Table S2 - overview of hepatic ontology search result and the selection of parent gene ontologies

included = ontology included
is part_of = ontology not included because it is part of another included parent ontology
not within scope = not included because not specific to adipose tissue in humans

| Selection | GO ID | GO term |
|-----------|-------|---------|
| is part_of | GO:0060344 | liver trabecula formation |
| is part_of | GO:0097421 | liver regeneration |
| not within scope | GO:1990402 | embryonic liver development |
| is part_of | GO:0071910 | determination of liver left/right asymmetry |
| is part_of | GO:0072575 | epithelial cell proliferation involved in liver morphogenesis |
| is part_of | GO:0072576 | liver morphogenesis |
| included | GO:0001889 | liver development |
| not within scope | GO:0015234 | thiamine transmembrane transporter activity |
| not within scope | GO:0015127 | bilirubin transmembrane transporter activity |
| is part_of | GO:0090320 | regulation of chylomicron remnant clearance |
| is part_of | GO:0090321 | positive regulation of chylomicron remnant clearance |
| not within scope | GO:0051413 | response to cortisone |
| included | GO:0036333 | hepatocyte homeostasis |
| not within scope | GO:0036378 | calcitriol biosynthetic process from calciol |
| not within scope | GO:0061011 | hepatic duct development |
| not within scope | GO:0061009 | common bile duct development |
| not within scope | GO:2001069 | glycogen binding |
| not within scope | GO:0014831 | gastro-intestinal system smooth muscle contraction |
| is part_of | GO:0035622 | intrahepatic bile duct development |
| not within scope | GO:0045122 | aflatoxin biosynthetic process |
| is part_of | GO:0070365 | hepatocyte differentiation |
| is part_of | GO:0070367 | negative regulation of hepatocyte differentiation |
| is part_of | GO:0070366 | regulation of hepatocyte differentiation |
| is part_of | GO:0070368 | positive regulation of hepatocyte differentiation |
| not within scope | GO:0030975 | thiamine binding |
| not within scope | GO:0048175 | hepatocyte growth factor biosynthetic process |
| not within scope | GO:0009228 | thiamine biosynthetic process |
| not within scope | GO:0009230 | thiamine catabolic process |
| not within scope | GO:0034363 | intermediate-density lipoprotein particle |
| not within scope | GO:0034362 | low-density lipoprotein particle |
| not within scope | GO:0034361 | very-low-density lipoprotein particle |
| not within scope | GO:0034360 | chylomicron remnant |
| not within scope | GO:0034364 | high-density lipoprotein particle |
| included | GO:0034382 | chylomicron remnant clearance |
| included | GO:0034379 | very-low-density lipoprotein particle assembly |
| not within scope | GO:0006772 | thiamine metabolic process |
| not within scope | GO:0004806 | triglyceride lipase activity |
| not within scope | GO:0097330 | response to 5-fluoro-2'-deoxyuridine |
| included | GO:0097284 | hepatocyte apoptotic process |
| not within scope | GO:0043639 | benzoate catabolic process |
| not within scope | GO:0043691 | reverse cholesterol transport |
| not within scope | GO:0018952 | parathion metabolic process |
| not within scope | GO:0018874 | benzoate metabolic process |
cyanuric acid metabolic process
hepatocyte dedifferentiation
hepatic stellate cell proliferation
regulation of systemic arterial blood pressure by stress relaxation
organ or tissue specific immune response
hepatocyte cell migration
hepatocyte proliferation
parathion catabolic process
hepatic stellate cell activation
negative regulation of hepatic stellate cell activation
regulation of hepatic stellate cell activation
positive regulation of hepatic stellate cell activation
regulation of very-low-density lipoprotein particle remodeling
negative regulation of very-low-density lipoprotein particle remodeling
positive regulation of very-low-density lipoprotein particle remodeling
plasma lipoprotein particle remodeling
low-density lipoprotein particle remodeling
very-low-density lipoprotein particle remodeling
high-density lipoprotein particle remodeling
ketohexokinase activity
negative regulation of hepatocyte proliferation
regulation of hepatocyte proliferation
negative regulation of cellular response to hepatocyte growth factor stimulus
positive regulation of cellular response to hepatocyte growth factor stimulus
regulation of cellular response to hepatocyte growth factor stimulus
not within scope GO:0035729 cellular response to hepatocyte growth factor stimulus
not within scope GO:0035728 response to hepatocyte growth factor
not within scope GO:0048178 negative regulation of hepatocyte growth factor biosynthetic process
not within scope GO:0048177 positive regulation of hepatocyte growth factor biosynthetic process
not within scope GO:0048176 regulation of hepatocyte growth factor biosynthetic process
not within scope GO:0048012 hepatocyte growth factor receptor signaling pathway
not within scope GO:0005008 hepatocyte growth factor-activated receptor activity
not within scope GO:0005171 hepatocyte growth factor receptor binding
not within scope GO:1902202 regulation of hepatocyte growth factor receptor signaling pathway
not within scope GO:1902203 negative regulation of hepatocyte growth factor receptor signaling pathway
not within scope GO:1902204 positive regulation of hepatocyte growth factor receptor signaling pathway
not within scope GO:0032676 positive regulation of hepatocyte growth factor production
not within scope GO:0032686 negative regulation of hepatocyte growth factor production
not within scope GO:0032605 hepatocyte growth factor production
is part_of GO:1903944 negative regulation of hepatocyte apoptotic process
is part_of GO:1903945 positive regulation of hepatocyte apoptotic process
is part_of GO:1903943 regulation of hepatocyte apoptotic process
is part_of GO:0015126 canaliculac bile acid transmembrane transporter activity
included GO:003675 pericanaliculac vesicle
is part_of GO:0061017 hepatoblast differentiation
included GO:0015722 canaliculac bile acid transport