Top 30 of GO Enrichment urea carboxylase activity putrescine-importing ATPase activity host cell surface receptor binding histidinol dehydrogenase activity -DNA ligase (ATP) activity carbon-halide lyase activity carbohydrate transmembrane transporter activity -Gene_number ATP-dependent DNA helicase activity -• 2.00 allophanate hydrolase activity -2.25 acetyl-CoA carboxylase activity -2.50 3-hydroxybutyryl-CoA dehydrogenase activity -2.75 3-hydroxybutyryl-CoA dehydratase activity -3.00 2,3-dimethylmalate lyase activity q_value acetyl-CoA carboxylase complex -0.25 urea catabolic process streptomycin biosynthetic process -0.20 regulation of triglyceride metabolic process -0.15 regulation of cholesterol metabolic process -0.10 protein secretion protein glycosylation in Golgi -GO_domain propionate catabolic process biological_process positive regulation of lipoprotein lipase activity cellular_component nitrogen utilization molecular_function negative regulation of sporulation resulting in formation of a cellula etc... modulation by symbiont of microbe-associated molecular pattern-induced etc... lagging strand elongation gamma-1,2,3,4,5,6-hexachlorocyclohexane metabolic process -ER to Golgi vesicle-mediated transport chylomicron remnant clearance cellular response to alkalinity -10 12 8 11 Rich Factor