

Appendix C Table 5.1 Protein ratios used as the normalization factors for OxycysDML data.

Sequence ^a	Acc. No. ^b	Protein Name	Protein AD/WT Ratio ^c	N ^d
AACICAEKEEKEEL	Q8VC81	Group XIIB phospholipase A2-like protein	0.92	6
AADKDTCFSTEGPNLVTR	P07724	Serum albumin	0.83	6
AAPLSLCAALTAVDQSVLLKPEAK	Q61838	Alpha-2-macroglobulin	1.62	6
AAVARGAQVIENCAVTGIR	Q99LB7	Sarcosine dehydrogenase, mitochondrial	1.02	6
ACGANLPENFSISQIFSQAMAAR	P34914-2	Isoform 2 of Bifunctional epoxide hydrolase 2	0.93	6
ADHQPLTEASYVNLPTIALCNTDSPLR	P14206	40S ribosomal protein SA	0.96	6
AFTTWTANAGIEEER	A2A848	Peroxisomal acyl-coenzyme A oxidase 1 (Fragment)	1.25	6
AGASIVGVNCHFDPSVSLQTVK	O35490	Betaine--homocysteine S-methyltransferase 1	0.86	6
AIAQSSVIFNPCLFGR	Q8VCC2	Liver carboxylesterase 1	0.84	6
AIGAVPLIQGEYMIPCEK	F6Y6L6	Cathepsin D (Fragment)	0.98	6
AIQDAGCQVLK	P40936	Indolethylamine N-methyltransferase	0.99	6
AISQTPGCVLLDQVADAGPSTNR	Q91XD4	Formimidoyltransferase-cyclodeaminase	1.01	6
ALAGCDFLTISPK	Q93092	Transaldolase	0.99	6
ALCDVGTAIASCSR	Q9CRC0	Vitamin K epoxide reductase complex subunit 1	1.19	6
ALCSEFQGSVATPR	P41317	Mannose-binding protein C	1.10	6
ALEDAQIPYSAVEQACVGYVYGDSTSGQR	P32020	Non-specific lipid-transfer protein	0.97	6
ALNVEPDGTGLTCSLAPNILSQL	P99029-2	Isoform Cytoplasmic+peroxisomal of Peroxiredoxin-5, mitochondri	0.90	6
ALTTCPYQLCALPR	Q9JKY7	Cytochrome P450 CYP2D22	1.14	6
ANVKGYLGPQLPDCLK	P08249	Malate dehydrogenase, mitochondrial	1.04	6
ATFHTPFSQLGQSPEACSSYTFPK	Q9WUR2-2	Isoform 2 of Enoyl-CoA delta isomerase 2, mitochondrial	1.27	6
AVCVLKGDPVQGTIHFQK	P08228	Superoxide dismutase [Cu-Zn]	0.71	6
AVLRIADQCPSSLAIQENANALAR	Q91Y97	Fructose-bisphosphate aldolase B	1.28	6
AVSSFFSGSCVPCADPVAFPK	Q921I1	Serotransferrin	1.01	6
AYLMSQPLAYHTPCGK	O35490	Betaine--homocysteine S-methyltransferase 1	0.86	6
DASINPPMCLQDVER	Q63880-2	Isoform 2 of Carboxylesterase 3A	1.20	6
DFTPVCTTELGR	D3Z0Y2	Peroxiredoxin-6	0.97	6
DVRPITEQIAVTAGCK	Q91WU0	Expressed sequence AU018778	0.80	6
EAIICKNIPR	O88844	Isocitrate dehydrogenase [NADP] cytoplasmic	1.03	6
EAPFTHFDPSCLFPACR	P16015	Carbonic anhydrase 3	1.62	6
ECCHGDLLECADDRAELAK	P07724	Serum albumin	0.83	6
ECDVLPDDTVSTLYNR	Q8R0Y6	Cytosolic 10-formyltetrahydrofolate dehydrogenase	0.99	6

EFGASECISPQDFSK	P28474	Alcohol dehydrogenase class-3	1.02	6
EIIAVSCGPSQCQETIR	Q9DCW4	Electron transfer flavoprotein subunit beta	1.20	6
EKPDDPLNYFIGGCAGGLTLGAR	Q9D8B4	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11	0.78	6
ELGSPPGISLETIDAAFSCPGSSR	Q91X72	Hemopexin	1.01	6
ENYGELADCCTK	P07724	Serum albumin	0.83	6
EYCGVPGDGYEELIR	Q07456	Protein AMBP	1.32	6
FCQEFQHYPAMGGVAPQALAVAASGPGSSFR	Q61838	Alpha-2-macroglobulin	1.62	6
FCYADKALLNR	Q8CHT0	Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial	1.19	6
