a>	
C00424	Lactaldehyde	<a href="#">HMDB0003052</a>	439231	<a href="#">C00424</a>	
C00479	Propanal	<a href="#">HMDB0003366</a>	527	<a href="#">C00479</a>	
C00937	D-Lactaldehyde	<a href="#">HMDB0006458</a>	439350	<a href="#">C00937</a>	
C05235	Hydroxyacetone	<a href="#">HMDB0006981</a>	8299	<a href="#">C05235</a>	
<b>C05999</b>		-	-	-	<a href="#">View</a>
C00385	Xanthine	<a href="#">HMDB0000292</a>	1188	<a href="#">C00385</a>	
C00246	Butyric acid	<a href="#">HMDB0000039</a>	264	<a href="#">C00246</a>	
C00116	Glycerol	<a href="#">HMDB0000131</a>	753	<a href="#">C00116</a>	
C00146	Phenol	<a href="#">HMDB0000228</a>	996	<a href="#">C00146</a>	
C04221	trans-1,2-Dihydrobenzene-1,2-diol	<a href="#">HMDB0001164</a>	149186	<a href="#">C04221</a>	

**No records?**

Query name: **CE0520**

Matched Name	HMDB	PubChem	KEGG
--------------	------	---------	------

No records found.

**OK**      **Cancel**

**Search unknown on KEGG to identify metabolite**

**Proceed to bottom of the table**

C00016	FAD	<a href="#">HMDB0001248</a>	643975	<a href="#">C00016</a>
C00016	FAD	<a href="#">HMDB0001248</a>	643975	<a href="#">C00016</a>
C01352	FADH	<a href="#">HMDB0001197</a>	446013	<a href="#">C01352</a>

You can download the result [here](#)

**Submit**

**Choose a species**

Please select a pathway library:

Mammals	<input type="radio"/> Homo sapiens (human) [80] <input checked="" type="radio"/> Mus musculus (mouse) [82] <input type="radio"/> Rattus norvegicus (rat) [81] <input type="radio"/> Bos taurus (cow) [81]
Birds	<input type="radio"/> Gallus gallus (chicken) [78]
Fish	<input type="radio"/> Danio rerio (zebrafish) [81]
Insects	<input type="radio"/> Drosophila melanogaster (fruit fly) [79]
Nematodes	<input type="radio"/> Caenorhabditis elegans (nematode) [78]
Fungi	<input type="radio"/> Saccharomyces cerevisiae (yeast) [65]
Plants	<input type="radio"/> Oryza sativa japonica (Japanese rice) [83] <input type="radio"/> Arabidopsis thaliana (thale cress) [87]
Parasites	<input type="radio"/> Schistosoma mansoni [69] <input type="radio"/> Plasmodium falciparum 3D7 (Malaria) [47] <input type="radio"/> Trypanosoma brucei [54]
Prokaryotes	<input type="radio"/> Escherichia coli K-12 MG1655 [87] <input type="radio"/> Bacillus subtilis [80] <input type="radio"/> Pseudomonas putida KT2440 [89] <input type="radio"/> Staphylococcus aureus N315 (MRSA/VSSA) [73] <input type="radio"/> Thermotoga maritima [57] <input type="radio"/> Synechococcus elongatus PCC7942 [75] <input type="radio"/> Mesorhizobium loti [86]

## Statistical analysis selection

Please specify pathway analysis algorithms:

