

Table 1: Differentially regulated proteins in CCl₄ treated BALB/c mice

Accession number	Protein	Functions and pathways	CCl ₄ vs. Oil (2xCCl ₄ inj.)	significance	CCl ₄ vs. Oil (mRNA level)
Q63836	Selenium binding protein-2	not known; binds selenium and acetaminophen	(-2.53) -3.8	(1.5E-4) 3,7E-4	-5.36
Q58ET5	Glutathione S-transferase	conjugation of reduced glutathione to exogenous and endogenous hydrophobic electrophiles	(-1.05) 2.12	(6.4E-1) 1.9E-4	3.86
Q9CZS1	Aldehyde dehydrogenase 1	detoxification of acetaldehyde, metabolism of corticosteroids, biogenic amines, neurotransmitters, and lipid peroxidation	(1.18) 2.26	(2.8E-1) 5.1E-4	2.26
P47738	Aldehyde dehydrogenase 2	converting retinaldehyde to retinoic acid	(-1.19) 1.69	(6.3E-2) 1.0E-3	1.62
Q8R0Y6	Formyltetrahydrofolate dehydrogenase	mediate the use of formate or methyl groups	(-1.75) -1.52	(2.9E-3) 1.0E-2	1.63
Q8C196	Carbamoyl-phosphate synthase	removing of excess ammonia from the cell	(4.03) 1.53	(5.7E-3) 9.1E-3	1.17
P07759	Serin proteinase inhibitor clade A	belongs to the serpin family	(-2.17) -3.24	(4.6E-2) 7.4E-3	-1.61
Q921I1	Transferrin	serum beta-globulin that binds and transports iron	(-1.03) -1.91	(9.4E-1) 1.3E-2	-1.73
Q61111	Quaking Type II	interacting selectively with any nucleic acid and mRNA	(-1.34) -2.29	(2.4E-1) 9.1E-5	n.d.
P16015	Carbonic anhydrase 3	reversible hydration of carbon dioxide	(-1.52) -1.56	(1.3E-2) 2.8E-5	n.d.
Q99LB7	Sarcosine Dehydrogenase	oxidative degradation of sarcosine	(-1.74) -1.64	(5.9E-4) 1.6E-4	n.d.
Q00623	apolipoprotein A-I precursor	participates in cholesterol transport	(-1.16) -2,32	(2.7E-1) 1.1E-6	n.d.
Q91X87	Selenium binding protein-1	molecular function: selenium binding	(-1.29) -1.81	(1.1E-2) 3.6E-5	n.d.
P54869	HMG-CoA synthase	condenses acetyl-CoA with acetoacetyl-CoA to form HMG-CoA	(-1.02) 1.66	(9.4E-1) 2.8E-5	n.d.
O35490 P16460	Mix: betaine-homocysteine methyltransferase, argininosuccinate synthetase 1	involved in the regulation of homocysteine metabolism synthesis of N(omega)-L-arginino)succinate	(1.08) 1.82	(5.0E-1) 1.6E-5	n.d.
Q9R1N4 Q7TPE1	Mix: Nitrilase 1 / Carbonic anhydrase 2	hydrolase activity, acting on C-N (but not peptide) bonds Carbonate dehydratase activity	(1.34) 3.33	(3.5E-3) 6.1E-4	n.d.
Q61176	Arginase	arginine degradation via the urea cycle; first step	(1.3) 1.65	(5.9E-2) 4.1E-4	n.d.
Q9DBT9	DMGDH precursor	oxidative degradation of N,N-dimethylglycine	(-1.31) -1.88	(3.4E-3) 5.2E-4	n.d.
Q8K0E8	fibrinogen, B beta polypeptide	involved in clotting	(-2.41) -1.89	(4.9E-2) 1.4E-4	n.d.
Q91VS8	FERM, RhoGEF and pleckstrin domain protein 2	plays a role in the response to class 3 semaphorins and remodeling of the actin cytoskeleton	(-1.29) 1.71	(1.2E-2) 2.6E-4	n.d.

Mouse liver proteins differentially regulated in CCl₄ induced hepatic injury analyzed by DIGE/MALDI-TOF-MS and peptide mass fingerprint database search. Statistical significance performed by DeCyder image analysis software of regulated spots is given for each value. Verification of DIGE results by RT-PCR was performed for proteins which were always found inter-individually reproducible and which were identified at least twice by MALDI-TOF-MS. Protein regulation in initiation phase of fibrosis is given in brackets. Underlined values indicate lack of significance or no regulation. Accession numbers were extracted from the SWISS-PROT database.