FELTCYSLAPQIK	J3QNG0	MCG15755	1.21	6
FLHDPSATQGFVGCALSSNIQR	G3UYY2	Selenium-binding protein 2	1.22	6
FLSCYDPINIQTSGTTGNPK	Q8VCW8	Acyl-CoA synthetase family member 2, mitochondrial	0.95	6
GAQVIENCAVTGIR	Q99LB7	Sarcosine dehydrogenase, mitochondrial	1.02	6
GAVHQLCQSLAGK	D3YWR7	Dihydropteridine reductase	0.95	6
GCDVVVIPAGVPR	P08249	Malate dehydrogenase, mitochondrial	1.04	6
GDFCIQVGR	Q5NC80	Nucleoside diphosphate kinase (Fragment)	1.00	6
GEVITTYCPANNEPIAR	G3UYR8	Alpha-aminoadipic semialdehyde dehydrogenase	0.89	6
GGCEAIVDTGTSLLVGPVVEEVKELQK	F6Y6L6	Cathepsin D (Fragment)	0.98	6
GGDVSVCEWYR	P56391	Cytochrome c oxidase subunit 6B1	0.94	6
GIQVSNNGPCLGSR	D3Z041	Long-chain-fatty-acid--CoA ligase 1	1.03	6
GKFPDVPGFVSWVTPCISAK	Q61176	Arginase-1	0.94	6
GLAVSDNGPCLGYR	Q8JZR0	Long-chain-fatty-acid--CoA ligase 5	1.19	6
GLCAIAQAESLR	D3YV43	40S ribosomal protein S3	0.90	6
GNDQVRFELTCYSLAPQIK	J3QNG0	MCG15755	1.21	6
GNDVLVIECNLR	Q8C196	Carbamoyl-phosphate synthase [ammonia], mitochondrial	0.89	6
GNPTKVVAVDCGIKNNVIR	Q8C196	Carbamoyl-phosphate synthase [ammonia], mitochondrial	0.89	6
GNVVAEKISGQKVNEAACDIAR	O35490	Betaine--homocysteine S-methyltransferase 1	0.86	6
GVLFGVPGAFTPGCSK	P99029-2	Isoform Cytoplasmic+peroxisomal of Peroxiredoxin-5, mitochondri	0.90	6
GVLFGVPGAFTPGCSK	Q01853	Transitional endoplasmic reticulum ATPase	1.03	6
GYGCAGVSSVAYGLLTR	Q60759	Glutaryl-CoA dehydrogenase, mitochondrial	1.14	6
GYLGPEQLPDCLK	P08249	Malate dehydrogenase, mitochondrial	1.04	6
GYVSCALGCPYEGK	P38060	Hydroxymethylglutaryl-CoA lyase, mitochondrial	0.98	6
IADQCPSLAIQENANALAR	Q91Y97	Fructose-bisphosphate aldolase B	1.28	6
IASVKPSDAGTYVCQAQNALGTAQK	B1B0C7	Basement membrane-specific heparan sulfate proteoglycan core pro	1.00	6
IAVIGAGASGLTCIK	P97872	Dimethylaniline monooxygenase [N-oxide-forming] 5	1.07	6

IIPGFMCQGGDFTR	P17742	Peptidyl-prolyl cis-trans isomerase A	0.96	6
ILADSINSEVGILCHALQK	P16331	Phenylalanine-4-hydroxylase	1.18	6
ISGQKVNEAACDIAR	O35490	Betaine--homocysteine S-methyltransferase 1	0.86	6
ISLGLPVGAVINCADNTGAK	A2A6F8	60S ribosomal protein L23 (Fragment)	1.06	6
ISSEYSDMIESFCK	Q8R084	Protein Ugt2b1	0.93	6
ITNKVFANPEDCAGFGK	D3YU60	Microsomal glutathione S-transferase 1	0.97	6
KITISDCGQL	P17742	Peptidyl-prolyl cis-trans isomerase A	0.96	6
LCAATATILDKPEDR	O35215	D-dopachrome decarboxylase	0.81	6
LCEAICPAQAITIEAEPR	Q8K3J1	NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrion	1.50	6
LCLTGQWEAAQELQHR	E9Q1R2	4-hydroxy-2-oxoglutarate aldolase, mitochondrial	0.41	6
LCNPPVNAISPTVITEVR	Q9DBM2	Peroxisomal bifunctional enzyme	1.16	6
LGPNYLQIPVNCOPYR	P24270	Catalase	0.95	6
LIGPNCPGVINPGECK	Q9WUM5	Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	1.16	6
LLCGGGAADRGYFIQPTVFGDVK	P47738	Aldehyde dehydrogenase, mitochondrial	1.04	6