Over Representation Analysis

Hypergeometric Test

Fisher's Exact Test

Pathway Topology Analysis

Relative-betweenness Centrality

Out-degree Centrality

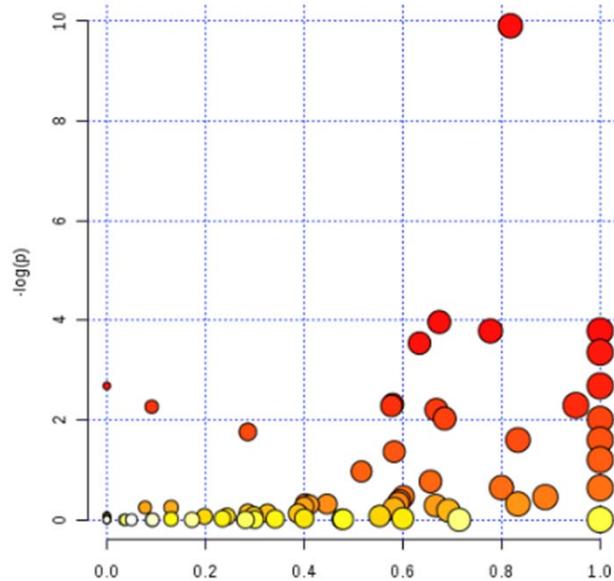
Please specify a reference metabolome:

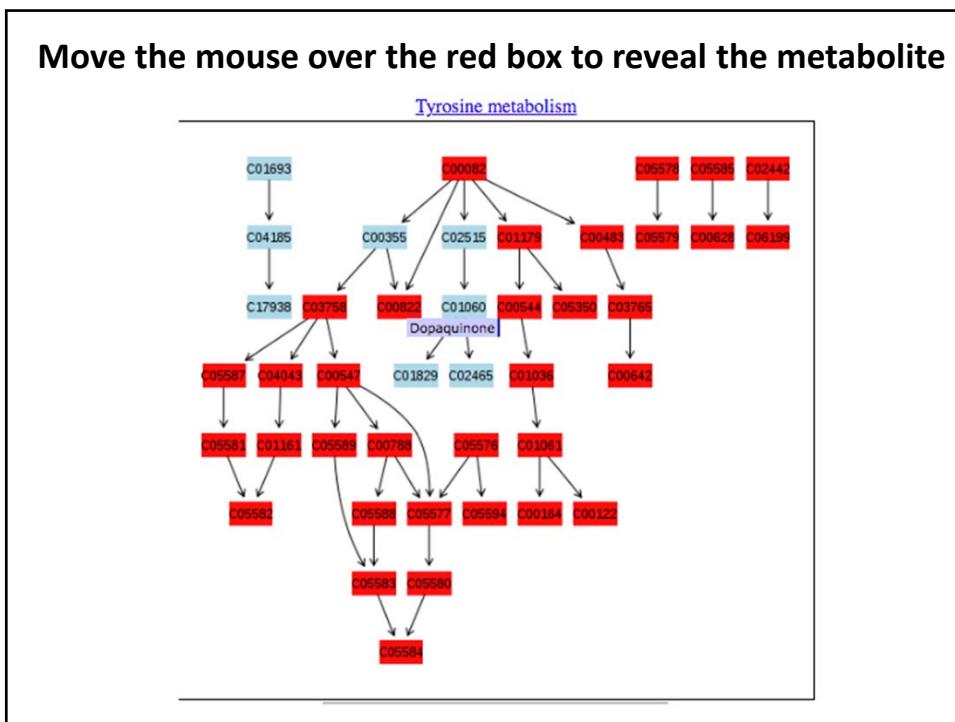
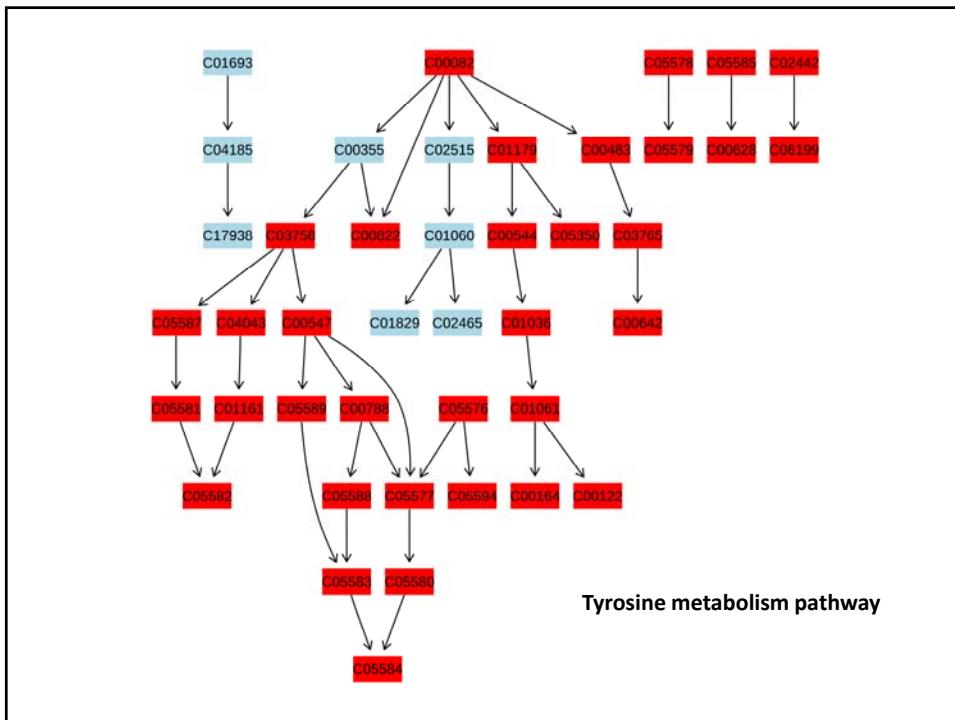
Use all compounds in the selected pathways

