Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
	KEGG_PATHWAY	Tyrosine metabolism	RT		6	0,3	6,2E-1	9,5E-1
	KEGG_PATHWAY	RNA polymerase	RT		5	0,2	6,2E-1	9,5E-1
	KEGG_PATHWAY	Glyoxylate and dicarboxylate metabolism	RT		3	0,1	6,4E-1	9,5E-1
	KEGG_PATHWAY	Alanine, aspartate and glutamate metabolism	RT		6	0,3	6,5E-1	9,5E-1
	KEGG_PATHWAY	N-Glycan biosynthesis	RT		7	0,3	6,7E-1	9,6E-1
	KEGG_PATHWAY	Progesterone-mediated oocyte maturation	RT		13	0,6	6,9E-1	9,6E-1
	KEGG_PATHWAY	Fructose and mannose metabolism	RT		7	0,3	6,9E-1	9,6E-1
	KEGG_PATHWAY	O-Glycan biosynthesis	RT		4	0,2	7,0E-1	9,6E-1
	KEGG_PATHWAY	Notch signaling pathway	RT		8	0,4	7,1E-1	9,6E-1
	KEGG_PATHWAY	Riboflavin metabolism	RT		3	0,1	7,3E-1	9,6E-1
	KEGG_PATHWAY	Homologous recombination	RT		4	0,2	7,3E-1	9,6E-1
	KEGG_PATHWAY	Synthesis and degradation of ketone bodies	RT		2	0,1	7,4E-1	9,6E-1
	KEGG_PATHWAY	Vitamin B6 metabolism	RT		2	0,1	7,4E-1	9,6E-1
	KEGG_PATHWAY	Steroid hormone biosynthesis	RT		4	0,2	7,6E-1	9,7E-1
	KEGG_PATHWAY	Nicotinate and nicotinamide metabolism	RT		3	0,1	7,6E-1	9,7E-1
	KEGG_PATHWAY	Inositol phosphate metabolism	RT		8	0,4	7,7E-1	9,7E-1
	KEGG_PATHWAY	Sphingolipid metabolism	RT		6	0,3	7,8E-1	9,7E-1
	KEGG_PATHWAY	Apoptosis	RT		11	0,5	7,8E-1	9,7E-1
	KEGG_PATHWAY	PPAR signaling pathway	RT		8	0,4	8,1E-1	9,7E-1
	KEGG_PATHWAY	Endocytosis	RT		26	1,2	8,1E-1	9,7E-1
	KEGG_PATHWAY	Glutathione metabolism	RT		5	0,2	8,1E-1	9,7E-1
	KEGG_PATHWAY	Porphyrin and chlorophyll metabolism	RT		4	0,2	8,1E-1	9,7E-1
	KEGG_PATHWAY	Lysine degradation	RT		6	0,3	8,2E-1	9,7E-1
	KEGG_PATHWAY	GnRH signaling pathway	RT		12	0,6	8,2E-1	9,7E-1
	KEGG_PATHWAY	Thiamine metabolism	RT		2	0,1	8,2E-1	9,7E-1
	KEGG_PATHWAY	Metabolism of xenobiotics by cytochrome P450	RT		3	0,1	8,2E-1	9,7E-1
	KEGG_PATHWAY	Drug metabolism	RT		3	0,1	8,2E-1	9,7E-1
	KEGG_PATHWAY	Wnt signaling pathway	RT		19	0,9	8,3E-1	9,7E-1
	KEGG_PATHWAY	Biosynthesis of unsaturated fatty acids	RT		3	0,1	8,5E-1	9,7E-1
	KEGG_PATHWAY	Intestinal immune network for IgA production	RT		3	0,1	8,5E-1	9,7E-1
	KEGG_PATHWAY	Folate biosynthesis	RT		2	0,1	8,5E-1	9,7E-1
	KEGG_PATHWAY	Arachidonic acid metabolism	RT		4	0,2	8,6E-1	9,7E-1
	KEGG_PATHWAY	Regulation of actin cytoskeleton	RT		24	1,1	8,6E-1	9,7E-1
	KEGG_PATHWAY	Pyrimidine metabolism	RT		12	0,6	8,7E-1	9,7E-1
	KEGG_PATHWAY	Dorso-ventral axis formation	RT		3	0,1	8,7E-1	9,7E-1
	KEGG_PATHWAY	Tight junction	RT		15	0,7	8,7E-1	9,7E-1
	KEGG_PATHWAY	Basal transcription factors	RT		4	0,2	8,7E-1	9,7E-1
	KEGG_PATHWAY	Cytosolic DNA-sensing pathway	RT		4	0,2	8,7E-1	9,7E-1
	KEGG_PATHWAY	Calcium signaling pathway	RT		20	0,9	8,8E-1	9,7E-1
	KEGG_PATHWAY	Valine, leucine and isoleucine biosynthesis	RT		2	0,1	8,8E-1	9,7E-1
	KEGG_PATHWAY	ECM-receptor interaction	RT		8	0,4	8,9E-1	9,8E-1
	KEGG_PATHWAY	Amino sugar and nucleotide sugar metabolism	RT		6	0,3	8,9E-1	9,7E-1
	KEGG_PATHWAY	NOD-like receptor signaling pathway	RT		6	0,3	8,9E-1	9,7E-1
	KEGG_PATHWAY	Pantothenate and CoA biosynthesis	RT		2	0,1	9,0E-1	9,8E-1
	KEGG_PATHWAY	Non-homologous end-joining	RT		2	0,1	9,0E-1	9,8E-1
	KEGG_PATHWAY	Cardiac muscle contraction	RT		9	0,4	9,0E-1	9,8E-1

1679 gene(s) from your list are not in the output.

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