LLGSTIPLCSAQWER	P97742	Carnitine O-palmitoyltransferase 1, liver isoform	1.25	6
LLLGPCTPVQYR	P97872	Dimethylaniline monooxygenase [N-oxide-forming] 5	1.07	6
LLQLACPGTGEADAR	Q8K1B3	Gltpd2 protein	2.03	6
LLQVTPTDSGEYVCR	B1B0C7	Basement membrane-specific heparan sulfate proteoglycan core protein 1	1.00	6
LLYECNPIAYVMEK	Q9QXD6	Fructose-1,6-bisphosphatase 1	1.25	6
LQTCCDKPLLK	P07724	Serum albumin	0.83	6
LQVTASPSLCGLR	P28666	Murinoglobulin-2	0.83	6
LSRLEAPCQQWMELR	Q9CRB3	5-hydroxyisourate hydrolase	1.09	6
LSYYPHCLASFTELVR	Q9QXF8	Glycine N-methyltransferase	1.21	6
LVILANNCPALR	P62889	60S ribosomal protein L30	0.93	6
LYILQASPADAGEYVCR	B1B0C7	Basement membrane-specific heparan sulfate proteoglycan core protein 1	1.00	6
MCHPSVDGFTPR	Q8C196	Carbamoyl-phosphate synthase [ammonia], mitochondrial	0.89	6
MLQGTCGAPIDPTIYLSK	P56593	Cytochrome P450 2A12	0.95	6
NALANPLYCPDYR	Q9DB77	Cytochrome b-c1 complex subunit 2, mitochondrial	1.00	6
NALVSHLDGTTVPCEDIGR	Q9CZ13	Cytochrome b-c1 complex subunit 1, mitochondrial	1.12	6
NCVILPHIGSATYK	Q91Z53	Glyoxylate reductase/hydroxypyruvate reductase	1.07	6
NCWQNYLDFHR	P56391	Cytochrome c oxidase subunit 6B1	0.94	6
NLDKEYLPIGGLAEFCK	P05202	Aspartate aminotransferase, mitochondrial	1.21	6
NNPAIVVIGNNGQINYDHQNDGATQALASCQI	D3Z5B9	Protein ERGIC-53 (Fragment)	2.03	6
NQQEGVCPEGSIDNSPVKWCALSHLER	Q921I1	Serotransferrin	1.01	6

NYDYILSTGCAPP GK	Q9QXF8	Glycine N-methyltransferase	1.21	6
QAAPCVLFFDELDSIAK	Q01853	Transitional endoplasmic reticulum ATPase	1.03	6
QALQDTSKPCLLNIMIEPQSTR	D3YZ54	2-hydroxyacyl-CoA lyase 1	1.07	6
QCSSGLQAVANIAGGIR	Q8VCH0	3-ketoacyl-CoA thiolase B, peroxisomal	1.22	6
QISKCLGLTEAQTR	Q8C196	Carbamoyl-phosphate synthase [ammonia], mitochondrial	0.89	6
QLVLLNPYAALCNR	Q8VBW8	Tetratricopeptide repeat protein 36	1.31	6
QVADEGDALVAGGVSQTPSYLSCK	O35490	Betaine--homocysteine S-methyltransferase 1	0.86	6
QVADEGDALVAGGVSQTPSYLSCKSEVEVK	O35490	Betaine--homocysteine S-methyltransferase 1	0.86	6
QVADEGDALVAGGVSQTPSYLSCKSEVEVKK	O35490	Betaine--homocysteine S-methyltransferase 1	0.86	6
QVEAELLPCLR	Q8CG76	Aflatoxin B1 aldehyde reductase member 2	1.07	6
QVIDCQLADVNNLGK	Q9CPY7-2	Isoform 2 of Cytosol aminopeptidase	1.02	6
RDPLHEELLGQGCVFQER	Q99LB7	Sarcosine dehydrogenase, mitochondrial	1.02	6
RPCFSALTVDETYVPK	P07724	Serum albumin	0.83	6
RPCFSALTVDETYVPKEFK	P07724	Serum albumin	0.83	6
SAGACTAAAF LR	Q9CPY7-2	Isoform 2 of Cytosol aminopeptidase	1.02	6
SAGWVPIGILLFCK	Q921I1	Serotransferrin	1.01	6
SALEHSVQCAVDVK	P24270	Catalase	0.95	6
SAPSIPKENFSC LTR	P14152	Malate dehydrogenase, cytoplasmic	1.24	6
SAYALGGLGSGICPNK	Q8C196	Carbamoyl-phosphate synthase [ammonia], mitochondrial	0.89	6
SAYALGGLGSGICPNKETLIDLGTK	Q8C196	Carbamoyl-phosphate synthase [ammonia], mitochondrial	0.89	6
