

Species	Category	Term ID	Term name	Treatment	P-value
Human	KEGG	hsa00240	Pyrimidine metabolism	Low - 24 h	0.0001855
Human	KEGG	hsa00982	Drug metabolism - cytochrome P450	Low - 24 h	0.00018996
Human	KEGG	hsa03030	DNA replication	Low - 24 h	1.10E-07
Human	KEGG	hsa04110	Cell cycle	Low - 24 h	1.25E-16
Human	KEGG	hsa04114	Oocyte meiosis	Low - 24 h	1.44E-05
Human	KEGG	hsa04115	p53 signaling pathway	Low - 24 h	4.98E-07
Human	KEGG	hsa00830	Retinol metabolism	Middle - 24 h	3.84E-05
Human	KEGG	hsa03030	DNA replication	Middle - 24 h	1.59E-12
Human	KEGG	hsa03420	Nucleotide excision repair	Middle - 24 h	5.47E-05
Human	KEGG	hsa03430	Mismatch repair	Middle - 24 h	4.99E-07
Human	KEGG	hsa03460	Fanconi anemia pathway	Middle - 24 h	2.99E-05
Human	KEGG	hsa04110	Cell cycle	Middle - 24 h	2.62E-17
Human	KEGG	hsa04115	p53 signaling pathway	Middle - 24 h	4.83E-07
Human	KEGG	hsa04141	Protein processing in endoplasmic reticulum	Middle - 24 h	1.41E-05
Human	KEGG	hsa05202	Transcriptional misregulation in cancer	Middle - 24 h	0.00011211
Human	KEGG	hsa04068	FoxO signaling pathway	High - 8 h	8.96E-07
Human	KEGG	hsa04110	Cell cycle	High - 8 h	1.87E-06
Human	KEGG	hsa04115	p53 signaling pathway	High - 8 h	3.66E-05
Human	KEGG	hsa00240	Pyrimidine metabolism	High - 24 h	0.00012092
Human	KEGG	hsa03030	DNA replication	High - 24 h	2.92E-12
Human	KEGG	hsa03430	Mismatch repair	High - 24 h	2.98E-05
Human	KEGG	hsa03460	Fanconi anemia pathway	High - 24 h	4.33E-05
Human	KEGG	hsa04110	Cell cycle	High - 24 h	2.43E-15
Human	KEGG	hsa04115	p53 signaling pathway	High - 24 h	3.20E-05
Human	KEGG	hsa04141	Protein processing in endoplasmic reticulum	High - 24 h	1.06E-08
Human	TOX	TOX:04	DNA Damage & Repair	Low - 24 h	4.86E-06
Human	TOX	TOX:08	Immunotoxicity	Low - 24 h	0.00026011
Human	TOX	TOX:02	Cholestasis	Middle - 8 h	0.0032688
Human	TOX	TOX:04	DNA Damage & Repair	Middle - 24 h	4.45E-09
Human	TOX	TOX:08	Immunotoxicity	Middle - 24 h	0.00087295
Human	TOX	TOX:11	Oxidative Stress & Antioxidant Response	Middle - 24 h	0.0016711
Human	TOX	TOX:07	Heat Shock Response	High - 8 h	8.55E-05
Human	TOX	TOX:04	DNA Damage & Repair	High - 24 h	5.10E-07
Human	TOX	TOX:05	ER Stress & Unfolded Protein Response	High - 24 h	0.00062041
Human	TOX	TOX:07	Heat Shock Response	High - 24 h	0.00031518
Human	TOX	TOX:08	Immunotoxicity	High - 24 h	0.0038211
Human	TOX	TOX:11	Oxidative Stress & Antioxidant Response	High - 24 h	0.0049039
Human	TOX	TOX:12	Phospholipidosis	High - 24 h	0.0014279
Human	GO (BP)	GO:0007091	metaphase/anaphase transition of mitotic cell cycle	Low - 24 h	1.16E-10

Species	Category	Term ID	Term name	Treatment	P-value
Human	GO (BP)	GO:0006271	DNA strand elongation involved in DNA replication	Low - 24 h	1.42E-09
Human	GO (BP)	GO:0034080	CENP-A containing nucleosome assembly	Low - 24 h	6.04E-08
Human	GO (BP)	GO:0051988	regulation of attachment of spindle microtubules to kinetochore	Low - 24 h	9.93E-08
Human	GO (BP)	GO:0006206	pyrimidine nucleobase metabolic process	Low - 24 h	1.80E-07
Human	GO (BP)	GO:0007076	mitotic chromosome condensation	Low - 24 h	7.54E-07
Human	GO (BP)	GO:0007094	mitotic spindle assembly checkpoint	Low - 24 h	8.99E-07
