

Differential urinary proteins used for OPLSDA found in DDA experiment

Uniprot ID	Protein description	Gene name	Average of WH	Average of DP	Average of SD	ANOVA-P	Fold change between WH and DP	P value between WH and DP	Fold change between WH and SD	P value between WH and SD	Fold change between DP and SD	P value between DP and SD
O43451	Maltase-glucoamylase, intestinal [Includes: Maltase (EC 3.2.1.20) (Alpha-glucosidase); Glucoamylase (EC 3.2.1.3) (Glucan 1,4-alpha-glucosidase)]	MGA	56.4	27.6	50.8	0.00057816	2.0435	0.00811753	1.1102	0.54954843	1.8406	0.02541692
P54802	Alpha-N-acetylglucosaminidase (EC 3.2.1.50) (N-acetyl-alpha-glucosaminidase) (NAG) [Cleaved into: Alpha-N-acetylglucosaminidase 82 kDa form; Alpha-N-acetylglucosaminidase 77 kDa form]	ANAG	51.2	21.6	24.8	0.00086056	2.3704	0.00947902	2.0645	0.01760228	1.1481	0.7446347
Q92820	Gamma-glutamyl hydrolase (EC 3.4.19.9) (Conjugase) (GH) (Gamma-Glu-X carboxypeptidase)	GGH	38.4	24.6	15	0.00112676	1.5610	0.03534555	2.5600	0.00169895	1.6400	0.12499841
Q13510	Acid ceramidase (AC) (ACDase) (Acid CDase) (EC 3.5.1.23) (Acylsphingosine deacylase) (N-acylethanolamine hydrolase ASAHI) (EC 3.5.1.-) (N-acylsphingosine amidohydrolase) (Putative 32 kDa heart protein) (PHP32) [Cleaved into: Acid ceramidase subunit alpha;	ASAHI	31.4	18	12.6	0.00139638	1.7444	0.06505807	2.4921	0.01465209	1.4286	0.42913251

Q7Z5L0	Vitelline membrane outer layer protein 1 homolog	VMO1	16	10	17.4	0.00176309	1.6000	0.03980505	1.0875	0.60045932	1.7400	0.01480435
P07686	Beta-hexosaminidase subunit beta (EC 3.2.1.52) (Beta-N-acetylhexosaminidase subunit beta) (Hexosaminidase subunit B) (Cervical cancer proto-oncogene 7 protein) (HCC-7) (N-acetyl-beta-glucosaminidase subunit beta) [Cleaved into: Beta-hexosaminidase subunit	HEXB	30.2	16.2	15.2	0.00214457	1.8642	0.03801899	1.9868	0.02805777	1.0658	0.87055005
P00558	Phosphoglycerate kinase 1 (EC 2.7.2.3) (Cell migration-inducing gene 10 protein) (Primer recognition protein 2) (PRP 2)	PGK1	21.6	10.8	15.2	0.0021978	2.0000	0.01516535	1.4211	0.11932585	1.4074	0.27131589
Q03154	Aminoacylase-1 (ACY-1) (EC 3.5.1.14) (N-acyl-L-amino-acid amidohydrolase)	ACY1	22	9.8	17.6	0.00261327	2.2449	0.01220306	1.2500	0.30870782	1.7959	0.08395723
P04406	Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (EC 1.2.1.12) (Peptidyl-cysteine S-nitrosylase GAPDH) (EC 2.6.99.-)	G3P	20	8.6	16.8	0.00278091	2.3256	0.00782769	1.1905	0.38868098	1.9535	0.04078596
P16870	Carboxypeptidase E (CPE) (EC 3.4.17.10) (Carboxypeptidase H) (CPH) (Enkephalin convertase) (Prohormone-processing carboxypeptidase)	CBPE	15.2	6.2	15.8	0.00301745	2.4516	0.0051284	1.0395	0.82375275	2.5484	0.00337343
P51688	N-sulphoglucosamine sulphohydrolase (EC 3.10.1.1) (Sulfoglucosamine sulfamidase) (Sulphamidase)	SPHM	24	14	7.2	0.00367352	1.7143	0.11405117	3.3333	0.01426705	1.9444	0.2690232

P06280	Alpha-galactosidase A (EC 3.2.1.22) (Alpha-D-galactosidase A) (Alpha-D-galactoside galactohydrolase) (Meliabiase) (Agalsidase)	AGAL	20.4	9.8	12.2	0.0038018	2.0816	0.01998261	1.6721	0.06022322	1.2449	0.55508205
O00468	Agrin [Cleaved into: Agrin N-terminal 110 kDa subunit; Agrin C-terminal 110 kDa subunit; Agrin C-terminal 90 kDa fragment (C90); Agrin C-terminal 22 kDa fragment (C22)]	AGRIN	7.8	17.4	10.2	0.00443212	2.2308	0.00372924	1.3077	0.38740077	1.7059	0.01964199
Q02818	Nucleobindin-1 (CALNUC)	NUCB1	18.2	8.8	8.2	0.00520281	2.0682	0.02412173	2.2195	0.01779549	1.0732	0.87196322
P06865	Beta-hexosaminidase subunit alpha (EC 3.2.1.52) (Beta-N-acetylhexosaminidase subunit alpha) (Hexosaminidase subunit A) (N-acetyl-beta-glucosaminidase subunit alpha)	HEXA	21.4	11	8	0.00533234	1.9455	0.0197552	2.6750	0.0046916	1.3750	0.45317829
O96009	Napsin-A (EC 3.4.23.-) (Aspartyl protease 4) (ASP4) (Asp 4) (Napsin-1) (TA01/TA02)	NAPSA	17.6	9.8	8.2	0.0053964	1.7959	0.03725861	2.1463	0.01539529	1.1951	0.63959252
P09668	Pro-cathepsin H [Cleaved into: Cathepsin H mini chain; Cathepsin H (EC 3.4.22.16); Cathepsin H heavy chain; Cathepsin H light chain]	CATH	16.2	9.4	7.2	0.00573126	1.7234	0.03659083	2.2500	0.00897546	1.3056	0.46141571
P18065	Insulin-like growth factor-binding protein 2 (IBP-2) (IGF-binding protein 2) (IGFBP-2)	IBP2	15.4	7	3.2	0.00576927	2.2000	0.032426	4.8125	0.00428535	2.1875	0.29545805