SCAEFVSGS QLR	B1ASE2	ATP synthase subunit d, mitochondrial (Fragment)	0.67	6
SCVITYLAQVDPK	G3V020	PCTP-like protein	0.91	6
SEGTYCCGPVSVR	P21981	Protein-glutamine gamma-glutamyltransferase 2	0.95	6
SFTSSCPVSAFV PK	Q8R0F8	Acylpyruvase FAHD1, mitochondrial	0.76	6
SIAQYWLGCPTSEK	P29788	Vitronectin	0.87	6
SIQFVDWCPTGFK	P68368	Tubulin alpha-4A chain	1.06	6
SLCPVSWVSAWDDR	P56391	Cytochrome c oxidase subunit 6B1	0.94	6
SLPQPQKVNSILGCSQ	Q91X72	Hemopexin	1.01	6
SLVANLAAANCYK	P55264-2	Isoform Short of Adenosine kinase	1.19	6
SLVANLAAANCYKK	P55264-2	Isoform Short of Adenosine kinase	1.19	6
SQTEEDCTEELFDLHAR	P99028	Cytochrome b-c1 complex subunit 6, mitochondrial	0.95	6
STCNVIASLIFAR	P11714	Cytochrome P450 2D9	0.93	6
STCTINYSTSLPLAQGIK	G3UYR8	Alpha-aminoadipic semialdehyde dehydrogenase	0.89	6
STCTINYSTSLPLAQGIKFQ	G3UYR8	Alpha-aminoadipic semialdehyde dehydrogenase	0.89	6

STEPCAHLLVSSIGVVGTAEQNR	O35215	D-dopachrome decarboxylase	0.81	6
SVKVIVVGNPANTNCLTASK	P14152	Malate dehydrogenase, cytoplasmic	1.24	6
SVSAFAPICNPVLCSWGK	H3BJP2	S-formylglutathione hydrolase (Fragment)	1.16	6
SVSAFAPICNPVLCSWGKK	H3BJP2	S-formylglutathione hydrolase (Fragment)	1.16	6
TAEVKSTVNTAVALTLACFGTQR	Q61176	Arginase-1	0.94	6
TCAEAVVPSYVPIVKK	P36552	Oxygen-dependent coproporphyrinogen-III oxidase, mitochondrial	0.69	6
TCLLNETGDEPFQYKN	P15105	Glutamine synthetase	0.76	6
TIAACNLPIVQGPCR	Q07456	Protein AMBP	1.32	6
TIPLISQCTPK	P08249	Malate dehydrogenase, mitochondrial	1.04	6
TIPLISQCTPKVDFPQDQLATLTGR	P08249	Malate dehydrogenase, mitochondrial	1.04	6
TIYAGNALCTVK	Q99LC5	Electron transfer flavoprotein subunit alpha, mitochondrial	0.91	6
TLTQCSWLLDGFPR	Q9WTP7	GTP:AMP phosphotransferase AK3, mitochondrial	0.86	6
TNCDLYEKLGEYGFQNAILVR	P07724	Serum albumin	0.83	6
TPADCPVIAIDFR	Q9D1Q6	Endoplasmic reticulum resident protein 44	0.58	6
TQSGTKNLRIQCEGGSFSLQSDPR	O35718	Suppressor of cytokine signaling 3	1.26	6
TSACFEPGLDYMVTK	Q8C196	Carbamoyl-phosphate synthase [ammonia], mitochondrial	0.89	6
TSACFEPGLDYMVTKIPR	Q8C196	Carbamoyl-phosphate synthase [ammonia], mitochondrial	0.89	6
TVMDDFAQFLDTCK	P07724	Serum albumin	0.83	6
VAVVAGYGDVGGKCAQALR	P50247	Adenosylhomocysteinase	0.89	6
VCIVGSGNWGSAIAK	E0CXN5	Glycerol-3-phosphate dehydrogenase [NAD(+)]	0.92	6
VCLIGCGFSTGYGSAVK	P00329	Alcohol dehydrogenase 1	1.28	6
VCLLGCGISTGYGAAVNTAK	P28474	Alcohol dehydrogenase class-3	1.02	6
VCNLIDSGTKEGASILLDGR	Q9EQ20	Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondr	1.09	6
VCTLAIDPGDSDIIR	P62889	60S ribosomal protein L30	0.93	6
VCYEQPVGFEFIR	E0CXN5	Glycerol-3-phosphate dehydrogenase [NAD(+)]	0.92	6
VFANAYLSDLGGCIK	P24549	Retinal dehydrogenase 1	1.08	6
VFANPEDCAGFGK	D3YU60	Microsomal glutathione S-transferase 1	0.97	6