Human	GO (BP)	GO:0008608	attachment of spindle microtubules to kinetochore	Low - 24 h	1.20E-06
Human	GO (BP)	GO:0000086	G2/M transition of mitotic cell cycle	Low - 24 h	1.48E-06
Human	GO (BP)	GO:0042493	response to drug	Low - 24 h	2.09E-06
Human	GO (BP)	GO:0045132	meiotic chromosome segregation	Low - 24 h	2.42E-06
Human	GO (BP)	GO:0006084	acetyl-CoA metabolic process	Low - 24 h	1.33E-05
Human	GO (BP)	GO:0007100	mitotic centrosome separation	Low - 24 h	2.14E-05
Human	GO (BP)	GO:0008283	cell proliferation	Low - 24 h	3.28E-05
Human	GO (BP)	GO:0055114	oxidation-reduction process	Low - 24 h	3.46E-05
Human	GO (BP)	GO:0006200	ATP catabolic process	Low - 24 h	3.64E-05
Human	GO (BP)	GO:1901606	alpha-amino acid catabolic process	Low - 24 h	4.91E-05
Human	GO (BP)	GO:0007131	reciprocal meiotic recombination	Low - 24 h	5.97E-05
Human	GO (BP)	GO:0009411	response to UV	Low - 24 h	7.00E-05
Human	GO (BP)	GO:0007018	microtubule-based movement	Low - 24 h	7.17E-05
Human	GO (BP)	GO:0015949	nucleobase-containing small molecule interconversion	Low - 24 h	8.60E-05
Human	GO (BP)	GO:0009636	response to toxic substance	Low - 24 h	9.46E-05
Human	GO (BP)	GO:0031570	DNA integrity checkpoint	Low - 24 h	0.00011555
Human	GO (BP)	GO:0090399	replicative senescence	Low - 24 h	0.00011972
Human	GO (BP)	GO:0000910	cytokinesis	Low - 24 h	0.00016247
Human	GO (BP)	GO:0006270	DNA replication initiation	Low - 24 h	0.00017279
Human	GO (BP)	GO:0009437	carnitine metabolic process	Low - 24 h	0.0001839
Human	GO (BP)	GO:0051382	kinetochore assembly	Low - 24 h	0.00026965
Human	GO (BP)	GO:0090068	positive regulation of cell cycle process	Low - 24 h	0.00031613
Human	GO (BP)	GO:0006366	transcription from RNA polymerase II promoter	Middle - 8 h	7.37E-07
Human	GO (BP)	GO:0031016	pancreas development	Middle - 8 h	4.88E-06
Human	GO (BP)	GO:0060412	ventricular septum morphogenesis	Middle - 8 h	1.59E-05
Human	GO (BP)	GO:0006271	DNA strand elongation involved in DNA replication	Middle - 24 h	4.43E-13
Human	GO (BP)	GO:0034080	CENP-A containing nucleosome assembly	Middle - 24 h	6.75E-12
Human	GO (BP)	GO:0007091	metaphase/anaphase transition of mitotic cell cycle	Middle - 24 h	5.31E-09
Human	GO (BP)	GO:0008283	cell proliferation	Middle - 24 h	2.30E-08
Human	GO (BP)	GO:0007076	mitotic chromosome condensation	Middle - 24 h	9.58E-08
Human	GO (BP)	GO:0006987	activation of signaling protein activity involved in unfolded protein response	Middle - 24 h	2.03E-07
Human	GO (BP)	GO:0000083	regulation of transcription involved in G1/S transition of mitotic cell cycle	Middle - 24 h	2.82E-07
Human	GO (BP)	GO:0006270	DNA replication initiation	Middle - 24 h	3.35E-07

Species	Category	Term ID	Term name	Treatment	P-value
Human	GO (BP)	GO:0008608	attachment of spindle microtubules to kinetochore	Middle - 24 h	8.49E-07
Human	GO (BP)	GO:0031100	organ regeneration	Middle - 24 h	9.09E-07
Human	GO (BP)	GO:0032201	telomere maintenance via semi-conservative replication	Middle - 24 h	3.24E-06
Human	GO (BP)	GO:0007094	mitotic spindle assembly checkpoint	Middle - 24 h	4.88E-06
Human	GO (BP)	GO:0051988	regulation of attachment of spindle microtubules to kinetochore	Middle - 24 h	5.33E-06