P14550	Aldo-keto reductase family 1 member A1 (EC 1.1.1.2) (EC 1.1.1.372) (EC 1.1.1.54) (Alcohol dehydrogenase [NADP (+)]) (Aldehyde reductase) (Glucuronate reductase) (EC 1.1.1.19) (Glucuronolactone reductase) (EC 1.1.1.20)	AK1A1	13.4	4.2	13.8	0.00603786	3.1905	0.00333854	1.0299	0.87661391	3.2857	0.00249941
O00584	Ribonuclease T2 (EC 4.6.1.19) (Ribonuclease 6)	RNT2	12.2	6.8	7.6	0.00742796	1.7941	0.00855276	1.6053	0.02027181	1.1176	0.65026266
P00352	Retinal dehydrogenase 1 (RALDH 1) (RalDH1) (EC 1.2.1.-) (EC 1.2.1.36) (ALDH-E1) (ALHDII) (Aldehyde dehydrogenase family 1 member A1) (Aldehyde dehydrogenase, cytosolic)	AL1A1	12	4.6	7	0.00750723	2.6087	0.01330081	1.7143	0.07361233	1.5217	0.36532407
P07148	Fatty acid-binding protein, liver (Fatty acid- binding protein 1) (Liver-type fatty acid- binding protein) (L-FABP)	FABPL	9.8	2.4	14	0.00830377	4.0833	0.09379109	1.4286	0.32200766	5.8333	0.01454583
P40189	Interleukin-6 receptor subunit beta (IL-6 receptor subunit beta) (IL-6R subunit beta) (IL-6R-beta) (IL-6RB) (CDw130) (Interleukin-6 signal transducer) (Membrane glycoprotein 130) (gp130) (Oncostatin-M receptor subunit alpha) (CD antigen CD130)	IL6RB	6.2	5	9	0.00850588	1.2400	0.41575468	1.4516	0.07275958	1.8000	0.0157565

Q9HD89	Resistin (Adipose tissue-specific secretory factor) (ADSF) (C/EBP-epsilon-regulated myeloid-specific secreted cysteine-rich protein) (Cysteine-rich secreted protein A12-alpha-like 2) (Cysteine-rich secreted protein FIZZ3)	RETN	11.4	3.6	7	0.00979157	3.1667	0.01100593	1.6286	0.11604229	1.9444	0.21505227
Q8TF66	Leucine-rich repeat-containing protein 15 (Leucine-rich repeat protein induced by beta-amyloid homolog) (hLib)	LRC15	8.4	3.4	4	0.01017688	2.4706	0.0181602	2.1000	0.03320385	1.1765	0.74857987
Q9HB40	Retinoid-inducible serine carboxypeptidase (EC 3.4.16.-) (Serine carboxypeptidase 1)	RISC	11.6	6	3.8	0.01053017	1.9333	0.05188652	3.0526	0.01094531	1.5789	0.41312538
P09210	Glutathione S-transferase A2 (EC 2.5.1.18) (GST HA subunit 2) (GST class-alpha member 2) (GST-gamma) (GSTA2-2) (GTH2)	GSTA2	11.6	1.4	7.6	0.01080269	8.2857	0.00001217	1.5263	0.01630058	5.4286	0.00098433
Q15375	Ephrin type-A receptor 7 (EC 2.7.10.1) (EPH homology kinase 3) (EHK-3) (EPH-like kinase 11) (EK11) (hEK11)	EPHA7	6.2	3.8	10.8	0.01162901	1.6316	0.31685436	1.7419	0.06842735	2.8421	0.01015318
P62258	14-3-3 protein epsilon (14-3-3E)	1433E	10	5	8.8	0.01200104	2.0000	0.00812219	1.1364	0.46194823	1.7600	0.03312108
Q9BRK5	45 kDa calcium-binding protein (Cab45) (Stromal cell-derived factor 4) (SDF-4)	CAB45	8.6	4.8	5	0.01223059	1.7917	0.01229253	1.7200	0.01638861	1.0417	0.87946013

O00754	Lysosomal alpha-mannosidase (Laman) (EC 3.2.1.24) (Lysosomal acid alpha-mannosidase) (Mannosidase alpha class 2B member 1) (Mannosidase alpha-B) [Cleaved into: Lysosomal alpha-mannosidase A peptide; Lysosomal alpha-mannosidase B peptide; Lysosomal alpha-m	MA2B1	14.4	4.2	1.8	0.01247006	3.4286	0.00416366	8.0000	0.00093196	2.3333	0.42271281
P21695	Glycerol-3-phosphate dehydrogenase [NAD(+)], cytoplasmic (GPD-C) (GPDH-C) (EC 1.1.1.8)	GPDA	9	1.4	6.4	0.0126893	6.4286	0.00352955	1.4063	0.23952372	4.5714	0.03475945
P00966	Argininosuccinate synthase (EC 6.3.4.5) (Citrulline--aspartate ligase)	ASSY	8.4	1.6	5.2	0.01286516	5.2500	0.01088062	1.6154	0.18218804	3.2500	0.13712994
Q06830	Peroxiredoxin-1 (EC 1.11.1.15) (Natural killer cell-enhancing factor A) (NKEF-A) (Proliferation-associated gene protein) (PAG) (Thioredoxin peroxidase 2) (Thioredoxin-dependent peroxide reductase 2)	PRDX1	9.6	3.8	5	0.01316329	2.5263	0.00502613	1.9200	0.01871584	1.3158	0.49201992
Q14914	Prostaglandin reductase 1 (PRG-1) (EC 1.3.1.-) (15-oxoprostaglandin 13-reductase) (EC 1.3.1.48) (NADP-dependent leukotriene B4 12-hydroxydehydrogenase) (EC 1.3.1.74)	PTGR1	10.8	2.4	4	0.01330424	4.5000	0.00891916	2.7000	0.02678304	1.6667	0.56383836