Upload a reference metabolome based on your technical platform

Submit

Overview of Pathway Analysis





## Summary table

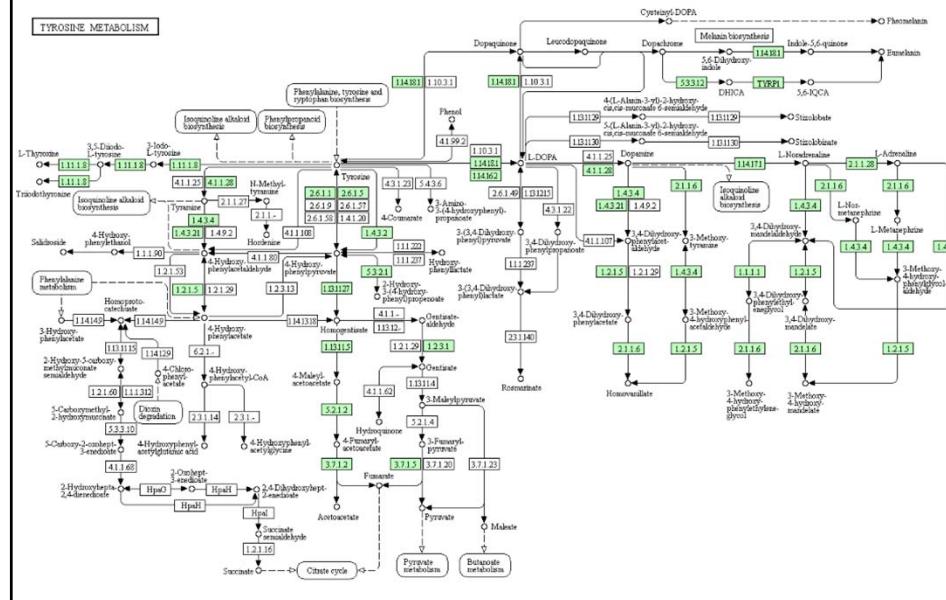
Pathway Name	Match Status	p	-log(p)	Holm p	FDR	Impact	Details
Tyrosine metabolism	34/42	4.9719E-5	9.9091	0.0040272	0.0040272	0.81825	KEGG
Arachidonic acid metabolism	25/36	0.018939	3.9665	1.0	0.45836	0.67402	KEGG
Phenylalanine metabolism	8/9	0.022635	3.7882	1.0	0.45836	0.77778	KEGG
One carbon pool by folate	8/9	0.022635	3.7882	1.0	0.45836	1.0	KEGG
Steroid hormone biosynthesis	44/70	0.028935	3.5427	1.0	0.46875	0.63389	KEGG
D-Glutamine and D-glutamate metabolism	5/5	0.034745	3.3597	1.0	0.46905	1.0	KEGG
D-Arginine and D-ornithine metabolism	4/4	0.068125	2.6864	1.0	0.6852	0.0	KEGG
Phenylalanine, tyrosine and tryptophan biosynthesis	4/4	0.068125	2.6864	1.0	0.6852	1.0	KEGG
Pentose phosphate pathway	13/19	0.098427	2.3184	1.0	0.6852	0.57963	KEGG
Vitamin B6 metabolism	7/9	0.10086	2.294	1.0	0.6852	0.95098	KEGG
Galactose metabolism	17/26	0.10173	2.2854	1.0	0.6852	0.57712	KEGG
Pentose and glucuronate interconversions	10/14	0.10339	2.2693	1.0	0.6852	0.09091	KEGG
Arginine and proline metabolism	27/44	0.10997	2.2075	1.0	0.6852	0.66803	KEGG
Tryptophan metabolism	25/41	0.13119	2.0311	1.0	0.72081	0.68487	KEGG
Ubiquinone and other terpenoid-quinone biosynthesis	3/3	0.13348	2.0138	1.0	0.72081	1.0	KEGG
Pantothenate and CoA biosynthesis	10/15	0.17143	1.7636	1.0	0.86788	0.28571	KEGG
Biotin metabolism	4/5	0.20165	1.6012	1.0	0.9074	0.83334	KEGG
Linoleic acid metabolism	4/5	0.20165	1.6012	1.0	0.9074	1.0	KEGG
Folate biosynthesis	10/16	0.25483	1.3671	1.0	1.0	0.58261	KEGG
Valine, leucine and isoleucine biosynthesis	7/11	0.29998	1.204	1.0	1.0	0.99999	KEGG