Human	GO (BP)	GO:0000722	telomere maintenance via recombination	Middle - 24 h	7.00E-06
Human	GO (BP)	GO:0007080	mitotic metaphase plate congression	Middle - 24 h	7.44E-06
Human	GO (BP)	GO:0000910	cytokinesis	Middle - 24 h	1.10E-05
Human	GO (BP)	GO:0070365	hepatocyte differentiation	Middle - 24 h	1.12E-05
Human	GO (BP)	GO:0051382	kinetochore assembly	Middle - 24 h	2.13E-05
Human	GO (BP)	GO:0045132	meiotic chromosome segregation	Middle - 24 h	2.20E-05
Human	GO (BP)	GO:0007019	microtubule depolymerization	Middle - 24 h	2.61E-05
Human	GO (BP)	GO:0014070	response to organic cyclic compound	Middle - 24 h	2.63E-05
Human	GO (BP)	GO:0006302	double-strand break repair	Middle - 24 h	4.12E-05
Human	GO (BP)	GO:0006206	pyrimidine nucleobase metabolic process	Middle - 24 h	4.63E-05
Human	GO (BP)	GO:0006297	nucleotide-excision repair, DNA gap filling	Middle - 24 h	4.77E-05
Human	GO (BP)	GO:0046394	carboxylic acid biosynthetic process	Middle - 24 h	4.80E-05
Human	GO (BP)	GO:0007584	response to nutrient	Middle - 24 h	6.01E-05
Human	GO (BP)	GO:0000086	G2/M transition of mitotic cell cycle	Middle - 24 h	6.59E-05
Human	GO (BP)	GO:0090307	spindle assembly involved in mitosis	Middle - 24 h	9.96E-05
Human	GO (BP)	GO:0006283	transcription-coupled nucleotide-excision repair	Middle - 24 h	0.0001042
Human	GO (BP)	GO:0016572	histone phosphorylation	Middle - 24 h	0.00010875
Human	GO (BP)	GO:0006268	DNA unwinding involved in DNA replication	Middle - 24 h	0.00010983
Human	GO (BP)	GO:0009411	response to UV	Middle - 24 h	0.00013072
Human	GO (BP)	GO:0071281	cellular response to iron ion	Middle - 24 h	0.00013533
Human	GO (BP)	GO:1901606	alpha-amino acid catabolic process	Middle - 24 h	0.00013547
Human	GO (BP)	GO:0006084	acetyl-CoA metabolic process	Middle - 24 h	0.00014285
Human	GO (BP)	GO:0006200	ATP catabolic process	Middle - 24 h	0.00014961
Human	GO (BP)	GO:0071479	cellular response to ionizing radiation	Middle - 24 h	0.00015656
Human	GO (BP)	GO:0009200	deoxyribonucleoside triphosphate metabolic process	Middle - 24 h	0.00022348
Human	GO (BP)	GO:0015949	nucleobase-containing small molecule interconversion	Middle - 24 h	0.00022348
Human	GO (BP)	GO:0008630	intrinsic apoptotic signaling pathway in response to DNA damage	Middle - 24 h	0.00024137
Human	GO (BP)	GO:0043065	positive regulation of apoptotic process	Middle - 24 h	0.00029346
Human	GO (BP)	GO:0010332	response to gamma radiation	Middle - 24 h	0.00030114
Human	GO (BP)	GO:0007100	mitotic centrosome separation	Middle - 24 h	0.00030171
Human	GO (BP)	GO:0051255	spindle midzone assembly	Middle - 24 h	0.00030171
Human	GO (BP)	GO:0060236	regulation of mitotic spindle organization	Middle - 24 h	0.00030171
Human	GO (BP)	GO:0045765	regulation of angiogenesis	Middle - 24 h	0.00030212
Human	GO (BP)	GO:0040001	establishment of mitotic spindle localization	Middle - 24 h	0.00031938

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Human	GO (BP)	GO:0070301	cellular response to hydrogen peroxide	Middle - 24 h	0.00036094
Human	GO (BP)	GO:0000725	recombinational repair	Middle - 24 h	0.000415
Human	GO (BP)	GO:0008283	cell proliferation	High - 8 h	1.78E-06
Human	GO (BP)	GO:0006366	transcription from RNA polymerase II promoter	High - 8 h	3.23E-06