Q8NCC3	Phospholipase A2 group XV (1-O-acylceramide synthase) (ACS) (LCAT-like lysophospholipase) (LPL) (EC 3.1.1.5) (Lysophospholipase 3) (Lysosomal phospholipase A and acyltransferase) (EC 2.3.1.-) (EC 3.1.1.32) (EC 3.1.1.4) (Lysosomal phospholipase A2) (LPLA2)	PAG15	8.8	4.4	4	0.01399608	2.0000	0.02865693	2.2000	0.01889666	1.1000	0.82502541
O75787	Renin receptor (ATPase H (+)-transporting lysosomal accessory protein 2) (ATPase H (+)-transporting lysosomal-interacting protein 2) (ER-localized type I transmembrane adaptor) (Embryonic liver differentiation factor 10) (N14F) (Renin/prorenin receptor) (Va)	RENR	6.8	2.8	4.6	0.01432497	2.4286	0.01315394	1.4783	0.13583525	1.6429	0.21532467
Q3LXA3	Triokinase/FMN cyclase (Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)) [Includes: ATP-dependent dihydroxyacetone kinase (DHA kinase) (EC 2.7.1.28) (EC 2.7.1.29) (Glycerone kinase) (Triokinase) (Triose kinase); FAD-AMP lyase]	TKFC	8	0.8	3.2	0.01438394	10.0000	0.00055037	2.5000	0.00907076	4.0000	0.14626503
P61586	Transforming protein RhoA (EC 3.6.5.2) (Rho cDNA clone 12) (h12)	RHOA	5	2.6	5.6	0.01473661	1.9231	0.03951905	1.1200	0.57437561	2.1538	0.01365828

Q15904	V-type proton ATPase subunit S1 (V-ATPase subunit S1) (Protein XAP-3) (V-ATPase Ac45 subunit) (V-ATPase S1 accessory protein) (Vacuolar proton pump subunit S1)	VAS1	4.8	2	5.4	0.01524927	2.4000	0.01891725	1.1250	0.5720257	2.7000	0.006435
O94760	N (G),N (G)-dimethylarginine dimethylaminohydrolase 1 (DDAH-1) (Dimethylarginine dimethylaminohydrolase 1) (EC 3.5.3.18) (DDAHI) (Dimethylargininase-1)	DDAH1	6.6	1.6	3.6	0.015625	4.1250	0.00837954	1.8333	0.08317508	2.2500	0.2316635
P13489	Ribonuclease inhibitor (Placental ribonuclease inhibitor) (Placental RNase inhibitor) (Ribonuclease/angiogenin inhibitor 1) (RAI)	RINI	4.2	1.6	5.2	0.015625	2.6250	0.014364	1.2381	0.29297111	3.2500	0.00189513
Q9BRT3	Migration and invasion enhancer 1 (HBV X-transactivated gene 4 protein) (HBV XAg-transactivated protein 4) (Protein C35)	MIEN1	3.6	2.2	5	0.01659621	1.6364	0.11209585	1.3889	0.11209585	2.2727	0.00499224
Q9Y653	Adhesion G-protein coupled receptor G1 (G-protein coupled receptor 56) (Protein TM7XN1) [Cleaved into: ADGRG1 N-terminal fragment (ADGRG1 NT) (GPR56 N-terminal fragment) (GPR56 NT) (GPR56 (N)) (GPR56 extracellular subunit) (GPR56 subunit alpha); ADGRG1 C-t	AGRG1	4.8	3	1.8	0.01783113	1.6000	0.11471849	2.6667	0.01504302	1.6667	0.27898397

P34896	Serine hydroxymethyltransferase, cytosolic (SHMT) (EC 2.1.2.1) (Glycine hydroxymethyltransferase) (Serine methylase)	GLYC	4	1	5	0.01788047	4.0000	0.04850302	1.2500	0.47826576	5.0000	0.01265795
O00592	Podocalyxin (GCTM-2 antigen) (Gp200) (Podocalyxin-like protein 1) (PC) (PCLP-1)	PODXL	4.4	2	2.2	0.01793985	2.2000	0.02418607	2.0000	0.03584348	1.1000	0.83350406
P21399	Cytoplasmic aconitate hydratase (Aconitase) (EC 4.2.1.3) (Citrate hydro-lyase) (Ferritin repressor protein) (Iron regulatory protein 1) (IRP1) (Iron-responsive element-binding protein 1) (IRE-BP 1)	ACOC	5	1	3.4	0.01877204	5.0000	0.01217045	1.4706	0.26104164	3.4000	0.10222676
Q04760	Lactoylglutathione lyase (EC 4.4.1.5) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (Methylglyoxalase) (S-D-lactoylglutathione methylglyoxal lyase)	LGUL	4.6	1	3	0.01969887	4.6000	0.0001532	1.5333	0.03278743	3.0000	0.01076019
P11766	Alcohol dehydrogenase class-3 (EC 1.1.1.1) (Alcohol dehydrogenase 5) (Alcohol dehydrogenase class chi chain) (Alcohol dehydrogenase class-III) (Glutathione-dependent formaldehyde dehydrogenase) (FALDH) (FDH) (GSH-FDH) (EC 1.1.1.-) (S- (hydroxymethyl)glutat	ADHX	4.6	1	3	0.02029742	4.6000	0.00148897	1.5333	0.09386827	3.0000	0.04211016