**Click on matched metabolites in the table**

Matched metabolites:

Pathway	Metabolites
Tyrosine metabolism	L-Dopachrome; Normetanephrine; 3-Methoxy-4-hydroxyphenylglycolaldehyde; Norepinephrine; Epinephrine; 3,4-Dihydroxymandelate; 3,4-Dihydroxymandelaldehyde; 3,4-Dihydroxyphenylglycol; Metanephrine; Dopamine; 3,4-Dihydroxyphenylacetaldehyde; 3,4-Dihydroxybenzeneacetic acid; Homovanillin; 3-Methoxytyramine; L-Dopa; 3,5-Diiodo-L-tyrosine; Iodotyrosine; L-Tyrosine; 4-Fumarylacetoin; Maleylacetoin; Homogentisic acid; 4-Hydroxyphenylpyruvic acid; 4-Hydroxyphenylacetaldehyde; Tyramine; 5,6-Dihydroxyindole; Gentisate aldehyde; N-Methyltyramine; 5,6-Dihydroxyindole-2-carboxylic acid; Vanillylmandelic acid; Vanylglucoside; Homovanillic acid; Liothryronine; Fumaric acid; Acetoacetic acid; 2-Hydroxy-3-(4-hydroxyphenyl)propenoic acid; p-Hydroxyphenylacetic acid; Indole-5,6-quinone; Dopaquinone; Thyroxine; Gentisic acid; Hordenine; 5,6-Indolequinone-2-carboxylic acid