Human	GO (BP)	GO:0033993	response to lipid	High - 8 h	7.54E-06
Human	GO (BP)	GO:0045736	negative regulation of cyclin-dependent protein serine/threonine kinase activity	High - 8 h	7.98E-06
Human	GO (BP)	GO:0014070	response to organic cyclic compound	High - 8 h	1.96E-05
Human	GO (BP)	GO:0009725	response to hormone	High - 8 h	7.34E-05
Human	GO (BP)	GO:0031016	pancreas development	High - 8 h	7.59E-05
Human	GO (BP)	GO:0045944	positive regulation of transcription from RNA polymerase II promoter	High - 8 h	7.98E-05
Human	GO (BP)	GO:0060412	ventricular septum morphogenesis	High - 8 h	9.00E-05
Human	GO (BP)	GO:0090009	primitive streak formation	High - 8 h	0.00010067
Human	GO (BP)	GO:0008285	negative regulation of cell proliferation	High - 8 h	0.00010913
Human	GO (BP)	GO:0048872	homeostasis of number of cells	High - 8 h	0.00012165
Human	GO (BP)	GO:0060537	muscle tissue development	High - 8 h	0.00019426
Human	GO (BP)	GO:0048661	positive regulation of smooth muscle cell proliferation	High - 8 h	0.00019805
Human	GO (BP)	GO:0070647	protein modification by small protein conjugation or removal	High - 8 h	0.0002139
Human	GO (BP)	GO:0055088	lipid homeostasis	High - 8 h	0.0002197
Human	GO (BP)	GO:0030518	intracellular steroid hormone receptor signaling pathway	High - 8 h	0.00026118
Human	GO (BP)	GO:0070848	response to growth factor	High - 8 h	0.00026479
Human	GO (BP)	GO:0006271	DNA strand elongation involved in DNA replication	High - 24 h	1.12E-12
Human	GO (BP)	GO:0034080	CENP-A containing nucleosome assembly	High - 24 h	1.12E-10
Human	GO (BP)	GO:0006987	activation of signaling protein activity involved in unfolded protein response	High - 24 h	2.42E-08
Human	GO (BP)	GO:0006270	DNA replication initiation	High - 24 h	3.57E-07
Human	GO (BP)	GO:0007076	mitotic chromosome condensation	High - 24 h	5.39E-07
Human	GO (BP)	GO:0007091	metaphase/anaphase transition of mitotic cell cycle	High - 24 h	7.41E-07
Human	GO (BP)	GO:0000086	G2/M transition of mitotic cell cycle	High - 24 h	1.86E-06
Human	GO (BP)	GO:0000083	regulation of transcription involved in G1/S transition of mitotic cell cycle	High - 24 h	2.21E-06
Human	GO (BP)	GO:0032201	telomere maintenance via semi-conservative replication	High - 24 h	2.21E-06
Human	GO (BP)	GO:1901606	alpha-amino acid catabolic process	High - 24 h	3.21E-06
Human	GO (BP)	GO:0000722	telomere maintenance via recombination	High - 24 h	5.25E-06
Human	GO (BP)	GO:0008608	attachment of spindle microtubules to kinetochore	High - 24 h	5.45E-06
Human	GO (BP)	GO:0015949	nucleobase-containing small molecule interconversion	High - 24 h	7.90E-06
Human	GO (BP)	GO:0007584	response to nutrient	High - 24 h	1.09E-05
Human	GO (BP)	GO:0040001	establishment of mitotic spindle localization	High - 24 h	1.33E-05
Human	GO (BP)	GO:0042493	response to drug	High - 24 h	1.84E-05
Human	GO (BP)	GO:0051988	regulation of attachment of spindle microtubules to kinetochore	High - 24 h	1.94E-05
Human	GO (BP)	GO:0060236	regulation of mitotic spindle organization	High - 24 h	3.15E-05
Human	GO (BP)	GO:0007080	mitotic metaphase plate congression	High - 24 h	3.22E-05