Q8IV08	5'-3' exonuclease PLD3 (EC 3.1.16.1) (Choline phosphatase 3) (HindIII K4L homolog) (Hu-K4) (Phosphatidylcholine-hydrolyzing phospholipase D3) (Phospholipase D3) (PLD 3)	PLD3	6.2	1.8	2.4	0.02043333	3.4444	0.00223197	2.5833	0.00587287	1.3333	0.60740175
O43570	Carbonic anhydrase 12 (EC 4.2.1.1) (Carbonate dehydratase XII) (Carbonic anhydrase XII) (CA-XII) (Tumor antigen HOM-RCC-3.1.3)	CAH12	3.4	1.6	3.8	0.02054038	2.1250	0.04399719	1.1176	0.62611748	2.3750	0.01760228
P09237	Matrilysin (EC 3.4.24.23) (Matrin) (Matrix metalloproteinase-7) (MMP-7) (Pump-1 protease) (Uterine metalloproteinase)	MMP7	5.8	1.4	2	0.02123255	4.1429	0.00658541	2.9000	0.01510963	1.4286	0.66268598
P50897	Palmitoyl-protein thioesterase 1 (PPT-1) (EC 3.1.2.22) (Palmitoyl-protein hydrolase 1)	PPT1	6	2.4	1.6	0.02201717	2.5000	0.0281132	3.7500	0.01006878	1.5000	0.58928935
O43852	Calumenin (Crocalbin) (IEF SSP 9302)	CALU	2	1.4	3.6	0.0226245	1.4286	0.45840452	1.8000	0.06365139	2.5714	0.01577436
P16930	Fumarylacetoacetate (FAA) (EC 3.7.1.2) (Beta-diketonase) (Fumarylacetoacetate hydrolase)	FAAA	3.2	1.2	4.2	0.02281438	2.6667	0.08640725	1.3125	0.36878748	3.5000	0.01599737
P18428	Lipopolysaccharide-binding protein (LBP)	LBP	4.2	0.8	2	0.02559254	5.2500	0.00238085	2.1000	0.02893517	2.5000	0.20100859
P31949	Protein S100-A11 (Calgizzarin) (Metastatic lymph node gene 70 protein) (MLN 70) (Protein S100-C) (S100 calcium-binding protein A11) [Cleaved into: Protein S100-A11, N-terminally processed]	S10AB	1.6	1.6	3.8	0.0263361	1.0000	1	2.3750	0.00614849	2.3750	0.00614849

Q9BTY2	Plasma alpha-L-fucosidase (EC 3.2.1.51) (Alpha-L-fucoside fucohydrolase 2) (Alpha-L-fucosidase 2)	FUCO2	6	1.8	0.4	0.02666495	3.3333	0.01761711	15.0000	0.00323017	4.5000	0.37744812
P52565	Rho GDP-dissociation inhibitor 1 (Rho GDI 1) (Rho-GDI alpha)	GDIR1	2.6	1	3.4	0.02731442	2.6000	0.03951905	1.3077	0.27068999	3.4000	0.0046816
Q9Y2S2	Lambda-crystallin homolog (EC 1.1.1.45) (L-gulonate 3-dehydrogenase) (Gul3DH)	CRYL1	4	0.6	3.6	0.02820538	6.6667	0.00668273	1.1111	0.70704631	6.0000	0.01365828
P25774	Cathepsin S (EC 3.4.22.27)	CATS	5.4	1.4	1	0.02873854	3.8571	0.00109967	5.4000	0.00052283	1.4000	0.67736449
Q9UBD6	Ammonium transporter Rh type C (Rh glycoprotein kidney) (Rhesus blood group family type C glycoprotein) (Rh family type C glycoprotein) (Rh type C glycoprotein) (Tumor-related protein DRC2)	RHCG	2	0.6	4	0.02933659	3.3333	0.22053086	2.0000	0.08963673	6.6667	0.00855043
P50053	Ketohexokinase (EC 2.7.1.3) (Hepatic fructokinase)	KHK	5.2	0.4	2	0.02940119	13.0000	0.00043354	2.6000	0.00763254	5.0000	0.13558051
P17813	Endoglin (CD antigen CD105)	EGLN	2	0.6	2.6	0.02951695	3.3333	0.06620025	1.3000	0.40345925	4.3333	0.01365828
Q8NI32	Ly6/PLAUR domain-containing protein 6B	LPD6B	2.4	1.4	2.6	0.02990883	1.7143	0.03915207	1.0833	0.65171105	1.8571	0.01672897
P07900	Heat shock protein HSP 90-alpha (Heat shock 86 kDa) (HSP 86) (HSP86) (Lipopolysaccharide-associated protein 2) (LAP-2) (LPS-associated protein 2) (Renal carcinoma antigen NY-REN-38)	HS90A	4	0.8	0.6	0.03045247	5.0000	0.01094649	6.6667	0.00772167	1.3333	0.85412001
P47972	Neuronal pentraxin-2 (NP2) (Neuronal pentraxin II) (NP-II)	NPTX2	2.2	0.6	2.6	0.03167635	3.6667	0.05622263	1.1818	0.60694322	4.3333	0.02151994
Q9UBQ7	Glyoxylate reductase/hydroxypyruvate reductase (EC 1.1.1.79) (EC 1.1.1.81)	GRHPR	3.4	1	1.4	0.03210392	3.4000	0.00700808	2.4286	0.01913126	1.4000	0.59840596

