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| **Description** | **Gene Count** | Adjusted P-Value | **Enriched Genes** |
| ***Biological Process*** |  |  |  |
| cellular amino acid catabolic process | 9 | 1.37242E-06 | AMT/AUH/IVD/OTC/PAH/ALDH5A1/ACAD8/GLS2/ASRGL1 |
| alpha-amino acid metabolic process | 11 | 3.66603E-06 | AMT/AUH/IVD/OTC/PAH/ALDH5A1/ACAD8/GLS2/SEPSECS/ASRGL1/MTHFD2L |
| alpha-amino acid catabolic process | 8 | 3.78617E-06 | AMT/AUH/IVD/OTC/PAH/ACAD8/GLS2/ASRGL1 |
| organic acid catabolic process | 12 | 4.87553E-06 | ACACB/AMT/AUH/IVD/OTC/PAH/ALDH5A1/ACAD8/GLS2/ASRGL1/MCEE/NUDT7 |
| carboxylic acid catabolic process | 12 | 4.87553E-06 | ACACB/AMT/AUH/IVD/OTC/PAH/ALDH5A1/ACAD8/GLS2/ASRGL1/MCEE/NUDT7 |
| cellular amino acid metabolic process | 12 | 8.17026E-05 | AMT/AUH/IVD/OTC/PAH/ALDH5A1/ACAD8/GLS2/SEPSECS/QRSL1/ASRGL1/MTHFD2L |
| fatty acid metabolic process | 12 | 0.000125275 | ACACB/AUH/CYP2C8/EPHX2/IVD/ACSM3/ALDH5A1/ACSL6/MCEE/NUDT7/ZADH2/CYP4V2 |
| small molecule catabolic process | 13 | 0.000131344 | ACACB/AMT/AUH/IVD/OTC/PAH/ALDH5A1/ACAD8/GLS2/ASRGL1/CDADC1/MCEE/NUDT7 |
| positive regulation of ion transport | 10 | 0.000140654 | ATP1B2/CACNB2/CAPN3/CHRNB2/KCNJ11/MLLT6/NPPA/RAMP3/ATP8A1/AMIGO1 |
| monocarboxylic acid catabolic process | 7 | 0.000148807 | ACACB/AUH/IVD/ALDH5A1/ASRGL1/MCEE/NUDT7 |
| positive regulation of cation transmembrane transport | 7 | 0.000254518 | ATP1B2/CACNB2/CAPN3/KCNJ11/NPPA/RAMP3/AMIGO1 |
| regulation of skeletal muscle adaptation | 3 | 0.000391621 | CAMK2B/GTF2IRD2/GTF2IRD2B |
| positive regulation of ion transmembrane transport | 7 | 0.000413753 | ATP1B2/CACNB2/CAPN3/KCNJ11/NPPA/RAMP3/AMIGO1 |
| branched-chain amino acid metabolic process | 3 | 0.000746814 | AUH/IVD/ACAD8 |
| branched-chain amino acid catabolic process | 3 | 0.000746814 | AUH/IVD/ACAD8 |
| ***Cellular Component*** |  |  |  |
| rough endoplasmic reticulum membrane | 3 | 0.002471542 | PLOD3, PLOD2, PLOD1 |
| mitochondrial matrix | 10 | 0.00439838 | ACAD8, MCEE, ALDH5A1, AUH, ACSM3, GLS2, IVD, MTHFD2L, AMT, OTC |
| neuronal cell body membrane | 3 | 0.012680811 | SLC4A8, AMIGO1, FLRT1 |
| intracellular | 22 | 0.016969865 | ZNF540, ZNF782, RAMP3, ZNF44, MYRIP, CLU, ZNF33B, ZNF33A, RDH12, RAB37, ZNF506, SEC14L5, ZNF30, DCX, TRIM68, CAPN3, RHOU, ZNF557, ZNF589, ZNF763, ZNF620, ZNF596 |
| myofibril | 3 | 0.029431117 | TMOD1, ANKRD23, CAPN3 |
| ***Molecular Function*** |  |  |  |
| alkali metal ion binding | 3 | 0.000429708 | ATP1A2/CAPN3/KCNJ11 |
| ATPase activity, coupled to transmembrane movement of substances | 6 | 0.000802459 | ABCC6/ATP1A2/ATP1B2/ATP8A1/ABCA5/ABCA11P |
| ATPase activity, coupled to movement of substances | 6 | 0.000802459 | ABCC6/ATP1A2/ATP1B2/ATP8A1/ABCA5/ABCA11P |
| P-P-bond-hydrolysis-driven transmembrane transporter activity | 6 | 0.001138934 | ABCC6/ATP1A2/ATP1B2/ATP8A1/ABCA5/ABCA11P |
| hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds | 6 | 0.001138934 | ADARB2/GLS2/QRSL1/ASRGL1/CDADC1/MTHFD2L |
| primary active transmembrane transporter activity | 6 | 0.001237839 | ABCC6/ATP1A2/ATP1B2/ATP8A1/ABCA5/ABCA11P |
| ***KEGG Pathway*** |  |  |  |
| Herpes simplex virus 1 infection | 13 | 0.00067523 | ZNF33A/ZNF33B/ZNF589/ZNF44/ZNF557/ZNF30/ZNF799/ZNF782/ZNF540/ZNF596/ZNF620/ZNF763/ZNF506 |
| Valine, leucine and isoleucine degradation | 4 | 0.001029969 | AUH/IVD/ACAD8/MCEE |
| Proximal tubule bicarbonate reclamation | 3 | 0.00123878 | ATP1A2/ATP1B2/GLS2 |
| Aldosterone synthesis and secretion | 5 | 0.002221761 | ATP1A2/ATP1B2/CAMK2B/KCNK3/NPPA |