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Human	GO (BP)	GO:0007094	mitotic spindle assembly checkpoint	High - 24 h	4.01E-05
Human	GO (BP)	GO:0006206	pyrimidine nucleobase metabolic process	High - 24 h	4.33E-05
Human	GO (BP)	GO:0006200	ATP catabolic process	High - 24 h	4.50E-05
Human	GO (BP)	GO:0031100	organ regeneration	High - 24 h	5.62E-05
Human	GO (BP)	GO:0051382	kinetochore assembly	High - 24 h	7.56E-05
Human	GO (BP)	GO:0055114	oxidation-reduction process	High - 24 h	8.31E-05
Human	GO (BP)	GO:0000910	cytokinesis	High - 24 h	8.57E-05
Human	GO (BP)	GO:0008283	cell proliferation	High - 24 h	9.44E-05
Human	GO (BP)	GO:0045132	meiotic chromosome segregation	High - 24 h	0.00010895
Human	GO (BP)	GO:0007019	microtubule depolymerization	High - 24 h	0.00014913
Human	GO (BP)	GO:0046394	carboxylic acid biosynthetic process	High - 24 h	0.00015846
Human	GO (BP)	GO:0006297	nucleotide-excision repair, DNA gap filling	High - 24 h	0.00019643
Human	GO (BP)	GO:0006081	cellular aldehyde metabolic process	High - 24 h	0.00021462
Human	GO (BP)	GO:0071479	cellular response to ionizing radiation	High - 24 h	0.00021462
Human	GO (BP)	GO:0030433	ER-associated ubiquitin-dependent protein catabolic process	High - 24 h	0.00021546
Human	GO (BP)	GO:0090068	positive regulation of cell cycle process	High - 24 h	0.00030154
Human	GO (BP)	GO:0006268	DNA unwinding involved in DNA replication	High - 24 h	0.00031637
Human	GO (BP)	GO:0009157	deoxyribonucleoside monophosphate biosynthetic process	High - 24 h	0.00032348
Human	GO (BP)	GO:0009221	pyrimidine deoxyribonucleotide biosynthetic process	High - 24 h	0.00032348
Human	GO (BP)	GO:0071281	cellular response to iron ion	High - 24 h	0.00032348
Human	GO (BP)	GO:0090307	spindle assembly involved in mitosis	High - 24 h	0.00034088
Human	GO (BP)	GO:0042060	wound healing	High - 24 h	0.00034532
Human	GO (CC)	GO:0032993	protein-DNA complex	Low - 24 h	6.19E-17
Human	GO (CC)	GO:0000922	spindle pole	Low - 24 h	1.28E-12
Human	GO (CC)	GO:0005829	cytosol	Low - 24 h	7.53E-11
Human	GO (CC)	GO:0030496	midbody	Low - 24 h	1.31E-08
Human	GO (CC)	GO:0005654	nucleoplasm	Low - 24 h	8.27E-08
Human	GO (CC)	GO:0005876	spindle microtubule	Low - 24 h	2.18E-07
Human	GO (CC)	GO:0072686	mitotic spindle	Low - 24 h	2.68E-07
Human	GO (CC)	GO:0000778	condensed nuclear chromosome kinetochore	Low - 24 h	3.33E-07
Human	GO (CC)	GO:0005871	kinesin complex	Low - 24 h	6.06E-06
Human	GO (CC)	GO:0000796	condensin complex	Low - 24 h	8.61E-06
Human	GO (CC)	GO:0000940	condensed chromosome outer kinetochore	Low - 24 h	1.12E-05
Human	GO (CC)	GO:0051233	spindle midzone	Low - 24 h	1.74E-05
Human	GO (CC)	GO:0005813	centrosome	Low - 24 h	4.51E-05
Human	GO (CC)	GO:0042555	MCM complex	Low - 24 h	0.00011022
Human	GO (CC)	GO:0008278	cohesin complex	Low - 24 h	0.00016939
Human	GO (CC)	GO:0005730	nucleolus	Low - 24 h	0.00020934
Human	GO (CC)	GO:0035371	microtubule plus-end	Low - 24 h	0.00064107

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Human	GO (CC)	GO:0045120	pronucleus	Low - 24 h	0.00083603
Human	GO (CC)	GO:0032993	protein-DNA complex	Middle - 24 h	1.76E-21
Human	GO (CC)	GO:0005654	nucleoplasm	Middle - 24 h	2.22E-12
Human	GO (CC)	GO:0000922	spindle pole	Middle - 24 h	1.17E-11