P09417	Dihydropteridine reductase (EC 1.5.1.34) (HDHPR) (Quinoid dihydropteridine reductase) (Short chain dehydrogenase/reductase family 33C member 1)	DHPR	3	0.6	2.8	0.033427625.0000	0.01991574	1.0714	0.82682472	4.6667	0.03005636
P22314	Ubiquitin-like modifier-activating enzyme 1 (EC 6.2.1.45) (Protein A1S9) (Ubiquitin-activating enzyme E1)	UBA1	4.2	0.8	1.2	0.033588135.2500	0.00549291	3.5000	0.01148153	1.5000	0.69807943
P20711	Aromatic-L-amino-acid decarboxylase (AADC) (EC 4.1.1.28) (DOPA decarboxylase) (DDC)	DDC	3.6	0.4	1.2	0.033643439.0000	0.00856592	3.0000	0.03648693	3.0000	0.44797711
O75629	Protein CREG1 (Cellular repressor of E1A-stimulated genes 1)	CREG1	3	1.4	1	0.034154452.1429	0.0224422	3.0000	0.00666273	1.4000	0.52504036
O75936	Gamma-butyrobetaine dioxygenase (EC 1.14.11.1) (Gamma-butyrobetaine hydroxylase) (Gamma-BBH) (Gamma-butyrobetaine,2-oxoglutarate dioxygenase)	BODG	3	0.4	1.2	0.034173137.5000	0.00072245	2.5000	0.00889287	3.0000	0.19106965
P63000	Ras-related C3 botulinum toxin substrate 1 (EC 3.6.5.2) (Cell migration-inducing gene 5 protein) (Ras-like protein TC25) (p21-Rac1)	RAC1	2.6	0.4	1.6	0.034270196.5000	0.00215217	1.6250	0.10249319	4.0000	0.05540462
Q9NZV1	Cysteine-rich motor neuron 1 protein (CRIM-1) (Cysteine-rich repeat-containing protein S52) [Cleaved into: Processed cysteine-rich motor neuron 1 protein]	CRIM1	0.6	0.4	2.2	0.034449271.5000	0.7242601	3.6667	0.01359479	5.5000	0.00695104

O75891	Cytosolic 10-formyltetrahydrofolate dehydrogenase (10-FTHFDH) (FDH) (EC 1.5.1.6) (Aldehyde dehydrogenase family 1 member L1)	AL1L1	3.4	0.8	1.2	0.03548601	4.2500	0.0018249	2.8333	0.00559035	1.5000	0.55171909
A6NL88	Protein shisa-7 (Cystine-knot AMPAR modulating protein of 59 kDa) (CKAMP59) (GABA (A) receptor auxiliary subunit Shisa7) (Protein shisa-6-like)	SHSA7	1	1	1.6	0.03570313	1.0000	1	1.6000	0.0110667	1.6000	0.0110667
Q8TAG5	V-set and transmembrane domain-containing protein 2A	VTM2A	0.6	0.2	2.2	0.03573358	3.0000	0.60274314	3.6667	0.05377391	11.0000	0.02031244
Q9UBI6	Guanine nucleotide-binding protein G (I)/G (S)/G (O) subunit gamma-12	GBG12	2	0.6	2	0.03574101	3.3333	0.02651165	1.0000	1	3.3333	0.02651165
Q96GW7	Brevican core protein (Brain-enriched hyaluronan-binding protein) (BEHAB) (Chondroitin sulfate proteoglycan 7)	PGCB	1	0.2	1.8	0.03617171	5.0000	0.13794653	1.8000	0.13794653	9.0000	0.00793772
Q9BRA2	Thioredoxin domain-containing protein 17 (14 kDa thioredoxin-related protein) (TRP14) (Protein 42-9-9) (Thioredoxin-like protein 5)	TXD17	2.4	0.8	1.2	0.03627092	3.0000	0.00566714	2.0000	0.0268843	1.5000	0.41723998
P54727	UV excision repair protein RAD23 homolog B (HR23B) (hHR23B) (XP-C repair-complementing complex 58 kDa protein) (p58)	RD23B	0.2	1	2	0.03627092	5.0000	0.16540671	10.0000	0.00607105	2.0000	0.08963673
Q7Z5N4	Protein sidekick-1	SDK1	2	0.2	0.6	0.03711017	10.0000	0.01473038	3.3333	0.04697615	3.0000	0.53895363

	3-hydroxybutyrate dehydrogenase type 2 (EC 1.1.1.-) (EC 1.1.1.30) (Dehydrogenase/reductase SDR family member 6) (Oxidoreductase UCPA) (R-beta-hydroxybutyrate dehydrogenase) (Short chain dehydrogenase/reductase family 15C member 1)	BDH2	2.2	0.4	1.2	0.037276525.5000	0.0110667	1.8333	0.12144718	3.0000	0.20718101
P02511	Alpha-crystallin B chain (Alpha (B)-crystallin) (Heat shock protein beta-5) (HspB5) (Renal carcinoma antigen NY-REN-27) (Rosenthal fiber component)	CRYAB	2.8	0.4	0.6	0.039073677.0000	0.0035266	4.6667	0.00614849	1.5000	0.76818569
Q96FV2	Secernin-2	SCRN2	1.4	0.2	0.4	0.040480997.0000	0.01377148	3.5000	0.03340135	2.0000	0.63959252
P07741	Adenine phosphoribosyltransferase (APRT) (EC 2.4.2.7)	APT	1.6	0.2	0.8	0.041007888.0000	0.00438187	2.0000	0.06865501	4.0000	0.1594575
Q13740	CD166 antigen (Activated leukocyte cell adhesion molecule) (CD antigen CD166)	CD166	1.6	0.6	0.4	0.042103742.6667	0.03915207	4.0000	0.01672897	1.5000	0.65171105
P00736	Complement C1r subcomponent (EC 3.4.21.41) (Complement component 1 subcomponent r) [Cleaved into: Complement C1r subcomponent heavy chain; Complement C1r subcomponent light chain]	C1R	2.4	0.8	1.8	0.042470293.0000	0.01204991	1.3333	0.28964936	2.2500	0.08963673