VIPLFSPQCGEGR	P00329	Alcohol dehydrogenase 1	1.28	6
VIVVGNPANTNCLTASK	P14152	Malate dehydrogenase, cytoplasmic	1.24	6
VLAACLTEKGAEQLR	O88451	Retinol dehydrogenase 7	1.15	6
VLCIINPGNPTGQVQSR	Q8BGT5	Alanine aminotransferase 2	1.22	6
VLCVINPGNPTGQVQTR	Q8QZR5	Alanine aminotransferase 1	1.44	6
VLTLDTMNPVCR	Q8QZR5	Alanine aminotransferase 1	1.44	6
VNKECCHGDLLECADDRAELAK	P07724	Serum albumin	0.83	6

VNPLGGAIALGHPLGCTGAR	Q8VCH0	3-ketoacyl-CoA thiolase B, peroxisomal	1.22	6
VNQAIWLLCTGAR	D3YYM6	40S ribosomal protein S5 (Fragment)	1.29	6
VVAVDCGIKNNVIR	Q8C196	Carbamoyl-phosphate synthase [ammonia], mitochondrial	0.89	6
VYKSLCPVSWWSAWDDR	P56391	Cytochrome c oxidase subunit 6B1	0.94	6
VYSYYNLEESCTR	P01027	Complement C3	1.06	6
YAICSALAASALPALVMSK	Q9D8E6	60S ribosomal protein L4	1.00	6
YCAGWADKIHGQTIPSDGDIFTYTR	P24549	Retinal dehydrogenase 1	1.08	6
YCNTWPMAISMLASK	Q64442	Sorbitol dehydrogenase	1.01	6
YIGGCCGFEPYHIR	O35490	Betaine--homocysteine S-methyltransferase 1	0.86	6
YKPVCNQVECHPYLNQGK	D3Z3P8	Estradiol 17 beta-dehydrogenase 5 (Fragment)	1.03	6
YLQDAGCPVFLYEFQHTPSSFAK	Q63880-2	Isoform 2 of Carboxylesterase 3A	1.20	6
YMCENQATISSK	P07724	Serum albumin	0.83	6
YVDIAIPCNNK	P14206	40S ribosomal protein SA	0.96	6
AAFGLSEAGFNTACLTK	Q8K2B3	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitoch	0.85	5
ACVDTALENLSTLK	P19096	Fatty acid synthase	1.08	5
ADFAQACQDAGVR	G5E8R3	Pyruvate carboxylase	0.84	5
AEACFVNCVER	Q9WVA2	Mitochondrial import inner membrane translocase subunit Tim8 A	0.99	5
AETFTFHSDICTLPEKEK	P07724	Serum albumin	0.83	5
AKVAPEEVSEVIFGHVLTAGCGQNPTR	F2Z459	Protein Acat3	1.21	5
ALQICELPGLADQVTR	Q8VCF0	Mitochondrial antiviral-signaling protein	1.19	5
ALSCLESSWK	P28666	Murinoglobulin-2	0.83	5
AQGTGELTQLLNSLCTAIK	Q9QXD6	Fructose-1,6-bisphosphatase 1	1.25	5
ATAEQLKTVMDDFAQFLDTCCCK	P07724	Serum albumin	0.83	5
AVLNPLCQVDYR	E9Q1S3	Protein transport protein Sec23A	1.02	5
DCLFASQSGSQPR	P27046	Alpha-mannosidase 2	0.47	5
EIEIDYTGTEPSSPCNK	Q8VEK0	Cell cycle control protein 50A	0.84	5
EIGFSDKQISKCLGLTEAQTR	Q8C196	Carbamoyl-phosphate synthase [ammonia], mitochondrial	0.89	5
ELKGKFPDVPGFVSWVTPCISAK	Q61176	Arginase-1	0.94	5
FEEGGYVVCNTK	O08573-2	Isoform Short of Galectin-9	0.89	5
GDLNDCFIPCTPK	Q922D8	C-1-tetrahydrofolate synthase, cytoplasmic	1.07	5
GLQGSFEELCR	D3Z041	Long-chain-fatty-acid--CoA ligase 1	1.03	5
GQNNPQVCPYNLYAEQLSGSAFTCPR	O09173	Homogentisate 1,2-dioxygenase	1.01	5
GSDCGIVNVNIPTSGAEIGGAFGGEK	G3UYR8	Alpha-aminoadipic semialdehyde dehydrogenase	0.89	5
HTTSYPPLCYQNPEAALR	Q8VCC2	Liver carboxylesterase 1	0.84	5

IALFGAGPASISCASFLAR	Q8CHR6	Dihydropyrimidine dehydrogenase [NADP(+)]	0.99	5
ICDFSNASKPQTIQUESTGGIVEVLHKVDSEGISI	P51660	Peroxisomal multifunctional enzyme type 2	1.16	5