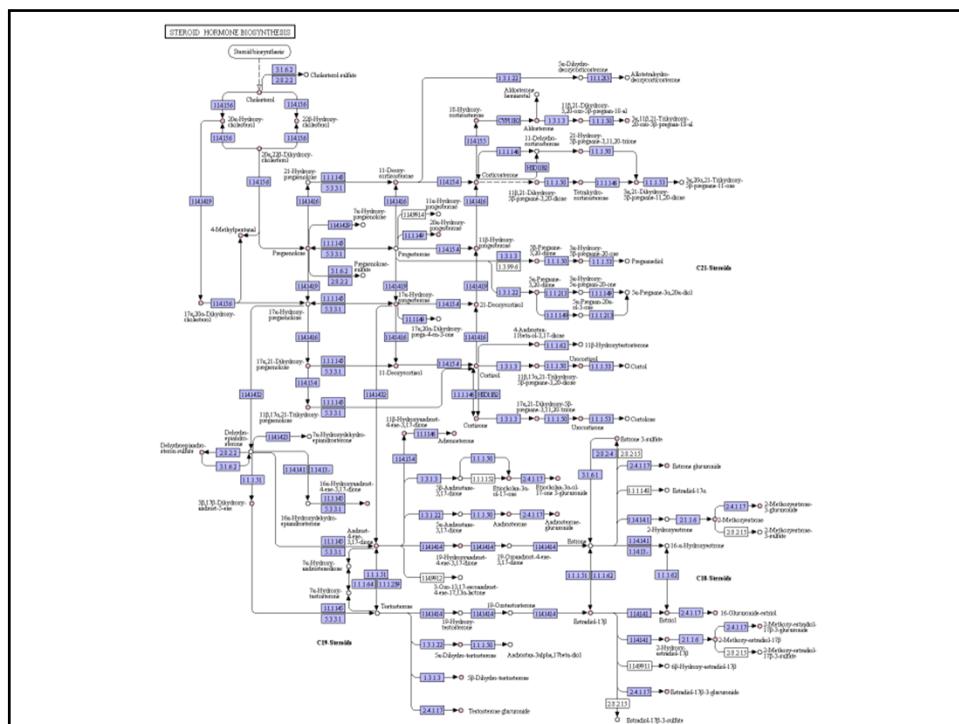
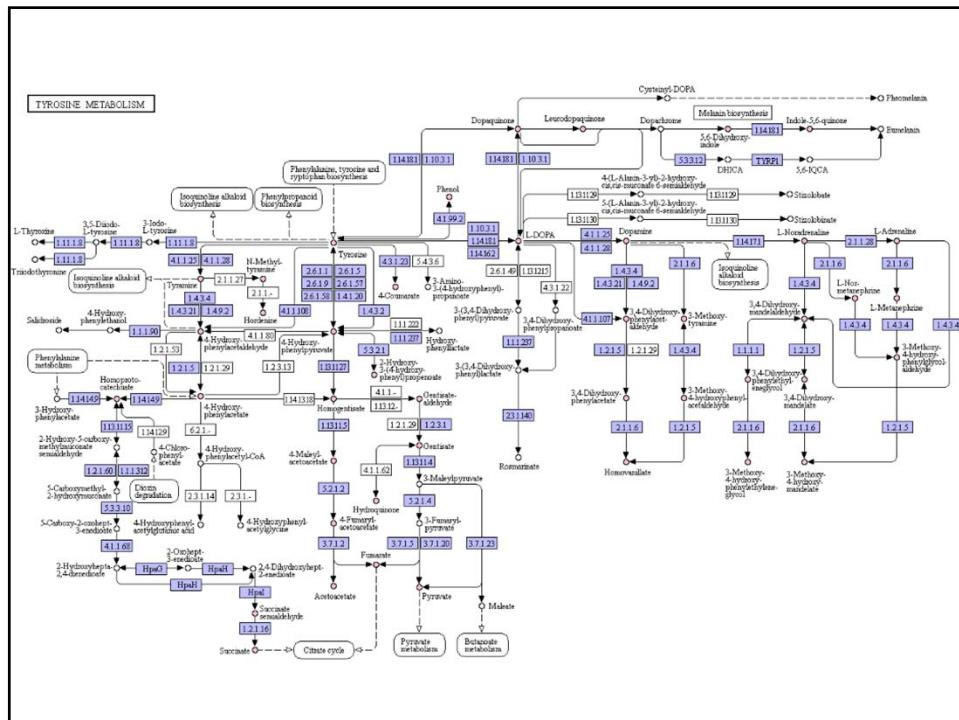
## Click on KEGG (right side of table)



## Pathway mapping with KEGG

- KEGG, Kyoto Encyclopedia of Genes and Genomes
- A comprehensive resource of genes, proteins and metabolites
- Has a Pathway tool
  
- [https://www.genome.jp/kegg/tool/map\\_pathway2.html](https://www.genome.jp/kegg/tool/map_pathway2.html)





**Questions?**