P50502	Hsc70-interacting protein (Hip) (Aging-associated protein 2) (Progesterone receptor-associated p48 protein) (Protein FAM10A1) (Putative tumor suppressor ST13) (Renal carcinoma antigen NY-REN-33) (Suppression of tumorigenicity 13 protein)	F10A1	1.4	0.2	0.2	0.04270113	7.0000	0.0268843	7.0000	0.0268843	1.0000	1
P01742	Immunoglobulin heavy variable 1-69 (Ig heavy chain V-I region EU) (Ig heavy chain V-I region SIE) (Ig heavy chain V-I region WOL)	HV169	1.8	0.4	1	0.046656	4.5000	0.00868387	1.8000	0.09889048	2.5000	0.20455005

The numbers represent the spectra counts. WH, wind-heat syndrome; DP, damp-poison syndrome; SD, spleen-deficiency syndrome

Differential urinary proteins used for OPLSDA found in DIA experiment

Uniprot ID	Protein description	Gene name	Average of WH	Average of DP	Average of SD	ANOVA-P	Fold change between WH and DP	P value between WH and DP	Fold change between WH and SD	P value between WH and SD	Fold change between DP and SD	P value between DP and SD
P08263	Glutathione S-transferase A1	GSTA1	2123366.91	1013444.75	2663714.93	0.02313493	2.09519751	0.0526814	1.25447699	0.34601025	2.62837706	0.00796901
O60449	Lymphocyte antigen 75	LY75	27668.4054	39712.4921	24364.3145	0.02514211	1.43530108	0.03301974	1.1356119	0.55401891	1.62994498	0.01119911
Q96C23	Galactose mutarotase	GALM	202850.429	100978.073	259036.127	0.04939513	2.00885621	0.09635631	1.27698092	0.36382813	2.56527104	0.01707568
O75874	Isocitrate dehydrogenase [NADP] cytoplasmic	IDH1	135339.963	105846.79	470167.169	0.00414506	1.27864022	0.77950935	3.47397147	0.00426549	4.44195964	0.00257559
P34896	Serine hydroxymethyltransferase, cytosolic	SHMT1	148590.176	104351.595	262834.289	0.03530954	1.42393775	0.43814444	1.76885375	0.0584942	2.51873763	0.01236019
Q5T2W1	Na (+)/H (+) exchange regulatory cofactor NHE-RF3	PDZK1	114110.73	32371.8148	94462.5189	0.0020435	3.52500255	0.00067809	1.20800007	0.37771603	2.91804829	0.00995636
P30046	D-dopachrome decarboxylase	DDT	193512.128	120153.918	284883.44	0.02640241	1.61053531	0.18769555	1.47217357	0.11331369	2.37098752	0.00757675
P09417	Dihydropteridine reductase	QDPR	131177.817	72660.3564	182880.777	0.01035125	1.8053561	0.07723361	1.39414407	0.12624445	2.51692651	0.00278715
O95967	EGF-containing fibulin-like extracellular matrix protein 2	EFEMP2	469752.727	720969.484	427399.165	0.02199313	1.5347851	0.02226328	1.09909603	0.69414473	1.68687621	0.01195946

P01008	Antithrombin-III	SERPINC1	521706.324	760602.456	398521.747	0.04202026	1.45791305	0.08158249	1.30910378	0.37251685	1.90855948	0.01467711
P05062	Fructose-bisphosphate aldolase B	ALDOB	1430111.88	898592.06	2130410.61	0.03697699	1.59150292	0.22617512	1.48968108	0.12431029	2.37083178	0.01102422
P01344	Insulin-like growth factor II	IGF2	73065.8746	113034.827	44708.788	0.0031231	1.54702626	0.0285819	1.63426203	0.12230167	2.52824628	0.00083213
P04004	Vitronectin	VTN	7826253.39	14919768.7	5475404.5	0.01626685	1.90637435	0.02793759	1.42934707	0.46063647	2.72487059	0.00662774
Q9BUT1	3-hydroxybutyrate dehydrogenase type 2	BDH2	90286.0149	61801.0632	109711.465	0.02603549	1.46091362	0.08459417	1.21515458	0.24557239	1.77523588	0.00800065
P07858	Cathepsin B	CTSB	7737011.2	10863219.8	4225132.15	0.04303693	1.40405894	0.19851384	1.83118798	0.16149896	2.57109586	0.0129335
P05089	Arginase-1	ARG1	47796.9809	25428.0002	16571.5778	0.01240471	1.87969878	0.03155864	2.8842746	0.00474954	1.53443447	0.40071806
P05155	Plasma protease C1 inhibitor	SERPING1	5470187.23	4399550.38	7007869.64	0.02987861	1.24335142	0.23349287	1.28110234	0.10033055	1.59286042	0.008816
P08294	Extracellular superoxide dismutase [Cu-Zn]	SOD3	1928216.5	895974.302	1600721.39	0.01794036	2.15208907	0.0055363	1.2045922	0.36065299	1.78657064	0.06069162
Q14894	Ketimine reductase mu-crystallin	CRYM	80675.0191	46905.5905	113015.182	0.01211035	1.71994464	0.0943298	1.4008696	0.11809707	2.40941817	0.00326177
P09211	Glutathione S-transferase P	GSTP1	432167.984	321279.726	604893.472	0.00755486	1.34514552	0.17180494	1.39967211	0.04284104	1.88276266	0.0020358
P42330	Aldo-keto reductase family 1 member C3	AKR1C3	70759.7301	48364.8964	111912.859	0.01514568	1.46303901	0.2605104	1.58158969	0.04987039	2.31392741	0.00447552
O43598	2'-deoxyribonucleoside 5'-phosphate N-hydrolase 1	DNPH1	112558.256	91291.8664	175629.611	0.01155179	1.23294945	0.41233693	1.5603441	0.02352549	1.9238254	0.00406327
P62258	14-3-3 protein epsilon	YWHAE	229831.834	174237.08	303515.174	0.02947034	1.31907533	0.21087205	1.32059675	0.11027369	1.7419666	0.00859434
P11684	Uteroglobin	SCGB1A1	1426745.36	4530121.23	1191030.61	0.00665247	3.17514349	0.0060273	1.19790822	0.82747568	3.80353047	0.00508677