Human	GO (CC)	GO:0005829	cytosol	Middle - 24 h	5.35E-10
Human	GO (CC)	GO:0000796	condensin complex	Middle - 24 h	2.70E-08
Human	GO (CC)	GO:0030496	midbody	Middle - 24 h	1.53E-07
Human	GO (CC)	GO:0000778	condensed nuclear chromosome kinetochore	Middle - 24 h	1.80E-07
Human	GO (CC)	GO:0005876	spindle microtubule	Middle - 24 h	2.98E-07
Human	GO (CC)	GO:0000940	condensed chromosome outer kinetochore	Middle - 24 h	9.16E-07
Human	GO (CC)	GO:0005663	DNA replication factor C complex	Middle - 24 h	2.84E-06
Human	GO (CC)	GO:0042555	MCM complex	Middle - 24 h	4.69E-06
Human	GO (CC)	GO:0072686	mitotic spindle	Middle - 24 h	9.32E-06
Human	GO (CC)	GO:0005871	kinesin complex	Middle - 24 h	4.48E-05
Human	GO (CC)	GO:0000785	chromatin	Middle - 24 h	0.00021058
Human	GO (CC)	GO:0005788	endoplasmic reticulum lumen	Middle - 24 h	0.0002234
Human	GO (CC)	GO:0005813	centrosome	Middle - 24 h	0.00051081
Human	GO (CC)	GO:0032300	mismatch repair complex	Middle - 24 h	0.00053004
Human	GO (CC)	GO:0000407	pre-autophagosomal structure	Middle - 24 h	0.00053852
Human	GO (CC)	GO:0051233	spindle midzone	Middle - 24 h	0.00071916
Human	GO (CC)	GO:0035371	microtubule plus-end	Middle - 24 h	0.00093564
Human	GO (CC)	GO:0005654	nucleoplasm	High - 8 h	1.40E-06
Human	GO (CC)	GO:0032993	protein-DNA complex	High - 24 h	5.80E-21
Human	GO (CC)	GO:0000922	spindle pole	High - 24 h	6.20E-11
Human	GO (CC)	GO:0005829	cytosol	High - 24 h	8.18E-10
Human	GO (CC)	GO:0000940	condensed chromosome outer kinetochore	High - 24 h	5.82E-09
Human	GO (CC)	GO:0005654	nucleoplasm	High - 24 h	2.02E-08
Human	GO (CC)	GO:0005876	spindle microtubule	High - 24 h	7.54E-08
Human	GO (CC)	GO:0000796	condensin complex	High - 24 h	1.02E-07
Human	GO (CC)	GO:0030496	midbody	High - 24 h	1.10E-07
Human	GO (CC)	GO:0000778	condensed nuclear chromosome kinetochore	High - 24 h	6.69E-07
Human	GO (CC)	GO:0070062	extracellular vesicular exosome	High - 24 h	6.20E-06
Human	GO (CC)	GO:0005813	centrosome	High - 24 h	7.40E-06
Human	GO (CC)	GO:0005663	DNA replication factor C complex	High - 24 h	8.43E-06
Human	GO (CC)	GO:0042555	MCM complex	High - 24 h	1.68E-05
Human	GO (CC)	GO:0005788	endoplasmic reticulum lumen	High - 24 h	0.00013482
Human	GO (CC)	GO:0005871	kinesin complex	High - 24 h	0.0003161
Human	GO (CC)	GO:0072686	mitotic spindle	High - 24 h	0.00035081
Human	GO (CC)	GO:0032155	cell division site part	High - 24 h	0.00051871

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Rat	KEGG	rno00051	Fructose and mannose metabolism - Rattus norvegicus (rat)	Middle - 24 h	7.38E-05
Rat	KEGG	rno00830	Retinol metabolism - Rattus norvegicus (rat)	Middle - 24 h	5.98E-05
Rat	KEGG	rno04610	Complement and coagulation cascades - Rattus norvegicus (rat)	Middle - 24 h	2.46E-06
Rat	KEGG	rno00260	Glycine, serine and threonine metabolism - Rattus norvegicus (rat)	High - 24 h	1.34E-08
Rat	KEGG	rno04610	Complement and coagulation cascades - Rattus norvegicus (rat)	High - 24 h	2.30E-12
Rat	TOX	TOX:04	DNA Damage & Repair	High - 8 h	0.00083009
Rat	GO (BP)	GO:0055114	oxidation-reduction process	Middle - 24 h	5.40E-08
Rat	GO (BP)	GO:0006805	xenobiotic metabolic process	Middle - 24 h	6.05E-06