ILPESSILFLCDLQEK	P85094	Isochorismatase domain-containing protein 2A, mitochondrial	1.23	5
ITNKVFANPEDCAGFGKGENAK	D3YU60	Microsomal glutathione S-transferase 1	0.97	5
KPVDQYEDCYLAR	Q921I1	Serotransferrin	1.01	5
LLEAGDFICQALNR	P38060	Hydroxymethylglutaryl-CoA lyase, mitochondrial	0.98	5
LLLEGVENKLTPCLK	D3Z041	Long-chain-fatty-acid--CoA ligase 1	1.03	5
LQTCCDKPLKK	P07724	Serum albumin	0.83	5
LSGCEAMDSQALVR	Q91WG0	Acylcarnitine hydrolase	0.92	5
LTAIPVSAFCDSK	Q71RI9-2	Isoform 2 of Kynurenine--oxoglutarate transaminase 3	0.92	5
LTESPCALVASQYGWSGNMER	F7C312	Endoplasmic reticulum chaperone protein 78 kDa glucose	0.92	5
LVNGCALNFFR	Q9DCJ5	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8	0.81	5
LVQEVTDFAKTCVADESAANCDK	P07724	Serum albumin	0.83	5
LVVPATQCGSLIGK	P60335	Poly(rC)-binding protein 1	0.73	5
MTNGFSGADLTEICQR	Q01853	Transitional endoplasmic reticulum ATPase	1.03	5
NKPEPTVEEIEAFQGNLCR	Q00519	Xanthine dehydrogenase/oxidase	0.85	5
NLVKTNCDLYEKLGEYGFQNAILVR	P07724	Serum albumin	0.83	5
NQEAMGAFQEFQVEACR	D3YZ54	2-hydroxyacyl-CoA lyase 1	1.07	5
NQEGVCPEGSIDNSPVK	Q921I1	Serotransferrin	1.01	5
QAAPCVLFFDELDSIAKAR	Q01853	Transitional endoplasmic reticulum ATPase	1.03	5
QLLCDLVGISR	Q99K67	Alpha-aminoadipic semialdehyde synthase, mitochondrial	1.06	5
RCLYASVLTAQPR	P58252	Elongation factor 2	1.01	5
RQLVLLNPYAALCNR	Q8VBW8	Tetratricopeptide repeat protein 36	1.31	5
SAFEYGGQKCSACSR	Q8CHT0	Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial	1.19	5
SCESDAPFPVHPGTPECCTKEGLER	P21614	Vitamin D-binding protein	0.97	5
SILEGSDEYLVCK	P01872	Ig mu chain C region	0.91	5
SITIANQTNCPYVTK	O08553	Dihydropyrimidinase-related protein 2	1.02	5
SLCAFRQAPLLIGSTK	P19096	Fatty acid synthase	1.08	5
SLHTLFGDKLCAIPNLRENYGELADCCTK	P07724	Serum albumin	0.83	5
SLLPGCQSVISR	Q9DCM0	Persulfide dioxygenase ETHE1, mitochondrial	1.09	5
SSFASCPQQWIK	Q8BGD8	Cytochrome c oxidase assembly factor 6 homolog	0.71	5
STVNTAVALTLACFGTQR	Q61176	Arginase-1	0.94	5
TCVADESAANCDK	P07724	Serum albumin	0.83	5
VAPEEVSEVIFGHVLTAGCGQNPTR	F2Z459	Protein Acat3	1.21	5

VCNLIDSGTKEGASILLDGR	Q9EQ20	Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondr	1.09	5
VDLSQPLIATCR	P52196	Thiosulfate sulfurtransferase	0.93	5
VFANPEDCAGFGKGENAK	D3YU60	Microsomal glutathione S-transferase 1	0.97	5
VKPKPEPEDLAICFTSGTTGNPK	D3Z041	Long-chain-fatty-acid--CoA ligase 1	1.03	5
VNEAACDIAR	O35490	Betaine--homocysteine S-methyltransferase 1	0.86	5
VYEEDAVPGLTPCR	Q9CZ13	Cytochrome b-c1 complex subunit 1, mitochondrial	1.12	5
YLAAAFPSACGK	Q9Z2V4	Phosphoenolpyruvate carboxykinase, cytosolic [GTP]	0.76	5
YNPNVLPVQCTGK	P14094	Sodium/potassium-transporting ATPase subunit beta-1	0.74	5
AADAHVDAHYYEQNEQPTGTCAACITGGNR	P55264-2	Isoform Short of Adenosine kinase	1.19	4