Q96DG6	Carboxymethylenebutyrylase homolog	CMBL	81920.6599	57451.6171	114285.287	0.0431894	1.42590695	0.23954168	1.39507283	0.13365237	1.98924404	0.01309484
P13489	Ribonuclease inhibitor	RNH1	138248.015	133877.494	248240.767	0.0290371	1.03264567	0.92022342	1.79561904	0.01997299	1.85423822	0.01813866
P07741	Adenine phosphoribosyltransferase	APRT	47464.4935	43537.9871	73587.1506	0.03830684	1.09018576	0.73302218	1.55036207	0.03432891	1.69018265	0.01844363
P15428	15-hydroxyprostaglandin dehydrogenase [NAD(+)]	HPGD	32872.5964	29273.4112	157257.446	0.00024917	1.12295066	0.90179292	4.78384622	0.00027105	5.37202327	0.000252
P15529	Membrane cofactor protein	CD46	149402.407	265667.127	129424.05	0.04059895	1.77819844	0.03717216	1.15436356	0.71708787	2.05268748	0.02139864
P16930	Fumarylacetoacetate	FAH	208204.062	154627.286	324700.189	0.01627684	1.34648979	0.32169442	1.5595286	0.04209273	2.09988934	0.00511416
O14745	Na (+)/H (+) exchange regulatory cofactor NHE-RF1	SLC9A3R1	195820.208	111104.008	161828.194	0.02576276	1.76249455	0.00752077	1.21005001	0.26964143	1.45654687	0.11152112
Q99497	Parkinson disease protein 7	PARK7	161535.582	114008.743	197698.289	0.04062441	1.41687012	0.12224957	1.22386837	0.2482483	1.73406252	0.01263654
Q9BRA2	Thioredoxin domain-containing protein 17	TXNDC17	90379.343	80157.0557	138231.108	0.02934474	1.12752823	0.62498587	1.52945466	0.03279932	1.72450331	0.01264737
P20333	Tumor necrosis factor receptor superfamily member 1B	TNFRSF1B	349751.23	665265.659	368444.254	0.0010072	1.90211099	0.00064024	1.05344663	0.82574434	1.80560737	0.00184205
P20851	C4b-binding protein beta chain	C4BPB	126454.953	281521.729	111997.15	0.04514833	2.22626099	0.03364246	1.12909082	0.8407543	2.51365084	0.02770962

P22692	Insulin-like growth factor-binding protein 4	IGFBP4	52011.8433	54032.3561	27181.8947	0.04756318	1.03884717	0.85363985	1.91347379	0.03462901	1.98780683	0.02612147
P00390	Glutathione reductase, mitochondrial	GSR	57697.4585	37401.0415	69723.3188	0.04300282	1.54266984	0.09543157	1.20842964	0.32845549	1.86420795	0.0143653
P25815	Protein S100-P	S100P	325581.536	274962.225	840987.813	0.04071564	1.18409551	0.82049942	2.58303288	0.03154987	3.05855764	0.02170937
P27824	Calnexin	CANX	54762.188	86177.1133	29080.8991	0.0239023	1.57366089	0.10259486	1.88309817	0.19051339	2.96335794	0.00697667
P27930	Interleukin-1 receptor type 2	IL1R2	158886.135	263393.577	202666.844	0.01182416	1.65775055	0.00320367	1.2755477	0.19874041	1.29963823	0.08505722
P26641	Elongation factor 1-gamma	EEF1G	27666.8367	34725.1074	18222.5706	0.02035572	1.25511665	0.1884325	1.51827298	0.09057924	1.9056097	0.00574448
P29966	Myristoylated alanine-rich C-kinase substrate	MARCKS	142352.975	187472.977	67674.8362	0.04792415	1.31695862	0.31362759	2.10348459	0.1101072	2.77020215	0.01519442
P30041	Peroxiredoxin-6	PRDX6	622054.661	496401.296	824201.681	0.03511229	1.2531286	0.27898449	1.32496665	0.09544117	1.6603536	0.01073391
P31431	Syndecan-4	SDC4	137026.322	1203215.97	49852.238	0.02573714	8.78091129	0.01996928	2.74864935	0.84562392	24.1356461	0.01698116
P31946	14-3-3 protein beta/alpha	YWHAB	266979.216	249944.066	446463.701	0.0004596	1.06815585	0.71021137	1.67227887	0.00066398	1.78625445	0.00032238
Q15435	Protein phosphatase 1 regulatory subunit 7	PPP1R7	26114.8944	14427.0351	23580.5436	0.0036392	1.81013591	0.00129586	1.10747635	0.45579329	1.63446914	0.01258197
P47755	F-actin-capping protein subunit alpha-2	CAPZA2	88342.5118	68247.2268	105209.758	0.02613197	1.29444837	0.11096676	1.19093012	0.18994298	1.54159756	0.00765018
P46940	Ras GTPase-activating-like protein IQGAP1	IQGAP1	48213.8932	74008.0506	20551.3343	0.03308398	1.53499429	0.16908543	2.34602252	0.15229477	3.60113117	0.00967202
P50395	Rab GDP dissociation inhibitor beta	GDI2	83670.608	53063.8823	107986.442	0.02726531	1.57679017	0.10541661	1.29061381	0.20667424	2.03502717	0.00809731

