

SUPPLEMENTARY TABLE 1
GENES DOWNREGULATED BY p38 INHIBITOR IN CELLS EXPRESSING ATP7B-H1069Q

BIOLOGICAL PROCESS	Number of genes	p-value	FDR
complement activation, classical pathway	18	3.50E-12	6.50E-09
humoral immune response mediated by circulating immunoglobulin	18	1.50E-11	2.80E-08
complement activation	20	7.90E-11	1.50E-07
activation of plasma proteins involved in acute inflammatory response	20	1.30E-10	2.40E-07
steroid metabolic process	46	1.40E-10	2.60E-07
protein maturation by peptide bond cleavage	28	2.30E-10	4.20E-07
acute inflammatory response	28	5.80E-09	1.10E-05
protein processing	30	7.50E-09	1.40E-05
protein maturation	31	1.50E-08	2.80E-05
lymphocyte mediated immunity	22	5.60E-08	1.00E-04
immunoglobulin mediated immune response	19	8.20E-08	1.50E-04
cholesterol metabolic process	25	1.30E-07	2.30E-04
B cell mediated immunity	19	1.50E-07	2.80E-04
response to wounding	77	2.40E-07	4.50E-04
humoral immune response	22	5.40E-07	1.00E-03
lipid biosynthetic process	53	6.30E-07	1.20E-03
activation of immune response	24	7.90E-07	1.50E-03
sterol metabolic process	25	8.10E-07	1.50E-03
adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	21	1.50E-06	2.80E-03
adaptive immune response	21	1.50E-06	2.80E-03
leukocyte mediated immunity	22	2.40E-06	4.50E-03
complement activation, alternative pathway	9	5.90E-06	1.10E-02
positive regulation of immune response	29	8.30E-06	1.50E-02
innate immune response	28	9.30E-06	1.70E-02
steroid biosynthetic process	20	2.80E-05	5.20E-02
fatty acid metabolic process	34	3.40E-05	6.30E-02
acylglycerol metabolic process	14	8.00E-05	1.50E-01
neutral lipid metabolic process	14	1.00E-04	1.80E-01
positive regulation of response to stimulus	37	1.00E-04	1.90E-01
cholesterol biosynthetic process	10	1.10E-04	2.00E-01
glycerol ether metabolic process	14	1.30E-04	2.30E-01
organic ether metabolic process	14	1.90E-04	3.50E-01
sterol biosynthetic process	11	2.70E-04	5.00E-01
inflammatory response	45	3.10E-04	5.70E-01
immune effector process	24	3.30E-04	6.00E-01
triglyceride metabolic process	12	4.00E-04	7.30E-01

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organic acid biosynthetic process	26	4.90E-04	9.00E-01
carboxylic acid biosynthetic process	26	4.90E-04	9.00E-01
response to oxidative stress	27	5.00E-04	9.20E-01
positive regulation of immune system process	35	5.60E-04	1.00E+00
response to hormone stimulus	48	7.00E-04	1.30E+00
lipid transport	24	1.00E-03	1.90E+00
response to endogenous stimulus	51	1.10E-03	2.00E+00
wound healing	29	1.10E-03	2.00E+00
carboxylic acid transport	24	1.20E-03	2.30E+00
organic acid transport	24	1.40E-03	2.50E+00
microtubule-based process	35	1.60E-03	3.00E+00
proteolysis	110	2.00E-03	3.70E+00
regulation of programmed cell death	88	2.10E-03	3.80E+00
glycerolipid metabolic process	25	2.10E-03	3.80E+00
negative regulation of transcription	55	2.10E-03	3.80E+00
oxidation reduction	72	2.10E-03	3.80E+00
regulation of cell death	88	2.30E-03	4.20E+00
regulation of apoptosis	87	2.30E-03	4.20E+00
regulation of immune effector process	18	2.30E-03	4.20E+00
cellular amino acid catabolic process	14	2.30E-03	4.20E+00
homeostatic process	82	2.50E-03	4.50E+00
liver development	12	2.50E-03	4.60E+00
blood coagulation	18	2.60E-03	4.70E+00
coagulation	18	2.60E-03	4.70E+00
carboxylic acid catabolic process	19	2.70E-03	4.80E+00
organic acid catabolic process	19	2.70E-03	4.80E+00
response to organic substance	79	2.70E-03	4.90E+00
CELLULAR COMPONENT	Number of genes	p-value	FDR
endoplasmic reticulum	121	8.80E-08	1.30E-04
membrane fraction	106	9.40E-08	1.40E-04
insoluble fraction	108	1.70E-07	2.50E-04
extracellular space	91	4.90E-07	7.00E-04
Golgi apparatus	108	1.20E-06	1.70E-03
cell fraction	128	1.30E-06	1.80E-03
extracellular region part	115	2.60E-06	3.70E-03
microsome	38	3.60E-05	5.20E-02
vesicular fraction	38	6.80E-05	9.80E-02
ER-Golgi intermediate compartment	11	9.60E-04	1.40E+00
membrane attack complex	5	1.10E-03	1.50E+00

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protein-lipid complex	10	1.10E-03	1.60E+00
plasma lipoprotein particle	10	1.10E-03	1.60E+00
microtubule cytoskeleton	64	1.20E-03	1.70E+00
microtubule	37	1.40E-03	2.00E+00
membrane-bounded vesicle	65	1.70E-03	2.40E+00
cytoplasmic membrane-bounded vesicle	63	1.90E-03	2.80E+00
vesicle	74	2.10E-03	2.90E+00
high-density lipoprotein particle	8	2.40E-03	3.40E+00
Golgi stack	11	2.40E-03	3.50E+00
vesicle lumen	11	2.40E-03	3.50E+00
endoplasmic reticulum part	43	2.90E-03	4.00E+00
endoplasmic reticulum lumen	15	3.30E-03	4.60E+00
MOLECULAR FUNCTION	Number of genes	p-value	FDR
peptidase inhibitor activity	29	3.00E-05	4.90E-02
endopeptidase inhibitor activity	28	3.00E-05	4.90E-02
cation binding	392	9.20E-05	1.50E-01
ion binding	397	9.40E-05	1.50E-01
enzyme inhibitor activity	41	1.10E-04	1.80E-01
solute:cation symporter activity	20	1.70E-04	2.70E-01
metal ion binding	386	1.80E-04	3.00E-01
oxidoreductase activity, acting on the CH-NH group of donors	10	3.10E-04	5.00E-01
serine-type endopeptidase inhibitor activity	19	3.30E-04	5.30E-01
magnesium ion binding	58	4.20E-04	6.80E-01
oxidoreductase activity, acting on the CH-CH group of donors, NAD or NADP as acceptor	8	4.50E-04	7.30E-01
steroid binding	15	4.50E-04	7.30E-01
ligase activity, forming carbon-sulfur bonds	9	9.40E-04	1.50E+00
oxidoreductase activity, acting on the CH-NH group of donors, NAD or NADP as acceptor	7	2.10E-03	3.40E+00
solute:sodium symporter activity	12	2.40E-03	3.80E+00
steroid dehydrogenase activity	9	2.50E-03	4.00E+00
anion:cation symporter activity	9	2.50E-03	4.00E+00
symporter activity	22	3.00E-03	4.70E+00
KEGG PATHWAY	Number of genes	p-value	FDR
Complement and coagulation cascades	33	5.00E-17	6.20E-14