

Pathway Name	Match status	Expected	P values	FDR
Aminoacyl-tRNA biosynthesis	16/22	0.362	4.86E-25	8.70E-23
Arginine and proline metabolism	9/136	2.24	0.000356	0.0227
Histidine metabolism	6/62	1.02	0.000492	0.0227
Valine, leucine and isoleucine biosynthesis	4/24	0.395	0.000566	0.0227
beta-Alanine metabolism	6/65	1.07	0.000635	0.0227
Alanine, aspartate and glutamate metabolism	7/98	1.61	0.00106	0.0286
Glyoxylate and dicarboxylate metabolism	8/128	2.11	0.00112	0.0286
Glutathione metabolism	6/76	1.25	0.00145	0.0325
Biosynthesis of unsaturated fatty acids	5/53	0.872	0.00166	0.033
Pantothenate and CoA biosynthesis	5/55	0.905	0.00196	0.0351
Synthesis and degradation of ketone bodies	2/5	0.0823	0.00259	0.0422
Glycolysis or Gluconeogenesis	3/23	0.378	0.00601	0.0897
Arginine biosynthesis	5/74	1.22	0.00712	0.098
Sphingolipid metabolism	4/51	0.839	0.0095	0.121
Taurine and hypotaurine metabolism	3/31	0.51	0.0139	0.166
Tyrosine metabolism	6/125	2.06	0.0165	0.184
Nicotinate and nicotinamide metabolism	5/98	1.61	0.0221	0.233
Pyrimidine metabolism	6/139	2.29	0.0263	0.257
D-Glutamine and D-glutamate metabolism	2/16	0.263	0.0277	0.257
Valine, leucine and isoleucine degradation	5/105	1.73	0.0287	0.257
Lysine degradation	5/108	1.78	0.0319	0.268
Phenylalanine, tyrosine and tryptophan biosynthesis	4/74	1.22	0.0329	0.268
Fatty acid biosynthesis	3/45	0.74	0.0372	0.289
Glycerophospholipid metabolism	4/82	1.35	0.0454	0.338

带格式表格[Charlies Wu]

Supplemental Table4: KEGG [Analysis of Genes](#) and [Metabolites](#) in AMD.

[FDR: false discovery rate; KEGG: Kyoto Encyclopedia of Genes and Genomes.](#)

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