Rat	GO (BP)	GO:0017144	drug metabolic process	Middle - 24 h	1.01E-05
Rat	GO (BP)	GO:0010043	response to zinc ion	Middle - 24 h	1.39E-05
Rat	GO (BP)	GO:0006790	sulfur compound metabolic process	Middle - 24 h	7.12E-05
Rat	GO (BP)	GO:0001889	liver development	Middle - 24 h	8.44E-05
Rat	GO (BP)	GO:0010468	regulation of gene expression	High - 8 h	8.90E-06
Rat	GO (BP)	GO:0072395	signal transduction involved in cell cycle checkpoint	High - 8 h	2.23E-05
Rat	GO (BP)	GO:0030330	DNA damage response, signal transduction by p53 class mediator	High - 8 h	2.67E-05
Rat	GO (BP)	GO:2000112	regulation of cellular macromolecule biosynthetic process	High - 8 h	2.82E-05
Rat	GO (BP)	GO:0019219	regulation of nucleobase-containing compound metabolic process	High - 8 h	3.00E-05
Rat	GO (BP)	GO:0016070	RNA metabolic process	High - 8 h	4.43E-05
Rat	GO (BP)	GO:0010467	gene expression	High - 8 h	5.87E-05
Rat	GO (BP)	GO:0055114	oxidation-reduction process	High - 24 h	5.09E-13
Rat	GO (BP)	GO:0009071	serine family amino acid catabolic process	High - 24 h	5.31E-07
Rat	GO (BP)	GO:0032787	monocarboxylic acid metabolic process	High - 24 h	1.82E-06
Rat	GO (BP)	GO:0006958	complement activation, classical pathway	High - 24 h	3.06E-06
Rat	GO (BP)	GO:0006544	glycine metabolic process	High - 24 h	3.35E-06
Rat	GO (BP)	GO:1901653	cellular response to peptide	High - 24 h	1.43E-05
Rat	GO (BP)	GO:0001889	liver development	High - 24 h	2.10E-05
Rat	GO (BP)	GO:0006805	xenobiotic metabolic process	High - 24 h	2.43E-05
Rat	GO (BP)	GO:0006006	glucose metabolic process	High - 24 h	2.62E-05
Rat	GO (BP)	GO:0006695	cholesterol biosynthetic process	High - 24 h	3.76E-05
Rat	GO (BP)	GO:0006733	oxidoreduction coenzyme metabolic process	High - 24 h	4.55E-05
Rat	GO (BP)	GO:0042632	cholesterol homeostasis	High - 24 h	4.74E-05
Rat	GO (BP)	GO:0044724	single-organism carbohydrate catabolic process	High - 24 h	5.51E-05
Rat	GO (BP)	GO:0051289	protein homotetramerization	High - 24 h	6.92E-05
Rat	GO (BP)	GO:0006790	sulfur compound metabolic process	High - 24 h	8.35E-05
Rat	GO (BP)	GO:0009070	serine family amino acid biosynthetic process	High - 24 h	8.37E-05
Rat	GO (BP)	GO:0009074	aromatic amino acid family catabolic process	High - 24 h	8.37E-05
Rat	GO (BP)	GO:0072524	pyridine-containing compound metabolic process	High - 24 h	9.02E-05
Rat	GO (BP)	GO:0043434	response to peptide hormone	High - 24 h	9.23E-05
Rat	GO (BP)	GO:0010878	cholesterol storage	High - 24 h	9.44E-05

Species	Category	Term ID	Term name	Treatment	P-value
Rat	GO (CC)	GO:0005615	extracellular space	Middle - 24 h	8.86E-05
Rat	GO (CC)	GO:0005634	nucleus	High - 8 h	3.42E-06
Rat	GO (CC)	GO:0070062	extracellular vesicular exosome	High - 24 h	7.36E-07
Rat	GO (CC)	GO:0005615	extracellular space	High - 24 h	0.00010594
Rat	GO (MF)	GO:0005506	iron ion binding	Middle - 24 h	4.35E-07
Rat	GO (MF)	GO:0005543	phospholipid binding	Middle - 24 h	5.16E-05
Rat	GO (MF)	GO:0016712	oxidoreductase activity, acting on paired donors, with incorporation or reduction of m	Middle - 24 h	5.45E-05
Rat	GO (MF)	GO:0030170	pyridoxal phosphate binding	High - 24 h	2.92E-05
Rat	GO (MF)	GO:0043546	molybdopterin cofactor binding	High - 24 h	2.95E-05