P51580	Thiopurine S-methyltransferase	TPMT	40329.0992	19979.6138	44616.9567	0.03331224	2.01851245	0.03487015	1.10632168	0.65267672	2.23312408	0.01645537
P52823	Stanniocalcin-1	STC1	126997.001	90987.5376	28651.9664	0.00888475	1.39576259	0.21817411	4.43240088	0.00241347	3.17561233	0.04759494
P54652	Heat shock-related 70 kDa protein 2	HSPA2	124537.525	103820.246	170643.189	0.00789181	1.1995495	0.28473613	1.37021504	0.0256911	1.64364076	0.00241123
P55017	Solute carrier family 12 member 3	SLC12A3	76749.8169	81498.989	150218.681	0.04039889	1.06187861	0.87142882	1.95725132	0.02071714	1.84319686	0.03292725
P55103	Inhibin beta C chain	INHBC	43035.8874	79437.2018	42096.9727	0.03125528	1.84583627	0.02046352	1.02230362	0.95121973	1.88700509	0.02344495
P60660	Myosin light polypeptide 6	MYL6	78015.3519	45290.6734	79212.3681	0.04722554	1.72254784	0.03062722	1.01534334	0.93594101	1.74897748	0.03287951
Q14393	Growth arrest-specific protein 6	GAS6	105991.937	61924.8923	168228.347	0.02377286	1.71162085	0.21270591	1.5871806	0.09107087	2.71665142	0.00685124
Q02388	Collagen alpha-1 (VII) chain	COL7A1	16310.643	36192.9769	15708.9087	0.0474699	2.21897915	0.03032205	1.03830529	0.94687275	2.3039778	0.03354386
Q04760	Lactoylglutathione lyase	GLO1	138524.692	128108.776	202842.811	0.02156586	1.08130525	0.68894145	1.46430797	0.02208068	1.58336389	0.01023845
Q04771	Activin receptor type-1	ACVR1	135370.797	183153.068	79891.3581	0.03187249	1.35297326	0.18403232	1.69443604	0.13548518	2.29252666	0.00928457
Q13938	Calcyphosin	CAPS	57674.8612	37448.8127	75502.8763	0.02275761	1.54009852	0.11103039	1.30911241	0.16944924	2.01616209	0.00652801
Q15366	Poly (rC)-binding protein 2	PCBP2	49457.786	41964.5654	63037.4527	0.02644695	1.17856066	0.29464913	1.27457086	0.07054163	1.50215907	0.00811066
Q96GP6	Scavenger receptor class F member 2	SCARF2	19690.7418	44154.3252	15665.393	0.00097147	2.24239014	0.00170052	1.25695805	0.58188597	2.81859033	0.00064249
Q6UXB4	C-type lectin domain family 4 member G	CLEC4G	903000.445	2263195.89	1356626.19	0.0226735	2.50630651	0.00696518	1.50235385	0.35202602	1.66825313	0.07507542

Q96DA0	Zymogen granule protein 16 homolog B	ZG16B	1073423.76	1636767.99	1930967	0.04064686	1.52481066	0.08857313	1.79888602	0.01444206	1.17974387	0.38800525
Q9NNX6	CD209 antigen	CD209	125053.282	213562.391	109985.894	0.04961777	1.70777119	0.04371457	1.13699382	0.72893248	1.94172528	0.0260621
Q96S96	Phosphatidylethanolamine-binding protein 4	PEBP4	261577.207	459499.195	88297.9622	0.00259247	1.75664845	0.0394958	2.96243765	0.07655463	5.20396149	0.00064175
Q99523	Sortilin	SORT1	60464.901	70228.2773	94062.724	0.00688392	1.1614718	0.31677905	1.55565828	0.00204585	1.33938532	0.02530841
Q9BS26	Endoplasmic reticulum resident protein 44	ERP44	111371.435	149083.132	75302.0938	0.00658714	1.33861193	0.07192447	1.4789952	0.0929752	1.97980062	0.00169852
P47972	Neuronal pentraxin-2	NPTX2	92767.4501	144916.508	185198.61	0.04990749	1.56214823	0.14763508	1.99637491	0.01606326	1.27796766	0.28319366
Q9BUP0	EF-hand domain-containing protein D1	EFHD1	9827.79437	9686.38031	6418.68047	0.03111489	1.01459927	0.91442718	1.53112379	0.01707499	1.50909215	0.02444703
P49747	Cartilage oligomeric matrix protein	COMP	2203564.59	5424410.67	2202763.52	0.04719619	2.46165268	0.02813343	1.00036366	0.99955655	2.46254789	0.03600958
Q7Z5L0	Vitelline membrane outer layer protein 1 homolog	VMO1	2096997.57	2521410.53	3816846.94	0.00598997	1.20239077	0.39109087	1.82014848	0.0019366	1.51377449	0.01754845
Q9Y2A9	N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase 3	B3GNT3	39282.3694	51637.9965	27879.5536	0.03450708	1.31453365	0.14268092	1.40900281	0.1867689	1.85218161	0.01023348

The numbers represent the abundance of each protein in each sample. WH, wind-heat syndrome; DP, damp-poison syndrome; SD, spleen-deficiency syndrome.