voltage-gated monoatomic cation channel activity -	0.0498186136006493	
RNA exonuclease activity, producing 5'-phosphomonoesters -	0.0479596488108672	
3'-5'-RNA exonuclease activity -	0.0456155621493888	
potassium channel activity - thiolester hydrolase activity -	0.0363899582452941 0.0363059841059394	
palmitoyltransferase activity -	0.0318975896077068	
prenyltransferase activity	0.0282976487112071 0.0275800762505213	
voltage-gated potassium channel activity - spectrin binding -	0.0269091091505795	
S-acyltransferase activity -	0.0211545830622581	
protein-cysteine S-palmitoyltransferase activity - protein-cysteine S-acyltransferase activity -	0.0211545830622581 0.0211545830622581	
acyltransferase activity -	0.017474979214187	
racemase and epimerase activity -	0.0170262964285934	
CoA hydrolase activity transferring groups other than aming any groups	0.0163913987720783 0.0139874809579844	
acyltransferase activity, transferring groups other than amino–acyl groups - racemase and epimerase activity, acting on carbohydrates and derivatives -	0.0129396827246718	
succinyl-CoA hydrolase activity -	0.00540647254160568	
hydroxymethylglutaryl–CoA hydrolase activity - acetyl–CoA hydrolase activity -	0.00540647254160568 0.00540647254160568	
GDP-mannose 3,5-epimerase activity	0.00328221588478676	
GDP-L-fucose synthase activity -	0.00328221588478676	
GDP-4-dehydro-D-rhamnose reductase activity - aspartate N-acetyltransferase activity -	0.00328221588478676 0.00269382460361153	
post–mRNA release spliceosomal complex -	0.0430903194234098	
catalytic step 1 spliceosome -	0.0399915890186259	
exosome (RNase complex) - exoribonuclease complex -	0.0285003996773363 0.0285003996773363	
voltage-gated potassium channel complex -	• 0.0225128369460014	
potassium channel complex -	0.0225128369460014	
nuclear exosome (RNase complex) - eukaryotic translation initiation factor 2B complex -	0.0220085262815948 0.0144620318382628	
post–spliceosomal complex -	0.012263223568865	
cytoplasmic exosome (RNase complex) -	0.0119706860816756	
positive regulation of oxidoreductase activity - mannosylation -	0.0447872546259135 0.0432492877303832	
purine–containing compound catabolic process -	0.0420190578547421	
cellular response to vascular endothelial growth factor stimulus	0.0417809213523253 0.0388155418378272	
positive regulation of potassium ion transport - ncRNA catabolic process -	0.0388155418378272 0.0380407661635993	
protein mannosylation -	0.0379238952751103	
dsRNA transport -	0.0371710761580389 0.0362360380911605	
nucleotide–sugar biosynthetic process - regulation of macrophage derived foam cell differentiation -	0.0344022041209231	
regulation of sterol transport -	0.0339576404543683	
regulation of cholesterol transport	0.0339576404543683 0.0338914107802637	
leukocyte cell–cell adhesion - negative regulation of lipid transport -	0.0337439235758186	
RNA surveillance -	0.0336303126049215	
snRNA processing -	0.0319094665044871 0.0312053291910627	
ribonucleotide catabolic process - nuclear RNA surveillance -	0.0310543912704912	
positive regulation of monoatomic ion transport -	0.0300741280075057	
acetyl–CoA metabolic process	0.0298387504248431 0.0296215801921826	
small molecule biosynthetic process - snRNA 3'-end processing -	0.0294195503413044	
mRNA 3'-splice site recognition -	0.0288816218219138	
positive regulation of monooxygenase activity - purine ribonucleotide catabolic process -	0.0286696578942469 0.0285722676132987	
purine nucleotide catabolic process -	0.0285722676132987	
nuclear mRNA surveillance -	0.025953402174049 0.0254776556134411	
positive regulation of nitric–oxide synthase activity - protein palmitoylation -	0.0242977793778354	
coenzyme A metabolic process -	0.0239630010142313	
rRNA 3'-end processing -	0.0231692069799049 0.022352805980717	
rRNA catabolic process - regulation of lipid localization -	0.0227046256710788	
negative regulation of macrophage derived foam cell differentiation -	0.0195147468624973	
regulation of neurotransmitter uptake - isoprenoid biosynthetic process -	0.0189260448018855 0.0181495177066751	
spliceosomal conformational changes to generate catalytic conformation -	0.0174869207981343	
vascular endothelial growth factor signaling pathway -	• 0.0166480420237679	
regulation of synaptic transmission, dopaminergic - brown fat cell differentiation -	0.0163854974693656 0.0163303818018596	
xonucleolytic trimming to generate mature 3'-end of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) -	0.015354796447054	
exonucleolytic trimming involved in rRNA processing	0.015354796447054 0.014902787472414	
generation of catalytic spliceosome for second transesterification step - polyadenylation-dependent RNA catabolic process -	0.014248092644573	
polyadenylation-dependent ncRNA catabolic process -	0.014248092644573	
nuclear polyadenylation-dependent ncRNA catabolic process - nuclear ncRNA surveillance -	0.014248092644573 0.014248092644573	
GDP-mannose metabolic process	0.0129004828908189	
tRNA catabolic process -	0.0127716150187045 0.011996956977528	
polyprenol metabolic process - nuclear polyadenylation-dependent rRNA catabolic process -	0.011796956977528	
equilibrioception -	0.0116337859439971	
nuclear–transcribed mRNA catabolic process, exonucleolytic, 3'–5' -	0.0116264266412744 0.0110854073453127	
positive regulation of synaptic transmission, dopaminergic - positive regulation of neurotransmitter uptake -	0.0110203466498867	
GDP-L-fucose metabolic process -	0.00949800471214295	
U5 snRNA 3'-end processing - U4 snRNA 3'-end processing -	0.009078524041514 0.009078524041514	
U1 snRNA 3'-end processing	0.009078524041514	
polyadenylation-dependent mRNA catabolic process -	0.009078524041514	
nuclear polyadenylation-dependent tRNA catabolic process - nuclear polyadenylation-dependent mRNA catabolic process -	0.009078524041514 0.009078524041514	
dolichol metabolic process -	0.00894333797493972	
cytolysis -	0.00860421669484748 0.00794759114353182	
regulation of lipid transport - polyprenol biosynthetic process -	0.00794759114353182 0.00696860125963724	
regulation of intracellular sterol transport -	0.00641686664286217	
regulation of intracellular lipid transport -	0.00641686664286217 0.00641686664286217	
regulation of intracellular cholesterol transport - GDP-L-fucose biosynthetic process -	0.00590615736269649	
'de novo' GDP-L-fucose biosynthetic process -	0.00590615736269649	
ribonucleoside bisphosphate catabolic process - purine nucleoside bisphosphate catabolic process -	0.00540647254160568 0.00540647254160568	
purine nucleoside bisphosphate catabolic process -	0.00540647254160568	
coenzyme A catabolic process	0.00540647254160568 0.00540647254160568	
acetyl-CoA catabolic process - dolichol biosynthetic process -	0.005406472541605680.00389996099365835	
regulation of dopamine uptake involved in synaptic transmission -	0.00269382460361153	
regulation of catecholamine uptake involved in synaptic transmission	0.00269382460361153 0.00269382460361153	
positive regulation of dopamine uptake involved in synaptic transmission - positive regulation of catecholamine uptake involved in synaptic transmission -	0.00269382460361153	
	0 100 200 30	0

ontology • BP CC MF