acetyltransferase activity -	•	0.0462486131938719			
N-acyltransferase activity -	•	0.0410476942321217			
N-acetyltransferase activity -	•	0.0364911594496703			
sulfotransferase activity -	•	0.027151352737722			
aryl sulfotransferase activity -	•	0.0133135546844079			
racemase and epimerase activity -	•	0.00977442314540206			
toxic substance binding -	•	0.00814138797450858			
racemase and epimerase activity, acting on carbohydrates and derivatives -	•	0.00724222762643581			
1-hydroxypyrene sulfotransferase activity -	•	0.00424925939472082			
GDP-mannose 3,5-epimerase activity -	•	0.00178626396087444			
GDP-L-fucose synthase activity -	•	0.00178626396087444			
GDP-4-dehydro-D-rhamnose reductase activity -	•	0.00178626396087444			
aspartate N-acetyltransferase activity -	•	0.0014910948730283			
Prp19 complex -	•	0.040598310930692			
post-mRNA release spliceosomal complex -	•	0.0253166872798408			
catalytic step 1 spliceosome -	•	0.0234980959339538			
post-spliceosomal complex -	•	0.00692692456783266			
positive regulation of neurotransmitter transport	•	0.0362988897088386			
positive regulation of response to drug-	•	0.0340630149153148			
nucleotide-sugar metabolic process-	•	0.0336138443961554			
positive regulation of amine transport -	•	0.032797347829002			
mRNA splice site selection -	•	0.0323132515914505			
RNA localization -	•	0.0215611009089999			
nucleotide-sugar biosynthetic process -	•	0.020436985968997			
dsRNA transport -	•	0.0193092162785791			ontology BP
leukocyte cell-cell adhesion -	•	0.0191412983968546			CCMF
mRNA 3'-splice site recognition -	•	0.0162892781962628			
sulfation -	•	0.014079056443192			
nucleobase-containing compound transport -	•	0.0116589397224186			
establishment of RNA localization -	•	0.0107507236124574			
ncRNA export from nucleus -	•	0.0105037886817195			
RNA transport -	•	0.0103540619261844			
nucleic acid transport -	•	0.0103540619261844			
regulation of neurotransmitter uptake -	•	0.010083978143109			
spliceosomal conformational changes to generate catalytic conformation -	•	0.0097361325568431			
regulation of synaptic transmission, dopaminergic -	•	0.00912480368404551			
generation of catalytic spliceosome for second transesterification step-	•	0.00837347284421309			
GDP-mannose metabolic process -	•	0.00744995428817656			
cytolysis -	•	0.00622105931109446			
positive regulation of synaptic transmission, dopaminergic -	•	0.00621079236735464			
positive regulation of neurotransmitter uptake -	•	0.00616842681255336			
GDP-L-fucose metabolic process -	•	0.00513612626084695			
snRNA transport -		0.00453447198967205			
GDP-L-fucose biosynthetic process	•	0.00317556070571431			
'de novo' GDP-L-fucose biosynthetic process -	•	0.00317556070571431			
snRNA export from nucleus -	•	0.00219496813142533			
regulation of dopamine uptake involved in synaptic transmission -		0.0014910948730283			
regulation of catecholamine uptake involved in synaptic transmission -		0.0014910948730283			
positive regulation of dopamine uptake involved in synaptic transmission -		0.0014910948730283 0.0014910948730283			
positive regulation of catecholamine uptake involved in synaptic transmission -	0	0.0014910948730283	200	300	
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