AKEFGASECISPQDFSK	P28474	Alcohol dehydrogenase class-3	1.02	4
AVLTSQETLFGGSDCTGNFCLFK	Q921I1	Serotransferrin	1.01	4
DCLIPMGITSENV AER	Q8VCH0	3-ketoacyl-CoA thiolase B, peroxisomal	1.22	4
EQGATVLCGGEVYVPEDPKLK	Q9JLJ2	4-trimethylaminobutyraldehyde dehydrogenase	0.99	4
FAELVYTGFWHSPECEFVR	J3QNG0	MCG15755	1.21	4
GALVTVGQLSCYDQAK	Q9QZD8	Mitochondrial dicarboxylate carrier	1.24	4
GCLELIKEAGVQIAGR	Q922D8	C-1-tetrahydrofolate synthase, cytoplasmic	1.07	4
GDDILLSPCFQR	P58710	L-gulonolactone oxidase	1.25	4
GVNEDTYSGLDCAR	E9Q6M6	Mitochondrial glutamate carrier 1	1.06	4
IAVAAQNCYK	P17751	Triosephosphate isomerase	0.84	4
IGPALSCGNTVVVKPAEQTPLTALHLASLIK	P24549	Retinal dehydrogenase 1	1.08	4
IICQGFTGKQGTFFHSQQALEYGTK	Q9WUM5	Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondr	1.16	4
IICRWDTVSNQVQR	Q64374	Regucalcin	0.96	4
IYGGSVTGATCKELASQPDVDGFLVGGASLK	P17751	Triosephosphate isomerase	0.84	4
ILADSINSEVGILCHALQKIKS	P16331	Phenylalanine-4-hydroxylase	1.18	4
IPFLEFSCPGVPPGLETLK	D3Z2P8	Sulfotransferase (Fragment)	1.10	4
KLVKEIIAVSCGPSQCQETIR	Q9DCW4	Electron transfer flavoprotein subunit beta	1.20	4
KVDLSQPLIATCR	P52196	Thiosulfate sulfurtransferase	0.93	4
LAAEGAAVAACDLDGAAAQDTVR	G3UX44	Estradiol 17-beta-dehydrogenase 8 (Fragment)	0.96	4
LADIGACAQIVHK	Q8VCN5	Cystathionine gamma-lyase	1.30	4
LICEATNFTPKPITVSWLK	P01872	Ig mu chain C region	0.91	4
LVNADGEAVYCK	P24270	Catalase	0.95	4
LYLGHNYVTAIRNQQEGVCPEGSIDNSPVK	Q921I1	Serotransferrin	1.01	4
METYCNSGSTDTSSVINAVTHALTAATPYTR	Q80XN0	D-beta-hydroxybutyrate dehydrogenase, mitochondrial	1.44	4
NILGGTVFREAIIICK	O88844	Isocitrate dehydrogenase [NADP] cytoplasmic	1.03	4

NILGGTVFREPIICK	P54071	Isocitrate dehydrogenase [NADP], mitochondrial	0.82	4
NLVKTNCDLYEK	P07724	Serum albumin	0.83	4
NTGIICTIGPASR	P52480	Pyruvate kinase PKM	0.80	4
QVIDCQLADVNNLGKYR	Q9CPY7-2	Isoform 2 of Cytosol aminopeptidase	1.02	4
SLHTLFGDKLCAIPNLR	P07724	Serum albumin	0.83	4
TACYGHFGRSEFPWEVPK	Q91X83	S-adenosylmethionine synthase isoform type-1	0.78	4
TIAECLADELINA AK	D3YYM6	40S ribosomal protein S5 (Fragment)	1.29	4
VAASDWTFLHCLPR	Q8R1A8	Ornithine carbamoyltransferase, mitochondrial	1.05	4
VFESTCSSGSPGSNQALLLR	Q6PB66	Leucine-rich PPR motif-containing protein, mitochondrial	0.95	4
VVGYFVSGCDPTIMGIGPVPAINGALKK	Q8BWT1	3-ketoacyl-CoA thiolase, mitochondrial	1.24	4
VYEGSILEADCILIPAASEK	P26443	Glutamate dehydrogenase 1, mitochondrial	1.18	4
YLLGTSLARPCAR	J3QNG0	MCG15755	1.21	4
YMCENQATISSKLTCCDKPLLK	P07724	Serum albumin	0.83	4
YVSHGATGKGNDQVRFELTCYSLAPQIK	J3QNG0	MCG15755	1.21	4
AAFGLSEAGFNTACLTKLFPTR	Q8K2B3	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitoch	0.85	3
AAGCDFNNVVK	P52760	Ribonuclease UK114	0.75	3
ADIPVVICDTPQK	Q8JZR0	Long-chain-fatty-acid--CoA ligase 5	1.19	3
AIGAVPLIQGEYMIPCEKVSSLPTVYLK	F6Y6L6	Cathepsin D (Fragment)	0.98	3
ASGAVGLSYGAHSNLCVNQIVR	Q9JHI5	Isovaleryl-CoA dehydrogenase, mitochondrial	1.03	3
AVQNACQILMK	G3X982	Aldehyde oxidase 3	1.02	3
DAGCPVFLYEFQHTPSSFAK	Q8VCU1	Carboxylesterase 3B	1.16	3
DICEGQVNSLPGSINK	P01027	Complement C3	1.06	3
DLAACIKGLPNVQR	O88844	Isocitrate dehydrogenase [NADP] cytoplasmic	1.03	3
EFGKGLGDCLVK	P51881	ADP/ATP translocase 2	1.21	3
EYCGVPGDGYEELIRS	Q07456	Protein AMBP	1.32	3
FAPPEPAEPWSFVKHTTSYPPLCYQNPEAALR	Q8VCC2	Liver carboxylesterase 1	0.84	3
FAQLCEEHGILRENIIDLSNANR	A2BIN0	Major urinary proteins 11 and 8	0.65	3
GATTNICYNVLR	D6RHA7	Acetyl-coenzyme A synthetase, cytoplasmic	0.78	3
GFGFPQGAFVTETCMSAVAAK	G3X982	Aldehyde oxidase 3	1.02	3
GICVADPYEIR	P01027	Complement C3	1.06	3
GMGLACGQDPELVR	Q8CHR6	Dihydropyrimidine dehydrogenase [NADP(+)]	0.99	3
GPCIYNEDNGIIK	Q9D8E6	60S ribosomal protein L4	1.00	3
GSGSGCVYLQTSLK	Q61838	Alpha-2-macroglobulin	1.62	3
LCGSGFQSIIVSGCQEICK	Q8BWT1	3-ketoacyl-CoA thiolase, mitochondrial	1.24	3

LIIAGTSCYSR	G3UZ26	Serine hydroxymethyltransferase (Fragment)	1.16	3
LKAYLMSQPLAYHTPDCGK	O35490	Betaine--homocysteine S-methyltransferase 1	0.86	3
NIAFFSTNCVEGTAR	Q8VDN2	Sodium/potassium-transporting ATPase subunit alpha-1	1.22	3
NLKQEDFELLCPDGTR	Q921I1	Serotransferrin	1.01	3
QALAWPDRVALVCTGSESSITNSQLDAR	Q4LDG0	Bile acyl-CoA synthetase	1.20	3
QATLGAGLPSTPCTTVNK	Q8QZT1	Acetyl-CoA acetyltransferase, mitochondrial	0.91	3
QATLGAGLPSTPCTTVNKCASGMK	Q8QZT1	Acetyl-CoA acetyltransferase, mitochondrial	0.91	3
QLAAGWGPCEVLVSNALAR	O09159	Lysosomal alpha-mannosidase	0.60	3
SAYALGGLGSGICPNKETLIDLGTAKAFAMTNC	Q8C196	Carbamoyl-phosphate synthase [ammonia], mitochondrial	0.89	3
SLCPVSWVSAWDDRIAEGTFPGKI	P56391	Cytochrome c oxidase subunit 6B1	0.94	3
SLVANLAAANCYKKEK	P55264-2	Isoform Short of Adenosine kinase	1.19	3
TAACLAAGNTVVIKPAQVTPLTALK	Q8R0Y6	Cytosolic 10-formyltetrahydrofolate dehydrogenase	0.99	3
TPYQIACGISQGLADNTVVAK	Q9D0R2	Threonine--tRNA ligase, cytoplasmic	0.56	3
TYSTINPTDGSVICQVSLAQVSDVDKAVAAAF	Q8R0Y6	Cytosolic 10-formyltetrahydrofolate dehydrogenase	0.99	3
VCKKDVELNGVYIPK	Q64459	Cytochrome P450 3A11	0.71	3
VGLIGSCTNSSYEDMGR	Q99KI0	Aconitate hydratase, mitochondrial	1.02	3
VTVAGLAGKDPVQCSR	A2A817	Protein DJ-1 (Fragment)	0.78	3
WFLTCINQPQFR	Q9D8N0	Elongation factor 1-gamma	1.05	3
WSSCNIFSTQDHAAAIAK	P50247	Adenosylhomocysteinase	0.89	3
YQVDPDACFSAK	Q60932-2	Isoform Mt-VDAC1 of Voltage-dependent anion-selective channel j	1.12	3

^a Peptides are grouped by sequence. ^b Accession number provided from the Uniprot mouse database (Jan 7, 2015; 52639 sequences). ^c Average protein AD/WT that obtained by cysDML and used for peptide ratio normalization in OxcysDML experiment. ^d Number of biological replicates quantified.